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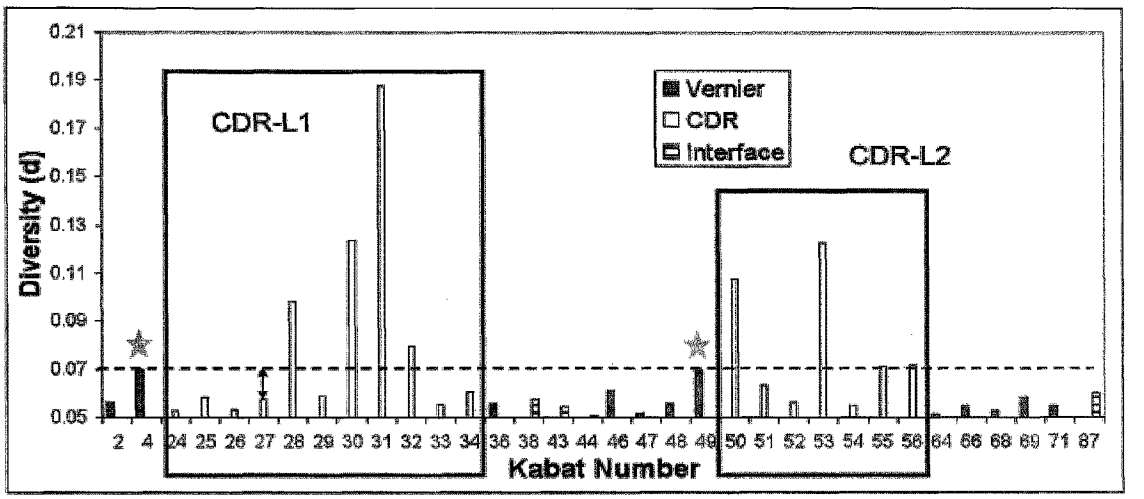
(72) **Inventeurs/Inventors:**
FELDHAUS, MICHAEL, US;
SIVASUBRAMANIAN, ARVIND, US;
VASQUEZ, MAXIMILIANO, US

(73) **Propriétaire/Owner:**
ADIMAB, LLC, US

(74) **Agent:** TORYS LLP

(54) **Titre : LIBRAIRIES RENFERMANT DES GROUPEMENTS DE SEGMENTATION ET LEURS METHODES DE PREPARATION ET UTILISATION**

(54) **Title: LIBRARIES COMPRISING SEGMENTAL POOLS, AND METHODS FOR THEIR PREPARATION AND USE**



(57) **Abrégé/Abstract:**
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ABSTRACT

Provided is a method that overcomes the inadequacies inherent in the known methods for generating libraries of antibody-encoding polynucleotides by specifically designing the libraries with directed sequence and length diversity.

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LIBRARIES COMPRISING SEGMENTAL POOLS, AND METHODS FOR THEIR PREPARATION AND USE

REFERENCE TO RELATED APPLICATIONS

This application is a national phase application under 35 U.S.C. § 371 of PCT International Application No. PCT/US2011/044063 filed July 14, 2011, which claims priority to U.S. Provisional Application No. 61/365,194 filed July 16, 2010.

BACKGROUND

Antibodies have profound relevance as research tools and in diagnostic and therapeutic applications. However, the identification of useful antibodies is difficult and once identified, antibodies often require considerable redesign or "humanization" before they are suitable for therapeutic applications in humans.

Many methods for identifying antibodies involve display of libraries of antibodies derived by amplification of nucleic acids from B cells or tissues. Some of these methods have utilized synthetic libraries. However, many of these approaches have limitations. For example, most human antibody libraries known in the art contain only the antibody sequence diversity that can be experimentally captured or cloned from a biological source (*e.g.*, B cells). Accordingly, such libraries may over-represent some sequences, while completely lacking or under-representing other sequences, particularly those binding human antigens. Most synthetic libraries known in the art have other limitations, such as the occurrence of unnatural (*i.e.*, non-human) amino acid sequence motifs that have the potential to be immunogenic.

Accordingly, a need exists for diverse antibody libraries that contain candidate antibodies that are non-immunogenic (*i.e.*, are human) and have desired properties (*e.g.*, the ability to recognize a broad variety of antigens). However, obtaining such libraries requires balancing the competing objectives of generating diverse libraries while still maintaining the human character of the sequences within the library. The current invention provides antibody libraries that have these and other desirable features, and methods of making and using such libraries.

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SUMMARY

The invention provides, among other things, improvements in the design and production of synthetic libraries that mimic the diversity of the natural human repertoire of CDRH3, CDRL3, heavy chain, light chain, and/or full-length (intact) antibody sequences. In some embodiments the invention defines and provides methods of generating theoretical segment pools of TN1, DH, N2, and H3-JH segments to consider for inclusion in a physical manifestation of a library (*e.g.,* polynucleotide or polypeptide) comprising or encoding CDRH3 sequences (*e.g.,* an antibody library). In certain embodiments the invention defines and provides methods of matching the individual members of these theoretical segment pools to a reference set of CDRH3 sequences, to determine the frequency of occurrence (or segment usage weight) of each of the segments in the theoretical segment pool in the reference set. While any set of CDRH3 sequences may be used as a reference set, the invention also defines and provides methods of generating particular reference sets or subsets of interest. For example, among other things, the present invention provides methods for filtering an original reference set to obtain a provided reference set with a preimmune character. Also provided are methods to define and/or identify segments that occur within the CDRH3 sequences in the reference set but not in the theoretical segment pool. Such segments can be added to a theoretical segment pool, for example in order to be considered for inclusion in a physical library. Although the frequency of occurrence of a particular segment in a reference set is useful to select segments for inclusion in a physical library, the invention also provides a number of physicochemical and biological properties that can be used (alone or together with any other criterion or criteria) to select segments for inclusion in a physical library.

In some embodiments the invention provides libraries that differ from certain other libraries known in the art in that they are not sitewise-stochastic in composition or sequence, and are therefore intrinsically less random than these certain other libraries of the art (*see e.g.,* Example 14 of US Pub. No. 2009/0181855, for a discussion of information content and randomness). In some embodiments, degenerate oligonucleotides may be used to further increase the diversity of the members of a library while further improving matching with a reference set of sequences (e.g., CDRH3, CDRL3, heavy chain, light chain, and/or full-length (intact) antibody sequences).

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The invention also provides libraries whose members have sequences that are related to one another in that they would be selected for inclusion in a physical library by performing the analyses described herein, for example by generating a CDRH3 reference set as in Example 3; generating theoretical segment pools as in Examples 5-7; matching the members of a theoretical segment pool to the reference set as in Examples 4 and 8; and selecting members of the theoretical segment pool for inclusion in a physical library as in Examples 8-9. Also provided are methods of further increasing diversity in certain sequences by utilizing degenerate oligonucleotides as in Examples 12-16.

In some embodiments, the present invention provides polynucleotide and polypeptide libraries comprising CDRH3, CDRL3, heavy chain, light chain, and/or full-length (intact) antibody sequences, and methods of making and using such libraries.

In some embodiments, the invention provides libraries comprising, consisting essentially of, or consisting of any of the libraries or theoretical segment pools described herein.

In some embodiments, the present invention recognizes that by mimicking the *in vivo* activity of the enzyme TdT computationally, theoretical segment pools can be generated and subsequently matched to large reference datasets of CDR sequences to choose, for inclusion in a library, those theoretical segments that best recapitulate the CDR sequences in the reference data sets.

In certain embodiments, the invention provides libraries of polynucleotides comprising at least about 10^4 polynucleotides encoding CDRH3 polypeptides with the structure: [TN1]-[DH]-[N2]-[H3-JH], wherein: TN1 is a polypeptide corresponding to any of the TN1 polypeptides of Tables 9-10 and 18-26, or a polypeptide produced by translation of any of the TN1 polynucleotides of Tables 25-26; DH is a polypeptide corresponding to any of the DH polypeptides of Tables 9, 11, 17-25 and 28, or a polypeptide produced by translation of any of the DH-encoding polynucleotides of Tables 16, 25 and 27; N2 is a polypeptide corresponding to any of the N2 polypeptides of Tables 9, 12, 18-25 and 30, or a polypeptide produced by translation of any of the N2-encoding polynucleotides of Tables 25 and 29; and H3-JH is a polypeptide corresponding to any of the H3-JH polypeptides of Tables 9, 13, 15, 18-25 and 32, or a polypeptide produced by translation of any of the H3-JH-encoding polynucleotides of Tables 14, 25 and 31.

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In some embodiments, the invention provides libraries wherein at least about 1%, 5%, or 10% of the sequences in the library have the structure provided above, or that of any of the libraries provided herein.

In certain embodiments, the invention provides libraries comprising polynucleotides encoding CDRH3 polypeptides produced by the sets of TN1, DH, N2, and H3-JH polypeptides provided in any one of Tables 23-25.

In some embodiments, the invention provides libraries comprising polynucleotides encoding CDRH3 polypeptides produced by the set of TN1 polypeptides provided in Table 26, the set of DH polypeptides provided in Table 28, the set of N2 polypeptides provided in Table 30 and the set of H3-JH polypeptides provided in Table 32.

In certain embodiments, the invention provides libraries whose members show (or encode polypeptides that show) at least a certain percent identity with the polypeptides described above, for example, a library comprising at least about 10^4 polynucleotides encoding CDRH3 polypeptides with the structure: [TN1]-[DH]-[N2]-[H3-JH], wherein: TN1 is a polypeptide at least about 80%, 90%, or 95% identical to any of the TN1 polypeptides of Tables 9-10 and 18-26, or a polypeptide at least about 80%, 90%, or 95% identical to a polypeptide produced by translation of any of the TN1 polynucleotides of Tables 25-26; DH is a polypeptide at least about 80%, 90%, or 95% identical to any of the DH polypeptides of Tables 9, 11, 17-25 and 28, or a polypeptide at least about 80%, 90%, or 95% identical to a polypeptide produced by translation of any of the DH-encoding polynucleotides of Tables 16, 25 and 27; N2 is a polypeptide at least about 80%, 90%, or 95% identical to any of the N2 polypeptides of Tables 9, 12, 18-25 and 30, or a polypeptide at least about 80%, 90%, or 95% identical to a polypeptide produced by translation of any of the N2-encoding polynucleotides of Tables 25 and 29; and H3-JH is a polypeptide at least about 80%, 90%, or 95% identical to any of the H3-JH polypeptides of Tables 9, 13, 15, 18-25 and 32, or a polypeptide at least about 80%, 90%, or 95% identical to a polypeptide produced by translation of any of the H3-JH-encoding polynucleotides of Tables 14, 25 and 31.

In some embodiments, the invention provides libraries comprising polynucleotides encoding light chain variable regions, wherein the light chain variable

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regions are selected from the group consisting of: (a) a VK1-05 sequence varied at one or more of positions 4, 49, and 46; (b) a VK1-12 sequence varied at one or more of positions 4, 49, 46, and 66; (c) a VK1-33 sequence varied at one or more of positions 4, 49, and 66; (d) a VK1-39 sequence varied at one or more of positions 4, 49, and 46; (e) a VK2-28 sequence varied at one or more of positions 2, 4, 46, and 49; (f) a VK3-11 sequence varied at one or more of positions 2, 4, 36, and 49; (g) a VK3-15 sequence varied at one or more of positions 2, 4, 48, and 49; (h) a VK3-20 sequence varied at one or more of positions 2, 4, 48, and 49; and/or (i) a VK4-1 sequence varied at one or more of positions 4, 46, 49, and 66.

In certain embodiments, the invention provides libraries comprising polynucleotides encoding light chain variable regions that comprise polypeptide sequences at least about 80%, 90%, or 95% identical to two or more of the light chain polypeptide sequences provided in Table 3.

In some embodiments, the invention provides libraries wherein the light chain variable regions comprise the polypeptide sequences provided in Table 3.

In certain embodiments, the invention provides libraries comprising polynucleotides encoding light chain variable regions, wherein the L3-VL polypeptide sequences of the light chain variable regions are varied at two or three residues between positions 89 to 94, inclusive, in comparison to an L3-VL germline sequence. In some embodiments, libraries containing a single light chain germline sequence and its variants are provided. In certain embodiments, variants produced from different light chain germline sequences can be combined to produce libraries encoding multiple light chain germline sequences and their variants. Any of the light chain L3-VL germline sequences provided herein may be varied at two or three residues between positions 89 to 94, inclusive, and one of ordinary skill in the art will recognize that any other L3-VL sequence can also be varied according to the principles described herein to produce libraries provided by the invention. In some embodiments, the present invention comprises libraries containing polynucleotides that encode antibody light chain variable regions, wherein the antibody light chain variable regions comprise one or more of the following L3-VL sequences: (i) an amino acid sequence that is identical to an L3-VL germline sequence (e.g., see Table 1); (ii) an amino acid sequence that contains two substitutions between residues 89-94, inclusive, in comparison to an L3-VL germline sequence; and (iii) an amino acid

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sequence that contains three substitutions between residues 89-94, inclusive, in comparison to an L3-VL germline sequence. In some embodiments, each antibody light chain variable region on a library includes one or more of the above L3-VL sequences. In some embodiments, such a library is combined with one or more sets of other nucleic acids that may or may not encode antibody light chain variable regions, and may or may not contain such L3-VL sequences. In some embodiments, the present invention comprises libraries containing polynucleotides that encode an antibody light chain variable region having an amino acid sequence as set forth in Table 4, or a polynucleotide sequence as set forth in one or more of Tables 5-7, wherein two or three residues at positions 89-94, inclusive, are varied.

In some embodiments, the present invention comprises libraries containing polynucleotides that encode an antibody light chain variable region, wherein, across the library, all encoded antibody light chain variable regions are identical to one another except for substitutions of residues at positions between residue 89 and residue 94, inclusive and further wherein, across the library, sequences of any two encoded antibody light chain variable regions differ from one another at not more than 3 positions.

In some embodiments, the invention provides libraries comprising polynucleotides encoding light chain variable regions comprising polypeptide sequences at least about 80%, 90%, or 95% identical to polypeptides produced by translation of two or more of the polynucleotide sequences provided in Tables 5-7. In certain embodiments all members of the library are at least about 80%, 90%, or 95% identical to polypeptides produced by translation of two or more of the polynucleotide sequences provided in Tables 5-7.

In certain embodiments, the invention provides a library comprising light chain variable regions that comprise the polypeptides produced by translation of the polynucleotide sequences provided in Tables 5-7. In certain embodiments, all members of the library comprise the polypeptides produced by translation of the polynucleotide sequences provided in Tables 5-7.

In some embodiments, any of the libraries described herein as containing or encoding CDRL3 and/or light chain variable regions, contains or encodes such CDRL3 and/or light chain variable regions in the context of complete light chains.

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Furthermore, in some embodiments, such libraries (and/or complete light chain libraries) further contain or encode one or more heavy chain CDRH3, variable domains, or intact heavy chains. In some embodiments, provided libraries include or encode intact antibodies such as, for example, intact intact IgGs.

In some embodiments, provided libraries include or encode human antibodies or antibody fragments; in some such embodiments, provided libraries include or encode intact human antibodies.

In certain embodiments, the invention provides libraries that comprise nucleic acid vectors containing library nucleic acids described herein. In many embodiments, each such library member comprises the same vector.

In some embodiments, the invention provides host cells containing one or more provided libraries, for example including a vector. In some embodiments the host cell is a yeast, and in certain embodiments the yeast is *Saccharomyces cerevisiae*.

In some embodiments, the invention provides antibodies isolated from the libraries described herein.

In certain embodiments, the invention provides kits containing any of the libraries described herein.

In some embodiments, the invention provides representations of libraries and/or theoretical segment pools in a computer readable format, for example, the TN1 polypeptides of Tables 10, 23-25 and 26; the DH polypeptides of Tables 11, 23-25 and 28; the N2 polypeptides of Tables 12, 23-25 and 30; the H3-JH polypeptides of Tables 13, 15, 17, 23-25 and 32; the TN1 polynucleotides of Tables 25-26; the DH polynucleotides of Tables 25 and 27; the N2 polynucleotides of Tables 25 and 29; and/or the H3-JH polynucleotides of Tables 25 and 31.

In certain embodiments, the invention provides a representation of the polynucleotide sequences of the Human Preimmune Set (Appendix A), or the polypeptide expression products thereof, in a computer readable format.

In some embodiments, the invention provides a method of making synthetic polynucleotides encoding a CDRH3 library, comprising: (a) providing a theoretical segment pool containing TN1, DH, N2, and H3-JH segments; (b) providing a reference set of CDRH3 sequences; (c) utilizing the theoretical segment pool of (a) to

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identify the closest match(es) to each CDRH3 sequence in the reference set of (b); (d) selecting segments from the theoretical segment pool for inclusion in a synthetic library; and (c) synthesizing the synthetic CDRH3 library. In certain embodiments, the invention provides libraries made by this method. In some embodiments, the segments selected for inclusion in the synthetic library are selected according to their segment usage weight in the reference set of CDRH3 sequences.

In certain embodiments, the invention provides a method of making synthetic polynucleotides encoding a CDRL3 library, comprising: (i) obtaining a reference set of light chain sequences, wherein the reference set contains light chain sequences with VL segments originating from the same IGVL germline gene and/or its allelic variants; (ii) determining which amino acids occur at each of the CDRL3 positions in the reference set that are encoded by the IGVL gene; (iii) synthesizing light chain variable domain encoding sequences wherein two positions between positions 89 and 94, inclusive, contain degenerate codons encoding two or more of the five most frequently occurring amino acid residues at the corresponding positions in the reference set; and (iv) synthesizing the polynucleotides encoding the CDRL3 library. In certain embodiments, the invention provides libraries made by this method.

In some embodiments, the invention provides a method of using any of the libraries of the invention to isolate an antibody binding an antigen, comprising contacting the polypeptide expression products of said libraries with an antigen and isolating polypeptide expression products that bind to the antigen.

In certain embodiments, the number of N-linked glycosylation sites, deamidation motifs, and/or Cys residues in the libraries of the invention are reduced or eliminated in comparison to libraries produced by amplification of a repertoire from a biological source.

The invention provides a number of polynucleotide and polypeptide sequences and segments that can be used to build larger polynucleotide and polypeptide sequences (e.g., TN1, DH, N2, and H3-JH segments that can be used to build CDRH3). One of ordinary skill in the art will readily recognize that in some instances these sequences can be more succinctly represented by providing consensus sequences after alignment of the sequences provided by the invention, and that these

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consensus sequences fall within the scope of the invention and may be used to more succinctly represent any of the sequences provided herein.

BRIEF DESCRIPTION OF THE DRAWING

Figure 1 shows that Vernier residues 4 and 49 (starred) in VK1-39 have a diversity index comparable to or greater than the diversity indices of the CDR positions (*i.e.,* at or above 0.07, in this example).

Figure 2 shows that clinically validated CDRL3 sequences deviate little from germline-like sequences (n=35).

Figure 3 shows the percent of sequences in the jumping dimer CDRL3 libraries of the invention and a previous CDRL3 library, VK-v1.0, with *X* or fewer mutations from germline. Here, F*X* is the percentage of sequences in a library with *X* or fewer mutations from germline.

Figure 4 shows the application of a provided method used to generate nucleotide sequences (SEQ ID NOS 8748-8759, respectively, in order of appearance) encoding the parent H3-JH segments.

Figure 5 shows the general schematic of an approach used to select segments from a theoretical segment pool for inclusion in a theoretical and/or synthetic library.

Figure 6 shows the frequency of "Good" and "Poor" expressing CDRH3 sequences isolated from yeast-based libraries described in US 2009/0181855, and their comparison to the sequences contained in the library design described therein ("Design"), as a function of the DH segment hydrophobicity (increasing to the right).

Figure 7 shows the percentage of CDRH3 sequences in the LUA-141 library and Exemplary Library Design 3 (ELD-3) that match CDRH3 sequences from Lee-666 and Boyd-3000 with zero, one, two, three, or more than three amino acid mismatches.

Figure 8 shows that Exemplary Library Design 3 (ELD-3) and the Extended Diversity Library Design both return better matches to clinically relevant CDRH3 sequences than the LUA-141 library.

Figure 9 shows that the combinatorial efficiency of Exemplary Library Design 3 (ELD-3) is greater than that of the LUA-141 library. Specifically, the ELD-3 segments are more likely to yield a unique CDRH3 than the LUA-141 library segments.

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Figure 10 shows the amino acid compositions of the Kabat-CDRH3s of LUA-141, Exemplary Library Design 3 (ELD-3), and Human CDRH3 sequences from the HPS (Human H3).

Figure 11 shows the Kabat-CDRH3 length distribution of LUA-141, Exemplary Library Design 3 (ELD-3), and Human CDRH3 sequences from the HPS (Human H3).

Figure 12 shows the percentage of CDRH3 sequences in the Extended Diversity library that match CDRH3 sequences from Boyd *et al.* with zero to thirty-two amino acid mismatches

Figure 13 shows the Kabat-CDRH3 length distribution of Exemplary Library Design 3 ("ELD-3"), the Extended Diversity Library Design ("Extended Diversity") and human CDRH3 sequences from the Boyd *et al.* data set ("Boyd 2009").

Figure 14 shows the amino acid compositions of the Kabat-CDRH3s of the Extended Diversity Library Design ("Extended Diversity") and human CDRH3 sequences from the Boyd *et al.* dataset ("Boyd 2009").

Figure 15 shows the combinatorial efficiency of the Extended Diversity Library Design by matching 20,000 randomly selected sequences from the (same) design. About 65% of the sequences appear only once in the design and about 17% appear twice.

DETAILED DESCRIPTION OF CERTAIN EMBODIMENTS OF THE INVENTION

The present invention provides, among other things, polynucleotide and polypeptide libraries, methods of producing and using the libraries, kits containing the libraries, and computer readable forms of representations of libraries and/or theoretical segment pools disclosed herein. Libraries taught in this application can be described, at least in part, in terms of components (*e.g.*., polynucleotide or polypeptide "segments") from which they are assembled. Among other things, the present invention specifically provides and contemplates these polynucleotide or polypeptide segments, methods of producing and using such segments, and kits and computer readable forms of representations that include such library segments.

In certain embodiments, the invention provides antibody libraries specifically designed based on sequences and CDR length distribution in a naturally occurring human antibody repertoire. It is estimated that, even in the absence of antigenic

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stimulation, an individual human makes at least about 10^7 different antibody molecules (Boyd *et al.,* Science Translational Medicine, 2009, 1: 1). The antigen-binding sites of many antibodies can cross-react with a variety of related but different epitopes. In addition, the human antibody repertoire is large enough to ensure that there is an antigen-binding site to fit almost any potential epitope, albeit potentially with low affinity.

The mammalian immune system has evolved unique genetic mechanisms that enable it to generate an almost unlimited number of different light and heavy chains in a remarkably economical way, by combinatorially joining chromosomally separated gene segments prior to transcription. Each type of immunoglobulin (Ig) chain (*i.e.,* kappa light, lambda light, and heavy) is synthesized by combinatorial assembly of DNA sequences, selected from two or more families of gene segments, to produce a single polypeptide chain. Specifically, the heavy chains and light chains each consist of a variable region and a constant (C) region. The variable regions of the heavy chains are encoded by DNA sequences assembled from three families of gene sequences: variable (IGHV), diversity (IGHD), and joining (IGHJ). The variable regions of light chains are encoded by DNA sequences assembled from two families of gene sequences for each of the kappa and lambda light chains: variable (IGLV) and joining (IGLJ). Each variable region (heavy and light) is also recombined with a constant region, to produce a full-length immunoglobulin chain.

While combinatorial assembly of the V, D and J gene segments make a substantial contribution to antibody variable region diversity, further diversity is introduced *in vivo*, at the pre-B cell stage, via imprecise joining of these gene segments and the introduction of non-templated nucleotides at the junctions between the gene segments (see *e.g.,* U.S. Pub. No. 2009/0181855,

for more information).

After a B cell recognizes an antigen, it is induced to proliferate. During proliferation, the B cell receptor locus undergoes an extremely high rate of somatic mutation that is far greater than the normal rate of genomic mutation. The mutations that occur are primarily localized to the Ig variable regions and comprise substitutions, insertions and deletions. This somatic hypermutation enables the production of B cells that express antibodies possessing enhanced affinity toward an antigen. Such antigen-driven somatic hypermutation fine-tunes antibody responses to a given antigen.

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Synthetic antibody libraries of the instant invention have the potential to recognize any antigen, including antigens of human origin. The ability to recognize antigens of human origin may not be present in other antibody libraries, such as antibody libraries prepared from human biological sources (*e.g.,* from human cDNA), because self-reactive antibodies are removed by the donor's immune system via negative selection.

Still further, the present invention provides strategies that streamline and/or simplify certain aspects of library development and/or screening. For example, in some embodiments, the present invention permits use of cell sorting technologies (*e.g.,* fluorescence activated cell sorting, FACS) to identify positive clones, and therefore bypasses or obviates the need for the standard and tedious methodology of generating a hybridoma library and supernatant screening.

Yet further, in some embodiments, the present invention provides libraries and/or sublibraries that accommodate multiple screening passes. For example, in some embodiments, provided libraries and/or sublibraries can be screened multiple times. In some such embodiments, individual provided libraries and/or sublibraries can be used to discover additional antibodies against many targets.

Before further description of the invention, certain terms are defined.

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by one of ordinary skill in the art relevant to the invention. Unless otherwise specified, the Kabat numbering system is used throughout the application. The definitions below supplement those in the art and are directed to the embodiments described in the current application.

The term "amino acid" or "amino acid residue," as would be understood by one of ordinary skill in the art, typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (Ile or I): leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); proline (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired.

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Generally, amino acids can be grouped as having a non-polar side chain (*e.g.*, Ala, Cys, Ile, Leu, Met, Phe, Pro, Val); a negatively charged side chain (*e.g.*, Asp, Glu); a positively charged side chain (*e.g.*, Arg, His, Lys); or an uncharged polar side chain (*e.g.*, Asn, Cys, Gln, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr).

As would be understood by those of ordinary skill in the art, the term "antibody" is used herein in the broadest sense and specifically encompasses at least monoclonal antibodies, polyclonal antibodies, multi-specific antibodies (*e.g.*, bispecific antibodies), chimeric antibodies, humanized antibodies, human antibodies, and antibody fragments. An antibody is a protein comprising one or more polypeptides substantially or partially encoded by immunoglobulin genes or fragments of immunoglobulin genes. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon and mu constant region genes, as well as myriad immunoglobulin variable region genes.

The term "antibody binding region" refers to one or more portions of an immunoglobulin or antibody variable region capable of binding an antigen(s). Typically, the antibody binding region is, for example, an antibody light chain (or variable region or one or more CDRs thereof), an antibody heavy chain (or variable region or one or more CDRs thereof), a heavy chain Fd region, a combined antibody light and heavy chain (or variable regions thereof) such as a Fab, $F(ab')_2$, single domain, or single chain antibodies (scFv), or any region of a full length antibody that recognizes an antigen, for example, an IgG (*e.g.*, an IgG1, IgG2, IgG3, or IgG4 subtype), IgA1, IgA2, IgD, IgE, or IgM antibody.

"Antibody fragments" comprise a portion of an intact antibody, for example, one or more portions of the antigen-binding region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments, diabodies, linear antibodies, single-chain antibodies, and multi-specific antibodies formed from intact antibodies and antibody fragments.

The term "antibody of interest" refers to an antibody that has a property of interest that is identified and/or isolated from a library of the invention. Exemplary properties of interest include, for example, but are not limited to, binding to a particular antigen or epitope, binding with a certain affinity, cross-reactivity, blocking a binding interaction between two molecules, and/or eliciting a certain biological effect.

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The term "canonical structure," as understood by those of ordinary skill in the art, refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol., 1996, 263: 800).

Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. As is known in the art, the conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (*i.e.,* outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues. The term "canonical structure" may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.,* in "Sequences of Proteins of Immunological Interest," 5th Edition, U.S. Department of Heath and Human Services, 1992). The Kabat numbering scheme is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner, and is used herein unless indicated otherwise. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia *et al.* and/or revealed by other techniques, for example, crystallography and two or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (*e.g.,* based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.*, and their implications for construing canonical aspects of antibody structure, are described in the literature.

The terms "CDR", and its plural "CDRs", refer to a complementarity determining region (CDR) of which three make up the binding character of a light

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chain variable region (CDRL1, CDRL2 and CDRL3) and three make up the binding character of a heavy chain variable region (CDRH1, CDRH2 and CDRH3). CDRs contribute to the functional activity of an antibody molecule and are separated by amino acid sequences that comprise framework regions. The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or other boundary definitions, including for example the CDRH3 numbering system described below. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable region. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See, for example Kabat *et al.*, in "Sequences of Proteins of Immunological Interest," 5th Edition, U.S. Department of Health and Human Services, 1992; Chothia *et al.*, J. Mol. Biol., 1987, 196: 901; and MacCallum *et al.*, J. Mol. Biol., 1996, 262: 732.

The "CDRH3 numbering system" used herein defines the first amino acid of CDRH3 as being at position 95 and the last amino acid of CDRH3 as position 102. Note that this is a custom numbering system that is not according to Kabat. The amino acid segment, beginning at position 95 is called "TN1" and, when present, is assigned numbers 95, 96, 96A, 96B, etc. Note that the nomenclature used in the current application is slightly different from that used in U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379. In those applications, position 95 was designated a "Tail" residue, while here, the Tail (T) has been combined with the N1 segment, to produce one segment, designated "TN1." The TN1 segment is followed by the "DH" segment, which is assigned numbers 97, 97A, 97B, 97C, etc. The DH segment is followed by the "N2" segment, which, when present, is numbered 98, 98A, 98B, etc. Finally, the most C-terminal amino acid residue of the "H3-JH" segment is designated as number 102. The residue directly before (N-terminal) it, when present, is 101, and the one before (if present) is 100. The rest of the H3-JH amino acids are numbered in reverse order, beginning with 99 for the amino acid just N-terminal to 100, 99A for the residue N-terminal to 99, and so forth for 99B, 99C, etc. Examples of CDRH3 sequence residue numbers may therefore include the following:

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13 Amino Acid CDR-H3 with TN1 and N2

(95)(96)(96A)(97)(97A)(97B)(97C)(97D) (98) (99)(100)(101)(102)

|----------|----------|----|----------|

TN1 DH N2 H3-JH

10 Amino Acid CDR-H3 without TN1 and N2

(97)(97A)(97B)(97C)(97D)(97E)(97F)(97G)(101)(102)

|----------|---------|

DH H3-JH

"Chassis" of the invention are portions of the antibody heavy chain variable (IGHV) or light chain variable (IGLV) domains that are not part of CDRH3 or CDRL3, respectively. A chassis of the invention is defined as the portion of the variable region of an antibody beginning with the first amino acid of FRM1 and ending with the last amino acid of FRM3. In the case of the heavy chain, the chassis includes the amino acids including from position 1 to position 94. In the case of the light chains (kappa and lambda), the chassis are defined as including from position 1 to position 88. The chassis of the invention may contain certain modifications relative to the corresponding germline variable domain sequences. These modifications may be engineered (*e.g.*, to remove N-linked glycosylation sites) or naturally occurring (*e.g.*, to account for naturally occurring allelic variation). For example, it is known in the art that the immunoglobulin gene repertoire is polymorphic (Wang *et al.*, Immunol. Cell. Biol., 2008, 86: 111; Collins *et al.*, Immunogenetics, 2008, 60: 669); chassis, CDRs and constant regions representative of these allelic variants are also encompassed by the invention. In some embodiments, the allelic variant(s) used in a particular embodiment of the invention may be selected based on the allelic variation present in different patient populations, for example, to identify antibodies that are non-immunogenic in these patient populations. In certain embodiments, the immunogenicity of an antibody of the invention may depend on allelic variation in the major histocompatibility complex (MHC) genes of a patient population. Such allelic variation may also be considered

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in the design of libraries of the invention. In certain embodiments of the invention, the chassis and constant regions are contained in a vector, and a CDR3 region is introduced between them via homologous recombination.

As used herein, a sequence designed with "directed diversity" has been specifically designed to contain both sequence diversity and length diversity. Directed diversity is not stochastic.

As used herein, the term "diversity" refers to a variety or a noticeable heterogeneity. The term "sequence diversity" refers to a variety of sequences which are collectively representative of several possibilities of sequences, for example, those found in natural human antibodies. For example, CDRH3 sequence diversity may refer to a variety of possibilities of combining the known human TN1, DH, N2, and H3-JH segments to form CDRH3 sequences. The CDRL3 sequence diversity (kappa or lambda) may refer to a variety of possibilities of combining the naturally occurring light chain variable region contributing to CDRL3 (*i.e.,* "L3-VL") and joining (*i.e.,* "L3-JL") segments, to form CDRL3 sequences. As used herein, "H3-JH" refers to the portion of the IGHJ gene contributing to CDRH3. As used herein, "L3-VL" and "L3-JL" refer to the portions of the IGLV and IGLJ genes (kappa or lambda) contributing to CDRL3, respectively.

As used herein, the term "expression" refers to steps involved in the production of a polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

The term "framework region" refers to the art-recognized portions of an antibody variable region that exist between the more divergent (*i.e.,* hypervariable) CDRs. Such framework regions are typically referred to as frameworks 1 through 4 (FRM1, FRM2, FRM3, and FRM4) and provide a scaffold for the presentation of the six CDRs (three from the heavy chain and three from the light chain) in three dimensional space, to form an antigen-binding surface.

The term "full-length heavy chain" refers to an immunoglobulin heavy chain that contains each of the canonical structural domains of an immunoglobulin heavy chain, including the four framework regions, the three CDRs, and the constant region.

The term "full-length light chain" refers to an immunoglobulin light chain that contains each of the canonical structural domains of an immunoglobulin light chain, including the four framework regions, the three CDRs, and the constant region.

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The term "germline-like," when used with respect to the CDRL3 sequences of the light chains of the invention, means those sequences consisting of combinations of: (i) the first six wild-type residues contributed to CDRL3 by the IGVL germline gene (*i.e.,* positions 89 to 94 in the Kabat numbering system; "L" is kappa or lambda); and (ii) one of several amino acid sequences, two one to four amino acids in length, largely, but not exclusively, derived from the JL segment ("L," again is kappa or lambda). For kappa CDRL3 sequences of the most common lengths (*i.e.,* 8, 9, and 10 residues), the sequences of (ii) number twenty and are: FT, LT, IT, RT, WT, YT, [X]T, [X]PT, [X]FT, [X]LT, [X]IT, [X]RT, [X]WT, [X]YT, [X]PFT, [X]PLT, [X]PIT, [X]PRT, [X]PWT and [X]PYT, where [X] corresponds to the amino acid residue found at position 95 (Kabat) in the respective VK germline sequence. X is most commonly P, but may also be S or any other amino acid residue found at position 95 of a VK germline sequence. For eight exemplified VK chassis exemplified herein, the corresponding 160 germline-like sequences, (*i.e.,* 20 sequences of two to four amino acids in length combined with positions 89 to 94 of each of eight VK germline sequences) are provided in Table 1. A similar approach is applied to define germline-like CDRL3 sequences for lambda light chains. As for the kappa sequences described above, the intact, un-mutated portions of CDRL3 encoded by the IGVL genes (in this case, IGV□) would be combined with the sequences largely, but not exclusively, derived from the J□ segment. Here, the latter sequences (corresponding to (ii), above), number five and are: YV, VV, WV, AV or V. In addition, and as described in Example 7 of US 2009/0818155, one could further allow for variation at the last position of the V□-gene-encoded portion of CDRL3 by considering partial codons, while still considering the resulting sequences "germline-like." More specifically, the entire "minimalist library" of Example 7 in US 2009/0818155 would be defined as "germline-like." One of ordinary skill in the art will readily recognize that these methods can be extended to other VK and V□ sequences.

The term "genotype-phenotype linkage," as understood by those of ordinary skill in the art, refers to the fact that the nucleic acid (genotype) encoding a protein with a particular phenotype (*e.g.,* binding an antigen) can be isolated from a library. For the purposes of illustration, an antibody fragment expressed on the surface of a phage can be isolated based on its binding to an antigen (*e.g.,* U.S. Patent No. 5,837,500). The binding of the antibody to the antigen simultaneously enables the

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isolation of the phage containing the nucleic acid encoding the antibody fragment. Thus, the phenotype (antigen-binding characteristics of the antibody fragment) has been "linked" to the genotype (nucleic acid encoding the antibody fragment). Other methods of maintaining a genotype-phenotype linkage include those of Wittrup *et al.* (U.S. Patent Nos. 6,300,065, 6,331,391, 6,423,538, 6,696,251, 6,699,658, and U.S. Pub. No. 20040146976), Miltenyi (US Patent No. 7,166,423), Fandl (U.S. Patent No. 6,919,183, US Pub No. 20060234311), Clausell-Tormos *et al.* (Chem. Biol., 2008, 15: 427), Love *et al.* (Nat. Biotechnol., 2006, 24: 703), and Kelly *et al.* (Chem. Commun., 2007, 14: 1773). The term can be used to refer to any method which localizes an antibody protein together with the gene encoding the antibody protein, in a way in which they can both be recovered while the linkage between them is maintained.

The term "heterologous moiety" is used herein to indicate the addition of a moiety to an antibody wherein the moiety is not part of a naturally-occurring antibody. Exemplary heterologous moieties include drugs, toxins, imaging agents, and any other compositions which might provide an activity that is not inherent in the antibody itself.

As used herein, the term "host cell" is intended to refer to a cell comprising a polynucleotide of the invention. It should be understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

As used herein, the term "human antibody CDR library" includes at least a polynucleotide or polypeptide library which has been designed to represent the sequence diversity and length diversity of naturally occurring CDRs in human antibodies (*e.g.*, the term "CDR" in "human antibody CDR library" may be substituted with "CDRL1," "CDRL2," "CDRL3," "CDRH1," "CDRH2," and/or "CDRH3"). Known human CDR sequences are represented in various data sets, including Jackson *et al.*, J. Immunol Methods, 2007, 324: 26; Martin, Proteins, 1996, 25: 130; Lee *et al.*, Immunogenetics, 2006, 57: 917, Boyd *et al.*, Science Translational

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Medicine, 2009, 1: 1, and WO/2009/036379,

and the HPS, which is provided in Appendix A.

The term "Human Preimmune Set," or "HPS," refers to a reference set of 3,571 curated human preimmune heavy chain sequences corresponding to the GI Nos. provided in Appendix A.

An "intact antibody" is one comprising full-length heavy- and light- chains (*i.e.*, four frameworks, three CDRs, and a constant region for each of the heavy and light chains). An intact antibody is also referred to as a "full-length" antibody.

The term "length diversity" refers to a variety in the length of a family of nucleotide or amino acid sequence. For example, in naturally occurring human antibodies, the heavy chain CDR3 sequence varies in length, for example, from about 2 amino acids to over about 35 amino acids, and the light chain CDR3 sequence varies in length, for example, from about 5 to about 16 amino acids.

The term "library" refers to a set of entities comprising two or more entities having diversity as described herein, and/or designed according to the methods of the invention. For example, a "library of polynucleotides" refers to a set of polynucleotides comprising two or more polynucleotides having diversity as described herein, and/or designed according to the methods of the invention. A "library of polypeptides" refers to a set of polypeptides comprising two or more polypeptides having diversity as described herein, and/or designed according to the methods of the invention. A "library of synthetic polynucleotides" refers to a set of polynucleotides comprising two or more synthetic polynucleotides having diversity as described herein, and/or designed according to the methods of the invention. Libraries where all members are synthetic are also encompassed by the invention. A "human antibody library" refers to a set of polypeptides comprising two or more polypeptides having diversity as described herein, and/or designed according to the methods of the invention, for example a library designed to represent the sequence diversity and length diversity of naturally occurring human antibodies. In some embodiments, the term "library" may refer to a set of entities sharing similar structural or sequence characteristics, for example, a "heavy chain library," "light chain library," "antibody library," and/or "CDRH3 library."

The term "physical realization" refers to a portion of a theoretical (*e.g.*, computer-based) or synthetic (*e.g.*, oligonucleotide-based) diversity that can actually be physically sampled, for example, by any display methodology. Exemplary display

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methodology include: phage display, ribosomal display, and yeast display. For synthetic sequences, the size of the physical realization of a library depends on (1) the fraction of the theoretical diversity that can actually be synthesized, and (2) the limitations of the particular screening method. Exemplary limitations of screening methods include the number of variants that can be screened in a particular assay (*e.g.,* ribosome display, phage display, yeast display) and the transformation efficiency of the host cells (*e.g.,* yeast, mammalian cells, bacteria) which are used in a screening assay. For the purposes of illustration, given a library with a theoretical diversity of 10^{12} members, an exemplary physical realization of the library (*e.g.,* in yeast, bacterial cells, or ribosome display) that can maximally include 10^{11} members will, therefore, sample about 10% of the theoretical diversity of the library. However, if fewer than 10^{11} members of the library with a theoretical diversity of 10^{12} are synthesized, and the physical realization of the library can maximally include 10^{11} members, less than 10% of the theoretical diversity of the library is sampled in the physical realization of the library. Similarly, a physical realization of the library that can maximally include more than 10^{12} members would "oversample" the theoretical diversity, meaning that each member may be present more than once (assuming that the entire 10^{12} theoretical diversity is synthesized).

The term "polynucleotide(s)" refers to nucleic acids such as DNA molecules and RNA molecules and analogs thereof (*e.g.*, DNA or RNA generated using nucleotide analogs or using nucleic acid chemistry). As desired, the polynucleotides may be made synthetically, *e.g.*, using art-recognized nucleic acid chemistry or enzymatically using, *e.g.*, a polymerase, and, if desired, be modified. Typical modifications include methylation, biotinylation, and other art-known modifications. In addition, the nucleic acid molecule can be single-stranded or double-stranded and, where desired, linked to a detectable moiety. The representation of nucleotide bases herein follows International Union of Pure and Applied Chemistry (IUPAC) nomenclature (see U.S. Pub. No. 2009/0181855).

"Preimmune" antibody libraries have sequence diversities and length diversities similar to naturally occurring human antibody sequences before these sequences have undergone negative selection and/or somatic hypermutation. For example, the set of sequences described in Lee *et al.* (Immunogenetics, 2006, 57: 917) and the Human Preimmune Set (HPS)

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described herein (see Appendix A) are believed to represent sequences from the preimmune repertoire. In certain embodiments of the invention, the sequences of the invention will be similar to these sequences (*e.g.*, in terms of composition and length).

As used herein, the term "sitewise stochastic" describes a process of generating a sequence of amino acids, where only the amino acid occurrences at the individual positions are considered, and higher order motifs (*e.g.*, pair-wise correlations) are not accounted for (*e.g.*, see Knappik, *et al.*, J Mol Biol, 2000, 296: 57, and analysis provided in U.S. Publication No. 2009/0181855).

The term "split-pool synthesis" refers to a procedure in which the products of a plurality of individual first reactions are combined (pooled) and then separated (split) before participating in a plurality of second reactions. For example, U.S. Publication No. 2009/0181855 describes the synthesis of 278 DH segments (products), each in a separate reaction. After synthesis, these 278 segments are combined (pooled) and then distributed (split) amongst 141 columns for the synthesis of the N2 segments. This enables the pairing of each of the 278 DH segments with each of 141 N2 segments.

As used herein, "stochastic" describes a process of generating a random sequence of nucleotides or amino acids, which is considered as a sample of one element from a probability distribution (*e.g.*, see U.S. Patent No. 5,723,323).

As used herein, the term "synthetic polynucleotide" refers to a molecule formed through a chemical process, as opposed to molecules of natural origin, or molecules derived via template-based amplification of molecules of natural origin (*e.g.*, immunoglobulin chains cloned from populations of B cells via PCR amplification are not "synthetic" as used herein). In some instances, for example, when referring to libraries of the invention that comprise multiple segments (*e.g.*, TN1, DH, N2, and/or H3-JH), the invention encompasses libraries in which at least one, two, three, or four of the aforementioned components is synthetic. By way of illustration, a library in which certain components are synthetic, while other components are of natural origin or derived via template-based amplification of molecules of natural origin, would be encompassed by the invention. Libraries that are fully synthetic would, of course, also be encompassed by the invention.

The term "theoretical diversity" refers to the maximum number of variants in a library design. For example, given an amino acid sequence of three residues, where

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residues one and three may each be any one of five amino acid types and residue two may be any one of 20 amino acid types, the theoretical diversity is 5×20×5=500 possible sequences. Similarly if sequence X is constructed by combination of 4 amino acid segments, where segment 1 has 100 possible sequences, segment 2 has 75 possible sequences, segment 3 has 250 possible sequences, and segment 4 has 30 possible sequences, the theoretical diversity of fragment X would be 100×75×200×30, or 5.6×10^5 possible sequences.

The term "theoretical segment pool" refers to a set of polynucleotide or polypeptide segments that can be used as building blocks to assemble a larger polynucleotide or polypeptide. For example, a theoretical segment pool containing TN1, DH, N2, and H3-JH segments can be used to assemble a library of CDRH3 sequences by concatenating them combinatorially to form a sequence represented by [TN1]-[DH]-[N2]-[H3-JH], and synthesizing the corresponding oligonucleotide(s). The term "theoretical segment pool" can apply to any set of polynucleotide or polypeptide segments. Thus, while a set of TN1, DH, N2, and H3-JH segments are collectively considered a theoretical segment pool, each of the individual sets of segments also comprise a theoretical segment pool, specifically a TN1 theoretical segment pool, a DH theoretical segment pool, an N2 theoretical segment pool, and an H3-JH theoretical segment pool. Any subsets of these theoretical segment pools containing two or more sequences can also be considered theoretical segment pools.

The term "unique," as used herein, refers to a sequence that is different (*e.g.*, has a different chemical structure) from every other sequence within the designed set (*e.g.*, the theoretical diversity). It should be understood that there are likely to be more than one copy of many unique sequences from the theoretical diversity in a particular physical realization. For example, a library comprising three unique sequences at the theoretical level may comprise nine total members if each sequence occurs three times in the physical realization of the library. However, in certain embodiments, each unique sequence may occur only once, less than once, or more than once.

The term "variable" refers to the portions of the immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (*i.e.*, the "variable domain(s)"). Variability is not evenly distributed throughout the variable domains of

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antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called "hypervariable" regions or "complementarity determining regions" (CDRs). The more conserved (*i.e.*, non-hypervariable) portions of the variable domains are called the "framework" regions (FRM). The variable domains of naturally occurring heavy and light chains each comprise four FRM regions, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.* Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991).

The constant domains are not directly involved in antigen binding, but exhibit various effector functions, such as, for example, antibody-dependent, cell-mediated cytotoxicity and complement activation.

Libraries of the invention containing "VKCDR3" sequences and "V□CDR3" sequences refer to the kappa and lambda sub-sets of the light chain CDR3 (CDRL3) sequences, respectively. Such libraries may be designed with directed diversity, to collectively represent the length and sequence diversity of the human antibody CDRL3 repertoire. "Preimmune" versions of these libraries have similar sequence diversities and length diversities as naturally occurring human antibody CDRL3 sequences before these sequences undergo negative selection and/or somatic hypermutation. Known human CDRL3 sequences are represented in various data sets, including the NCBI database, WO/2009/036379, and Martin, Proteins, 1996, 25: 130.

General Design of Libraries

Antibody libraries provided by the present invention may be designed to reflect certain aspects of the preimmune repertoire as created by the human immune system. Certain libraries of the invention are based on rational design informed by collections of human V, D, and J genes, and large databases of human heavy and light chain sequences (*e.g.*, publicly known germline sequences and sequences from Jackson *et al.*, J. Immunol Methods, 2007, 324: 26; Lee *et al.*, Immunogenetics, 2006, 57: 917; Boyd *et al.*, Science Translational Medicine, 2009, 1: 1-8,

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and sequences compiled from rearranged VK and V□ sequences (see WO/2009/036379).

Additional information may be found, for example, in Scaviner *et al.*, Exp. Clin. Immunogenet., 1999, 16: 234; Tomlinson *et al.*, J. Mol. Biol., 1992, 227: 799; and Matsuda *et al.*, J. Exp. Med., 1998, 188: 2151.

In certain embodiments of the invention, segments representing the possible V, D, and J diversity found in the human repertoire, as well as junctional diversity (*i.e.*, TN1 and N2), are synthesized *de novo* as single or double-stranded DNA oligonucleotides. In certain embodiments of the invention, oligonucleotides encoding CDR sequences are introduced into yeast along with one or more acceptor vectors containing heavy or light chain chassis sequences and constant domains. No primer-based PCR amplification or template-directed cloning steps from mammalian cDNA or mRNA are employed. Through standard homologous recombination, the recipient yeast recombines the CDR segments with the acceptor vectors containing the chassis sequences and constant regions, to create a properly ordered synthetic, full-length human heavy chain and/or light chain immunoglobulin library that can be genetically propagated, expressed, presented, and screened. One of ordinary skill in the art will readily recognize that the acceptor vector can be designed so as to produce constructs other than full-length human heavy chains and/or light chains. For example, in certain embodiments of the invention, the chassis may be designed to encode portions of a polypeptide encoding an antibody fragment or subunit of an antibody fragment, so that a sequence encoding an antibody fragment, or subunit thereof, is produced when the oligonucleotide cassette containing the CDR is recombined with the acceptor vector.

Thus, in certain embodiments, the invention provides a synthetic, preimmune human antibody repertoire the repertoire comprising:

(a) one or more selected human antibody heavy chain chassis (*i.e.*, amino acids 1 to 94 of the heavy chain variable region, using Kabat's definition);

(b) a CDRH3 repertoire (described more fully below), designed based on the human IGHD and IGHJ germline sequences, and the extraction of TN1 and N2 sequences from reference sets of human CDRH3 sequences, the CDRH3 repertoire comprising (i) a TN1 segment; (ii) a DH segment; (iii) an N2 segment; (iv) an H3-JH segment.

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(c) one or more selected human antibody kappa and/or lambda light chain chassis; and

(d) a CDRL3 repertoire designed based on the human IGLV and IGLJ germline sequences, wherein "L" may be a kappa or lambda light chain.

The instant invention also provides methods for producing and using such libraries, as well as libraries comprising one or more immunoglobulin domains or antibody fragments. Design and synthesis of each component of the antibody libraries of the invention is provided in more detail below.

Design of Antibody Library Chassis Sequences

In certain embodiments, provided libraries are constructed from selected chassis sequences that are based on naturally occurring variable domain sequences (*e.g.,* IGHV and IGLV genes). The selection of such chassis sequences can be done arbitrarily, or through the definition of certain pre-determined criteria. For example, the Kabat database, an electronic database containing non-redundant rearranged antibody sequences, can be queried for those heavy and light chain germline sequences that are most frequently represented. An algorithm such as BLAST, or a more specialized tool such as SoDA (Volpe *et al.*, Bioinformatics, 2006, 22: 438-44). can be used to compare rearranged antibody sequences with germline sequences (*e.g.,* using the V BASE2 database; see, for example, Retter *et al.,* Nucleic Acids Res., 2005, 33: D671-D674), or similar collections of human V, D, and J genes, to identify germline families that are most frequently used to generate functional antibodies.

Several criteria can be utilized for the selection of chassis for inclusion in the libraries of the invention. For example, sequences that are known (or have been determined) to express poorly in yeast, or other organisms used in the invention (*e.g.,* bacteria, mammalian cells, fungi, or plants) can be excluded from the libraries. Chassis may also be chosen based on the representation of their corresponding germline genes in the peripheral blood of humans. In certain embodiments of the invention, it may be desirable to select chassis that correspond to germline sequences that are highly represented in the peripheral blood of humans. In some embodiments, it may be desirable to select chassis that correspond to germline sequences that are less frequently represented, for example, to increase the canonical diversity of the

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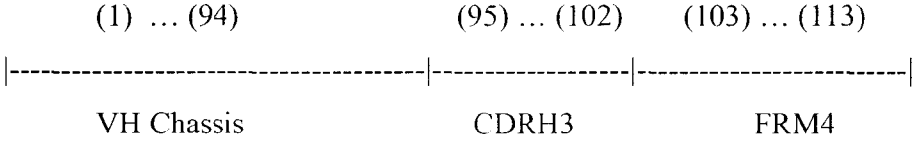
library. Therefore, chassis may be selected to produce libraries that represent the largest and most structurally diverse group of functional human antibodies.

In certain embodiments of the invention, less diverse chassis may be utilized, for example, if it is desirable to produce a smaller, more focused library with less chassis variability and greater CDR variability. In some embodiments of the invention, chassis may be selected based on both their expression in a cell of the invention (*e.g.*, a yeast cell) and the diversity of canonical structures represented by the selected sequences. One may therefore produce a library with a diversity of canonical structures that express well in a cell of the invention.

Design of Heavy Chain Chassis Sequences

The design and selection of heavy chain chassis sequences that can be used in the current invention is described in detail in U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379.

In general, VH domains of the library comprise three components: (1) a VH "chassis," which includes amino acids 1 to 94 (using Kabat numbering), (2) the CDRH3, which is defined herein to include the Kabat CDRH3 proper (positions 95-102), and (3) the FRM4 region, including amino acids 103 to 113 (Kabat numbering). The overall VH domain structure may therefore be depicted schematically (not to scale) as:



In certain embodiments of the invention, the VH chassis of the libraries may comprise from about Kabat residue 1 to about Kabat residue 94 of one or more of the following IGHV germline sequences: IGHV1-2, IGHV1-3, IGHV1-8, IGHV1-18, IGHV1-24, IGHV1-45, IGHV1-46, IGHV1-58, IGHV1-69, IGH8, IGH56, IGH100, IGHV3-7, IGHV3-9, IGHV3-11, IGHV3-13, IGHV3-15, IGHV3-20, IGHV3-21, IGHV3-23, IGHV3-30, IGHV3-33, IGHV3-43, IGHV3-48, IGHV3-49, IGHV3-53, IGHV3-64, IGHV3-66, IGHV3-72, IGHV3-73, IGHV3-74, IGHV4-4, IGHV4-28, IGHV4-31, IGHV4-34, IGHV4-39, IGHV4-59, IGHV4-61, IGHV4-B, IGHV5-51,

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IGHV6-1, and/or IGHV7-4-1. In some embodiments of the invention, a library may contain one or more of these sequences, one or more allelic variants of these sequences, or encode an amino acid sequence at least about 99.9%, 99.5%, 99%, 98.5%, 98%, 97.5%, 97%, 96.5%, 96%, 95.5%, 95%, 94.5%, 94%, 93.5%, 93%, 92.5%, 92%, 91.5%, 91%, 90.5%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 77.5%, 75%, 73.5%, 70%, 65%, 60%, 55%, or 50% identical to one or more of these sequences. One of ordinary skill in the art will recognize that given the chassis definition provided above, any IGHV-encoding sequence can be adapted for use as a chassis of the invention. As exemplified in U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379),

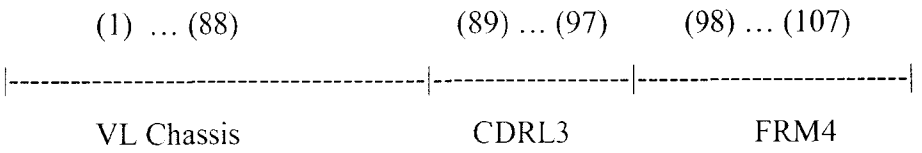
these chassis can also be varied, particularly by altering the amino acid residues in the CDRH1 and CDRH2 regions, further increasing the diversity of the library.

Design of Light Chain Chassis Sequences

The design and selection of light chain chassis sequences that can be used in the current invention is described in detail in U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379.

The light chain chassis of the invention may be based on kappa and/or lambda light chain sequences.

The VL domains of the library comprise three primary components: (1) a VL "chassis", which includes amino acids 1 to 88 (using Kabat numbering), (2) the CDRL3, which is defined herein to include the Kabat CDRL3 proper (positions 89-97), and (3) the FRM4 region, including amino acids 98 to 107 (Kabat numbering). The overall VL domain structure may therefore be depicted schematically (not to scale) as:



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In certain embodiments of the invention, the VL chassis of the libraries include one or more chassis based on IGKV germline sequences. In certain embodiments of the invention, the VL chassis of the libraries may comprise from about Kabat residue 1 to about Kabat residue 88 of one or more of the following IGKV germline sequences: IGKV1-05, IGKV1-06, IGKV1-08, IGKV1-09, IGKV1-12, IGKV1-13, IGKV1-16, IGKV1-17, IGKV1-27, IGKV1-33, IGKV1-37, IGKV1-39, IGKV1D-16, IGKV1D-17, IGKV1D-43, IGKV1D-8, IGK54, IGK58, IGK59, IGK60, IGK70, IGKV2D-26, IGKV2D-29, IGKV2D-30, IGKV3-11, IGKV3-15, IGKV3-20, IGKV3D-07, IGKV3D-11, IGKV3D-20, IGKV4-1, IGKV5-2, IGKV6-21, and/or IGKV6D-41. In some embodiments of the invention, a library may contain one or more of these sequences, one or more allelic variants of these sequences, or encode an amino acid sequence at least about 99.9%, 99.5%, 99%, 98.5%, 98%, 97.5%, 97%, 96.5%, 96%, 95.5%, 95%, 94.5%, 94%, 93.5%, 93%, 92.5%, 92%, 91.5%, 91%, 90.5%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80%, 77.5%, 75%, 73.5%, 70%, 65%, 60%, 55%, or 50% identical to one or more of these sequences.

In certain embodiments of the invention, the VL chassis of the libraries include one or more chassis based on IG□V germline sequences. In certain embodiments of the invention, the VL chassis of the libraries may comprise from about Kabat residue 1 to about Kabat residue 88 of one or more of the following IG□V germline sequences: IG□V3-1, IG□V3-21, IG□44, IG□V1-40, IG□V3-19, IG□V1-51, IG□V1-44, IG□V6-57, IG□11, IG□V3-25, IG□53, IG□V3-10, IG□V4-69, IG□V1-47, IG□41, IG□V7-43, IG□V7-46, IG□V5-45, IG□V4-60, IG□V10-54, IG□V8-61, IG□V3-9, IG□V1-36, IG□48, IG□V3-16, IG□V3-27, IG□V4-3, IG□V5-39, IG□V9-49, and/or IG□V3-12. In some embodiments of the invention, a library may contain one or more of these sequences, one or more allelic variants of these sequences, or encode an amino acid sequence at least about 99.9%, 99.5%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, or 50% identical to one or more of these sequences.

One of ordinary skill in the art will recognize that given the chassis definition provided above, any IGKV- or IG□V-encoding sequence can be adapted for use as a chassis of the invention.

Design and Selection of TN1, DH, N2, and H3-JH Segments

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The human germline repertoire contains at least six IGHJ genes (IGHJ1, IGHJ2, IGHJ3, IGHJ4, IGHJ5, and IGHJ6; included in Table 14, where the primary allele is designated "01," and selected allelic variants are designated "02" or "03"), and at least 27 IGHD genes (Table 16, including allelic variants). In some embodiments, the invention comprises a library of CDRH3 polypeptide sequences, or polynucleotide sequences encoding CDRH3 sequences, the library comprising members of any of the theoretical segment pools disclosed herein.

A person of ordinary skill in the art will recognize that not every segment in a theoretical segment pool provided herein is necessary to produce a functional CDRH3 library of the invention. Therefore, in certain embodiments, a CDRH3 library of the invention will contain a subset of the segments of any of the theoretical segment pools described herein. For example, in certain embodiments of the invention, at least about 15, 30, 45, 60, 75, 90, 100, 105, 120, 135, 150, 165, 180, 195, 200, 210, 225, 240, 255, 270, 285, 300, 320, 340, 360, 380, 400, 420, 440, 460, 480, 500, 520, 540, 560, 580, 600, 620, 640, or 643 of the H3-JH segments of any of the theoretical segment pools provided herein, or generated by the methods described herein, are included in a library. In some embodiments of the invention, at least about 15, 30, 45, 60, 75, 90, 100, 105, 120, 135, 150, 165, 180, 195, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1111, 2000, 3000, 4000, 5000, 6000, 7000, 14000, 21000, 28000, 35000, 42000, 49000, 56000, 63000, or 68374 of the DH segments of any of the theoretical segment pools provided herein, or generated by the methods described herein, are included in a library. In some embodiments of the invention, at least about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 141, 150, 160, 170, 180, 190, or 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 420, 424, 440, 460, 480, 500, 550, 600, 650, 700, 727, 750, 800, 850, 900, 950, or 1000 of the TN1 and/or N2 segments of any of the theoretical segment pools provided herein, or generated by the methods described herein, are included in a library. In certain embodiments, a library of the invention may contain less than a particular number of polynucleotide or polypeptide segments, where the number of segments is defined using any one of the integers provided above for the respective segment. In some embodiments of the invention, a particular numerical range is defined, using any two of the integers provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the integers provided, which define an upper and lower boundary, are contemplated.

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In certain embodiments, the invention provides CDRH3 libraries comprising at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the segments from any of the theoretical segment pools provided herein. For example, the invention provides libraries comprising at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the TN1, DH, N2, and/or H3-JH segments from any of the theoretical segment pools provided herein. In some embodiments of the invention, a particular percentage range is defined, using any two of the percentages provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the percentages provided, which define an upper and lower boundary, are contemplated.

In some embodiments of the invention, at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the H3-JH, DH, TN1, and/or N2 segments in a CDRH3 library are H3-JH, DH, TN1, and/or N2 segments of any of the theoretical segment pools provided herein, or generated by the methods described herein,. In some embodiments of the invention, at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the H3-JH, DH, TN1, and/or N2 segments of antibodies isolated from a CDRH3 library (*e.g.,* by binding to a particular antigen and/or generic ligand through one or more rounds of selection) are H3-JH, DH, TN1, and/or N2 segments of any of the theoretical segment pools provided herein, or generated by methods described herein. In certain embodiments, a CDRH3 library of the invention may contain less than a particular percentage of H3-JH, DH, TN1, and/or N2 segments of any of the theoretical segment pools provided herein, or generated by the methods described herein, where the number of segments is defined using any one of the percentages provided above for the respective segment. In some embodiments of the invention, a particular percentage range is defined, using any two of the percentages provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the percentages provided, which define an upper and lower boundary, are contemplated.

One of ordinary skill in the art will appreciate, upon reading the disclosure herein. that given the TN1, DH, N2, and/or H3-JH segments of any of the theoretical segment pools provided herein, or generated by the methods described herein, similar

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TN1, DH, N2, and/or H3-JH segments, and corresponding CDRH3 libraries, could be produced which, while not 100% identical to those provided in terms of their sequences, may be functionally very similar. Such theoretical segment pools and CDRH3 libraries also fall within the scope of the invention. A variety of techniques well-known in the art could be used to obtain these additional sequences, including the mutagenesis techniques provided herein. Therefore, each of the explicitly enumerated embodiments of the invention can also be practiced using segments that share a particular percent identity to any of the segments of any of the theoretical segment pools provided herein, or generated by the methods described herein. For example, each of the previously described embodiments of the invention can be practiced using TN1, DH, N2, and/or H3-JH segments that are at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% identical to the TN1, DH, N2, and/or H3-JH segments of any of the theoretical segment pools provided herein, or generated by the methods described herein.

In some embodiments, the invention provides libraries produced from one or more VH chassis sequences combined with one or more TN1 segments, one or more DH segments, one or more N2 segments, and one or more H3-JH segments. In certain embodiments at least 1, 2, 5, 10, 20, 50, 75, or 100, of each chassis, TN1, DH, N2, or H3-JH segments are included in a library of the invention.

In some embodiments, the invention provides a method of selecting TN1, DH, N2, and H3-JH segments from a theoretical segment pool for inclusion in a synthetic CDRH3 library, comprising:

(i) providing a theoretical segment pool containing one or more of TN1, DH, N2, and H3-JH segments;

(ii) providing a reference set of CDRH3 sequences;

(iii) utilizing the theoretical segment pool of (i) to identify the closest match(es) to each CDRH3 sequence in the reference set of (ii); and

(iv) selecting segments from the theoretical segment pool for inclusion in a synthetic library.

In some embodiments, the selection process of (iv) can optionally involve any number of additional criteria, including the frequency of occurrence of the segments of (i) in the reference set of (ii); the corresponding segmental usage weights; and any

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physicochemical properties (see all numerical indices at www.genome.jp/aaindex/) of the segments (*e.g.*, hydrophobicity, alpha-helical propensity, and/or isoelectric point). Optionally, TN1 and/or N2 segments that do not occur in the theoretical segment pool of (i) but that are found in the reference set of (ii) may be identified and added to prospective theoretical segment pools to produce theoretical segment pools with increased TN1 and/or N2 diversity in the prospective theoretical segment pools and/or synthetic libraries of the invention.

Any characteristic or set of characteristics of the segments can be used to choose them for inclusion in the library, including for example one or more biological properties (e.g., immunogenicity, stability, half-life) and/or one or more physicochemical properties such as the numerical indices provided above. In some embodiments, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more such properties is used to select segments for inclusion in a library of the invention. Physiochemical properties included in the index provided above can include, for example, ANDN920101 alpha-CH chemical shifts (Andersen et al., 1992); ARGP820101 Hydrophobicity index (Argos et al., 1982); ARGP820102 Signal sequence helical potential (Argos et al., 1982); ARGP820103 Membrane-buried preference parameters (Argos et al., 1982); BEGF750101 Conformational parameter of inner helix (Beghin-Dirkx, 1975); BEGF750102 Conformational parameter of beta-structure (Beghin-Dirkx, 1975); BEGF750103 Conformational parameter of beta-turn (Beghin-Dirkx, 1975); BHAR880101 Average flexibility indices (Bhaskaran-Ponnuswamy, 1988); BIGC670101 Residue volume (Bigelow, 1967); BIOV880101 Information value for accessibility; average fraction 35% (Biou et al., 1988); BIOV880102 Information value for accessibility; average fraction 23% (Biou et al., 1988); BROC820101 Retention coefficient in TFA (Browne et al., 1982); BROC820102 Retention coefficient in HFBA (Browne et al., 1982); BULH740101 Transfer free energy to surface (Bull-Breese, 1974); BULH740102 Apparent partial specific volume (Bull-Breese, 1974); BUNA790101 alpha-NH chemical shifts (Bundi-Wuthrich, 1979); BUNA790102 alpha-CH chemical shifts (Bundi-Wuthrich, 1979); BUNA790103 Spin-spin coupling constants 3JHalpha-NH (Bundi-Wuthrich, 1979); BURA740101 Normalized frequency of alpha-helix (Burgess et al., 1974); BURA740102 Normalized frequency of extended structure (Burgess et al., 1974); CHAM810101 Steric parameter (Charton, 1981); CHAM820101 Polarizability parameter (Charton-Charton, 1982); CHAM820102 Free energy of solution in water,

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kcal/mole (Charton-Charton, 1982); CHAM830101 The Chou-Fasman parameter of the coil conformation (Charton-Charton, 1983); CHAM830102 A parameter defined from the residuals obtained from the best correlation of the Chou-Fasman parameter of beta-sheet (Charton-Charton, 1983); CHAM830103 The number of atoms in the side chain labelled 1+1 (Charton-Charton, 1983); CHAM830104 The number of atoms in the side chain labelled 2+1 (Charton-Charton, 1983); CHAM830105 The number of atoms in the side chain labelled 3+1 (Charton-Charton, 1983); CHAM830106 The number of bonds in the longest chain (Charton-Charton, 1983); CHAM830107 A parameter of charge transfer capability (Charton-Charton, 1983); CHAM830108 A parameter of charge transfer donor capability (Charton-Charton, 1983); CHOC750101 Average volume of buried residue (Chothia, 1975); CHOC760101 Residue accessible surface area in tripeptide (Chothia, 1976); CHOC760102 Residue accessible surface area in folded protein (Chothia, 1976); CHOC760103 Proportion of residues 95% buried (Chothia, 1976); CHOC760104 Proportion of residues 100% buried (Chothia, 1976); CHOP780101 Normalized frequency of beta-turn (Chou-Fasman, 1978a); CHOP780201 Normalized frequency of alpha-helix (Chou-Fasman, 1978b); CHOP780202 Normalized frequency of beta-sheet (Chou-Fasman, 1978b); CHOP780203 Normalized frequency of beta-turn (Chou-Fasman, 1978b); CHOP780204 Normalized frequency of N-terminal helix (Chou-Fasman, 1978b); CHOP780205 Normalized frequency of C-terminal helix (Chou-Fasman, 1978b); CHOP780206 Normalized frequency of N-terminal non helical region (Chou-Fasman, 1978b); CHOP780207 Normalized frequency of C-terminal non helical region (Chou-Fasman, 1978b); CHOP780208 Normalized frequency of N-terminal beta-sheet (Chou-Fasman, 1978b); CHOP780209 Normalized frequency of C-terminal beta-sheet (Chou-Fasman, 1978b); CHOP780210 Normalized frequency of N-terminal non beta region (Chou-Fasman, 1978b); CHOP780211 Normalized frequency of C-terminal non beta region (Chou-Fasman, 1978b); CHOP780212 Frequency of the 1st residue in turn (Chou-Fasman, 1978b); CHOP780213 Frequency of the 2nd residue in turn (Chou-Fasman, 1978b); CHOP780214 Frequency of the 3rd residue in turn (Chou-Fasman, 1978b); CHOP780215 Frequency of the 4th residue in turn (Chou-Fasman, 1978b); CHOP780216 Normalized frequency of the 2nd and 3rd residues in turn (Chou-Fasman, 1978b); CIDH920101 Normalized hydrophobicity scales for alpha-proteins (Cid et al., 1992); CIDH920102 Normalized hydrophobicity scales for beta-proteins

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(Cid et al., 1992); CIDH920103 Normalized hydrophobicity scales for alpha+beta-proteins (Cid et al., 1992); CIDH920104 Normalized hydrophobicity scales for alpha/beta-proteins (Cid et al., 1992); CIDH920105 Normalized average hydrophobicity scales (Cid et al., 1992); COHE430101 Partial specific volume (Cohn-Edsall, 1943); CRAJ730101 Normalized frequency of middle helix (Crawford et al., 1973); CRAJ730102 Normalized frequency of beta-sheet (Crawford et al., 1973); CRAJ730103 Normalized frequency of turn (Crawford et al., 1973); DAWD720101 Size (Dawson, 1972); DAYM780101 Amino acid composition (Dayhoff et al., 1978a); DAYM780201 Relative mutability (Dayhoff et al., 1978b); DESM900101 Membrane preference for cytochrome b: MPH89 (Degli Esposti et al., 1990); DESM900102 Average membrane preference: AMP07 (Degli Esposti et al., 1990); EISD840101 Consensus normalized hydrophobicity scale (Eisenberg, 1984); EISD860101 Solvation free energy (Eisenberg-McLachlan, 1986); EISD860102 Atom-based hydrophobic moment (Eisenberg-McLachlan, 1986); EISD860103 Direction of hydrophobic moment (Eisenberg-McLachlan, 1986); FASG760101 Molecular weight (Fasman, 1976); FASG760102 Melting point (Fasman, 1976); FASG760103 Optical rotation (Fasman, 1976); FASG760104 pK-N (Fasman, 1976); FASG760105 pK-C (Fasman, 1976); FAUJ830101 Hydrophobic parameter pi (Fauchere-Pliska, 1983); FAUJ880101 Graph shape index (Fauchere et al., 1988); FAUJ880102 Smoothed upsilon steric parameter (Fauchere et al., 1988); FAUJ880103 Normalized van der Waals volume (Fauchere et al., 1988); FAUJ880104 STERIMOL length of the side chain (Fauchere et al., 1988); FAUJ880105 STERIMOL minimum width of the side chain (Fauchere et al., 1988); FAUJ880106 STERIMOL maximum width of the side chain (Fauchere et al., 1988); FAUJ880107 N.m.r. chemical shift of alpha-carbon (Fauchere et al., 1988); FAUJ880108 Localized electrical effect (Fauchere et al., 1988); FAUJ880109 Number of hydrogen bond donors (Fauchere et al., 1988); FAUJ880110 Number of full nonbonding orbitals (Fauchere et al., 1988); FAUJ880111 Positive charge (Fauchere et al., 1988); FAUJ880112 Negative charge (Fauchere et al., 1988); FAUJ880113 pK-a(RCOOH) (Fauchere et al., 1988); FINA770101 Helix-coil equilibrium constant (Finkelstein-Ptitsyn, 1977); FINA910101 Helix initiation parameter at posision i-1 (Finkelstein et al., 1991); FINA910102 Helix initiation parameter at posision i,i+1,i+2 (Finkelstein et al., 1991); FINA910103 Helix termination parameter at posision j-2,j-1,j (Finkelstein et al., 1991); FINA910104

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Helix termination parameter at posision j+1 (Finkelstein et al., 1991); GARJ730101 Partition coefficient (Garel et al., 1973); GEIM800101 Alpha-helix indices (Geisow-Roberts, 1980); GEIM800102 Alpha-helix indices for alpha-proteins (Geisow-Roberts, 1980); GEIM800103 Alpha-helix indices for beta-proteins (Geisow-Roberts, 1980); GEIM800104 Alpha-helix indices for alpha/beta-proteins (Geisow-Roberts, 1980); GEIM800105 Beta-strand indices (Geisow-Roberts, 1980); GEIM800106 Beta-strand indices for beta-proteins (Geisow-Roberts, 1980); GEIM800107 Beta-strand indices for alpha/beta-proteins (Geisow-Roberts, 1980)
GEIM800108 Aperiodic indices (Geisow-Roberts, 1980);GEI M800109 Aperiodic indices for alpha-proteins (Geisow-Roberts, 1980); GEIM800110 Aperiodic indices for beta-proteins (Geisow-Roberts, 1980); GEIM800111 Aperiodic indices for alpha/beta-proteins (Geisow-Roberts, 1980); GOLD730101 Hydrophobicity factor (Goldsack-Chalifoux, 1973); GOLD730102 Residue volume (Goldsack-Chalifoux, 1973); GRAR740101 Composition (Grantham, 1974); GRAR740102 Polarity (Grantham, 1974)
GRAR740103 Volume (Grantham, 1974); GUYH850101 Partition energy (Guy, 1985); HOPA770101 Hydration number (Hopfinger, 1971), Cited by Charton-Charton (1982)
HOPT810101 Hydrophilicity value (Hopp-Woods, 1981); HUTJ700101 Heat capacity (Hutchens, 1970); HUTJ700102 Absolute entropy (Hutchens, 1970); HUTJ700103 Entropy of formation (Hutchens, 1970); ISOY800101 Normalized relative frequency of alpha-helix (Isogai et al., 1980); ISOY800102 Normalized relative frequency of extended structure (Isogai et al., 1980); ISOY800103 Normalized relative frequency of bend (Isogai et al., 1980); ISOY800104 Normalized relative frequency of bend R (Isogai et al., 1980); ISOY800105 Normalized relative frequency of bend S (Isogai et al., 1980); ISOY800106 Normalized relative frequency of helix end (Isogai et al., 1980); ISOY800107 Normalized relative frequency of double bend (Isogai et al., 1980); ISOY800108 Normalized relative frequency of coil (Isogai et al., 1980); JANJ780101 Average accessible surface area (Janin et al., 1978); JANJ780102 Percentage of buried residues (Janin et al., 1978); JANJ780103 Percentage of exposed residues (Janin et al., 1978); JANJ790101 Ratio of buried and accessible molar fractions (Janin, 1979); JANJ790102 Transfer free energy (Janin, 1979); JOND750101 Hydrophobicity (Jones, 1975); JOND750102 pK (-COOH)

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(Jones, 1975); JOND920101 Relative frequency of occurrence (Jones et al., 1992); JOND920102 Relative mutability (Jones et al., 1992)

JUKT750101 Amino acid distribution (Jukes et al., 1975); JUNJ780101 Sequence frequency (Jungck, 1978); KANM800101 Average relative probability of helix (Kanehisa-Tsong, 1980); KANM800102 Average relative probability of beta-sheet (Kanehisa-Tsong, 1980); KANM800103 Average relative probability of inner helix (Kanehisa-Tsong, 1980); KANM800104 Average relative probability of inner beta-sheet (Kanehisa-Tsong, 1980); KARP850101 Flexibility parameter for no rigid neighbors (Karplus-Schulz, 1985); KARP850102 Flexibility parameter for one rigid neighbor (Karplus-Schulz, 1985); KARP850103 Flexibility parameter for two rigid neighbors (Karplus-Schulz, 1985); KHAG800101 The Kerr-constant increments (Khanarian-Moore, 1980); KLEP840101 Net charge (Klein et al., 1984); KRIW710101 Side chain interaction parameter (Krigbaum-Rubin, 1971); KRIW790101 Side chain interaction parameter (Krigbaum-Komoriya, 1979); KRIW790102 Fraction of site occupied by water (Krigbaum-Komoriya, 1979); KRIW790103 Side chain volume (Krigbaum-Komoriya, 1979); KYTJ820101 Hydropathy index (Kyte-Doolittle, 1982); LAWE840101 Transfer free energy, CHP/water (Lawson et al., 1984); LEVM760101 Hydrophobic parameter (Levitt, 1976); LEVM760102 Distance between C-alpha and centroid of side chain (Levitt, 1976); LEVM760103 Side chain angle theta(AAR) (Levitt, 1976); LEVM760104 Side chain torsion angle phi(AAAR) (Levitt, 1976); LEVM760105 Radius of gyration of side chain (Levitt, 1976); LEVM760106 van der Waals parameter R0 (Levitt, 1976)

LEVM760107 van der Waals parameter epsilon (Levitt, 1976); LEVM780101 Normalized frequency of alpha-helix, with weights (Levitt, 1978); LEVM780102 Normalized frequency of beta-sheet, with weights (Levitt, 1978); LEVM780103 Normalized frequency of reverse turn, with weights (Levitt, 1978); LEVM780104 Normalized frequency of alpha-helix, unweighted (Levitt, 1978); LEVM780105 Normalized frequency of beta-sheet, unweighted (Levitt, 1978); LEVM780106 Normalized frequency of reverse turn, unweighted (Levitt, 1978); LEWP710101 Frequency of occurrence in beta-bends (Lewis et al., 1971); LIFS790101 Conformational preference for all beta-strands (Lifson-Sander, 1979); LIFS790102 Conformational preference for parallel beta-strands (Lifson-Sander, 1979); LIFS790103 Conformational preference for antiparallel beta-strands (Lifson-Sander,

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1979); MANP780101 Average surrounding hydrophobicity (Manavalan-Ponnuswamy, 1978); MAXF760101 Normalized frequency of alpha-helix (Maxfield-Scheraga, 1976); MAXF760102 Normalized frequency of extended structure (Maxfield-Scheraga, 1976); MAXF760103 Normalized frequency of zeta R (Maxfield-Scheraga, 1976); MAXF760104 Normalized frequency of left-handed alpha-helix (Maxfield-Scheraga, 1976); MAXF760105 Normalized frequency of zeta L (Maxfield-Scheraga, 1976); MAXF760106 Normalized frequency of alpha region (Maxfield-Scheraga, 1976); MCMT640101 Refractivity (McMeekin et al., 1964), Cited by Jones (1975); MEEJ800101 Retention coefficient in HPLC, pH7.4 (Meek, 1980); MEEJ800102 Retention coefficient in HPLC, pH2.1 (Meek, 1980); MEEJ810101 Retention coefficient in NaClO4 (Meek-Rossetti, 1981); MEEJ810102 Retention coefficient in NaH2PO4 (Meek-Rossetti, 1981); MEIH800101 Average reduced distance for C-alpha (Meirovitch et al., 1980); MEIH800102 Average reduced distance for side chain (Meirovitch et al., 1980); MEIH800103 Average side chain orientation angle (Meirovitch et al., 1980); MIYS850101 Effective partition energy (Miyazawa-Jernigan, 1985); NAGK730101 Normalized frequency of alpha-helix (Nagano, 1973); NAGK730102 Normalized frequency of bata-structure (Nagano, 1973)

NAGK730103 Normalized frequency of coil (Nagano, 1973); NAKH900101 AA composition of total proteins (Nakashima et al., 1990); NAKH900102 SD of AA composition of total proteins (Nakashima et al., 1990); NAKH900103 AA composition of mt-proteins (Nakashima et al., 1990); NAKH900104 Normalized composition of mt-proteins (Nakashima et al., 1990); NAKH900105 AA composition of mt-proteins from animal (Nakashima et al., 1990); NAKH900106 Normalized composition from animal (Nakashima et al., 1990); NAKH900107 AA composition of mt-proteins from fungi and plant (Nakashima et al., 1990); NAKH900108 Normalized composition from fungi and plant (Nakashima et al., 1990); NAKH900109 AA composition of membrane proteins (Nakashima et al., 1990); NAKH900110 Normalized composition of membrane proteins (Nakashima et al., 1990); NAKH900111 Transmembrane regions of non-mt-proteins (Nakashima et al., 1990); NAKH900112 Transmembrane regions of mt-proteins (Nakashima et al., 1990); NAKH900113 Ratio of average and computed composition (Nakashima et al., 1990); NAKH920101 AA composition of CYT of single-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920102 AA composition of CYT2 of single-spanning

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proteins (Nakashima-Nishikawa, 1992); NAKH920103 AA composition of EXT of single-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920104 AA composition of EXT2 of single-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920105 AA composition of MEM of single-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920106 AA composition of CYT of multi-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920107 AA composition of EXT of multi-spanning proteins (Nakashima-Nishikawa, 1992); NAKH920108 AA composition of MEM of multi-spanning proteins (Nakashima-Nishikawa, 1992); NISK800101 8 A contact number (Nishikawa-Ooi, 1980); NISK860101 14 A contact number (Nishikawa-Ooi, 1986); NOZY710101 Transfer energy, organic solvent/water (Nozaki-Tanford, 1971); OOBM770101 Average non-bonded energy per atom (Oobatake-Ooi, 1977); OOBM770102 Short and medium range non-bonded energy per atom (Oobatake-Ooi, 1977); OOBM770103 Long range non-bonded energy per atom (Oobatake-Ooi, 1977)

OOBM770104 Average non-bonded energy per residue (Oobatake-Ooi, 1977); OOBM770105 Short and medium range non-bonded energy per residue (Oobatake-Ooi, 1977); OOBM850101 Optimized beta-structure-coil equilibrium constant (Oobatake et al., 1985); OOBM850102 Optimized propensity to form reverse turn (Oobatake et al., 1985); OOBM850103 Optimized transfer energy parameter (Oobatake et al., 1985); OOBM850104 Optimized average non-bonded energy per atom (Oobatake et al., 1985); OOBM850105 Optimized side chain interaction parameter (Oobatake et al., 1985); PALJ810101 Normalized frequency of alpha-helix from LG (Palau et al., 1981); PALJ810102 Normalized frequency of alpha-helix from CF (Palau et al., 1981); PALJ810103 Normalized frequency of beta-sheet from LG (Palau et al., 1981); PALJ810104 Normalized frequency of beta-sheet from CF (Palau et al., 1981); PALJ810105 Normalized frequency of turn from LG (Palau et al., 1981); PALJ810106 Normalized frequency of turn from CF (Palau et al., 1981); PALJ810107 Normalized frequency of alpha-helix in all-alpha class (Palau et al., 1981); PALJ810108 Normalized frequency of alpha-helix in alpha+beta class (Palau et al., 1981); PALJ810109 Normalized frequency of alpha-helix in alpha/beta class (Palau et al., 1981); PALJ810110 Normalized frequency of beta-sheet in all-beta class (Palau et al., 1981); PALJ810111 Normalized frequency of beta-sheet in alpha+beta class (Palau et al., 1981); PALJ810112 Normalized frequency of beta-sheet in alpha/beta class (Palau et al., 1981); PALJ810113 Normalized frequency of turn in

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all-alpha class (Palau et al., 1981); PALJ810114 Normalized frequency of turn in all-beta class (Palau et al., 1981); PALJ810115 Normalized frequency of turn in alpha+beta class (Palau et al., 1981); PALJ810116 Normalized frequency of turn in alpha/beta class (Palau et al., 1981); PARJ860101 HPLC parameter (Parker et al., 1986); PLIV810101 Partition coefficient (Pliska et al., 1981); PONP800101 Surrounding hydrophobicity in folded form (Ponnuswamy et al., 1980); PONP800102 Average gain in surrounding hydrophobicity (Ponnuswamy et al., 1980); PONP800103 Average gain ratio in surrounding hydrophobicity (Ponnuswamy et al., 1980); PONP800104 Surrounding hydrophobicity in alpha-helix (Ponnuswamy et al., 1980); PONP800105 Surrounding hydrophobicity in beta-sheet (Ponnuswamy et al., 1980); PONP800106 Surrounding hydrophobicity in turn (Ponnuswamy et al., 1980); PONP800107 Accessibility reduction ratio (Ponnuswamy et al., 1980); PONP800108 Average number of surrounding residues (Ponnuswamy et al., 1980); PRAM820101 Intercept in regression analysis (Prabhakaran-Ponnuswamy, 1982); PRAM820102 Slope in regression analysis x 1.0E1 (Prabhakaran-Ponnuswamy, 1982); PRAM820103 Correlation coefficient in regression analysis (Prabhakaran-Ponnuswamy, 1982); PRAM900101 Hydrophobicity (Prabhakaran, 1990); PRAM900102 Relative frequency in alpha-helix (Prabhakaran, 1990); PRAM900103 Relative frequency in beta-sheet (Prabhakaran, 1990); PRAM900104 Relative frequency in reverse-turn (Prabhakaran, 1990); PTIO830101 Helix-coil equilibrium constant (Ptitsyn-Finkelstein, 1983); PTIO830102 Beta-coil equilibrium constant (Ptitsyn-Finkelstein, 1983); QIAN880101 Weights for alpha-helix at the window position of -6 (Qian-Sejnowski, 1988); QIAN880102 Weights for alpha-helix at the window position of -5 (Qian-Sejnowski, 1988); QIAN880103 Weights for alpha-helix at the window position of -4 (Qian-Sejnowski, 1988); QIAN880104 Weights for alpha-helix at the window position of -3 (Qian-Sejnowski, 1988); QIAN880105 Weights for alpha-helix at the window position of -2 (Qian-Sejnowski, 1988); QIAN880106 Weights for alpha-helix at the window position of -1 (Qian-Sejnowski, 1988); QIAN880107 Weights for alpha-helix at the window position of 0 (Qian-Sejnowski, 1988); QIAN880108 Weights for alpha-helix at the window position of 1 (Qian-Sejnowski, 1988); QIAN880109 Weights for alpha-helix at the window position of 2 (Qian-Sejnowski, 1988); QIAN880110 Weights for alpha-helix at the window position of 3 (Qian-Sejnowski, 1988); QIAN880111 Weights for alpha-helix at the window position of 4 (Qian-Sejnowski, 1988); QIAN880112 Weights for alpha-

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helix at the window position of 5 (Qian-Sejnowski, 1988); QIAN880113 Weights for alpha-helix at the window position of 6 (Qian-Sejnowski, 1988); QIAN880114 Weights for beta-sheet at the window position of -6 (Qian-Sejnowski, 1988); QIAN880115 Weights for beta-sheet at the window position of -5 (Qian-Sejnowski, 1988); QIAN880116 Weights for beta-sheet at the window position of -4 (Qian-Sejnowski, 1988); QIAN880117 Weights for beta-sheet at the window position of -3 (Qian-Sejnowski, 1988); QIAN880118 Weights for beta-sheet at the window position of -2 (Qian-Sejnowski, 1988); QIAN880119 Weights for beta-sheet at the window position of -1 (Qian-Sejnowski, 1988); QIAN880120 Weights for beta-sheet at the window position of 0 (Qian-Sejnowski, 1988); QIAN880121 Weights for beta-sheet at the window position of 1 (Qian-Sejnowski, 1988); QIAN880122 Weights for beta-sheet at the window position of 2 (Qian-Sejnowski, 1988); QIAN880123 Weights for beta-sheet at the window position of 3 (Qian-Sejnowski, 1988); QIAN880124 Weights for beta-sheet at the window position of 4 (Qian-Sejnowski, 1988); QIAN880125 Weights for beta-sheet at the window position of 5 (Qian-Sejnowski, 1988); QIAN880126 Weights for beta-sheet at the window position of 6 (Qian-Sejnowski, 1988); QIAN880127 Weights for coil at the window position of -6 (Qian-Sejnowski, 1988); QIAN880128 Weights for coil at the window position of -5 (Qian-Sejnowski, 1988); QIAN880129 Weights for coil at the window position of -4 (Qian-Sejnowski, 1988); QIAN880130 Weights for coil at the window position of -3 (Qian-Sejnowski, 1988); QIAN880131 Weights for coil at the window position of -2 (Qian-Sejnowski, 1988); QIAN880132 Weights for coil at the window position of -1 (Qian-Sejnowski, 1988); QIAN880133 Weights for coil at the window position of 0 (Qian-Sejnowski, 1988); QIAN880134 Weights for coil at the window position of 1 (Qian-Sejnowski, 1988); QIAN880135 Weights for coil at the window position of 2 (Qian-Sejnowski, 1988); QIAN880136 Weights for coil at the window position of 3 (Qian-Sejnowski, 1988); QIAN880137 Weights for coil at the window position of 4 (Qian-Sejnowski, 1988); QIAN880138 Weights for coil at the window position of 5 (Qian-Sejnowski, 1988); QIAN880139 Weights for coil at the window position of 6 (Qian-Sejnowski, 1988); RACS770101 Average reduced distance for C-alpha (Rackovsky-Scheraga, 1977); RACS770102 Average reduced distance for side chain (Rackovsky-Scheraga, 1977); RACS770103 Side chain orientational preference (Rackovsky-Scheraga, 1977); RACS820101 Average relative fractional occurrence in A0(i) (Rackovsky-Scheraga, 1982); RACS820102 Average relative fractional occurrence in

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AR(i) (Rackovsky-Scheraga, 1982); RACS820103 Average relative fractional occurrence in AL(i) (Rackovsky-Scheraga, 1982); RACS820104 Average relative fractional occurrence in EL(i) (Rackovsky-Scheraga, 1982); RACS820105 Average relative fractional occurrence in E0(i) (Rackovsky-Scheraga, 1982); RACS820106 Average relative fractional occurrence in ER(i) (Rackovsky-Scheraga, 1982); RACS820107 Average relative fractional occurrence in A0(i-1) (Rackovsky-Scheraga, 1982); RACS820108 Average relative fractional occurrence in AR(i-1) (Rackovsky-Scheraga, 1982); RACS820109 Average relative fractional occurrence in AL(i-1) (Rackovsky-Scheraga, 1982); RACS820110 Average relative fractional occurrence in EL(i-1) (Rackovsky-Scheraga, 1982); RACS820111 Average relative fractional occurrence in E0(i-1) (Rackovsky-Scheraga, 1982); RACS820112 Average relative fractional occurrence in ER(i-1) (Rackovsky-Scheraga, 1982); RACS820113 Value of theta(i) (Rackovsky-Scheraga, 1982); RACS820114 Value of theta(i-1) (Rackovsky-Scheraga, 1982); RADA880101 Transfer free energy from chx to wat (Radzicka-Wolfenden, 1988); RADA880102 Transfer free energy from oct to wat (Radzicka-Wolfenden, 1988); RADA880103 Transfer free energy from vap to chx (Radzicka-Wolfenden, 1988); RADA880104 Transfer free energy from chx to oct (Radzicka-Wolfenden, 1988); RADA880105 Transfer free energy from vap to oct (Radzicka-Wolfenden, 1988); RADA880106 Accessible surface area (Radzicka-Wolfenden, 1988); RADA880107 Energy transfer from out to in(95%buried) (Radzicka-Wolfenden, 1988); RADA880108 Mean polarity (Radzicka-Wolfenden, 1988); RICJ880101 Relative preference value at N" (Richardson-Richardson, 1988); RICJ880102 Relative preference value at N' (Richardson-Richardson, 1988); RICJ880103 Relative preference value at N-cap (Richardson-Richardson, 1988); RICJ880104 Relative preference value at N1 (Richardson-Richardson, 1988); RICJ880105 Relative preference value at N2 (Richardson-Richardson, 1988); RICJ880106 Relative preference value at N3 (Richardson-Richardson, 1988); RICJ880107 Relative preference value at N4 (Richardson-Richardson, 1988); RICJ880108 Relative preference value at N5 (Richardson-Richardson, 1988); RICJ880109 Relative preference value at Mid (Richardson-Richardson, 1988); RICJ880110 Relative preference value at C5 (Richardson-Richardson, 1988); RICJ880111 Relative preference value at C4 (Richardson-Richardson, 1988); RICJ880112 Relative preference value at C3 (Richardson-Richardson, 1988); RICJ880113 Relative preference value at C2 (Richardson-Richardson, 1988);

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RICJ880114 Relative preference value at C1 (Richardson-Richardson, 1988); RICJ880115 Relative preference value at C-cap (Richardson-Richardson, 1988); RICJ880116 Relative preference value at C' (Richardson-Richardson, 1988); RICJ880117 Relative preference value at C" (Richardson-Richardson, 1988); ROBB760101 Information measure for alpha-helix (Robson-Suzuki, 1976); ROBB760102 Information measure for N-terminal helix (Robson-Suzuki, 1976); ROBB760103 Information measure for middle helix (Robson-Suzuki, 1976); ROBB760104 Information measure for C-terminal helix (Robson-Suzuki, 1976); ROBB760105 Information measure for extended (Robson-Suzuki, 1976); ROBB760106 Information measure for pleated-sheet (Robson-Suzuki, 1976); ROBB760107 Information measure for extended without H-bond (Robson-Suzuki, 1976); ROBB760108 Information measure for turn (Robson-Suzuki, 1976); ROBB760109 Information measure for N-terminal turn (Robson-Suzuki, 1976); ROBB760110 Information measure for middle turn (Robson-Suzuki, 1976); ROBB760111 Information measure for C-terminal turn (Robson-Suzuki, 1976); ROBB760112 Information measure for coil (Robson-Suzuki, 1976); ROBB760113 Information measure for loop (Robson-Suzuki, 1976); ROBB790101 Hydration free energy (Robson-Osguthorpe, 1979); ROSG850101 Mean area buried on transfer (Rose et al., 1985); ROSG850102 Mean fractional area loss (Rose et al., 1985); ROSM880101 Side chain hydropathy, uncorrected for solvation (Roseman, 1988); ROSM880102 Side chain hydropathy, corrected for solvation (Roseman, 1988); ROSM880103 Loss of Side chain hydropathy by helix formation (Roseman, 1988); SIMZ760101 Transfer free energy (Simon, 1976), Cited by Charton-Charton (1982); SNEP660101 Principal component I (Sneath, 1966); SNEP660102 Principal component II (Sneath, 1966); SNEP660103 Principal component III (Sneath, 1966); SNEP660104 Principal component IV (Sneath, 1966); SUEM840101 Zimm-Bragg parameter s at 20 C (Sueki et al., 1984); SUEM840102 Zimm-Bragg parameter sigma x 1.0E4 (Sueki et al., 1984); SWER830101 Optimal matching hydrophobicity (Sweet-Eisenberg, 1983); TANS770101 Normalized frequency of alpha-helix (Tanaka-Scheraga, 1977); TANS770102 Normalized frequency of isolated helix (Tanaka-Scheraga, 1977); TANS770103 Normalized frequency of extended structure (Tanaka-Scheraga, 1977); TANS770104 Normalized frequency of chain reversal R (Tanaka-Scheraga, 1977); TANS770105 Normalized frequency of chain reversal S (Tanaka-Scheraga, 1977); TANS770106 Normalized frequency of chain reversal D (Tanaka-

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Scheraga, 1977); TANS770107 Normalized frequency of left-handed helix (Tanaka-Scheraga, 1977); TANS770108 Normalized frequency of zeta R (Tanaka-Scheraga, 1977); TANS770109 Normalized frequency of coil (Tanaka-Scheraga, 1977) TANS770110 Normalized frequency of chain reversal (Tanaka-Scheraga, 1977); VASM830101 Relative population of conformational state A (Vasquez et al., 1983); VASM830102 Relative population of conformational state C (Vasquez et al., 1983); VASM830103 Relative population of conformational state E (Vasquez et al., 1983); VELV850101 Electron-ion interaction potential (Veljkovic et al., 1985); VENT840101 Bitterness (Venanzi, 1984); VHEG790101 Transfer free energy to lipophilic phase (von Heijne-Blomberg, 1979); WARP780101 Average interactions per side chain atom (Warme-Morgan, 1978); WEBA780101 RF value in high salt chromatography (Weber-Lacey, 1978); WERD780101 Propensity to be buried inside (Wertz-Scheraga, 1978); WERD780102 Free energy change of epsilon(i) to epsilon(ex) (Wertz-Scheraga, 1978); WERD780103 Free energy change of alpha(Ri) to alpha(Rh) (Wertz-Scheraga, 1978); WERD780104 Free energy change of epsilon(i) to alpha(Rh) (Wertz-Scheraga, 1978); WOEC730101 Polar requirement (Woese, 1973); WOLR810101 Hydration potential (Wolfenden et al., 1981); WOLS870101 Principal property value z1 (Wold et al., 1987); WOLS870102 Principal property value z2 (Wold et al., 1987); WOLS870103 Principal property value z3 (Wold et al., 1987); YUTK870101 Unfolding Gibbs energy in water, pH7.0 (Yutani et al., 1987); YUTK870102 Unfolding Gibbs energy in water, pH9.0 (Yutani et al., 1987); YUTK870103 Activation Gibbs energy of unfolding, pH7.0 (Yutani et al., 1987); YUTK870104 Activation Gibbs energy of unfolding, pH9.0 (Yutani et al., 1987); ZASB820101 Dependence of partition coefficient on ionic strength (Zaslavsky et al., 1982); ZIMJ680101 Hydrophobicity (Zimmerman et al., 1968); ZIMJ680102 Bulkiness (Zimmerman et al., 1968); ZIMJ680103 Polarity (Zimmerman et al., 1968); ZIMJ680104 Isoelectric point (Zimmerman et al., 1968); ZIMJ680105 RF rank (Zimmerman et al., 1968); AURR980101 Normalized positional residue frequency at helix termini N4'(Aurora-Rose, 1998); AURR980102 Normalized positional residue frequency at helix termini N''' (Aurora-Rose, 1998); AURR980103 Normalized positional residue frequency at helix termini N'' (Aurora-Rose, 1998); AURR980104 Normalized positional residue frequency at helix termini N'(Aurora-Rose, 1998); AURR980105 Normalized positional residue frequency at helix termini Nc (Aurora-Rose, 1998); AURR980106 Normalized positional residue frequency at helix termini

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N1 (Aurora-Rose, 1998); AURR980107 Normalized positional residue frequency at helix termini N2 (Aurora-Rose, 1998); AURR980108 Normalized positional residue frequency at helix termini N3 (Aurora-Rose, 1998); AURR980109 Normalized positional residue frequency at helix termini N4 (Aurora-Rose, 1998); AURR980110 Normalized positional residue frequency at helix termini N5 (Aurora-Rose, 1998); AURR980111 Normalized positional residue frequency at helix termini C5 (Aurora-Rose, 1998); AURR980112 Normalized positional residue frequency at helix termini C4 (Aurora-Rose, 1998); AURR980113 Normalized positional residue frequency at helix termini C3 (Aurora-Rose, 1998); AURR980114 Normalized positional residue frequency at helix termini C2 (Aurora-Rose, 1998); AURR980115 Normalized positional residue frequency at helix termini C1 (Aurora-Rose, 1998); AURR980116 Normalized positional residue frequency at helix termini Cc (Aurora-Rose, 1998); AURR980117 Normalized positional residue frequency at helix termini C' (Aurora-Rose, 1998); AURR980118 Normalized positional residue frequency at helix termini C" (Aurora-Rose, 1998); AURR980119 Normalized positional residue frequency at helix termini C"' (Aurora-Rose, 1998); AURR980120 Normalized positional residue frequency at helix termini C4' (Aurora-Rose, 1998); ONEK900101 Delta G values for the peptides extrapolated to 0 M urea (O'Neil-DeGrado, 1990); ONEK900102 Helix formation parameters (delta delta G) (O'Neil-DeGrado, 1990); VINM940101 Normalized flexibility parameters (B-values), average (Vihinen et al., 1994); VINM940102 Normalized flexibility parameters (B-values) for each residue surrounded by none rigid neighbours (Vihinen et al., 1994); VINM940103 Normalized flexibility parameters (B-values) for each residue surrounded by one rigid neighbours (Vihinen et al., 1994); VINM940104 Normalized flexibility parameters (B-values) for each residue surrounded by two rigid neighbours (Vihinen et al., 1994); MUNV940101 Free energy in alpha-helical conformation (Munoz-Serrano, 1994); MUNV940102 Free energy in alpha-helical region (Munoz-Serrano, 1994); MUNV940103 Free energy in beta-strand conformation (Munoz-Serrano, 1994); MUNV940104 Free energy in beta-strand region (Munoz-Serrano, 1994); MUNV940105 Free energy in beta-strand region (Munoz-Serrano, 1994) WIMW960101 Free energies of transfer of AcWl-X-LL peptides from bilayer interface to water (Wimley-White, 1996); KIMC930101 Thermodynamic beta sheet propensity (Kim-Berg, 1993); MONM990101 Turn propensity scale for transmembrane helices (Monne et al., 1999); BLAM930101 Alpha helix propensity of

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position 44 in T4 lysozyme (Blaber et al., 1993); PARS000101 p-Values of mesophilic proteins based on the distributions of B values (Parthasarathy-Murthy, 2000); PARS000102 p-Values of thermophilic proteins based on the distributions of B values (Parthasarathy-Murthy, 2000); KUMS000101 Distribution of amino acid residues in the 18 non-redundant families of thermophilic proteins (Kumar et al., 2000); KUMS000102 Distribution of amino acid residues in the 18 non-redundant families of mesophilic proteins (Kumar et al., 2000); KUMS000103 Distribution of amino acid residues in the alpha-helices in thermophilic proteins (Kumar et al., 2000); KUMS000104 Distribution of amino acid residues in the alpha-helices in mesophilic proteins (Kumar et al., 2000); TAKK010101 Side-chain contribution to protein stability (kJ/mol) (Takano-Yutani, 2001); FODM020101 Propensity of amino acids within pi-helices (Fodje-Al-Karadaghi, 2002); NADH010101 Hydropathy scale based on self-information values in the two-state model (5% accessibility) (Naderi-Manesh et al., 2001); NADH010102 Hydropathy scale based on self-information values in the two-state model (9% accessibility) (Naderi-Manesh et al., 2001); NADH010103 Hydropathy scale based on self-information values in the two-state model (16% accessibility) (Naderi-Manesh et al., 2001); NADH010104 Hydropathy scale based on self-information values in the two-state model (20% accessibility) (Naderi-Manesh et al., 2001); NADH010105 Hydropathy scale based on self-information values in the two-state model (25% accessibility) (Naderi-Manesh et al., 2001); NADH010106 Hydropathy scale based on self-information values in the two-state model (36% accessibility) (Naderi-Manesh et al., 2001); NADH010107 Hydropathy scale based on self-information values in the two-state model (50% accessibility) (Naderi-Manesh et al., 2001); MONM990201 Averaged turn propensities in a transmembrane helix (Monne et al., 1999); KOEP990101 Alpha-helix propensity derived from designed sequences (Koehl-Levitt, 1999); KOEP990102 Beta-sheet propensity derived from designed sequences (Koehl-Levitt, 1999); CEDJ970101 Composition of amino acids in extracellular proteins (percent) (Cedano et al., 1997); CEDJ970102 Composition of amino acids in anchored proteins (percent) (Cedano et al., 1997); CEDJ970103 Composition of amino acids in membrane proteins (percent) (Cedano et al., 1997); CEDJ970104 Composition of amino acids in intracellular proteins (percent) (Cedano et al., 1997); CEDJ970105 Composition of amino acids in nuclear proteins (percent) (Cedano et al., 1997); FUKS010101 Surface composition of amino acids in intracellular proteins of

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thermophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010102 Surface composition of amino acids in intracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010103 Surface composition of amino acids in extracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010104 Surface composition of amino acids in nuclear proteins (percent) (Fukuchi-Nishikawa, 2001); FUKS010105 Interior composition of amino acids in intracellular proteins of thermophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010106 Interior composition of amino acids in intracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010107 Interior composition of amino acids in extracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010108 Interior composition of amino acids in nuclear proteins (percent) (Fukuchi-Nishikawa, 2001); FUKS010109 Entire chain composition of amino acids in intracellular proteins of thermophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010110 Entire chain composition of amino acids in intracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010111 Entire chain composition of amino acids in extracellular proteins of mesophiles (percent) (Fukuchi-Nishikawa, 2001); FUKS010112 Entire chain compositino of amino acids in nuclear proteins (percent) (Fukuchi-Nishikawa, 2001); AVBF000101 Screening coefficients gamma, local (Avbelj, 2000); AVBF000102 Screening coefficients gamma, non-local (Avbelj, 2000); AVBF000103 Slopes tripeptide, FDPB VFF neutral (Avbelj, 2000); AVBF000104 Slopes tripeptides, LD VFF neutral (Avbelj, 2000); AVBF000105 Slopes tripeptide, FDPB VFF noside (Avbelj, 2000); AVBF000106 Slopes tripeptide FDPB VFF all (Avbelj, 2000); AVBF000107 Slopes tripeptide FDPB PARSE neutral (Avbelj, 2000); AVBF000108 Slopes dekapeptide, FDPB VFF neutral (Avbelj, 2000); AVBF000109 Slopes proteins, FDPB VFF neutral (Avbelj, 2000); YANJ020101 Side-chain conformation by gaussian evolutionary method (Yang et al., 2002); MITS020101 Amphiphilicity index (Mitaku et al., 2002); TSAJ990101 Volumes including the crystallographic waters using the ProtOr (Tsai et al., 1999); TSAJ990102 Volumes not including the crystallographic waters using the ProtOr (Tsai et al., 1999); COSI940101 Electron-ion interaction potential values (Cosic, 1994); PONP930101 Hydrophobicity scales (Ponnuswamy, 1993); WILM950101 Hydrophobicity coefficient in RP-HPLC, C18 with 0.1%TFA/MeCN/H2O (Wilce et al. 1995); WILM950102 Hydrophobicity coefficient in RP-HPLC, C8 with 0.1%TFA/MeCN/H2O (Wilce et al. 1995); WILM950103

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Hydrophobicity coefficient in RP-HPLC, C4 with 0.1%TFA/MeCN/H2O (Wilce et al. 1995); WILM950104 Hydrophobicity coefficient in RP-HPLC, C18 with 0.1%TFA/2-PrOH/MeCN/H2O (Wilce et al. 1995); KUHL950101 Hydrophilicity scale (Kuhn et al., 1995); GUOD860101 Retention coefficient at pH 2 (Guo et al., 1986); JURD980101 Modified Kyte-Doolittle hydrophobicity scale (Juretic et al., 1998); BASU050101 Interactivity scale obtained from the contact matrix (Bastolla et al., 2005); BASU050102 Interactivity scale obtained by maximizing the mean of correlation coefficient over single-domain globular proteins (Bastolla et al., 2005); BASU050103 Interactivity scale obtained by maximizing the mean of correlation coefficient over pairs of sequences sharing the TIM barrel fold (Bastolla et al., 2005); SUYM030101 Linker propensity index (Suyama-Ohara, 2003); PUNT030101 Knowledge-based membrane-propensity scale from 1D_Helix in MPtopo databases (Punta-Maritan, 2003); PUNT030102 Knowledge-based membrane-propensity scale from 3D_Helix in MPtopo databases (Punta-Maritan, 2003); GEOR030101 Linker propensity from all dataset (George-Heringa, 2003); GEOR030102 Linker propensity from 1-linker dataset (George-Heringa, 2003); GEOR030103 Linker propensity from 2-linker dataset (George-Heringa, 2003); GEOR030104 Linker propensity from 3-linker dataset (George-Heringa, 2003); GEOR030105 Linker propensity from small dataset (linker length is less than six residues) (George-Heringa, 2003); GEOR030106 Linker propensity from medium dataset (linker length is between six and 14 residues) (George-Heringa, 2003); GEOR030107 Linker propensity from long dataset (linker length is greater than 14 residues) (George-Heringa, 2003); GEOR030108 Linker propensity from helical (annotated by DSSP) dataset (George-Heringa, 2003); GEOR030109 Linker propensity from non-helical (annotated by DSSP) dataset (George-Heringa, 2003); ZHOH040101 The stability scale from the knowledge-based atom-atom potential (Zhou-Zhou, 2004); ZHOH040102 The relative stability scale extracted from mutation experiments (Zhou-Zhou, 2004); ZHOH040103 Buriability (Zhou-Zhou, 2004); BAEK050101 Linker index (Bae et al., 2005); HARY940101 Mean volumes of residues buried in protein interiors (Harpaz et al., 1994); PONJ960101 Average volumes of residues (Pontius et al., 1996); DIGM050101 Hydrostatic pressure asymmetry index, PAI (Di Giulio, 2005); WOLR790101 Hydrophobicity index (Wolfenden et al., 1979); OLSK800101 Average internal preferences (Olsen, 1980); KIDA850101 Hydrophobicity-related index (Kidera et al., 1985); GUYH850102 Apparent partition energies calculated

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from Wertz-Scheraga index (Guy, 1985); GUYH850103 Apparent partition energies calculated from Robson-Osguthorpe index (Guy, 1985); GUYH850104 Apparent partition energies calculated from Janin index (Guy, 1985); GUYH850105 Apparent partition energies calculated from Chothia index (Guy, 1985); ROSM880104 Hydropathies of amino acid side chains, neutral form (Roseman, 1988); ROSM880105 Hydropathies of amino acid side chains, pi-values in pH 7.0 (Roseman, 1988); JACR890101 Weights from the IFH scale (Jacobs-White, 1989); COWR900101 Hydrophobicity index, 3.0 pH (Cowan-Whittaker, 1990) BLAS910101 Scaled side chain hydrophobicity values (Black-Mould, 1991); CASG920101 Hydrophobicity scale from native protein structures (Casari-Sippl, 1992); CORJ870101 NNEIG index (Cornette et al., 1987); CORJ870102 SWEIG index (Cornette et al., 1987); CORJ870103 PRIFT index (Cornette et al., 1987); CORJ870104 PRILS index (Cornette et al., 1987); CORJ870105 ALTFT index (Cornette et al., 1987)
CORJ870106 ALTLS index (Cornette et al., 1987); CORJ870107 TOTFT index (Cornette et al., 1987); CORJ870108 TOTLS index (Cornette et al., 1987); MIYS990101 Relative partition energies derived by the Bethe approximation (Miyazawa-Jernigan, 1999); MIYS990102 Optimized relative partition energies - method A (Miyazawa-Jernigan, 1999); MIYS990103 Optimized relative partition energies - method B (Miyazawa-Jernigan, 1999); MIYS990104 Optimized relative partition energies - method C (Miyazawa-Jernigan, 1999); MIYS990105 Optimized relative partition energies - method D (Miyazawa-Jernigan, 1999); ENGD860101 Hydrophobicity index (Engelman et al., 1986); and FASG890101 Hydrophobicity index (Fasman, 1989)

In some embodiments of the invention, degenerate oligonucleotides are used to synthesize one or more of the TN1, DH, N2, and/or H3-JH segments of the invention. In certain embodiments of the invention, the codon at or near the 5' end of the oligonucleotide encoding the H3-JH segment is a degenerate codon. Such degenerate codons may be the first codon from the 5' end, the second codon from the 5' end, the third codon from the 5' end, the fourth codon from the 5' end, the fifth codon from the 5' end, and/or any combination of the above. In some embodiments of the invention, one or more of the codons at or near the 5' and/or 3' ends of the DH segment are degenerate. Such degenerate codons may be the first codon from the 5' and/or 3' end(s), the second codon from the 5' and/or 3' end(s), the third codons from

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the 5' and/or 3' end(s), the fourth codon from the 5' and/or 3' end(s), the fifth codon from the 5' and/or 3' end(s), and/or any combination of the above. Degenerate codons used in each of the oligonucleotides encoding the segments may be selected for their ability to optimally recapitulate sequences in a theoretical segment pool and/or CDRH3 reference set.

In some embodiments, the invention provides methods of producing a theoretical segment pool of H3-JH segments, as described in the Examples. Theoretical segment pools generated utilizing NNN triplets, instead of or in addition to the NN doublets described in Example 5 also fall within the scope of the invention, as do synthetic libraries incorporating segments from these theoretical segment pools.

In some embodiments, the invention provides methods of producing a theoretical segment pool of DH segments, as described in the Examples. In particular, for example, the invention provides methods of producing a theoretical segment pool of DH segments described by the PYTHON program of Example 6. Example 6 describes the application of this program to produce the 68K theoretical segment pool (minimum length of DNA sequences after progressive deletions = 4 bases; and minimum length of peptide sequences for inclusion in the theoretical segment pool = 2). An alternative example is provided wherein the minimum length of the DNA sequences after progressive deletions was one base and the minimum length of the peptide sequence is one amino acid. It is also contemplated that other values could be used for these parameters. For example, the minimum length of the DNA sequences after progressive deletions could be set as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15, and the minimum length of the peptide sequences in the theoretical segment pool could be set as 1, 2, 3, 4, or 5.

Design of CDRH3 Libraries Using the TN1, DH, N2, and H3-JH Segments

The CDRH3 libraries of the invention comprise TN1, DH, N2, and H3-JH segments. Thus, in certain embodiments of the invention, the overall design of the CDRH3 libraries can be represented by the following formula:

[TN1]-[DH]-[N2]-[H3-JH].

In certain embodiments of the invention, a synthetic CDRH3 repertoire is combined with selected VH chassis sequences and heavy chain constant regions, via homologous recombination. Therefore, in certain embodiments of the invention, it may be desirable to include DNA sequences flanking the 5' and 3' ends of the

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synthetic CDRH3 libraries, to facilitate homologous recombination between the synthetic CDRH3 libraries and vectors containing the selected chassis and constant regions. In certain embodiments, the vectors also contain a sequence encoding at least a portion of the non-truncated region of the IGHJ gene (*i.e.,* FRM4-JH). Thus, a polynucleotide encoding an N-terminal sequence (*e.g.,* CA(K/R/T)) may be added to the synthetic CDRH3 sequences, wherein the N-terminal polynucleotide is homologous with FRM3 of the chassis, while a polynucleotide encoding a C-terminal sequence (*e.g.,* WG(Q/R/K)G) may be added to the synthetic CDRH3, wherein the C-terminal polynucleotide is homologous with FRM4-JH. Although the sequence WG(Q/R)G is presented in this exemplary embodiment, additional amino acids, C-terminal to this sequence in FRM4-JH may also be included in the polynucleotide encoding the C-terminal sequence. The purpose of the polynucleotides encoding the N-terminal and C-terminal sequences, in this case, is to facilitate homologous recombination, and one of ordinary skill in the art would recognize that these sequences may be longer or shorter than depicted below. Accordingly, in certain embodiments of the invention, the overall design of the CDRH3 repertoire, including the sequences required to facilitate homologous recombination with the selected chassis, can be represented by the following formula (regions homologous with vector underlined):

CA[R/K/T]-[TN1]-[DH]-[N2]-[H3-JH]-[WG(Q/R/K)G].

In some embodiments of the invention, the CDRH3 repertoire can be represented by the following formula, which excludes the T residue presented in the schematic above:

CA[R/K]-[TN1]-[DH]-[N2]-[H3-JH]-[WG(Q/R/K)G].

References describing collections of V, D, and J genes include Scaviner *et al.,* Exp. Clin, Immunogenet., 1999, 16: 243 and Ruiz *et al.,* Exp. Clin. Immunogenet, 1999, 16: 173.

Although homologous recombination is one method of producing the libraries of the invention, a person of ordinary skill in the art will readily recognize that other methods of DNA assembly, such as ligation or site-specific recombination, and/or DNA synthesis, can also be used to produce the libraries of the invention.

CDRH3 Lengths

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The lengths of the segments may also be varied, for example, to produce libraries with a particular distribution of CDRH3 lengths. In one embodiment of the invention, the H3-JH segments are about 0 to about 10 amino acids in length, the DH segments are about 0 to about 12 amino acids in length, the TN1 segments are about 0 to about 4 amino acids in length, and the N2 segments are about 0 to about 4 amino acids in length. In certain embodiments, the H3-JH segments are at least about 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, and/or 10 amino acids in length. In some embodiments, the DH segments are at least about 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and/or 12 amino acids in length. In certain embodiments, the TN1 segments are at least about 0, 1, 2, 3, or 4 amino acids in length. In some embodiments, the N2 amino acids are at least about 0, 1, 2, 3, or 4 amino acids in length. In certain embodiments of the invention, the CDRH3 is about 2 to about 35, about 2 to about 28, or about 5 to about 26 amino acids in length. In some embodiments, the CDRH3 is at least about 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, and/or 35 amino acids in length. In some embodiments, the length of any of the segments or CDRH3s of the invention may be less than a particular number of amino acids, where the number of amino acids is defined using any one of the integers provided above for the respective segment or CDRH3. In certain embodiments of the invention, a particular numerical range is defined, using any two of the integers provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the integers provided, which define an upper and lower boundary, are contemplated.

Design of CDRL3 Libraries

The design of CDRL3 libraries, and light chain sequences, is described in detail in U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379.

Libraries described herein are designed according to similar principles, with three important differences, namely that the libraries of the current invention contain (1) variability in CDRL1 and CDRL2; (2) variability in the framework regions; and/or (3) variability in CDRL3 that is designed to produce light chain libraries with CDRL3s that closely resemble human germline-like CDRL3 sequences, as defined above (Table 1).

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A CDRL3 library of the invention may be a VKCDR3 library and/or a V□CDR3 library. In certain embodiments of the invention, patterns of occurrence of particular amino acids at defined positions within VL sequences are determined by analyzing data available in public or other databases, for example, the NCBI database (see, for example, WO/2009/036379). In certain embodiments of the invention, these sequences are compared on the basis of identity and assigned to families on the basis of the germline genes from which they are derived. The amino acid composition at each position of the sequence, in each germline family, may then be determined. This process is illustrated in the Examples provided herein.

Light Chains with Framework Variability

In some embodiments, the invention provides a library of light chain variable domains wherein the light chain variable domains are varied at one or more of framework positions 2, 4, 36, 46, 48, 49, and 66. In some embodiments, the invention provides a library of light chain variable domains comprising at least a plurality of light chain variable domains whose amino acid sequences are identical to one another except for substitutions at one or more of positions 2, 4, 36, 46, 48, 49, and 66. In certain embodiments, the invention provides a library of light chain variable domains comprising at least a plurality of light chain variable domains whose amino acid sequences are at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, and/or 99.5% to any of the light chain variable domain sequences disclosed herein, and further have substitutions at one or more of positions 2, 4, 36, 46, 48, 49, and 66. In some embodiments, the amino acids selected for inclusion in these positions are selected from amongst about the most 2, 3, 4, 5, 6, 7, 8, 9, and/or 10 most frequently occurring amino acids at the corresponding position in a reference set of light chain variable domains.

In some embodiments, the invention provides systems and methods of selecting framework positions to be varied in a light chain variable domain, comprising:

(i) obtaining a reference set of light chain sequences, wherein the reference set contains light chain sequences with VL segments selected from the group consisting of sequences found in, or encoded by, a single IGVL germline gene and/or sequences

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found in, or encoded by, allelic variants of the single IGVL germline gene;

(ii) determining which framework positions within the reference set have a degree of variability that is similar to the degree of variability occurring in one more CDR positions of the sequences in the reference set (*e.g.*, the variability in a framework position is at least about 70%, 80%, 90%, or 95%, 100%, or more of the variability found in a CDR position of the sequences in the reference set);

(iii) determining the frequency of occurrence of amino acid residues for each of the framework positions identified in (ii);

(iv) synthesizing light chain variable domain encoding sequences wherein the framework positions identified in (ii) are varied to include the 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 most frequently occurring amino acid residues (identified in (iii)) at the corresponding position.

One of ordinary skill in the art, reading the present disclosure will appreciate that the present invention provides analogous methods for developing framework variants of heavy chain sequences.

Light Chains with CDR1 and/or CDR2 Variability

In some embodiments, the invention provides a library of light chain variable domains wherein the light chain variable domains are varied at one or more of CDRL1 positions 28, 29, 30, 30A, 30B, 30E, 31, and 32 (Chothia-Lesk numbering scheme; Chothia and Lesk, J. Mol. Biol., 1987, 196: 901). In some embodiments, the invention provides a library of light chain variable domains wherein the light chain variable domains are varied at one or more of CDRL2 positions 50, 51, 53, and 55. In some embodiments, the amino acids selected for inclusion in these CDRL1 and/or CDRL2 positions are selected from amongst about the most 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, and/or 20 most frequently occurring amino acids at the corresponding position in a reference set of light chain variable domains.

In some embodiments, the invention provides systems and methods for selecting CDRL1 and/or CDRL2 positions to be varied in a light chain variable domain, comprising:

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(i) obtaining a reference set of light chain sequences, wherein the reference set contains light chain sequences with VL segments selected from the group consisting of sequences found in, or encoded by, a single IGVL germline gene and sequences found in, or encoded by, allelic variants of the single IGVL germline gene;

(ii) determining which CDRL1 and/or CDRL2 positions are variable within the reference set;

(iii) synthesizing light chain variable domain encoding sequences wherein the CDRL1 and/or CDRL2 positions identified in (ii) are varied to include the 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 most frequently occurring amino acid residues at the corresponding position.

One of ordinary skill in the art, reading the present disclosure will appreciate that the present invention provides analogous methods for developing CDRH2 and/or CDRH2 variants of heavy chain sequences.

Light Chain Sequences

In some embodiments, the invention provides a light chain library comprising one or more of any of the light chain sequences provided herein, for example, the polypeptide sequences of Table 3 and/or Table 4 and/or the polynucleotide sequences of Table 5, Table 6, and/or Table 7. A person of ordinary skill in the art will recognize that not every light chain sequence provided herein is necessary to produce a functional light chain library of the invention. Therefore, in certain embodiments, a light chain library of the invention will contain a subset of the sequences described above. For example, in certain embodiments of the invention, at least about 10, 100, 200, 300, 400, 500, 600, 700, 800, 900, 10^3, 10^4, and/or 10^5 of the light chain polynucleotide and/or polypeptide sequences provided herein are included in a library. In some embodiments, a library of the invention may contain less than a particular number of polynucleotide or polypeptide segments, where the number of segments is defined using any one of the integers provided above for the respective segment. In certain embodiments of the invention, a particular numerical range is defined, using any two of the integers provided above as lower and upper boundaries

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of the range, inclusive or exclusive. All combinations of the integers provided, which define an upper and lower boundary, are contemplated.

In certain embodiments, the invention provides light chain libraries comprising at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the sequences from any of the sets of light chain sequences provided herein. For example, the invention provides libraries comprising at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the light chain sequences provided in Table 3, Table 4, Table 5, Table 6, and/or Table 7. In some embodiments of the invention, a particular percentage range is defined, using any two of the percentages provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the percentages provided, which define an upper and lower boundary, are contemplated.

In some embodiments of the invention, at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the light chain sequences in a library are light chain sequences provided herein. In certain embodiments of the invention, at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% of the light chain sequences isolated from a light chain library (*e.g.*, by binding to a particular antigen and/or generic ligand) are light chain sequences provided herein. In some embodiments, a light chain library of the invention may contain less than a particular percentage of light chain sequences provided herein, where the percentage of light chain sequences is defined using any one of the percentages provided above. In certain embodiments of the invention, a particular percentage range is defined, using any two of the percentages provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the percentages provided, which define an upper and lower boundary, are contemplated.

One of ordinary skill in the art will further recognize that given the light chain sequences provided herein, similar light chain sequences could be produced which share a designated level of overall sequence identity and/or one or more characteristic sequence elements described herein, which overall degree of sequence identity and/or characteristic sequence elements may confer common functional attributes. Those of ordinary skill in the art will be well familiar with a variety of techniques for preparing

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such related sequences, , including the mutagenesis techniques provided herein. Therefore, each of the explicitly enumerated embodiments of the invention can also be practiced using light chain sequences that share a particular percent identity to any of the light chain sequences provided herein. For example, each of the previously described embodiments of the invention can be practiced using light chain sequences that are at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% identical to the light chain sequences provided herein. For example, in some embodiments, light chain libraries provided by the invention comprise light chain variable domains at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% identical to the light chain sequences provided herein, with substitutions in one or more of framework positions 2, 4, 36, 46, 48, 49, and 66, CDRL1 positions 28, 29, 30, 30A, 30B, 30E, 31, and 32 (Chothia-Lesk numbering scheme), and/or CDRL2 positions 50, 51, 53, and 55.

In some embodiments, the invention provides systems and methods for varying positions within the portion of CDRL3s encoded by a particular IGVL germline gene, comprising:

(i) obtaining a reference set of light chain sequences, wherein the reference set contains light chain sequences with VL segments originating from the same IGVL germline gene and/or its allelic variants;

(ii) determining which amino acids occur at each of the CDRL3 positions in the reference set that are encoded by the IGVL gene (*i.e.*, positions 89-94, inclusive);

(iii) synthesizing light chain variable domain encoding sequences wherein two positions in each light chain variable domain encoding sequence contain degenerate codons encoding the 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 most frequently occurring amino acid residues at the corresponding positions in the reference set.

As described in the examples, the degenerate codons of (iii) can be chosen to best reproduce the amino acid diversity contained in the reference set for each of the two positions varied in each light chain. Finally, while the methods and systems described above are described with respect to CDRL3, one of ordinary skill in the art

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will readily recognize that the same principles can be applied to CDRH1 and/or CDRH2 of the heavy chain, which are encoded entirely by the IGHV gene.

CDRL3 Lengths

In some embodiments, as an alternative or in addition to other features described herein, the present invention provides libraries in which lengths of CDRL3s may be varied. The present invention therefore provides, among other things, libraries with a particular distribution of CDRL3 lengths. Although CDRL3 libraries of lengths 8, 9, and 10 are exemplified, one of ordinary skill in the art will readily recognize that the methods described herein can be applied to produce light chains with CDRL3s of different lengths (*e.g.,* about 5, 6, 7, 11, 12, 13, 14, 15, and/or 16) that also fall within the scope of the invention. In some embodiments, the length of any of the CDRL3s of the invention may be less than a particular number of amino acids, where the number of amino acids is defined using any one of the integers provided above. In some embodiments of the invention, a particular numerical range is defined, using any two of the integers provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the integers provided, which define an upper and lower boundary, are contemplated.

Synthetic Antibody Libraries

In some embodiments of the invention, provided libraries include one or more synthetic polynucleotides. In some embodiments, provided libraries may comprise synthetic polynucleotides selected from (a) heavy chain chassis polynucleotides; (b) light chain chassis polynucleotides; (c) CDR3 polynucleotides; (d) constant domain polynucleotides; and (e) combinations thereof. Those of ordinary skill in the art will appreciate that such synthetic polynucleotides may be linked to other synthetic or non-synthetic polynucleotides in provided libraries.

Synthetic polynucleotides provided herein may be prepared by any available method. For example, in some embodiments, synthetic polynucleotides can be synthesized by split pool DNA synthesis as described in Feldhaus *et al.*, Nucleic Acids Research, 2000, 28: 534; Omstein *et al.,* Biopolymers, 1978, 17: 2341; Brenner and Lerner, PNAS, 1992, 87: 6378, U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379.

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In some embodiments of the invention, segments representing the possible TN1, DH, N2, and JH diversity found in the human repertoire are synthesized *de novo* either as double-stranded DNA oligonucleotides, single-stranded DNA oligonucleotides representative of the coding strand, or single-stranded DNA oligonucleotides representative of the non-coding strand. Such sequences can then be introduced into a host cell along with an acceptor vector containing a chassis sequence and, in some cases a portion of FRM4 and a constant region. No primer-based PCR amplification from mammalian cDNA or mRNA or template-directed cloning steps from mammalian cDNA or mRNA need be employed.

Construction of Libraries by Yeast Homologous Recombination

In certain embodiments, the invention exploits the inherent ability of yeast cells to facilitate homologous recombination at high efficiency. The mechanism of homologous recombination in yeast and its applications are briefly described below (also see *e.g.*, U.S. Patent Nos. 6,406,863; 6,410,246; 6,410,271; 6,610,472; and 7,700,302).

As an illustrative embodiment, homologous recombination can be carried out in, for example, *Saccharomyces cerevisiae*, which has genetic machinery designed to carry out homologous recombination with high efficiency. Exemplary *S. cerevisiae* strains include EM93, CEN.PK2, RM11-1a, YJM789, and BJ5465. This mechanism is believed to have evolved for the purpose of chromosomal repair, and is also called "gap repair" or "gap filling". By exploiting this mechanism, mutations can be introduced into specific loci of the yeast genome. For example, a vector carrying a mutant gene can contain two sequence segments that are homologous to the 5' and 3' open reading frame (ORF) sequences of a gene that is intended to be interrupted or mutated. The vector may also encode a positive selection marker, such as a nutritional enzyme allele (*e.g.*, URA3) and/or an antibiotic resistant marker (*e.g.*, Geneticin / G418), flanked by the two homologous DNA segments. Other selection markers and antibiotic resistance markers are known to one of ordinary skill in the art.

In some embodiments of the invention, this vector (*e.g.*, a plasmid) is linearized and transformed into the yeast cells. Through homologous recombination between the plasmid and the yeast genome, at the two homologous recombination sites, a reciprocal exchange of the DNA content occurs between the wild type gene in the yeast genome and the mutant gene (including the selection marker gene(s)) that is

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flanked by the two homologous sequence segments. By selecting for the one or more selection markers, the surviving yeast cells will be those cells in which the wild-type gene has been replaced by the mutant gene (Pearson *et al.*, Yeast, 1998, 14: 391).

This mechanism has been used to make systematic mutations in all 6,000 yeast genes, or open reading frames (ORFs), for functional genomics studies. Because the exchange is reciprocal, a similar approach has also been used successfully to clone yeast genomic DNA fragments into a plasmid vector (Iwasaki *et al.*, Gene, 1991, 109: 81).

By utilizing the endogenous homologous recombination machinery present in yeast, gene fragments or synthetic oligonucleotides can also be cloned into a plasmid vector without a ligation step. In this application of homologous recombination, a target gene fragment (*i.e.*, the fragment to be inserted into a plasmid vector, *e.g.*, a CDR3) is obtained (*e.g.*, by oligonucleotides synthesis, PCR amplification, restriction digestion out of another vector, etc.). DNA sequences that are homologous to selected regions of the plasmid vector are added to the 5' and 3' ends of the target gene fragment. These homologous regions may be fully synthetic, or added via PCR amplification of a target gene fragment with primers that incorporate the homologous sequences. The plasmid vector may include a positive selection marker, such as a nutritional enzyme allele (*e.g.*, URA3), or an antibiotic resistance marker (*e.g.*, Geneticin / G418). The plasmid vector is then linearized by a unique restriction cut located in-between the regions of sequence homology shared with the target gene fragment, thereby creating an artificial gap at the cleavage site. The linearized plasmid vector and the target gene fragment flanked by sequences homologous to the plasmid vector are co-transformed into a yeast host strain. The yeast is then able to recognize the two stretches of sequence homology between the vector and target gene fragment and facilitate a reciprocal exchange of DNA content through homologous recombination at the gap. As a consequence, the target gene fragment is inserted into the vector without ligation.

The method described above has also been demonstrated to work when the target gene fragments are in the form of single stranded DNA, for example, as a circular M13 phage derived form, or as single stranded oligonucleotides (Simon and Moore, Mol. Cell Biol., 1987, 7: 2329; Ivanov *et al.*, Genetics, 1996, 142: 693; and DeMarini *et al.*, 2001, 30: 520). Thus, the form of the target that can be recombined into the gapped vector can be double

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stranded or single stranded, and derived from chemical synthesis, PCR, restriction digestion, or other methods.

Several factors may influence the efficiency of homologous recombination in yeast. For example, the efficiency of the gap repair is correlated with the length of the homologous sequences flanking both the linearized vector and the target gene. In certain embodiments, about 20 or more base pairs may be used for the length of the homologous sequence, and about 80 base pairs may give a near-optimized result (Hua *et al.,* Plasmid, 1997, 38: 91; Raymond *et al.,* Genome Res., 2002, 12: 190).

In certain embodiments of the invention, at least about 5, 10, 15, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34 35, 36, 37, 38, 39, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 187, 190, or 200 homologous base pairs may be used to facilitate recombination. In certain embodiments, between about 20 and about 40 base pairs are utilized. In addition, the reciprocal exchange between the vector and gene fragment is strictly sequence-dependent, *i.e.* it does not cause a frame shift. Therefore, gap-repair cloning assures the insertion of gene fragments with both high efficiency and precision. The high efficiency makes it possible to clone two, three, or more targeted gene fragments simultaneously into the same vector in one transformation attempt (Raymond *et al.,* Biotechniques, 1999, 26: 134).

Moreover, the nature of precision sequence conservation through homologous recombination makes it possible to clone selected genes or gene fragments into expression or fusion vectors for direct functional examination (El-Deiry *et al.,* Nature Genetics, 1992, 1: 4549; Ishioka *et al.,* PNAS, 1997, 94: 2449).

Libraries of gene fragments have also been constructed in yeast using homologous recombination. For example, a human brain cDNA library was constructed as a two-hybrid fusion library in vector pJG4-5 (Guidotti and Zervos, Yeast, 1999, 15: 715). It has also been reported that a total of 6,000 pairs of PCR primers were used for amplification of 6,000 known yeast ORFs for a study of yeast genomic protein interactions (Hudson *et al.,* Genome Res., 1997, 7: 1169). In 2000, Uetz *et al.* conducted a comprehensive analysis-of protein-protein interactions in *Saccharomyces cerevisiae* (Uetz *et al.,* Nature, 2000, 403: 623).

The protein-protein interaction map of the budding yeast

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was studied by using a comprehensive system to examine two-hybrid interactions in all possible combinations between the yeast proteins (Ito *et al.*, PNAS, 2000, 97: 1143), and the genomic protein linkage map of Vaccinia virus was studied using this system (McCraith *et al.*, PNAS, 2000, 97: 4879).

In certain embodiments of the invention, a synthetic CDR3 (heavy or light chain) may be joined by homologous recombination with a vector encoding a heavy or light chain chassis, a portion of FRM4, and a constant region, to form a full-length heavy or light chain. In certain embodiments of the invention, the homologous recombination is performed directly in yeast cells. In some embodiments, such a method comprises:

(a) transforming into yeast cells:

(i) a linearized vector encoding a heavy or light chain chassis, a portion of FRM4, and a constant region, wherein the site of linearization is between the end of FRM3 of the chassis and the beginning of the constant region; and

(ii) a library of CDR3 insert nucleotide sequences that are linear and double stranded, wherein each of the CDR3 insert sequences comprises a nucleotide sequence encoding CDR3 and 5'- and 3'-flanking sequences that are sufficiently homologous to the termini of the vector of (i) at the site of linearization to enable homologous recombination to occur between the vector and the library of CDR3 insert sequences; and

(b) allowing homologous recombination to occur between the vector and the CDR3 insert sequences in the transformed yeast cells, such that the CDR3 insert sequences are incorporated into the vector, to produce a vector encoding full-length heavy chain or light chain.

As specified above, CDR3 inserts may have a 5' flanking sequence and a 3' flanking sequence that are homologous to the termini of the linearized vector. When the CDR3 inserts and the linearized vectors are introduced into a host cell, for example, a yeast cell, the "gap" (the linearization site) created by linearization of the vector is filled by the CDR3 fragment insert through recombination of the homologous sequences at the 5' and 3' termini of these two linear double-stranded DNAs (*i.e.*, the vector and the insert). Through this event of homologous

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recombination, libraries of circular vectors encoding full-length heavy or light chains comprising variable CDR3 inserts is generated. Particular instances of these methods are presented in the Examples.

Subsequent analysis may be carried out to determine, for example, the efficiency of homologous recombination that results in correct insertion of the CDR3 sequences into the vectors. For example, PCR amplification of the CDR3 inserts directly from selected yeast clones may reveal how many clones are recombinant. In certain embodiments, libraries with minimum of about 90% recombinant clones are utilized. In certain embodiments libraries with a minimum of about 1%, 5% 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% recombinant clones are utilized. The same PCR amplification of selected clones may also reveal the insert size.

To verify the sequence diversity of the inserts in the selected clones, a PCR amplification product with the correct size of insert may be "fingerprinted" with restriction enzymes known to cut or not cut within the amplified region. From a gel electrophoresis pattern, it may be determined whether the clones analyzed are of the same identity or of the distinct or diversified identity. The PCR products may also be sequenced directly to reveal the identity of inserts and the fidelity of the cloning procedure, and to prove the independence and diversity of the clones.

Expression and Screening Systems

Libraries of polynucleotides generated by any of the techniques described herein, or other suitable techniques, can be expressed and screened to identify antibodies having desired structure and/or activity. Expression of the antibodies can be carried out, for example, using cell-free extracts (and *e.g.*, ribosome display), phage display, prokaryotic cells (*e.g.*, bacterial display), or eukaryotic cells (*e.g.*, yeast display). In certain embodiments of the invention, the antibody libraries are expressed in yeast.

In some embodiments, polynucleotides are engineered to serve as templates that can be expressed in a cell-free extract. Vectors and extracts as described, for example in U.S. Patent Nos. 5,324,637; 5,492,817; 5,665,563, can be used and many are commercially available. Ribosome display and other cell-free techniques for linking a polynucleotide (*i.e.*, a genotype) to

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a polypeptide (*i.e.*, a phenotype) can be used, *e.g.*, Profusion™ (see, *e.g.*, U.S. Patent Nos. 6,348,315; 6,261,804; 6,258,558; and 6,214,553).

Alternatively or additionally, polynucleotides of the invention can be expressed in an *E. coli* expression system, such as that described by Pluckthun and Skerra. (Meth. Enzymol., 1989, 178: 476; Biotechnology, 1991, 9: 273).

Mutant proteins can be expressed for secretion in the medium and/or in the cytoplasm of the bacteria, as described by Better and Horwitz, Meth. Enzymol., 1989, 178: 476.

In some embodiments, the single domains encoding VH and VL are each attached to the 3' end of a sequence encoding a signal sequence, such as the ompA, phoA or pelB signal sequence (Lei *et al.*, J. Bacteriol., 1987, 169: 4379.

These gene fusions are assembled in a dicistronic construct, so that they can be expressed from a single vector, and secreted into the periplasmic space of *E. coli* where they will refold and can be recovered in active form. (Skerra *et al.*, Biotechnology, 1991, 9: 273).

For example, antibody heavy chain genes can be concurrently expressed with antibody light chain genes to produce antibodies or antibody fragments.

In some embodiments of the invention, antibody sequences are expressed on the membrane surface of a prokaryote, *e.g.*, *E. coli*, using a secretion signal and lipidation moiety as described, *e.g.*, in US2004/0072740; US2003/0100023; and US2003/0036093.

Higher eukaryotic cells, such as mammalian cells, for example myeloma cells (*e.g.*, NS/0 cells), hybridoma cells, Chinese hamster ovary (CHO), and human embryonic kidney (HEK) cells, can also be used for expression of the antibodies of the invention. Typically, antibodies expressed in mammalian cells are designed to be secreted into the culture medium, or expressed on the surface of the cell. Antibody or antibody fragments can be produced, for example, as intact antibody molecules or as individual VH and VL fragments, Fab fragments, single domains, or as single chains (scFv) (Huston *et al.*, PNAS, 1988, 85: 5879).

Alternatively or additionally, antibodies can be expressed and screened by anchored periplasmic expression (APEx 2-hybrid surface display), as described, for example, in Jeong *et al.*, PNAS, 2007, 104: 8247

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or by other anchoring methods as described, for example, in Mazor *et al.*, Nature Biotechnology, 2007, 25: 563.

In some embodiments of the invention, antibodies can be selected using mammalian cell display (Ho *et al.*, PNAS, 2006, 103: 9637).

Screening of the antibodies derived from the libraries of the invention can be carried out by any appropriate means. For example, binding activity can be evaluated by standard immunoassay and/or affinity chromatography. Screening of antibodies of the invention for catalytic function, *e.g.*, proteolytic function can be accomplished using a standard assays, *e.g.*, the hemoglobin plaque assay as described in U.S. Patent No. 5,798,208. Determining the ability of candidate antibodies to bind therapeutic targets can be assayed *in vitro* using, *e.g.*, a BIACORE™ instrument, which measures binding rates of an antibody to a given target or antigen based on surface plasmon resonance. *In vivo* assays can be conducted using any of a number of animal models and then subsequently tested, as appropriate, in humans. Cell-based biological assays are also contemplated.

One feature of the instant invention is the speed at which the antibodies of the library can be expressed and screened. In certain embodiments of the invention, the antibody library can be expressed in yeast, which have a doubling time of less than about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 hours. In some embodiments, the doubling times are about 1 to about 3 hours, about 2 to about 4, about 3 to about 8 hours, about 3 to about 24, about 5 to about 24, about 4 to about 6 about 5 to about 22, about 6 to about 8, about 7 to about 22, about 8 to about 10 hours, about 7 to about 20, about 9 to about 20, about 9 to about 18, about 11 to about 18, about 11 to about 16, about 13 to about 16, about 16 to about 20, or about 20 to about 30 hours. In certain embodiments of the invention, an antibody library is expressed in yeast with a doubling time of about 16 to about 20 hours, about 8 to about 16 hours, or about 4 to about 8 hours. Thus, an antibody library of the instant invention can be expressed and screened in a matter of hours, as compared to previously known techniques which take several days to express and screen antibody libraries. A limiting step in the throughput of such screening processes in mammalian cells is typically the time required to iteratively regrow populations of isolated cells, which, in some cases, have doubling times greater than the doubling times of the yeast used in the current invention.

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In certain embodiments of the invention, the composition of a library may be defined after one or more enrichment steps (for example by screening for antigen binding, binding to a generic ligand, or other properties). For example, a library with a composition comprising about x% sequences or libraries of the invention may be enriched to contain about 2x%, 3x%, 4x%, 5x%, 6x%, 7x%, 8x%, 9x%, 10x%, 20x%, 25x%, 40x%, 50x%, 60x% 75x%, 80x%, 90x%, 95x%,or 99x% sequences or libraries of the invention, after one or more screening steps. In some embodiments of the invention, the sequences or libraries of the invention may be enriched about 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 100-fold, 1,000-fold, or more, relative to their occurrence prior to the one or more enrichment steps. In certain embodiments of the invention, a library may contain at least a certain number of a particular type of sequence(s), such as CDRH3s, CDRL3s, heavy chains, light chains, or whole antibodies (*e.g.,* at least about 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, or 10^{20}). In certain embodiments, these sequences may be enriched during one or more enrichment steps, to provide libraries comprising at least about 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, or 10^{19} of the respective sequence(s).

Mutagenesis Approaches for Affinity Maturation

As described above, antibody leads can be identified through a selection process that involves screening the antibodies of a library of the invention for binding to one or more antigens, or for a biological activity. Coding sequences of these antibody leads may be further mutagenized *in vitro* or *in vivo* to generate secondary libraries with diversity introduced in the context of the initial antibody leads. Such mutagenized antibody leads can then be further screened for binding to target antigens or biological activity, *in vitro* or *in vivo*, following procedures similar to those used for the selection of the initial antibody lead from the primary library. Such mutagenesis and selection of primary antibody leads effectively mimics the affinity maturation process naturally occurring in a mammal that produces antibodies with progressive increases in the affinity to an antigen.

In some embodiments of the invention, only the CDRH3 region is mutagenized. In some embodiments of the invention, the whole variable region is mutagenized. In some embodiments of the invention one or more of CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, and/ CDRL3 may be mutagenized. In some

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embodiments of the invention, "light chain shuffling" may be used as part of the affinity maturation protocol. In certain embodiments, this may involve pairing one or more heavy chains with a number of light chains, to select light chains that enhance the affinity and/or biological activity of an antibody. In certain embodiments of the invention, the number of light chains to which the one or more heavy chains can be paired is at least about 2, 5, 10, 100, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, or 10^{10}. In certain embodiments of the invention, these light chains are encoded by plasmids. In some embodiments of the invention, the light chains may be integrated into the genome of the host cell.

Coding sequences of antibody leads may be mutagenized using any of wide variety of methods. Examples of methods of mutagenesis include, but are not limited to site-directed mutagenesis, error-prone PCR mutagenesis, cassette mutagenesis, and random PCR mutagenesis. Alternatively or additionally, oligonucleotides encoding regions with the desired mutations can be synthesized and introduced into the sequence to be mutagenized, for example, via recombination or ligation.

Site-directed mutagenesis or point mutagenesis may be used to gradually change the CDR sequences in specific regions. For example, this may be accomplished by using oligonucleotide-directed mutagenesis or PCR. For example, a short sequence of an antibody lead may be replaced with a synthetically mutagenized oligonucleotide in either the heavy chain or light chain region, or both. Such a method may not be efficient for mutagenizing large numbers of CDR sequences, but may be used for fine tuning of a particular lead to achieve higher affinity toward a specific target protein.

Cassette mutagenesis may alternatively or additionally be used to mutagenize the CDR sequences in specific regions. In a typical cassette mutagenesis, a sequence block, or a region, of a single template is replaced by a completely or partially randomized sequence. However, the maximum information content that can be obtained may be statistically limited by the number of random sequences of the oligonucleotides. Similar to point mutagenesis, this method may also be used for fine tuning of a particular lead to achieve higher affinity towards a specific target protein.

Error-prone PCR, or "poison" PCR, may be used to mutagenize the CDR sequences, for example, by following protocols described in U.S. Patent No. 6,153,745; Caldwell and Joyce, PCR Methods and Applications, 1992, 2: 28; Leung *et al.,* Technique, 1989, 1: 11; Shafikhani *et al.,* Biotechniques, 1997, 23: 304; and

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Stemmer *et al.*, PNAS, 1994, 91: 10747.

Conditions for error prone PCR may include, for example, (a) high concentrations of Mn^{2-} (*e.g.*, about 0.4 to about 0.6 mM) that efficiently induces malfunction of Taq DNA polymerase; and/or (b) a disproportionally high concentration of one nucleotide substrate (*e.g.*, dGTP) in the PCR reaction that causes incorrect incorporation of this high concentration substrate into the template and produces mutations. Alternatively or additionally, other factors such as, the number of PCR cycles, the species of DNA polymerase used, and the length of the template, may affect the rate of misincorporation of "wrong" nucleotides into the PCR product. Commercially available kits may be utilized for the mutagenesis of the selected antibody library, such as the "Diversity PCR random mutagenesis kit" (CLONTECH™).

Primer pairs used in PCR-based mutagenesis may, in certain embodiments, include regions matched with the homologous recombination sites in the expression vectors. Such a design allows facile re-introduction of the PCR products back into the heavy or light chain chassis vectors, after mutagenesis, via homologous recombination.

Other PCR-based mutagenesis methods can also be used, alone or in conjunction with the error prone PCR described above. For example, the PCR amplified CDR segments may be digested with DNase to create nicks in the double stranded DNA. These nicks can be expanded into gaps by other exonucleases such as Bal 31. Gaps may then be filled by random sequences by using DNA Klenow polymerase at a low concentration of regular substrates dGTP, dATP, dTTP, and dCTP with one substrate (e.g., dGTP) at a disproportionately high concentration. This fill-in reaction should produce high frequency mutations in the filled gap regions. Such methods of DNase digestion may be used in conjunction with error prone PCR to create a high frequency of mutations in the desired CDR segments.

CDR or antibody segments amplified from the primary antibody leads may also be mutagenized *in vivo* by exploiting the inherent ability of mutation in pre-B cells. The Ig genes in pre-B cells are specifically susceptible to a high-rate of mutation. The Ig promoter and enhancer facilitate such high rate mutations in a pre-B cell environment while the pre-B cells proliferate. Accordingly, CDR gene segments may be cloned into a mammalian expression vector that contains a human Ig enhancer

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and promoter. Such a construct may be introduced into a pre-B cell line, such as 38B9, which allows the mutation of the VH and VL gene segments naturally in the pre-B cells (Liu and Van Ness, Mol. Immunol., 1999, 36: 461).

The mutagenized CDR segments can be amplified from the cultured pre-B cell line and re-introduced back into the chassis-containing vector(s) via, for example, homologous recombination.

In some embodiments, a CDR "hit" isolated from screening the library can be re-synthesized, for example using degenerate codons or trinucleotides, and re-cloned into the heavy or light chain vector using gap repair.

Other Variants of Polynucleotide Sequences of the Invention

In certain embodiments, the invention provides a polynucleotide that hybridizes with a polynucleotide taught herein, or that hybridizes with the complement of a polynucleotide taught herein. For example, an isolated polynucleotide that remains hybridized after hybridization and washing under low, medium, or high stringency conditions to a polynucleotide taught herein or the complement of a polynucleotide taught herein is encompassed by the present invention.

Exemplary low stringency conditions include hybridization with a buffer solution of about 30% to about 35% formamide, about 1 M NaCl, about 1% SDS (sodium dodecyl sulphate) at about 37°C, and a wash in about 1X to about 2X SSC (20X SSC=3.0 M NaCl/0.3 M trisodium citrate) at about 50°C to about 55°C.

Exemplary moderate stringency conditions include hybridization in about 40% to about 45% formamide, about 1 M NaCl, about 1% SDS at about 37°C, and a wash in about 0.5X to about 1X SSC at abut 55°C to about 60°C.

Exemplary high stringency conditions include hybridization in about 50% formamide, about 1 M NaCl, about 1% SDS at about 37°C, and a wash in about 0.1X SSC at about 60° C to about 65° C.

Optionally, wash buffers may comprise about 0.1% to about 1% SDS.

The duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

Sublibraries and Larger Libraries Comprising Libraries or Sub-Libraries of the Invention

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Libraries comprising combinations of the libraries described herein (*e.g.*, CDRH3 and CDRL3 libraries) are encompassed by the invention. Sublibraries comprising portions of the libraries described herein are also encompassed by the invention (*e.g.*, a CDRH3 library in a particular heavy chain chassis or a sub-set of the CDRH3 libraries, for example based on length).

Moreover, libraries containing one of the libraries or sublibraries of the invention also fall within the scope of the invention. For example, in certain embodiments of the invention, one or more libraries or sublibraries of the invention may be contained within a larger library (theoretical or physical), which may include sequences derived by other means, for example, non-human or human sequence derived by stochastic or sitewise-stochastic synthesis. In certain embodiments of the invention, at least about 1% of the sequences in a polynucleotide library may be those of the invention (*e.g.*, CDRH3 sequences, CDRL3 sequences, VH sequences, VL sequences), regardless of the composition of the other 99% of sequences. For the purposes of illustration only, one of ordinary skill in the art would readily recognize that a library containing 10^9 total members, where 10^7 members are members of the libraries of the invention (*i.e.*, 1%) would have utility, and that members of the libraries of the invention could be isolated from such a library. In some embodiments of the invention, at least about 0.001%, 0.01%, 0.1%, 2%, 5%, 10%, 20%, 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% of the sequences in any polynucleotide library may be those of the invention, regardless of the composition of the other sequences. In some embodiments, the sequences of the invention may comprise about 0.001% to about 1%, about 1% to about 2%, about 2% to about 5%, about 5% to about 10%, about 10% to about 15%, about 15% to about 20%, about 20% to about 25%, about 25% to about 30%, about 30% to about 35%, about 35% to about 40%, about 40% to about 45%, about 45% to about 50%, about 50% to about 55%, about 55% to about 60%, about 60% to about 65%, about 65% to about 70%, about 70% to about 75%, about 75% to about 80%, about 80% to about 85%, about 85% to about 90%, about 90% to about 95%, or about 95% to about 99% of the sequences in any polynucleotide library, regardless of the composition of the other sequences. Thus, libraries more diverse than one or more libraries or sublibraries of the invention, but yet still comprising one or more libraries or sublibraries of the invention, in an amount in which the one or more libraries or sublibraries of the

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invention can be effectively screened and from which sequences encoded by the one or more libraries or sublibraries of the invention can be isolated, also fall within the scope of the invention.

Alternative Scaffolds

As would be evident to one of ordinary skill in the art, the CDRH3 and/or CDRL3 polypeptides provided by the invention may also be displayed on alternative scaffolds. Several such scaffolds have been shown to yield molecules with specificities and affinities that rival those of antibodies. Exemplary alternative scaffolds include those derived from fibronectin (*e.g.,* AdNectin), the □-sandwich (*e.g.,* iMab), lipocalin (*e.g.,* Anticalin), EETI-II/AGRP, BPTI/LACI-D1/ITI-D2 (*e.g.,* Kunitz domain), thioredoxin (*e.g.,* peptide aptamer), protein A (*e.g.,* Affibody), ankyrin repeats (*e.g.,* DARPin), □B-crystallin/ubiquitin (*e.g.,* Affilin), $CTLD_3$ (*e.g.,* Tetranectin), and $(LDLR\text{-}A\ module)_3$ (*e.g.,* Avimers). Additional information on alternative scaffolds is provided, for example, in Binz *et al.,* Nat. Biotechnol., 2005 23: 1257 and Skerra, Current Opin. in Biotech., 2007 18: 295-304.

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Additional Embodiments of the Invention

Library Sizes

In some embodiments of the invention, a library comprises about 10^1 to about 10^{20} different polynucleotide or polypeptide sequences (encoding or comprising *e.g.*, antibodies, heavy chains, CDRH3s, light chains, and/or CDRL3s). In some embodiments, the libraries of the invention are designed to include at least about 10^1, 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, 10^{17}, 10^{18}, 10^{19}, or 10^{20}, or more different antibody, heavy chain, CDRH3, light chain, and/or CDRL3 polynucleotide or polypeptide sequences. In some embodiments, a library of the invention may contain less than a particular number of polynucleotide or polypeptide sequences, where the number of sequences is defined using any one of the integers provided above. In certain embodiments of the invention, a particular numerical range is defined, using any two of the integers provided above as lower and upper boundaries of the range, inclusive or exclusive. All combinations of the integers provided, which define an upper and lower boundary, are contemplated.

In some embodiments, the invention provides libraries wherein a fraction of the members of the library are members produced according to the methods, systems, and compositions provided herein. One important property of the libraries of the invention is that they favorably mimic certain aspects of the human preimmune repertoire, including length diversity and sequence diversity. One or ordinary skill in the art will readily recognize that libraries provided by the invention include libraries where a subset of the members of the library are members produced according to the methods, systems, and compositions provided herein. For example, a library containing 10^8 members wherein 10^6 members are produced according to the methods, systems, and compositions provided herein, would contain 1% sequences produced according to the methods, systems, and compositions provided herein. One of ordinary skill in the art would recognize that one or more of the 10^6 members could readily be isolated using screening techniques known in the art. Therefore, said libraries fall within the scope of the invention. More specifically, libraries comprising at least about 1%, 2.5%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% CDRH3, CDRL3, light chain, or heavy chain, and/or full-length antibody sequences provided herein fall within the scope of the invention. Libraries comprising at least about 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15} CDRH3, CDRL3, light chain, heavy chain,

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and/or full-length antibody sequences provided herein also fall within the scope of the invention.

Human Preimmune Set

In some embodiments, the invention comprises the set of 3,571 curated human preimmune antibody sequences contained within the HPS, their corresponding CDRH3 sequences (Appendix A), and/or a representation of these CDRH3 sequences (and/or TN1, DH, N2, and/or H3-JH segments thereof) in a computer readable format. In certain embodiments, the invention comprises a method of producing a CDRH3 library, the method comprising matching candidate segments (*i.e.,* TN1, DH, N2, and H3-JH) from a theoretical segment pool with CDRH3 sequences in the HPS and/or any other repertoire of CDRH3 sequences. In some embodiments, the invention comprises the candidate segments from the theoretical segment pools disclosed herein and/or the segments selected for inclusion in a physical library.

Embodiments

While the methods described herein demonstrate the production of theoretical segment pools of H3-JH and DH segments using a limited number of allelic variants, one of ordinary skill in the art will recognize that methods taught herein may be applied to any IGHJ and IGHD genes, including any other allelic variants and all non-human IGHJ and IGHD genes. Alternatively or additionally, methods described herein may be applied to any reference set of CDRH3 sequences, for example to extract additional TN1 and/or N2 segments. Alternatively or additionally, one of ordinary skill in the art will recognize that each of the described embodiments of the invention may be in polynucleotide or polypeptide form, within a vector, virus, or microorganism (*e.g.,* a yeast or bacteria). Furthermore, since the invention involves synthetic libraries that are fully enumerated, certain embodiments of the invention relate to any of the embodiments described above in a computer readable format, and uses thereof.

Non-human antibody libraries also fall within the scope of the invention.

The present disclosure describes the removal of sequences containing Cys residues, N-linked glycosylation motifs, deamidation motifs, and highly hydrophobic sequences from the libraries of the invention. One of ordinary skill in the art will recognize that one or more of these criteria (*i.e.,* not necessarily all) can be applied to

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remove undesirable sequences from any library of the invention. However, libraries containing one or more of these types of sequences also fall within the scope of the invention. Other criteria can also be used; those described herein are not limiting.

In certain embodiments, the invention provides libraries in which the number of times a particular sequence is repeated within the library (either theoretical, synthetic, or physical realization) is limited. For example, in some embodiments, the invention provides libraries wherein the frequency of occurrence of any of the sequences in the library (*e.g.,* CDRH3, CDRL3, heavy chain, light chain, full-length antibody) is less than about 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000. In some embodiments, the frequency of occurrence of any of the sequences in the library is less than a multiple of the frequency of occurrence of any other sequence in the library, for examples less than about 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000 times the frequency of occurrence of any other sequence in the library.

In some embodiments, libraries are defined by the combinatorial diversity of the segments used to produce CDRH3 sequences, in particular the number of non-degenerate segment combinations that can be used to produce a particular CDRH3 sequence. In some embodiments, this metric may be calculated using, for example, a sample of about 2000, 5000, 10000, 20000, 50000, 100000, or more sequences from the CDRH3 library and "self-matching" using the segments used to generate the CDRH3 sequences of that library. In certain embodiments, the invention provides libraries wherein at least about 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of the CDRH3 sequences in the library may be formed by a single combination of segments.

In certain embodiments of the invention, a statistical bootstrap analysis was used to generate CDRH3 reference sets. While it may be advantageous to use this method, it is not required for every embodiment of the invention.

In some embodiments, the invention provides methods and systems of selecting polynucleotides to encode polypeptides of the invention, comprising selecting polynucleotide segments lacking (or containing) certain restriction sites individually and/or after combinatorial concatenation with other segments (*e.g.,* see Example 9.3.7).

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The exemplary libraries provided herein are not limiting and provided for exemplification only.

EXAMPLES

This invention is further illustrated by the following examples which should not be construed as limiting.

In general, the practice of the present invention employs, unless otherwise indicated, conventional techniques of chemistry, molecular biology, recombinant DNA technology, PCR technology, immunology (especially, *e.g.*, antibody technology), expression systems (*e.g.*, yeast expression, cell-free expression, phage display, ribosome display, and PROFUSION^{TM}), and any necessary cell culture that are within the skill of the art and are explained in the literature. See, *e.g.*, Sambrook, Fritsch and Maniatis, *Molecular Cloning: Cold Spring Harbor Laboratory Press* (1989); *DNA Cloning*, Vols. 1 and 2, (D.N. Glover, Ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait, Ed. 1984); *PCR Handbook Current Protocols in Nucleic Acid Chemistry*, Beaucage, Ed. John Wiley & Sons (1999) (Editor); *Oxford Handbook of Nucleic Acid Structure*, Neidle, Ed., Oxford Univ Press (1999); *PCR Protocols: A Guide to Methods and Applications*, Innis *et al.*, Academic Press (1990); *PCR Essential Techniques: Essential Techniques*, Burke, Ed., John Wiley & Son Ltd (1996); *The PCR Technique: RT-PCR,* Siebert, Ed., Eaton Pub. Co. (1998); *Antibody Engineering Protocols (Methods in Molecular Biology),* 510, Paul, S., Humana Pr (1996); *Antibody Engineering: A Practical Approach (Practical Approach Series, 169)*, McCafferty, Ed., Irl Pr (1996); *Antibodies: A Laboratory Manual,* Harlow *et al.*, C.S.H.L. Press, Pub. (1999); *Current Protocols in Molecular Biology*, eds. Ausubel *et al.*, John Wiley & Sons (1992); *Large-Scale Mammalian Cell Culture Technology,* Lubiniecki, A., Ed., Marcel Dekker, Pub., (1990); *Phage Display: A Laboratory Manual*, C. Barbas (Ed.), CSHL Press, (2001); *Antibody Phage Display*, P O'Brien (Ed.), Humana Press (2001); Border *et al.*, Nature Biotechnology, 1997, 15: 553; Border *et al.*, Methods Enzymol., 2000, 328: 430; ribosome display as described by Pluckthun *et al.* in U.S. Patent No. 6,348,315, and Profusion^{TM} as described by Szostak *et al.* in U.S. Patent Nos. 6,258,558; 6,261,804; and 6,214,553; and bacterial

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periplasmic expression as described in US20040058403A1.

Further details regarding antibody sequence analysis using Kabat conventions and programs to analyze aligned nucleotide and amino acid sequences may be found, *e.g.*, in Johnson *et al.*, Methods Mol. Biol., 2004, 248: 11; Johnson *et al.*, Int. Immunol., 1998, 10: 1801; Johnson *et al.*, Methods Mol. Biol., 1995, 51: 1; Wu *et al.*, Proteins, 1993, 16: 1; and Martin, Proteins, 1996, 25: 130.

Further details regarding antibody sequence analysis using Chothia conventions may be found, *e.g.*, in Chothia *et al.*, J. Mol. Biol., 1998, 278: 457; Morea *et al.*, Biophys. Chem., 1997, 68: 9; Morea *et al.*, J. Mol. Biol., 1998, 275: 269; Al-Lazikani *et al.*, J. Mol. Biol., 1997, 273: 927. Barre *et al.*, Nat. Struct. Biol., 1994, 1: 915; Chothia *et al.*, J. Mol. Biol., 1992, 227: 799; Chothia *et al.*, Nature, 1989, 342: 877; and Chothia *et al.*, J. Mol. Biol., 1987, 196: 901. Further analysis of CDRH3 conformation may be found in Shirai *et al.*, FEBS Lett., 1999, 455: 188 and Shirai *et al.*, FEBS Lett., 1996, 399: 1. Further details regarding Chothia analysis are described, for example, in Chothia *et al.*, Cold Spring Harb. Symp. Quant Biol., 1987, 52: 399.

Further details regarding CDR contact considerations are described, for example, in MacCallum *et al.*, J. Mol. Biol., 1996, 262: 732.

Further details regarding the antibody sequences and databases referred to herein are found, *e.g.*, in Tomlinson *et al.*, J. Mol. Biol., 1992, 227: 776, VBASE2 (Retter *et al.*, Nucleic Acids Res., 2005, 33: D671); BLAST (www.ncbi.nlm.nih.gov/BLAST/); CDHIT (bioinformatics.ljcrf.edu/cd-hi/); EMBOSS (www.hgmp.mrc.ac.uk/Software/EMBOSS/); PHYLIP (evolution.genetics.washington.edu/phylip.html); and FASTA (fasta.bioch.virginia.edu).

LIGHT CHAIN LIBRARIES

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Example 1. Light Chain Libraries with Framework and/or CDRL1 and/or CDRL2 Variability

Although the diversity in antibody sequences is concentrated in the CDRs, certain residues in the framework regions can also influence antigen recognition and/or modulate affinity (Queen *et al.,* Proc. Natl. Acad. Sci. USA, 1989, 86: 10029; Carter *et al.,* Proc. Natl. Acad. Sci. USA, 1992, 89: 4285).

These residues have been cataloged and used to make framework substitutions that improve antibody affinity, for example, during the process of antibody humanization (*e.g.,* see the "Vernier" residues in Foote and Winter, J. Mol. Biol., 1992, 224: 487). In the heavy chain, the Vernier residues include Kabat-numbered residues 2, 27-30, 47-49, 67, 69, 71, 73, 78, 93-94, and 103. In the light chain, the Vernier residues include Kabat residues 2, 4, 35-36, 46-49, 64, 66, 68-69, 71, and 98. The Vernier residue numbers are the same for kappa and lambda light chain sequences (*see* Table 4 in Chothia et al., J. Mol. Biol., 1985, 186: 651).

Additionally, framework positions at the VL-VH interface may also influence affinity. In the heavy chain, the interface residues include Kabat residues 35, 37, 39, 45, 47, 91, 93, 95, 100, and 103 (Chothia et al., J. Mol. Biol., 1985, 186: 651).

In the light chain, the interface residues include Kabat residues 34, 36, 38 44, 46, 87, 89, 91, 96, and 98.

The following procedure was used to select the framework residues to be varied and the amino acids to which they should be varied:

a. A collection of human VK light chain DNA sequences was obtained from NCBI (*see* Appendix A of WO/2009/036379 for GI Nos.). These sequences were classified according to the germline origin of their VK germline segment.
b. Patterns of variation at each of the Vernier and interface positions were examined as follows:
    i. Equation 1 (from Makowski & Soares, Bioinformatics, 2003, 19: 483) was used to calculate a diversity index for the Vernier positions, interface positions, CDRL1, and CDRL2.

$$d = \frac{1}{N \quad p_i^2} \qquad \textit{Equation 1}$$

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Here, d is the diversity index, N is 20, the total number of amino acid types, and p_i is the fraction of amino acid of type "i" at the position of interest. The sum is carried out over the 20 amino acid types. The parameter d will attain its minimum value of 0.05 or 1/20, when a single amino acid type is observed at a given position: p_i is 1 for one type and zero for all the rest. Conversely, when all the amino acid types are equally probable (*e.g.*, p_i is 0.05 for all i), d will attain its maximum value of 1.0.

ii. The diversity index for each of the Vernier and interface positions were compared to the diversity index for the positions in CDRL1 and CDRL2.

iii. The interface positions were found to be relatively invariant, with d values very close to the minimum of 0.05, and were thus not altered. The Vernier residues with a diversity index comparable to or larger than that of the CDR positions (*i.e.*, at or above 0.07 for the particular example provided in Figure 1) were selected as candidates for variance (see Figure 1). The amino acid residues included in these positions were selected from amongst the two to three amino acids most frequently occurring in that position in the sequences in the collection of human VK light chains, for each particular VK germline.

iv. Table 2 shows the positions selected for variance in each of nine exemplified light chain germlines. The alternative framework positions represent positions with a diversity index less than the primary framework positions, but where variability may still be incorporated to influence antigen binding.

v. The amino acid residues in the framework positions selected for variance were varied as follows (Table 3 provides the polypeptide sequences of these variants):

1. **Position 2**: Germline I was optionally changed to V.
2. **Position 4:** Germline M or L was optionally changed to L or M. In some embodiments, changes from M to L, but not the reverse, may be preferred, because M may undergo oxidation during production, processing, or

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storage, potentially altering the properties of the antibody.

3. **Position 36:** Germline Y was optionally changed to F and H.
4. **Position 46:** Germline L was optionally changed to V.
5. **Position 48:** Germline I was optionally changed to L.
6. **Position 49:** Germline Y was optionally changed to S, F, and H.
7. **Position 66:** Germline G was optionally changed to R and E.

One of ordinary skill in the art would readily recognize that the procedure outlined above could also be used to select positions to vary in V□ germline sequences, and that libraries containing V□ chains also fall within the scope of the invention.

In addition to the framework mutations, variability was also introduced into CDRL1 and CDRL2. This was performed by determining which residues in CDRL1 and CDRL2 were variable, within a particular germline, in the VK dataset used above and incorporating the most frequently occurring 2 to 4 variants into CDRL1 and CDRL2 in the synthetic libraries of the invention. With the exception of position 50 of CDRL2 of the V□1-5 germline, these alternatives did not arise from allelic variation. Table 3 shows the polypeptide sequences of nine light chain chassis and their framework and CDR L1/L2 variants for the currently exemplified embodiment of the invention. The amino acid residues in the CDRL1/L2 positions selected for variance were varied as follows (using the Chothia-Lesk numbering system; Chothia and Lesk, J. Mol. Biol., 1987, 196: 901):

1. **Position 28:** Germline S or G were optionally changed to G, A, or D.
2. **Position 29:** Germline V was optionally changed to I.
3. **Position 30:** Germline S was optionally changed to N, D, G, T, A, or R.
4. **Position 30A:** Germline H was optionally changed to Y
5. **Position 30B:** Germline S was optionally changed to R or T.
6. **Position 30E:** Germline Y was optionally changed to N.

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7. **Position 31:** Germline S was optionally changed to D, R, I, N, or T.
8. **Position 32:** Germline Y or N were optionally changed to F, S, or D.
9. **Position 50:** Germline A, D, or G were optionally changed to G, S, E, K, or D.
10. **Position 51:** Germline G or A were optionally changed to A, S, or T.
11. **Position 53:** Germline S or N were optionally changed to N, H, S, K, or R.
12. **Position 55:** Germline E was optionally changed to A or Q.

Example 2. Light Chain Libraries with Enhanced Diversity in CDRL3

A variety of methods of producing light chain libraries are known in the art (*e.g.,* see U.S. Publication Nos. 2009/0181855, 2010/0056386, and WO/2009/036379). An analysis of clinically validated antibody sequences indicated that these sequences have very little deviation from germline-like VL-JL (where "L" can be a kappa or lambda germline sequence) rearrangements prior to somatic mutation (Figure 2). Here, a germline-like rearrangement is one where neither the V nor J portion differ from the respective germline genes and, for the purposes of this particular example, where the length of CDRL3 is restricted to 8, 9 or 10 amino acids (*see* U.S. Publication Nos. 2009/0181855, 2010/0056386, and WO/2009/036379). For the IGHJK1 gene, however, both WT (Trp-Thr) and RT (Arg-Thr) sequences (the first two N-terminal residues) are considered "germline-like" and so are full L3 rearrangements containing such sequences. Therefore, new light chain libraries were designed and constructed with the objectives of simultaneously (1) minimizing deviation from germline-like sequences, as defined above; and (2) generating maximal diversity. In particular, the overarching goal was to maximize the *type* of diversity that is indicated to be most favorable by clinically validated antibody sequences. In particular, the designed library sought to maximize the diversity of CDRL3 sequences that differ from length-matched germline sequences by two amino acids or fewer.

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This was accomplished by utilizing a "jumping dimer" or "jumping trimer" approach to light chain oligonucleotide design. The jumping dimer approach involves the incorporation of degenerate codons at each of the six positions of CDRL3 encoded by the VL segment (L3-VL). At most two positions vary from germline in each individual L3-VL sequence, but the two positions do not have to be adjacent to one another. Thus, the total number of designed degenerate oligonucleotides synthesized per VL chassis is 6!/(4!2!), or fifteen (accounting for six of the most commonly occurring amino acids at the junction (position 96) between VL and JL for each kappa germline chassis (namely F, L, I, R, W, Y, and P; see U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379, for more details on the junctional amino acids at position 96). The jumping trimer approach is analogous to the jumping dimer approach, but with three positions varying from germline in each individual L3-VL sequence, instead of two as in the jumping dimer. The degenerate codons selected for each position in the jumping dimer and trimer approaches were chosen to (1) to reproduce the diversity contained in the known repertoire of publicly available human VK sequences (see Appendix A of WO/2009/036379); and (2) to minimize or eliminate undesirable sequences within the CDRL3s of the resulting synthetic light chains, such as N-linked glycosylation motifs (NXS/NXT), Cys residues, stop codons, and deamidation-prone NG motifs. Table 4 shows the fifteen degenerate oligonucleotides encoding the VK1-39 CDRL3 sequences with a length of nine amino acids and F or Y as the junctional amino acid, and the corresponding degenerate polypeptide sequences. Table 5, Table 6, and Table 7 provide the oligonucleotide sequences for each of the VK sequences of the exemplary jumping dimer and trimer libraries, for CDRL3 lengths of 8, 9, and 10, respectively, and the sequences for the corresponding CDRL3s.

The number of unique CDRL3 sequences within each germline library was then enumerated and compared to the number of unique CDRL3 sequences in a different light chain library, designated "VK-v1.0" (see Example 6.2 in US Publication No. 2009/0181855), for each of the three lengths. Table 8 provides the number of unique CDRL3 sequences in each of the respective germline libraries.

Figure 3 provides the percentage of sequences in the jumping dimer and VK-v1.0 libraries with CDRL3 length of nine amino acids that contain no mutations from germline-like sequences (Table 1) or 1, 2, 3, or 4 or fewer mutations from germline-

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like sequences. Naturally-occurring VK1-05 sequences are almost as likely to have Ser (germline amino acid type) as Pro at Kabat position 95, thus both residues (S and P) were incorporated in the synthetic libraries representing VK1-05 repertoires. However, as indicated in Table 1, only Ser was considered to be a germline-like residue at position 95 for the purposes of this analysis when the VK gene is VK1-05. The plot for VK3-20 is representative of the remaining chassis in the library for a length nine. All of the sequences in the VK1-05 library were within three amino acids of human germline sequences, and approximately 63% of the sequences were within two amino acids of human germline-like sequences. For the rest of the libraries, and as designed, 100% of the sequences were within two amino acids of human germline-like sequences; thus, over 95% of the sequences of length 9 in the jumping dimer library considered as a whole were within 2 amino acids of germline-like sequences. By comparison, only 16% of the members of the VK-v1.0 libraries of length nine amino acids are within two amino acids of the corresponding human germline-like sequences. For length 8, about 98% of the sequences in the jumping dimer libraries were within two amino acids of germline-like, versus about 19% for VK-v1.0. For length 10, more than 95% of the sequences of the jumping dimer library were within two amino acids of germline-like, versus about 8% for VK-v1.0.

In some embodiments, to concentrate the diversity in positions most likely to be solvent-exposed in the folded antibody, positions 89 and 90 (Kabat numbering) are not modified from germline – these are most often QQ, but the sequence is MQ for the VK2-28 chassis. Other VK germline genes have different sequences at positions 88-89, and the use of these genes as chassis also falls within the scope of the invention. For example, VK1-27 has QK, VK1-17 and VK1-6 both have LQ, and so on. The sequences in these positions are known in the art and can be obtained, for example, from Scaviner *et al.,* Exp. Clin. Immunogenet., 1999, 16: 234 (see Figure 2).

CDRH3 LIBRARIES

The following examples describe methods and compositions useful for the design and synthesis of antibody libraries with improved CDRH3 sequences in comparison to libraries known in the art. The CDRH3 sequences of the invention have enhanced diversity in comparison to libraries known in the art, while retaining

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the character of human sequences, improving combinatorial efficiency of the synthetic CDRH3 segments, and/or improving the matching between synthetic CDRH3 sequences and human CDRH3 sequences in one or more reference sets.

Example 3. Generating a Curated Reference Set of Human Preimmune CDRH3 Sequences

A file containing approximately 84,000 human and mouse heavy chain DNA sequences was downloaded from the BLAST public resource (ftp.ncbi.nih.gov/blast/db/FASTA/; filename: igSeqNt.gz; download date: Aug 29, 2008). Of these approximately 84,000 sequences, approximately 34,000 sequences were identified as human heavy chain sequences based on analysis of the sequence header annotation. These sequences were then filtered as follows: First, all sequences were classified, via their VH-region, according to their corresponding (closest matched) VH germline. Sequences that were of an incorrect or insufficient length, or that could not be matched due to extensive mutation, were discarded. Second, any sequences containing more than five mutations, at the DNA level, when compared to their corresponding germline VH sequence were also discarded. It was assumed, consistent with Rada and Milstein, EMBO J., 2001, 20: 4570, that mutations (or lack thereof) in the N-terminal portion of the variable region may be used as conservative surrogates for mutations (or lack thereof) in the C-terminal portion of the variable region, in particular in CDRH3. Therefore, selecting only sequences with five or fewer nucleotide mutations in VH, which is N-terminal to CDRH3 is highly likely to also select for CDRH3 sequences that are either lightly mutated or not mutated at all (*i.e.,* having preimmune character).

After translating the remaining DNA sequences into their amino acid counterparts, the appropriate reading frame containing the heavy chain germline amino acid sequence was identified and used to identify the sequences of the CDRs, including that of the CDRH3. The list of CDRH3 sequences obtained at this point was further filtered to eliminate members that did not differ from any other sequence in the set by at least three amino acids (after matching for length). This process yielded 11,411 CDRH3 sequences, with 3,571 sequences annotated as originating from healthy adults ("Healthy Preimmune Set" or "HPS"; *see* Appendix A for GI Nos.) and the other 7,840 sequences annotated as originating from individuals suffering from disease, of fetal origin, or of antigen-specific origin. The methods described below

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were then used to deconvolute each of the sequences in the HPS into the four segments that constitute the CDRH3: (1) TN1, (2) DH, (3) N2, and (4) H3-JH.

Example 4. Method to Match Segments from a Theoretical Segment Pool to CDRH3s in a Reference Set

This example describes the method used to identify the TN1, DH, N2, and H3-JH segments of the CDRH3s in the HPS. The currently exemplified approach to the design and synthesis of human CDRH3 sequences mimics the segmental V-D-J gene recombination processes by which the human immune system generates the preimmune CDRH3 repertoire. The matching method described here determines which TN1, DH, N2 and H3-JH segments have been used to produce a particular CDRH3 across a reference set of CDRH3s (*e.g.,* the HPS). This information is then used, optionally in conjunction with other information described below (*e.g.,* physicochemical properties), to determine which TN1, DH, N2, and H3-JH segments from a theoretical segment pool (or segments extracted from the CDRH3 sequences in the reference set, in the case of the TN1 and N2) should be included in a synthetic CDRH3 library.

The inputs to the matching method are: (1) a reference set of CDRH3 sequences (*e.g.,* the human CDRH3 sequences in the HPS), and (2) a theoretical segment pool, containing a plurality of TN1, DH, N2 and/or H3-JH segments. Methods by which the members of the theoretical segment pool are generated are more fully described below. For each CDRH3 in the reference set, the matching method generates two outputs: (i) a list of the closest matched CDRH3 sequences that can be generated using the segments of the theoretical segment pool, and (ii) the one or more segment combinations from the theoretical segment pool that can be used to create these closest matched CDRH3 sequences.

The matching method was performed as follows: Each TN1 segment in the theoretical segment pool was aligned at its first amino acid with the first amino acid (position 95) of the CDRH3 sequence from the reference set. For each segment length, all (*i.e.,* one or more) of the segments returning the best matches are retained, and the remaining segments are discarded. The retained TN1 segments are then concatenated with all DH segments from the theoretical segment pool, to create [TN1]-[DH] segments. These segments are then aligned as above, and all the best matches for each of the [TN1]-[DH] segments are retained. The procedure is repeated

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with [TN1]-[DH]-[N2] and [TN1]-[DH]-[N2]-[H3-JH] segments until the length of the CDRH3 sequence from the reference set is identically recapitulated by the segment combinations from the theoretical segment pool. All segment combinations returning the best match to the CDRH3s in the reference set are retained as the output of the matching method.

Table 9 provides an example of the output of the matching method, specifically the output for four individual sequences from the HPS, using a theoretical segment pool designated "Theoretical Segment Pool 1," or "TSP1". TSP1 contains several theoretical segment pools, namely: 212 TN1 segments (Table 10), 1,111 DH segments (Table 11), 141 N2 segments (Table 12), and 285 H3-JH segments (Table 13). The CDRH3 sequence in Test Case 1 contains an identical match in TSP1 that is reached via a unique combination of the four segments. Test Cases 2.1 and 2.2 each return an identical match, but via two distinct combinations that differ in the TN1 and DH segments. In Test Cases 3.1, 4.1, and 4.2, the closest matches are all a single amino acid away from the reference CDRH3, and can be reached via one (3.1) or two (4.1 and 4.2) combinations of segments from TSP1. This approach can be generalized to find all of the closest matches to any reference CDRH3 sequence within any theoretical segment pool and all combinations of the segments within the theoretical segment pool that can produce the reference CDRH3 sequence exactly and/or its closest matches.

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Example 5. Deriving Theoretical Segment Pools of H3-JH Segments

In order to produce theoretical segment pools of H3-JH segments for consideration for inclusion in a synthetic CDRH3 library, the following method was applied to generate mutants of seven (IGHJ1-01, IGHJ2-01, IGHJ3-02, IGHJ4-02, IGHJ5-02, IGHJ6-02 and IGHJ6-03) of the twelve germline IGHJ sequences of Table 14. These seven alleles were chosen because they were among the most commonly occurring alleles in human sequences. Libraries where all sequences of Table 14 (some differing only in FRM4) are used to generate H3-JH and/or JH (*i.e.,* H3-JH and FRM4) also fall within the scope of the invention. The method is intended to simulate the creation of junctional diversity during the V-D-J recombination process *in vivo*, which occurs via enzyme-mediated addition and deletion of nucleotides to the germline gene segments. The method proceeds as follows, and results in a fully enumerated theoretical segment pool of H3-JH segments:

1. A pre-treatment was applied to the IGHJ genes that contain a partial codon consisting of two nucleotide bases at their 5' terminus (IGHJ3-02, IGHJ4-02, IGHJ5-02, IGHJ6-02 and IGHJ6-03), prior to the first nucleotide encoding the translation of the JH segment that produces the well-known JH framework regions. For example, the IGHJ3-02 gene contains an AT dinucleotide sequence prior to the first nucleotide encoding the translation of the JH segment that produces the JH framework region (Figure 4, top). All partial codons consisting of two nucleotide bases were completed, using all possible nucleotide doublets (*i.e.,* NN) at their two most 5' positions (Figure 4, top, second row for IGHJ3-02). More specifically, the most 5' nucleotide in the germline sequence was mutated to N and an additional N was added 5' to that nucleotide.
2. IGHJ genes IGHJ1-01 (Figure 4, center) and IGHJ2-01 (Figure 4, bottom) contain zero and one nucleotide base(s) at their 5' termini, prior to the first nucleotide encoding the translation of the JH segment that produces the JH framework region. For these genes, the pre-treatment described in step 1 was not performed. Instead, the 5' doublets were mutated to NN (Figure 4, middle and bottom, second row of each). Therefore, after performing this step, each of the seven IGHJ genes enumerated above was converted to a variant with an NN doublet as its first two 5' positions.

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3. The 5' codons of the sequences produced via steps 1 and 2 were then deleted, and the first two bases of the resulting DNA sequence were subsequently mutated to an NN doublet (Figure 4, rows 3-4 for all).
4. The 5' codons of the sequences produced in step 3 were then deleted, and the first two bases of the resulting DNA sequence were subsequently mutated to an NN doublet (Figure 4, rows 5-6 for all).
5. Each of the polynucleotide sequences generated by steps (1) – (4) were then translated, to obtain a theoretical segment pool consisting of 248 parent H3-JH polypeptide segments (Table 15) from the reading frame for each sequence that produced the JH framework region.
6. The parent H3-JH polypeptide segments were truncated at their N-termini, by removing one amino acid at a time until only the portion of the JH segment comprising FW4 remains (*i.e.*, an H3-JH segment with a length of zero amino acids).

The methods described above resulted in the production of a theoretical segment pool of 285 H3-JH segments (Table 13).

Example 6. Deriving Theoretical Segment Pools of DH Segments

Two theoretical pools of DH segments were generated, using one or more of two translation methods, designated "Translation Method 0" (TM0), or "Translation Method 1" ("TM1"), each performed in the three forward reading frames of 27 human germline IGHD DNA sequences or segments derived therefrom (Table 16).

The 1K DH Theoretical Segment Pool (1K DH)

TM1 was used to generate the "1K DH Theoretical Segment Pool" ("1K DH"; see the 1,111 DH segments of Table 11). In TM1, IGHD sequences that had a partial codon containing two untranslated bases after translation in any of the three forward reading frames were completed to produce a full codon only if the two bases could encode only a single amino acid upon completion. For example, a DNA sequence such as TTA-GCT-CG has two full codons that would be translated to LA, and a remaining partial codon (CG) that can only encode R, as any of CGA, CGC, CGG, or CGT will encode R. Thus, applying TM1 to this sequence will yield LAR. For sequences with partial codons that could encode more than one amino acid (*e.g.*, GA

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or AG), the partial codons were ignored. Applying TM1 to the 27 IGHD sequences of Table 16 generated a theoretical segment pool containing the 73 DH parent segments of Table 17 (some containing stop codons ("Z") and unpaired Cys residues). These sequences were then progressively deleted at the amino acid level, at their N- and C-termini, until only two amino acids remained. Truncated segments were discarded if they contained a stop codon, unpaired Cys residues, N-linked glycosylation motifs, or deamidation motifs. This process yielded the 1,111 DH segments of Table 11.

The 68K DH Theoretical Segment Pool (68K DH)

The 27 IGHD genes and alleles of Table 16 were progressively deleted on either or both of their 5' and 3' ends until four bases remained, yielding 5,076 unique polynucleotide sequences of four or more nucleotides. These 5,076 sequences were subjected to systematic addition of 0, 1 and/or 2 N nucleotides their 5' and/or 3' ends. The resulting sequences were translated using TM0. In TM0, only full codons are translated; partial codons (*i.e.,* 1 or 2 bases) are ignored. This method yielded 68,374 unique DH polypeptide segments after elimination of segments with stop codons, unpaired Cys residues, Asn in the last or next to last position that can lead to N-linked glycosylation motifs, and deamidation motifs (the "68K DH Theoretical Segment Pool"). Using the IGHD genes of Table 16 as an input for the PYTHON computer code provided below will reproduce the exact theoretical segment pool of 68,374 DH segments. There are two free parameters in this program: (1) the minimum length of the DNA sequences remaining after progressive deletions (4 bases in this example), and (2) the minimum length of the peptide sequences (2 amino acids in this example) acceptable for inclusion in the theoretical segment pool. These parameters can be changed to alter the output of the program. For example, changing the first parameter to one base and the second parameter to one amino acid would lead to a larger theoretical segment pool with 68,396 unique sequences, including 18 single-amino acid segments. DH segments progressively truncated to different lengths also fall within the scope of the invention; for example those truncated to 1, 2, 3, or 4 or more amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides prior to translation.

PYTHON Computer Program to Generate 68,374 DH Segments

```
import math, sys, string
```


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```
class genes:
      name = 'x'
      seq = 'x'
      progdel = set()
class table:
   name = 'x'
   dna = 'x'
   dna_n = 20 * ['x']
   prot = 60 * ['x']
   uprot = set()

pepcod = { 'A':0, 'C':1, 'D':2, 'E': 3, 'F': 4, 'G': 5, 'H': 6,
'I':7, 'K':8, 'L': 9, 'M': 10,
'N':11, 'P':12, 'Q':13, 'R': 14, 'S': 15, 'T': 16, 'V':17,
'W':18, 'Y': 19, 'Z': 20}
codpep = 21 * ['']
codpep[0] = 'A'
codpep[1] = 'C'
codpep[2] = 'D'
codpep[3] = 'E'
codpep[4] = 'F'
codpep[5] = 'G'
codpep[6] = 'H'
codpep[7] = 'I'
codpep[8] = 'K'
codpep[9] = 'L'
codpep[10] = 'M'
codpep[11] = 'N'
codpep[12] = 'P'
codpep[13] = 'Q'
codpep[14] = 'R'
codpep[15] = 'S'
codpep[16] = 'T'
codpep[17] = 'V'
codpep[18] = 'W'
codpep[19] = 'Y'
# Z represents a stop codon
codpep[20] = 'Z'

bases = 'ACGT'

def translate_dna(sequence):
# Translation of input DNA sequence using standard genetic code
```


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```
# Only full codons are considered with any remaining 1 or 2 bp
being ignored
# Z represents a stop codon
          code = {
          'AIA':'I', 'ATC':'I', 'ATT':'I', 'ATG':'M',
          'ACA':'T', 'ACC':'T', 'ACG':'T', 'ACT':'T',
          'AAC':'N', 'AAT':'N', 'AAA':'K', 'AAG':'K',
          'AGC':'S', 'AGT':'S', 'AGA':'R', 'AGG':'R',
          'CTA':'L', 'CTC':'L', 'CTG':'L', 'CTT':'L',
          'CCA':'P', 'CCC':'P', 'CCG':'P', 'CCT':'P',
          'CAC':'H', 'CAT':'H', 'CAA':'Q', 'CAG':'Q',
          'CGA':'R', 'CGC':'R', 'CGG':'R', 'CGT':'R',
          'GTA':'V', 'GTC':'V', 'GTG':'V', 'GTT':'V',
          'GCA':'A', 'GCC':'A', 'GCG':'A', 'GCT':'A',
          'GAC':'D', 'GAT':'D', 'GAA':'E', 'GAG':'E',
          'GGA':'G', 'GGC':'G', 'GGG':'G', 'GGT':'G',
          'TCA':'S', 'TCC':'S', 'TCG':'S', 'TCT':'S',
          'TTC':'F', 'TTT':'F', 'TTA':'L', 'TTG':'L',
          'TAC':'Y', 'TAT':'Y', 'TAA':'Z', 'TAG':'Z',
          'TGC':'C', 'TGT':'C', 'TGA':'Z', 'TGG':'W',
          }
          proteinseq = ''
          for n in range(0,len(sequence),3):
              if code.has_key(sequence[n:n+3]) == True:
                  proteinseq += code[sequence[n:n+3]]
          return proteinseq


# main body starts here

# open input and output files
in1 = open(sys.argv[1], 'r')
ou1 = open(sys.argv[2], 'w')

# read DNA sequences for input DH segments
data = in1.readlines()
nseg = len(data)

seqs = [ genes() for i in range(nseg) ]
for i in range(nseg):
  line = data[i]
  words = string.split(line)
  seqs[i].name = words[0]
```


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```
  seqs[i].seq = words[1]
  seqs[i].progdel = set()

# Define here minimum length for DNA (4) and for protein (2)
minlen = 4
minp = 2

# Implement progressive base by base deletion from 5' or 3' or
both ends
alln = 0
for i in range(nseq):
      seq = seqs[i].seq
      lseq = len(seq)
      nt = ct = lseq
      for n in range(nt):
            for c in range(ct):
                  nseq = seq[n:lseq-c]
                  if (len(nseq) >= minlen):
                        seqs[i].progdel.add(nseq)
      alln += len(seqs[i].progdel)

# Collect unique DNA sequences across all DH genes of origin
and ignore redundant ones
progdel = [ table() for i in range(alln) ]
n = 0
for i in range(nseq):
      for kk in seqs[i].progdel:
            unix = 1
            for j in range(n):
                  if (kk == progdel[j].dna):
                        unix = 0
                        break
            if (unix == 1):
                  progdel[n].name = seqs[i].name
                  progdel[n].dna = kk
                  n +=1

# Add none, 1 or 2 bp on one or both ends
# extras 20 + 20 * (21) + 20 + 420 = 440
# allocate memory for all variants
for i in range(n):
      progdel[i].dna_n = 440 * ['x']
      progdel[i].prot = 441 *3 * ['x']
```


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```
        progdel[i].uprot = set()

# add 1 or 2 bases at each end of input segment
tot = 0
for i in range(n):
# Step over each unique DNA sequence
  k = 0
# One base on 5' end combined with 1 or 2 bases added to 3' end
  for l5 in range(4):
    progdel[i].dna_n[k] = bases[l5] + progdel[i].dna
    k +=1
    for l3 in range(4):
      progdel[i].dna_n[k] = bases[l5] + progdel[i].dna +
bases[l3]
      k +=1
    for l3 in range(4):
      for m3 in range(4):
        progdel[i].dna_n[k] = bases[l5] + progdel[i].dna +
bases[l3] + bases[m3]
        k +=1
# One or two bases added to 3' only in this part
  for l3 in range(4):
    progdel[i].dna_n[k] = progdel[i].dna + bases[l3]
    k +=1
  for l3 in range(4):
    for m3 in range(4):
      progdel[i].dna_n[k] = progdel[i].dna + bases[l3] +
bases[m3]
      k +=1
# Two bases on 5' end combined with 1 or 2 bp on 3' end
  for l5 in range(4):
    for m5 in range(4):
      progdel[i].dna_n[k] = bases[l5] + bases[m5] +
progdel[i].dna
      k +=1
      for l3 in range(4):
        progdel[i].dna_n[k] = bases[l5] + bases[m5] +
progdel[i].dna + bases[l3]
        k +=1
      for l3 in range(4):
        for m3 in range(4):
          progdel[i].dna_n[k] = bases[l5] + bases[m5] +
progdel[i].dna + bases[l3] + bases[m3]
```


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```
            k +=1
# Now translate in all 3 forwared reading frames
# Save unique peptide sequences
  for fr in range(3):
    piece = progdel[i].dna
    piece = piece[fr:]
    tpiece = translate_dna(piece)
    progdel[i].prot[fr] = tpiece
    progdel[i].uprot.add(tpiece)

    for k in range(440):
      piece = progdel[i].dna_n[k]
      piece = piece[fr:]
      tpiece = translate_dna(piece)
      progdel[i].uprot.add(tpiece)
      progdel[i].prot[3+440*fr +k] = tpiece
  tot += len(progdel[i].uprot)

# Collect unique sequences with no ASN at last or next to last
position, no unpaired or consecutive CYS, no stops
unset = set()
segm = [ genes() for i in range(tot) ]
lux = 0
nn = 0
for i in range(n):
       k = 0
       for kk in progdel[i].uprot:
# Filter out sequences with undesired features, including
length being too short (under "minp" defined above)
             if (len(kk) < minp): continue
             if (kk[len(kk)-1] == "N"  or kk[len(kk)-2] ==
"N"): continue
             if (kk.count("Z") > 0 or kk.count("CC") >0 or
kk.count("C") % 2 >0): continue
             unset.add(kk)
             lux1 = len(unset)
             if (lux1 > lux):
                    segm[nn].name = progdel[i].name + "_" +
str(nn)
                    segm[nn].seq = kk
                    nn += 1
             lux = lux1
             k +=1
```


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```
# Print out unique peptide sequences that pass all the filters
for i in range(nn):
        oul.write("%s\t%s\n" % (segm[i].name, segm[i].seq))
```

Example 7. Deriving Theoretical Segment Pools of TN1 and N2 Segments

The libraries of this example are designed to, in some instances, have a greater diversity in their TN1 and N2 segments in comparison to other libraries known in the art. The diversity of the TN1 and N2 segments was increased by using the matching method described in Example 4 to deconvolute the CDRH3 sequences in the HPS into their constituent segments (*i.e.,* TN1, DH, N2, and H3-JH), followed by extraction of "novel" TN1 and N2 segments in the manner described below. For the purposes of the invention, "novel" TN1 and N2 segments are TN1 and N2 segments that do not appear in a theoretical segment pool that is matched to a reference set of CDRH3 sequences. Following is an example of the method used to extract novel TN1 and N2 segments from the HPS. This method can be generalized to extract novel TN1 and N2 segments from any reference set of CDRH3 sequences, using any theoretical segment pool containing TN1, DH, N2, and/or H3-JH segments.

Table 9 provides the matching results for the reference CDRH3 sequence ERTINWGWGVYAFDI (SEQ ID NO: 8760) (Test Cases 5.1-5.4) from the HPS, using Theoretical Segment Pool 1 ("TSP1"). The best matches to the reference CDRH3 are four CDRH3 sequences, each within three amino acids of the reference CDRH3 sequence. In each of these matches, the TN1, DH, N2 and H3-JH segments are of length 4, 3, 3 and 5 amino acids, respectively. Thus the reference CDRH3 can be deconvoluted into the following segments: ERTI-NWG-WGW-YAFDI (SEQ ID NO: 8761) (*i.e.* [TN1]-[DH]-[N2]-[H3-JH], respectively). The DH and H3-JH segments from the reference CDRH3, NWG and YAFDI (SEQ ID NO: 4540) respectively, are identically present in TSP1. However, the TN1 (ERTI) (SEQ ID NO: 8718) and N2 (WGW) segments from the reference CDRH3 are absent in TSP1 and match TSP1 segments with one or more amino acid mismatches. These "novel" TN1 and N2 segments are extracted from the reference CDRH3 and considered for inclusion prospective theoretical segment pools and/or synthetic libraries. Additional novel TN1 and N2 segments were accumulated by applying this analysis to all

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members of the HPS. In order to robustly identify TN1 and N2 sequences, the extraction was performed only for those CDRH3 sequences in which the DH and H3-JH segments in the reference CDRH3 and TSP1 cumulatively return no more than 3 amino acid mismatches, implying that the DH and H3-JH segments of the reference CDRH3 had been reliably assigned.

Example 8. Calculation of Segment Usage Weights

Segment usage weights were calculated for their utility in determining which segments from the theoretical segment pools (*e.g.,* TSP1 and TSP1 plus novel TN1 and N2 segments identified as described in Example 7) should be included in a synthetic library. Segment usage weights were obtained by utilization of the matching method described above and Equation 2:

Equation 2

$$w(i) = \frac{1}{S_m} \sum_{j=1}^{S_m} \frac{1}{g(j)} \sum_{k=1}^{g(j)} f_i(k)$$

where,

- w(i): Weight for segment i. $0 \leq w(i) \leq 1$.
- S_m: Number of sequences (out of total S in the reference CDRH3 set) which contain one or more best matches with no more than m amino acid mismatches in the specified region of the reference CDRH3 sequence. Here, the mismatches are computed over the Kabat-CDRH3 region, but other fragments of the CDRH3 sequences may also be considered. A constant value of $m=3$ was used here, but other values may be used, or the value may depend on the length of the reference CDRH3 sequence.
- $g(j)$: Total number of degenerate segment combinations producing the best match to the reference CDRH3 sequence j.
- $f_i(k)$: Fractional amino acid identity of TN1, DH, N2 or H3-JH segment in degenerate match k, relative to the corresponding sequence fragment in the reference CDRH3 sequence j. The fractional amino acid identity equals zero if the segment does not appear in match k. Other definitions of f, such as amino acid similarity (*e.g.,* based on physicochemical properties of the amino acids such as hydrophobicity), instead of identity, may be also used.

The procedure for calculating segment usage weights will be further exemplified below. In each of these examples, the best match combinations from TSP1 are

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provided for a single CDRH3 sequence (S_m = 1) and the degeneracy (k) and fractional mismatch (f) dependent weight calculations are explained.

Example 8.1. Segment usage weights for Test Case 1 in Table 9

Refer to Test Case 1 in Table 9. The CDRH3 sequence RTAHHFDY (SEQ ID NO: 3660) is identically located in TSP1 (f = 1, subscripts dropped for simplicity) via a unique segment combination (g = 1). Table 18 provides the usage weights for the segments corresponding to the best match from TSP1 for the CDRH3 of Test Case 1.

Example 8.2. Segment usage weights for Test Cases 2.1 and 2.2 in Table 9

Refer to Test Cases 2.1 and 2.2 in Table 9. The CDRH3 sequence VGIVGAASY (SEQ ID NO: 3661) may be identically located in TSP1 (f = 1) via two distinct segment combinations (g = 2). Table 19 provides the usage weights for the segments corresponding to the best match from TSP1 for the CDRH3 of Test Cases 2.1 and 2.2.

Example 8.3. Segment usage weights for Test Case 3.1 in Table 9

Refer to Test Case 3.1 in Table 9. The CDRH3 sequence DRYSGHDLGY (SEQ ID NO: 3662) may be identically located in TSP1 via a unique segment combination (g = 1) with a single amino acid difference. As provided below, the TN1, N2 and H3-JH segments match the corresponding reference sequence fragments identically, while four of the five DH amino acids match identically.

Sequence from the HPS: DR-YSG**H**D-LG-Y (SEQ ID NO: 3662)

Nearest Neighbor in TSP1: DR-YSG**Y**D-LG-Y (SEQ ID NO: 8719)

Thus, here

f = 4/5 for the DH segment; and

= 1 for the TN1, N2, and H3-JH segments (Table 20).

Example 8.4. Matching of Test Cases 4.1 and 4.2 in Table 9.

Refer to test cases 4.1 and 4.2 in Table 9. The CDRH3 sequence GIAAADSNWLDP (SEQ ID NO: 3663) may be located in TSP1 via two distinct

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segment combinations ($g = 2$), each with a single amino acid difference. As provided below, the TN1, DH and N2 segments match the corresponding reference sequence fragments identically, while five of the six H3-JH amino acids match identically.

Sequence from HPS: (-)-GIAAA-D-SNW**L**DP (SEQ ID NO: 3663)

Nearest Neighbor in TSP1: (-)-GIAAA-D-SNW**F**DP (SEQ ID NO: 8720)

Sequence from HPS: G-IAAA-D-SNW**L**DP (SEQ ID NO: 3663)

Nearest Neighbor in TSP1: G-IAAA-D-SNW**F**DP (SEQ ID NO: 8720)

Here, (-) represents the "empty" TN1 segment.

Applying Equation 2 results in the segment usage weights provided in Table 21.

Example 8.5. Calculating the Segment usage weights for Test Cases 1 to 4.2 of Table 9

Extending the individual calculations described above to simultaneously include all of Test Cases 1 to 4.2 of Table 9 results in the segment usage weights of Table 22.

Example 8.6. Calculating the Segment usage weights for Test Cases 5.1 to 5.4 of Table 9

Refer to the CDRH3 sequence ERTINWGWGVYAFDI (SEQ ID NO: 8760) and the novel TN1 and N2 segments extracted from the CDRH3 sequence, in Example 7. In this case, the novel TN1 and N2 segments (ERTI (SEQ ID NO: 8718) and WGV respectively), and the DH and H3-JH segments from TSP1 (NWG and YAFDI (SEQ ID NO: 4540) respectively) are each assigned usage weights of unity.

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Example 9. Selection of TN1, DH, N2 and JH Segments for Inclusion in Synthetic Libraries

Figure 5 provides the general method used for the design of synthetic CDRH3 libraries. The method uses as input: (1) a theoretical segment pool containing TN1, DH, N2, and H3-JH segments (*e.g.,* TSP plus novel TN1 and N2 segments); and (2) a collection of reference CDRH3 sequences (*e.g.,* the HPS). From these inputs, a particular subset of segments from the theoretical segment pool is selected for inclusion in a physical CDRH3 library.

First, the best matches to the CDRH3s of the HPS were obtained, from within the TSP1 set, with or without the novel TN1 and N2 segments, using the matching method described above. This data was then used to compute the segment usage weights via Equation 2. Segments were prioritized for inclusion in the physical library based on their relative frequency of occurrence in the CDRH3 sequences of the HPS (as indicated by the segment usage weights), as well as other factors (more fully described below), such as hydrophobicity, alpha-helical propensity, and expressibility in yeast.

Example 9.1. Exemplary Library Design (ELD-1)

ELD-1 uses the HPS and the segments from TSP1 1 (9.5×10^9 members) as inputs and produces an output of 100 TN1, 200 DH, 141 N2 and 100 H3-JH segments, each from TSP1, ranked in order by their usage weights in the HPS, to produce a library with theoretical complexity of 2.82×10^8. The segments corresponding to ELD-1 are provided in Table 23. Note that here the combination of all of the segments (*i.e.,* TN1, DH, N2, and H3-JH), and the individual sets of segments (*i.e.,* TN1 only, DH only, N2 only, and H3-JH only) each constitute theoretical segment pools.

Example 9.2. Exemplary Library Design 2 (ELD-2)

The inputs for this design are the HPS and the segments from TSP1 plus the novel TN1 and N2 segments extracted from the HPS (Example 7). The outputs are (1) 200 DH and 100 H3-JH segments, each from TSP1; and (2) 100 TN1 and 200 N2 segments including TN1 and N2 segments originally in TSP1 and those extracted from the sequences in the HPS. Applying the method described in Example 7 to extract novel TN1 and N2 segments (*i.e.,* those not included in TSP1) resulted in the identification of 1,710 novel TN1 segments and 1,024 novel N2 segments. The

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segments corresponding to ELD-2 are provided in Table 24. Note that here the combination of all of the segments (*i.e.,* TN1, DH, N2, and H3-JH), and the individual sets of segments (*i.e.,* TN1 only, DH only, N2 only, and H3-JH only) each constitute theoretical segment pools. As in ELD-1, all segments in ELD-2 were selected for inclusion based solely on their usage weights in the HPS.

Example 9.3. Exemplary Library Design 3 (ELD-3)

The inputs for this design are identical to those for ELD-2. As in ELD-2, the outputs are (1) a set of 200 DH and 100 H3-JH segments,, each from TSP1; and (2) a set of 100 TN1 and 200 N2 segments, including TN1 and N2 segments originally in TSP1 and those extracted from the sequences in the HPS (Example 7). However, the approach used for the selection of the segments for ELD-3 differs in two respects. First, selected physicochemical properties of the segments (hydrophobicity, isoelectric point, and alpha-helix propensity) were used, in addition to the segment usage weights, to prioritize segments for inclusion in the physical library. Hydrophobicity was used to de-prioritize hydrophobic DH segments that are empirically over-represented in poorly expressed antibodies isolated from yeast-based libraries. Isoelectric point and propensity for alpha-helix formation were utilized to identify segments located in regions of physicochemical property space that were relatively unexplored in CDRH3 libraries known in the art (*e.g.,* U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379). Second, the segment usage weights were calculated via a bootstrap analysis of the HPS dataset. These methods are more fully described below. The segments corresponding to ELD-3 are provided in Table 25. Note that here the combination of all of the segments (*i.e.,* TN1, DH, N2, and H3-JH), and the individual sets of segments (*i.e.,* TN1 only, DH only, N2 only, and H3-JH only) each constitute theoretical segment pools.

Example 9.3.1. Generation of Segment Usage Weights via Bootstrap Analysis

Bootstrap analysis (Efron & Tibshirani, An Introduction to the Bootstrap, 1994 Chapman Hill, New York) is a widely used statistical procedure for estimating the variability of a statistic of a given sample. This estimate is based on the value of the statistic calculated for several sub-samples, equal in size to the original sample and derived from it via sampling with replacement. Members of the original sample

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are chosen at random to form the sub-samples, and are typically included multiple times in each sub-sample (hence, "sampling with replacement").

Here, the original sample is the HPS dataset with n= 3,571 members and the statistic is the segment usage weight. One-thousand sub-samples, each with 3,571 members, were generated by randomly choosing sequences from the HPS dataset (no more than 10 repeats of a given sequence were allowed in each sub-sample). The matching method described above was then applied to each sub-sample, and the final segment usage weights were calculated as the average of the values obtained for the individual sub-samples. Average values derived via this bootstrap procedure are more robust than values calculated from the parent HPS dataset alone. Unless indicated otherwise, these average values of the 1,000 sub-samples were used in the selection of segments for ELD-3.

Example 9.3.2. Amino Acid Property Indices

The *AAindex* database, available online at www.genome.jp/aaindex/, provides more than 500 numerical indices representing various physicochemical and biochemical properties of amino acids and pairs of amino acids. These properties include hydrophobicity, electrostatic behavior, secondary structure propensities and other characteristics, with several indices often available for a given property. The following three indices were chosen by starting with the well-understood Kyte-Doolittle hydropathy index (KYJT820101) and adding the indices most numerically de-correlated from it and each other. They thus potentially describe non-overlapping regions of amino acid property space and were used for analysis and selection of the DH and H3-JH segments for ELD-3:

1. KYTJ820101 (hydropathy index)
2. LEVM780101(normalized frequency of alpha helix)
3. ZIMJ680104 (isoelectric point)

Example 9.3.3. Hydrophobic DH Segments are Over-Represented in Poorly Expressed Antibodies Isolated from Yeast-Based Libraries

Based on protein expression levels from approximately 1200 antibodies expressed in *S. cerevisiae,* antibodies were classified as either "Good" or "Poor" expressors. The CDRH3 sequence of each antibody in each category was examined to

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identify sequence features that correlated with the expression level. One such sequence feature is the hydrophobicity of the DH segments calculated using the KYTJ820101 index. Figure 6 provides the frequency of "Good" and "Poor" expressors as a function of the DH segment hydrophobicity (increasing to the right). The distribution expected from the synthetic library used to isolate these antibodies is also provided as a reference ("Design"). DH segments with the highest hydrophobicity values (far right of the plot) are over-represented (relative to the expectation based on the design) among "Poor" expressors and under-represented among "Good" expressors. Similarly, hydrophilic DH segments (far left) are over-represented among "Good" expressors and under-represented among "Poor" expressors. From this data, it was inferred that the overall expressibility of the antibodies of the library may be improved by synthesizing CDRH3 sequences with fewer hydrophobic DH segments.

Example 9.3.4. Selection of the 200 DH Segments for Inclusion in ELD-3

A set of 71 DH segments from TSP1 were designated as "core" DH segments for automatic inclusion in ELD-3. These segments had the following desirable properties:

1. Fifty-three of seventy-one were present within the top 7% of DH segments rank-ordered by segment usage weights from the bootstrap analysis.
2. Eighteen of seventy-one were present within the top 7% of DH segments rank-ordered by usage weights derived from antibodies isolated from libraries expressed in *S. cerevisiae*.

The remaining 1,040 segments were designated as "non-core." To complete the set of 200 segments in ELD-3, 129 segments were chosen from the "non-core" pool of segments in the following manner:

1. Sixty-five segments were eliminated because they contain either (a) an Asn residue at the last or next-to-last position with the potential to form N-linked glycosylation motifs via combination with N2 amino acids or (b) the amino acid sequence NG, implicated in de-amidation.
2. Segments with higher than median values for the KYTJ820101 hydropathy index (median=2.9 for 1K DH) were eliminated from further consideration. In view of the known importance of Tyr for antigen recognition (Fellouse *et al.*, PNAS, 2004, 101: 12467; and Hofstadter *et al.*, J. Mol. Biol., 1999, 285: 805) segments containing at least

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one Tyr residue were retained unless located in the highest hydrophobicity quartile (KYTJ820101 value higher than 9.4). This eliminated 443 segments.

3. The final set of 129 segments was obtained by using an objective function that aimed to maximize the Euclidean distance, between the "core" and the remaining 443 "non-core" segments, in a multi-dimensional space defined by the following variables: (1) amino acid mismatches to nearest neighbor; and (2) values of the three physicochemical property indices.

Example 9.3.5. Selection of the 100 H3-JH Segments for Inclusion in ELD-3

One-hundred H3-JH segments were chosen for inclusion in ELD-3 in the following manner.

1. Twenty-eight H3-JH segments were selected after being experimentally validated in other libraries containing only these H3-JH segments (*see* U.S. Publication Nos. 2009/0181855 and 2010/0056386, and WO/2009/036379).
2. Fifty-seven segments were selected based on their presence within the top 25% of H3-JH segments rank-ordered by usage weights from the bootstrap analysis described above. These 57 H3-JH segments, plus the 28 H3-JH segments of (1) (*i.e.,* 85 segments total) were designated as the "core" H3-JH segments, which, like the core DH segments, were automatically included in ELD-3.
4. Fifteen additional segments were chosen by using an objective function that aimed to maximize the Euclidian distance, between the "core" and the remaining 200 "non-core" segments, in a multi-dimensional space defined by the following variables: (1) amino acid mismatches to nearest neighbor; and (2) values of the three physicochemical property indices.

Example 9.3.6. Selection of 100 TN1 and 200 N2 segments for Inclusion in ELD-3

TN1 and N2 segments were extracted from the sequences in each sub-sample of the bootstrap procedure, and the 100 TN1 and 200 N2 segments with the highest

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average segment usage weights were chosen for inclusion into the library, after elimination of sequences with undesirable motifs, namely Cys and Asn residues.

Example 9.3.7. Selection of Nucleotide Sequences to Encode the Segments Chosen for Inclusion in ELD-3

Each of the polypeptide segments chosen for inclusion in the library must be back translated (polypeptide to DNA) into a corresponding oligonucleotide sequence. While a large number of oligonucleotides could possibly encode each polypeptide segment, due to the degeneracy of the genetic code, certain constraints were imposed to select oligonucleotides that were more desirable. First, since ELD-3 was expressed in yeast (*S. cerevisiae*), codons that are rarely used in yeast were avoided. For example, of the six possible codons for Arg, three: CGA, CGC and CGG are used to encode yeast proteins at rates of under 10% (see, for example, Nakamura et al., Nucleic Acids Res., 2000, 28:292), and therefore those three codons were avoided to the extent possible. Second, since many antibodies are produced in Chinese Hamster Ovary (CHO) cells (after discovery *e.g.,* in yeast), the CCG codon (encoding Pro) was also avoided, since it is rarely used by hamsters (Nakamura et al.)

A number of restriction enzymes are employed during the actual construction of the CDRH3 oligonucleotide library (see Example 10 of U.S. Pub. No. 2009/0181855). It is thus desirable to avoid the occurrence of recognition motifs for these restriction enzymes within the CDRH3 polynucleotide sequences. Codons are selected at the individual segment level to avoid introducing recognition motifs for restriction enzymes that may be used downstream. Since such motifs may also be generated by combinatorial assembly of the segments, the segment combinations are also checked and, whenever possible, codons are changed to eliminate the occurrence of such motifs. Specifically, three restriction enzymes were used during the construction of the currently exemplified CDRH3 library: BsrDI, BbsI, and AvrII. The first two are type II enzymes with non-palindromic recognition sites. The reverse strand of the oligonucleotides encoding the segments was checked explicitly for recognition sites for these two enzymes. In particular, the reverse strands were checked for the motifs GCAATG and CATTGC (for BsrDI) and GAAGAC and GTCTTC (for BbsI). The recognition motif for AvrII is palindromic so the oligonucleotides were only checked for the sequence CCTAGG. However, AvrII is

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used only to treat TN1 segments, and thus it is not necessary to evaluate its presence in the other segments or their combinations.

An additional constraint that was imposed to improve engineering of the polypeptide to polynucleotide conversion was avoidance of consecutive runs of 6 or more of the same type of base, as this is believed to increase errors during solid phase oligonucleotide synthesis. Therefore, DNA sequences for the segments of ELD-3 were chosen to avoid such motifs. The DNA sequences for the ELD-3 segments are included, with the respective polypeptide sequences, in Table 25. One of ordinary skill in the art will readily recognize that these methods can also be applied to any other library, any restriction sites, any number of nucleotide repeats, and/or to avoid the occurrence of any codons considered undesirable in any organism.

Example 10. Matching of ELD-3 to Human CDRH3 Datasets and Clinically Relevant Antibodies

Among the objectives of the invention is to mimic the V-D-J recombination processes underlying the creation of the human CDRH3 repertoire *in vivo*, thereby increasing the diversity of the CDRH3 library in comparison to other libraries known in the art, while maintaining the human character of CDRH3. One measure of success is the extent to which collections of human reference CDRH3 sequences are represented identically, or via close matches (*e.g.*, less than about 5, 4, 3, or 2 amino acid differences) in any library of the invention. We evaluated this metric using two human CDRH3 sequence reference datasets, both non-overlapping with each other and the HPS: (1) a collection of 666 human CDRH3 sequences (Lee *et al.*, Immunogenetics, 2006, 57: 917; "Lee-666"); and (2) a collection of 3,000 human CDRH3 sequences randomly chosen from the over 200,000 sequences disclosed in Boyd *et al.*, Science Translational Medicine, 2009, 1: 1-8 ("Boyd-3000"). The results of the random sample of the 3,000 human CDRH3 sequences from Boyd *et al.* was representative of the results of the same analysis as applied to all members of the Boyd *et al.* set (>200,000 CDRH3 sequences).

Figure 7 provides the percentage of CDRH3 sequences in two synthetic libraries, "LUA-141" and ELD-3, that match a sequence from the Lee-666 or Boyd-3000 sets with zero, one, two, three, or more than three amino acid mismatches. Here, "LUA-141" represents a library containing 212 TN1, 278 DH, 141 N2, and 28 H3-JH (*see* U.S. Publication No. 2009/0181855 for details). In particular, it is notable

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that ELD-3 exhibits a higher percentage of sequences (12.9% and 12.1% for the Lee-666 and Boyd-3000 sets, respectively) that identically match a reference CDRH3 sequence than LUA-141 (8.4% and 6.3% for the Lee-666 and Boyd-3000 sets, respectively). It is also notable that ELD-3 exhibits a higher cumulative percentage of human CDRH3 sequences found with no more than two amino acid mismatches (54.1% and 52.5% for the Lee-666 and Boyd-3000 sets, respectively) relative to LUA-141 (41.2% and 43.7% for the Lee-666 and Boyd-3000 sets, respectively).

Another metric by which antibody libraries can be evaluated is their ability to match "clinically relevant" reference CDRH3 sequences. Figure 8 demonstrates that ELD-3 returns better matches to clinically relevant CDRH3 sequences than the LUA-141 library. Specifically, ELD-3 matches 34 of 55 (62%) clinically validated antibodies within one amino acid, while the LUA-141 library only matches 20 of 55 (37%).

Example 11. Comparison of ELD-3 to LUA-141

ELD-3 has 73 TN1, 92 DH, 119 N2, and 28 H3-JH in common with LUA-141. Thus, 94.5% of the sequences in ELD-3 (4.0×10^8 members) are different from the LUA-141 library (2.3×10^8 members). Figure 9 demonstrates that the combinatorial efficiency of the segments in ELD-3 is greater than that of the segments in LUA-141. Specifically, the ELD-3 segments are more likely to yield a unique CDRH3 than the LUA-141 library segments. This is advantageous, because it allows one to synthesize libraries with increased CDRH3 diversity using fewer segments.

Figure 10 provides the amino acid compositions of the Kabat-CDRH3s of LUA-141, ELD-3, and Human CDRH3 sequences from the HPS.

Figure 11 provides the Kabat-CDRH3 length distribution of LUA-141, ELD-3, and Human CDRH3 sequences from the HPS.

CDRH3 Libraries Synthesized with Degenerate Oligonucleotides

Example 12. Further Increasing CDRH3 Diversity by Utilizing Degenerate Oligonucleotides

The methods described in this example extend the methods taught above, to produce CDRH3 libraries with more members than those of the libraries described

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above. In particular, one or two degenerate codons were introduced into the DH and or N2 polynucleotide segments, and (generally) no degenerate codon or one degenerate codon were introduced into the H3-JH segments. Segments with different numbers of degenerate codons are also contemplated; for example DH segments with 0, 1, 2, 3, 4, 5, 6, 7, 8, or more degenerate codons, and H3-JH segments with 0, 1, 2, 3, 4, 5, or more degenerate codons. This results in CDRH3 libraries containing greater than about 10^{11} (about 2×10^{11}) distinct CDRH3 amino acid sequences that closely reflect properties, such as length and composition among others, of a reference set of human CDRH3 sequences. As described below, the degenerate positions in the DH segments are usually, but not always, the very N- and/or C-terminal positions, or 5' and 3' end codons (*i.e.,* not necessarily only the first or last base), respectively, when considering the corresponding oligonucleotide sequences. Degenerate codons were similarly used to synthesize N2 segments. Two hundred of the TN1 segments were as described in ELD-3, although libraries with degenerate TN1 segments, or with alternative choices of TN1 segment sequences, fall within the scope of the invention. An additional one hundred TN1 segments complete the set of 300 TN1 segments for this library. The amino acid and nucleotide sequences are listed in Table 26. It is also possible to use mixtures of trinucleotides instead of, or in addition to, degenerate oligonucleotides in order to allow amino acid type variation at one or more selected positions within "base" or "seed" segment sequences (defined below).

Example 13. Selection of DH Segments for Synthesis by Degenerate Oligonucleotides

The segment usage weights were calculated for the 68K DH Theoretical Segment Pool by comparison to the sequences contained in Boyd *et al.* The DH segments with a length of three or more amino acids were ranked according to their segment usage weights (as described above), and the top 201 were designated as "seed" sequences. These seed sequences were then varied by selecting certain positions to incorporate degenerate codons. The positions selected for variance, the amino acids types to which they were varied, were determined by comparing the seed sequences to a reference set of 9,171 DH segments that were a subset of the 68K DH Theoretical Segment Pool. These 9,171 DH segments were selected because their segment usage weight in Boyd *et al.* was significant, meaning that the cumulative segment usage weight (Example 8) is at least 1.0.

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Each of the 201 seed sequences was compared to each of the sequences in the reference set of 9,171 DH segments, and those of identical length and differing at a single position were further considered to inform possible variants of the seed. In this manner, the most variable position for each seed was identified and a set of candidate amino acid types was also identified for each position. Finally, a set of degenerate codons was considered, to identify the codon that most faithfully represented the set of candidate amino acid types for each particular position. Degenerate codons encoding stop codons, Cys residues, N-linked glycosylation motifs (*i.e.,* NXS or NXT, where X is any amino acid type), or deamidation motifs (NG) were eliminated from consideration. This process generated 149 unique degenerate oligonucleotide sequences, which collectively encode 3,566 unique polypeptide sequences. Alternative designs generated according to the same principles were also considered, and those having a larger diversity (in terms of the number of unique polypeptide sequences) and smaller RMAX values (see below) were given preference for inclusion in the libraries of the invention. However, it is also conceivable that different criteria could be used to select DH segments from the 68K DH Theoretical Segment Pool, and that libraries including DH segments selected by these different criteria would also fall within the scope of the invention.

Because not all degenerate oligonucleotides encode an identical number of polypeptides, the latter do not occur with uniformly identical weights over the entirety of a given theoretical segment pool (*i.e.,* TN1, DH, N2 and H3-JH) contained within a CDRH3 library of the invention. For example, an individual amino acid sequence X encoded by an oligonucleotide of total degeneracy 4 will have a "weight" of 1/4, while another individual amino acid sequence, Y, encoded by an oligonucleotide of degeneracy 6 will have a weight of 1/6. Moreover, certain amino acid sequences could be encoded by more than one degenerate oligonucleotide, so their weights will be the sum of the individual contributions by each oligonucleotide. Within a given theoretical segment pool, the ratio of the weight of the most heavily weighted polypeptide to that of the least heavily weighted one, RMAX, is an important design criterion that one would ideally like to minimize. The RMAX value may be defined by length, or overall for all of the segments of any given type (*i.e.,* all the DH segments, or all the H3-JH segments, and so on for the TN1, and/or the N2 segments). Table 27 lists the degenerate oligonucleotide sequences, while Table 28 lists the

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unique polypeptide sequences resulting from these oligonucleotides. These two tables include the DH dimer segments the design of which is detailed below.

Example 13.1. Selection of DH Dimer Segments

A different method was employed to design a set of degenerate oligonucleotides encoding DH dimer sequences. The method aimed to include all of the 45 dimer sequences in ELD-3 plus as many of the other 400 theoretically possible dimer sequences (*i.e.,* 20 residues possible in each of 2 positions = 20 * 20), minus segments containing Asn (N) residues and excessively hydrophobic dimers (*i.e.,* any dimer combination comprising only F, I, L, M, and/or V residues). This design process ultimately yielded 35 degenerate oligonucleotide sequences encoding 213 unique peptide dimer sequences. As with the selection processes used for all of the other segments of the invention, one or ordinary skill in the art will readily recognize that other criteria could be used to select the DH dimer segments, and that libraries including these segments also fall within the scope of the invention.

Combining the DH dimer segments with the longer DH segments of Example 13, yielded the final set of DH segments of the currently exemplified library, encoded by a total of 184 oligonucleotides (35 encoding dimers and 149 encoding segments having three or more amino acids) versus the 200 oligonucleotides of ELD-3. The 184 oligonucleotides encode a total of 3,779 unique polypeptide sequences: 213 dimers and 3,566 longer segments of three amino acids or greater.

Example 14. Generation of Expanded N2 Diversity

As described above, ELD-3 contains 200 N2 segments. In the currently exemplified library, the empty N2 segment (*i.e.,* no N2, so that the DH segments are joined directly to the H3-JH segments) and monomer N2 segments were the same as in ELD-3. However, degenerate oligonucleotides were used to generate sets of two-, three-, and four-mers that not only recapitulated all of the corresponding sequences in ELD-3 but also resulted in additional diversity. As with the DH segments, these degenerate oligonucleotides were designed to eliminate Asn (in unsuitable positions) and Cys residues, and stop codons. More specifically, Asn residues were allowed at the first position of trimers and at the first or second position of tetramers whenever the subsequent amino acid was not Gly and the next amino acid was not Ser or Thr, thus avoiding deamidation or N-linked glycosylation motifs within the candidate N2

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segments. The N2 theoretical segment pool for the currently exemplified library contains one zero-mer (*i.e.,* no N2 segment), 18 monomer, 279 dimer, 339 trimers, and 90 tetramer N2 amino acid sequences, or 727 segments in total. These amino acid sequences are encoded by 1, 18, 81, 36, and 10 oligonucleotides, respectively, for a total of 146 oligonucleotides. All but the first 19 oligonucleotides, those encoding the zero- and one-mers, are degenerate. Table 29 lists the 146 oligonucleotide sequences, while Table 30 lists the resulting 727 unique polypeptide sequences.

Example 15. Generation of Expanded H3-JH Diversity

Application of nucleotide-level progressive deletions on the 5' end of the human IGHJ polynucleotide segments down to the point where only the DNA sequence corresponding to FRM4 remained (*i.e.,* no H3-JH remained), followed by systematic 1- or 2-bp completions on the same 5' end, resulted in 643 unique H3-JH peptide segments after translation ("643 H3-JH Set"). As done with the DH segments, it is possible to rank order each of the 643 segments by their usage weights obtained after comparison to the approximately 237,000 human sequences from Boyd *et al.,* and the top 200 individual sequences, from those devoid of the undesired motifs described above, were chosen to provide the set of H3-JH segments for the currently exemplified library.

In an alternatively exemplified embodiment, 46 of the 200 H3-JH segments were designed with a two-fold degenerate codon in the first position (*i.e.,* N-terminal or 5' end, respectively, at the peptide and oligonucleotide level), so that, overall, 200 oligonucleotides would encode 246 unique peptide sequences.

In yet other alternatively exemplified embodiments, further use of degenerate codons may be conceived to produce libraries encoded by 90, 100, 200 or more oligonucleotides representing up to 500 distinct polypeptide sequences. Preferably, but not necessarily, these up to 500 unique sequences could be a subset of the sequences in the 643 H3-JH reference set described above, or a subset of variants of these sequences. As exemplified above, H3-JH segments containing undesirable polypeptide motifs may be eliminated from the design. The oligonucleotide sequences for the JH segments are listed on Table 31, while the resulting unique polypeptide sequences are provided in Table 32. In Table 31, nucleotide sequences corresponding to the FRM4 region are also provided, but the "peptide length" value

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refers to the H3-JH portion only. For simplicity, only the H3-JH peptide sequences are included in Table 32.

Example 16. Extended Diversity Library Design (EDLD)

The TN1, DH, H3-JH, and N2 segments selected above, and provided in Tables 26 to 32, were combined to generate an Extended Diversity Library Design (EDLD) with theoretical diversity of about 2×10^{11} (300 TN1 × 3,779 DH × 727 N2 × 246 H3-JH). The oligonucleotides encoding the selected segments were chosen according to the principles of Example 9.3.7.

Figures 12 - 15 illustrate certain characteristics of this design indicating, for example, that about 50% of the approximately 237,000 CDRH3 sequences in Boyd *et al.* may be recapitulated by library sequences with either one or no mismatches (*i.e.,* by summing the "0" and "1" bins of Figure 12) . The theoretical length distributions (Figure 13) and amino acid compositions (Figure 14) of these libraries also match closely the respective characteristics observed in the same set of human CDRH3 sequences. Figure 15 shows the combinatorial efficiency of the Extended Diversity Library Design. Approximately 65% of the sequences appear only once in the design (*i.e.,* are generated via one non-degenerate combination of segments). Figure 8, previously presented, shows that the Extended Diversity Library Design outperforms both LUA-141 and ELD-3 in terms of matching to clinically relevant human antibody sequences.

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Table 1. Germline-like sequences for eight of the VK chassis provided by the invention.

Germline	Junction	Germline-Like CDRL3 Sequence	SEQ ID NO	Germline	Junction	Germline-Like CDRL3 Sequence	SEQ ID NO
VK1-05	1	QQYNSYST	1	VK2-28	1	MQALQTPT	101
VK1-05	2	QQYNSYFT	2	VK2-28	2	MQALQTFT	102
VK1-05	3	QQYNSYLT	3	VK2-28	3	MQALQTLT	103
VK1-05	4	QQYNSYIT	4	VK2-28	4	MQALQTIT	104
VK1-05	5	QQYNSYRT	5	VK2-28	5	MQALQTRT	105
VK1-05	6	QQYNSYWT	6	VK2-28	6	MQALQTWT	106
VK1-05	7	QQYNSYYT	7	VK2-28	7	MQALQTYT	107
VK1-05	8	QQYNSYSPT	8	VK2-28	8	MQALQTPPT	108
VK1-05	9	QQYNSYSFT	9	VK2-28	9	MQALQTPFT	109
VK1-05	10	QQYNSYSLT	10	VK2-28	10	MQALQTPLT	110
VK1-05	11	QQYNSYSIT	11	VK2-28	11	MQALQTPIT	111
VK1-05	12	QQYNSYSRT	12	VK2-28	12	MQALQTPRT	112
VK1-05	13	QQYNSYSWT	13	VK2-28	13	MQALQTPWT	113
VK1-05	14	QQYNSYSYT	14	VK2-28	14	MQALQTPYT	114
VK1-05	15	QQYNSYSPFT	15	VK2-28	15	MQALQTPPFT	115
VK1-05	16	QQYNSYSPLT	16	VK2-28	16	MQALQTPPLT	116
VK1-05	17	QQYNSYSPIT	17	VK2-28	17	MQALQTPPIT	117
VK1-05	18	QQYNSYSPRT	18	VK2-28	18	MQALQTPPRT	118
VK1-05	19	QQYNSYSPWT	19	VK2-28	19	MQALQTPPWT	119
VK1-05	20	QQYNSYSPYT	20	VK2-28	20	MQALQTPPYT	120
VK1-12	1	QQANSFPT	21	VK3-11	1	QQRSNWPT	121
VK1-12	2	QQANSFFT	22	VK3-11	2	QQRSNWFT	122
VK1-12	3	QQANSFLT	23	VK3-11	3	QQRSNWLT	123
VK1-12	4	QQANSFIT	24	VK3-11	4	QQRSNWIT	124
VK1-12	5	QQANSFRT	25	VK3-11	5	QQRSNWRT	125
VK1-12	6	QQANSFWT	26	VK3-11	6	QQRSNWWT	126
VK1-12	7	QQANSFYT	27	VK3-11	7	QQRSNWYT	127
VK1-12	8	QQANSFPPT	28	VK3-11	8	QQRSNWPPT	128
VK1-12	9	QQANSFPFT	29	VK3-11	9	QQRSNWPFT	129
VK1-12	10	QQANSFPLT	30	VK3-11	10	QQRSNWPLT	130

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VK1-12	11	QQANSFPIT	31	VK3-11	11	QQRSNWPIT	131
VK1-12	12	QQANSFPRT	32	VK3-11	12	QQRSNWPRT	132
VK1-12	13	QQANSFPWT	33	VK3-11	13	QQRSNWPWT	133
VK1-12	14	QQANSFPYT	34	VK3-11	14	QQRSNWPYT	134
VK1-12	15	QQANSFPPFT	35	VK3-11	15	QQRSNWPPFT	135
VK1-12	16	QQANSFPPLT	36	VK3-11	16	QQRSNWPPLT	136
VK1-12	17	QQANSFPPIT	37	VK3-11	17	QQRSNWPPIT	137
VK1-12	18	QQANSFPPRT	38	VK3-11	18	QQRSNWPPRT	138
VK1-12	19	QQANSFPPWT	39	VK3-11	19	QQRSNWPPWI	139
VK1-12	20	QQANSFPPYT	40	VK3-11	20	QQRSNWPPYT	140
VK1-33	1	QQYDNLPT	41	VK3-15	1	QQYNNWPT	141
VK1-33	2	QQYDNLFT	42	VK3-15	2	QQYNNWFT	142
VK1-33	3	QQYDNLLT	43	VK3-15	3	QQYNNWLT	143
VK1-33	4	QQYDNLIT	44	VK3-15	4	QQYNNWIT	144
VK1-33	5	QQYDNLRT	45	VK3-15	5	QQYNNWRT	145
VK1-33	6	QQYDNLWT	46	VK3-15	6	QQYNNWWT	146
VK1-33	7	QQYDNLYT	47	VK3-15	7	QQYNNWYT	147
VK1-33	8	QQYDNLPPT	48	VK3-15	8	QQYNNWPPT	148
VK1-33	9	QQYDNLPFT	49	VK3-15	9	QQYNNWPFT	149
VK1-33	10	QQYDNLPLT	50	VK3-15	10	QQYNNWPLT	150
VK1-33	11	QQYDNLPIT	51	VK3-15	11	QQYNNWPIT	151
VK1-33	12	QQYDNLPRT	52	VK3-15	12	QQYNNWPRT	152
VK1-33	13	QQYDNLPWT	53	VK3-15	13	QQYNNWPWT	153
VK1-33	14	QQYDNLPYT	54	VK3-15	14	QQYNNWPYT	154
VK1-33	15	QQYDNLPPFT	55	VK3-15	15	QQYNNWPPFT	155
VK1-33	16	QQYDNLPPLT	56	VK3-15	16	QQYNNWPPLT	156
VK1-33	17	QQYDNLPPIT	57	VK3-15	17	QQYNNWPPIT	157
VK1-33	18	QQYDNLPPRT	58	VK3-15	18	QQYNNWPPRT	158
VK1-33	19	QQYDNLPPWT	59	VK3-15	19	QQYNNWPPWT	159
VK1-33	20	QQYDNLPPYT	60	VK3-15	20	QQYNNWPPYT	160
VK1-39	1	QQSYSTPT	61	VK3-20	1	QQYGSSPT	161
VK1-39	2	QQSYSTFT	62	VK3-20	2	QQYGSSFT	162
VK1-39	3	QQSYSTLT	63	VK3-20	3	QQYGSSLT	163
VK1-39	4	QQSYSTIT	64	VK3-20	4	QQYGSSIT	164

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VK1-39	5	QQSYSTRT	65	VK3-20	5	QQYGSSRT	165
VK1-39	6	QQSYSTWT	66	VK3-20	6	QQYGSSWT	166
VK1-39	7	QQSYSTYT	67	VK3-20	7	QQYGSSYT	167
VK1-39	8	QQSYSIPPT	68	VK3-20	8	QQYGSSPPT	168
VK1-39	9	QQSYSTPFT	69	VK3-20	9	QQYGSSPFT	169
VK1-39	10	QQSYSTPLT	70	VK3-20	10	QQYGSSPLT	170
VK1-39	11	QQSYSTPIT	71	VK3-20	11	QQYGSSPIT	171
VK1-39	12	QQSYSTPRT	72	VK3-20	12	QQYGSSPRT	172
VK1-39	13	QQSYSTPWT	73	VK3-20	13	QQYGSSPWT	173
VK1-39	14	QQSYSTPYT	74	VK3-20	14	QQYGSSPYT	174
VK1-39	15	QQSYSTPPFT	75	VK3-20	15	QQYGSSPPFT	175
VK1-39	16	QQSYSTPPLT	76	VK3-20	16	QQYGSSPPLT	176
VK1-39	17	QQSYSTPPIT	77	VK3-20	17	QQYGSSPPIT	177
VK1-39	18	QQSYSTPPRT	78	VK3-20	18	QQYGSSPPRT	178
VK1-39	19	QQSYSTPPWT	79	VK3-20	19	QQYGSSPPWT	179
VK1-39	20	QQSYSTPPYT	80	VK3-20	20	QQYGSSPPYT	180
VK4-01	1	QQYYSTPT	81				
VK4-01	2	QQYYSTFT	82				
VK4-01	3	QQYYSTLT	83				
VK4-01	4	QQYYSTIT	84				
VK4-01	5	QQYYSTRT	85				
VK4-01	6	QQYYSTWT	86				
VK4-01	7	QQYYSTYT	87				
VK4-01	8	QQYYSTPPT	88				
VK4-01	9	QQYYSTPFT	89				
VK4-01	10	QQYYSTPLT	90				
VK4-01	11	QQYYSTPIT	91				
VK4-01	12	QQYYSTPRT	92				
VK4-01	13	QQYYSTPWT	93				
VK4-01	14	QQYYSTPYT	94				
VK4-01	15	QQYYSTPPFT	95				
VK4-01	16	QQYYSTPPLT	96				
VK4-01	17	QQYYSTPPIT	97				
VK4-01	18	QQYYSTPPRT	98				

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VK4-01	19	QQYYSTPPWT	99				
VK4-01	20	QQYYSTPPYT	100				

Table 2. Summary of framework variants for exemplified light chain germlines.

Light Chain Germline	Number of Sequences Analyzed	Primary Framework Positions Selected for Variance	Alternative Framework Positions Selected for Variance
VK1-5	307	4, 49	46
VK1-12	113	4, 49	46, 66
VK1-33	188	4, 66	49
VK1-39	656	4, 49	46
VK2-28	275	46, 49	2, 4
VK3-11	375	4, 36	2, 49
VK3-15	202	4, 49	2, 48
VK3-20	867	4, 49	2, 48
VK4-1	368	4, 49	46, 66

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Table 3. Polypeptide sequences of exemplified light chain chassis with variability in CDRL1, CDRL2, and frameworks. The Kabat numbers for segment boundaries are indicated. Here, L1 and L2 (in the "Category" column) indicate variability in CDRL1 and CDRL2, respectively, while "F" indicates a framework variant. Sequences designated with both L1 or L2 and F contain variability in both a CDR and framework region.

Name	Chassis	Category	FRM1: 1-23	CDR1: 24-34	FRM2: 35-49	CDR2: 50-56	FRM3: 57-88	SEQ ID NOs:
VK1-39	VK1-39	Germline	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	181
VK1-39.1	VK1-39	L1	DIQMTQSPSSLSASVGDRVTITC	RASQSINSYLN	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	182
VK1-39.2	VK1-39	L1	DIQMTQSPSSLSASVGDRVTITC	RASQSIDSYLN	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	183
VK1-39.3	VK1-39	L1	DIQMTQSPSSLSASVGDRVTITC	RASQSISRYLN	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	184
VK1-39.6	VK1-39	L2	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY	GASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	185
VK1-39.7	VK1-39	L2	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY	SASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	186
VK1-39.8	VK1-39	L2	DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY	AASNLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	187

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VK1-39.10	VK1-39	F	DIQLTQSPSSLSAS VGDRVTITC	RASQSISSYL N	WYQQKPGKAPK LLIY	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	188
VK1-39.11	VK1-39	FL1	DIQLTQSPSSLSAS VGDRVTITC	RASQSINSYL N	WYQQKPGKAPK LLIY	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	189
VK1-39.12	VK1-39	FL1	DIQLTQSPSSLSAS VGDRVTITC	RASQSIDSYL N	WYQQKPGKAPK LLIY	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	190
VK1-39.15	VK1-39	FL1	DIQLTQSPSSLSAS VGDRVTITC	RASQSISSFL N	WYQQKPGKAPK LLIY	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	191
VK1-39.17	VK1-39	FL2	DIQLTQSPSSLSAS VGDRVTITC	RASQSISSYL N	WYQQKPGKAPK LLIY	SASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	192
VK1-39.18	VK1-39	FL2	DIQLTQSPSSLSAS VGDRVTITC	RASQSISSYL N	WYQQKPGKAPK LLIY	AASNLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	193
VK1-39.20	VK1-39	F	DIQMTQSPSSLSAS VGDRVTITC	RASQSISSYL N	WYQQKPGKAPK LLIS	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	194
VK1-39.23	VK1-39	FL1	DIQMTQSPSSLSAS VGDRVTITC	RASQSISRYL N	WYQQKPGKAPK LLIS	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY YC	195
VK1-39.24	VK1-39	FL1	DIQMTQSPSSLSAS VGDRVTITC	RASQSISIYL N	WYQQKPGKAPK LLIS	AASSLQS	GVPSRFSGSG SGTDFTLTIS SLQPEDFATY	196

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							YC	
VK1-39.25	VK1-39	FL1	DIQMTQSPSSLSASVGDRVTITC	RASQSISSFLN	WYQQKPGKAPKLLIS	AASSLQS	GVPSRFSGSGSGIDFTLTISSLQPEDFATYYC	197
VK1-05	VK1-05	Germline	DIQMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	198
VK1-05.1	VK1-05	L1	DIQMTQSPSTLSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	199
VK1-05.5	VK1-05	L2	DIQMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIY	EASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	200
VK1-05.6	VK1-05	L2	DIQMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIY	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	201
VK1-05.7	VK1-05	L12	DIQMTQSPSTLSASVGDRVTITC	RASQAISSWLA	WYQQKPGKAPKLLIY	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	202
VK1-05.8	VK1-05	L12	DIQMTQSPSTLSASVGDRVTITC	RASQSINSWLA	WYQQKPGKAPKLLIY	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	203
VK1-05.9	VK1-05	L12	DIQMTQSPSTLSASVGDRVTITC	RASQSIGSWLA	WYQQKPGKAPKLLIY	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATY	204

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							YC	
VK1-05.10	VK1-05	F	DIQLTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	205
VK1-05.11	VK1-05	FL1	DIQLTQSPSTLSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	206
VK1-05.12	VK1-05	FL1	DIQLTQSPSTLSASVGDRVTITC	RASQAISSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	207
VK1-05.14	VK1-05	FL1	DIQLTQSPSTLSASVGDRVTITC	RASQSIGSWLA	WYQQKPGKAPKLLIY	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	208
VK1-05.20	VK1-05	F	DIQMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIS	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	209
VK1-05.21	VK1-05	FL1	DIQMTQSPSTLSASVGDRVTITC	RASQSINSWLA	WYQQKPGKAPKLLIS	DASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	210
VK1-05.25	VK1-05	FL2	DIQLTQSPSTLSASVGDRVTITC	RASQSIGSWLA	WYQQKPGKAPKLLIY	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	211
VK1-05.26	VK1-05	FL2	DIQMTQSPSTLSASVGDRVTITC	RASQSISSWLA	WYQQKPGKAPKLLIS	KASSLES	GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC	212

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VK1-12	VK1-12	Germline	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	213
VK1-12.2	VK1-12	L1	DIQMTQSPSSVSASVGDRVTITC	RASQGIGSWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	214
VK1-12.3	VK1-12	L1	DIQMTQSPSSVSASVGDRVTITC	RASQGIDSWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	215
VK1-12.4	VK1-12	L1	DIQMTQSPSSVSASVGDRVTITC	RASQGISRWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	216
VK1-12.5	VK1-12	L2	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	GASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	217
VK1-12.6	VK1-12	L2	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	SASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	218
VK1-12.7	VK1-12	L2	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	AASNLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	219
VK1-12.10	VK1-12	F	DIQLTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	220

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VK1-12.11	VK1-12	FL1	DIQLTQSPSSVSASVGDRVTITC	RASQDISSWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	221
VK1-12.14	VK1-12	FL1	DIQLTQSPSSVSASVGDRVTITC	RASQGISRWLA	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	222
VK1-12.15	VK1-12	FL2	DIQLTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	GASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	223
VK1-12.16	VK1-12	FL2	DIQLTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	SASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	224
VK1-12.17	VK1-12	FL2	DIQLTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIY	AASNLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	225
VK1-12.20	VK1-12	F	DIQMTQSPSSVSASVGDRVTITC	RASQGISSWLA	WYQQKPGKAPKLLIS	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	226
VK1-12.21	VK1-12	FL1	DIQMTQSPSSVSASVGDRVTITC	RASQDISSWLA	WYQQKPGKAPKLLIS	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	227
VK1-12.23	VK1-12	FL1	DIQMTQSPSSVSASVGDRVTITC	RASQGIDSWLA	WYQQKPGKAPKLLIS	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	228
VK1-12.24	VK1-12	FL1	DIQMTQSPSSVSASVGDRVTITC	RASQGISRWLA	WYQQKPGKAPKLLIS	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATY	229

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							YC	
VK1-33	VK1-33	Germline	DIQMTQSPSSLSASVGDRVTITC	QASQDISNYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	230
VK1-33.1	VK1-33	L1	DIQMTQSPSSLSASVGDRVTITC	QASQDITNYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	231
VK1-33.2	VK1-33	L1	DIQMTQSPSSLSASVGDRVTITC	QASQDIANYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	232
VK1-33.8	VK1-33	L2	DIQMTQSPSSLSASVGDRVTITC	QASQDISNYLN	WYQQKPGKAPKLLIY	DASNLAT	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	233
VK1-33.10	VK1-33	F	DIQLTQSPSSLSASVGDRVTITC	QASQDISNYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	234
VK1-33.13	VK1-33	FL1	DIQLTQSPSSLSASVGDRVTITC	QASQDISNSLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	235
VK1-33.14	VK1-33	FL1	DIQLTQSPSSLSASVGDRVTITC	QASQDISNFLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	236
VK1-33.17	VK1-33	FL2	DIQLTQSPSSLSASVGDRVTITC	QASQDISNYLN	WYQQKPGKAPKLLIY	DASNLQT	GVPSRFSGSGSGTDFTFTISSLQPEDIATY	237

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							YC	
VK1-33.20	VK1-33	F	DIQMTQSPSSLSASVGDRVTITC	QASQDISNYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSRSGTDFTFTISSLQPEDIATYYC	238
VK1-33.21	VK1-33	FL1	DIQMTQSPSSLSASVGDRVTITC	QASQDITNYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSRSGTDFTFTISSLQPEDIATYYC	239
VK1-33.22	VK1-33	FL1	DIQMTQSPSSLSASVGDRVTITC	QASQDIANYLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSRSGTDFTFTISSLQPEDIATYYC	240
VK1-33.23	VK1-33	FL1	DIQMTQSPSSLSASVGDRVTITC	QASQDISNSLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSRSGTDFTFTISSLQPEDIATYYC	241
VK1-33.24	VK1-33	FL1	DIQMTQSPSSLSASVGDRVTITC	QASQDISNFLN	WYQQKPGKAPKLLIY	DASNLET	GVPSRFSGSRSGTDFTFTISSLQPEDIATYYC	242
VK2-28	VK2-28	Germline	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQLLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	243
VK2-28.1	VK2-28	L1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLYSNGYNYLD	WYLQKPGQSPQLLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	244
VK2-28.2	VK2-28	L1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHRNGYNYLD	WYLQKPGQSPQLLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVY	245

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							YC	
VK2-28.3	VK2-28	L1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHTNGYNYLD	WYLQKPGQSPQLLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	246
VK2-28.4	VK2-28	L1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGNNYLD	WYLQKPGQSPQLLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	247
VK2-28.5	VK2-28	L2	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQLLIY	LASNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	248
VK2-28.6	VK2-28	L2	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQLLIY	LGSHRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	249
VK2-28.10	VK2-28	F	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQVLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	250
VK2-28.11	VK2-28	L1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLYSNGYNYLD	WYLQKPGQSPQVLIY	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	251
VK2-28.15	VK2-28	FL2	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQVLIY	LASNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	252
VK2-28.17	VK2-28	FL2	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQVLIY	LGSSRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	253

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VK2-28.20	VK2-28	F	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQLLIF	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	254
VK2-28.24	VK2-28	FL1	DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGNNYLD	WYLQKPGQSPQLLIF	LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	255
VK3-11	VK3-11	Germline	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	256
VK3-11.2	VK3-11	L1	EIVLTQSPATLSLSPGERATLSC	RASQSVSRYLA	WYQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	257
VK3-11.3	VK3-11	L1	EIVLTQSPATLSLSPGERATLSC	RASQSVSNYLA	WYQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	258
VK3-11.4	VK3-11	L2	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DSSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	259
VK3-11.5	VK3-11	L2	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DTSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	260
VK3-11.6	VK3-11	L2	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DASKRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	261

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VK3-11.10	VK3-11	F	EIVMTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	262
VK3-11.13	VK3-11	FL1	EIVMTQSPATLSLSPGERATLSC	RASQSVSNYLA	WYQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	263
VK3-11.14	VK3-11	FL2	EIVMTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DSSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	264
VK3-11.15	VK3-11	FL2	EIVMTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DTSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	265
VK3-11.16	VK3-11	FL2	EIVMTQSPATLSLSPGERATLSC	RASQSVSSYLA	WYQQKPGQAPRLLIY	DASKRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	266
VK3-11.20	VK3-11	F	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WFQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	267
VK3-11.21	VK3-11	FL1	EIVLTQSPATLSLSPGERATLSC	RASQSISSYLA	WFQQKPGQAPRLLIY	DASNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	268
VK3-11.24	VK3-11	FL2	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WFQQKPGQAPRLLIY	DSSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	269
VK3-11.25	VK3-11	FL2	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLA	WFQQKPGQAPRLLIY	DTSNRAT	GIPARFSGSGSGTDFTLTISSLEPEDFAVY	270

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							YC	
VK3-15	VK3-15	Germline	EIVMTQSPATLSVSPGERATLSC	RASQSVSSNLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	271
VK3-15.1	VK3-15	L1	EIVMTQSPATLSVSPGERATLSC	RASQSVGSNLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	272
VK3-15.6	VK3-15	L1	EIVMTQSPATLSVSPGERATLSC	RASQSVSSSLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	273
VK3-15.7	VK3-15	L2	EIVMTQSPATLSVSPGERATLSC	RASQSVSSNLA	WYQQKPGQAPRLLIY	DASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	274
VK3-15.8	VK3-15	L2	EIVMTQSPATLSVSPGERATLSC	RASQSVSSNLA	WYQQKPGQAPRLLIY	SASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	275
VK3-15.10	VK3-15	F	EIVLTQSPATLSVSPGERATLSC	RASQSVSSNLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	276
VK3-15.11	VK3-15	FL1	EIVLTQSPATLSVSPGERATLSC	RASQSVGSNLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	277
VK3-15.14	VK3-15	FL1	EIVLTQSPATLSVSPGERATLSC	RASQSVSTNLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVY	278

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							YC	
VK3-15.16	VK3-15	FL1	EIVLTQSPATLSVSPGERATLSC	RASQSVSSDLA	WYQQKPGQAPRLLIY	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	279
VK3-15.20	VK3-15	F	EIVMTQSPATLSVSPGERATLSC	RASQSVSSNLA	WYQQKPGQAPRLLIF	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	280
VK3-15.21	VK3-15	FL1	EIVMTQSPATLSVSPGERATLSC	RASQSVGSNLA	WYQQKPGQAPRLLIF	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	281
VK3-15.25	VK3-15	FL1	EIVMTQSPATLSVSPGERATLSC	RASQSVSSDLA	WYQQKPGQAPRLLIF	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	282
VK3-15.26	VK3-15	FL1	EIVMTQSPATLSVSPGERATLSC	RASQSVSSSLA	WYQQKPGQAPRLLIF	GASTRAT	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	283
VK3-20	VK3-20	Germline	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	284
VK3-20.1	VK3-20	L1	EIVLTQSPGTLSLSPGERATLSC	RASQSVRSSYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	285
VK3-20.4	VK3-20	L1	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSDYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVY	286

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							YC	
VK3-20.7	VK3-20	L2	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASNRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	287
VK3-20.8	VK3-20	L2	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASRRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	288
VK3-20.10	VK3-20	F	EIVMTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	289
VK3-20.17	VK3-20	FL2	EIVMTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASNRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	290
VK3-20.20	VK3-20	F	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIS	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	291
VK3-20.22	VK3-20	FL1	EIVLTQSPGTLSLSPGERATLSC	RASQSVSSNYLA	WYQQKPGQAPRLLIS	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	292
VK4-01	VK4-01	Germline	DIVMTQSPDSLAVSLGERATINC	KSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	293
VK4-01.1	VK4-01	L1	DIVMTQSPDSLAVSLGERATINC	KSSQSLLYSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVY	294

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							YC	
VK4-01.2	VK4-01	L1	DIVMTQSPDSLAVSLGERATINC	KSSQSILYSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	295
VK4-01.3	VK4-01	L1	DIVMTQSPDSLAVSLGERATINC	KSSQSVLHSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	296
VK4-01.4	VK4-01	L1	DIVMTQSPDSLAVSLGERATINC	KSSQSVLFSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	297
VK4-01.5	VK4-01	L1	DIVMTQSPDSLAVSLGERATINC	KSSQSVLYTSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	298
VK4-01.7	VK4-01	L2	DIVMTQSPDSLAVSLGERATINC	KSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIY	WASSRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	299
VK4-01.10	VK4-01	F	DIVLTQSPDSLAVSLGERATINC	KSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	300
VK4-01.13	VK4-01	FL1	DIVLTQSPDSLAVSLGERATINC	KSSQSVLHSSNNKNYLA	WYQQKPGQPPKLLIY	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	301
VK4-01.17	VK4-01	FL2	DIVLTQSPDSLAVSLGERATINC	KSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIY	WASSRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	302

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VK4-01.20	VK4-01	F	DIVMTQSPDSLAVSLGERATINC	KSSQSVLYSSNNKNYLA	WYQQKPGQPPKLLIS	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	303
VK4-01.23	VK4-01	FL1	DIVMTQSPDSLAVSLGERATINC	KSSQSVLHSSNNKNYLA	WYQQKPGQPPKLLIS	WASTRES	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	304

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Table 4. Jumping dimer and trimer oligonucleotides for the VK1-39 sequences with CDRL3 length nine and F as the junctional amino acid. *i.e.*, The sequences depicted below occur between YYC and FGG, to yield: …YYC-[89-97]-FGG… . The sequences in this table encompassed by positions "[89-97]" are disclosed as SEQ ID NOS 8721-8745, respectively, in order of appearance.

Name	Oligo	SEQ ID NO	89	90	91	92	93	94	95	96	97
		Jumping Dimer									
VK1-39_1	SWMSWMAGC TACAGTACT CCTTWCACT	305	DEHLQV	DEHLQV	S	Y	S	T	P	FY	T
VK1-39_2	SWMCAAVNA TACAGTACT CCTTWCACT	306	DEHLQV	Q	AEGIKLPQR TV	Y	S	T	P	FY	T
VK1-39_3	SWMCAAAGC BHCAGTACT CCTTWCACT	307	DEHLQV	Q	S	ADFHLPS VY	S	T	P	FY	T
VK1-39_4	SWMCAAAGC TACNHCACT CCTTWCACT	308	DEHLQV	Q	S	Y	ADFHILNP STVY	T	P	FY	T
VK1-39_5	SWMCAAAGC TACAGTBHC CCTTWCACT	309	DEHLQV	Q	S	Y	S	ADFHL PSVY	P	FY	T
VK1-39_6	CAGSWMVNA TACAGTACT CCTTWCACT	310	Q	DEHLQV	AEGIKLPQR TV	Y	S	T	P	FY	T
VK1-39_7	CAGSWMAGC BHCAGTACT CCTTWCACT	311	Q	DEHLQV	S	ADFHLPS VY	S	T	P	FY	T

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VK1-39_8	CAGSWMAGC TACNHCACT CCTTWCACT	312	Q	DEHLQV	S	Y	ADFHILNP STVY	T	P	FY	T
VK1-39_9	CAGSWMAGC TACAGTBHC CCTTWCACT	313	Q	DEHLQV	S	Y	S	ADFHL PSVY	P	FY	T
VK1-39_10	CAGCAAVNA BHCAGTACT CCTTWCACT	314	Q	Q	AEGIKLPQR TV	ADFHLPS VY	S	T	P	FY	T
VK1-39_11	CAGCAAVNA TACNHCACT CCTTWCACT	315	Q	Q	AEGIKLPQR TV	Y	ADFHILNP STVY	T	P	FY	T
VK1-39_12	CAGCAAVNA TACAGTBHC CCTTWCACT	316	Q	Q	AEGIKLPQR TV	Y	S	ADFHL PSVY	P	FY	T
VK1-39_13	CAGCAAAGC BHCNHCACT CCTTWCACT	317	Q	Q	S	ADFHLPS VY	ADFHILNP STVY	T	P	FY	T
VK1-39_14	CAGCAAAGC BHCAGTBHC CCTTWCACT	318	Q	Q	S	ADFHLPS VY	S	ADFHL PSVY	P	FY	T
VK1-39_15	CAGCAAAGC TACNHCBHC CCTTWCACT	319	Q	Q	S	Y	ADFHILNP SIVY	ADFHL PSVY	P	FY	T
		Jumping Trimer									
VK1-39_10_0_9	CAGCAAVNA BHCAGTACT CCTTWCACT	314	Q	Q	AEGIKLPQR TV	ADFHLPS VY	S	T	P	FY	T

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VK1-39_11_0_9	CAGCAAVNATACNHCACTCCTTWCACT	315	Q	Q	AEGIKLPQRTV	Y	ADFHILNPSTVY	T	P	FY	T
VK1-39_12_0_9	CAGCAAVNATACAGTBHCCCTTWCACT	316	Q	Q	AEGIKLPQRTV	Y	S	ADFHLPSVY	P	FY	T
VK1-39_13_0_9	CAGCAAAGCBHCNHCACTCCTTWCACT	317	Q	Q	S	ADFHLPSVY	ADFHILNPSTVY	T	P	FY	T
VK1-39_14_0_9	CAGCAAAGCBHCAGTBHCCCTTWCACT	318	Q	Q	S	ADFHLPSVY	S	ADFHLPSVY	P	FY	T
VK1-39_15_0_9	CAGCAAAGCTACNHCBHCCCTTWCACT	319	Q	Q	S	Y	ADFHILNPSTVY	ADFHLPSVY	P	FY	T
VK1-39_t1_0_9	CAGCAAVNABHCNHCACTCCTTWCACT	320	Q	Q	AEGIKLPQRTV	ADFHLPSVY	ADFHILNPSTVY	T	P	FY	T
VK1-39_t2_0_9	CAGCAAVNABHCAGTBHCCCTTWCACT		Q	Q	AEGIKLPQRTV	ADFHLPSVY	S	ADFHLPSVY	P	FY	T
VK1-39_t3_0_9	CAGCAAVNATACNHCBHCCCTTWCACT		Q	Q	AEGIKLPQRTV	Y	ADFHILNPSTVY	ADFHLPSVY	P	FY	T
VK1-39_t4_0_9	CAGCAAAGCBHCNHCBHCCCTTWCACT		Q	Q	S	ADFHLPSVY	ADFHILNPSTVY	ADFHLPSVY	P	FY	T

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Table 5. Oligonucleotide sequences for exemplary VK jumping dimer and trimer sequences with CDRL3 length 8.

Name	Sequence of Synthesized Oligonucleotide	Portion of Oligonucleotide Corresponding to CDRL3 Proper	SEQ ID NO (Oligo)	SEQ ID NO (CDRL3 Portion)
Jumping Dimer				
VK1-05_1_0_8	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACA ATAGTTACTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACTWCACT	324	948
VK1-05_10_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTTACTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACTWCACT	325	949
VK1-05_11_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCTACTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACTWCACT	326	950
VK1-05_12_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCTWCACT	327	951
VK1-05_13_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCTACTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACTWCACT	328	952
VK1-05_14_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCTWCACT	329	953
VK1-05_15_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACA ATMBCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCTWCACT	330	954
VK1-05_2_0_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCA ATAGTTACTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACTWCACT	331	955
VK1-05_3_0_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACV RMAGTTACTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACTWCACT	332	956
VK1-05_4_0_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATMBCTACTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACTWCACT	333	957
VK1-05_5_0_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCTWCACT	334	958
VK1-05_6_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCA ATAGTTACTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACTWCACT	335	959
VK1-05_7_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACV RMAGTTACTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACTWCACT	336	960

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VK1-05_8_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATMBCTACTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACTWCACT	337	961
VK1-05_9_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCTWCACT	338	962
VK1-05_1_1_8	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACA ATAGTTACMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACMTCACT	339	963
VK1-05_10_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTTACMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACMTCACT	340	964
VK1-05_11_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCTACMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACMTCACT	341	965
VK1-05_12_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCMTCACT	342	966
VK1-05_13_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCTACMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACMTCACT	343	967
VK1-05_14_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCMTCACT	344	968
VK1-05_15_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACA ATMBCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCMTCACT	345	969
VK1-05_2_1_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCA ATAGTTACMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACMTCACT	346	970
VK1-05_3_1_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACV RMAGTTACMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACMTCACT	347	971
VK1-05_4_1_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATMBCTACMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACMTCACT	348	972
VK1-05_5_1_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCMTCACT	349	973
VK1-05_6_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCA ATAGTTACMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACMTCACT	350	974
VK1-05_7_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACV RMAGTTACMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACMTCACT	351	975
VK1-05_8_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATMBCTACMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACMTCACT	352	976
VK1-05_9_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCMTCACT	353	977

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VK1-05_1_2_8	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACA ATAGTTACWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACWGGACT	354	978
VK1-05_10_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTTACWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACWGGACT	355	979
VK1-05_11_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCTACWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACWGGACT	356	980
VK1-05_12_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCWGGACT	357	981
VK1-05_13_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCTACWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACWGGACT	358	982
VK1-05_14_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCWGGACT	359	983
VK1-05_15_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACA ATMBCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCWGGACT	360	984
VK1-05_2_2_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCA ATAGTTACWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACWGGACT	361	985
VK1-05_3_2_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACV RMAGTTACWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACWGGACT	362	986
VK1-05_4_2_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATMBCTACWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACWGGACT	363	987
VK1-05_5_2_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCWGGACT	364	988
VK1-05_6_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCA ATAGTTACWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACWGGACT	365	989
VK1-05_7_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACV RMAGTTACWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACWGGACT	366	990
VK1-05_8_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATMBCTACWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACWGGACT	367	991
VK1-05_9_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCWGGACT	368	992
VK1-05_1_3_8	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACA ATAGTTACCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACCCTACT	369	993
VK1-05_10_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTTACCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACCCTACT	370	994

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VK1-05_11_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCTACCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACCCTACT	371	995
VK1-05_12_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCCCTACT	372	996
VK1-05_13_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCTACCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACCCTACT	373	997
VK1-05_14_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCCCTACT	374	998
VK1-05_15_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACA ATMBCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCCCTACT	375	999
VK1-05_2_3_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCA ATAGTTACCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACCCTACT	376	1000
VK1-05_3_3_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACV RMAGTTACCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACCCTACT	377	1001
VK1-05_4_3_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATMBCTACCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACCCTACT	378	1002
VK1-05_5_3_8	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCCCTACT	379	1003
VK1-05_6_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCA ATAGTTACCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACCCTACT	380	1004
VK1-05_7_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACV RMAGTTACCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACCCTACT	381	1005
VK1-05_8_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATMBCTACCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACCCTACT	382	1006
VK1-05_9_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCCCTACT	383	1007
VK1-12_1_0_8	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAA ATAGTTTCTWCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCTWCACT	384	1008
VK1-12_10_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTTTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCTWCACT	385	1009
VK1-12_11_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCTTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCTWCACT	386	1010
VK1-12_12_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCTWCACT	387	1011

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VK1-12_13_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCTTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCTWCACT	388	1012
VK1-12_14_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCTWCACT	389	1013
VK1-12_15_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAA ATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCTWCACT	390	1014
VK1-12_2_0_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAA ATAGTTTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCTWCACT	391	1015
VK1-12_3_0_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAN HCAGTTTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCTWCACT	392	1016
VK1-12_4_0_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATNHCTTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCTWCACT	393	1017
VK1-12_5_0_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCTWCACT	394	1018
VK1-12_6_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAA ATAGTTTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCTWCACT	395	1019
VK1-12_7_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAN HCAGTTTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCTWCACT	396	1020
VK1-12_8_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATNHCTTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCTWCACT	397	1021
VK1-12_9_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCTWCACT	398	1022
VK1-12_1_1_8	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAA ATAGTTTCMTCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCMTCACT	399	1023
VK1-12_10_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTTTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCMTCACT	400	1024
VK1-12_11_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCTTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCMTCACT	401	1025
VK1-12_12_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCMTCACT	402	1026
VK1-12_13_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCTTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCMTCACT	403	1027
VK1-12_14_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCMTCACT	404	1028

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VK1-12_15_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCMTCACT	405	1029
VK1-12_2_1_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAGTTTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCMTCACT	406	1030
VK1-12_3_1_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCAGTTTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCMTCACT	407	1031
VK1-12_4_1_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATNHCTTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCMTCACT	408	1032
VK1-12_5_1_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCMTCACT	409	1033
VK1-12_6_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATAGTTTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCMTCACT	410	1034
VK1-12_7_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCAGTTTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCMTCACT	411	1035
VK1-12_8_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATNHCTTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCMTCACT	412	1036
VK1-12_9_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCMTCACT	413	1037
VK1-12_1_2_8	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAGTTTCWGGACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCWGGACT	414	1038
VK1-12_10_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTTTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCWGGACT	415	1039
VK1-12_11_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCTTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCWGGACT	416	1040
VK1-12_12_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCWGGACT	417	1041
VK1-12_13_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCTTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCWGGACT	418	1042
VK1-12_14_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCWGGACT	419	1043
VK1-12_15_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCWGGACT	420	1044
VK1-12_2_2_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAGTTTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCWGGACT	421	1045

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VK1-12_3_2_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAN HCAGTTTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCWGGACT	422	1046
VK1-12_4_2_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATNHCTTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCWGGACT	423	1047
VK1-12_5_2_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCWGGACT	424	1048
VK1-12_6_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAA ATAGTTTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCWGGACT	425	1049
VK1-12_7_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAN HCAGTTTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCWGGACT	426	1050
VK1-12_8_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATNHCTTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCWGGACT	427	1051
VK1-12_9_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCWGGACT	428	1052
VK1-12_1_3_8	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAA ATAGTTTCCCTACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCCTACT	429	1053
VK1-12_10_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTTTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCCTACT	430	1054
VK1-12_11_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCTTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCCTACT	431	1055
VK1-12_12_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCCTACT	432	1056
VK1-12_13_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCTTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCCTACT	433	1057
VK1-12_14_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCCTACT	434	1058
VK1-12_15_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAA ATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCCTACT	435	1059
VK1-12_2_3_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAA ATAGTTTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCCTACT	436	1060
VK1-12_3_3_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAN HCAGTTTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCCTACT	437	1061
VK1-12_4_3_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATNHCTTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCCTACT	438	1062

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VK1-12_5_3_8	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCCTACT	439	1063
VK1-12_6_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAA ATAGTTTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCCTACT	440	1064
VK1-12_7_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAN HCAGTTTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCCTACT	441	1065
VK1-12_8_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATNHCTTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCCTACT	442	1066
VK1-12_9_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAA ATAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCCTACT	443	1067
VK1-33_1_0_8	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACG ATAATCTCTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCTWCACT	444	1068
VK1-33_10_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATCTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCTWCACT	445	1069
VK1-33_11_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCCTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCTWCACT	446	1070
VK1-33_12_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCTWCACT	447	1071
VK1-33_13_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCCTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCTWCACT	448	1072
VK1-33_14_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCTWCACT	449	1073
VK1-33_15_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACG ATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCTWCACT	450	1074
VK1-33_2_0_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCG ATAATCTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCTWCACT	451	1075
VK1-33_3_0_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACN HCAATCTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCTWCACT	452	1076
VK1-33_4_0_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATNHCCTCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCTWCACT	453	1077
VK1-33_5_0_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATAATYWCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCTWCACT	454	1078
VK1-33_6_0_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCG ATAATCTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCTWCACT	455	1079

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VK1-33_7_0_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACN HCAATCTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCTWCACT	456	1080
VK1-33_8_0_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATNHCCTCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCTWCACT	457	1081
VK1-33_9_0_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCTWCACT	458	1082
VK1-33_1_1_8	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACG ATAATCTCMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCMTCACT	459	1083
VK1-33_10_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATCTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCMTCACT	460	1084
VK1-33_11_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCCTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCMTCACT	461	1085
VK1-33_12_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCMTCACT	462	1086
VK1-33_13_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCCTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCMTCACT	463	1087
VK1-33_14_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCMTCACT	464	1088
VK1-33_15_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACG ATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCMTCACT	465	1089
VK1-33_2_1_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCG ATAATCTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCMTCACT	466	1090
VK1-33_3_1_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACN HCAATCTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCMTCACT	467	1091
VK1-33_4_1_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATNHCCTCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCMTCACT	468	1092
VK1-33_5_1_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATAATYWCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCMTCACT	469	1093
VK1-33_6_1_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCG ATAATCTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCMTCACT	470	1094
VK1-33_7_1_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACN HCAATCTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCMTCACT	471	1095
VK1-33_8_1_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATNHCCTCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCMTCACT	472	1096

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VK1-33_9_1_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCMTCACT	473	1097
VK1-33_1_2_8	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACG ATAATCTCWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCWGGACT	474	1098
VK1-33_10_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATCTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCWGGACT	475	1099
VK1-33_11_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCCTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCWGGACT	476	1100
VK1-33_12_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCWGGACT	477	1101
VK1-33_13_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCCTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCWGGACT	478	1102
VK1-33_14_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCWGGACT	479	1103
VK1-33_15_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACG ATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCWGGACT	480	1104
VK1-33_2_2_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCG ATAATCTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCWGGACT	481	1105
VK1-33_3_2_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACN HCAATCTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCWGGACT	482	1106
VK1-33_4_2_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATNHCCTCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCWGGACT	483	1107
VK1-33_5_2_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATAATYWCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCWGGACT	484	1108
VK1-33_6_2_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCG ATAATCTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCWGGACT	485	1109
VK1-33_7_2_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACN HCAATCTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCWGGACT	486	1110
VK1-33_8_2_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATNHCCTCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCWGGACT	487	1111
VK1-33_9_2_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCWGGACT	488	1112
VK1-33_1_3_8	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACG ATAATCTCCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCCTACT	489	1113

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VK1-33_10_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATCTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCCTACT	490	1114
VK1-33_11_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCCTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCCTACT	491	1115
VK1-33_12_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCCTACT	492	1116
VK1-33_13_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCCTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCCTACT	493	1117
VK1-33_14_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTACT	494	1118
VK1-33_15_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACG ATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCCTACT	495	1119
VK1-33_2_3_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCG ATAATCTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCCTACT	496	1120
VK1-33_3_3_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACN HCAATCTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCCTACT	497	1121
VK1-33_4_3_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATNHCCTCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCCTACT	498	1122
VK1-33_5_3_8	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACG ATAATYWCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCCTACT	499	1123
VK1-33_6_3_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCG ATAATCTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCCTACT	500	1124
VK1-33_7_3_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACN HCAATCTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCCTACT	501	1125
VK1-33_8_3_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATNHCCTCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCCTACT	502	1126
VK1-33_9_3_8	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACG ATAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCCTACT	503	1127
VK1-39_1_0_8	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCT ACAGTACTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTTWCACT	504	1128
VK1-39_10_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTACTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTTWCACT	505	1129
VK1-39_11_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCACTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTTWCACT	506	1130

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VK1-39_12_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCTWCACT	507	1131
VK1-39_13_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCACTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTTWCACT	508	1132
VK1-39_14_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCTWCACT	509	1133
VK1-39_15_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCT ACNHCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCTWCACT	510	1134
VK1-39_2_0_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNAT ACAGTACTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTTWCACT	511	1135
VK1-39_3_0_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCB HCAGTACTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTTWCACT	512	1136
VK1-39_4_0_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACNHCACTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTTWCACT	513	1137
VK1-39_5_0_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACAGTBHCTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCTWCACT	514	1138
VK1-39_6_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNAT ACAGTACTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTTWCACT	515	1139
VK1-39_7_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCB HCAGTACTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTTWCACT	516	1140
VK1-39_8_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACNHCACTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTTWCACT	517	1141
VK1-39_9_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCTWCACT	518	1142
VK1-39_1_1_8	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCT ACAGTACTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTMTCACT	519	1143
VK1-39_10_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTACTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTMTCACT	520	1144
VK1-39_11_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCACTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTMTCACT	521	1145
VK1-39_12_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCMTCACT	522	1146
VK1-39_13_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCACTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTMTCACT	523	1147

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VK1-39_14_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCMTCACT	524	1148
VK1-39_15_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCT ACNHCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCMTCACT	525	1149
VK1-39_2_1_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNAT ACAGTACTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTMTCACT	526	1150
VK1-39_3_1_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCB HCAGTACTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTMTCACT	527	1151
VK1-39_4_1_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACNHCACTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTMTCACT	528	1152
VK1-39_5_1_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACAGTBHCMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCMTCACT	529	1153
VK1-39_6_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNAT ACAGTACTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTMTCACT	530	1154
VK1-39_7_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCB HCAGTACTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTMTCACT	531	1155
VK1-39_8_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACNHCACTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTMTCACT	532	1156
VK1-39_9_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCMTCACT	533	1157
VK1-39_1_2_8	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCT ACAGTACTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTWGGACT	534	1158
VK1-39_10_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTACTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTWGGACT	535	1159
VK1-39_11_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCACTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTWGGACT	536	1160
VK1-39_12_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCWGGACT	537	1161
VK1-39_13_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCACTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTWGGACT	538	1162
VK1-39_14_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCWGGACT	539	1163
VK1-39_15_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCT ACNHCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCWGGACT	540	1164

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VK1-39_2_2_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNAT ACAGTACTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTWGGACT	541	1165
VK1-39_3_2_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCB HCAGTACTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTWGGACT	542	1166
VK1-39_4_2_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACNHCACTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTWGGACT	543	1167
VK1-39_5_2_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACAGTBHCWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCWGGACT	544	1168
VK1-39_6_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNAT ACAGTACTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTWGGACT	545	1169
VK1-39_7_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCB HCAGTACTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTWGGACT	546	1170
VK1-39_8_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACNHCACTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTWGGACT	547	1171
VK1-39_9_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCWGGACT	548	1172
VK1-39_1_3_8	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCT ACAGTACTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCCTACT	549	1173
VK1-39_10_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTACTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCCTACT	550	1174
VK1-39_11_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCACTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCCTACT	551	1175
VK1-39_12_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCCTACT	552	1176
VK1-39_13_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCACTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCCTACT	553	1177
VK1-39_14_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCCTACT	554	1178
VK1-39_15_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCT ACNHCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCCTACT	555	1179
VK1-39_2_3_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNAT ACAGTACTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCCTACT	556	1180
VK1-39_3_3_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCB HCAGTACTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCCTACT	557	1181

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VK1-39_4_3_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACNHCACTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCCTACT	558	1182
VK1-39_5_3_8	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCT ACAGTBHCCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCCTACT	559	1183
VK1-39_6_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNAT ACAGTACTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCCTACT	560	1184
VK1-39_7_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCB HCAGTACTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCCTACT	561	1185
VK1-39_8_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACNHCACTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCCTACT	562	1186
VK1-39_9_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCT ACAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCCTACT	563	1187
VK2-28_1_0_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCAC TCCAGACTTWCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTTWCACT	564	1188
VK2-28_10_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGACTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTTWCACT	565	1189
VK2-28_11_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMACTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTTWCACT	566	1190
VK2-28_12_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCCAGVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCTWCACT	567	1191
VK2-28_13_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMACTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTTWCACT	568	1192
VK2-28_14_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NACAGVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCTWCACT	569	1193
VK2-28_15_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAC TCSRMVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCTWCACT	570	1194
VK2-28_2_0_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNAC TCCAGACTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTTWCACT	571	1195
VK2-28_3_0_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAM NACAGACTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTTWCACT	572	1196
VK2-28_4_0_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCSRMACTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTTWCACT	573	1197
VK2-28_5_0_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCCAGVBCTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCTWCACT	574	1198

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VK2-28_6_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNAC TCCAGACTIWCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTTWCACT	575	1199
VK2-28_7_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAM NACAGACTIWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTTWCACT	576	1200
VK2-28_8_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCSRMACTIWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTTWCACT	577	1201
VK2-28_9_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCCAGVBCIWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCTWCACT	578	1202
VK2-28_1_1_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCAC TCCAGACTMTCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTMTCACT	579	1203
VK2-28_10_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGACTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTMTCACT	580	1204
VK2-28_11_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMACTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTMTCACT	581	1205
VK2-28_12_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCCAGVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCMTCACT	582	1206
VK2-28_13_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMACTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTMTCACT	583	1207
VK2-28_14_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NACAGVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCMTCACT	584	1208
VK2-28_15_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAC TCSRMVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCMTCACT	585	1209
VK2-28_2_1_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNAC TCCAGACTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTMTCACT	586	1210
VK2-28_3_1_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAM NACAGACTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTMTCACT	587	1211
VK2-28_4_1_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCSRMACTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTMTCACT	588	1212
VK2-28_5_1_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCCAGVBCMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCMTCACT	589	1213
VK2-28_6_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNAC TCCAGACTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTMTCACT	590	1214
VK2-28_7_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAM NACAGACTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTMTCACT	591	1215

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VK2-28_8_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCSRMACTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTMTCACT	592	1216
VK2-28_9_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCCAGVBCMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCMTCACT	593	1217
VK2-28_1_2_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCAC TCCAGACTWGGACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTWGGACT	594	1218
VK2-28_10_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGACTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTWGGACT	595	1219
VK2-28_11_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMACTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTWGGACT	596	1220
VK2-28_12_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCCAGVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCWGGACT	597	1221
VK2-28_13_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMACTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTWGGACT	598	1222
VK2-28_14_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NACAGVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCWGGACT	599	1223
VK2-28_15_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAC TCSRMVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCWGGACT	600	1224
VK2-28_2_2_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNAC TCCAGACTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTWGGACT	601	1225
VK2-28_3_2_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAM NACAGACTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTWGGACT	602	1226
VK2-28_4_2_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCSRMACTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTWGGACT	603	1227
VK2-28_5_2_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCCAGVBCWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCWGGACT	604	1228
VK2-28_6_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNAC TCCAGACTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTWGGACT	605	1229
VK2-28_7_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAM NACAGACTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTWGGACT	606	1230
VK2-28_8_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCSRMACTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTWGGACT	607	1231
VK2-28_9_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCCAGVBCWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCWGGACT	608	1232

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VK2-28_1_3_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCAC TCCAGACTCCTACTTTTGGCGGAGGGACCAAG	DISSWMGCACTCCAGACTCCTACT	609	1233
VK2-28_10_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGACTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCCTACT	610	1234
VK2-28_11_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMACTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCCTACT	611	1235
VK2-28_12_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCCAGVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCCTACT	612	1236
VK2-28_13_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMACTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCCTACT	613	1237
VK2-28_14_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NACAGVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCCTACT	614	1238
VK2-28_15_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAC TCSRMVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCCTACT	615	1239
VK2-28_2_3_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNAC TCCAGACTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCCTACT	616	1240
VK2-28_3_3_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAM NACAGACTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCCTACT	617	1241
VK2-28_4_3_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCSRMACTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCCTACT	618	1242
VK2-28_5_3_8	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAC TCCAGVBCCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCCTACT	619	1243
VK2-28_6_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNAC TCCAGACTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCCTACT	620	1244
VK2-28_7_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAM NACAGACTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCCTACT	621	1245
VK2-28_8_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCSRMACTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCCTACT	622	1246
VK2-28_9_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAC TCCAGVBCCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCCTACT	623	1247
VK3-11_1_0_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAA GTAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGTWCACT	624	1248
VK3-11_10_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGTWCACT	625	1249

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VK3-11_11_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGTWCACT	626	1250
VK3-11_12_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCTWCACT	627	1251
VK3-11_13_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGTWCACT	628	1252
VK3-11_14_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCTWCACT	629	1253
VK3-11_15_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAA GTNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCTWCACT	630	1254
VK3-11_2_0_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA GTAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGTWCACT	631	1255
VK3-11_3_0_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAN HCAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGTWCACT	632	1256
VK3-11_4_0_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTNHCTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGTWCACT	633	1257
VK3-11_5_0_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTAATYWCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCTWCACT	634	1258
VK3-11_6_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA GTAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGTWCACT	635	1259
VK3-11_7_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAN HCAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGTWCACT	636	1260
VK3-11_8_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGTWCACT	637	1261
VK3-11_9_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCTWCACT	638	1262
VK3-11_1_1_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAA GTAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGMTCACT	639	1263
VK3-11_10_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGMTCACT	640	1264
VK3-11_11_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGMTCACT	641	1265
VK3-11_12_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCMTCACT	642	1266

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VK3-11_13_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGMTCACT	643	1267
VK3-11_14_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCMTCACT	644	1268
VK3-11_15_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAA GTNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCMTCACT	645	1269
VK3-11_2_1_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA GTAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGMTCACT	646	1270
VK3-11_3_1_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAN HCAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGMTCACT	647	1271
VK3-11_4_1_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTNHCTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGMTCACT	648	1272
VK3-11_5_1_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTAATYWCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCMTCACT	649	1273
VK3-11_6_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA GTAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGMTCACT	650	1274
VK3-11_7_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAN HCAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGMTCACT	651	1275
VK3-11_8_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGMTCACT	652	1276
VK3-11_9_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCMTCACT	653	1277
VK3-11_1_2_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAA GTAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGWGGACT	654	1278
VK3-11_10_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGWGGACT	655	1279
VK3-11_11_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGWGGACT	656	1280
VK3-11_12_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCWGGACT	657	1281
VK3-11_13_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGWGGACT	658	1282
VK3-11_14_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCWGGACT	659	1283

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VK3-11_15_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAA GTNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCWGGACT	660	1284
VK3-11_2_2_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA GTAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGWGGACT	661	1285
VK3-11_3_2_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAN HCAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGWGGACT	662	1286
VK3-11_4_2_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTNHCTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGWGGACT	663	1287
VK3-11_5_2_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTAATYWCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCWGGACT	664	1288
VK3-11_6_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA GTAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGWGGACT	665	1289
VK3-11_7_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAN HCAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGWGGACT	666	1290
VK3-11_8_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGWGGACT	667	1291
VK3-11_9_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCWGGACT	668	1292
VK3-11_1_3_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAA GTAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCCTACT	669	1293
VK3-11_10_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTACT	670	1294
VK3-11_11_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCCTACT	671	1295
VK3-11_12_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCCTACT	672	1296
VK3-11_13_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCCTACT	673	1297
VK3-11_14_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCCTACT	674	1298
VK3-11_15_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAA GTNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCCTACT	675	1299
VK3-11_2_3_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA GTAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCCTACT	676	1300

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VK3-11_3_3_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAN HCAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCCTACT	677	1301
VK3-11_4_3_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTNHCTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCCTACT	678	1302
VK3-11_5_3_8	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAA GTAATYWCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCCTACT	679	1303
VK3-11_6_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA GTAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCCTACT	680	1304
VK3-11_7_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAN HCAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCCTACT	681	1305
VK3-11_8_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCCTACT	682	1306
VK3-11_9_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAA GTAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCCTACT	683	1307
VK3-15_1_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMT ACAATAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGTWCACT	684	1308
VK3-15_10_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGTWCACT	685	1249
VK3-15_11_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGTWCACT	686	1309
VK3-15_12_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCTWCACT	687	1310
VK3-15_13_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGTWCACT	688	1311
VK3-15_14_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCTWCACT	689	1073
VK3-15_15_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACAATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCTWCACT	690	1312
VK3-15_2_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGB HCAATAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGTWCACT	691	1313
VK3-15_3_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACNHCAATTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGTWCACT	692	1314
VK3-15_4_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATNHCTGGTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGTWCACT	693	1315

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VK3-15_5_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATAATYWCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCTWCACT	694	1316
VK3-15_6_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMB HCAATAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGTWCACT	695	1317
VK3-15_7_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACNHCAATTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGTWCACT	696	1318
VK3-15_8_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGTWCACT	697	1319
VK3-15_9_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCTWCACT	698	1320
VK3-15_1_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMT ACAATAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGMTCACT	699	1321
VK3-15_10_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGMTCACT	700	1264
VK3-15_11_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGMTCACT	701	1322
VK3-15_12_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCMTCACT	702	1323
VK3-15_13_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGMTCACT	703	1324
VK3-15_14_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCMTCACT	704	1088
VK3-15_15_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACAATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCMTCACT	705	1325
VK3-15_2_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGB HCAATAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGMTCACT	706	1326
VK3-15_3_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACNHCAATTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGMTCACT	707	1327
VK3-15_4_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATNHCTGGMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGMTCACT	708	1328
VK3-15_5_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATAATYWCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCMTCACT	709	1329
VK3-15_6_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMB HCAATAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGMTCACT	710	1330

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VK3-15_7_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACNHCAATTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGMTCACT	711	1331
VK3-15_8_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGMTCACT	712	1332
VK3-15_9_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCMTCACT	713	1333
VK3-15_1_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMT ACAATAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGWGGACT	714	1334
VK3-15_10_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGWGGACT	715	1279
VK3-15_11_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGWGGACT	716	1335
VK3-15_12_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCWGGACT	717	1336
VK3-15_13_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGWGGACT	718	1337
VK3-15_14_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCWGGACT	719	1103
VK3-15_15_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACAATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCWGGACT	720	1338
VK3-15_2_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGB HCAATAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGWGGACT	721	1339
VK3-15_3_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACNHCAATTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGWGGACT	722	1340
VK3-15_4_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATNHCTGGWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGWGGACT	723	1341
VK3-15_5_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATAATYWCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCWGGACT	724	1342
VK3-15_6_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMB HCAATAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGWGGACT	725	1343
VK3-15_7_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACNHCAATTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGWGGACT	726	1344
VK3-15_8_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGWGGACT	727	1345

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VK3-15_9_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCWGGACT	728	1346
VK3-15_1_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMT ACAATAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCCTACT	729	1347
VK3-15_10_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTACT	730	1294
VK3-15_11_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCCTACT	731	1348
VK3-15_12_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCCTACT	732	1349
VK3-15_13_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCCTACT	733	1350
VK3-15_14_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTACT	734	1118
VK3-15_15_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACAATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCCTACT	735	1351
VK3-15_2_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGB HCAATAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCCTACT	736	1352
VK3-15_3_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACNHCAATTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCCTACT	737	1353
VK3-15_4_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATNHCTGGCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCCTACT	738	1354
VK3-15_5_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGT ACAATAATYWCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCCTACT	739	1355
VK3-15_6_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMB HCAATAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCCTACT	740	1356
VK3-15_7_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACNHCAATTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCCTACT	741	1357
VK3-15_8_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCCTACT	742	1358
VK3-15_9_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMT ACAATAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCCTACT	743	1359
VK3-20_1_0_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACG GAAGTAGTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTTWCACT	744	1360

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VK3-20_10_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTAGTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTTWCACT	745	1361
VK3-20_11_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCAGTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTTWCACT	746	1362
VK3-20_12_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCTWCACT	747	1363
VK3-20_13_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCAGTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTTWCACT	748	1364
VK3-20_14_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCTWCACT	749	1365
VK3-20_15_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACG GAVNCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCTWCACT	750	1366
VK3-20_2_0_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCG GAAGTAGTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTTWCACT	751	1367
VK3-20_3_0_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACB HCAGTAGTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTTWCACT	752	1368
VK3-20_4_0_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAVNCAGTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTTWCACT	753	1369
VK3-20_5_0_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAAGTBHCTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCTWCACT	754	1370
VK3-20_6_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCG GAAGTAGTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTTWCACT	755	1371
VK3-20_7_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACB HCAGTAGTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTTWCACT	756	1372
VK3-20_8_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAVNCAGTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTTWCACT	757	1373
VK3-20_9_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCTWCACT	758	1374
VK3-20_1_1_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACG GAAGTAGTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTMTCACT	759	1375
VK3-20_10_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTAGTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTMTCACT	760	1376
VK3-20_11_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCAGTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTMTCACT	761	1377

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VK3-20_12_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCMTCACT	762	1378
VK3-20_13_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCAGTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTMTCACT	763	1379
VK3-20_14_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCMTCACT	764	1380
VK3-20_15_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVNCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCMTCACT	765	1381
VK3-20_2_1_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAGTAGTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTMTCACT	766	1382
VK3-20_3_1_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAGTAGTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTMTCACT	767	1383
VK3-20_4_1_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVNCAGTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTMTCACT	768	1384
VK3-20_5_1_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAGTBHCMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCMTCACT	769	1385
VK3-20_6_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAGTAGTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTMTCACT	770	1386
VK3-20_7_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAGTAGTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTMTCACT	771	1387
VK3-20_8_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVNCAGTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTMTCACT	772	1388
VK3-20_9_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCMTCACT	773	1389
VK3-20_1_2_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAGTAGTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTWGGACT	774	1390
VK3-20_10_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTAGTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTWGGACT	775	1391
VK3-20_11_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCAGTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTWGGACT	776	1392
VK3-20_12_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCWGGACT	777	1393
VK3-20_13_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCAGTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTWGGACT	778	1394

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VK3-20_14_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCWGGACT	779	1395
VK3-20_15_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACG GAVNCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCWGGACT	780	1396
VK3-20_2_2_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCG GAAGTAGTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTWGGACT	781	1397
VK3-20_3_2_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACB HCAGTAGTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTWGGACT	782	1398
VK3-20_4_2_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAVNCAGTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTWGGACT	783	1399
VK3-20_5_2_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAAGTBHCWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCWGGACT	784	1400
VK3-20_6_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCG GAAGTAGTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTWGGACT	785	1401
VK3-20_7_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACB HCAGTAGTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTWGGACT	786	1402
VK3-20_8_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAVNCAGTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTWGGACT	787	1403
VK3-20_9_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCWGGACT	788	1404
VK3-20_1_3_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACG GAAGTAGTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCCTACT	789	1405
VK3-20_10_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTAGTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCCTACT	790	1406
VK3-20_11_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCAGTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCCTACT	791	1407
VK3-20_12_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCCTACT	792	1408
VK3-20_13_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCAGTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCCTACT	793	1409
VK3-20_14_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCCTACT	794	1410
VK3-20_15_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACG GAVNCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCCTACT	795	1411

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VK3-20_2_3_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCG GAAGTAGTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCCTACT	796	1412
VK3-20_3_3_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACB HCAGTAGTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCCTACT	797	1413
VK3-20_4_3_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAVNCAGTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCCTACT	798	1414
VK3-20_5_3_8	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACG GAAGTBHCCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCCTACT	799	1415
VK3-20_6_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCG GAAGTAGTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCCTACT	800	1416
VK3-20_7_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACB HCAGTAGTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCCTACT	801	1417
VK3-20_8_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAVNCAGTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCCTACT	802	1418
VK3-20_9_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACG GAAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCCTACT	803	1419
Jumping Trimer				
VK1-05_t1_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMMBCTACTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACTWCACT	804	1420
VK1-05_t1_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMMBCTACMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACMTCACT	805	1421
VK1-05_t1_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMMBCTACWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACWGGACT	806	1422
VK1-05_t1_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMMBCTACYCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTACT	807	1423
VK1-05_t2_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCTWCACT	808	1424
VK1-05_t2_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCMTCACT	809	1425
VK1-05_t2_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCWGGACT	810	1426
VK1-05_t2_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCA ATMBCYWCYCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTACT	811	1427

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VK1-05_t3_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCTWCACT	812	1428
VK1-05_t3_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCMTCACT	813	1429
VK1-05_t3_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCWGGACT	814	1430
VK1-05_t3_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCV RMAGTYWCYCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTACT	815	1431
VK1-05_t4_0_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCTWCACT	816	1432
VK1-05_t4_1_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCMTCACT	817	1433
VK1-05_t4_2_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCWGGACT	818	1434
VK1-05_t4_3_8	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACV RMMBCYWCYCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTACT	819	1435
VK1-12_t1_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCNHCTTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCTWCACT	820	1436
VK1-12_t1_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCNHCTTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCMTCACT	821	1437
VK1-12_t1_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCNHCTTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCWGGACT	822	1438
VK1-12_t1_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCNHCTTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTACT	823	1439
VK1-12_t2_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCTWCACT	824	1440
VK1-12_t2_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCMTCACT	825	1441
VK1-12_t2_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCWGGACT	826	1442
VK1-12_t2_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAN HCAGTYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTACT	827	1443
VK1-12_t3_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCTWCACT	828	1444

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VK1-12_t3_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCMTCACT	829	1445
VK1-12_t3_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCWGGACT	830	1446
VK1-12_t3_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAA ATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTACT	831	1447
VK1-12_t4_0_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCTWCACT	832	1448
VK1-12_t4_1_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCMTCACT	833	1449
VK1-12_t4_2_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCWGGACT	834	1450
VK1-12_t4_3_8	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAN HCNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTACT	835	1451
VK1-33_t1_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCNHCCTCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCTWCACT	836	1452
VK1-33_t1_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCNHCCTCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCMTCACT	837	1453
VK1-33_t1_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCNHCCTCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCWGGACT	838	1454
VK1-33_t1_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCNHCCTCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTACT	839	1455
VK1-33_t2_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCTWCACT	840	1456
VK1-33_t2_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCMTCACT	841	1457
VK1-33_t2_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCWGGACT	842	1458
VK1-33_t2_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCN HCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTACT	843	1459
VK1-33_t3_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCTWCACT	844	1460
VK1-33_t3_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCMTCACT	845	1461

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VK1-33_t3_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCWGGACT	846	1462
VK1-33_t3_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCG ATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTACT	847	1463
VK1-33_t4_0_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCTWCACT	848	1464
VK1-33_t4_1_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCMTCACT	849	1465
VK1-33_t4_2_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCWGGACT	850	1466
VK1-33_t4_3_8	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACN HCNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTACT	851	1467
VK1-39_t1_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCNHCACTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTTWCACT	852	1468
VK1-39_t1_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCNHCACTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTMTCACT	853	1469
VK1-39_t1_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCNHCACTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTWGGACT	854	1470
VK1-39_t1_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCNHCACTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTACT	855	1471
VK1-39_t2_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCTWCACT	856	1472
VK1-39_t2_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCMTCACT	857	1473
VK1-39_t2_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCWGGACT	858	1474
VK1-39_t2_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAB HCAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTACT	859	1475
VK1-39_t3_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCTWCACT	860	1476
VK1-39_t3_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCMTCACT	861	1477
VK1-39_t3_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCWGGACT	862	1478

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VK1-39_t3_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNAT ACNHCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTACT	863	1479
VK1-39_t4_0_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCTWCACT	864	1480
VK1-39_t4_1_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCMTCACT	865	1481
VK1-39_t4_2_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCWGGACT	866	1482
VK1-39_t4_3_8	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCB HCNHCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTACT	867	1483
VK2-28_t1_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NASRMACTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTTWCACT	868	1484
VK2-28_t1_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NASRMACTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTMTCACT	869	1485
VK2-28_t1_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NASRMACTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTWGGACT	870	1486
VK2-28_t1_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NASRMACTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTACT	871	1487
VK2-28_t2_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCTWCACT	872	1488
VK2-28_t2_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCMTCACT	873	1489
VK2-28_t2_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCWGGACT	874	1490
VK2-28_t2_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAM NACAGVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTACT	875	1491
VK2-28_t3_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCTWCACT	876	1492
VK2-28_t3_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCMTCACT	877	1493
VK2-28_t3_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCWGGACT	878	1494
VK2-28_t3_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAC TCSRMVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTACT	879	1495

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VK2-28_t4_0_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMVBCTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCTWCACT	880	1496
VK2-28_t4_1_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMVBCMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCMTCACT	881	1497
VK2-28_t4_2_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMVBCWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCWGGACT	882	1498
VK2-28_t4_3_8	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAM NASRMVBCCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTACT	883	1499
VK3-11_t1_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGTWCACT	884	1500
VK3-11_t1_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGMTCACT	885	1501
VK3-11_t1_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGWGGACT	886	1502
VK3-11_t1_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTACT	887	1503
VK3-11_t2_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCTWCACT	888	1456
VK3-11_t2_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCMTCACT	889	1457
VK3-11_t2_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCWGGACT	890	1458
VK3-11_t2_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTACT	891	1459
VK3-11_t3_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCTWCACT	892	1504
VK3-11_t3_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCMTCACT	893	1505
VK3-11_t3_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCWGGACT	894	1506
VK3-11_t3_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA GTNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTACT	895	1507
VK3-11_t4_0_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCTWCACT	896	1508

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VK3-11_t4_1_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCMTCACT	897	1509
VK3-11_t4_2_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCWGGACT	898	1510
VK3-11_t4_3_8	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAN HCNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTACT	899	1511
VK3-15_t1_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCNHCTGGTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGTWCACT	900	1500
VK3-15_t1_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCNHCTGGMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGMTCACT	901	1501
VK3-15_t1_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCNHCTGGWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGWGGACT	902	1502
VK3-15_t1_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCNHCTGGCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTACT	903	1503
VK3-15_t2_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCTWCACT	904	1456
VK3-15_t2_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCMTCACT	905	1457
VK3-15_t2_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCWGGACT	906	1458
VK3-15_t2_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCNHCAATYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTACT	907	1459
VK3-15_t3_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCTWCACT	908	1512
VK3-15_t3_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCMTCACT	909	1513
VK3-15_t3_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCWGGACT	910	1514
VK3-15_t3_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGB HCAATNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTACT	911	1515
VK3-15_t4_0_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCYWCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCTWCACT	912	1464
VK3-15_t4_1_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCYWCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCMTCACT	913	1465

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VK3-15_t4_2_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCYWCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCWGGACT	914	1466
VK3-15_t4_3_8	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ACNHCNHCYWCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTACT	915	1467
VK3-20_t1_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCVNCAGTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTTWCACT	916	1516
VK3-20_t1_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCVNCAGTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTMTCACT	917	1517
VK3-20_t1_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCVNCAGTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTWGGACT	918	1518
VK3-20_t1_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCVNCAGTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTACT	919	1519
VK3-20_t2_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCTWCACT	920	1520
VK3-20_t2_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCMTCACT	921	1521
VK3-20_t2_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCWGGACT	922	1522
VK3-20_t2_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCB HCAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTACT	923	1523
VK3-20_t3_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCTWCACT	924	1524
VK3-20_t3_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCMTCACT	925	1525
VK3-20_t3_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCWGGACT	926	1526
VK3-20_t3_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCG GAVNCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTACT	927	1527
VK3-20_t4_0_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCTWCACT	928	1528
VK3-20_t4_1_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCMTCACT	929	1529
VK3-20_t4_2_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCWGGACT	930	1530

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VK3-20_t4_3_8	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACB HCVNCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTACT	931	1531
VK4-01_t1_0_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCNHCACTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTTWCACT	932	1532
VK4-01_t1_1_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCNHCACTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTMTCACT	933	1533
VK4-01_t1_2_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCNHCACTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTWGGACT	934	1534
VK4-01_t1_3_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCNHCACTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTACT	935	1535
VK4-01_t2_0_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCAGTBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCTWCACT	936	1520
VK4-01_t2_1_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCAGTBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCMTCACT	937	1521
VK4-01_t2_2_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCAGTBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCWGGACT	938	1522
VK4-01_t2_3_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCB HCAGTBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTACT	939	1523
VK4-01_t3_0_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCT ACNHCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCTWCACT	940	1536
VK4-01_t3_1_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCT ACNHCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCMTCACT	941	1537
VK4-01_t3_2_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCT ACNHCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCWGGACT	942	1538
VK4-01_t3_3_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCT ACNHCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTACT	943	1539
VK4-01_t4_0_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACB HCNHCBHCTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCTWCACT	944	1540
VK4-01_t4_1_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACB HCNHCBHCMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCMTCACT	945	1541
VK4-01_t4_2_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACB HCNHCBHCWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCWGGACT	946	1542
VK4-01_t4_3_8	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACB HCNHCBHCCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTACT	947	1543

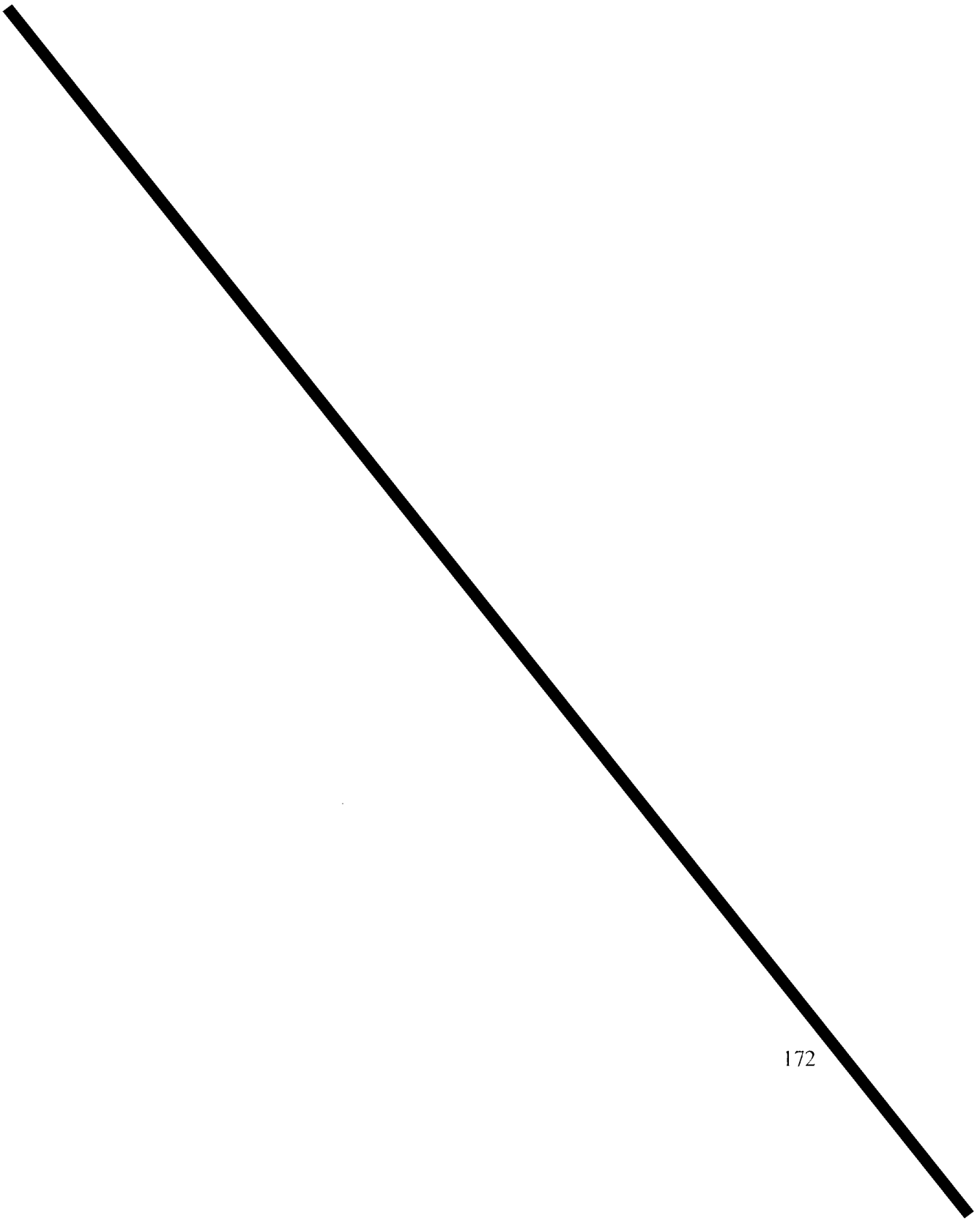

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Table 6. Oligonucleotide sequences for exemplary VK jumping dimer and trimer sequences with CDRL3 length 9.

Name	Sequence of Synthesized Oligonucleotide	Portion of Oligonucleotide Corresponding to CDRL3 Proper	SEQ ID NO (Oligo)	SEQ ID NO (CDRL3 Portion)
Jumping Dimer				
VK1-05_1_0_9	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYCTT WCACT	1544	2168
VK1-05_10_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYCTT WCACT	1545	2169
VK1-05_11_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATM BCTACYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYCTT WCACT	1546	2170
VK1-05_12_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATA GTYWCYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYCTT WCACT	1547	2171
VK1-05_13_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMM BCTACYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYCTT WCACT	1548	2172
VK1-05_14_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMA GTYWCYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYCTT WCACT	1549	2173
VK1-05_15_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATM BCYWCYCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYCTT WCACT	1550	2174
VK1-05_2_0_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYCTT WCACT	1551	2175
VK1-05_3_0_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYCTT WCACT	1552	2176
VK1-05_4_0_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATM BCTACYCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYCTT WCACT	1553	2177
VK1-05_5_0_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATA GTYWCYCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYCTT WCACT	1554	2178
VK1-05_6_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYCTT WCACT	1555	2179
VK1-05_7_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMA GTTACYCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYCTT WCACT	1556	2180

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VK1-05_8_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATM BCTACYCTIWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYCTT WCACT	1557	2181
VK1-05_9_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATA GTYWCYCTIWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYCTT WCACT	1558	2182
VK1-05_1_1_9	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYCTM TCACT	1559	2183
VK1-05_10_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYCTM TCACT	1560	2184
VK1-05_11_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATM BCTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYCTM TCACT	1561	2185
VK1-05_12_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATA GTYWCYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYCTM TCACT	1562	2186
VK1-05_13_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMM BCTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYCTM TCACT	1563	2187
VK1-05_14_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMA GTYWCYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYCTM TCACT	1564	2188
VK1-05_15_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATM BCYWCYCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYCTM TCACT	1565	2189
VK1-05_2_1_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYCTM TCACT	1566	2190
VK1-05_3_1_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYCTM TCACT	1567	2191
VK1-05_4_1_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATM BCTACYCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYCTM TCACT	1568	2192
VK1-05_5_1_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATA GTYWCYCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYCTM TCACT	1569	2193
VK1-05_6_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYCTM TCACT	1570	2194
VK1-05_7_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMA GTTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYCTM TCACT	1571	2195
VK1-05_8_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATM BCTACYCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYCTM TCACT	1572	2196
VK1-05_9_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATA GTYWCYCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYCTM TCACT	1573	2197

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VK1-05_1_2_9	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYCTW GGACT	1574	2198
VK1-05_10_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYCTW GGACT	1575	2199
VK1-05_11_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATM BCTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYCTW GGACT	1576	2200
VK1-05_12_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATA GTYWCYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYCTW GGACT	1577	2201
VK1-05_13_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMM BCTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYCTW GGACT	1578	2202
VK1-05_14_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMA GTYWCYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYCTW GGACT	1579	2203
VK1-05_15_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATM BCYWCYCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYCTW GGACT	1580	2204
VK1-05_2_2_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYCTW GGACT	1581	2205
VK1-05_3_2_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYCTW GGACT	1582	2206
VK1-05_4_2_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATM BCTACYCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYCTW GGACT	1583	2207
VK1-05_5_2_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATA GTYWCYCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYCTW GGACT	1584	2208
VK1-05_6_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYCTW GGACT	1585	2209
VK1-05_7_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMA GTTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYCTW GGACT	1586	2210
VK1-05_8_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATM BCTACYCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYCTW GGACT	1587	2211
VK1-05_9_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATA GTYWCYCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYCTW GGACT	1588	2212
VK1-05_1_3_9	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATA GTTACYCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYCTC CTACT	1589	2213
VK1-05_10_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMA GTTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYCTC CTACT	1590	2214

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VK1-05_11_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYCTCCTACT	1591	2215
VK1-05_12_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATAGTYWCYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYCTCCTACT	1592	2216
VK1-05_13_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYCTCCTACT	1593	2217
VK1-05_14_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMAGTYWCYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYCTCCTACT	1594	2218
VK1-05_15_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATMBCYWCYCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYCTCCTACT	1595	2219
VK1-05_2_3_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATAGTTACYCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYCTCCTACT	1596	2220
VK1-05_3_3_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMAGTTACYCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYCTCCTACT	1597	2221
VK1-05_4_3_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATMBCTACYCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYCTCCTACT	1598	2222
VK1-05_5_3_9	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATAGTYWCYCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYCTCCTACT	1599	2223
VK1-05_6_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATAGTTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYCTCCTACT	1600	2224
VK1-05_7_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMAGTTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYCTCCTACT	1601	2225
VK1-05_8_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATMBCTACYCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYCTCCTACT	1602	2226
VK1-05_9_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATAGTYWCYCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYCTCCTACT	1603	2227
VK1-12_1_0_9	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCCTTWCACT	1604	2228
VK1-12_10_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCCTTWCACT	1605	2229
VK1-12_11_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCTTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCCTTWCACT	1606	2230
VK1-12_12_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAGTYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCCTTWCACT	1607	2231

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VK1-12_13_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCTTCCCTTWCACT	CAGCAGGCANHCNHCTTCCCTTWCACT	1608	2232
VK1-12_14_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAGTYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCCTTWCACT	1609	2233
VK1-12_15_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNHCYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCCTTWCACT	1610	2234
VK1-12_2_0_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCCTTWCACT	1611	2235
VK1-12_3_0_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCCTTWCACT	1612	2236
VK1-12_4_0_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATNHCTTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCCTTWCACT	1613	2237
VK1-12_5_0_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATAGTYWCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCCTTWCACT	1614	2238
VK1-12_6_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCCTTWCACT	1615	2239
VK1-12_7_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCAGTTTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCCTTWCACT	1616	2240
VK1-12_8_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATNHCTTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCCTTWCACT	1617	2241
VK1-12_9_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATAGTYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCCTTWCACT	1618	2242
VK1-12_1_1_9	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAGTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCCTMTCACT	1619	2243
VK1-12_10_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCCTMTCACT	1620	2244
VK1-12_11_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCCTMTCACT	1621	2245
VK1-12_12_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAGTYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCCTMTCACT	1622	2246
VK1-12_13_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCCTMTCACT	1623	2247
VK1-12_14_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAGTYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCCTMTCACT	1624	2248

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VK1-12_15_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATN HCYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCCTM TCACT	1625	2249
VK1-12_2_1_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATA GTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCCTM TCACT	1626	2250
VK1-12_3_1_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCA GTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCCTM TCACT	1627	2251
VK1-12_4_1_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATN HCTTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCCTM TCACT	1628	2252
VK1-12_5_1_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATA GTYWCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCCTM TCACT	1629	2253
VK1-12_6_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATA GTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCCTM TCACT	1630	2254
VK1-12_7_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCA GTTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCCTM TCACT	1631	2255
VK1-12_8_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATN HCTTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCCTM TCACT	1632	2256
VK1-12_9_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATA GTYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCCTM TCACT	1633	2257
VK1-12_1_2_9	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCCTW GGACT	1634	2258
VK1-12_10_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCCTW GGACT	1635	2259
VK1-12_11_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATN HCTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCCTW GGACT	1636	2260
VK1-12_12_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATA GTYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCCTW GGACT	1637	2261
VK1-12_13_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCN HCTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCCTW GGACT	1638	2262
VK1-12_14_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCA GTYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCCTW GGACT	1639	2263
VK1-12_15_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATN HCYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCCTW GGACT	1640	2264
VK1-12_2_2_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCCTW GGACT	1641	2265

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VK1-12_3_2_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCCTW GGACT	1642	2266
VK1-12_4_2_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATN HCTTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCCTW GGACT	1643	2267
VK1-12_5_2_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATA GTYWCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCCTW GGACT	1644	2268
VK1-12_6_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCCTW GGACT	1645	2269
VK1-12_7_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCA GTTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCCTW GGACT	1646	2270
VK1-12_8_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATN HCTTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCCTW GGACT	1647	2271
VK1-12_9_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATA GTYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCCTW GGACT	1648	2272
VK1-12_1_3_9	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCCTC CTACT	1649	2273
VK1-12_10_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCCTC CTACT	1650	2274
VK1-12_11_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATN HCTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCCTC CTACT	1651	2275
VK1-12_12_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATA GTYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCCTC CTACT	1652	2276
VK1-12_13_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCN HCTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCCTC CTACT	1653	2277
VK1-12_14_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCA GTYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCCTC CTACT	1654	2278
VK1-12_15_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATN HCYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCCTC CTACT	1655	2279
VK1-12_2_3_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCCTC CTACT	1656	2280
VK1-12_3_3_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCCTC CTACT	1657	2281
VK1-12_4_3_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATN HCTTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCCTC CTACT	1658	2282

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VK1-12_5_3_9	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATA GTYWCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCCTC CTACT	1659	2283
VK1-12_6_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCCTC CTACT	1660	2284
VK1-12_7_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCA GTTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCCTC CTACT	1661	2285
VK1-12_8_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATN HCTTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCCTC CTACT	1662	2286
VK1-12_9_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATA GTYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCCTC CTACT	1663	2287
VK1-33_1_0_9	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCCTT WCACT	1664	2288
VK1-33_10_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCCTT WCACT	1665	2289
VK1-33_11_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATN HCCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCCTT WCACT	1666	2290
VK1-33_12_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATA ATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCCTT WCACT	1667	2291
VK1-33_13_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCN HCCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCCTT WCACT	1668	2292
VK1-33_14_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCA ATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTT WCACT	1669	2293
VK1-33_15_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATN HCYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCCTT WCACT	1670	2294
VK1-33_2_0_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCCTT WCACT	1671	2295
VK1-33_3_0_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCCTT WCACT	1672	2296
VK1-33_4_0_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATN HCCTCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCCTT WCACT	1673	2297
VK1-33_5_0_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATA ATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCCTT WCACT	1674	2298
VK1-33_6_0_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCCTT WCACT	1675	2299

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VK1-33_7_0_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCA ATCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCCTT WCACT	1676	2300
VK1-33_8_0_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATN HCCTCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCCTT WCACT	1677	2301
VK1-33_9_0_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATA ATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCCTT WCACT	1678	2302
VK1-33_1_1_9	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCCTM TCACT	1679	2303
VK1-33_10_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCCTM TCACT	1680	2304
VK1-33_11_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATN HCCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCCTM TCACT	1681	2305
VK1-33_12_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATA ATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCCTM TCACT	1682	2306
VK1-33_13_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCN HCCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCCTM TCACT	1683	2307
VK1-33_14_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCA ATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTM TCACT	1684	2308
VK1-33_15_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATN HCYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCCTM TCACT	1685	2309
VK1-33_2_1_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCCTM TCACT	1686	2310
VK1-33_3_1_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCCTM TCACT	1687	2311
VK1-33_4_1_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATN HCCTCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCCTM TCACT	1688	2312
VK1-33_5_1_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATA ATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCCTM TCACT	1689	2313
VK1-33_6_1_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCCTM TCACT	1690	2314
VK1-33_7_1_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCA ATCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCCTM TCACT	1691	2315
VK1-33_8_1_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATN HCCTCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCCTM TCACT	1692	2316

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VK1-33_9_1_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATA ATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCCTM TCACT	1693	2317
VK1-33_1_2_9	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCCTW GGACT	1694	2318
VK1-33_10_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCCTW GGACT	1695	2319
VK1-33_11_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATN HCCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCCTW GGACT	1696	2320
VK1-33_12_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCCTW GGACT	1697	2321
VK1-33_13_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCN HCCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCCTW GGACT	1698	2322
VK1-33_14_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTW GGACT	1699	2323
VK1-33_15_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATN HCYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCCTW GGACT	1700	2324
VK1-33_2_2_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCCTW GGACT	1701	2325
VK1-33_3_2_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCCTW GGACT	1702	2326
VK1-33_4_2_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATN HCCTCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCCTW GGACT	1703	2327
VK1-33_5_2_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCCTW GGACT	1704	2328
VK1-33_6_2_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCCTW GGACT	1705	2329
VK1-33_7_2_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCA ATCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCCTW GGACT	1706	2330
VK1-33_8_2_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATN HCCTCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCCTW GGACT	1707	2331
VK1-33_9_2_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCCTW GGACT	1708	2332
VK1-33_1_3_9	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATA ATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCCTC CTACT	1709	2333

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VK1-33_10_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCCTCCTACT	1710	2334
VK1-33_11_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCCTCCTACT	1711	2335
VK1-33_12_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCCTCCTACT	1712	2336
VK1-33_13_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCCTCCTACT	1713	2337
VK1-33_14_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTCCTACT	1714	2338
VK1-33_15_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATNHCYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCCTCCTACT	1715	2339
VK1-33_2_3_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATAATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCCTCCTACT	1716	2340
VK1-33_3_3_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCAATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCCTCCTACT	1717	2341
VK1-33_4_3_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATNHCCTCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCCTCCTACT	1718	2342
VK1-33_5_3_9	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCCTCCTACT	1719	2343
VK1-33_6_3_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATAATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCCTCCTACT	1720	2344
VK1-33_7_3_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCAATCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCCTCCTACT	1721	2345
VK1-33_8_3_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATNHCCTCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCCTCCTACT	1722	2346
VK1-33_9_3_9	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCCTCCTACT	1723	2347
VK1-39_1_0_9	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAGTACTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCCTTWCACT	1724	305
VK1-39_10_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTACTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCCTTWCACT	1725	314
VK1-39_11_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCACTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCCTTWCACT	1726	315

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VK1-39_12_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAGTBHCCCTTWCACT	CAGCAAVNATACAGTBHCCCTTWCACT	1727	316
VK1-39_13_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCACTCCTTWCACT	CAGCAAAGCBHCNHCACTCCTTWCACT	1728	317
VK1-39_14_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAGTBHCCCTTWCACT	CAGCAAAGCBHCAGTBHCCCTTWCACT	1729	318
VK1-39_15_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNHCBHCCCTTWCACT	CAGCAAAGCTACNHCBHCCCTTWCACT	1730	319
VK1-39_2_0_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACAGTACTCCTTWCACT	SWMCAAVNATACAGTACTCCTTWCACT	1731	306
VK1-39_3_0_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCAGTACTCCTTWCACT	SWMCAAAGCBHCAGTACTCCTTWCACT	1732	307
VK1-39_4_0_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACNHCACTCCTTWCACT	SWMCAAAGCTACNHCACTCCTTWCACT	1733	308
VK1-39_5_0_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACAGTBHCCCTTWCACT	SWMCAAAGCTACAGTBHCCCTTWCACT	1734	309
VK1-39_6_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACAGTACTCCTTWCACT	CAGSWMVNATACAGTACTCCTTWCACT	1735	310
VK1-39_7_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCAGTACTCCTTWCACT	CAGSWMAGCBHCAGTACTCCTTWCACT	1736	311
VK1-39_8_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACNHCACTCCTTWCACT	CAGSWMAGCTACNHCACTCCTTWCACT	1737	312
VK1-39_9_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACAGTBHCCCTTWCACT	CAGSWMAGCTACAGTBHCCCTTWCACT	1738	313
VK1-39_1_1_9	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAGTACTCCTMTCACT	SWMSWMAGCTACAGTACTCCTMTCACT	1739	2348
VK1-39_10_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTACTCCTMTCACT	CAGCAAVNABHCAGTACTCCTMTCACT	1740	2349
VK1-39_11_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCACTCCTMTCACT	CAGCAAVNATACNHCACTCCTMTCACT	1741	2350
VK1-39_12_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAGTBHCCCTMTCACT	CAGCAAVNATACAGTBHCCCTMTCACT	1742	2351
VK1-39_13_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCACTCCTMTCACT	CAGCAAAGCBHCNHCACTCCTMTCACT	1743	2352

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VK1-39_14_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCCTMTCACT	1744	2353
VK1-39_15_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNHCBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCCTMTCACT	1745	2354
VK1-39_2_1_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACAGTACTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCCTMTCACT	1746	2355
VK1-39_3_1_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCAGTACTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCCTMTCACT	1747	2356
VK1-39_4_1_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACNHCACTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCCTMTCACT	1748	2357
VK1-39_5_1_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCCTMTCACT	1749	2358
VK1-39_6_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACAGTACTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCCTMTCACT	1750	2359
VK1-39_7_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCAGTACTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCCTMTCACT	1751	2360
VK1-39_8_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACNHCACTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCCTMTCACT	1752	2361
VK1-39_9_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCCTMTCACT	1753	2362
VK1-39_1_2_9	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAGTACTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCCTWGGACT	1754	2363
VK1-39_10_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCCTWGGACT	1755	2364
VK1-39_11_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCCTWGGACT	1756	2365
VK1-39_12_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCCTWGGACT	1757	2366
VK1-39_13_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCCTWGGACT	1758	2367
VK1-39_14_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCCTWGGACT	1759	2368
VK1-39_15_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNHCBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCCTWGGACT	1760	2369

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VK1-39_2_2_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACA GTACTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCCTW GGACT	1761	2370
VK1-39_3_2_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCA GTACTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCCTW GGACT	1762	2371
VK1-39_4_2_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACN HCACTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCCTW GGACT	1763	2372
VK1-39_5_2_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACA GTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCCTW GGACT	1764	2373
VK1-39_6_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACA GTACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCCTW GGACT	1765	2374
VK1-39_7_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCA GTACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCCTW GGACT	1766	2375
VK1-39_8_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACN HCACTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCCTW GGACT	1767	2376
VK1-39_9_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACA GTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCCTW GGACT	1768	2377
VK1-39_1_3_9	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCCTC CTACT	1769	2378
VK1-39_10_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCCTC CTACT	1770	2379
VK1-39_11_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACN HCACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCCTC CTACT	1771	2380
VK1-39_12_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCCTC CTACT	1772	2381
VK1-39_13_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCN HCACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCCTC CTACT	1773	2382
VK1-39_14_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCCTC CTACT	1774	2383
VK1-39_15_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACN HCBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCCTC CTACT	1775	2384
VK1-39_2_3_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCCTC CTACT	1776	2385
VK1-39_3_3_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCCTC CTACT	1777	2386

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VK1-39_4_3_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACN HCACTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCCTC CTACT	1778	2387
VK1-39_5_3_9	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCCTC CTACT	1779	2388
VK1-39_6_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCCTC CTACT	1780	2389
VK1-39_7_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCA GTACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCCTC CTACT	1781	2390
VK1-39_8_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACN HCACTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCCTC CTACT	1782	2391
VK1-39_9_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCCTC CTACT	1783	2392
VK2-28_1_0_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCCTT WCACT	1784	2393
VK2-28_10_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNAC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCCTT WCACT	1785	2394
VK2-28_11_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCS RMACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCCTT WCACT	1786	2395
VK2-28_12_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCC AGVBCCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCCTT WCACT	1787	2396
VK2-28_13_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAS RMACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCCTT WCACT	1788	2397
VK2-28_14_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAC AGVBCCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCCTT WCACT	1789	2398
VK2-28_15_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCS RMVBCCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCCTT WCACT	1790	2399
VK2-28_2_0_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCCTT WCACT	1791	2400
VK2-28_3_0_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNAC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCCTT WCACT	1792	2401
VK2-28_4_0_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCS RMACTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCCTT WCACT	1793	2402
VK2-28_5_0_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCC AGVBCCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCCTT WCACT	1794	2403

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VK2-28_6_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCCTT WCACT	1795	2404
VK2-28_7_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNAC AGACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCCTT WCACT	1796	2405
VK2-28_8_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCS RMACTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCCTT WCACT	1797	2406
VK2-28_9_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCC AGVBCCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCCTT WCACT	1798	2407
VK2-28_1_1_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCCTM TCACT	1799	2408
VK2-28_10_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNAC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCCTM TCACT	1800	2409
VK2-28_11_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCS RMACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCCTM TCACT	1801	2410
VK2-28_12_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCC AGVBCCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCCTM TCACT	1802	2411
VK2-28_13_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAS RMACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCCTM TCACT	1803	2412
VK2-28_14_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAC AGVBCCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCCTM TCACT	1804	2413
VK2-28_15_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCS RMVBCCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCCTM TCACT	1805	2414
VK2-28_2_1_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCCTM TCACT	1806	2415
VK2-28_3_1_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNAC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCCTM TCACT	1807	2416
VK2-28_4_1_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCS RMACTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCCTM TCACT	1808	2417
VK2-28_5_1_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCC AGVBCCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCCTM TCACT	1809	2418
VK2-28_6_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCCTM TCACT	1810	2419
VK2-28_7_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNAC AGACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCCTM TCACT	1811	2420

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VK2-28_8_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCS RMACTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCCTM TCACT	1812	2421
VK2-28_9_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCC AGVBCCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCCTM TCACT	1813	2422
VK2-28_1_2_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCCTW GGACT	1814	2423
VK2-28_10_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNAC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCCTW GGACT	1815	2424
VK2-28_11_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCS RMACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCCTW GGACT	1816	2425
VK2-28_12_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCC AGVBCCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCCTW GGACT	1817	2426
VK2-28_13_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAS RMACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCCTW GGACT	1818	2427
VK2-28_14_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAC AGVBCCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCCTW GGACT	1819	2428
VK2-28_15_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCS RMVBCCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCCTW GGACT	1820	2429
VK2-28_2_2_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCCTW GGACT	1821	2430
VK2-28_3_2_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNAC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCCTW GGACT	1822	2431
VK2-28_4_2_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCS RMACTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCCTW GGACT	1823	2432
VK2-28_5_2_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCC AGVBCCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCCTW GGACT	1824	2433
VK2-28_6_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCCTW GGACT	1825	2434
VK2-28_7_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNAC AGACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCCTW GGACT	1826	2435
VK2-28_8_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCS RMACTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCCTW GGACT	1827	2436
VK2-28_9_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCC AGVBCCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCCTW GGACT	1828	2437

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VK2-28_1_3_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCCTC CTACT	1829	2438
VK2-28_10_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNAC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCCTC CTACT	1830	2439
VK2-28_11_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCS RMACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCCTC CTACT	1831	2440
VK2-28_12_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCC AGVBCCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCCTC CTACT	1832	2441
VK2-28_13_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAS RMACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCCTC CTACT	1833	2442
VK2-28_14_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNAC AGVBCCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCCTC CTACT	1834	2443
VK2-28_15_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCS RMVBCCCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCCTC CTACT	1835	2444
VK2-28_2_3_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCCTC CTACT	1836	2445
VK2-28_3_3_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNAC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCCTC CTACT	1837	2446
VK2-28_4_3_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCS RMACTCCTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCCTC CTACT	1838	2447
VK2-28_5_3_9	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCC AGVBCCCTCCTACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCCTC CTACT	1839	2448
VK2-28_6_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCCTC CTACT	1840	2449
VK2-28_7_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNAC AGACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCCTC CTACT	1841	2450
VK2-28_8_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCS RMACTCCTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCCTC CTACT	1842	2451
VK2-28_9_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCC AGVBCCCTCCTACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCCTC CTACT	1843	2452
VK3-11_1_0_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTA ATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCCTT WCACT	1844	2453
VK3-11_10_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCA ATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTT WCACT	1845	2454

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VK3-11_11_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCCTTWCACT	1846	2455
VK3-11_12_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCCTTWCACT	1847	2456
VK3-11_13_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCCTTWCACT	1848	2457
VK3-11_14_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCCTTWCACT	1849	2458
VK3-11_15_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTNHCYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCCTTWCACT	1850	2459
VK3-11_2_0_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCCTTWCACT	1851	2460
VK3-11_3_0_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCCTTWCACT	1852	2461
VK3-11_4_0_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCCTTWCACT	1853	2462
VK3-11_5_0_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCCTTWCACT	1854	2463
VK3-11_6_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCCTTWCACT	1855	2464
VK3-11_7_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCCTTWCACT	1856	2465
VK3-11_8_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCCTTWCACT	1857	2466
VK3-11_9_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCCTTWCACT	1858	2467
VK3-11_1_1_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCCTMTCACT	1859	2468
VK3-11_10_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTMTCACT	1860	2469
VK3-11_11_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCCTMTCACT	1861	2470
VK3-11_12_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCCTMTCACT	1862	2471

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VK3-11_13_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCCTMTCACT	1863	2472
VK3-11_14_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCCTMTCACT	1864	2473
VK3-11_15_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTNHCYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCCTMTCACT	1865	2474
VK3-11_2_1_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCCTMTCACT	1866	2475
VK3-11_3_1_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCCTMTCACT	1867	2476
VK3-11_4_1_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCCTMTCACT	1868	2477
VK3-11_5_1_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCCTMTCACT	1869	2478
VK3-11_6_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCCTMTCACT	1870	2479
VK3-11_7_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCCTMTCACT	1871	2480
VK3-11_8_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCCTMTCACT	1872	2481
VK3-11_9_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCCTMTCACT	1873	2482
VK3-11_1_2_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCCTWGGACT	1874	2483
VK3-11_10_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTWGGACT	1875	2484
VK3-11_11_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCCTWGGACT	1876	2485
VK3-11_12_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCCTWGGACT	1877	2486
VK3-11_13_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCCTWGGACT	1878	2487
VK3-11_14_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCCTWGGACT	1879	2488

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VK3-11_15_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTN HCYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCCTW GGACT	1880	2489
VK3-11_2_2_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTA ATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCCTW GGACT	1881	2490
VK3-11_3_2_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCA ATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCCTW GGACT	1882	2491
VK3-11_4_2_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTN HCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCCTW GGACT	1883	2492
VK3-11_5_2_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCCTW GGACT	1884	2493
VK3-11_6_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTA ATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCCTW GGACT	1885	2494
VK3-11_7_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCA ATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCCTW GGACT	1886	2495
VK3-11_8_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTN HCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCCTW GGACT	1887	2496
VK3-11_9_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTA ATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCCTW GGACT	1888	2497
VK3-11_1_3_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCCTC CTACT	1889	2498
VK3-11_10_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTC CTACT	1890	2499
VK3-11_11_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTN HCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCCTC CTACT	1891	2500
VK3-11_12_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTA ATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCCTC CTACT	1892	2501
VK3-11_13_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCN HCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCCTC CTACT	1893	2502
VK3-11_14_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCA ATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCCTC CTACT	1894	2503
VK3-11_15_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTN HCYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCCTC CTACT	1895	2504
VK3-11_2_3_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCCTC CTACT	1896	2505

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VK3-11_3_3_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCCTC CTACT	1897	2506
VK3-11_4_3_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTN HCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCCTC CTACT	1898	2507
VK3-11_5_3_9	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTA ATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCCTC CTACT	1899	2508
VK3-11_6_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCCTC CTACT	1900	2509
VK3-11_7_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCA ATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCCTC CTACT	1901	2510
VK3-11_8_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTN HCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCCTC CTACT	1902	2511
VK3-11_9_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTA ATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCCTC CTACT	1903	2512
VK3-15_1_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACA ATAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCCTT WCACT	1904	2513
VK3-15_10_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTT WCACT	1905	2454
VK3-15_11_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCCTT WCACT	1906	2514
VK3-15_12_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCCTT WCACT	1907	2515
VK3-15_13_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCCTT WCACT	1908	2516
VK3-15_14_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTT WCACT	1909	2293
VK3-15_15_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACA ATNHCYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCCTT WCACT	1910	2517
VK3-15_2_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA ATAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCCTT WCACT	1911	2518
VK3-15_3_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACN HCAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCCTT WCACT	1912	2519
VK3-15_4_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCCTT WCACT	1913	2520

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VK3-15_5_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCCTT WCACT	1914	2521
VK3-15_6_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA ATAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCCTT WCACT	1915	2522
VK3-15_7_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACN HCAATTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCCTT WCACT	1916	2523
VK3-15_8_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATNHCTGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCCTT WCACT	1917	2524
VK3-15_9_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATAATYWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCCTT WCACT	1918	2525
VK3-15_1_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACA ATAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCCTM TCACT	1919	2526
VK3-15_10_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTM TCACT	1920	2469
VK3-15_11_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCCTM TCACT	1921	2527
VK3-15_12_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCCTM TCACT	1922	2528
VK3-15_13_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCCTM TCACT	1923	2529
VK3-15_14_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTM TCACT	1924	2308
VK3-15_15_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACA ATNHCYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCCTM TCACT	1925	2530
VK3-15_2_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA ATAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCCTM TCACT	1926	2531
VK3-15_3_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACN HCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCCTM TCACT	1927	2532
VK3-15_4_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCCTM TCACT	1928	2533
VK3-15_5_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCCTM TCACT	1929	2534
VK3-15_6_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA ATAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCCTM TCACT	1930	2535

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VK3-15_7_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACN HCAATTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCCTM TCACT	1931	2536
VK3-15_8_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATNHCTGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCCTM TCACT	1932	2537
VK3-15_9_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATAATYWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCCTM TCACT	1933	2538
VK3-15_1_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACA ATAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCCTW GGACT	1934	2539
VK3- 15_10_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTW GGACT	1935	2484
VK3- 15_11_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCCTW GGACT	1936	2540
VK3- 15_12_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATAATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCCTW GGACT	1937	2541
VK3- 15_13_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCCTW GGACT	1938	2542
VK3- 15_14_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCAATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTW GGACT	1939	2323
VK3- 15_15_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACA ATNHCYWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCCTW GGACT	1940	2543
VK3-15_2_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA ATAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCCTW GGACT	1941	2544
VK3-15_3_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACN HCAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCCTW GGACT	1942	2545
VK3-15_4_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCCTW GGACT	1943	2546
VK3-15_5_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATAATYWCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCCTW GGACT	1944	2547
VK3-15_6_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA ATAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCCTW GGACT	1945	2548
VK3-15_7_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACN HCAATTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCCTW GGACT	1946	2549
VK3-15_8_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATNHCTGGCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCCTW GGACT	1947	2550

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VK3-15_9_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATAATYWCCCIWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCCTW GGACT	1948	2551
VK3-15_1_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACA ATAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCCTC CTACT	1949	2552
VK3-15_10_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCN HCAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCCTC CTACT	1950	2499
VK3-15_11_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATNHCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCCTC CTACT	1951	2553
VK3-15_12_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCA ATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCCTC CTACT	1952	2554
VK3-15_13_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCNHCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCCTC CTACT	1953	2555
VK3-15_14_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACN HCAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCCTC CTACT	1954	2338
VK3-15_15_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACA ATNHCYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCCTC CTACT	1955	2556
VK3-15_2_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCA ATAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCCTC CTACT	1956	2557
VK3-15_3_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACN HCAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCCTC CTACT	1957	2558
VK3-15_4_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATNHCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCCTC CTACT	1958	2559
VK3-15_5_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACA ATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCCTC CTACT	1959	2560
VK3-15_6_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCA ATAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCCTC CTACT	1960	2561
VK3-15_7_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACN HCAATTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCCTC CTACT	1961	2562
VK3-15_8_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATNHCTGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCCTC CTACT	1962	2563
VK3-15_9_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACA ATAATYWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCCTC CTACT	1963	2564
VK3-20_1_0_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCCTT WCACT	1964	2565

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VK3-20_10_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCCTT WCACT	1965	2566
VK3-20_11_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAV NCAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCCTT WCACT	1966	2567
VK3-20_12_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAA GTBHCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCCTT WCACT	1967	2568
VK3-20_13_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCV NCAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCCTT WCACT	1968	2569
VK3-20_14_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCA GTBHCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCCTT WCACT	1969	2570
VK3-20_15_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAV NCBHCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCCTT WCACT	1970	2571
VK3-20_2_0_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCCTT WCACT	1971	2572
VK3-20_3_0_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCCTT WCACT	1972	2573
VK3-20_4_0_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAV NCAGTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCCTT WCACT	1973	2574
VK3-20_5_0_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAA GTBHCCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCCTT WCACT	1974	2575
VK3-20_6_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCCTT WCACT	1975	2576
VK3-20_7_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCA GTAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCCTT WCACT	1976	2577
VK3-20_8_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAV NCAGTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCCTT WCACT	1977	2578
VK3-20_9_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAA GTBHCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCCTT WCACT	1978	2579
VK3-20_1_1_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAA GTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCCTM TCACT	1979	2580
VK3-20_10_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCA GTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCCTM TCACT	1980	2581
VK3-20_11_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAV NCAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCCTM TCACT	1981	2582

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VK3-20_12_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCCTMTCACT	1982	2583
VK3-20_13_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCCTMTCACT	1983	2584
VK3-20_14_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCCTMTCACT	1984	2585
VK3-20_15_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVNCBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCCTMTCACT	1985	2586
VK3-20_2_1_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAGTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCCTMTCACT	1986	2587
VK3-20_3_1_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAGTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCCTMTCACT	1987	2588
VK3-20_4_1_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVNCAGTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCCTMTCACT	1988	2589
VK3-20_5_1_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCCTMTCACT	1989	2590
VK3-20_6_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAGTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCCTMTCACT	1990	2591
VK3-20_7_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAGTAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCCTMTCACT	1991	2592
VK3-20_8_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVNCAGTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCCTMTCACT	1992	2593
VK3-20_9_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAGTBHCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCCTMTCACT	1993	2594
VK3-20_1_2_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCCTWGGACT	1994	2595
VK3-20_10_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCCTWGGACT	1995	2596
VK3-20_11_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCCTWGGACT	1996	2597
VK3-20_12_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCCTWGGACT	1997	2598
VK3-20_13_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCCTWGGACT	1998	2599

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VK3-20_14_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCCTWGGACT	1999	2600
VK3-20_15_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVNCBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCCTWGGACT	2000	2601
VK3-20_2_2_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCCTWGGACT	2001	2602
VK3-20_3_2_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCCTWGGACT	2002	2603
VK3-20_4_2_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVNCAGTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCCTWGGACT	2003	2604
VK3-20_5_2_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCCTWGGACT	2004	2605
VK3-20_6_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCCTWGGACT	2005	2606
VK3-20_7_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAGTAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCCTWGGACT	2006	2607
VK3-20_8_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVNCAGTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCCTWGGACT	2007	2608
VK3-20_9_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAGTBHCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCCTWGGACT	2008	2609
VK3-20_1_3_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAGTAGTCCTCCTACTTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCCTCCTACT	2009	2610
VK3-20_10_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCCTCCTACT	2010	2611
VK3-20_11_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCCTCCTACT	2011	2612
VK3-20_12_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAGTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCCTCCTACT	2012	2613
VK3-20_13_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCCTCCTACT	2013	2614
VK3-20_14_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAGTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCCTCCTACT	2014	2615
VK3-20_15_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVNCBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCCTCCTACT	2015	2616

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VK3-20_2_3_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAA GTAGTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCCTC CTACT	2016	2617
VK3-20_3_3_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCA GTAGTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCCTC CTACT	2017	2618
VK3-20_4_3_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAV NCAGTCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCCTC CTACT	2018	2619
VK3-20_5_3_9	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCCTC CTACT	2019	2620
VK3-20_6_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAA GTAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCCTC CTACT	2020	2621
VK3-20_7_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCA GTAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCCTC CTACT	2021	2622
VK3-20_8_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAV NCAGTCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCCTC CTACT	2022	2623
VK3-20_9_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAA GTBHCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCCTC CTACT	2023	2624
Jumping Trimer				
VK1-05_t1_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTAC YCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTTWC ACT	2024	2625
VK1-05_t1_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTAC YCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTMTC ACT	2025	2626
VK1-05_t1_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTAC YCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTWGG ACT	2026	2627
VK1-05_t1_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTAC YCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTCCT ACT	2027	2628
VK1-05_t2_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWC YCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTTWC ACT	2028	2629
VK1-05_t2_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWC YCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTMTC ACT	2029	2630
VK1-05_t2_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWC YCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTWGG ACT	2030	2631
VK1-05_t2_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWC YCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTCCT ACT	2031	2632
VK1-05_t3_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWC YCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTTWC ACT	2032	2633
VK1-05_t3_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWC YCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTMTC ACT	2033	2634

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VK1-05_t3_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWC YCTWCGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTWGG ACT	2034	2635
VK1-05_t3_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWC YCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTCCT ACT	2035	2636
VK1-05_t4_0_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWC YCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTTWC ACT	2036	2637
VK1-05_t4_1_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWC YCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTMTC ACT	2037	2638
VK1-05_t4_2_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWC YCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTWGG ACT	2038	2639
VK1-05_t4_3_9	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWC YCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTCCT ACT	2039	2640
VK1-12_t1_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTTWC ACT	2040	2641
VK1-12_t1_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTMTC ACT	2041	2642
VK1-12_t1_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTWGG ACT	2042	2643
VK1-12_t1_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTCCT ACT	2043	2644
VK1-12_t2_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTTWC ACT	2044	2645
VK1-12_t2_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTMTC ACT	2045	2646
VK1-12_t2_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTWGG ACT	2046	2647
VK1-12_t2_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTCCT ACT	2047	2648
VK1-12_t3_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTTWC ACT	2048	2649
VK1-12_t3_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTMTC ACT	2049	2650
VK1-12_t3_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTWGG ACT	2050	2651
VK1-12_t3_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTCCT ACT	2051	2652
VK1-12_t4_0_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTTWC ACT	2052	2653
VK1-12_t4_1_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTMTC ACT	2053	2654

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VK1-12_t4_2_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTWGG ACT	2054	2655
VK1-12_t4_3_9	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTCCT ACT	2055	2656
VK1-33_t1_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTTWC ACT	2056	2657
VK1-33_t1_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTMTC ACT	2057	2658
VK1-33_t1_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTWGG ACT	2058	2659
VK1-33_t1_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTCCT ACT	2059	2660
VK1-33_t2_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTTWC ACT	2060	2661
VK1-33_t2_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTMTC ACT	2061	2662
VK1-33_t2_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTWGG ACT	2062	2663
VK1-33_t2_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCCT ACT	2063	2664
VK1-33_t3_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTTWC ACT	2064	2665
VK1-33_t3_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTMTC ACT	2065	2666
VK1-33_t3_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTWGG ACT	2066	2667
VK1-33_t3_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTCCT ACT	2067	2668
VK1-33_t4_0_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTTWC ACT	2068	2669
VK1-33_t4_1_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTMTC ACT	2069	2670
VK1-33_t4_2_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTWGG ACT	2070	2671
VK1-33_t4_3_9	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCCT ACT	2071	2672
VK1-39_t1_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACT CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTTWC ACT	2072	320
VK1-39_t1_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACT CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTMTC ACT	2073	2673

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VK1-39_t1_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACT CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTWGG ACT	2074	2674
VK1-39_t1_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACT CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTCCT ACT	2075	2675
VK1-39_t2_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTTWC ACT	2076	321
VK1-39_t2_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTMTC ACT	2077	2676
VK1-39_t2_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTWGG ACT	2078	2677
VK1-39_t2_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTCCT ACT	2079	2678
VK1-39_t3_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTTWC ACT	2080	322
VK1-39_t3_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTMTC ACT	2081	2679
VK1-39_t3_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTWGG ACT	2082	2680
VK1-39_t3_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTCCT ACT	2083	2681
VK1-39_t4_0_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTTWC ACT	2084	323
VK1-39_t4_1_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTMTC ACT	2085	2682
VK1-39_t4_2_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTWGG ACT	2086	2683
VK1-39_t4_3_9	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTCCT ACT	2087	2684
VK2-28_t1_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACT CCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTTWC ACT	2088	2685
VK2-28_t1_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACT CCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTMTC ACT	2089	2686
VK2-28_t1_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACT CCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTWGG ACT	2090	2687
VK2-28_t1_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACT CCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTCCT ACT	2091	2688
VK2-28_t2_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBC CCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTTWC ACT	2092	2689
VK2-28_t2_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBC CCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTMTC ACT	2093	2690

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VK2-28_t2_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBC CCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTWGG ACT	2094	2691
VK2-28_t2_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBC CCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTCCT ACT	2095	2692
VK2-28_t3_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBC CCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTTWC ACT	2096	2693
VK2-28_t3_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBC CCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTMTC ACT	2097	2694
VK2-28_t3_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBC CCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTWGG ACT	2098	2695
VK2-28_t3_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBC CCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTCCT ACT	2099	2696
VK2-28_t4_0_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBC CCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTTWC ACT	2100	2697
VK2-28_t4_1_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBC CCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTMTC ACT	2101	2698
VK2-28_t4_2_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBC CCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTWGG ACT	2102	2699
VK2-28_t4_3_9	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBC CCTCCTACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTCCT ACT	2103	2700
VK3-11_t1_0_9	CCTCAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGG CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTTWC ACT	2104	2701
VK3-11_t1_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGG CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTMTC ACT	2105	2702
VK3-11_t1_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGG CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTWGG ACT	2106	2703
VK3-11_t1_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGG CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCCT ACT	2107	2704
VK3-11_t2_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTTWC ACT	2108	2661
VK3-11_t2_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTMTC ACT	2109	2662
VK3-11_t2_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTWGG ACT	2110	2663
VK3-11_t2_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCCT ACT	2111	2664
VK3-11_t3_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTTWC ACT	2112	2705
VK3-11_t3_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTMTC ACT	2113	2706

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VK3-11_t3_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTWGG ACT	2114	2707
VK3-11_t3_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTCCT ACT	2115	2708
VK3-11_t4_0_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWC CCTTWCACTTTTGCCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTTWC ACT	2116	2709
VK3-11_t4_1_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTMTC ACT	2117	2710
VK3-11_t4_2_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTWGG ACT	2118	2711
VK3-11_t4_3_9	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTCCT ACT	2119	2712
VK3-15_t1_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHC TGGCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTTWC ACT	2120	2701
VK3-15_t1_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHC TGGCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTMTC ACT	2121	2702
VK3-15_t1_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHC TGGCCTWGCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTWGG ACT	2122	2703
VK3-15_t1_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHC TGGCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCCT ACT	2123	2704
VK3-15_t2_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAAT YWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTTWC ACT	2124	2661
VK3-15_t2_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAAT YWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTMTC ACT	2125	2662
VK3-15_t2_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAAT YWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTWGG ACT	2126	2663
VK3-15_t2_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAAT YWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCCT ACT	2127	2664
VK3-15_t3_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHC YWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTTWC ACT	2128	2713
VK3-15_t3_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHC YWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTMTC ACT	2129	2714
VK3-15_t3_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHC YWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTWGG ACT	2130	2715
VK3-15_t3_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHC YWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTCCT ACT	2131	2716
VK3-15_t4_0_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHC YWCCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTTWC ACT	2132	2669
VK3-15_t4_1_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHC YWCCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTMTC ACT	2133	2670

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VK3-15_t4_2_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHC YWCCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTWGG ACT	2134	2671
VK3-15_t4_3_9	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHC YWCCCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCCT ACT	2135	2672
VK3-20_t1_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGT CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTTWC ACT	2136	2717
VK3-20_t1_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGT CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTMTC ACT	2137	2718
VK3-20_t1_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGT CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTWGG ACT	2138	2719
VK3-20_t1_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGT CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTCCT ACT	2139	2720
VK3-20_t2_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTTWC ACT	2140	2721
VK3-20_t2_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTMTC ACT	2141	2722
VK3-20_t2_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTWGG ACT	2142	2723
VK3-20_t2_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCCT ACT	2143	2724
VK3-20_t3_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTTWC ACT	2144	2725
VK3-20_t3_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTMTC ACT	2145	2726
VK3-20_t3_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTWGG ACT	2146	2727
VK3-20_t3_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTCCT ACT	2147	2728
VK3-20_t4_0_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTTWC ACT	2148	2729
VK3-20_t4_1_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTMTC ACT	2149	2730
VK3-20_t4_2_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTWGG ACT	2150	2731
VK3-20_t4_3_9	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTCCT ACT	2151	2732
VK4-01_t1_0_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACT CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTTWC ACT	2152	2733
VK4-01_t1_1_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACT CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTMTC ACT	2153	2734

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VK4-01_t1_2_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACT CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTWGG ACT	2154	2735
VK4-01_t1_3_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACT CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTCCT ACT	2155	2736
VK4-01_t2_0_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTTWC ACT	2156	2721
VK4-01_t2_1_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTMTC ACT	2157	2722
VK4-01_t2_2_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTWGG ACT	2158	2723
VK4-01_t2_3_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCCT ACT	2159	2724
VK4-01_t3_0_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTTWC ACT	2160	2737
VK4-01_t3_1_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTMTC ACT	2161	2738
VK4-01_t3_2_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTWGG ACT	2162	2739
VK4-01_t3_3_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTCCT ACT	2163	2740
VK4-01_t4_0_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHC CCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTTWC ACT	2164	2741
VK4-01_t4_1_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHC CCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTMTC ACT	2165	2742
VK4-01_t4_2_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHC CCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTWGG ACT	2166	2743
VK4-01_t4_3_9	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHC CCTCCTACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTCCT ACT	2167	2744

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Table 7. Oligonucleotide sequences for exemplary VK jumping dimer and trimer sequences with CDRL3 length 10.

Name	Sequence of Synthesized Oligonucleotide	Portion of Oligonucleotide Corresponding to CDRL3 Proper	SEQ ID NO (Oligo)	SEQ ID NO (CDRL3 Portion)
Jumping Dimer				
VK1-05_1_0_10	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYC TCCTTWCACT	2745	3213
VK1-05_10_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYC TCCTTWCACT	2746	3214
VK1-05_11_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMB CTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYC TCCTTWCACT	2747	3215
VK1-05_12_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATAG TYWCYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYC TCCTTWCACT	2748	3216
VK1-05_13_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMB CTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYC TCCTTWCACT	2749	3217
VK1-05_14_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMAG TYWCYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYC TCCTTWCACT	2750	3218
VK1-05_15_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATMB CYWCYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYC TCCTTWCACT	2751	3219
VK1-05_2_0_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYC TCCTTWCACT	2752	3220
VK1-05_3_0_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYC TCCTTWCACT	2753	3221
VK1-05_4_0_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATMB CTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYC TCCTTWCACT	2754	3222
VK1-05_5_0_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATAG TYWCYCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYC TCCTTWCACT	2755	3223
VK1-05_6_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYC TCCTTWCACT	2756	3224
VK1-05_7_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMAG TTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYC TCCTTWCACT	2757	3225

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VK1-05_8_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATMB CTACYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYC TCCTTWCACT	2758	3226
VK1-05_9_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATAG TYWCYCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYC TCCTTWCACT	2759	3227
VK1-05_1_1_10	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYC TCCTMTCACT	2760	3228
VK1-05_10_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYC TCCTMTCACT	2761	3229
VK1-05_11_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMB CTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYC TCCTMTCACT	2762	3230
VK1-05_12_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATAG TYWCYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYC TCCTMTCACT	2763	3231
VK1-05_13_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMB CTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYC TCCTMTCACT	2764	3232
VK1-05_14_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMAG TYWCYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYC TCCTMTCACT	2765	3233
VK1-05_15_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATMB CYWCYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYC TCCTMTCACT	2766	3234
VK1-05_2_1_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYC TCCTMTCACT	2767	3235
VK1-05_3_1_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYC TCCTMTCACT	2768	3236
VK1-05_4_1_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATMB CTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYC TCCTMTCACT	2769	3237
VK1-05_5_1_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATAG TYWCYCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYC TCCTMTCACT	2770	3238
VK1-05_6_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYC TCCTMTCACT	2771	3239
VK1-05_7_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMAG TTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYC TCCTMTCACT	2772	3240
VK1-05_8_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATMB CTACYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYC TCCTMTCACT	2773	3241
VK1-05_9_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATAG TYWCYCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYC TCCTMTCACT	2774	3242

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VK1-05_1_2_10	CCTGATGATTTTGCAACTTATTACTGCSWMSWMTACAATAG ITTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAGTTACYC TCCTWGGACT	2775	3243
VK1-05_10_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAG ITTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTTACYC TCCTWGGACT	2776	3244
VK1-05_11_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMB CTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCTACYC TCCTWGGACT	2777	3245
VK1-05_12_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATAG TYWCYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAGTYWCYC TCCTWGGACT	2778	3246
VK1-05_13_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMB CTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCTACYC TCCTWGGACT	2779	3247
VK1-05_14_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMAG TYWCYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMAGTYWCYC TCCTWGGACT	2780	3248
VK1-05_15_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACAATMB CYWCYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATMBCYWCYC TCCTWGGACT	2781	3249
VK1-05_2_2_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGBHCAATAG TTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAGTTACYC TCCTWGGACT	2782	3250
VK1-05_3_2_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACVRMAG TTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACVRMAGTTACYC TCCTWGGACT	2783	3251
VK1-05_4_2_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATMB CTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATMBCTACYC TCCTWGGACT	2784	3252
VK1-05_5_2_10	CCTGATGATTTTGCAACTTATTACTGCSWMCAGTACAATAG TYWCYCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAGTYWCYC TCCTWGGACT	2785	3253
VK1-05_6_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMBHCAATAG TTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAGTTACYC TCCTWGGACT	2786	3254
VK1-05_7_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACVRMAG TTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACVRMAGTTACYC TCCTWGGACT	2787	3255
VK1-05_8_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATMB CTACYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATMBCTACYC TCCTWGGACT	2788	3256
VK1-05_9_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGSWMTACAATAG TYWCYCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAGTYWCYC TCCTWGGACT	2789	3257
VK1-12_1_0_10	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCC TCCTTWCACT	2790	3258
VK1-12_10_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCC TCCTTWCACT	2791	3259

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VK1-12_11_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNH CTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCC TCCTTWCACT	2792	3260
VK1-12_12_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAG TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCC TCCTTWCACT	2793	3261
VK1-12_13_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNH CTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCC TCCTTWCACT	2794	3262
VK1-12_14_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAG TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCC TCCTTWCACT	2795	3263
VK1-12_15_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNH CYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCC TCCTTWCACT	2796	3264
VK1-12_2_0_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCC TCCTTWCACT	2797	3265
VK1-12_3_0_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCC TCCTTWCACT	2798	3266
VK1-12_4_0_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATNH CTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCC TCCTTWCACT	2799	3267
VK1-12_5_0_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATAG TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCC TCCTTWCACT	2800	3268
VK1-12_6_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCC TCCTTWCACT	2801	3269
VK1-12_7_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCAG TTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCC TCCTTWCACT	2802	3270
VK1-12_8_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATNH CTTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCC TCCTTWCACT	2803	3271
VK1-12_9_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATAG TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCC TCCTTWCACT	2804	3272
VK1-12_1_1_10	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCC TCCTMTCACT	2805	3273
VK1-12_10_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCC TCCTMTCACT	2806	3274
VK1-12_11_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNH CTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCC TCCTMTCACT	2807	3275
VK1-12_12_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAG TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCC TCCTMTCACT	2808	3276

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VK1-12_13_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNH CTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCC TCCTMTCACT	2809	3277
VK1-12_14_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAG TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCC TCCTMTCACT	2810	3278
VK1-12_15_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNH CYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCC TCCTMTCACT	2811	3279
VK1-12_2_1_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCC TCCTMTCACT	2812	3280
VK1-12_3_1_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCC TCCTMTCACT	2813	3281
VK1-12_4_1_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATNH CTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCC TCCTMTCACT	2814	3282
VK1-12_5_1_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATAG TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCC TCCTMTCACT	2815	3283
VK1-12_6_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCC TCCTMTCACT	2816	3284
VK1-12_7_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCAG TTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCC TCCTMTCACT	2817	3285
VK1-12_8_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATNH CTTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCC TCCTMTCACT	2818	3286
VK1-12_9_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATAG TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCC TCCTMTCACT	2819	3287
VK1-12_1_2_10	CCTGAAGATTTTGCAACTTATTACTGTSWMSWMGCAAATAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMGCAAATAGTTTCCC TCCTWGGACT	2820	3288
VK1-12_10_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTTTCCC TCCTWGGACT	2821	3289
VK1-12_11_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNH CTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCTTCCC TCCTWGGACT	2822	3290
VK1-12_12_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATAG TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATAGTYWCCC TCCTWGGACT	2823	3291
VK1-12_13_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNH CTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCTTCCC TCCTWGGACT	2824	3292
VK1-12_14_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCAG TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCAGTYWCCC TCCTWGGACT	2825	3293

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VK1-12_15_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCAAATNH CYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCAAATNHCYWCCC TCCTWGGACT	2826	3294
VK1-12_2_2_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGRNAAATAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGRNAAATAGTTTCCC TCCTWGGACT	2827	3295
VK1-12_3_2_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCANHCAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCANHCAGTTTCCC TCCTWGGACT	2828	3296
VK1-12_4_2_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATNH CTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATNHCTTCCC TCCTWGGACT	2829	3297
VK1-12_5_2_10	CCTGAAGATTTTGCAACTTATTACTGTSWMCAGGCAAATAG TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGGCAAATAGTYWCCC TCCTWGGACT	2830	3298
VK1-12_6_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMRNAAATAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMRNAAATAGTTTCCC TCCTWGGACT	2831	3299
VK1-12_7_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCANHCAG TTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCANHCAGTTTCCC TCCTWGGACT	2832	3300
VK1-12_8_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATNH CTTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATNHCTTCCC TCCTWGGACT	2833	3301
VK1-12_9_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGSWMGCAAATAG TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMGCAAATAGTYWCCC TCCTWGGACT	2834	3302
VK1-33_1_0_10	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCC TCCTTWCACT	2835	3303
VK1-33_10_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCC TCCTTWCACT	2836	3304
VK1-33_11_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNH CCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCC TCCTTWCACT	2837	3305
VK1-33_12_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCC TCCTTWCACT	2838	3306
VK1-33_13_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNH CCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCC TCCTTWCACT	2839	3307
VK1-33_14_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTTWCACT	2840	3308
VK1-33_15_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATNH CYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCC TCCTTWCACT	2841	3309
VK1-33_2_0_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCC TCCTTWCACT	2842	3310

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VK1-33_3_0_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCC TCCTTWCACT	2843	3311
VK1-33_4_0_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATNH CCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCC TCCTTWCACT	2844	3312
VK1-33_5_0_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCC TCCTTWCACT	2845	3313
VK1-33_6_0_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCC TCCTTWCACT	2846	3314
VK1-33_7_0_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCAA TCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCC TCCTTWCACT	2847	3315
VK1-33_8_0_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATNH CCTCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCC TCCTTWCACT	2848	3316
VK1-33_9_0_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATAA IYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCC TCCTTWCACT	2849	3317
VK1-33_1_1_10	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCC TCCTMTCACT	2850	3318
VK1-33_10_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCC TCCTMTCACT	2851	3319
VK1-33_11_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNH CCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCC TCCTMTCACT	2852	3320
VK1-33_12_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCC TCCTMTCACT	2853	3321
VK1-33_13_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNH CCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCC TCCTMTCACT	2854	3322
VK1-33_14_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTMTCACT	2855	3323
VK1-33_15_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATNH CYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCC TCCTMTCACT	2856	3324
VK1-33_2_1_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCC TCCTMTCACT	2857	3325
VK1-33_3_1_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCC TCCTMTCACT	2858	3326
VK1-33_4_1_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATNH CCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCC TCCTMTCACT	2859	3327

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VK1-33_5_1_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCC TCCTMTCACT	2860	3328
VK1-33_6_1_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCC TCCTMTCACT	2861	3329
VK1-33_7_1_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCAA TCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCC TCCTMTCACT	2862	3330
VK1-33_8_1_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATNH CCTCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCC TCCTMTCACT	2863	3331
VK1-33_9_1_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCC TCCTMTCACT	2864	3332
VK1-33_1_2_10	CCTGAAGATATTGCAACATATTACTGTSWMSWMTACGATAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGATAATCTCCC TCCTWGGACT	2865	3333
VK1-33_10_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATCTCCC TCCTWGGACT	2866	3334
VK1-33_11_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNH CCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCCTCCC TCCTWGGACT	2867	3335
VK1-33_12_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATAATYWCCC TCCTWGGACT	2868	3336
VK1-33_13_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNH CCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCCTCCC TCCTWGGACT	2869	3337
VK1-33_14_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTWGGACT	2870	3338
VK1-33_15_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACGATNH CYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGATNHCYWCCC TCCTWGGACT	2871	3339
VK1-33_2_2_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGBHCGATAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGATAATCTCCC TCCTWGGACT	2872	3340
VK1-33_3_2_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACNHCAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATCTCCC TCCTWGGACT	2873	3341
VK1-33_4_2_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATNH CCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATNHCCTCCC TCCTWGGACT	2874	3342
VK1-33_5_2_10	CCTGAAGATATTGCAACATATTACTGTSWMCAGTACGATAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGATAATYWCCC TCCTWGGACT	2875	3343
VK1-33_6_2_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMBHCGATAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGATAATCTCCC TCCTWGGACT	2876	3344

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VK1-33_7_2_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACNHCAA TCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATCTCCC TCCTWGGACT	2877	3345
VK1-33_8_2_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATNH CCTCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATNHCCTCCC TCCTWGGACT	2878	3346
VK1-33_9_2_10	CCTGAAGATATTGCAACATATTACTGTCAGSWMTACGATAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGATAATYWCCC TCCTWGGACT	2879	3347
VK1-39_1_0_10	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCC TCCTTWCACT	2880	3348
VK1-39_10_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCC TCCTTWCACT	2881	3349
VK1-39_11_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNH CACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCC TCCTTWCACT	2882	3350
VK1-39_12_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCC TCCTTWCACT	2883	3351
VK1-39_13_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNH CACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCC TCCTTWCACT	2884	3352
VK1-39_14_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCC TCCTTWCACT	2885	3353
VK1-39_15_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNH CBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCC TCCTTWCACT	2886	3354
VK1-39_2_0_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCC TCCTTWCACT	2887	3355
VK1-39_3_0_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCC TCCTTWCACT	2888	3356
VK1-39_4_0_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACNH CACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCC TCCTTWCACT	2889	3357
VK1-39_5_0_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCC TCCTTWCACT	2890	3358
VK1-39_6_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCC TCCTTWCACT	2891	3359
VK1-39_7_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCAG TACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCC TCCTTWCACT	2892	3360
VK1-39_8_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACNH CACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCC TCCTTWCACT	2893	3361

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VK1-39_9_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCC TCCTTWCACT	2894	3362
VK1-39_1_1_10	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCC TCCTMTCACT	2895	3363
VK1-39_10_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCC TCCTMTCACT	2896	3364
VK1-39_11_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNH CACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCC TCCTMTCACT	2897	3365
VK1-39_12_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCC TCCTMTCACT	2898	3366
VK1-39_13_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNH CACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCC TCCTMTCACT	2899	3367
VK1-39_14_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCC TCCTMTCACT	2900	3368
VK1-39_15_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNH CBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCC TCCTMTCACT	2901	3369
VK1-39_2_1_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCC TCCTMTCACT	2902	3370
VK1-39_3_1_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCC TCCTMTCACT	2903	3371
VK1-39_4_1_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACNH CACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCC TCCTMTCACT	2904	3372
VK1-39_5_1_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCC TCCTMTCACT	2905	3373
VK1-39_6_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCC TCCTMTCACT	2906	3374
VK1-39_7_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCAG TACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCC TCCTMTCACT	2907	3375
VK1-39_8_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACNH CACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCC TCCTMTCACT	2908	3376
VK1-39_9_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCC TCCTMTCACT	2909	3377
VK1-39_1_2_10	CCTGAAGATTTTGCAACTTACTACTGTSWMSWMAGCTACAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGCTACAGTACTCC TCCTWGGACT	2910	3378

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VK1-39_10_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTACTCC TCCTWGGACT	2911	3379
VK1-39_11_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNH CACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCACTCC TCCTWGGACT	2912	3380
VK1-39_12_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACAGTBHCCC TCCTWGGACT	2913	3381
VK1-39_13_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNH CACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCACTCC TCCTWGGACT	2914	3382
VK1-39_14_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCAGTBHCCC TCCTWGGACT	2915	3383
VK1-39_15_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCTACNH CBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCTACNHCBHCCC TCCTWGGACT	2916	3384
VK1-39_2_2_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAVNATACAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAVNATACAGTACTCC TCCTWGGACT	2917	3385
VK1-39_3_2_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCBHCAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCBHCAGTACTCC TCCTWGGACT	2918	3386
VK1-39_4_2_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACNH CACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACNHCACTCC TCCTWGGACT	2919	3387
VK1-39_5_2_10	CCTGAAGATTTTGCAACTTACTACTGTSWMCAAAGCTACAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAAAGCTACAGTBHCCC TCCTWGGACT	2920	3388
VK1-39_6_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMVNATACAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMVNATACAGTACTCC TCCTWGGACT	2921	3389
VK1-39_7_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCBHCAG TACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCBHCAGTACTCC TCCTWGGACT	2922	3390
VK1-39_8_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACNH CACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACNHCACTCC TCCTWGGACT	2923	3391
VK1-39_9_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGSWMAGCTACAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGCTACAGTBHCCC TCCTWGGACT	2924	3392
VK2-28_1_0_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCCA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCC TCCTTWCACT	2925	3393
VK2-28_10_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCC TCCTTWCACT	2926	3394
VK2-28_11_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSR MACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCC TCCTTWCACT	2927	3395

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VK2-28_12_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCCA GVBCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCC TCCTTWCACT	2928	3396
VK2-28_13_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASR MACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCC TCCTTWCACT	2929	3397
VK2-28_14_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNACA GVBCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCC TCCTTWCACT	2930	3398
VK2-28_15_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCSR MVBCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCC TCCTTWCACT	2931	3399
VK2-28_2_0_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCCA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCC TCCTTWCACT	2932	3400
VK2-28_3_0_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNACA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCC TCCTTWCACT	2933	3401
VK2-28_4_0_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCSR MACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCC TCCTTWCACT	2934	3402
VK2-28_5_0_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCCA GVBCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCC TCCTTWCACT	2935	3403
VK2-28_6_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCCA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCC TCCTTWCACT	2936	3404
VK2-28_7_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNACA GACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCC TCCTTWCACT	2937	3405
VK2-28_8_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCSR MACTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCC TCCTTWCACT	2938	3406
VK2-28_9_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCCA GVBCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCC TCCTTWCACT	2939	3407
VK2-28_1_1_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCCA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCC TCCTMTCACT	2940	3408
VK2-28_10_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCC TCCTMTCACT	2941	3409
VK2-28_11_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSR MACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCC TCCTMTCACT	2942	3410
VK2-28_12_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCCA GVBCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCC TCCTMTCACT	2943	3411
VK2-28_13_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASR MACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCC TCCTMTCACT	2944	3412

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VK2-28_14_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNACA GVBCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCC TCCTMTCACT	2945	3413
VK2-28_15_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCSR MVBCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCC TCCTMTCACT	2946	3414
VK2-28_2_1_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCCA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCC TCCTMTCACT	2947	3415
VK2-28_3_1_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNACA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCC TCCTMTCACT	2948	3416
VK2-28_4_1_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCSR MACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCC TCCTMTCACT	2949	3417
VK2-28_5_1_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCCA GVBCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCC TCCTMTCACT	2950	3418
VK2-28_6_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCCA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCC TCCTMTCACT	2951	3419
VK2-28_7_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNACA GACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCC TCCTMTCACT	2952	3420
VK2-28_8_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCSR MACTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCC TCCTMTCACT	2953	3421
VK2-28_9_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCCA GVBCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCC TCCTMTCACT	2954	3422
VK2-28_1_2_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSSWMGCACTCCA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSSWMGCACTCCAGACTCC TCCTWGGACT	2955	3423
VK2-28_10_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGACTCC TCCTWGGACT	2956	3424
VK2-28_11_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSR MACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMACTCC TCCTWGGACT	2957	3425
VK2-28_12_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCCA GVBCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCCAGVBCCC TCCTWGGACT	2958	3426
VK2-28_13_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASR MACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMACTCC TCCTWGGACT	2959	3427
VK2-28_14_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNACA GVBCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNACAGVBCCC TCCTWGGACT	2960	3428
VK2-28_15_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCACTCSR MVBCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGGCACTCSRMVBCCC TCCTWGGACT	2961	3429

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VK2-28_2_2_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGVNACTCCA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGVNACTCCAGACTCC TCCTWGGACT	2962	3430
VK2-28_3_2_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCAMNACA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCAMNACAGACTCC TCCTWGGACT	2963	3431
VK2-28_4_2_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCSR MACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCSRMACTCC TCCTWGGACT	2964	3432
VK2-28_5_2_10	GCTGAGGATGTTGGGGTTTATTACTGCDTSCAGGCACTCCA GVBCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	DTSCAGGCACTCCAGVBCCC TCCTWGGACT	2965	3433
VK2-28_6_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMVNACTCCA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMVNACTCCAGACTCC TCCTWGGACT	2966	3434
VK2-28_7_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCAMNACA GACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCAMNACAGACTCC TCCTWGGACT	2967	3435
VK2-28_8_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCSR MACTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCSRMACTCC TCCTWGGACT	2968	3436
VK2-28_9_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGSWMGCACTCCA GVBCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGSWMGCACTCCAGVBCCC TCCTWGGACT	2969	3437
VK3-11_1_0_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCC TCCTTWCACT	2970	3438
VK3-11_10_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTTWCACT	2971	3439
VK3-11_11_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNH CTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCC TCCTTWCACT	2972	3440
VK3-11_12_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCC TCCTTWCACT	2973	3441
VK3-11_13_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNH CTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCC TCCTTWCACT	2974	3442
VK3-11_14_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCC TCCTTWCACT	2975	3443
VK3-11_15_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTNH CYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCC TCCTTWCACT	2976	3444
VK3-11_2_0_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCC TCCTTWCACT	2977	3445
VK3-11_3_0_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCC TCCTTWCACT	2978	3446

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VK3-11_4_0_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTNH CTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCC TCCTTWCACT	2979	3447
VK3-11_5_0_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCC TCCTTWCACT	2980	3448
VK3-11_6_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCC TCCTTWCACT	2981	3449
VK3-11_7_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCAA TTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCC TCCTTWCACT	2982	3450
VK3-11_8_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTNH CTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCC TCCTTWCACT	2983	3451
VK3-11_9_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTAA TYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCC TCCTTWCACT	2984	3452
VK3-11_1_1_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCC TCCTMTCACT	2985	3453
VK3-11_10_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTMTCACT	2986	3454
VK3-11_11_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNH CTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCC TCCTMTCACT	2987	3455
VK3-11_12_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCC TCCTMTCACT	2988	3456
VK3-11_13_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNH CTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCC TCCTMTCACT	2989	3457
VK3-11_14_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCC TCCTMTCACT	2990	3458
VK3-11_15_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTNH CYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCC TCCTMTCACT	2991	3459
VK3-11_2_1_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCC TCCTMTCACT	2992	3460
VK3-11_3_1_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCC TCCTMTCACT	2993	3461
VK3-11_4_1_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTNH CTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCC TCCTMTCACT	2994	3462
VK3-11_5_1_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCC TCCTMTCACT	2995	3463

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VK3-11_6_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCC TCCTMTCACT	2996	3464
VK3-11_7_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCAA TTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCC TCCTMTCACT	2997	3465
VK3-11_8_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTNH CTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCC TCCTMTCACT	2998	3466
VK3-11_9_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTAA TYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCC TCCTMTCACT	2999	3467
VK3-11_1_2_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMSWMAGAAGTAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMAGAAGTAATTGGCC TCCTWGGACT	3000	3468
VK3-11_10_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTWGGACT	3001	3469
VK3-11_11_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNH CTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCTGGCC TCCTWGGACT	3002	3470
VK3-11_12_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTAATYWCCC TCCTWGGACT	3003	3471
VK3-11_13_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNH CTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCTGGCC TCCTWGGACT	3004	3472
VK3-11_14_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCAATYWCCC TCCTWGGACT	3005	3473
VK3-11_15_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGAAGTNH CYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGAAGTNHCYWCCC TCCTWGGACT	3006	3474
VK3-11_2_2_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAGTAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAGTAATTGGCC TCCTWGGACT	3007	3475
VK3-11_3_2_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGANHCAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGANHCAATTGGCC TCCTWGGACT	3008	3476
VK3-11_4_2_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTNH CTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTNHCTGGCC TCCTWGGACT	3009	3477
VK3-11_5_2_10	CCTGAAGATTTTGCAGTTTATTACTGTSWMCAGAGAAGTAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGAGAAGTAATYWCCC TCCTWGGACT	3010	3478
VK3-11_6_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAGTAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAGTAATTGGCC TCCTWGGACT	3011	3479
VK3-11_7_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGANHCAA TTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGANHCAATTGGCC TCCTWGGACT	3012	3480

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VK3-11_8_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTNH CTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTNHCTGGCC TCCTWGGACT	3013	3481
VK3-11_9_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGSWMAGAAGTAA TYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMAGAAGTAATYWCCC TCCTWGGACT	3014	3482
VK3-15_1_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACAA TAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCC TCCTTWCACT	3015	3483
VK3-15_10_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNH CAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTTWCACT	3016	3439
VK3-15_11_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA INHCTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCC TCCTTWCACT	3017	3484
VK3-15_12_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA IAATYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCC TCCTTWCACT	3018	3485
VK3-15_13_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CNHCTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCC TCCTTWCACT	3019	3486
VK3-15_14_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CAATYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTTWCACT	3020	3308
VK3-15_15_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACAA INHCYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCC TCCTTWCACT	3021	3487
VK3-15_2_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAA TAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCC TCCTTWCACT	3022	3488
VK3-15_3_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACNH CAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCC TCCTTWCACT	3023	3489
VK3-15_4_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TNHCTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCC TCCTTWCACT	3024	3490
VK3-15_5_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TAATYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCC TCCTTWCACT	3025	3491
VK3-15_6_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAA TAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCC TCCTTWCACT	3026	3492
VK3-15_7_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACNH CAATTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCC TCCTTWCACT	3027	3493
VK3-15_8_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA INHCTGGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCC TCCTTWCACT	3028	3494
VK3-15_9_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA TAATYWCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCC TCCTTWCACT	3029	3495

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VK3-15_1_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACAA TAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCC TCCTMTCACT	3030	3496
VK3-15_10_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNH CAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTMTCACT	3031	3454
VK3-15_11_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA TNHCTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCC TCCTMTCACT	3032	3497
VK3-15_12_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA TAATYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCC TCCTMTCACT	3033	3498
VK3-15_13_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CNHCTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCC TCCTMTCACT	3034	3499
VK3-15_14_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CAATYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTMTCACT	3035	3323
VK3-15_15_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACAA TNHCYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCC TCCTMTCACT	3036	3500
VK3-15_2_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAA TAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCC TCCTMTCACT	3037	3501
VK3-15_3_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACNH CAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCC TCCTMTCACT	3038	3502
VK3-15_4_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TNHCTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCC TCCTMTCACT	3039	3503
VK3-15_5_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TAATYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCC TCCTMTCACT	3040	3504
VK3-15_6_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAA TAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCC TCCTMTCACT	3041	3505
VK3-15_7_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACNH CAATTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCC TCCTMTCACT	3042	3506
VK3-15_8_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA TNHCTGGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCC TCCTMTCACT	3043	3507
VK3-15_9_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA TAATYWCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCC TCCTMTCACT	3044	3508
VK3-15_1_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMSWMTACAA TAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACAATAATTGGCC TCCTWGGACT	3045	3509
VK3-15_10_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNH CAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATTGGCC TCCTWGGACT	3046	3469

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VK3-15_11_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA TNHCTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCTGGCC TCCTWGGACT	3047	3510
VK3-15_12_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAA TAATYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATAATYWCCC TCCTWGGACT	3048	3511
VK3-15_13_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CNHCTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCTGGCC TCCTWGGACT	3049	3512
VK3-15_14_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNH CAATYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCAATYWCCC TCCTWGGACT	3050	3338
VK3-15_15_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACAA TNHCYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACAATNHCYWCCC TCCTWGGACT	3051	3513
VK3-15_2_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGBHCAA TAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCAATAATTGGCC TCCTWGGACT	3052	3514
VK3-15_3_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACNH CAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACNHCAATTGGCC TCCTWGGACT	3053	3515
VK3-15_4_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TNHCTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATNHCTGGCC TCCTWGGACT	3054	3516
VK3-15_5_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTSWMCAGTACAA TAATYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACAATAATYWCCC TCCTWGGACT	3055	3517
VK3-15_6_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMBHCAA TAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCAATAATTGGCC TCCTWGGACT	3056	3518
VK3-15_7_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACNH CAATTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACNHCAATTGGCC TCCTWGGACT	3057	3519
VK3-15_8_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA TNHCTGGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATNHCTGGCC TCCTWGGACT	3058	3520
VK3-15_9_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGSWMTACAA TAATYWCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACAATAATYWCCC TCCTWGGACT	3059	3521
VK3-20_1_0_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCC TCCTTWCACT	3060	3522
VK3-20_10_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCC TCCTTWCACT	3061	3523
VK3-20_11_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVN CAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCC TCCTTWCACT	3062	3524
VK3-20_12_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCC TCCTTWCACT	3063	3525

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VK3-20_13_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVN CAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCC TCCTTWCACT	3064	3526
VK3-20_14_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCC TCCTTWCACT	3065	3527
VK3-20_15_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVN CBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCC TCCTTWCACT	3066	3528
VK3-20_2_0_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCC TCCTTWCACT	3067	3529
VK3-20_3_0_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCC TCCTTWCACT	3068	3530
VK3-20_4_0_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVN CAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCC TCCTTWCACT	3069	3531
VK3-20_5_0_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCC TCCTTWCACT	3070	3532
VK3-20_6_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCC TCCTTWCACT	3071	3533
VK3-20_7_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAG TAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCC TCCTTWCACT	3072	3534
VK3-20_8_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVN CAGTCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCC TCCTTWCACT	3073	3535
VK3-20_9_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAG TBHCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCC TCCTTWCACT	3074	3536
VK3-20_1_1_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCC TCCTMTCACT	3075	3537
VK3-20_10_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCC TCCTMTCACT	3076	3538
VK3-20_11_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVN CAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCC TCCTMTCACT	3077	3539
VK3-20_12_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCC TCCTMTCACT	3078	3540
VK3-20_13_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVN CAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCC TCCTMTCACT	3079	3541
VK3-20_14_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCC TCCTMTCACT	3080	3542

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VK3-20_15_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVN CBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCC TCCTMTCACT	3081	3543
VK3-20_2_1_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCC TCCTMTCACT	3082	3544
VK3-20_3_1_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCC TCCTMTCACT	3083	3545
VK3-20_4_1_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVN CAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCC TCCTMTCACT	3084	3546
VK3-20_5_1_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCC TCCTMTCACT	3085	3547
VK3-20_6_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCC TCCTMTCACT	3086	3548
VK3-20_7_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAG TAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCC TCCTMTCACT	3087	3549
VK3-20_8_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVN CAGTCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCC TCCTMTCACT	3088	3550
VK3-20_9_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAG TBHCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCC TCCTMTCACT	3089	3551
VK3-20_1_2_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMSWMTACGGAAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMSWMTACGGAAGTAGTCC TCCTWGGACT	3090	3552
VK3-20_10_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTAGTCC TCCTWGGACT	3091	3553
VK3-20_11_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVN CAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCAGTCC TCCTWGGACT	3092	3554
VK3-20_12_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAAGTBHCCC TCCTWGGACT	3093	3555
VK3-20_13_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVN CAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCAGTCC TCCTWGGACT	3094	3556
VK3-20_14_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCAGTBHCCC TCCTWGGACT	3095	3557
VK3-20_15_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACGGAVN CBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACGGAVNCBHCCC TCCTWGGACT	3096	3558
VK3-20_2_2_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGBHCGGAAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGBHCGGAAGTAGTCC TCCTWGGACT	3097	3559

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VK3-20_3_2_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACBHCAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACBHCAGTAGTCC TCCTWGGACT	3098	3560
VK3-20_4_2_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAVN CAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAVNCAGTCC TCCTWGGACT	3099	3561
VK3-20_5_2_10	CCTGAAGATTTTGCAGTGTATTACTGTSWMCAGTACGGAAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	SWMCAGTACGGAAGTBHCCC TCCTWGGACT	3100	3562
VK3-20_6_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMBHCGGAAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMBHCGGAAGTAGTCC TCCTWGGACT	3101	3563
VK3-20_7_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACBHCAG TAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACBHCAGTAGTCC TCCTWGGACT	3102	3564
VK3-20_8_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAVN CAGTCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAVNCAGTCC TCCTWGGACT	3103	3565
VK3-20_9_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGSWMTACGGAAG TBHCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGSWMTACGGAAGTBHCCC TCCTWGGACT	3104	3566
Jumping Trimer				
VK1-05_t1_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTACY CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTCC TTWCACT	3105	3567
VK1-05_t1_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTACY CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTCC TMTCACT	3106	3568
VK1-05_t1_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMMBCTACY CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMMBCTACYCTCC TWGGACT	3107	3569
VK1-05_t2_0_10	CCTGATCATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWCY CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTCC TTWCACT	3108	3570
VK1-05_t2_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWCY CTCCTMTCACTTTTGGCCGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTCC TMTCACT	3109	3571
VK1-05_t2_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCAATMBCYWCY CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATMBCYWCYCTCC TWGGACT	3110	3572
VK1-05_t3_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWCY CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTCC TTWCACT	3111	3573
VK1-05_t3_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWCY CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTCC TMTCACT	3112	3574
VK1-05_t3_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGBHCVRMAGTYWCY CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCVRMAGTYWCYCTCC TWGGACT	3113	3575
VK1-05_t4_0_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWCY CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTCC TTWCACT	3114	3576
VK1-05_t4_1_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWCY CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTCC TMTCACT	3115	3577

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VK1-05_t4_2_10	CCTGATGATTTTGCAACTTATTACTGCCAGCAGTACVRMMBCYWCY CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACVRMMBCYWCYCTCC TWGGACT	3116	3578
VK1-12_t1_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTCC TTWCACT	3117	3579
VK1-12_t1_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTCC CTCCTMTCACTTTTGGCGGCAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTCC TMTCACT	3118	3580
VK1-12_t1_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCNHCTTCC CTCCTWGGACTTTTGGCGGCAGGGACCAAG	CAGCAGRNANHCNHCTTCCCTCC TWGGACT	3119	3581
VK1-12_t2_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTCC TTWCACT	3120	3582
VK1-12_t2_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTCC TMTCACT	3121	3583
VK1-12_t2_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNANHCAGTYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNANHCAGTYWCCCTCC TWGGACT	3122	3584
VK1-12_t3_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTCC TTWCACT	3123	3585
VK1-12_t3_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTCC TMTCACT	3124	3586
VK1-12_t3_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGRNAAATNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGRNAAATNHCYWCCCTCC TWGGACT	3125	3587
VK1-12_t4_0_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTCC TTWCACT	3126	3588
VK1-12_t4_1_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTCC TMTCACT	3127	3589
VK1-12_t4_2_10	CCTGAAGATTTTGCAACTTATTACTGTCAGCAGGCANHCNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGGCANHCNHCYWCCCTCC TWGGACT	3128	3590
VK1-33_t1_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTCC TTWCACT	3129	3591
VK1-33_t1_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTCC TMTCACT	3130	3592
VK1-33_t1_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCNHCCTCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCCTCCCTCC TWGGACT	3131	3593
VK1-33_t2_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TTWCACT	3132	3594
VK1-33_t2_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TMTCACT	3133	3595
VK1-33_t2_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCNHCAATYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TWGGACT	3134	3596
VK1-33_t3_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTCC TTWCACT	3135	3597

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VK1-33_t3_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTCC TMTCACT	3136	3598
VK1-33_t3_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGBHCGATNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGATNHCYWCCCTCC TWGGACT	3137	3599
VK1-33_t4_0_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TTWCACT	3138	3600
VK1-33_t4_1_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TMTCACT	3139	3601
VK1-33_t4_2_10	CCTGAAGATATTGCAACATATTACTGTCAGCAGTACNHCNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TWGGACT	3140	3602
VK1-39_t1_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACTC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTCC TTWCACT	3141	3603
VK1-39_t1_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACTC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTCC TMTCACT	3142	3604
VK1-39_t1_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCNHCACTC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCNHCACTCCTCC TWGGACT	3143	3605
VK1-39_t2_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTCC TTWCACT	3144	3606
VK1-39_t2_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTCC TMTCACT	3145	3607
VK1-39_t2_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNABHCAGTBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNABHCAGTBHCCCTCC TWGGACT	3146	3608
VK1-39_t3_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTCC TTWCACT	3147	3609
VK1-39_t3_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTCC TMTCACT	3148	3610
VK1-39_t3_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAVNATACNHCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAVNATACNHCBHCCCTCC TWGGACT	3149	3611
VK1-39_t4_0_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTCC TTWCACT	3150	3612
VK1-39_t4_1_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTCC TMTCACT	3151	3613
VK1-39_t4_2_10	CCTGAAGATTTTGCAACTTACTACTGTCAGCAAAGCBHCNHCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAAAGCBHCNHCBHCCCTCC TWGGACT	3152	3614
VK2-28_t1_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACTC CTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTCC TTWCACT	3153	3615
VK2-28_t1_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACTC CTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTCC TMTCACT	3154	3616
VK2-28_t1_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNASRMACTC CTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNASRMACTCCTCC TWGGACT	3155	3617

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VK2-28_t2_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTCC TTWCACT	3156	3618
VK2-28_t2_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTCC TMTCACT	3157	3619
VK2-28_t2_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNAMNACAGVBCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	ATGCAGVNAMNACAGVBCCCTCC TWGGACT	3158	3620
VK2-28_t3_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTCC TTWCACT	3159	3621
VK2-28_t3_1_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTCC TMTCACT	3160	3622
VK2-28_t3_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGVNACTCSRMVBCC CTCCTWGCACTTTTGGCGGAGGGACCAAG	ATGCAGVNACTCSRMVBCCCTCC TWGGACT	3161	3623
VK2-28_t4_0_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	ATGCAGGCAMNASRMVBCCCTCC TTWCACT	3162	3624
VK2-28_t4_1_10	GCTCAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	ATCCAGGCAMNASRMVBCCCTCC TMTCACT	3163	3625
VK2-28_t4_2_10	GCTGAGGATGTTGGGGTTTATTACTGCATGCAGGCAMNASRMVBCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	ATCCAGGCAMNASRMVBCCCTCC TWGGACT	3164	3626
VK3-11_t1_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGGC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TTWCACT	3165	3627
VK3-11_t1_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGGC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TMTCACT	3166	3628
VK3-11_t1_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCTGGC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TWGGACT	3167	3629
VK3-11_t2_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TTWCACT	3168	3594
VK3-11_t2_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TMTCACT	3169	3595
VK3-11_t2_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TWGGACT	3170	3596
VK3-11_t3_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTCC TTWCACT	3171	3630
VK3-11_t3_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTCC TMTCACT	3172	3631
VK3-11_t3_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAGTNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAGTNHCYWCCCTCC TWGGACT	3173	3632
VK3-11_t4_0_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTCC TTWCACT	3174	3633
VK3-11_t4_1_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTCC TMTCACT	3175	3634

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VK3-11_t4_2_10	CCTGAAGATTTTGCAGTTTATTACTGTCAGCAGAGANHCNHCYWCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGAGANHCNHCYWCCCTCC TWGGACT	3176	3635
VK3-15_t1_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCT GGCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TTWCACT	3177	3627
VK3-15_t1_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCT GGCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TMTCACT	3178	3628
VK3-15_t1_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCNHCT GGCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCNHCTGGCCTCC TWGGACT	3179	3629
VK3-15_t2_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATY WCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TTWCACT	3180	3594
VK3-15_t2_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATY WCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TMTCACT	3181	3595
VK3-15_t2_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCNHCAATY WCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCNHCAATYWCCCTCC TWGGACT	3182	3596
VK3-15_t3_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHCY WCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTCC TTWCACT	3183	3636
VK3-15_t3_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHCY WCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTCC TMTCACT	3184	3637
VK3-15_t3_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGBHCAATNHCY WCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCAATNHCYWCCCTCC TWGGACT	3185	3638
VK3-15_t4_0_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHCY WCCCTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TTWCACT	3186	3600
VK3-15_t4_1_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHCY WCCCTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TMTCACT	3187	3601
VK3-15_t4_2_10	CAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACNHCNHCY WCCCTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACNHCNHCYWCCCTCC TWGGACT	3188	3602
VK3-20_t1_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGTC CTCCTTWCACTTTTGGCGGAGGACCAAG	CAGCAGBHCBHCVNCAGTCCTCC TTWCACT	3189	3639
VK3-20_t1_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGTC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTCC TMTCACT	3190	3640
VK3-20_t1_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCVNCAGTC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCVNCAGTCCTCC TWGGACT	3191	3641
VK3-20_t2_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TTWCACT	3192	3642
VK3-20_t2_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TMTCACT	3193	3643
VK3-20_t2_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TWGGACT	3194	3644
VK3-20_t3_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTCC TTWCACT	3195	3645

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VK3-20_t3_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTCC TMTCACT	3196	3646
VK3-20_t3_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGBHCGGAVNCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCGGAVNCBHCCCTCC TWGGACT	3197	3647
VK3-20_t4_0_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTCC TTWCACT	3198	3648
VK3-20_t4_1_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTCC TMTCACT	3199	3649
VK3-20_t4_2_10	CCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACBHCVNCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCVNCBHCCCTCC TWGGACT	3200	3650
VK4-01_t1_0_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACTC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTCC TTWCACT	3201	3651
VK4-01_t1_1_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACTC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTCC TMTCACT	3202	3652
VK4-01_t1_2_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCNHCACTC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCNHCACTCCTCC TWGGACT	3203	3653
VK4-01_t2_0_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TTWCACT	3204	3642
VK4-01_t2_1_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TMTCACT	3205	3643
VK4-01_t2_2_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCBHCAGTBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCBHCAGTBHCCCTCC TWGGACT	3206	3644
VK4-01_t3_0_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTCC TTWCACT	3207	3654
VK4-01_t3_1_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTCC TMTCACT	3208	3655
VK4-01_t3_2_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGBHCTACNHCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGBHCTACNHCBHCCCTCC TWGGACT	3209	3656
VK4-01_t4_0_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHCC CTCCTTWCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTCC TTWCACT	3210	3657
VK4-01_t4_1_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHCC CTCCTMTCACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTCC TMTCACT	3211	3658
VK4-01_t4_2_10	GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTACBHCNHCBHCC CTCCTWGGACTTTTGGCGGAGGGACCAAG	CAGCAGTACBHCNHCBHCCCTCC TWGGACT	3212	3659

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Table 8. Number of unique CDRL3 amino acid sequences in exemplary jumping dimer ("JD") and jumping trimer ("JT") VK libraries and comparison to VK-v1.0.

	L = 8 aa		L = 9 aa		L = 10 aa	
Jumping Dimer						
Germline	JD	VK-v1.0	JD	VK-v1.0	JD	VK-v1.0
VK1-05	3549	3072	7098	6144	6084	13824
VK1-12	5250	2016	5250	2016	4500	5184
VK1-33	5502	4032	5502	4032	4716	10368
VK1-39	7224	3024	7224	3024	6192	7776
VK2-28	4396	2016	4396	2016	3768	5184
VK3-11	6048	2352	6048	2016	5184	6048
VK3-15	5789	2016	5789	2352	4962	5184
VK3-20	6405	2016	6671	2016	5490	5184
VK4-01	NPE*	2016	6405	2592	NPE*	5184
Total	$4.42*10^4$	$2.26*10^4$	$5.44*10^4$	$2.62*10^4$	$4.09*10^4$	$6.39*10^4$
Jumping Trimer						
Germline	JT	VK-v1.0	JT	VK-v1.0	JT	VK-v1.0
VK1-05	7872	3072	13776	6144	11808	13824
VK1-12	14469	2016	14469	2016	12402	5184
VK1-33	15960	4032	15960	4032	13680	10368
VK1-39	28980	3024	28980	3024	24840	7776
VK2-28	12306	2016	12306	2016	10548	5184
VK3-11	18900	2352	18900	2016	16200	6048
VK3-15	18256	2016	18256	2352	15648	5184
VK3-20	23688	2016	23688	2016	20304	5184
VK4-01	23688	2016	23688	2592	20304	5184
Total	$1.64*10^5$	$2.26*10^4$	$1.70*10^5$	$2.62*10^4$	$1.46*10^5$	$6.39*10^4$

* Not Presently Exemplified. However, given the teachings of the specification, a person of ordinary skill in the art could readily produce a library of such lengths, and these lengths are included within the scope of the invention.

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Table 9. Matching output for exemplary CDRH3 sequences from the HPS and TSP1. Amino acid mismatches in the theoretical design are indicated in bold.

Test Case	CDRH3 Sequence from HPS	SEQ ID NO	Mismatches	TN1	SEQ ID NO	DH	SEQ ID NO	N2	H3-JH	SEQ ID NO
1	RTAHHFDY	3660	0	R		TA		H	HFDY	4582
2.1	VGIVGAASY	3661	0	V		GIVGA	3751	AS	Y	
2.2	VGIVGAASY	3661	0	VG		IVGA	3755	AS	Y	
3.1	DRYSGHDLGY	3662	1	DR		YSG**Y**D	4389	LG	Y	
4.1	GIAAADSNWLDP	3663	1	-		GIAAA	4448	D	SNW**F**DP	4600
4.2	GIAAADSNWLDP	3663	1	-		IAAA	4452	D	SNW**F**DP	4600
5.1	ERTINWGWGGVYAFDI	3664	3	E**G**T**G**	3707	NWG		**G**GV	YAFDI	4540
5.2	ERTINWGWGGVYAFDI	3664	3	E**G**T**G**	3707	NWG		WG**T**	YAFDI	4540
5.3	ERTINWGWGGVYAFDI	3664	3	ER**GG**	3719	NWG		**G**GV	YAFDI	4540

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5.4	ERTINWGWGGVYAFDI	3664	3	ERGG	3719	NWG		WGT	YAFDI	4540

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Table 10. Theoretical segment pool of 212 TN1 sequences contained in Theoretical Segment Pool 1 (TSP1).

TN1 Segment Name	Amino Acid Sequence	TN1 Segment Name	Amino Acid Sequence	SEQ ID NO
P000	-	P107	PT	n/a
P001	E	P108	EPT	n/a
P002	D	P109	DPT	n/a
P003	G	P110	GPT	n/a
P004	EG	P111	PV	n/a
P005	DG	P112	EPV	n/a
P006	GG	P113	DPV	n/a
P007	R	P114	GPV	n/a
P008	ER	P115	RP	n/a
P009	DR	P116	ERP	n/a
P010	GR	P117	DRP	n/a
P011	S	P118	GRP	n/a
P012	ES	P119	SP	n/a
P013	DS	P120	ESP	n/a
P014	GS	P121	DSP	n/a
P015	P	P122	GSP	n/a
P016	EP	P123	LP	n/a
P017	DP	P124	ELP	n/a
P018	GP	P125	DLP	n/a
P019	L	P126	GLP	n/a
P020	EL	P127	AP	n/a
P021	DL	P128	EAP	n/a
P022	GL	P129	DAP	n/a
P023	A	P130	GAP	n/a
P024	EA	P131	TP	n/a
P025	DA	P132	ETP	n/a
P026	GA	P133	DTP	n/a
P027	T	P134	GTP	n/a

P028	ET	P135	VP	n/a
P029	DT	P136	EVP	n/a
P030	GT	P137	DVP	n/a
P031	V	P138	GVP	n/a
P032	EV	P139	AGG	n/a
P033	DV	P140	EAGG	3665
P034	GV	P141	DAGG	3666
P035	EGG	P142	GAGG	3667
P036	DGG	P143	EGAG	3668
P037	GGG	P144	DGAG	3669
P038	EGR	P145	GGAG	3670
P039	DGR	P146	EGGA	3671
P040	GGR	P147	DGGA	3672
P041	EGS	P148	GGGA	3673
P042	DGS	P149	EGGG	3674
P043	GGS	P150	DGGG	3675
P044	EGP	P151	GGGG	3676
P045	DGP	P152	EGGL	3677
P046	GGP	P153	DGGL	3678
P047	EGL	P154	GGGL	3679
P048	DGL	P155	EGGP	3680
P049	GGL	P156	DGGP	3681
P050	EGA	P157	GGGP	3682
P051	DGA	P158	EGGR	3683
P052	GGA	P159	DGGR	3684
P053	EGT	P160	GGGR	3685
P054	DGT	P161	EGGS	3686
P055	GGT	P162	DGGS	3687
P056	EGV	P163	GGGS	3688
P057	DGV	P164	EGGT	3689
P058	GGV	P165	DGGT	3690
P059	RG	P166	GGGT	3691

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P060	ERG	P167	EGGV	3692
P061	DRG	P168	DGGV	3693
P062	GRG	P169	GGGV	3694
P063	SG	P170	EGLG	3695
P064	ESG	P171	DGLG	3696
P065	DSG	P172	GGLG	3697
P066	GSG	P173	EGPG	3698
P067	PG	P174	DGPG	3699
P068	EPG	P175	GGPG	3700
P069	DPG	P176	EGRG	3701
P070	GPG	P177	DGRG	3702
P071	LG	P178	GGRG	3703
P072	ELG	P179	EGSG	3704
P073	DLG	P180	DGSG	3705
P074	GLG	P181	GGSG	3706
P075	AG	P182	EGTG	3707
P076	EAG	P183	DGTG	3708
P077	DAG	P184	GGTG	3709
P078	GAG	P185	EGVG	3710
P079	TG	P186	DGVG	3711
P080	ETG	P187	GGVG	3712
P081	DTG	P188	LGG	n/a
P082	GTG	P189	ELGG	3713
P083	VG	P190	DLGG	3714
P084	EVG	P191	GLGG	3715
P085	DVG	P192	PGG	n/a
P086	GVG	P193	EPGG	3716
P087	PR	P194	DPGG	3717
P088	EPR	P195	GPGG	3718
P089	DPR	P196	RGG	n/a
P090	GPR	P197	ERGG	3719
P091	PS	P198	DRGG	3720

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P092	EPS	P199	GRGG	3721
P093	DPS	P200	SGG	n/a
P094	GPS	P201	ESGG	3722
P095	PP	P202	DSGG	3723
P096	EPP	P203	GSGG	3724
P097	DPP	P204	TGG	n/a
P098	GPP	P205	ETGG	3725
P099	PL	P206	DTGG	3726
P100	EPL	P207	GTGG	3727
P101	DPL	P208	VGG	n/a
P102	GPL	P209	EVGG	3728
P103	PA	P210	DVGG	3729
P104	EPA	P211	GVGG	3730
P105	DPA			
P106	GPA			

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Table 11. 1K DH Theoretical Segment Pool sequences (1,111 DH segments).

DH Segment Name	Amino Acid Sequence	SEQ ID NO	DH Segment Name	Amino Acid Sequence	SEQ ID NO
DHUNIV_001	GTTGTT	3731	DHUNIV_557	YDYV	4107
DHUNIV_002	GTTGT	3732	DHUNIV_558	DYVW	4108
DHUNIV_003	TTGTT	3733	DHUNIV_559	YVWG	4109
DHUNIV_004	GTTG	3734	DHUNIV_560	VWGS	4110
DHUNIV_005	TTGT	3735	DHUNIV_561	WGSY	4111
DHUNIV_006	TGTT	3736	DHUNIV_562	GSYA	4112
DHUNIV_007	GTT	n/a	DHUNIV_563	SYAY	4113
DHUNIV_008	TTG	n/a	DHUNIV_564	YAYT	4114
DHUNIV_009	TGT	n/a	DHUNIV_565	YYD	n/a
DHUNIV_010	GT	n/a	DHUNIV_566	YDY	n/a
DHUNIV_011	TT	n/a	DHUNIV_567	DYV	n/a
DHUNIV_012	TG	n/a	DHUNIV_568	YVW	n/a
DHUNIV_013	VQLER	3737	DHUNIV_569	VWG	n/a
DHUNIV_014	VQLE	3738	DHUNIV_570	WGS	n/a
DHUNIV_015	QLER	3739	DHUNIV_571	SYA	n/a
DHUNIV_016	VQL	n/a	DHUNIV_572	YAY	n/a
DHUNIV_017	QLE	n/a	DHUNIV_573	AYT	n/a
DHUNIV_018	LER	n/a	DHUNIV_574	YD	n/a
DHUNIV_019	VQ	n/a	DHUNIV_575	DY	n/a
DHUNIV_020	QL	n/a	DHUNIV_576	YV	n/a
DHUNIV_021	LE	n/a	DHUNIV_577	VW	n/a
DHUNIV_022	ER	n/a	DHUNIV_578	WG	n/a
DHUNIV_023	YNWND	3740	DHUNIV_579	IMITFGGVMLIP	4115
DHUNIV_024	YNWN	3741	DHUNIV_580	IMITFGGVMLI	4116
DHUNIV_025	NWND	3742	DHUNIV_581	MITFGGVMLIP	4117
DHUNIV_026	YNW	n/a	DHUNIV_582	IMITFGGVML	4118
DHUNIV_027	NWN	n/a	DHUNIV_583	MITFGGVMLI	4119
DHUNIV_028	WND	n/a	DHUNIV_584	ITFGGVMLIP	4120
DHUNIV_029	YN	n/a	DHUNIV_585	IMITFGGVM	4121

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DHUNIV_030	NW	n/a	DHUNIV_586	MITFGGVML	4122
DHUNIV_031	WN	n/a	DHUNIV_587	ITFGGVMLI	4123
DHUNIV_032	ND	n/a	DHUNIV_588	TFGGVMLIP	4124
DHUNIV_033	GITGTT	3743	DHUNIV_589	IMITFGGV	4125
DHUNIV_034	GITGT	3744	DHUNIV_590	MITFGGVM	4126
DHUNIV_035	ITGTT	3745	DHUNIV_591	ITFGGVML	4127
DHUNIV_036	GITG	3746	DHUNIV_592	TFGGVMLI	4128
DHUNIV_037	ITGT	3747	DHUNIV_593	FGGVMLIP	4129
DHUNIV_038	GIT	n/a	DHUNIV_594	IMITFGG	4130
DHUNIV_039	ITG	n/a	DHUNIV_595	MITFGGV	4131
DHUNIV_040	GI	n/a	DHUNIV_596	ITFGGVM	4132
DHUNIV_041	IT	n/a	DHUNIV_597	TFGGVML	4133
DHUNIV_042	GIVGATT	3748	DHUNIV_598	FGGVMLI	4134
DHUNIV_043	GIVGAT	3749	DHUNIV_599	GGVMLIP	4135
DHUNIV_044	IVGATT	3750	DHUNIV_600	IMITFG	4136
DHUNIV_045	GIVGA	3751	DHUNIV_601	MITFGG	4137
DHUNIV_046	IVGAT	3752	DHUNIV_602	ITFGGV	4138
DHUNIV_047	VGATT	3753	DHUNIV_603	TFGGVM	4139
DHUNIV_048	GIVG	3754	DHUNIV_604	FGGVML	4140
DHUNIV_049	IVGA	3755	DHUNIV_605	GGVMLI	4141
DHUNIV_050	VGAT	3756	DHUNIV_606	GVMLIP	4142
DHUNIV_051	GATT	3757	DHUNIV_607	IMITF	4143
DHUNIV_052	GIV	n/a	DHUNIV_608	MITFG	4144
DHUNIV_053	IVG	n/a	DHUNIV_609	ITFGG	4145
DHUNIV_054	VGA	n/a	DHUNIV_610	TFGGV	4146
DHUNIV_055	GAT	n/a	DHUNIV_611	FGGVM	4147
DHUNIV_056	ATT	n/a	DHUNIV_612	GGVML	4148
DHUNIV_057	IV	n/a	DHUNIV_613	GVMLI	4149
DHUNIV_058	VG	n/a	DHUNIV_614	VMLIP	4150
DHUNIV_059	GA	n/a	DHUNIV_615	IMIT	4151
DHUNIV_060	AT	n/a	DHUNIV_616	MITF	4152
DHUNIV_061	WELL	3758	DHUNIV_617	ITFG	4153

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DHUNIV_062	WEL	n/a	DHUNIV_618	TFGG	4154
DHUNIV_063	ELL	n/a	DHUNIV_619	FGGV	4155
DHUNIV_064	WE	n/a	DHUNIV_620	GGVM	4156
DHUNIV_065	EL	n/a	DHUNIV_621	GVML	4157
DHUNIV_066	LL	n/a	DHUNIV_622	VMLI	4158
DHUNIV_067	YSGSYY	3759	DHUNIV_623	MLIP	4159
DHUNIV_068	YSGSY	3760	DHUNIV_624	IMI	n/a
DHUNIV_069	SGSYY	3761	DHUNIV_625	MIT	n/a
DHUNIV_070	YSGS	3762	DHUNIV_626	ITF	n/a
DHUNIV_071	SGSY	3763	DHUNIV_627	TFG	n/a
DHUNIV_072	GSYY	3764	DHUNIV_628	FGG	n/a
DHUNIV_073	YSG	n/a	DHUNIV_629	GGV	n/a
DHUNIV_074	SGS	n/a	DHUNIV_630	GVM	n/a
DHUNIV_075	GSY	n/a	DHUNIV_631	VML	n/a
DHUNIV_076	SYY	n/a	DHUNIV_632	MLI	n/a
DHUNIV_077	YS	n/a	DHUNIV_633	LIP	n/a
DHUNIV_078	SG	n/a	DHUNIV_634	IM	n/a
DHUNIV_079	GS	n/a	DHUNIV_635	MI	n/a
DHUNIV_080	SY	n/a	DHUNIV_636	TF	n/a
DHUNIV_081	YY	n/a	DHUNIV_637	VM	n/a
DHUNIV_082	LEL	n/a	DHUNIV_638	LI	n/a
DHUNIV_083	YNWNY	3765	DHUNIV_639	WLLL	4160
DHUNIV_084	NWNY	3766	DHUNIV_640	WLL	n/a
DHUNIV_085	WNY	n/a	DHUNIV_641	WL	n/a
DHUNIV_086	NY	n/a	DHUNIV_642	YYYDSSGYYY	4161
DHUNIV_087	RIL	n/a	DHUNIV_643	YYYDSSGYY	4162
DHUNIV_088	LLL	n/a	DHUNIV_644	YYDSSGYYY	4163
DHUNIV_089	RI	n/a	DHUNIV_645	YYYDSSGY	4164
DHUNIV_090	IL	n/a	DHUNIV_646	YYDSSGYY	4165
DHUNIV_091	WW	n/a	DHUNIV_647	YDSSGYYY	4166
DHUNIV_092	GYCSGGSCYS	3767	DHUNIV_648	YYYDSSG	4167
DHUNIV_093	GYCSGGSCY	3768	DHUNIV_649	YYDSSGY	4168

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DHUNIV_094	YCSGGSCYS	3769	DHUNIV_650	YDSSGYY	4169
DHUNIV_095	GYCSGGSC	3770	DHUNIV_651	DSSGYYY	4170
DHUNIV_096	YCSGGSCY	3771	DHUNIV_652	YYYDSS	4171
DHUNIV_097	CSGGSCYS	3772	DHUNIV_653	YYDSSG	4172
DHUNIV_098	YCSGGSC	3773	DHUNIV_654	YDSSGY	4173
DHUNIV_099	CSGGSCY	3774	DHUNIV_655	DSSGYY	4174
DHUNIV_100	CSGGSC	3775	DHUNIV_656	SSGYYY	4175
DHUNIV_101	SGGS	3776	DHUNIV_657	YYYDS	4176
DHUNIV_102	SGG	n/a	DHUNIV_658	YYDSS	4177
DHUNIV_103	GGS	n/a	DHUNIV_659	YDSSG	4178
DHUNIV_104	GY	n/a	DHUNIV_660	DSSGY	4179
DHUNIV_105	GG	n/a	DHUNIV_661	SSGYY	4180
DHUNIV_106	DIVVVVAATP	3777	DHUNIV_662	SGYYY	4181
DHUNIV_107	DIVVVVAAT	3778	DHUNIV_663	YYYD	4182
DHUNIV_108	IVVVVAATP	3779	DHUNIV_664	YYDS	4183
DHUNIV_109	DIVVVVAA	3780	DHUNIV_665	YDSS	4184
DHUNIV_110	IVVVVAAT	3781	DHUNIV_666	DSSG	4185
DHUNIV_111	VVVVAATP	3782	DHUNIV_667	SSGY	4186
DHUNIV_112	DIVVVVA	3783	DHUNIV_668	SGYY	4187
DHUNIV_113	IVVVVAA	3784	DHUNIV_669	GYYY	4188
DHUNIV_114	VVVVAAT	3785	DHUNIV_670	YDS	n/a
DHUNIV_115	VVVAATP	3786	DHUNIV_671	DSS	n/a
DHUNIV_116	DIVVVV	3787	DHUNIV_672	SSG	n/a
DHUNIV_117	IVVVVA	3788	DHUNIV_673	SGY	n/a
DHUNIV_118	VVVVAA	3789	DHUNIV_674	GYY	n/a
DHUNIV_119	VVVAAT	3790	DHUNIV_675	DS	n/a
DHUNIV_120	VVAATP	3791	DHUNIV_676	ITMIVVVITT	4189
DHUNIV_121	DIVVV	3792	DHUNIV_677	ITMIVVVIT	4190
DHUNIV_122	IVVVV	3793	DHUNIV_678	TMIVVVITT	4191
DHUNIV_123	VVVVA	3794	DHUNIV_679	ITMIVVVI	4192
DHUNIV_124	VVVAA	3795	DHUNIV_680	TMIVVVIT	4193
DHUNIV_125	VVAAT	3796	DHUNIV_681	MIVVVITT	4194

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DHUNIV_126	VAATP	3797	DHUNIV_682	ITMIVVV	4195
DHUNIV_127	DIVV	3798	DHUNIV_683	TMIVVVI	4196
DHUNIV_128	IVVV	3799	DHUNIV_684	MIVVVIT	4197
DHUNIV_129	VVVV	3800	DHUNIV_685	IVVVITT	4198
DHUNIV_130	VVVA	3801	DHUNIV_686	ITMIVV	4199
DHUNIV_131	VVAA	3802	DHUNIV_687	TMIVVV	4200
DHUNIV_132	VAAT	3803	DHUNIV_688	MIVVVI	4201
DHUNIV_133	AATP	3804	DHUNIV_689	IVVVIT	4202
DHUNIV_134	DIV	n/a	DHUNIV_690	VVVITT	4203
DHUNIV_135	IVV	n/a	DHUNIV_691	ITMIV	4204
DHUNIV_136	VVV	n/a	DHUNIV_692	TMIVV	4205
DHUNIV_137	VVA	n/a	DHUNIV_693	MIVVV	4206
DHUNIV_138	VAA	n/a	DHUNIV_694	VVVIT	4207
DHUNIV_139	AAT	n/a	DHUNIV_695	VVITT	4208
DHUNIV_140	ATP	n/a	DHUNIV_696	ITMI	4209
DHUNIV_141	DI	n/a	DHUNIV_697	TMIV	4210
DHUNIV_142	VV	n/a	DHUNIV_698	MIVV	4211
DHUNIV_143	VA	n/a	DHUNIV_699	VVIT	4212
DHUNIV_144	AA	n/a	DHUNIV_700	VITT	4213
DHUNIV_145	TP	n/a	DHUNIV_701	TMI	n/a
DHUNIV_146	YQLL	3805	DHUNIV_702	MIV	n/a
DHUNIV_147	YQL	n/a	DHUNIV_703	VIT	n/a
DHUNIV_148	QLL	n/a	DHUNIV_704	ITT	n/a
DHUNIV_149	YQ	n/a	DHUNIV_705	VLRFLEWLLY	4214
DHUNIV_150	GYCSSTSCYA	3806	DHUNIV_706	VLRFLEWLL	4215
DHUNIV_151	GYCSSTSCY	3807	DHUNIV_707	LRFLEWLLY	4216
DHUNIV_152	YCSSTSCYA	3808	DHUNIV_708	VLRFLEWL	4217
DHUNIV_153	GYCSSTSC	3809	DHUNIV_709	LRFLEWLL	4218
DHUNIV_154	YCSSTSCY	3810	DHUNIV_710	RFLEWLLY	4219
DHUNIV_155	CSSTSCYA	3811	DHUNIV_711	VLRFLEW	4220
DHUNIV_156	YCSSTSC	3812	DHUNIV_712	LRFLEWL	4221
DHUNIV_157	CSSTSCY	3813	DHUNIV_713	RFLEWLL	4222

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DHUNIV_158	CSSISC	3814	DHUNIV_714	FLEWLLY	4223
DHUNIV_159	SSIS	3815	DHUNIV_715	VLRFLE	4224
DHUNIV_160	SSI	n/a	DHUNIV_716	LRFLEW	4225
DHUNIV_161	SIS	n/a	DHUNIV_717	RFLEWL	4226
DHUNIV_162	SS	n/a	DHUNIV_718	FLEWLL	4227
DHUNIV_163	ST	n/a	DHUNIV_719	LEWLLY	4228
DHUNIV_164	TS	n/a	DHUNIV_720	VLRFL	4229
DHUNIV_165	YA	n/a	DHUNIV_721	LRFLE	4230
DHUNIV_166	DIVVVPAAMP	3816	DHUNIV_722	RFLEW	4231
DHUNIV_167	DIVVVPAAM	3817	DHUNIV_723	FLEWL	4232
DHUNIV_168	IVVVPAAMP	3818	DHUNIV_724	LEWLL	4233
DHUNIV_169	DIVVVPAA	3819	DHUNIV_725	EWLLY	4234
DHUNIV_170	IVVVPAAM	3820	DHUNIV_726	VLRF	4235
DHUNIV_171	VVVPAAMP	3821	DHUNIV_727	LRFL	4236
DHUNIV_172	DIVVVPA	3822	DHUNIV_728	RFLE	4237
DHUNIV_173	IVVVPAA	3823	DHUNIV_729	FLEW	4238
DHUNIV_174	VVVPAAM	3824	DHUNIV_730	LEWL	4239
DHUNIV_175	VVPAAMP	3825	DHUNIV_731	EWLL	4240
DHUNIV_176	DIVVVP	3826	DHUNIV_732	WLLY	4241
DHUNIV_177	IVVVPA	3827	DHUNIV_733	VLR	n/a
DHUNIV_178	VVVPAA	3828	DHUNIV_734	LRF	n/a
DHUNIV_179	VVPAAM	3829	DHUNIV_735	RFL	n/a
DHUNIV_180	VPAAMP	3830	DHUNIV_736	FLE	n/a
DHUNIV_181	IVVVP	3831	DHUNIV_737	LEW	n/a
DHUNIV_182	VVVPA	3832	DHUNIV_738	EWL	n/a
DHUNIV_183	VVPAA	3833	DHUNIV_739	RF	n/a
DHUNIV_184	VPAAM	3834	DHUNIV_740	FL	n/a
DHUNIV_185	PAAMP	3835	DHUNIV_741	EW	n/a
DHUNIV_186	VVVP	3836	DHUNIV_742	YYDFWSGYYT	4242
DHUNIV_187	VVPA	3837	DHUNIV_743	YYDFWSGYY	4243
DHUNIV_188	VPAA	3838	DHUNIV_744	YDFWSGYYT	4244
DHUNIV_189	PAAM	3839	DHUNIV_745	YYDFWSGY	4245

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DHUNIV_190	AAMP	3840	DHUNIV_746	YDFWSGYY	4246
DHUNIV_191	VVP	n/a	DHUNIV_747	DFWSGYYT	4247
DHUNIV_192	VPA	n/a	DHUNIV_748	YYDFWSG	4248
DHUNIV_193	PAA	n/a	DHUNIV_749	YDFWSGY	4249
DHUNIV_194	AAM	n/a	DHUNIV_750	DFWSGYY	4250
DHUNIV_195	AMP	n/a	DHUNIV_751	FWSGYYT	4251
DHUNIV_196	VP	n/a	DHUNIV_752	YYDFWS	4252
DHUNIV_197	PA	n/a	DHUNIV_753	YDFWSG	4253
DHUNIV_198	AM	n/a	DHUNIV_754	DFWSGY	4254
DHUNIV_199	MP	n/a	DHUNIV_755	FWSGYY	4255
DHUNIV_200	YQLLY	3841	DHUNIV_756	WSGYYT	4256
DHUNIV_201	QLLY	3842	DHUNIV_757	YYDFW	4257
DHUNIV_202	LLY	n/a	DHUNIV_758	YDFWS	4258
DHUNIV_203	LY	n/a	DHUNIV_759	DFWSG	4259
DHUNIV_204	GYCSSTSCYT	3843	DHUNIV_760	FWSGY	4260
DHUNIV_205	YCSSTSCYT	3844	DHUNIV_761	WSGYY	4261
DHUNIV_206	CSSTSCYT	3845	DHUNIV_762	SGYYT	4262
DHUNIV_207	YT	n/a	DHUNIV_763	YYDF	4263
DHUNIV_208	DIVVVPAAIP	3846	DHUNIV_764	YDFW	4264
DHUNIV_209	DIVVVPAAI	3847	DHUNIV_765	DFWS	4265
DHUNIV_210	IVVVPAAIP	3848	DHUNIV_766	FWSG	4266
DHUNIV_211	IVVVPAAI	3849	DHUNIV_767	WSGY	4267
DHUNIV_212	VVVPAAIP	3850	DHUNIV_768	GYYT	4268
DHUNIV_213	VVVPAAI	3851	DHUNIV_769	YDF	n/a
DHUNIV_214	VVPAAIP	3852	DHUNIV_770	DFW	n/a
DHUNIV_215	VVPAAI	3853	DHUNIV_771	FWS	n/a
DHUNIV_216	VPAAIP	3854	DHUNIV_772	WSG	n/a
DHUNIV_217	VPAAI	3855	DHUNIV_773	YYT	n/a
DHUNIV_218	PAAIP	3856	DHUNIV_774	DF	n/a
DHUNIV_219	PAAI	3857	DHUNIV_775	FW	n/a
DHUNIV_220	AAIP	3858	DHUNIV_776	WS	n/a
DHUNIV_221	AAI	n/a	DHUNIV_777	ITIFGVVIIP	4269

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DHUNIV_222	AIP	n/a	DHUNIV_778	ITIFGVVII	4270
DHUNIV_223	AI	n/a	DHUNIV_779	TIFGVVIIP	4271
DHUNIV_224	IP	n/a	DHUNIV_780	ITIFGVVI	4272
DHUNIV_225	WIL	n/a	DHUNIV_781	TIFGVVII	4273
DHUNIV_226	WI	n/a	DHUNIV_782	IFGVVIIP	4274
DHUNIV_227	SILWW	3859	DHUNIV_783	ITIFGVV	4275
DHUNIV_228	SILW	3860	DHUNIV_784	TIFGVVI	4276
DHUNIV_229	ILWW	3861	DHUNIV_785	IFGVVII	4277
DHUNIV_230	SIL	n/a	DHUNIV_786	FGVVIIP	4278
DHUNIV_231	ILW	n/a	DHUNIV_787	ITIFGV	4279
DHUNIV_232	LWW	n/a	DHUNIV_788	TIFGVV	4280
DHUNIV_233	LLF	n/a	DHUNIV_789	IFGVVI	4281
DHUNIV_234	SI	n/a	DHUNIV_790	FGVVII	4282
DHUNIV_235	LW	n/a	DHUNIV_791	GVVIIP	4283
DHUNIV_236	LF	n/a	DHUNIV_792	ITIFG	4284
DHUNIV_237	AYCGGDCYS	3862	DHUNIV_793	TIFGV	4285
DHUNIV_238	AYCGGDCY	3863	DHUNIV_794	IFGVV	4286
DHUNIV_239	YCGGDCYS	3864	DHUNIV_795	FGVVI	4287
DHUNIV_240	AYCGGDC	3865	DHUNIV_796	GVVII	4288
DHUNIV_241	YCGGDCY	3866	DHUNIV_797	VVIIP	4289
DHUNIV_242	CGGDCYS	3867	DHUNIV_798	ITIF	4290
DHUNIV_243	YCGGDC	3868	DHUNIV_799	TIFG	4291
DHUNIV_244	CGGDCY	3869	DHUNIV_800	IFGV	4292
DHUNIV_245	CGGDC	3870	DHUNIV_801	FGVV	4293
DHUNIV_246	GGD	n/a	DHUNIV_802	GVVI	4294
DHUNIV_247	AY	n/a	DHUNIV_803	VVII	4295
DHUNIV_248	GD	n/a	DHUNIV_804	VIIP	4296
DHUNIV_249	HIVVVIAIP	3871	DHUNIV_805	ITI	n/a
DHUNIV_250	HIVVVIAI	3872	DHUNIV_806	TIF	n/a
DHUNIV_251	IVVVIAIP	3873	DHUNIV_807	IFG	n/a
DHUNIV_252	HIVVVIA	3874	DHUNIV_808	FGV	n/a
DHUNIV_253	IVVVIAI	3875	DHUNIV_809	GVV	n/a

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DHUNIV_254	VVVIAIP	3876	DHUNIV_810	IIP	n/a
DHUNIV_255	HIVVVI	3877	DHUNIV_811	TI	n/a
DHUNIV_256	IVVVIA	3878	DHUNIV_812	IF	n/a
DHUNIV_257	VVVIAI	3879	DHUNIV_813	VLRYFDWLL	4297
DHUNIV_258	VVIAIP	3880	DHUNIV_814	VLRYFDWL	4298
DHUNIV_259	HIVVV	3881	DHUNIV_815	LRYFDWLL	4299
DHUNIV_260	IVVVI	3882	DHUNIV_816	VLRYFDW	4300
DHUNIV_261	VVVIA	3883	DHUNIV_817	LRYFDWL	4301
DHUNIV_262	VVIAI	3884	DHUNIV_818	RYFDWLL	4302
DHUNIV_263	VIAIP	3885	DHUNIV_819	VLRYFD	4303
DHUNIV_264	HIVV	3886	DHUNIV_820	LRYFDW	4304
DHUNIV_265	VVVI	3887	DHUNIV_821	RYFDWL	4305
DHUNIV_266	VVIA	3888	DHUNIV_822	YFDWLL	4306
DHUNIV_267	VIAI	3889	DHUNIV_823	VLRYF	4307
DHUNIV_268	IAIP	3890	DHUNIV_824	LRYFD	4308
DHUNIV_269	HIV	n/a	DHUNIV_825	RYFDW	4309
DHUNIV_270	VVI	n/a	DHUNIV_826	YFDWL	4310
DHUNIV_271	VIA	n/a	DHUNIV_827	FDWLL	4311
DHUNIV_272	IAI	n/a	DHUNIV_828	VLRY	4312
DHUNIV_273	HI	n/a	DHUNIV_829	LRYF	4313
DHUNIV_274	VI	n/a	DHUNIV_830	RYFD	4314
DHUNIV_275	IA	n/a	DHUNIV_831	YFDW	4315
DHUNIV_276	HIVVVTAIP	3891	DHUNIV_832	FDWL	4316
DHUNIV_277	HIVVVTAI	3892	DHUNIV_833	DWLL	4317
DHUNIV_278	IVVVTAIP	3893	DHUNIV_834	LRY	n/a
DHUNIV_279	HIVVVTA	3894	DHUNIV_835	RYF	n/a
DHUNIV_280	IVVVTAI	3895	DHUNIV_836	YFD	n/a
DHUNIV_281	VVVTAIP	3896	DHUNIV_837	FDW	n/a
DHUNIV_282	HIVVVT	3897	DHUNIV_838	DWL	n/a
DHUNIV_283	IVVVTA	3898	DHUNIV_839	RY	n/a
DHUNIV_284	VVVTAI	3899	DHUNIV_840	YF	n/a
DHUNIV_285	VVTAIP	3900	DHUNIV_841	FD	n/a

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DHUNIV_286	IVVVT	3901	DHUNIV_842	DW	n/a
DHUNIV_287	VVVTA	3902	DHUNIV_843	YYDILTGYYN	4318
DHUNIV_288	VVTAI	3903	DHUNIV_844	YYDILTGYY	4319
DHUNIV_289	VTAIP	3904	DHUNIV_845	YDILTGYYN	4320
DHUNIV_290	VVVT	3905	DHUNIV_846	YYDILTGY	4321
DHUNIV_291	VVTA	3906	DHUNIV_847	YDILTGYY	4322
DHUNIV_292	VTAI	3907	DHUNIV_848	DILTGYYN	4323
DHUNIV_293	TAIP	3908	DHUNIV_849	YYDILTG	4324
DHUNIV_294	VVT	n/a	DHUNIV_850	YDILTGY	4325
DHUNIV_295	VTA	n/a	DHUNIV_851	DILTGYY	4326
DHUNIV_296	TAI	n/a	DHUNIV_852	ILTGYYN	4327
DHUNIV_297	VT	n/a	DHUNIV_853	YYDILT	4328
DHUNIV_298	TA	n/a	DHUNIV_854	YDILTG	4329
DHUNIV_299	RILY	3909	DHUNIV_855	DILTGY	4330
DHUNIV_300	ILY	n/a	DHUNIV_856	ILTGYY	4331
DHUNIV_301	MLY	n/a	DHUNIV_857	LTGYYN	4332
DHUNIV_302	ML	n/a	DHUNIV_858	YYDIL	4333
DHUNIV_303	GYCTNGVCYT	3910	DHUNIV_859	YDILT	4334
DHUNIV_304	GYCTNGVCY	3911	DHUNIV_860	DILTG	4335
DHUNIV_305	YCTNGVCYT	3912	DHUNIV_861	ILTGY	4336
DHUNIV_306	GYCTNGVC	3913	DHUNIV_862	LTGYY	4337
DHUNIV_307	YCTNGVCY	3914	DHUNIV_863	TGYYN	4338
DHUNIV_308	CTNGVCYT	3915	DHUNIV_864	YYDI	4339
DHUNIV_309	YCTNGVC	3916	DHUNIV_865	YDIL	4340
DHUNIV_310	CTNGVCY	3917	DHUNIV_866	DILT	4341
DHUNIV_311	CTNGVC	3918	DHUNIV_867	ILTG	4342
DHUNIV_312	TNGV	3919	DHUNIV_868	LTGY	4343
DHUNIV_313	TNG	n/a	DHUNIV_869	TGYY	4344
DHUNIV_314	NGV	n/a	DHUNIV_870	GYYN	4345
DHUNIV_315	TN	n/a	DHUNIV_871	YDI	n/a
DHUNIV_316	NG	n/a	DHUNIV_872	DIL	n/a
DHUNIV_317	GV	n/a	DHUNIV_873	ILT	n/a

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DHUNIV_318	DIVLMVYAIP	3920	DHUNIV_874	LTG	n/a
DHUNIV_319	DIVLMVYAI	3921	DHUNIV_875	TGY	n/a
DHUNIV_320	IVLMVYAIP	3922	DHUNIV_876	LT	n/a
DHUNIV_321	DIVLMVYA	3923	DHUNIV_877	LVIIT	4346
DHUNIV_322	IVLMVYAI	3924	DHUNIV_878	LVII	4347
DHUNIV_323	VLMVYAIP	3925	DHUNIV_879	LVI	n/a
DHUNIV_324	DIVLMVY	3926	DHUNIV_880	LV	n/a
DHUNIV_325	IVLMVYA	3927	DHUNIV_881	DYGDY	4348
DHUNIV_326	VLMVYAI	3928	DHUNIV_882	DYGD	4349
DHUNIV_327	LMVYAIP	3929	DHUNIV_883	YGDY	4350
DHUNIV_328	DIVLMV	3930	DHUNIV_884	DYG	n/a
DHUNIV_329	IVLMVY	3931	DHUNIV_885	YGD	n/a
DHUNIV_330	VLMVYA	3932	DHUNIV_886	GDY	n/a
DHUNIV_331	LMVYAI	3933	DHUNIV_887	TTVTT	4351
DHUNIV_332	MVYAIP	3934	DHUNIV_888	TTVT	4352
DHUNIV_333	DIVLM	3935	DHUNIV_889	TVTT	4353
DHUNIV_334	IVLMV	3936	DHUNIV_890	TTV	n/a
DHUNIV_335	VLMVY	3937	DHUNIV_891	TVT	n/a
DHUNIV_336	LMVYA	3938	DHUNIV_892	VTT	n/a
DHUNIV_337	MVYAI	3939	DHUNIV_893	TV	n/a
DHUNIV_338	VYAIP	3940	DHUNIV_894	LRW	n/a
DHUNIV_339	DIVL	3941	DHUNIV_895	RW	n/a
DHUNIV_340	IVLM	3942	DHUNIV_896	DYGGNS	4354
DHUNIV_341	VLMV	3943	DHUNIV_897	DYGGN	4355
DHUNIV_342	LMVY	3944	DHUNIV_898	YGGNS	4356
DHUNIV_343	MVYA	3945	DHUNIV_899	DYGG	4357
DHUNIV_344	VYAI	3946	DHUNIV_900	YGGN	4358
DHUNIV_345	YAIP	3947	DHUNIV_901	GGNS	4359
DHUNIV_346	IVL	n/a	DHUNIV_902	YGG	n/a
DHUNIV_347	VLM	n/a	DHUNIV_903	GGN	n/a
DHUNIV_348	LMV	n/a	DHUNIV_904	GNS	n/a
DHUNIV_349	MVY	n/a	DHUNIV_905	GN	n/a

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DHUNIV_350	VYA	n/a	DHUNIV_906	NS	n/a
DHUNIV_351	YAI	n/a	DHUNIV_907	TIVVTP	4360
DHUNIV_352	VL	n/a	DHUNIV_908	TIVVT	4361
DHUNIV_353	LM	n/a	DHUNIV_909	TVVTP	4362
DHUNIV_354	MV	n/a	DHUNIV_910	TIVV	4363
DHUNIV_355	VY	n/a	DHUNIV_911	TVVT	4364
DHUNIV_356	VLLWFGELL	3948	DHUNIV_912	VVIP	4365
DHUNIV_357	VLLWFGEL	3949	DHUNIV_913	TVV	n/a
DHUNIV_358	LLWFGELL	3950	DHUNIV_914	VTP	n/a
DHUNIV_359	VLLWFGE	3951	DHUNIV_915	LQ	n/a
DHUNIV_360	LLWFGEL	3952	DHUNIV_916	DYSNY	4366
DHUNIV_361	LWFGELL	3953	DHUNIV_917	DYSN	4367
DHUNIV_362	VLLWFG	3954	DHUNIV_918	YSNY	4368
DHUNIV_363	LLWFGE	3955	DHUNIV_919	DYS	n/a
DHUNIV_364	LWFGEL	3956	DHUNIV_920	YSN	n/a
DHUNIV_365	WFGELL	3957	DHUNIV_921	SNY	n/a
DHUNIV_366	VLLWF	3958	DHUNIV_922	SN	n/a
DHUNIV_367	LLWFG	3959	DHUNIV_923	VDIVATIT	4369
DHUNIV_368	LWFGE	3960	DHUNIV_924	VDIVATI	4370
DHUNIV_369	WFGEL	3961	DHUNIV_925	DIVATIT	4371
DHUNIV_370	FGELL	3962	DHUNIV_926	VDIVAT	4372
DHUNIV_371	VLLW	3963	DHUNIV_927	DIVATI	4373
DHUNIV_372	LLWF	3964	DHUNIV_928	IVATIT	4374
DHUNIV_373	LWFG	3965	DHUNIV_929	VDIVA	4375
DHUNIV_374	WFGE	3966	DHUNIV_930	DIVAT	4376
DHUNIV_375	FGEL	3967	DHUNIV_931	IVATI	4377
DHUNIV_376	GELL	3968	DHUNIV_932	VATIT	4378
DHUNIV_377	VLL	n/a	DHUNIV_933	VDIV	4379
DHUNIV_378	LLW	n/a	DHUNIV_934	DIVA	4380
DHUNIV_379	LWF	n/a	DHUNIV_935	IVAT	4381
DHUNIV_380	WFG	n/a	DHUNIV_936	VATI	4382
DHUNIV_381	FGE	n/a	DHUNIV_937	ATIT	4383

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DHUNIV_382	GEL	n/a	DHUNIV_938	VDI	n/a
DHUNIV_383	WF	n/a	DHUNIV_939	IVA	n/a
DHUNIV_384	FG	n/a	DHUNIV_940	VAT	n/a
DHUNIV_385	GE	n/a	DHUNIV_941	ATI	n/a
DHUNIV_386	YYYGSGSYYN	3969	DHUNIV_942	TII	n/a
DHUNIV_387	YYYGSGSYY	3970	DHUNIV_943	VD	n/a
DHUNIV_388	YYGSGSYYN	3971	DHUNIV_944	WLRL	4384
DHUNIV_389	YYYGSGSY	3972	DHUNIV_945	WLR	n/a
DHUNIV_390	YYGSGSYY	3973	DHUNIV_946	GYSGYDY	4385
DHUNIV_391	YGSGSYYN	3974	DHUNIV_947	GYSGYD	4386
DHUNIV_392	YYYGSGS	3975	DHUNIV_948	YSGYDY	4387
DHUNIV_393	YYGSGSY	3976	DHUNIV_949	GYSGY	4388
DHUNIV_394	YGSGSYY	3977	DHUNIV_950	YSGYD	4389
DHUNIV_395	GSGSYYN	3978	DHUNIV_951	SGYDY	4390
DHUNIV_396	YYYGSG	3979	DHUNIV_952	GYSG	4391
DHUNIV_397	YYGSGS	3980	DHUNIV_953	YSGY	4392
DHUNIV_398	YGSGSY	3981	DHUNIV_954	SGYD	4393
DHUNIV_399	GSGSYY	3982	DHUNIV_955	GYDY	4394
DHUNIV_400	SGSYYN	3983	DHUNIV_956	GYS	n/a
DHUNIV_401	YYYGS	3984	DHUNIV_957	GYD	n/a
DHUNIV_402	YYGSG	3985	DHUNIV_958	VEMATIT	4395
DHUNIV_403	YGSGS	3986	DHUNIV_959	VEMATI	4396
DHUNIV_404	GSGSY	3987	DHUNIV_960	EMATIT	4397
DHUNIV_405	GSYYN	3988	DHUNIV_961	VEMAT	4398
DHUNIV_406	YYYG	3989	DHUNIV_962	EMATI	4399
DHUNIV_407	YYGS	3990	DHUNIV_963	MATIT	4400
DHUNIV_408	YGSG	3991	DHUNIV_964	VEMA	4401
DHUNIV_409	GSGS	3992	DHUNIV_965	EMAT	4402
DHUNIV_410	SYYN	3993	DHUNIV_966	MATI	4403
DHUNIV_411	YYY	n/a	DHUNIV_967	VEM	n/a
DHUNIV_412	YYG	n/a	DHUNIV_968	EMA	n/a
DHUNIV_413	YGS	n/a	DHUNIV_969	MAT	n/a

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DHUNIV_414	GSG	n/a	DHUNIV_970	VE	n/a
DHUNIV_415	YYN	n/a	DHUNIV_971	EM	n/a
DHUNIV_416	YG	n/a	DHUNIV_972	MA	n/a
DHUNIV_417	ITMVRGVIIT	3994	DHUNIV_973	RWLQL	4404
DHUNIV_418	ITMVRGVII	3995	DHUNIV_974	RWLQ	4405
DHUNIV_419	TMVRGVIIT	3996	DHUNIV_975	WLQL	4406
DHUNIV_420	ITMVRGVI	3997	DHUNIV_976	RWL	n/a
DHUNIV_421	TMVRGVII	3998	DHUNIV_977	WLQ	n/a
DHUNIV_422	MVRGVIIT	3999	DHUNIV_978	LQL	n/a
DHUNIV_423	ITMVRGV	4000	DHUNIV_979	RDGYNY	4407
DHUNIV_424	TMVRGVI	4001	DHUNIV_980	RDGYN	4408
DHUNIV_425	MVRGVII	4002	DHUNIV_981	DGYNY	4409
DHUNIV_426	VRGVIIT	4003	DHUNIV_982	RDGY	4410
DHUNIV_427	ITMVRG	4004	DHUNIV_983	DGYN	4411
DHUNIV_428	TMVRGV	4005	DHUNIV_984	GYNY	4412
DHUNIV_429	MVRGVI	4006	DHUNIV_985	RDG	n/a
DHUNIV_430	VRGVII	4007	DHUNIV_986	DGY	n/a
DHUNIV_431	RGVIIT	4008	DHUNIV_987	GYN	n/a
DHUNIV_432	ITMVR	4009	DHUNIV_988	YNY	n/a
DHUNIV_433	TMVRG	4010	DHUNIV_989	RD	n/a
DHUNIV_434	MVRGV	4011	DHUNIV_990	DG	n/a
DHUNIV_435	VRGVI	4012	DHUNIV_991	VDTAMVT	4413
DHUNIV_436	RGVII	4013	DHUNIV_992	VDTAMV	4414
DHUNIV_437	GVIIT	4014	DHUNIV_993	DTAMVT	4415
DHUNIV_438	ITMV	4015	DHUNIV_994	VDTAM	4416
DHUNIV_439	TMVR	4016	DHUNIV_995	DTAMV	4417
DHUNIV_440	MVRG	4017	DHUNIV_996	TAMVT	4418
DHUNIV_441	VRGV	4018	DHUNIV_997	VDTA	4419
DHUNIV_442	RGVI	4019	DHUNIV_998	DTAM	4420
DHUNIV_443	GVII	4020	DHUNIV_999	TAMV	4421
DHUNIV_444	VIIT	4021	DHUNIV_1000	AMVT	4422
DHUNIV_445	ITM	n/a	DHUNIV_1001	VDT	n/a

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DHUNIV_446	TMV	n/a	DHUNIV_1002	DTA	n/a
DHUNIV_447	MVR	n/a	DHUNIV_1003	TAM	n/a
DHUNIV_448	VRG	n/a	DHUNIV_1004	AMV	n/a
DHUNIV_449	RGV	n/a	DHUNIV_1005	MVT	n/a
DHUNIV_450	GVI	n/a	DHUNIV_1006	DT	n/a
DHUNIV_451	VII	n/a	DHUNIV_1007	WIQLWL	4423
DHUNIV_452	IIT	n/a	DHUNIV_1008	WIQLW	4424
DHUNIV_453	TM	n/a	DHUNIV_1009	IQLWL	4425
DHUNIV_454	VR	n/a	DHUNIV_1010	WIQL	4426
DHUNIV_455	RG	n/a	DHUNIV_1011	IQLW	4427
DHUNIV_456	II	n/a	DHUNIV_1012	QLWL	4428
DHUNIV_457	VLLWFRELL	4022	DHUNIV_1013	WIQ	n/a
DHUNIV_458	VLLWFREL	4023	DHUNIV_1014	IQL	n/a
DHUNIV_459	LLWFRELL	4024	DHUNIV_1015	QLW	n/a
DHUNIV_460	VLLWFRE	4025	DHUNIV_1016	LWL	n/a
DHUNIV_461	LLWFREL	4026	DHUNIV_1017	IQ	n/a
DHUNIV_462	LWFRELL	4027	DHUNIV_1018	GYSYGY	4429
DHUNIV_463	VLLWFR	4028	DHUNIV_1019	GYSYG	4430
DHUNIV_464	LLWFRE	4029	DHUNIV_1020	YSYGY	4431
DHUNIV_465	LWFREL	4030	DHUNIV_1021	GYSY	4432
DHUNIV_466	WFRELL	4031	DHUNIV_1022	YSYG	4433
DHUNIV_467	LLWFR	4032	DHUNIV_1023	SYGY	4434
DHUNIV_468	LWFRE	4033	DHUNIV_1024	YSY	n/a
DHUNIV_469	WFREL	4034	DHUNIV_1025	SYG	n/a
DHUNIV_470	FRELL	4035	DHUNIV_1026	YGY	n/a
DHUNIV_471	LWFR	4036	DHUNIV_1027	GYSSSWY	4435
DHUNIV_472	WFRE	4037	DHUNIV_1028	GYSSSW	4436
DHUNIV_473	FREL	4038	DHUNIV_1029	YSSSWY	4437
DHUNIV_474	RELL	4039	DHUNIV_1030	GYSSS	4438
DHUNIV_475	WFR	n/a	DHUNIV_1031	YSSSW	4439
DHUNIV_476	FRE	n/a	DHUNIV_1032	SSSWY	4440
DHUNIV_477	REL	n/a	DHUNIV_1033	GYSS	4441

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DHUNIV_478	FR	n/a	DHUNIV_1034	YSSS	4442
DHUNIV_479	RE	n/a	DHUNIV_1035	SSSW	4443
DHUNIV_480	ITMVQGVIIT	4040	DHUNIV_1036	SSWY	4444
DHUNIV_481	ITMVQGVII	4041	DHUNIV_1037	YSS	n/a
DHUNIV_482	TMVQGVIIT	4042	DHUNIV_1038	SSS	n/a
DHUNIV_483	ITMVQGVI	4043	DHUNIV_1039	SSW	n/a
DHUNIV_484	TMVQGVII	4044	DHUNIV_1040	SWY	n/a
DHUNIV_485	MVQGVIIT	4045	DHUNIV_1041	SW	n/a
DHUNIV_486	ITMVQGV	4046	DHUNIV_1042	WY	n/a
DHUNIV_487	TMVQGVI	4047	DHUNIV_1043	GIAAAGT	4445
DHUNIV_488	MVQGVII	4048	DHUNIV_1044	GIAAAG	4446
DHUNIV_489	VQGVIIT	4049	DHUNIV_1045	IAAAGT	4447
DHUNIV_490	ITMVQG	4050	DHUNIV_1046	GIAAA	4448
DHUNIV_491	TMVQGV	4051	DHUNIV_1047	IAAAG	4449
DHUNIV_492	MVQGVI	4052	DHUNIV_1048	AAAGT	4450
DHUNIV_493	VQGVII	4053	DHUNIV_1049	GIAA	4451
DHUNIV_494	QGVIIT	4054	DHUNIV_1050	IAAA	4452
DHUNIV_495	ITMVQ	4055	DHUNIV_1051	AAAG	4453
DHUNIV_496	TMVQG	4056	DHUNIV_1052	AAGT	4454
DHUNIV_497	MVQGV	4057	DHUNIV_1053	GIA	n/a
DHUNIV_498	VQGVI	4058	DHUNIV_1054	IAA	n/a
DHUNIV_499	QGVII	4059	DHUNIV_1055	AAA	n/a
DHUNIV_500	TMVQ	4060	DHUNIV_1056	AAG	n/a
DHUNIV_501	MVQG	4061	DHUNIV_1057	AGT	n/a
DHUNIV_502	VQGV	4062	DHUNIV_1058	AG	n/a
DHUNIV_503	QGVI	4063	DHUNIV_1059	QQLV	4455
DHUNIV_504	MVQ	n/a	DHUNIV_1060	QQL	n/a
DHUNIV_505	VQG	n/a	DHUNIV_1061	QLV	n/a
DHUNIV_506	QGV	n/a	DHUNIV_1062	QQ	n/a
DHUNIV_507	QG	n/a	DHUNIV_1063	GYSSGWY	4456
DHUNIV_508	LRLGEL	4064	DHUNIV_1064	GYSSGW	4457
DHUNIV_509	LRLGE	4065	DHUNIV_1065	YSSGWY	4458

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DHUNIV_510	RLGEL	4066	DHUNIV_1066	GYSSG	4459
DHUNIV_511	LRLG	4067	DHUNIV_1067	YSSGW	4460
DHUNIV_512	RLGE	4068	DHUNIV_1068	SSGWY	4461
DHUNIV_513	LGEL	4069	DHUNIV_1069	YSSG	4462
DHUNIV_514	LRL	n/a	DHUNIV_1070	SSGW	4463
DHUNIV_515	RLG	n/a	DHUNIV_1071	SGWY	4464
DHUNIV_516	LGE	n/a	DHUNIV_1072	SGW	n/a
DHUNIV_517	LR	n/a	DHUNIV_1073	GWY	n/a
DHUNIV_518	RL	n/a	DHUNIV_1074	GW	n/a
DHUNIV_519	LG	n/a	DHUNIV_1075	GIAVAGT	4465
DHUNIV_520	YYDYVWGSYAYT	4070	DHUNIV_1076	GIAVAG	4466
DHUNIV_521	YYDYVWGSYAY	4071	DHUNIV_1077	IAVAGT	4467
DHUNIV_522	YDYVWGSYAYT	4072	DHUNIV_1078	GIAVA	4468
DHUNIV_523	YYDYVWGSYA	4073	DHUNIV_1079	IAVAG	4469
DHUNIV_524	YDYVWGSYAY	4074	DHUNIV_1080	AVAGT	4470
DHUNIV_525	DYVWGSYAYT	4075	DHUNIV_1081	GIAV	4471
DHUNIV_526	YYDYVWGSY	4076	DHUNIV_1082	IAVA	4472
DHUNIV_527	YDYVWGSYA	4077	DHUNIV_1083	AVAG	4473
DHUNIV_528	DYVWGSYAY	4078	DHUNIV_1084	VAGT	4474
DHUNIV_529	YVWGSYAYT	4079	DHUNIV_1085	IAV	n/a
DHUNIV_530	YYDYVWGS	4080	DHUNIV_1086	AVA	n/a
DHUNIV_531	YDYVWGSY	4081	DHUNIV_1087	VAG	n/a
DHUNIV_532	DYVWGSYA	4082	DHUNIV_1088	AV	n/a
DHUNIV_533	YVWGSYAY	4083	DHUNIV_1089	QWLV	4475
DHUNIV_534	VWGSYAYT	4084	DHUNIV_1090	QWL	n/a
DHUNIV_535	YYDYVWG	4085	DHUNIV_1091	WLV	n/a
DHUNIV_536	YDYVWGS	4086	DHUNIV_1092	QW	n/a
DHUNIV_537	DYVWGSY	4087	DHUNIV_1093	EYSSSS	4476
DHUNIV_538	YVWGSYA	4088	DHUNIV_1094	EYSSS	4477
DHUNIV_539	VWGSYAY	4089	DHUNIV_1095	YSSSS	4478
DHUNIV_540	WGSYAYT	4090	DHUNIV_1096	EYSS	4479
DHUNIV_541	YYDYVW	4091	DHUNIV_1097	SSSS	4480

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DHUNIV_542	YDYVWG	4092	DHUNIV_1098	EYS	n/a
DHUNIV_543	DYVWGS	4093	DHUNIV_1099	EY	n/a
DHUNIV_544	YVWGSY	4094	DHUNIV_1100	SIAARP	4481
DHUNIV_545	VWGSYA	4095	DHUNIV_1101	SIAAR	4482
DHUNIV_546	WGSYAY	4096	DHUNIV_1102	IAARP	4483
DHUNIV_547	GSYAYT	4097	DHUNIV_1103	SIAA	4484
DHUNIV_548	YYDYV	4098	DHUNIV_1104	IAAR	4485
DHUNIV_549	YDYVW	4099	DHUNIV_1105	AARP	4486
DHUNIV_550	DYVWG	4100	DHUNIV_1106	SIA	n/a
DHUNIV_551	YVWGS	4101	DHUNIV_1107	AAR	n/a
DHUNIV_552	VWGSY	4102	DHUNIV_1108	ARP	n/a
DHUNIV_553	WGSYA	4103	DHUNIV_1109	AR	n/a
DHUNIV_554	GSYAY	4104	DHUNIV_1110	RP	n/a
DHUNIV_555	SYAYT	4105	DHUNIV_1111	NWG	n/a
DHUNIV_556	YYDY	4106			

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Table 12. Theoretical segment pool of 141 N2 segments in Theoretical Segment Pool 1 (TSP1).

Segment Type	Sequences	Number
"Zero"	(no addition) V segment joins directly to D segment	1
Monomers	G, P, R, A, S, L, T, V, D, E, F, H, I, K, M, Q, W, Y	18
Dimers	GG, GP, GR, GA, GS, GL, GT, GV, PG, RG, AG, SG, LG, TG, VG, PP, PR, PA, PS, PL, PT, PV, RP, AP, SP, LP, TP, VP, AR, AS, AT, AY, DL, DT, EA, EK, FH, FS, HL, HW, IS, KV, LD, LE, LR, LS, LT, NR, NT, QE, QL, QT, RA, RD, RE, RF, RH, RL, RR, RS, RV, SA, SD, SE, SF, SI, SK, SL, SQ, SR, SS, ST, SV, TA, TR, TS, TT, TW, VD, VS, WS, YS	82
Trimers	GGG, GPG, GRG, GAG, GSG, GLG, GTG, GVG, PGG, RGG, AGG, SGG, LGG, TGG, VGG, GGP, GGR, GGA, GGS, GGL, GGT, GGV , AAE, AYH, DTL, EKR, ISR, NIP, PKS, PRP, PTA, PTQ, REL, RPL, SAA, SAL, SGL, SSE, TGL, WGT	40

Table 13. Theoretical segment pool of 285 H3-JH segments.

H3-JH Segment Name	Amino Acid Sequence	SEQ ID NO	H3-JH Segment Name	Amino Acid Sequence	SEQ ID NO
JHUNIV_001	IEYFQH	4487	JHUNIV_144	ADY	n/a
JHUNIV_002	EYFQH	4488	JHUNIV_145	YDY	n/a
JHUNIV_003	YFQH	4489	JHUNIV_146	NYFDY	4593
JHUNIV_004	FQH	n/a	JHUNIV_147	DNWFDP	4594
JHUNIV_005	QH	n/a	JHUNIV_148	NWFDP	4595
JHUNIV_006	H	n/a	JHUNIV_149	WFDP	4596
JHUNIV_007		n/a	JHUNIV_150	FDP	n/a
JHUNIV_008	SEYFQH	4490	JHUNIV_151	DP	n/a
JHUNIV_009	PEYFQH	4491	JHUNIV_152	P	n/a
JHUNIV_010	FEYFQH	4492	JHUNIV_153	YNWFDP	4597
JHUNIV_011	HEYFQH	4493	JHUNIV_154	HNWFDP	4598
JHUNIV_012	REYFQH	4494	JHUNIV_155	FNWFDP	4599
JHUNIV_013	LEYFQH	4495	JHUNIV_156	SNWFDP	4600
JHUNIV_014	NEYFQH	4496	JHUNIV_157	RNWFDP	4601
JHUNIV_015	IEYFQE	4497	JHUNIV_158	LNWFDP	4602
JHUNIV_016	DEYFQH	4498	JHUNIV_159	PNWFDP	4603
JHUNIV_017	GEYFQH	4499	JHUNIV_160	INWFDP	4604
JHUNIV_018	VEYFQH	4500	JHUNIV_161	TNWFDP	4605
JHUNIV_019	YEYFQH	4501	JHUNIV_162	GNWFDP	4606
JHUNIV_020	KYFQH	4502	JHUNIV_163	VNWFDP	4607
JHUNIV_021	QYFQH	4503	JHUNIV_164	ANWFDP	4608
JHUNIV_022	LYFQH	4504	JHUNIV_165	DWFDP	4609
JHUNIV_023	SYFQH	4505	JHUNIV_166	YWFDP	4610
JHUNIV_024	RYFQH	4506	JHUNIV_167	HWFDP	4611
JHUNIV_025	PYFQH	4507	JHUNIV_168	FWFDP	4612
JHUNIV_026	IYFQH	4508	JHUNIV_169	SWFDP	4613

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JHUNIV_027	TYFQH	4509	JHUNIV_170	RWFDP	4614
JHUNIV_028	GYFQH	4510	JHUNIV_171	LWFDP	4615
JHUNIV_029	VYFQH	4511	JHUNIV_172	PWFDP	4616
JHUNIV_030	AYFQH	4512	JHUNIV_173	IWFDP	4617
JHUNIV_031	NFQH	4513	JHUNIV_174	TWFDP	4618
JHUNIV_032	DFQH	4514	JHUNIV_175	GWFDP	4619
JHUNIV_033	HFQH	4515	JHUNIV_176	VWFDP	4620
JHUNIV_034	FFQH	4516	JHUNIV_177	AWFDP	4621
JHUNIV_035	SFQH	4517	JHUNIV_178	RFDP	4622
JHUNIV_036	RFQH	4518	JHUNIV_179	GFDP	4623
JHUNIV_037	LFQH	4519	JHUNIV_180	LFDP	4624
JHUNIV_038	PFQH	4520	JHUNIV_181	SFDP	4625
JHUNIV_039	IFQH	4521	JHUNIV_182	QFDP	4626
JHUNIV_040	TFQH	4522	JHUNIV_183	PFDP	4627
JHUNIV_041	GFQH	4523	JHUNIV_184	KFDP	4628
JHUNIV_042	VFQH	4524	JHUNIV_185	MFDP	4629
JHUNIV_043	AFQH	4525	JHUNIV_186	TFDP	4630
JHUNIV_044	AEYFQH	4526	JHUNIV_187	EFDP	4631
JHUNIV_045	YWYFDL	4527	JHUNIV_188	VFDP	4632
JHUNIV_046	WYFDL	4528	JHUNIV_189	AFDP	4633
JHUNIV_047	YFDL	4529	JHUNIV_190	NNWFDP	4634
JHUNIV_048	FDL	n/a	JHUNIV_191	DYYYYYGMDV	4635
JHUNIV_049	DL	n/a	JHUNIV_192	YYYYYGMDV	4636
JHUNIV_050	L	n/a	JHUNIV_193	YYYYGMDV	4637
JHUNIV_051	DWYFDL	4530	JHUNIV_194	YYYGMDV	4638
JHUNIV_052	HWYFDL	4531	JHUNIV_195	YYGMDV	4639
JHUNIV_053	NWYFDL	4532	JHUNIV_196	YGMDV	4640
JHUNIV_054	GYFDL	4533	JHUNIV_197	GMDV	4641
JHUNIV_055	RYFDL	4534	JHUNIV_198	MDV	n/a
JHUNIV_056	HFDL	4535	JHUNIV_199	DV	n/a

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JHUNIV_057	NFDL	4536	JHUNIV_200	V	n/a
JHUNIV_058	DFDL	4537	JHUNIV_201	YYYYYYGMDV	4642
JHUNIV_059	DAFDI	4538	JHUNIV_202	HYYYYYGMDV	4643
JHUNIV_060	AFDI	4539	JHUNIV_203	FYYYYYGMDV	4644
JHUNIV_061	FDI	n/a	JHUNIV_204	SYYYYYGMDV	4645
JHUNIV_062	DI	n/a	JHUNIV_205	RYYYYYGMDV	4646
JHUNIV_063	I	n/a	JHUNIV_206	LYYYYYGMDV	4647
JHUNIV_064	YAFDI	4540	JHUNIV_207	PYYYYYGMDV	4648
JHUNIV_065	HAFDI	4541	JHUNIV_208	IYYYYYGMDV	4649
JHUNIV_066	FAFDI	4542	JHUNIV_209	TYYYYYGMDV	4650
JHUNIV_067	SAFDI	4543	JHUNIV_210	GYYYYYGMDV	4651
JHUNIV_068	RAFDI	4544	JHUNIV_211	VYYYYYGMDV	4652
JHUNIV_069	LAFDI	4545	JHUNIV_212	AYYYYYGMDV	4653
JHUNIV_070	PAFDI	4546	JHUNIV_213	NYYYYGMDV	4654
JHUNIV_071	IAFDI	4547	JHUNIV_214	DYYYYGMDV	4655
JHUNIV_072	TAFDI	4548	JHUNIV_215	HYYYYGMDV	4656
JHUNIV_073	GAFDI	4549	JHUNIV_216	FYYYYGMDV	4657
JHUNIV_074	VAFDI	4550	JHUNIV_217	SYYYYGMDV	4658
JHUNIV_075	AAFDI	4551	JHUNIV_218	RYYYYGMDV	4659
JHUNIV_076	TFDI	4552	JHUNIV_219	LYYYYGMDV	4660
JHUNIV_077	SFDI	4553	JHUNIV_220	PYYYYGMDV	4661
JHUNIV_078	PFDI	4554	JHUNIV_221	IYYYYGMDV	4662
JHUNIV_079	FFDI	4555	JHUNIV_222	TYYYYGMDV	4663
JHUNIV_080	HFDI	4556	JHUNIV_223	GYYYYGMDV	4664
JHUNIV_081	RFDI	4557	JHUNIV_224	VYYYYGMDV	4665
JHUNIV_082	LFDI	4558	JHUNIV_225	AYYYYGMDV	4666
JHUNIV_083	NFDI	4559	JHUNIV_226	NYYYGMDV	4667
JHUNIV_084	IFDI	4560	JHUNIV_227	DYYYGMDV	4668
JHUNIV_085	DFDI	4561	JHUNIV_228	HYYYGMDV	4669
JHUNIV_086	GFDI	4562	JHUNIV_229	FYYYGMDV	4670

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JHUNIV_087	VFDI	4563	JHUNIV_230	SYYYGMDV	4671
JHUNIV_088	YFDI	4564	JHUNIV_231	RYYYGMDV	4672
JHUNIV_089	IDI	n/a	JHUNIV_232	LYYYGMDV	4673
JHUNIV_090	VDI	n/a	JHUNIV_233	PYYYGMDV	4674
JHUNIV_091	LDI	n/a	JHUNIV_234	IYYYGMDV	4675
JHUNIV_092	SDI	n/a	JHUNIV_235	TYYYGMDV	4676
JHUNIV_093	HDI	n/a	JHUNIV_236	GYYYGMDV	4677
JHUNIV_094	RDI	n/a	JHUNIV_237	VYYYGMDV	4678
JHUNIV_095	PDI	n/a	JHUNIV_238	AYYYGMDV	4679
JHUNIV_096	NDI	n/a	JHUNIV_239	NYYYYYGMDV	4680
JHUNIV_097	TDI	n/a	JHUNIV_240	DYYYYYYMDV	4681
JHUNIV_098	DDI	n/a	JHUNIV_241	YYYYYYMDV	4682
JHUNIV_099	GDI	n/a	JHUNIV_242	YYYYYMDV	4683
JHUNIV_100	ADI	n/a	JHUNIV_243	YYYYMDV	4684
JHUNIV_101	YDI	n/a	JHUNIV_244	YYYMDV	4685
JHUNIV_102	NAFDI	4565	JHUNIV_245	YYMDV	4686
JHUNIV_103	DYFDY	4566	JHUNIV_246	YMDV	4687
JHUNIV_104	YFDY	4567	JHUNIV_247	YYYYYYYMDV	4688
JHUNIV_105	FDY	n/a	JHUNIV_248	HYYYYYYMDV	4689
JHUNIV_106	DY	n/a	JHUNIV_249	FYYYYYYMDV	4690
JHUNIV_107	Y	n/a	JHUNIV_250	SYYYYYYMDV	4691
JHUNIV_108	YYFDY	4568	JHUNIV_251	RYYYYYYMDV	4692
JHUNIV_109	HYFDY	4569	JHUNIV_252	LYYYYYYMDV	4693
JHUNIV_110	FYFDY	4570	JHUNIV_253	PYYYYYYMDV	4694
JHUNIV_111	SYFDY	4571	JHUNIV_254	IYYYYYYMDV	4695
JHUNIV_112	RYFDY	4572	JHUNIV_255	TYYYYYYMDV	4696
JHUNIV_113	LYFDY	4573	JHUNIV_256	GYYYYYYMDV	4697
JHUNIV_114	PYFDY	4574	JHUNIV_257	VYYYYYYMDV	4698
JHUNIV_115	IYFDY	4575	JHUNIV_258	AYYYYYYMDV	4699
JHUNIV_116	TYFDY	4576	JHUNIV_259	NYYYYYMDV	4700

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JHUNIV_117	GYFDY	4577	JHUNIV_260	DYYYYYMDV	4701
JHUNIV_118	VYFDY	4578	JHUNIV_261	HYYYYYMDV	4702
JHUNIV_119	AYFDY	4579	JHUNIV_262	FYYYYYMDV	4703
JHUNIV_120	NFDY	4580	JHUNIV_263	SYYYYYMDV	4704
JHUNIV_121	DFDY	4581	JHUNIV_264	RYYYYYMDV	4705
JHUNIV_122	HFDY	4582	JHUNIV_265	LYYYYYMDV	4706
JHUNIV_123	FFDY	4583	JHUNIV_266	PYYYYYMDV	4707
JHUNIV_124	SFDY	4584	JHUNIV_267	IYYYYYMDV	4708
JHUNIV_125	RFDY	4585	JHUNIV_268	TYYYYYMDV	4709
JHUNIV_126	LFDY	4586	JHUNIV_269	GYYYYYMDV	4710
JHUNIV_127	PFDY	4587	JHUNIV_270	VYYYYYMDV	4711
JHUNIV_128	IFDY	4588	JHUNIV_271	AYYYYYMDV	4712
JHUNIV_129	TFDY	4589	JHUNIV_272	NYYYYMDV	4713
JHUNIV_130	GFDY	4590	JHUNIV_273	DYYYYMDV	4714
JHUNIV_131	VFDY	4591	JHUNIV_274	HYYYYMDV	4715
JHUNIV_132	AFDY	4592	JHUNIV_275	FYYYYMDV	4716
JHUNIV_133	IDY	n/a	JHUNIV_276	SYYYYMDV	4717
JHUNIV_134	VDY	n/a	JHUNIV_277	RYYYYMDV	4718
JHUNIV_135	LDY	n/a	JHUNIV_278	LYYYYMDV	4719
JHUNIV_136	SDY	n/a	JHUNIV_279	PYYYYMDV	4720
JHUNIV_137	HDY	n/a	JHUNIV_280	IYYYYMDV	4721
JHUNIV_138	RDY	n/a	JHUNIV_281	TYYYYMDV	4722
JHUNIV_139	PDY	n/a	JHUNIV_282	GYYYYMDV	4723
JHUNIV_140	NDY	n/a	JHUNIV_283	VYYYYMDV	4724
JHUNIV_141	TDY	n/a	JHUNIV_284	AYYYYMDV	4725
JHUNIV_142	DDY	n/a	JHUNIV_285	NYYYYYYMDV	4726
JHUNIV_143	GDY	n/a			

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Table 14. Twelve germline IGHJ genes and alleles.

IGHJ Gene	DNA Sequence	SEQ ID NO
IGHJ1-01	GCTGAATACTTCCAGCACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCAG	4727
IGHJ2-01	CTACTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCAG	4728
IGHJ3-01	ATGCTTTTGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG	4729
IGHJ3-02	ATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG	4730
IGHJ4-01	ACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAG	4731
IGHJ4-02	ACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	4732
IGHJ4-03	GCTACTTTGACTACTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCAG	4733
IGHJ5-01	ACAACTGGTTCGACTCCTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAG	4734
IGHJ5-02	ACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG	4735
IGHJ6-01	ATTACTACTACTACTACGGTATGGACGTCTGGGGGCAAGGGACCACGGTCACCGTCTCCTCAG	4736
IGHJ6-02	ATTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG	4737
IGHJ6-03	ATTACTACTACTACTACATGGACGTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCAG	4738

Table 15. Theoretical segment pool of 248 parent H3-JH segments.

H3-JH Parent Segment Name	Amino Acid Sequence	SEQ ID NO	H3-JH Parent Segment Name	Amino Acid Sequence	SEQ ID NO
JHparent001	ADI	n/a	JHparent125	TAFDI	4548
JHparent002	ADY	n/a	JHparent126	TWFDP	4618
JHparent003	DDI	n/a	JHparent127	TYFDY	4576
JHparent004	DDY	n/a	JHparent128	TYFQH	4509
JHparent005	GDI	n/a	JHparent129	VAFDI	4550
JHparent006	GDY	n/a	JHparent130	VWFDP	4620
JHparent007	HDI	n/a	JHparent131	VYFDY	4578
JHparent008	HDY	n/a	JHparent132	VYFQH	4511
JHparent009	IDI	n/a	JHparent133	WYFDL	4528
JHparent010	IDY	n/a	JHparent134	YAFDI	4540
JHparent011	LDI	n/a	JHparent135	YWFDP	4610
JHparent012	LDY	n/a	JHparent136	YYFDY	4568
JHparent013	NDI	n/a	JHparent137	AEYFQH	4526
JHparent014	NDY	n/a	JHparent138	ANWFDP	4608
JHparent015	PDI	n/a	JHparent139	DEYFQH	4498
JHparent016	PDY	n/a	JHparent140	DNWFDP	4594
JHparent017	RDI	n/a	JHparent141	DWYFDL	4530
JHparent018	RDY	n/a	JHparent142	FEYFQH	4492
JHparent019	SDI	n/a	JHparent143	FNWFDP	4599
JHparent020	SDY	n/a	JHparent144	GEYFQH	4499
JHparent021	TDI	n/a	JHparent145	GNWFDP	4606
JHparent022	TDY	n/a	JHparent146	HEYFQH	4493
JHparent023	VDI	n/a	JHparent147	HNWFDP	4598
JHparent024	VDY	n/a	JHparent148	HWYFDL	4531
JHparent025	YDI	n/a	JHparent149	IEYFQH	4497
JHparent026	YDY	n/a	JHparent150	INWFDP	4604
JHparent027	AFDP	4633	JHparent151	LEYFQH	4495

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JHparent028	AFDY	4592	JHparent152	LNWFDP	4602
JHparent029	AFQH	4525	JHparent153	NEYFQH	4496
JHparent030	DFDI	4561	JHparent154	NNWFDP	4634
JHparent031	DFDL	4537	JHparent155	NWYFDL	4532
JHparent032	DFDY	4581	JHparent156	PEYFQH	4491
JHparent033	DFQH	4514	JHparent157	PNWFDP	4603
JHparent034	EFDP	4631	JHparent158	REYFQH	4494
JHparent035	FFDI	4555	JHparent159	RNWFDP	4601
JHparent036	FFDY	4583	JHparent160	SEYFQH	4490
JHparent037	FFQH	4516	JHparent161	SNWFDP	4600
JHparent038	GFDI	4562	JHparent162	TEYFQH	4487
JHparent039	GFDP	4623	JHparent163	TNWFDP	4605
JHparent040	GFDY	4590	JHparent164	VEYFQH	4500
JHparent041	GFQH	4523	JHparent165	VNWFDP	4607
JHparent042	HFDI	4556	JHparent166	YEYFQH	4501
JHparent043	HFDL	4535	JHparent167	YNWFDP	4597
JHparent044	HFDY	4582	JHparent168	YWYFDL	4527
JHparent045	HFQH	4515	JHparent169	AYYYGMDV	4679
JHparent046	IFDI	4560	JHparent170	AYYYYMDV	4725
JHparent047	IFDY	4588	JHparent171	DYYYGMDV	4668
JHparent048	IFQH	4521	JHparent172	DYYYYMDV	4714
JHparent049	KFDP	4628	JHparent173	FYYYGMDV	4670
JHparent050	LFDI	4558	JHparent174	FYYYYMDV	4716
JHparent051	LFDP	4624	JHparent175	GYYYGMDV	4677
JHparent052	LFDY	4586	JHparent176	GYYYYMDV	4723
JHparent053	LFQH	4519	JHparent177	HYYYGMDV	4669
JHparent054	MFDP	4629	JHparent178	HYYYYMDV	4715
JHparent055	NFDI	4559	JHparent179	IYYYGMDV	4675
JHparent056	NFDL	4536	JHparent180	IYYYYMDV	4721
JHparent057	NFDY	4580	JHparent181	LYYYGMDV	4673
JHparent058	NFQH	4513	JHparent182	LYYYYMDV	4719
JHparent059	PFDI	4554	JHparent183	NYYYGMDV	4667

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JHparent060	PFDP	4627	JHparent184	NYYYYMDV	4713
JHparent061	PFDY	4587	JHparent185	PYYYGMDV	4674
JHparent062	PFQH	4520	JHparent186	PYYYYMDV	4720
JHparent063	QFDP	4626	JHparent187	RYYYGMDV	4672
JHparent064	RFDI	4557	JHparent188	RYYYYMDV	4718
JHparent065	RFDP	4622	JHparent189	SYYYGMDV	4671
JHparent066	RFDY	4585	JHparent190	SYYYYMDV	4717
JHparent067	RFQH	4518	JHparent191	TYYYGMDV	4676
JHparent068	SFDI	4553	JHparent192	TYYYYMDV	4722
JHparent069	SFDP	4625	JHparent193	VYYYGMDV	4678
JHparent070	SFDY	4584	JHparent194	VYYYYMDV	4724
JHparent071	SFQH	4517	JHparent195	AYYYYGMDV	4666
JHparent072	TFDI	4552	JHparent196	AYYYYYMDV	4712
JHparent073	TFDP	4630	JHparent197	DYYYYGMDV	4655
JHparent074	TFDY	4589	JHparent198	DYYYYYMDV	4701
JHparent075	TFQH	4522	JHparent199	FYYYYGMDV	4657
JHparent076	VFDI	4563	JHparent200	FYYYYYMDV	4703
JHparent077	VFDP	4632	JHparent201	GYYYYGMDV	4664
JHparent078	VFDY	4591	JHparent202	GYYYYYMDV	4710
JHparent079	VFQH	4524	JHparent203	HYYYYGMDV	4656
JHparent080	YFDI	4564	JHparent204	HYYYYYMDV	4702
JHparent081	YFDL	4529	JHparent205	IYYYYGMDV	4662
JHparent082	AAFDI	4551	JHparent206	IYYYYYMDV	4708
JHparent083	AWFDP	4621	JHparent207	LYYYYGMDV	4660
JHparent084	AYFDY	4579	JHparent208	LYYYYYMDV	4706
JHparent085	AYFQH	4512	JHparent209	NYYYYGMDV	4654
JHparent086	DAFDI	4538	JHparent210	NYYYYYMDV	4700
JHparent087	DWFDP	4609	JHparent211	PYYYYGMDV	4661
JHparent088	DYFDY	4566	JHparent212	PYYYYYMDV	4707
JHparent089	FAFDI	4542	JHparent213	RYYYYGMDV	4659
JHparent090	FWFDP	4612	JHparent214	RYYYYYMDV	4705
JHparent091	FYFDY	4570	JHparent215	SYYYYGMDV	4658

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JHparent092	GAFDI	4549	JHparent216	SYYYYYMDV	4704
JHparent093	GWFDP	4619	JHparent217	TYYYYGMDV	4663
JHparent094	GYFDL	4533	JHparent218	TYYYYYMDV	4709
JHparent095	GYFDY	4577	JHparent219	VYYYYGMDV	4665
JHparent096	GYFQH	4510	JHparent220	VYYYYYMDV	4711
JHparent097	HAFDI	4541	JHparent221	AYYYYYGMDV	4653
JHparent098	HWFDP	4611	JHparent222	AYYYYYYMDV	4699
JHparent099	HYFDY	4569	JHparent223	DYYYYYGMDV	4635
JHparent100	IAFDI	4547	JHparent224	DYYYYYYMDV	4681
JHparent101	IWFDP	4617	JHparent225	FYYYYYGMDV	4644
JHparent102	IYFDY	4575	JHparent226	FYYYYYYMDV	4690
JHparent103	IYFQH	4508	JHparent227	GYYYYYGMDV	4651
JHparent104	KYFQH	4502	JHparent228	GYYYYYYMDV	4697
JHparent105	LAFDI	4545	JHparent229	HYYYYYGMDV	4643
JHparent106	LWFDP	4615	JHparent230	HYYYYYYMDV	4689
JHparent107	LYFDY	4573	JHparent231	IYYYYYGMDV	4649
JHparent108	LYFQH	4504	JHparent232	IYYYYYYMDV	4695
JHparent109	NAFDI	4565	JHparent233	LYYYYYGMDV	4647
JHparent110	NYFDY	4593	JHparent234	LYYYYYYMDV	4693
JHparent111	PAFDI	4546	JHparent235		4680

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				NYYYYYGMDV	
JHparent112	PWFDP	4616	JHparent236	NYYYYYYMDV	4726
JHparent113	PYFDY	4574	JHparent237	PYYYYYGMDV	4648
JHparent114	PYFQH	4507	JHparent238	PYYYYYYMDV	4694
JHparent115	QYFQH	4503	JHparent239	RYYYYYGMDV	4646
JHparent116	RAFDI	4544	JHparent240	RYYYYYYMDV	4692
JHparent117	RWFDP	4614	JHparent241	SYYYYYGMDV	4645
JHparent118	RYFDL	4534	JHparent242	SYYYYYYMDV	4691
JHparent119	RYFDY	4572	JHparent243	TYYYYYGMDV	4650
JHparent120	RYFQH	4506	JHparent244	TYYYYYYMDV	4696
JHparent121	SAFDI	4543	JHparent245	VYYYYYGMDV	4652
JHparent122	SWFDP	4613	JHparent246	VYYYYYYMDV	4698
JHparent123	SYFDY	4571	JHparent247	YYYYYYGMDV	4642
JHparent124	SYFQH	4505	JHparent248	YYYYYYYMDV	4688

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Table 16. Polynucleotide sequences of 27 human IGHD genes and alleles.

IGHD Gene	Polynucleotide Sequence	SEQ ID NO
IGHD1-(1)-01	GGTACAACTGGAACGAC	4739
IGHD1-20	GGTATAACTGGAACGAC	4740
IGHD1-26	GGTATAGTGGGAGCTACTAC	4741
IGHD1-7	GGTATAACTGGAACTAC	4742
IGHD2-15-01	AGGATATTGTAGTGGTGGTAGCTGCTACTCC	4743
IGHD2-2-x	AGGATATTGTAGTAGTACCAGCTGCTATGCC	4744
IGHD2-2-y	AGGATATTGTAGTAGTACCAGCTGCTATACC	4745
IGHD2-2-z	TGGATATTGTAGTAGTACCAGCTGCTATGCC	4746
IGHD2-21-01	AGCATATTGTGGTGGTGATTGCTATTCC	4747
IGHD2-21-02	AGCATATTGTGGTGGTGACTGCTATTCC	4748
IGHD2-8-01	AGGATATTGTACTAATGGTGTATGCTATACC	4749
IGHD3-10-01	GTATTACTATGGTTCGGGGAGTTATTATAAC	4750
IGHD3-10-03	GTATTACTATGGTTCAGGGAGTTATTATAAC	4751
IGHD3-16-02	GTATTATGATTACGTTTGGGGGAGTTATGCTTATACC	4752
IGHD3-22-01	GTATTACTATGATAGTAGTGGTTATTACTAC	4753
IGHD3-3-01	GTATTACGATTTTTGGAGTGGTTATTATACC	4754
IGHD3-9-01	GTATTACGATATTTTGACTGGTTATTATAAC	4755
IGHD4-17	TGACTACGGTGACTAC	4756
IGHD4-23-01	TGACTACGGTGGTAACTCC	4757
IGHD4-4/11-01	TGACTACAGTAACTAC	4758
IGHD5-12-01	GTGGATATAGTGGCTACGATTAC	4759
IGHD5-24-01	GTAGAGATGGCTACAATTAC	4760
IGHD5-5/18-01	GTGGATACAGCTATGGTTAC	4761
IGHD6-13-01	GGGTATAGCAGCAGCTGGTAC	4762
IGHD6-19-01	GGGTATAGCAGTGGCTGGTAC	4763
IGHD6-6-01	GAGTATAGCAGCTCGTCC	4764
IGHD7-27-01	CTAACTGGGGA	4765

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Table 17. Theoretical segment pool of 73 DH parent Segments. "Z" represents a stop codon.

DH Parent Segment Name	Amino Acid Sequence	SEQ ID NO	DH Parent Segment Name	Amino Acid Sequence	SEQ ID NO
DHparent001	LTG	n/a	DHparent038	WIZWLRL	4776
DHparent002	NWG	n/a	DHparent039	VDIVATIT	4369
DHparent003	ZLG	n/a	DHparent040	AYCGGDCYS	3862
DHparent004	DYGDY	4348	DHparent041	HIVVVIAIP	3871
DHparent005	DYSNY	4366	DHparent042	HIVVVTAIP	3891
DHparent006	TTVTI	4351	DHparent043	SILWWZLLF	4777
DHparent007	VQLER	3737	DHparent044	DIVLMVYAIP	3920
DHparent008	VZLEL	4766	DHparent045	DIVVVPAAIP	3846
DHparent009	VZLER	4767	DHparent046	DIVVVPAAMP	3816
DHparent010	VZQLV	4768	DHparent047	DIVVVVAATP	3777
DHparent011	YNWND	3740	DHparent048	GYCSGGSCYS	3767
DHparent012	YNWNY	3765	DHparent049	GYCSSTSCYA	3806
DHparent013	ZLQZL	4769	DHparent050	GYCSSTSCYT	3843
DHparent014	ZLRZL	4770	DHparent051	GYCTNGVCYT	3910
DHparent015	DYGGNS	4354	DHparent052	ITIFGVVIIP	4269
DHparent016	EYSSSS	4476	DHparent053	ITIFZLVIIT	4778 & 8746
DHparent017	GITGTT	3743	DHparent054	ITMIVVVITT	4189
DHparent018	GTTGTT	3731	DHparent055	ITMVQGVIIT	4040
DHparent019	GYSYGY	4429	DHparent056	ITMVRGVIIT	3994
DHparent020	RDGYNY	4407	DHparent057	RILYZWCMLY	4779 & 8747
DHparent021	SIAARP	4481	DHparent058	RILZWWZLLL	4780
DHparent022	ITVVTP	4360	DHparent059	RILZZYQLLC	4781
DHparent023	VZQQLV	4771	DHparent060	RILZZYQLLY	4782
DHparent024	VZQWLV	4772	DHparent061	VLLWFGELLZ	4783
DHparent025	VZWELL	4773	DHparent062	VLLWFRELLZ	4784
DHparent026	WIQLWL	4423	DHparent063	VLLZZZWLLL	4785
DHparent027	YSGSYY	3759	DHparent064	VLRFLEWLLY	4214
DHparent028	ZLRWZL	4774	DHparent065	VLRYFDWLLZ	4786

DHparent029	ZRWLQL	4775	DHparent066	WILZZYQLLC	4787
DHparent030	GIAAAGI	4445	DHparent067	YYDFWSGYYT	4242
DHparent031	GIAVAGI	4465	DHparent068	YYDILTGYYN	4318
DHparent032	GIVGATI	3748	DHparent069	YYYDSSGYYY	4161
DHparent033	GYSGYDY	4385	DHparent070	YYYGSGSYYN	3969
DHparent034	GYSSGWY	4456	DHparent071	IMITFGGVMLIP	4115
DHparent035	GYSSSWY	4435	DHparent072	VLZLRLGELCLY	4788
DHparent036	VDTAMVT	4413	DHparent073	YYDYVWGSYAYT	4070
DHparent037	VEMATIT	4395			

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Table 18. Application of Equation 1 to Test Case 1.

Type	Segment	Weight
TN1	R	1.0
DH	TA	1.0
N2	E	1.0
H3-JH	EFDY (SEQ ID NO: 4582)	1.0

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Table 19. Application of Equation 1 to Test Cases 2.1 and 2.1.

Type	Segment	Weight
TN1	V and VG	0.5 each
DH	GIVGA (SEQ ID NO: 3751) and IVGA (SEQ ID NO: 3755)	0.5 each
N2	AS	1.0
H3-JH	Y	1.0

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Table 20. Application of Equation 1 to Test Case 3.1.

Type	Segment	Weight
TN1	DR	1.0
DH	YSGYD (SEQ ID NO: 4389)	0.8
N2	LG	1.0
H3-JH	Y	1.0

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Table 21. Application of Equation 1 to Test Cases 4.1 and 4.2.

Type	Segment	Weight
TN1	"-" and G	0.5 each
DH	GIAAA (SEQ ID NO: 4448) and IAAA (SEQ ID NO: 4452)	0.5 each
N2	D	1.0
H3-JH	SNWFDP (SEQ ID NO: 4600)	0.83

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Table 22. Application of Equation 1 to all Test Cases.

Type	Segments	Weight
TN1	DR, R, VG, V, G and "-"	0.25, 0.25, 0.125, 0.125, 0.125 and 0.125 respectively
DH	TA, YSGYD (SEQ ID NO: 4389), IAAA (SEQ ID NO: 4452), GIAAA (SEQ ID NO: 4448), IVGA (SEQ ID NO: 3755) and GIVGA (SEQ ID NO: 3751)	0.25, 0.20, 0.125, 0.125, 0.125 and 0.125 respectively
N2	AS, H, D and LG	0.25 each
H3-JH	Y, HFDY (SEQ ID NO: 4582) and SNWFDP (SEQ ID NO: 4600)	0.50, 0.25 and 0.209

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Table 23. Segments used in Exemplary Library Design 1 (ELD-1). The sequences collectively form a theoretical segment pool that comprises individual theoretical segment pools of TN1, DH, N2, and H3-JH segments.

Segment No.	TN1	SEQ ID NO	DH	SEQ ID NO	N2	H3-JH	SEQ ID NO
1	-	n/a	YYYDSSGYY	4162	-	DAFDI	4538
2	G	n/a	YGDY	4350	Y	YYFDY	4568
3	D	n/a	DYGDY	4348	G	Y	n/a
4	A	n/a	YYYDSSGY	4164	D	FDY	n/a
5	V	n/a	YCSSTSCY	3810	S	DY	n/a
6	DR	n/a	YYDSSGY	4168	P	YGMDV	4640
7	S	n/a	YCSGGSCY	3771	F	-	n/a
8	L	n/a	YCSSTSC	3812	L	LDY	n/a
9	DL	n/a	GG	n/a	A	GAFDI	4549
10	R	n/a	RG	n/a	E	YFDY	4567
11	GR	n/a	SGSY	3763	V	YYGMDV	4639
12	T	n/a	YYDSSGYY	4165	H	AFDI	4539
13	GG	n/a	SS	n/a	T	PFDY	4587
14	E	n/a	YDFWSGY	4249	R	GMDV	4641
15	DS	n/a	GYCSSTSC	3809	W	GWFDP	4619
16	VG	n/a	DY	n/a	SG	YYYYGMDV	4637
17	DG	n/a	YYYDSSG	4167	I	IDY	n/a
18	AP	n/a	CSSTSCY	3813	RG	GYFDY	4577
19	GL	n/a	YYDFWSGY	4245	K	GFDY	4590
20	GS	n/a	SSGWY	4461	LG	MDV	n/a
21	DRG	n/a	AG	n/a	Q	VDY	n/a
22	DLG	n/a	DSSGY	4179	GP	YYYGMDV	4638
23	VP	n/a	SSSW	4443	PG	NWFDP	4595
24	DP	n/a	VGAT	3756	LP	PDY	n/a
25	P	n/a	SY	n/a	AG	WFDP	4596
26	EG	n/a	DTAM	4420	GS	NFDY	4580
27	GA	n/a	IAAAG	4449	TS	YWYFDL	4527

28	AG	n/a	YSSSW	4439	SS	NAFDI	4565
29	GV	n/a	GS	n/a	GG	HFDY	4582
30	GP	n/a	YYDSSG	4172	YS	SFDY	4584
31	ER	n/a	VG	n/a	M	YYYYYGMDV	4636
32	DV	n/a	YSSSWY	4437	SL	DYYYGMDV	4668
33	VGG	n/a	YCSGGSC	3773	SP	DFDY	4581
34	SG	n/a	YDSSGYY	4169	SD	YNWFDP	4597
35	GRG	n/a	GI	n/a	AP	DYYYYGMDV	4655
36	DA	n/a	GYCSGGSCY	3768	GR	YYYMDV	4685
37	DRP	n/a	YSSS	4442	TG	LFDY	4586
38	DSG	n/a	SSGW	4463	SR	DYFDY	4566
39	GPR	n/a	TA	n/a	LD	NYYYYGMDV	4654
40	DT	n/a	DSSGYY	4174	LS	GDY	n/a
41	GGG	n/a	GYCSSTSCY	3807	GA	YDY	n/a
42	DRGG	3720	TTVT	4352	VG	SYFDY	4571
43	PL	n/a	YSSGWY	4458	PP	YYMDV	4686
44	DPS	n/a	GW	n/a	RR	TFDY	4589
45	LP	n/a	LG	n/a	GSG	YYYYYYGMDV	4642
46	RG	n/a	DYGD	4349	GT	FFDY	4583
47	GT	n/a	TVTT	4353	TP	SYYYYGMDV	4658
48	LG	n/a	AAA	n/a	RP	VFDY	4591
49	DLP	n/a	YSSGW	4460	RD	YAFDI	4540
50	DGR	n/a	LV	n/a	QL	SDY	n/a
51	ERG	n/a	YYDFWSGYY	4243	TT	WYFDL	4528
52	DGS	n/a	YYDSSGYYY	4163	PL	DWFDP	4609
53	ES	n/a	YYDFWSG	4248	RS	AFDY	4592
54	PS	n/a	YGD	n/a	WS	PYYYYGMDV	4661
55	GGS	n/a	YG	n/a	RV	HYFDY	4569
56	DPR	n/a	GT	n/a	RF	DV	n/a
57	EA	n/a	YSGSY	3760	SF	RFDY	4585
58	GGR	n/a	YYYGSGSY	3972	PT	NYFDY	4593
59	DGG	n/a	LR	n/a	PS	IFDY	4588

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60	SP	n/a	SSS	n/a	AT	ADY	n/a
61	DPG	n/a	GD	n/a	RL	HYYYGMDV	4669
62	DSGG	3723	CSGGSCY	3774	SV	GYYYYYGMDV	4651
63	DPL	n/a	GY	n/a	RA	DWYFDL	4530
64	TP	n/a	YCGGDCY	3866	GRG	GYYYGMDV	4677
65	AGG	n/a	QWLV	4475	VP	YYYYMDV	4684
66	PR	n/a	IAAA	4452	SQ	V	n/a
67	DGT	n/a	QG	n/a	AS	FDP	n/a
68	GLG	n/a	YCSSTSCYT	3844	PR	DDY	n/a
69	DSP	n/a	SG	n/a	VD	GYYYYGMDV	4664
70	GGV	n/a	TTVTT	4351	GV	YMDV	4687
71	GPS	n/a	QQL	n/a	LT	NWYFDL	4532
72	GVG	n/a	IAVA	4472	TR	PYFDY	4574
73	GGA	n/a	GDY	n/a	VS	FDI	n/a
74	RP	n/a	YYYDSSGYYY	4161	SGL	NDY	n/a
75	DPP	n/a	DGYN	4411	RGG	HYYYYYGMDV	4643
76	DPT	n/a	CSSTSC	3814	LR	VYYYGMDV	4678
77	EV	n/a	IVVVPAAI	3849	SGG	VYFDY	4578
78	GAP	n/a	AVAG	4473	SA	SNWFDP	4600
79	DGRG	3702	AA	n/a	AY	NYYYGMDV	4667
80	GPP	n/a	DSSG	4185	LE	LYYYYGMDV	4660
81	DLGG	3714	VR	n/a	TGG	DYYYYYGMDV	4635
82	ET	n/a	YDFWSG	4253	GL	AAFDI	4551
83	DGGP	3681	GYSSSWY	4435	GAG	SWFDP	4613
84	DGGR	3684	SGW	n/a	TA	SYYYYYGMDV	4645
85	DGSG	3705	WG	n/a	IS	SYYYGMDV	4671
86	GTG	n/a	SGSYY	3761	ST	P	n/a
87	DPGG	3717	RY	n/a	SSE	YYYYYMDV	4683
88	DGGS	3687	DS	n/a	GLG	RAFDI	4544
89	GGT	n/a	TT	n/a	PRP	RYFDY	4572
90	GGRG	3703	YCSGGSCYS	3769	RPL	FYYYYGMDV	4657
91	EGR	n/a	PA	n/a	EA	GNWFDP	4606

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92	DGA	n/a	IVVVPAA	3823	LGG	RWFDP	4614
93	DGL	n/a	IAAAGT	4447	FS	GFDP	4623
94	EL	n/a	AAAG	4453	DL	DYYYYMDV	4714
95	EGG	n/a	GYCSGGSC	3770	GGG	PYYYGMDV	4674
96	LGG	n/a	SGWY	4464	AR	DP	n/a
97	DPA	n/a	DYGGN	4355	RE	HAFDI	4541
98	EGV	n/a	YYYDS	4176	PA	DNWFDP	4594
99	GSG	n/a	YSSG	4462	PTQ	LNWFDP	4602
100	GGP	n/a	YDSSGY	4173	AGG	AYYYYGMDV	4666
101			VAG	n/a	GGV		
102			SSW	n/a	SI		
103			GSGSY	3987	SAA		
104			SSSS	4480	GGS		
105			NW	n/a	GGA		
106			DFWSGY	4254	GPG		
107			QQLV	4455	PGG		
108			YGGN	4358	AAE		
109			YDSSG	4178	GGR		
110			GYSYG	4430	TW		
111			TV	n/a	GGP		
112			NG	n/a	GGL		
113			IVGAT	3752	VGG		
114			IVGA	3755	GTG		
115			YGSGSY	3981	NR		
116			SSWY	4444	NTP		
117			ST	n/a	PV		
118			DFWSGYY	4250	EK		
119			GSY	n/a	GVG		
120			YYDSS	4177	KV		
121			VGA	n/a	EKR		

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122			AT	n/a	QT		
123			RP	n/a	SE		
124			YYYGSGS	3975	SAL		
125			GIAAAG	4446	FH		
126			SGY	n/a	RH		
127			TG	n/a	PTA		
128			LT	n/a	HL		
129			RD	n/a	WGT		
130			WEL	n/a	REL		
131			YSYG	4433	NT		
132			TVT	n/a	HW		
133			GYCSGGSCYS	3767	PKS		
134			AR	n/a	DT		
135			YYGSGSY	3976	DTL		
136			RW	n/a	SK		
137			DIVVVPA	3822	TGL		
138			YSGS	3762	AYH		
139			GYSSSW	4436	ISR		
140			YSSSS	4478	GGT		
141			YYYDSS	4171	QE		
142			QL	n/a			
143			GYSGYD	4386			
144			GE	n/a			
145			MA	n/a			
146			DSS	n/a			
147			RF	n/a			
148			DTAMV	4417			
149			YYGSGSYY	3973			

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150			VDTAMV	4414			
151			FGVV	4293			
152			EYSSS	4477			
153			TTV	n/a			
154			SWY	n/a			
155			IAARP	4483			
156			VE	n/a			
157			SIAA	4484			
158			YSGYD	4389			
159			DIVVVPAA	3819			
160			CSGGSC	3775			
161			DW	n/a			
162			TS	n/a			
163			RL	n/a			
164			YSS	n/a			
165			GN	n/a			
166			SN	n/a			
167			GYSY	4432			
168			YYDS	4183			
169			VDTAM	4416			
170			LE	n/a			
171			AVAGT	4470			
172			YSY	n/a			
173			SW	n/a			
174			SSG	n/a			
175			FGV	n/a			
176			VP	n/a			
177			VA	n/a			

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178			SYY	n/a			
179			QWL	n/a			
180			GSG	n/a			
181			TIFGVV	4280			
182			AVA	n/a			
183			FWSGY	4260			
184			YSGSYY	3759			
185			IAVAG	4469			
186			YS	n/a			
187			YQL	n/a			
188			SIAAR	4482			
189			YCGGDC	3868			
190			NWNY	3766			
191			SSSWY	4440			
192			GIAVA	4468			
193			YSYGY	4431			
194			GIAAA	4448			
195			YYG	n/a			
196			AAG	n/a			
197			AV	n/a			
198			AYCGGDCY	3863			
199			YYGSGS	3980			
200			EY	n/a			

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Table 24. Segments used in Exemplary Library Design 2 (ELD-2). The sequences collectively form a theoretical segment pool that comprises individual theoretical segment pools of TN1, DH, N2, and H3-JH segments.

Segment No.	TN1	SEQ ID NO	DH	SEQ ID NO	N2	SEQ ID NO	H3-JH	SEQ ID NO
1	-	n/a	YYYDSSGYY	4162	-	n/a	DAFDI	4538
2	G	n/a	YGDY	4350	G	n/a	YYFDY	4568
3	D	n/a	DYGDY	4348	D	n/a	Y	n/a
4	A	n/a	YYYDSSGY	4164	A	n/a	FDY	n/a
5	V	n/a	YCSSTSCY	3810	V	n/a	DY	n/a
6	S	n/a	YYDSSGY	4168	S	n/a	YGMDV	4640
7	DR	n/a	YCSGGSCY	3771	DR	n/a	-	n/a
8	L	n/a	YCSSTSC	3812	L	n/a	LDY	n/a
9	R	n/a	GG	n/a	R	n/a	GAFDI	4549
10	DL	n/a	RG	n/a	DL	n/a	YFDY	4567
11	T	n/a	SGSY	3763	T	n/a	YYGMDV	4639
12	E	n/a	YYDSSGYY	4165	E	n/a	AFDI	4539
13	GR	n/a	SS	n/a	GR	n/a	PFDY	4587
14	GG	n/a	YDFWSGY	4249	GG	n/a	GMDV	4641
15	DG	n/a	GYCSSTSC	3809	DG	n/a	GWFDP	4619
16	DS	n/a	DY	n/a	DS	n/a	YYYYGMDV	4637
17	VG	n/a	YYYDSSG	4167	VG	n/a	IDY	n/a
18	EG	n/a	CSSTSCY	3813	EG	n/a	GYFDY	4577
19	P	n/a	YYDFWSGY	4245	P	n/a	GFDY	4590
20	GL	n/a	SSGWY	4461	GL	n/a	MDV	n/a
21	GS	n/a	AG	n/a	GS	n/a	VDY	n/a
22	DP	n/a	DSSGY	4179	DP	n/a	YYYGMDV	4638
23	GP	n/a	SSSW	4443	GP	n/a	NWFDP	4595
24	GA	n/a	VGAT	3756	GA	n/a	PDY	n/a
25	GV	n/a	SY	n/a	GV	n/a	WFDP	4596
26	H	n/a	DTAM	4420	H	n/a	NFDY	4580
27	DRG	n/a	IAAAG	4449	DRG	n/a	YWYFDL	4527

28	DQ	n/a	YSSSW	4439	DQ	n/a	NAFDI	4565
29	AG	n/a	GS	n/a	AG	n/a	HFDY	4582
30	DLG	n/a	YYDSSG	4172	DLG	n/a	SFDY	4584
31	DV	n/a	VG	n/a	DV	n/a	YYYYYGMDV	4636
32	Q	n/a	YSSSWY	4437	Q	n/a	DYYYGMDV	4668
33	N	n/a	YCSGGSC	3773	N	n/a	DFDY	4581
34	AP	n/a	YDSSGYY	4169	AP	n/a	YNWFDP	4597
35	GGG	n/a	GI	n/a	GGG	n/a	DYYYYGMDV	4655
36	DH	n/a	GYCSGGSCY	3768	DH	n/a	YYYMDV	4685
37	VP	n/a	YSSS	4442	VP	n/a	LFDY	4586
38	SG	n/a	SSGW	4463	SG	n/a	DYFDY	4566
39	GRG	n/a	TA	n/a	GRG	n/a	NYYYYGMDV	4654
40	AR	n/a	DSSGYY	4174	AR	n/a	GDY	n/a
41	RG	n/a	GYCSSTSCY	3807	RG	n/a	YDY	n/a
42	ER	n/a	TTVT	4352	ER	n/a	SYFDY	4571
43	DA	n/a	YSSGWY	4458	DA	n/a	YYMDV	4686
44	AS	n/a	GW	n/a	AS	n/a	TFDY	4589
45	PL	n/a	LG	n/a	PL	n/a	YYYYYYGMDV	4642
46	DQG	n/a	DYGD	4349	DQG	n/a	FFDY	4583
47	VL	n/a	TVTT	4353	VL	n/a	SYYYYGMDV	4658
48	GT	n/a	AAA	n/a	GT	n/a	VFDY	4591
49	DGG	n/a	YSSGW	4460	DGG	n/a	YAFDI	4540
50	DSG	n/a	LV	n/a	DSG	n/a	SDY	n/a
51	VGG	n/a	YYDFWSGYY	4243	VGG	n/a	WYFDL	4528
52	F	n/a	YYDSSGYYY	4163	F	n/a	DWFDP	4609
53	AL	n/a	YYDFWSG	4248	AL	n/a	AFDY	4592
54	PS	n/a	YGD	n/a	PS	n/a	PYYYYGMDV	4661
55	ES	n/a	YG	n/a	ES	n/a	HYFDY	4569
56	ERG	n/a	GT	n/a	ERG	n/a	DV	n/a
57	GGV	n/a	YSGSY	3760	GGV	n/a	RFDY	4585
58	DRP	n/a	YYYGSGSY	3972	DRP	n/a	NYFDY	4593
59	EA	n/a	LR	n/a	EA	n/a	IFDY	4588

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60	TP	n/a	SSS	n/a	TP	n/a	ADY	n/a
61	GPR	n/a	GD	n/a	GPR	n/a	HYYYGMDV	4669
62	LE	n/a	CSGGSCY	3774	LH	n/a	GYYYYYGMDV	4651
63	SR	n/a	GY	n/a	SR	n/a	DWYFDL	4530
64	LP	n/a	YCGGDCY	3866	LP	n/a	GYYYGMDV	4677
65	LG	n/a	QWLV	4475	LG	n/a	YYYYMDV	4684
66	DI	n/a	IAAA	4452	DT	n/a	V	n/a
67	VA	n/a	QG	n/a	VA	n/a	FDP	n/a
68	SL	n/a	YCSSTSCYT	3844	SL	n/a	DDY	n/a
69	EGG	n/a	SG	n/a	EGG	n/a	GYYYYGMDV	4664
70	DRS	n/a	TTVTT	4351	DRS	n/a	YMDV	4687
71	K	n/a	QQL	n/a	K	n/a	NWYFDL	4532
72	DPG	n/a	IAVA	4472	DPG	n/a	PYFDY	4574
73	I	n/a	GDY	n/a	I	n/a	FDI	n/a
74	GD	n/a	YYYDSSGYYY	4161	GD	n/a	NDY	n/a
75	DGT	n/a	DGYN	4411	DGT	n/a	HYYYYYGMDV	4643
76	GPP	n/a	CSSTSC	3814	GPP	n/a	VYYYGMDV	4678
77	DPP	n/a	IVVVPAAI	3849	DPP	n/a	VYFDY	4578
78	RR	n/a	AVAG	4473	RR	n/a	SNWFDP	4600
79	EGV	n/a	AA	n/a	EGV	n/a	NYYYGMDV	4667
80	GF	n/a	DSSG	4185	GF	n/a	LYYYYGMDV	4660
81	GVG	n/a	VR	n/a	GVG	n/a	DYYYYYGMDV	4635
82	DPS	n/a	YDFWSG	4253	DPS	n/a	AAFDI	4551
83	VD	n/a	GYSSSWY	4435	VD	n/a	SWFDP	4613
84	GGT	n/a	SGW	n/a	GGT	n/a	SYYYYYGMDV	4645
85	DK	n/a	WG	n/a	DK	n/a	SYYYGMDV	4671
86	GTG	n/a	SGSYY	3761	GTG	n/a	P	n/a
87	DF	n/a	RY	n/a	DF	n/a	YYYYYMDV	4683
88	GQ	n/a	DS	n/a	GQ	n/a	RAFDI	4544
89	SP	n/a	TT	n/a	SP	n/a	RYFDY	4572
90	QG	n/a	YCSGGSCYS	3769	QG	n/a	FYYYYGMDV	4657
91	DLT	n/a	PA	n/a	DLT	n/a	GNWFDP	4606

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92	AK	n/a	IVVVPAA	3823	AK	n/a	RWFDP	4614
93	GPS	n/a	IAAAGT	4447	GPS	n/a	GFDP	4623
94	QR	n/a	AAAG	4453	QR	n/a	DYYYYMDV	4714
95	VR	n/a	GYCSGGSC	3770	VR	n/a	PYYYGMDV	4674
96	DSP	n/a	SGWY	4464	DSP	n/a	DP	n/a
97	DPL	n/a	DYGGN	4355	DPL	n/a	HAFDI	4541
98	EGR	n/a	YYYDS	4176	EGR	n/a	DNWFDP	4594
99	GRRG	4789	YSSG	4462	GRRG	4789	LNWFDP	4602
100	EV	n/a	YDSSGY	4173	EV	n/a	AYYYYGMDV	4666
101			VAG	n/a	RP	n/a		
102			SSW	n/a	GH	n/a		
103			GSGSY	3987	DGR	n/a		
104			SSSS	4480	AA	n/a		
105			NW	n/a	DD	n/a		
106			DFWSGY	4254	W	n/a		
107			QQLV	4455	GGS	n/a		
108			YGGN	4358	DIS	n/a		
109			YDSSG	4178	GGA	n/a		
110			GYSYG	4430	GK	n/a		
111			TV	n/a	DGP	n/a		
112			NG	n/a	DLK	n/a		
113			IVGAT	3752	ET	n/a		
114			IVGA	3755	TT	n/a		
115			YGSGSY	3981	VH	n/a		
116			SSWY	4444	AE	n/a		
117			ST	n/a	VS	n/a		
118			DFWSGYY	4250	LGG	n/a		
119			GSY	n/a	C	n/a		
120			YYDSS	4177	DKG	n/a		
121			VGA	n/a	HA	n/a		

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122			AT	n/a	VI	n/a		
123			RP	n/a	HP	n/a		
124			YYYGSGS	3975	GGE	n/a		
125			GIAAAG	4446	EP	n/a		
126			SGY	n/a	EF	n/a		
127			TG	n/a	DRN	n/a		
128			LT	n/a	DWG	n/a		
129			RD	n/a	GE	n/a		
130			WEL	n/a	DRA	n/a		
131			YSYG	4433	VN	n/a		
132			TVT	n/a	DRE	n/a		
133			GYCSGGSCYS	3767	DLA	n/a		
134			AR	n/a	EN	n/a		
135			YYGSGSY	3976	VT	n/a		
136			RW	n/a	HG	n/a		
137			DIVVVPA	3822	RA	n/a		
138			YSGS	3762	M	n/a		
139			GYSSSW	4436	DVP	n/a		
140			YSSSS	4478	GAP	n/a		
141			YYYDSS	4171	GLG	n/a		
142			QL	n/a	GPG	n/a		
143			GYSGYD	4386	PG	n/a		
144			GE	n/a	DSS	n/a		
145			MA	n/a	SS	n/a		
146			DSS	n/a	AGG	n/a		
147			RF	n/a	GGR	n/a		
148			DTAMV	4417	GPN	n/a		
149			YYGSGSYY	3973	DRL	n/a		

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150			VDTAMV	4414	GRR	n/a		
151			FGVV	4293	DSGG	3723		
152			EYSSS	4477	TR	n/a		
153			TTV	n/a	DLS	n/a		
154			SWY	n/a	RGG	n/a		
155			IAARP	4483	Y	n/a		
156			VE	n/a	EVR	n/a		
157			SIAA	4484	LI	n/a		
158			YSGYD	4389	TF	n/a		
159			DIVVVPAA	3819	LK	n/a		
160			CSGGSC	3775	DLE	n/a		
161			DW	n/a	GY	n/a		
162			TS	n/a	DGS	n/a		
163			RL	n/a	GVR	n/a		
164			YSS	n/a	GQR	n/a		
165			GN	n/a	EGL	n/a		
166			SN	n/a	VLG	n/a		
167			GYSY	4432	QP	n/a		
168			YYDS	4183	VM	n/a		
169			VDTAM	4416	VE	n/a		
170			LE	n/a	DQGG	4790		
171			AVAGT	4470	PN	n/a		
172			YSY	n/a	DGL	n/a		
173			SW	n/a	PV	n/a		
174			SSG	n/a	HR	n/a		
175			FGV	n/a	AD	n/a		
176			VP	n/a	DLF	n/a		
177			VA	n/a	LD	n/a		

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178			SYY	n/a	GGD	n/a		
179			QWL	n/a	DRR	n/a		
180			GSG	n/a	DHH	n/a		
181			TIFGVV	4280	DW	n/a		
182			AVA	n/a	DAS	n/a		
183			FWSGY	4260	GW	n/a		
184			YSGSYY	3759	SV	n/a		
185			IAVAG	4469	GLR	n/a		
186			YS	n/a	DGA	n/a		
187			YQL	n/a	LA	n/a		
188			SIAAR	4482	EEG	n/a		
189			YCGGDC	3868	AV	n/a		
190			NWNY	3766	VQ	n/a		
191			SSSWY	4440	AH	n/a		
192			GIAVA	4468	RS	n/a		
193			YSYGY	4431	WA	n/a		
194			GIAAA	4448	LR	n/a		
195			YYG	n/a	GSG	n/a		
196			AAG	n/a	GGSG	3706		
197			AV	n/a	DLR	n/a		
198			AYCGGDCY	3863	VWG	n/a		
199			YYGSGS	3980	HL	n/a		
200			EY	n/a	EH	n/a		

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Table 25. Segments used in Exemplary Library Design 3 (ELD-3). The sequences collectively form a theoretical segment pool that comprises individual theoretical segment pools of TN1, DH, N2, and H3-JH segments.

Segment No.	TN1 (plus AR or AK)[1]	SEQ ID NO	TN1 Nucleotides (plus AR or AK)[1]	SEQ ID NO	DH	SEQ ID NO	DH Nucleotides	SEQ ID NO	N2	N2 Nucleotides	H3-JH	SEQ ID NO	H3-JH Nucleotides	SEQ ID NO
1	AR	n/a	GCCAGA	n/a	GT	n/a	GGTACT	n/a	-	-	-	n/a	-	n/a
2	ARE	n/a	GCCAGAGAG	n/a	TT	n/a	ACTACT	n/a	A	GCT	Y	n/a	TAT	n/a
3	ARD	n/a	GCCAGAGAC	n/a	TG	n/a	ACAGGC	n/a	D	GAT	DI	n/a	GATATT	n/a
4	ARG	n/a	GCCAGAGGA	n/a	ER	n/a	GAGCGT	n/a	E	GAG	DL	n/a	GACTTG	n/a
5	AREG	4791	GCCAGAGAGGGA	4963	QLE	n/a	CAATTAGAG	n/a	F	TTC	DP	n/a	GATCCT	n/a
6	ARDG	4792	GCCAGAGACGGA	4964	LER	n/a	TTAGAGCGT	n/a	G	GGC	DV	n/a	GATGTA	n/a
7	ARGG	4793	GCCAGAGGTGGA	4965	VGAT	3756	GTTGGCGCAACT	5135	H	CAT	DY	n/a	GACTAT	n/a
8	ARR	n/a	GCCAGGAGA	n/a	YSG	n/a	TATAGTGGT	n/a	I	ATC	QH	n/a	CAGCAC	n/a
9	ARER	4794	GCCAGAGAGAGA	4966	YSGSY	3760	TACTCTGGCTCTTAT	5136	K	AAA	ADY	n/a	GCTGATTAT	n/a
10	ARDR	4795	GCCAGAGACAGA	4967	VG	n/a	GTAGGC	n/a	L	CTG	DDY	n/a	GATGACTAT	n/a
11	ARGR	4796	GCCAGAGGCAGA	4968	AT	n/a	GCCACT	n/a	M	ATG	FDI	n/a	TTTGACATT	n/a
12	ARS	n/a	GCCAGATCT	n/a	WEL	n/a	TGGGAGCTT	n/a	P	CCT	FDL	n/a	TTCGACTTA	n/a
13	ARES	4797	GCCAGAGAATCT	4969	YS	n/a	TACAGC	n/a	Q	CAG	FDP	n/a	TTTGACCCT	n/a
14	ARDS	4798	GCCAGAGACTCT	4970	SG	n/a	AGTGGT	n/a	R	AGG	FDY	n/a	TTCGACTAT	n/a
15	ARGS	4799	GCCAGAGGTTCT	4971	GS	n/a	GGTTCT	n/a	S	TCA	FQH	n/a	TTCCAGCAC	n/a
16	ARP	n/a	GCCAGACCT	n/a	SY	n/a	AGCTAC	n/a	T	ACC	GDY	n/a	GGTGACTAC	n/a
17	ARDP	4800	GCCAGAGACCCT	4972	CSSTSC	3814	TGTAGTAGTACAAGTTGC	5137	V	GTT	IDY	n/a	ATCGACTAT	n/a
18	ARGP	4801	GCCAGAGGGCCT	4973	CSSTSCY	3813	TGCTCATCTACATCATGCTAT	5138	W	TGG	LDY	n/a	TTGGACTAT	n/a
19	ARL	n/a	GCCAGATTG	n/a	YCSSTSC	3812	TATTGTTCAAGTACATCTTGT	5139	Y	TAC	MDV	n/a	ATGGATGTG	n/a
20	ARDL	4802	GCCAGAGACTTG	4974	GYCSSTSC	3809	GGGTATTGCTCCAGTACCTCATGT	5140	AD	GCTGAT	PDY	n/a	CCAGATTAT	n/a
21	ARGL	4803	GCCAGAGGGTTG	4975	YCSSTSCY	3810	TACTGCAGCAGCACAAGTTGTTAC	5141	AG	GCAGGC	SDY	n/a	TCTGATTAC	n/a
22	ARA	n/a	GCCAGAGCT	n/a	GYCSSTSCY	3807	GGGTATTGCAGTTCAACTAGTTGTTAT	5142	AP	GCCCCA	VDY	n/a	GTTGACTAC	n/a
23	AREA	4804	GCCAGAGAGGCT	4976	YCSSTSCYT	3844	TACTGTTCATCAACCTCCTGTTATACT	5143	AQ	GCTCAG	YDY	n/a	TATGATTAC	n/a
24	ARDA	4805	GCCAGAGATGCT	4977	PAA	n/a	CCTGCCGCT	n/a	AR	GCTAGG	AFDI	4539	GCCTTCGATATC	5251
25	ARGA	4806	GCCAGAGGTGCT	4978	CSGGSCY	3774	TGCTCTGGGGGTAGCTGCTAT	5144	AS	GCTAGT	AFDY	4592	GCCTTCGATTAC	5252
26	ART	n/a	GCCAGAACT	n/a	YCSGGSC	3773	TACTGTAGCGGTGGTAGTTGC	5145	AT	GCTACC	DFDY	4581	GATTTCGACTAT	5253
27	ARET	4807	GCCAGAGAGACT	4979	GYCSGGSC	3770	GGATACTGTAGTGGCGGATCCTGC	5146	AY	GCCTAC	FFDY	4583	TTTTCGATTAC	5254
28	ARDT	4808	GCCAGAGATACT	4980	YCSGGSCY	3771	TACTGCTCCGGAGGAAGTTGTTAT	5147	DA	GACGCC	GFDP	4623	GGGTTTGACCCA	5255
29	ARGT	4809	GCCAGAGGCACT	4981	GYCSGGSCY	3768	GGTTATTGCAGTGGGGGTTCATGTTAC	5148	DS	GACGAT	GFDY	4590	GGGTTCGACTAC	5256
30	ARV	n/a	GCCAGAGTG	n/a	YCSGGSCYS	3769	TACTGTTCCGGAGGTAGCTGTTACTCT	5149	DE	GACGAG	GMDV	4641	GGCATGGATGTA	5257
31	AREV	4810	GCCAGAGAGGTG	4982	RI	n/a	AGAATC	n/a	DG	GATGGT	HFDY	4582	CACTTTGACTAT	5258
32	ARDV	4811	GCCAGAGATGTG	4983	GY	n/a	GGATAT	n/a	DL	GACTTG	IFDY	4588	ATATTCGATTAC	5259
33	ARGV	4812	GCCAGAGGGTG	4984	GG	n/a	GGCGGT	n/a	DP	GACCCT	LFDY	4586	TTATTTGATTAT	5260
34	AREGG	4813	GCCAGAGAGGGAGGA	4985	ATP	n/a	GCTACCCCT	n/a	DS	GACTCC	MFDY	4580	AACTTTGATTAT	5261
35	ARDGG	4814	GCCAGAGATGGTGGA	4986	DI	n/a	GACATC	n/a	DY	GATTAT	PFDY	4587	CCCTTCGACTAT	5262
36	ARGGG	4815	GCCAGAGGTGGAGGA	4987	TP	n/a	ACTCCT	n/a	EA	GAGGCC	RFDY	4585	AGATTTGACTAT	5263
37	ARGGR	4816	GCCAGAGAGGGAGGA	4988	GE	n/a	GGAGAT	n/a	EG	GAGGAC	SFDY	4584	AGTTTCGATTAC	5264
38	ARGS	4817	GCCAGAGGTGGTTCT	4989	AYCGGDCY	3863	GCCTATTGCGGTGGTGACTGCTAT	5150	EG	GAAGGA	TFDY	4589	ACATTTGATTAC	5265
39	ARGSP	4818	GCCAGAGGTGGACCT	4990	AYCGGEC	3865	GCATATTGCGGAGGGGATTGC	5151	EK	GAGAAA	VFDY	4591	GTTTTGATTAT	5266
40	APGA	4819	GCCAGAGGAGGTACT	4991	YCGGDCY	3866	TATTGTGGTGGGGACTCCTAT	5152	ER	GAAAGA	WFDP	4596	TGGTTTGATCCA	5267
41	APDGT	4820	GCCAGAGACGGTACT	4992	YCGGDC	3868	TACTGCGGAGGCGATTGC	5153	ES	GAATCT	YFDL	4529	TATTTCGACTTA	5268
42	ARGGT	4821	GCCAGAGGTGGACCT	4993	HI	n/a	CACATC	n/a	ET	GAAACA	YFDY	4567	TACTTCGATTAC	5269
43	AREGV	4822	GCCAGAGAGGGAGTG	4994	TA	n/a	ACAGCT	n/a	FA	TTTGCT	YFQH	4489	TATTTCCAGCAC	5270
44	ARAGV	4823	GCCAGAGATGGCTTG	4995	GYCSSTSCYA	3806	GGGTATTGCTCTAGCACTTCATGCTATGCA	5154	FH	TTTCAT	YMDV	4687	TATATGGATGTA	5271
45	ARRG	4824	GCCAGAAGAGG	4996	SS	n/a	AGTTCT	n/a	FL	TTTCTC	DAFDI	4538	GATGCCTTCGATATA	5272
46	AREAG	4825	GCCAGAGAAGCTGGA	4997	GT	n/a	AGTACT	n/a	FR	TTTAGG	DWFDP	4609	GACTGGTTTGACCCC	5273

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57	ARDRG	4826	GCCAGAGATCGTGGA	4998	TS	n/a	ACCAGC	n/a	FS	TTTAGT	DYFDY	4566	GACTACTTTGATTAC	5274
58	ARGRG	4827	GCCAGAGGCAGGGGA	4999	PAAMP	3835	CCAGCAGCTATGCCT	5155	GA	GGAGCC	EYFQH	4488	GAATACTTCCAACAC	5275
59	ARGG	4828	GCCAGATCAGGA	5000	PA	n/a	CCCGCC	n/a	GD	GGTGAT	GAFDI	4549	GGCGCATTCGATATT	5276
60	ARDSG	4829	GCCAGAGACTCAGGA	5001	MP	n/a	ATGCCT	n/a	GE	GGTGAG	GWFDP	4619	GGGTGGTTTGATCCA	5277
61	ARDPG	4830	GCCAGAGATCCAGGA	5002	VYAIP	3940	GTCTATGCAATTCCT	5156	GG	GGAGGC	GYFDY	4577	GGCTATTTTGACTAC	5278
62	ARLG	4831	GCCAGATTGGGA	5003	WFGE	3966	TGGTTTGGGGAG	5157	GL	GGATTG	HAFDI	4541	CATGCTTTTGATATA	5279
63	ARDLG	4832	GCCAGAGACTTGGGA	5004	FGE	n/a	TTTGGAGAG	n/a	GP	GGACCA	HYFDY	4569	CATTACTTCGATTAC	5280
64	ARAG	4833	GCCAGAGCTGGA	5005	GEL	n/a	GGCGAGCTT	n/a	GR	GGTAGG	NAFDI	4565	AACGCATTCGATATT	5281
65	ARVG	4834	GCCAGAGTGGGA	5006	WFG	n/a	TGGTTCGGT	n/a	GS	GGCAGT	NWFDP	4595	AACTGGTTCGATCCA	5282
66	ARGVG	4835	GCCAGAGGCGTAGGA	5007	GSG	n/a	GGTTCAGGC	n/a	GT	GGAACA	NYFDY	4593	AATTATTTCGACTAT	5283
67	ARPP	4836	GCCAGACCCAGA	5008	SGSY	3763	AGTGGATCTTAT	5158	GV	GGAGTT	PYFDY	4574	CCCTACTTTGACTAT	5284
68	ARGPR	4837	GCCAGAGGACCAAGA	5009	YYGS	3990	TATTATGGCAGT	5159	GW	GGATGG	RAFDI	4544	AGAGCCTTTGATATC	5285
69	ARPS	4838	GCCAGACCATCT	5010	YYYG	3989	TACTACTATGGC	5160	GY	GGATAT	RYFDY	4572	AGGTACTTCGATTAC	5286
70	ARDPS	4839	GCCAGAGATCCCTCT	5011	GSGSY	3987	GGCAGCGGTTCCTAC	5161	HE	CATGAG	SWFDP	4613	TCATGGTTCGACCCC	5287
71	ARGPS	4840	GCAAGAGGACCTTCT	5012	SGSYY	3761	AGTGGATCCTATTAC	5162	HL	CATTTG	SYFDY	4571	AGTTACTTTGACTAT	5288
72	ARDPP	4841	GCCAGAGACCCACCT	5013	YYYGSG	3979	TATTACTACGGGTCTGGC	5163	HP	CATCCT	TYFDY	4576	ACTTATTTCGACTAC	5289
73	ARGPP	4842	GCCAGAGGACCGCCT	5014	SGS	n/a	AGCGGCAGT	n/a	HS	CACTCC	VAFDI	4550	GTGGCCTTCGACATT	5290
74	ARPL	4843	GCCAGACCGTTG	5015	YYYGSGS	3975	TATTACTACGGATCTGGCTCT	5164	IF	ATCTTC	VYFDY	4578	GTCTATTTTGATTAT	5291
75	ARDPL	4844	GCCAGAGATCCTTTG	5016	YYYGSGSY	3972	TATTACTATGGCTCTGGTAGCTAC	5165	IG	ATCGGC	WYFDL	4528	TGGTATTTCGATTTG	5292
76	ARRP	4845	GCCAGAAGGCCT	5017	YGS	n/a	TATGGCTCC	n/a	IR	ATAAGG	YAFDI	4540	TACGCATTTGACATC	5293
77	ARDRP	4846	GCCAGAGACCGTCCT	5018	YYG	n/a	TACTATGGT	n/a	IS	ATCAGT	YGMDV	4640	TACGGCATGGACGTC	5294
78	ARSP	4847	GCCAGATCACCT	5019	YYY	n/a	TATTATTAT	n/a	KG	AAAGGA	YYFDY	4568	TATTATTTTGATTAC	5295
79	ARLP	4848	GCCAGACTTCCT	5020	MVRG	4017	ATGGTAAGAGGT	5166	KR	AAGAGA	YYMDV	4686	TATTATATGGACGTC	5296
80	ARAP	4849	GCCAGAGCCCCT	5021	TMVRG	4010	ACCATGGTGAGGGGT	5167	KV	AAAGTG	AEYFQH	4526	GCAGAGTACTTCCAGCAC	5297
81	ARTP	4850	GCCAGAACTCCT	5022	RGV	n/a	AGAGGAGTT	n/a	LD	TTGGAT	DNWFDP	4594	GACAATTGGTTTGATCCC	5298
82	ARVP	4851	GCCAGAGTCCCT	5023	VRG	n/a	GTCAGAGGC	n/a	LE	TTAGAG	DWYFDL	4530	GATTGGTACTTCGACTTG	5299
83	ARVGG	4852	GCCAGAGTTGGAGGA	5024	FG	n/a	TTCGGC	n/a	LG	TTAGGT	GNWFDP	4606	GGGAATTGGTTTGATCCT	5300
84	ARQ	n/a	GCAAGACAG	n/a	GE	n/a	GGCGAG	n/a	LH	TTACAT	NWYFDL	4532	AACTGGTATTTCGACTTA	5301
85	ARH	n/a	GCCAGACAC	n/a	YG	n/a	TACGGC	n/a	LL	TTATTG	PNWFDP	4603	CCCAATTGGTTTGATCCA	5302
86	ARDQ	4853	GCCAGGGACCAG	5025	VR	n/a	GTGCGT	n/a	LP	TTACCA	SNWFDP	4600	AGTAATTGGTTTGACCCT	5303
87	ARDH	4854	GCAAGAGACCAC	5026	RG	n/a	AGAGGT	n/a	LR	TTGAGG	YNWFDP	4597	TATAATTGGTTTGATCCT	5304
88	ARAR	4855	GCAAGGGCTAGA	5027	FRE	n/a	TTCAGGGAG	n/a	LS	TTAAGC	YWYFDL	4527	TATTGGTATTTCGATTTG	5305
89	ARAS	4856	GCTAGGGCACCT	5028	RE	n/a	AGAGAG	n/a	LT	TTGACA	YYGMDV	4639	TACTATGGGATGGACGTG	5306
90	ARDQG	4857	GCTAGGGATCAGGGA	5029	QG	n/a	CAAGGT	n/a	LV	TTGGTA	YYYMDV	4685	TACTATTACATGGACGTT	5307
91	ARSR	4858	GCTAGATCAAGA	5030	LR	n/a	TTACGT	n/a	LW	TTGTGG	YYYGMDV	4638	TATTATTACGGTATGGACGTC	5308
92	ARDRS	4859	GCCAGGGACAGGTCT	5031	YYDYVWGSYAYT	4070	TACTATGATTACGTCTGGGGGTCTTATGCTTACACT	5168	LY	TTGTAC	YYYYMDV	4684	TACTATTATTACATGGATGTC	5309
93	ARSL	4860	GCTAGATCTTTG	5032	YYDYVWGSYAY	4071	TACTACGACTATGTATGGGGCTCATATGCTTAC	5169	MG	ATGGGC	DYYYGMDV	4668	GATTATTATTACGGTATGGATCTT	5310
94	ARLH	4861	GCTAGGTGCAC	5033	YYDYVWGSYA	4073	TACTACGATTACGTATGGGGAAGCTACGCT	5170	MT	ATGACC	GYYYGMDV	4677	GGGTACTATTATGGTATGGACTTC	5311
95	ARDLT	4862	GCCAGGGATTTGACT	5034	YDYVWGSYAY	4074	TATGATTATGTGTGGGGGTCATACGCATAC	5171	PA	CCTGCT	HYYYGMDV	4669	CATTATTACTATGGGATGGACGTA	5312
96	ARK	n/a	GCAGAAAG	n/a	DY	n/a	GATTAC	n/a	PE	CCTGAG	NYYYYMDV	4713	AACTATTACTATTATATGGATGTC	5313
97	ARAE	4863	GCAAGAGCCTAG	5035	WG	n/a	TGGGGC	n/a	PE	CCTGAG	PYYYYMDV	4720	CCCTATTACTATTATATGGATGTG	5314
98	ARDLS	4864	GCAAGGGATTTTGCT	5036	DYVWGSYAYT	4075	GATTATGTGTGGGGGTCTTACGCCTACACC	5172	PF	CCTTTC	RYYYGMDV	4718	AGGTATTACTATGGTATGGACGTC	5315
99	ARGD	4865	GCTAGAGGGCAC	5037	YDYVWGSYA	4077	TACGACTATGTGTGGGGTTCCTATGCT	5173	PG	CCTGGT	YYYYGMDV	4637	TACTATTATTACGGGATGGACGTA	5316
100	ARRR	4866	GCTAGAGGAGA	5038	YYES	4183	TACTAGGATTCC	5174	PH	CCACAT	DYYYGMDV	4655	GATTACTATTATTACGGGATGGATGTT	5317
101	ARSK	4867	GCTAGAGATAAG	5039	YYG	4182	TATTATTATGAC	5175	PL	CCATTA	GYYYGMDV	4664	GGGTATTACTATTACGGATGGACGTA	5318
102	ARAS	4868	GCTAGAGTACCT	5040	DSSGY	4179	GACAGTTCCGGGTAC	5176	PP	CCTCCA	HYYYGMDV	4654	AATTACTATTACTATGGATGGACGTG	5319
103	ARERL	4869	GCTAGAGACAGATTG	5041	YDSSG	4178	TATGATAGTTCAGGT	5177	PQ	CCTCAG	PYYYGMDV	4661	CCATATTACTATTACGGATGGACGTG	5320
104	ARGQ	4870	GCTAGGGCCAG	5042	YYGS	4177	TACTATGACTCATCC	5178	PR	CCAAGG	GYYYGMDV	4658	AGCTACTACTACTACGGAATGGACGTC	5321
105	ARTR	4871	GCCAGGGTTAGA	5043	YYYDS	4176	TATTATTACGATAGT	5179	PS	CCTTCT	YYYYYGMDV	4636	TACTATTATTATTACGGTATGGACGTA	5322
106	ARAP	4872	GCTAGAGCTAAG	5044	GYY	n/a	GGATATTAC	n/a	PT	CCTACA	DYYYYYMDV	4681	GATTACTATTACTACTATTATTACGGTATGGACGTA	5323
107	ARGK	4873	GCCAGGGCTAAG	5045	DSSGYY	4174	GATTCTTCCGGGTACTAC	5180	PY	CCTGTT	GYYYYGMDV	4651	GGTTATTACTATTACTATTATTACGGTATGGACGTA	5324
108	ARSIS	4874	GCAAGGGATATTTCT	5046	YDSSGY	4173	TATGATTCCAGCGGATAC	5181	QG	CAGGGC	HYYYYGMDV	4643	CCATTACTATTATTACGGGTATGGACGTA	5325
109	AREPT	4875	GCTAGGGATTTCACT	5047	YYDSSG	4172	TACTACGATAGCTCCGGT	5182	QL	CAATTA	RYYYYYYMDV	4692	AGATACTACTACTATTATTACGACTATGGTA	5326
110	ARGG	4876	GCCAGGCAGGGA	5048	YYYDSS	4171	TATTATTACGACTCTTCC	5183	QP	CAGCCA	YYYYYYSMDV	4642	TATTACTACTACTACTATGATAGTGGTTAC	5327
111	AK	n/a	GCCAAG	n/a	YDSSGYY	4169	TACGACTCTTCTGGTTATTAC	5184	QS	CAGTCA				
112	AKE	n/a	GCCAAGGAG	n/a	YYDSSGY	4168	TATTATGACAGCAGCGGGTAT	5185	QT	CAGACT				

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103	AKD	n/a	GCCAAGGAC	n/a	YYYDSSG	4167	TACTACTACGATTCCAGCGGT	5186	RA	AGGGCT				
104	AKG	n/a	GCCAAGGGA	n/a	YDSSGYYY	4166	TACGACAGTTCCGGATATTATTAC	5187	RD	AGGGAC				
105	AKEG	4877	GCCAAGGAAGGA	5049	SGY	n/a	AGCGGATAT	n/a	RE	AGGGAG				
106	AKDG	4878	GCCAAGGACGGA	5050	YYDSSGYY	4165	TACTATGATAGTAGTGGGTACTAT	5188	RF	AGATTC				
107	AKGG	4879	GCCAAGGGCGGA	5051	YYYDSSGY	4164	TACTACTATGACAGCTCAGGGTAT	5189	RG	AGGGGA				
108	AKR	n/a	GCCAAGAGA	n/a	YYDSSGYYY	4163	TATTACGACAGCAGTGGCTACTACTAT	5190	RH	AGGCAT				
109	AKER	4880	GCCAAGGAAAGA	5052	YYYDSSGYY	4162	TACTACTACGATAGCTCTGGATACTAT	5191	RL	AGATTA				
110	AKDR	4881	GCCAAGGACAGA	5053	YYYDSSGYYY	4161	TATTATTACGATTCCAGTGGTTATTATTAT	5192	RM	AGGATG				
111	AKGR	4882	GCCAAGGGCAGA	5054	YDS	n/a	TACGACTCC	n/a	RP	AGGCCA				
112	AKS	n/a	GCCAAGTCT	n/a	YYD	n/a	TACTATGAC	n/a	RR	CGTAGA				
113	AKES	4883	GCCAAGGAATCT	5055	DSSG	4185	GACTCATCCGGT	5193	RS	AGAAGT				
114	AKDS	4884	GCCAAGGATTCT	5056	GYYY	4188	GGTTACTATTAC	5194	RV	AGAGTG				
115	AKGS	4885	GCCAAGGGATCT	5057	SGYY	4187	AGCGGCTACTAT	5195	RY	AGATAT				
116	AKP	n/a	GCCAAGCCT	n/a	DS	n/a	GACTCT	n/a	SA	TCAGCC				
117	AKDP	4886	GCCAAGGATCCT	5058	RFLEW	4231	AGATTTTTGGAGTGG	5196	SD	TCAGAC				
118	AKGP	4887	GCCAAGGGTCCT	5059	EWL	n/a	GAATGGCTT	n/a	SE	TCCGAG				
119	AKL	n/a	GCCAAGTTG	n/a	RF	n/a	AGATTC	n/a	SF	TCATTC				
120	AKDL	4888	GCCAAGGACTTG	5060	YYDFWSGYYT	4242	TACTATGATTTTTGGAGTGGATATTATACC	5197	SG	AGCGGA				
121	AKGL	4889	GCCAAGGGGTTG	5061	YDFWSG	4253	TATGATTTTTGGTCTGGT	5198	SH	AGTCAC				
122	AKA	n/a	GCCAAGGCT	n/a	DFWSGY	4254	GATTTTTGGAGCGGCTAT	5199	SI	TCTATC				
123	AKEA	4890	GCCAAGGAAGCT	5062	FWSGY	4260	TTTTGGAGCGGGTAT	5200	SK	AGTAAA				
124	AKDA	4891	GCCAAGGACGCT	5063	YYDFWSGYY	4243	TACTACGACTTCTGGAGCGGGTATTAC	5201	SL	TCCTTG				
125	AKGA	4892	GCCAAGGGCGCT	5064	YYDFWSGY	4245	TACTACGATTTTGGTCTGGATAT	5202	SP	AGCCCA				
126	AKT	n/a	GCCAAGACT	n/a	YDFWSGYY	4246	TATGACTTTTGGAGTGGTTACTAC	5203	SQ	AGCCAA				
127	AKET	4893	GCCAAGGAAACT	5065	YYDFWSG	4248	TACTACGATTTCTGGTCAGGC	5204	SR	TCAAGA				
128	AKDT	4894	GCCAAGGATACT	5066	YDFWSGY	4249	TATGACTTCTGGAGTGGTTAC	5205	SS	TCCTCA				
129	AKGT	4895	GCCAAGGGAACT	5067	DFWSGYY	4250	GACTTCTGGTCAGGATACTAC	5206	ST	AGTACA				
130	AKV	n/a	GCCAAGGTG	n/a	VLRYF	4307	GTGTTGAGGTACTTC	5207	SV	TCAGTA				
131	AKEV	4896	GCCAAGGAAGTG	5068	LRYFD	4308	TTAAGATACTTTGAT	5208	SW	TCATGG				
132	AKDV	4897	GCCAAGGACGTG	5069	RYFDW	4309	AGATACTTTGATTGG	5209	SY	TCTTAC				
133	AKGV	4898	GCCAAGGGCGTG	5070	VLRY	4312	GTGTTGAGGTAT	5210	TA	ACCGCC				
134	AKEGG	4899	GCCAAGGAGGGAGGA	5071	LRYF	4313	TTGAGATATTTC	5211	TG	ACTGGC				
135	AKDGG	4900	GCCAAGGACGGTGGA	5072	RYFD	4314	AGATACTTTGAT	5212	TF	ACACCA				
136	AKGGG	4901	GCCAAGGGAGGAGGA	5073	VLRYFDWL	4298	GTCTTAAGGTACTTCGATTGGCTT	5213	TR	ACAAGA				
137	AKEGR	4902	GCCAAGGAACGGTAGA	5074	LRY	n/a	TTAAGATAC	n/a	TS	ACATCT				
138	AKGGS	4903	GCCAAGGGAGGTTCT	5075	RYF	n/a	AGATACTTC	n/a	TT	ACTACT				
139	AKGGP	4904	GCCAAGGGAGGTCCT	5076	RY	n/a	AGATAT	n/a	TV	ACAGTT				
140	AKGGA	4905	GCCAAGGAGGGGCT	5077	FD	n/a	TTCGAT	n/a	TW	ACTTGG				
141	AKDGT	4906	GCCAAGGATGGTACT	5078	DW	n/a	GATTGG	n/a	TY	ACTTAT				
142	AKDGT	4907	GCCAAGGATGGTACT	5079	VLRYFDW	4300	GTCTTAAGATACTTTGATTGG	5214	VA	GTAGCC				
143	AKEGV	4908	GCCAAGGAAGGTAGTG	5080	VLRYFD	4303	GTCTTGAGGTACTTTGAC	5215	VC	GTCGAC				
144	AKGGV	4909	GCCAAGGGTGGTGTT	5081	LRYFDW	4304	TTAAGATACTTCGATTGG	5216	VG	GTTGGA				
145	AKRG	4910	GCCAAGAGAGGA	5082	RYFDWL	4305	AGATATTTCGACTGGTTT	5217	VL	GTCTTG				
146	AKERG	4911	GCCAAGGAGAGAGGA	5083	YDLLTGYY	4322	TATGACATATTGACTGGCTACTAC	5218	VP	GTTCCT				
147	AKDRG	4912	GCCAAGGATAGGGGA	5084	YDLLTGY	4325	TATGATATATTAACTGGGTAC	5219	VR	GTGAGA				
148	AKGRG	4913	GCCAAGGGTAGGGGA	5085	DLLTGYY	4326	GATATCTTAACCGGGTATTAT	5220	VS	GTTTCA				
149	AKGT	4914	GCCAAGTGTGGA	5086	GYG	n/a	GATTATGGT	n/a	VT	GTTACC				
150	AKGGG	4915	GCCAAGGATAGTGGA	5087	GDY	n/a	GGGGACTAC	n/a	VW	GTAGTA				
151	AKGPG	4916	GCCAAGGACCCCGGA	5088	YGD	n/a	TACGGTGAC	n/a	WG	TGGGGT				
152	AKLG	4917	GCCAAGTTAGGA	5089	RYGD	4349	GATTACGGCGAT	5221	WS	TGGTCA				
153	AKELG	4918	GCCAAGGATCTTGGA	5090	YGDY	4350	TACGGCGATTAT	5222	YA	TACGCT				
154	AKAG	4919	GCCAAGGCTGGA	5091	RYGDY	4348	GACTACGGAGATTAT	5223	YD	TATGAC				
155	AKVG	4920	GCCAAGGTAGGA	5092	TTYTT	4351	ACCACAGTAACCACC	5224	YE	TATGAG				
156	AKGVG	4921	GCCAAGGGTGTCGGA	5093	TTYT	4352	ACAACTGTGACT	5225	YS	TATTCT				
157	AKPR	4922	GCCAAGCCTAGA	5094	TYTT	4353	ACAGTAACTACT	5226	AAA	GCTGCCGCT				
158	AKGPR	4923	GCCAAGGGCCCAGA	5095	RW	n/a	AGATGG	n/a	AGM	GCAGGCATG				

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159	AKPS	4924	GCCAAGCCTTCT	5096	VTP	n/a	GTAACTCCT	n/a	DGG	GATGGGGGT				
160	AKDPS	4925	GCCAAGGATCCCTCT	5097	VD	n/a	GTTGAC	n/a	DGV	GATGGTGTA				
161	AKGPS	4926	GCCAAAGGCCATCT	5098	GYSGYD	4386	GGCTACTCAGGATACGAC	5227	FGG	TTCGGGGGC				
162	AKDPP	4927	GCCAAGGATCCACCT	5099	YSGYD	4389	TATAGCGGATATGAC	5228	GAG	GGAGCTGGA				
163	AKGPP	4928	GCCAAGGGCCCTCCT	5100	RD	n/a	AGAGAT	n/a	GGA	GGAGGGGCC				
164	AKPL	4929	GCCAAGCCGTTG	5101	RDGY	4410	AGAGATGGTTAC	5229	GCG	GGAGGCGGT				
165	AKDPL	4930	GCCAAGGACCCTTTG	5102	RDG	n/a	AGAGATGGT	n/a	GGL	GGAGGCTTA				
166	AKRP	4931	GCCAAGAGGCCT	5103	DTAM	4420	GATACTGCTATG	5230	GGR	GGTGGTAGA				
167	AKDRP	4932	GCCAAGGACCGTCCT	5104	YGY	n/a	TACGGCTAC	n/a	GGS	GGCGGGAGC				
168	AKSP	4933	GCCAAGAGTCCT	5105	YSY	n/a	TATTCTTAC	n/a	GGV	GGTGGGGTA				
169	AKLP	4934	GCCAAGCTACCT	5106	YSYG	4433	TATTCATATGGT	5231	GIG	GGATTAGGC				
170	AKAP	4935	GCCAAGGCTCCT	5107	GYSYG	4430	GGATATAGTTATGGC	5232	GFG	GGCCCCGGC				
171	AKTP	4936	GCCAAGACGCCT	5108	SSS	n/a	AGTTCAAGC	n/a	GFP	GGACCACCT				
172	AKVP	4937	GCCAAGGTACCT	5109	YSSSWY	4437	TACAGTAGCTCTTGGTAC	5233	GRG	GGAAGGGGC				
173	AKVGG	4938	GCCAAGGTGGGTGGA	5110	GYSSSWY	4435	GGCTACAGTTCAAGCTGGTAT	5234	GSG	GGATCTGGC				
174	AKQ	n/a	GCAAAACAG	n/a	SSW	n/a	AGTTCCTGG	n/a	GTG	GGAACTGGC				
175	AKH	n/a	GCCAAACAC	n/a	SWY	n/a	AGCTGGTAC	n/a	GVG	GGAGTAGGT				
176	AKDQ	4939	GCCAAGGATCAG	5111	SSSW	4443	AGTAGCTCTTGG	5235	LGG	TTGGGAGGC				
177	AKDH	4940	GCTAAAGACCAC	5112	YSSS	4442	TACAGCAGCTCC	5236	LGH	TTGGGCCAC				
178	AKAR	4941	GCCAAGGCAAGA	5113	YSSSW	4439	TACTCTTCCTCATGG	5237	PGG	CCTGGCGGC				
179	AKAS	4942	GCCAAGGCATCT	5114	SW	n/a	AGCTGG	n/a	PKQ	CCAAAGCAG				
180	AKDQG	4943	GCAAAGGATCAGGGA	5115	AG	n/a	GCTGGT	n/a	PKR	CCTAAAAGG				
181	AKGR	4944	GCCAAGAGTAGA	5116	QQLV	4455	CAGCAATTGGTT	5238	PTQ	CCAACTCAG				
182	AKDRS	4945	GCAAAAGACAGGCCT	5117	QQL	n/a	CAGCAACTT	n/a	RPE	AGGTTTGAG				
183	AKSL	4946	GCAAAGAGCTTG	5118	GWY	n/a	GGTTGGTAC	n/a	RGG	AGGGGAGGT				
184	AKLH	4947	GCTAAATTGCAC	5119	SSGWY	4461	AGCTCTGGATGGTAC	5239	RGL	AGGGGATTG				
185	AKDLT	4948	GCCAAGGACTTGACT	5120	YSSGW	4460	TATAGTAGCGGATGG	5240	RGS	AGGGGTAGT				
186	AKK	n/a	GCTAAAAAG	n/a	YSSGWY	4458	TATAGCAGCGGTTGGTAC	5241	RPL	AGGCCATTA				
187	AKAE	4949	GCTAAAGCAGAG	5121	GYSSGWY	4456	GGTTATTCATCAGGTTGGTAT	5242	RPY	AGGCCATAT				
188	AKDLS	4950	GCAAAAGACTTGTCT	5122	SGW	n/a	AGTGGTTGG	n/a	SAA	TCTGCCGCC				
189	AKGD	4951	GCAAAAGGGAC	5123	YSS	n/a	TACAGTTCC	n/a	SGE	AGCGGGGAG				
190	AKRR	4952	GCAAAAAGGAGG	5124	SGWY	4464	AGTGGTTGGTAT	5243	SGS	TCTGGCGGC				
191	AKDK	4953	GCAAAAGACAAG	5125	SSGW	4463	AGTTCCGGTTGG	5244	SKL	TCAGGGTTA				
192	AKVS	4954	GCCAAAGTATCT	5126	YSSG	4462	TACTCAAGTGGT	5245	SGW	AGCGGTTGG				
193	AKDRL	4955	GCAAAAGACAGGTTG	5127	GW	n/a	GGTTGG	n/a	SGV	AGCGGCTAC				
194	AKGQ	4956	GCCAAAGTACAG	5128	QWLV	4475	CAGTGGTTAGTT	5246	SRG	TCAAGAGGT				
195	AKVR	4957	GCAAAAGTCAGA	5129	EYSS	4479	GAGTACTCATCC	5247	SSE	TCATCAGAG				
196	AKAR	4958	GCAAAGCAAAG	5130	GTAAPP	4481	AGCATAGCAGCAAGGCCT	5248	SSW	AGCTCATGG				
197	AKSP	4959	GCAAATGGCAG	5131	RP	n/a	CGTCCT	n/a	TGG	ACCGGTGGC				
198	AKSG	4960	GCAAAGCACATTTCT	5132	TAARP	4483	ATAGCAGCAAGGCCT	5249	VGR	GTTGGCAGA				
199	AKDST	4961	GCTAAAGATTCAGCT	5133	AARP	4486	GCCGCAAGACCT	5250	VGG	GTGCAAGGA				
200	AKQG	4962	GCCAAGCAAGGA	5134	ARP	n/a	GCTAGACCT	n/a	VTA	GTCACAGCT				

[1] "AR" and "AK" refer to the last two C-terminal amino acids of the heavy chain chassis used in the current example. They are not part of the TN1 segment.

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Table 26. Theoretical segment pool of 300 TN1 segments (plus AR/AK; which is not part of TN1) used in the library of Example 12.

Peptide (plus AR or AK)[1]	SEQ ID NO	Nucleotide (plus AR or AK)[1]	SEQ ID NO	In ELD-3?
AR	n/a	GCCAGA	n/a	YES
AK	n/a	GCCAAG	n/a	YES
ARE	n/a	GCCAGAGAG	n/a	YES
AKE	n/a	GCCAAGGAG	n/a	YES
ARD	n/a	GCCAGAGAC	n/a	YES
AKD	n/a	GCCAAGGAC	n/a	YES
ARG	n/a	GCCAGAGGA	n/a	YES
AKG	n/a	GCCAAGGGA	n/a	YES
AREG	4791	GCCAGAGAGGGA	4963	YES
AKEG	4877	GCCAAGGAAGGA	5049	YES
ARDG	4792	GCCAGAGACGGA	4964	YES
AKDG	4878	GCCAAGGACGGA	5050	YES
ARGG	4793	GCCAGAGGTGGA	4965	YES
AKGG	4879	GCCAAGGGCGGA	5051	YES
ARR	n/a	GCCAGGAGA	n/a	YES
AKR	n/a	GCCAAGAGA	n/a	YES
ARER	4794	GCCAGAGAGAGA	4966	YES
AKER	4880	GCCAAGGAAAGA	5052	YES
ARDR	4795	GCCAGAGACAGA	4967	YES
AKDR	4881	GCCAAGGACAGA	5053	YES
ARGR	4796	GCCAGAGGCAGA	4968	YES
AKGR	4882	GCCAAGGGCAGA	5054	YES
ARS	n/a	GCCAGATCT	n/a	YES
AKS	n/a	GCCAAGTCT	n/a	YES
ARES	4797	GCCAGAGAATCT	4969	YES
AKES	4883	GCCAAGGAATCT	5055	YES
ARDS	4798	GCCAGAGACTCT	4970	YES
AKDS	4884	GCCAAGGATTCT	5056	YES

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ARGS	4799	GCCAGAGGTTCT	4971	YES
AKGS	4885	GCCAAGGGATCT	5057	YES
ARP	n/a	GCCAGACCT	n/a	YES
AKP	n/a	GCCAAGCCT	n/a	YES
AREP	5328	GCCAGAGAGCCT	5428	NO
AKEP	5329	GCCAAGGAGCCT	5429	NO
ARDP	4800	GCCAGAGACCCT	4972	YES
AKDP	4886	GCCAAGGATCCT	5058	YES
ARGP	4801	GCCAGAGGGCCT	4973	YES
AKGP	4887	GCCAAGGGTCCT	5059	YES
ARL	n/a	GCCAGATTG	n/a	YES
AKL	n/a	GCCAAGTTG	n/a	YES
AREL	5330	GCCAGAGAGTTG	5430	NO
AKEL	5331	GCCAAGGAATTG	5431	NO
ARDL	4802	GCCAGAGACTTG	4974	YES
AKDL	4888	GCCAAGGACTTG	5060	YES
ARGL	4803	GCCAGAGGGTTG	4975	YES
AKGL	4889	GCCAAGGGGTTG	5061	YES
ARA	n/a	GCCAGAGCT	n/a	YES
AKA	n/a	GCCAAGGCT	n/a	YES
AREA	4804	GCCAGAGAGGCT	4976	YES
AKEA	4890	GCCAAGGAAGCT	5062	YES
ARDA	4805	GCCAGAGATGCT	4977	YES
AKDA	4891	GCCAAGGACGCT	5063	YES
ARGA	4806	GCCAGAGGTGCT	4978	YES
AKGA	4892	GCCAAGGGCGCT	5064	YES
ART	n/a	GCCAGAACT	n/a	YES
AKT	n/a	GCCAAGACT	n/a	YES
ARET	4807	GCCAGAGAGACT	4979	YES
AKET	4893	GCCAAGGAAACT	5065	YES
ARDT	4808	GCCAGAGATACT	4980	YES
AKDT	4894	GCCAAGGATACT	5066	YES

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ARGT	4809	GCCAGAGGCACT	4981	YES
AKGT	4895	GCCAAGGGAACT	5067	YES
ARV	n/a	GCCAGAGTG	n/a	YES
AKV	n/a	GCCAAGGTG	n/a	YES
AREV	4810	GCCAGAGAGGTG	4982	YES
AKEV	4896	GCCAAGGAAGTG	5068	YES
ARDV	4811	GCCAGAGATGTG	4983	YES
AKDV	4897	GCCAAGGACGTG	5069	YES
ARGV	4812	GCCAGAGGGGTG	4984	YES
AKGV	4898	GCCAAGGGCGTG	5070	YES
AREGG	4813	GCCAGAGAGGGAGGA	4985	YES
AKEGG	4899	GCCAAGGAGGGAGGA	5071	YES
ARDGG	4814	GCCAGAGATGGTGGA	4986	YES
AKDGG	4900	GCCAAGGACGGTGGA	5072	YES
ARGGG	4815	GCCAGAGGTGGAGGA	4987	YES
AKGGG	4901	GCCAAGGGAGGAGGA	5073	YES
AREGR	5332	GCCAGAGAAGGGAGA	5432	NO
AKEGR	5333	GCCAAGGAAGGCAGA	5433	NO
ARDGR	4816	GCCAGAGACGGCAGA	4988	YES
AKDGR	4902	GCCAAGGACGGTAGA	5074	YES
ARGGR	5334	GCCAGAGGAGGTAGA	5434	NO
AKGGR	5335	GCCAAGGGAGGTAGA	5435	NO
AREGS	5336	GCCAGAGAAGGATCT	5436	NO
AKEGS	5337	GCCAAGGAAGGATCT	5437	NO
ARDGS	5338	GCCAGAGACGGATCT	5438	NO
AKDGS	5339	GCCAAGGATGGTTCT	5439	NO
ARGGS	4817	GCCAGAGGCGGTTCT	4989	YES
AKGGS	4903	GCCAAGGGAGGTTCT	5075	YES
AREGP	5340	GCCAGAGAAGGTCCT	5440	NO
AKEGP	5341	GCCAAGGAGGGGCCT	5441	NO
ARDGP	5342	GCCAGAGACGGTCCT	5442	NO
AKDGP	5343	GCCAAGGACGGTCCT	5443	NO

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ARGGP	4818	GCCAGAGGTGGGCCT	4990	YES
AKGGP	4904	GCCAAGGGAGGTCCT	5076	YES
AREGL	5344	GCCAGAGAGGGCTTG	5444	NO
AKEGL	5345	GCCAAGGAAGGGTTG	5445	NO
ARDGL	5346	GCCAGAGATGGGTTG	5446	NO
AKDGL	5347	GCCAAGGACGGTTTG	5447	NO
ARGGL	5348	GCCAGAGGTGGATTG	5448	NO
AKGGL	5349	GCCAAGGGAGGGTTG	5449	NO
AREGA	5350	GCCAGAGAAGGAGCT	5450	NO
AKEGA	5351	GCCAAGGAGGGAGCT	5451	NO
ARDGA	5352	GCCAGAGATGGCGCT	5452	NO
AKDGA	5353	GCCAAGGATGGAGCT	5453	NO
ARGGA	4819	GCCAGAGGAGGTGCT	4991	YES
AKGGA	4905	GCCAAGGGAGGCGCT	5077	YES
ARDGT	4820	GCCAGAGACGGTACT	4992	YES
AKDGT	4906	GCCAAGGATGGCACT	5078	YES
ARGGT	4821	GCCAGAGGTGGAACT	4993	YES
AKGGT	4907	GCCAAGGGAGGCACT	5079	YES
AREGV	4822	GCCAGAGAGGGAGTG	4994	YES
AKEGV	4908	GCCAAGGAAGGAGTG	5080	YES
ARDGV	5354	GCCAGAGATGGTGTG	5454	NO
AKDGV	5355	GCCAAGGATGGTGTG	5455	NO
ARGGV	4823	GCCAGAGGTGGCGTG	4995	YES
AKGGV	4909	GCCAAGGGCGGTGTG	5081	YES
ARRG	4824	GCCAGAAGAGGA	4996	YES
AKRG	4910	GCCAAGAGAGGA	5082	YES
ARERG	4825	GCCAGAGAGCGTGGA	4997	YES
AKERG	4911	GCCAAGGAGAGAGGA	5083	YES
ARDRG	4826	GCCAGAGATCGTGGA	4998	YES
AKDRG	4912	GCCAAGGATAGGGGA	5084	YES
ARGRG	4827	GCCAGAGGCAGGGGA	4999	YES
AKGRG	4913	GCCAAGGGTAGGGGA	5085	YES

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ARSG	4828	GCCAGATCAGGA	5000	YES
AKSG	4914	GCCAAGTCTGGA	5086	YES
ARESG	5356	GCCAGAGAGTCTGGA	5456	NO
AKESG	5357	GCCAAGGAAAGTGGA	5457	NO
ARDSG	4829	GCCAGAGACTCAGGA	5001	YES
AKDSG	4915	GCCAAGGATAGTGGA	5087	YES
ARGSG	5358	GCCAGAGGCTCTGGA	5458	NO
AKGSG	5359	GCCAAGGGGTCTGGA	5459	NO
ARPG	5360	GCCAGACCAGGA	5460	NO
AKPG	5361	GCCAAGCCCGGA	5461	NO
ARDPG	4830	GCCAGAGATCCAGGA	5002	YES
AKDPG	4916	GCCAAGGACCCCGGA	5088	YES
ARGPG	5362	GCCAGAGGACCTGGA	5462	NO
AKGPG	5363	GCCAAGGGGCCTGGA	5463	NO
ARLG	4831	GCCAGATTGGGA	5003	YES
AKLG	4917	GCCAAGTTAGGA	5089	YES
ARDLG	4832	GCCAGAGACTTGGGA	5004	YES
AKDLG	4918	GCCAAGGATCTTGGA	5090	YES
ARGLG	5364	GCCAGAGGACTAGGA	5464	NO
AKGLG	5365	GCCAAGGGTTTGGGA	5465	NO
ARAG	4833	GCCAGAGCTGGA	5005	YES
AKAG	4919	GCCAAGGCTGGA	5091	YES
AREAG	5366	GCCAGAGAAGCCGGA	5466	NO
AKEAG	5367	GCCAAGGAGGCTGGA	5467	NO
ARDAG	5368	GCCAGAGACGCAGGA	5468	NO
AKDAG	5369	GCCAAGGATGCCGGA	5469	NO
ARGAG	5370	GCCAGAGGTGCCGGA	5470	NO
AKGAG	5371	GCCAAGGGAGCAGGA	5471	NO
ARTG	5372	GCCAGAACTGGA	5472	NO
AKTG	5373	GCCAAGACCGGA	5473	NO
ARDTG	5374	GCCAGAGACACGGGA	5474	NO
AKDTG	5375	GCCAAGGATACGGGA	5475	NO

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ARVG	4834	GCCAGAGTGGGA	5006	YES
AKVG	4920	GCCAAGGTAGGA	5092	YES
AREVG	5376	GCCAGAGAAGTCGGA	5476	NO
AKEVG	5377	GCCAAGGAGGTAGGA	5477	NO
ARDVG	5378	GCCAGAGATGTAGGA	5478	NO
AKDVG	5379	GCCAAGGACGTAGGA	5479	NO
ARGVG	4835	GCCAGAGGCGTAGGA	5007	YES
AKGVG	4921	GCCAAGGGTGTCGGA	5093	YES
ARPR	4836	GCCAGACCCAGA	5008	YES
AKPR	4922	GCCAAGCCTAGA	5094	YES
ARDPR	5380	GCCAGAGATCCAAGA	5480	NO
AKDPR	5381	GCCAAGGATCCTAGA	5481	NO
ARGPR	4837	GCCAGAGGACCAAGA	5009	YES
AKGPR	4923	GCCAAGGGCCCCAGA	5095	YES
ARPS	4838	GCCAGACCATCT	5010	YES
AKPS	4924	GCCAAGCCTTCT	5096	YES
ARDPS	4839	GCCAGAGATCCCTCT	5011	YES
AKDPS	4925	GCCAAGGATCCCTCT	5097	YES
ARGPS	4840	GCAAGAGGACCTTCT	5012	YES
AKGPS	4926	GCCAAAGGGCCATCT	5098	YES
ARPP	5382	GCCAGACCACCT	5482	NO
AKPP	5383	GCCAAGCCACCT	5483	NO
ARDPP	4841	GCCAGAGACCCACCT	5013	YES
AKDPP	4927	GCCAAGGATCCACCT	5099	YES
ARGPP	4842	GCCAGAGGACCGCCT	5014	YES
AKGPP	4928	GCCAAGGGCCCTCCT	5100	YES
ARPL	4843	GCCAGACCGTTG	5015	YES
AKPL	4929	GCCAAGCCGTTG	5101	YES
ARDPL	4844	GCCAGAGATCCTTTG	5016	YES
AKDPL	4930	GCCAAGGACCCTTTG	5102	YES
ARGPL	5384	GCCAGAGGTCCCTTG	5484	NO
AKGPL	5385	GCCAAGGGGCCGTTG	5485	NO

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ARPA	5386	GCCAGACCAGCT	5486	NO
AKPA	5387	GCCAAGCCGGCT	5487	NO
ARDPA	5388	GCCAGAGATCCCGCT	5488	NO
AKDPA	5389	GCCAAGGACCCCGCT	5489	NO
ARPT	5390	GCCAGACCTACT	5490	NO
AKPT	5391	GCCAAGCCTACT	5491	NO
ARDPT	5392	GCCAGAGATCCGACT	5492	NO
AKDPT	5393	GCCAAGGACCCTACT	5493	NO
ARGPT	5394	GCCAGAGGACCCACT	5494	NO
AKGPT	5395	GCCAAGGGGCCCACT	5495	NO
ARPV	5396	GCCAGACCGGTG	5496	NO
AKPV	5397	GCCAAGCCAGTG	5497	NO
ARDPV	5398	GCCAGAGATCCGGTG	5498	NO
AKDPV	5399	GCCAAGGACCCTGTG	5499	NO
ARRP	4845	GCCAGAAGGCCT	5017	YES
AKRP	4931	GCCAAGAGGCCT	5103	YES
ARDRP	4846	GCCAGAGACCGTCCT	5018	YES
AKDRP	4932	GCCAAGGACCGTCCT	5104	YES
ARGRP	5400	GCCAGAGGAAGGCCT	5500	NO
AKGRP	5401	GCCAAGGGCCGTCCT	5501	NO
ARSP	4847	GCCAGATCACCT	5019	YES
AKSP	4933	GCCAAGAGTCCT	5105	YES
ARDSP	5402	GCCAGAGACTCTCCT	5502	NO
AKDSP	5403	GCCAAGGACTCCCCT	5503	NO
ARGSP	5404	GCCAGAGGTTCCCCT	5504	NO
AKGSP	5405	GCCAAGGGTTCACCT	5505	NO
ARLP	4848	GCCAGACTTCCT	5020	YES
AKLP	4934	GCCAAGCTACCT	5106	YES
ARDLP	5406	GCCAGAGATCTTCCT	5506	NO
AKDLP	5407	GCCAAGGATCTACCT	5507	NO
ARAP	4849	GCCAGAGCCCCT	5021	YES
AKAP	4935	GCCAAGGCTCCT	5107	YES

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ARDAP	5408	GCCAGAGATGCTCCT	5508	NO
AKDAP	5409	GCCAAGGATGCTCCT	5509	NO
ARGAP	5410	GCCAGAGGGGCCCCT	5510	NO
AKGAP	5411	GCCAAGGGTGCCCCT	5511	NO
ARTP	4850	GCCAGAACTCCT	5022	YES
AKTP	4936	GCCAAGACGCCT	5108	YES
ARDTP	5412	GCCAGAGATACCCCT	5512	NO
AKDTP	5413	GCCAAGGACACGCCT	5513	NO
ARVP	4851	GCCAGAGTCCCT	5023	YES
AKVP	4937	GCCAAGGTACCT	5109	YES
ARAGG	5414	GCCAGAGCTGGCGGA	5514	NO
AKAGG	5415	GCCAAGGCCGGTGGA	5515	NO
ARDGGG	5416	GCCAGAGATGGTGGCGGA	5516	NO
AKDGGG	5417	GCCAAGGACGGCGGTGGA	5517	NO
ARLGG	5418	GCCAGATTGGGCGGA	5518	NO
AKLGG	5419	GCCAAGCTAGGCGGA	5519	NO
ARDLGG	5420	GCCAGAGATTTGGGTGGA	5520	NO
AKDLGG	5421	GCCAAGGATTTGGGTGGA	5521	NO
ARRGG	5422	GCCAGAAGAGGTGGA	5522	NO
AKRGG	5423	GCCAAGAGAGGAGGA	5523	NO
ARDRGG	5424	GCCAGAGACCGTGGCGGA	5524	NO
AKDRGG	5425	GCCAAGGACAGAGGTGGA	5525	NO
ARSGG	5426	GCCAGATCAGGCGGA	5526	NO
AKSGG	5427	GCCAAGTCCGGTGGA	5527	NO
ARVGG	4852	GCCAGAGTTGGAGGA	5024	YES
AKVGG	4938	GCCAAGGTGGGTGGA	5110	YES
ARQ	n/a	GCAAGACAG	n/a	YES
AKQ	n/a	GCAAAACAG	n/a	YES
ARH	n/a	GCCAGACAC	n/a	YES
AKH	n/a	GCCAAACAC	n/a	YES
ARDQ	4853	GCCAGGGACCAG	5025	YES
AKDQ	4939	GCCAAGGATCAG	5111	YES

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ARDH	4854	GCAAGAGACCAC	5026	YES
AKDH	4940	GCTAAAGACCAC	5112	YES
ARAR	4855	GCAAGGGCTAGA	5027	YES
AKAR	4941	GCCAAGGCAAGA	5113	YES
ARAS	4856	GCTAGGGCATCT	5028	YES
AKAS	4942	GCCAAGGCATCT	5114	YES
ARDQG	4857	GCTAGGGATCAGGGA	5029	YES
AKDQG	4943	GCAAAGGATCAGGGA	5115	YES
ARSR	4858	GCTAGATCAAGA	5030	YES
AKSR	4944	GCCAAGAGTAGA	5116	YES
ARDRS	4859	GCCAGGGACAGGTCT	5031	YES
AKDRS	4945	GCAAAAGACAGGTCT	5117	YES
ARSL	4860	GCTAGATCTTTG	5032	YES
AKSL	4946	GCAAAGAGCTTG	5118	YES
ARLH	4861	GCTAGGTTGCAC	5033	YES
AKLH	4947	GCTAAATTGCAC	5119	YES
ARDLT	4862	GCCAGGGATTTGACT	5034	YES
AKDLT	4948	GCCAAGGACTTGACT	5120	YES
ARK	n/a	GCCAGAAAG	n/a	YES
AKK	n/a	GCTAAAAAG	n/a	YES
ARAE	4863	GCAAGAGCCGAG	5035	YES
AKAE	4949	GCTAAAGCAGAG	5121	YES
ARDLS	4864	GCAAGGGATTTGTCT	5036	YES
AKDLS	4950	GCAAAAGACTTGTCT	5122	YES
ARGD	4865	GCTAGAGGGGAC	5037	YES
AKGD	4951	GCAAAAGGGGAC	5123	YES
ARRR	4866	GCTAGGAGGAGA	5038	YES
AKRR	4952	GCAAAAAGGAGA	5124	YES
ARDK	4867	GCTAGAGATAAG	5039	YES
AKDK	4953	GCAAAAGACAAG	5125	YES
ARVS	4868	GCTAGAGTATCT	5040	YES
AKVS	4954	GCCAAAGTATCT	5126	YES

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ARDRL	4869	GCCAGAGACAGGTTG	5041	YES
AKDRL	4955	GCAAAAGACAGGTTG	5127	YES
ARGQ	4870	GCTAGGGGCCAG	5042	YES
AKGQ	4956	GCCAAAGGACAG	5128	YES
ARVR	4871	GCCAGGGTCAGA	5043	YES
AKVR	4957	GCAAAAGTCAGA	5129	YES
ARAK	4872	GCTAGGGCTAAG	5044	YES
AKAK	4958	GCAAAGGCAAAG	5130	YES
ARGK	4873	GCCAGGGGTAAG	5045	YES
AKGK	4959	GCAAAGGGCAAG	5131	YES
ARDIS	4874	GCAAGGGATATTTCT	5046	YES
AKDIS	4960	GCAAAGGACATTTCT	5132	YES
ARDFT	4875	GCTAGGGATTTCACT	5047	YES
AKDFT	4961	GCTAAAGATTTCACT	5133	YES
ARQG	4876	GCCAGGCAGGGA	5048	YES
AKQG	4962	GCCAAGCAAGGA	5134	YES

[i] "AR" and "AK" refer to the last two C-terminal amino acids of the heavy chain chassis used in the current example. They are not part of the TN1 segment.

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Table 27. Theoretical segment pool of degenerate oligonucleotide sequences encoding DH segments of Example 13.

Name	Degenerate Oligo	Peptide Length	SEQ ID NO
DH_001	KHTGAK	2	n/a
DH_002	KHTKGG	2	n/a
DH_003	KHTCMT	2	n/a
DH_004	KHTMCT	2	n/a
DH_005	GVCWSG	2	n/a
DH_006	SVCYAT	2	n/a
DH_007	BYCSAG	2	n/a
DH_008	SBAMAG	2	n/a
DH_009	VSCMAA	2	n/a
DH_010	GRABYT	2	n/a
DH_011	GRAKBG	2	n/a
DH_012	RDAGAK	2	n/a
DH_013	RDAGRT	2	n/a
DH_014	YHTSAC	2	n/a
DH_015	YHTKAC	2	n/a
DH_016	YHTMCG	2	n/a
DH_017	MHAGAW	2	n/a
DH_018	MHAGRT	2	n/a
DH_019	MHAMCT	2	n/a
DH_020	MBCYAT	2	n/a
DH_021	CVACNG	2	n/a
DH_022	MSCAHG	2	n/a
DH_023	CRGKBG	2	n/a
DH_024	WSGHCT	2	n/a
DH_025	WGGKHT	2	n/a
DH_026	BGGSAK	2	n/a
DH_027	BWCAMA	2	n/a
DH_028	BHCTGG	2	n/a

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DH_029	TGGVBT	2	n/a
DH_030	BHCAGT	2	n/a
DH_031	SRTATT	2	n/a
DH_032	ACABHT	2	n/a
DH_033	SVCGCT	2	n/a
DH_034	ATGSVT	2	n/a
DH_035	SWGAGG	2	n/a
DH_036	GTAGCAVBT	3	n/a
DH_037	DBGSWACTT	3	n/a
DH_038	VNCBCAGGT	3	n/a
DH_039	VNCDCATAT	3	n/a
DH_040	VHAKKGTTG	3	n/a
DH_041	CCAGCABHT	3	n/a
DH_042	VHASRACTT	3	n/a
DH_043	BHCAGCRST	3	n/a
DH_044	BHCGGAKMT	3	n/a
DH_045	BHCGGAGDT	3	n/a
DH_046	BHCAGCKMT	3	n/a
DH_047	NHCCRACTT	3	n/a
DH_048	NHCAGCKGG	3	n/a
DH_049	BHCGGAKSG	3	n/a
DH_050	VBCGGAGNT	3	n/a
DH_051	NHCAGCGVT	3	n/a
DH_052	NHCTACGVT	3	n/a
DH_053	NHCAGCGVG	3	n/a
DH_054	VHATGGSYG	3	n/a
DH_055	VNCGHCTAT	3	n/a
DH_056	GGTRNACTT	3	n/a
DH_057	NHCABAGGT	3	n/a
DH_058	VHAGCAGNT	3	n/a
DH_059	DBGKYCGGT	3	n/a
DH_060	BHCGGARKT	3	n/a

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DH_061	NHCGTAGVT	3	n/a
DH_062	VNTTHCTAT	3	n/a
DH_063	GTAGTABHT	3	n/a
DH_064	VBCGNCCTT	3	n/a
DH_065	BHCGGAGNG	3	n/a
DH_066	VNCGHCGGT	3	n/a
DH_067	AGGBHCGGT	3	n/a
DH_068	VNCTBGTAT	3	n/a
DH_069	VNCTBGCTT	3	n/a
DH_070	NHCKACTAT	3	n/a
DH_071	CTARNACTT	3	n/a
DH_072	NHCBCAGGT	3	n/a
DH_073	NHCTACBAT	3	n/a
DH_074	BHCACAGCCAKS	4	5528
DH_075	VHGGBAGCAACT	4	5529
DH_076	DBGTTCGGAGNG	4	5530
DH_077	BHCGGAKMCTAT	4	5531
DH_078	TACAGCAGCVBT	4	5532
DH_079	VHGGTARSAGGT	4	5533
DH_080	VBCGACGGATHT	4	5534
DH_081	NHCTACGGAGVT	4	5535
DH_082	VHGRYGGCAACT	4	5536
DH_083	VHATACAGCRST	4	5537
DH_084	CAGTGGCTABHT	4	5538
DH_085	VHAGTAGCAGNT	4	5539
DH_086	VBCACAGTARMG	4	5540
DH_087	AGCAGCAGCDBG	4	5541
DH_088	NHCTMCTACGGT	4	5542
DH_089	BHCAGCTGGTHT	4	5543
DH_090	VHACAACTAGNT	4	5544
DH_091	BHCGGAAGCKMT	4	5545
DH_092	BHCGGATSGTAT	4	5546

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DH_093	NHCAGCGGABGG	4	5547
DH_094	BHCGGATACKMT	4	5548
DH_095	VHAGTAACARMG	4	5549
DH_096	GCAGCAGCAVBT	4	5550
DH_097	VBCAYATTCGGT	4	5551
DH_098	GTAGCAGCAVHA	4	5552
DH_099	NHCTACTACGVT	4	5553
DH_100	VBCKMCGGATAT	4	5554
DH_101	VHACAACTAKKG	4	5555
DH_102	VHGGGARKCGCT	4	5556
DH_103	VBTBTCGGAGAG	4	5557
DH_104	BHCTACAGCKMT	4	5558
DH_105	VHAGTASSAGCT	4	5559
DH_106	VBTCDAGGAGTT	4	5560
DH_107	GACAGCAGCDBG	4	5561
DH_108	VBCGVCTACAGT	4	5562
DH_109	NHCTACGGAKCT	4	5563
DH_110	NHCTACTACTHT	4	5564
DH_111	BHCVGCTACAGT	4	5565
DH_112	VBCTGGTTCGGT	4	5566
DH_113	VNCTACTACTHT	4	5567
DH_114	VHABTCGGAGGT	4	5568
DH_115	NHCATGGTAAGAGVT	5	5569
DH_116	NHCTACGGAGACTHT	5	5570
DH_117	VBCTACAGCTACGNT	5	5571
DH_118	VNCAGCGGAAGCTHT	5	5572
DH_119	VBCTTTCTAGAATBG	5	5573
DH_120	BHCGGAAGCTACKMT	5	5574
DH_121	NHCAGCGGAAGCTHT	5	5575
DH_122	BHCAGCAGCAGCTBG	5	5576
DH_123	BHCAGCAGCGGATBG	5	5577
DH_124	VBCACAGTAACAANA	5	5578

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DH_125	BHCAGCAGCAGCTHT	5	5579
DH_126	NHCAGCGGATGGTHT	5	5580
DH_127	NHCAGCGGATACGVT	5	5581
DH_128	NHCTACTACGACABT	5	5582
DH_129	BHCAGCAGCGGATHT	5	5583
DH_130	VHAGCAGCAAGACNT	5	5584
DH_131	VHGTACTACTACGVT	5	5585
DH_132	VBCACAATGGTACRG	5	5586
DH_133	NHCATGGTACRAGGT	5	5587
DH_134	NHCTSGGGAAGCTAT	5	5588
DH_135	BHCAGCAGCAGCTGGTHT	6	5589
DH_136	NHCTACTACGACAGCABT	6	5590
DH_137	VBCTACAGCGGATACGNT	6	5591
DH_138	BHCAGCAGCGGATGGTHT	6	5592
DH_139	NHCTACTACGGAAGCGVT	6	5593
DH_140	BHCAGCAGCGGATACTHT	6	5594
DH_141	NHCTACGACAGCAGCGVT	6	5595
DH_142	NHCGACTTCTGGAGCGVT	6	5596
DH_143	BHCGACAGCAGCGGATHT	6	5597
DH_144	SNATACTTCGACTGGYYT	6	5598
DH_145	TGTRGCRGCACAAGCTGT	6	5599
DH_146	NHCTACTACGGAAGCGVG	6	5600
DH_147	TGTRGCRGCGGAAGCTGT	6	5601
DH_148	NHCTTTTGGAGCGGATHT	6	5602
DH_149	NHCTACTACGACAGCAGCGVT	7	5603
DH_150	NHCGACATACTAACAGGATHT	7	5604
DH_151	NHCTACGACTTCTGGAGCGVT	7	5605
DH_152	BHCTGTAGCAGCACAAGCTGT	7	5606
DH_153	DBGTACAGCAGCAGCTGGTHT	7	5607
DH_154	NHCTACGACAGCAGCGGATHT	7	5608
DH_155	NHCTACTACGGAAGCGGAABT	7	5609
DH_156	DBGTACAGCAGCGGATGGTHT	7	5610

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DH_157	BHCTGTAGCGGAGGAAGCTGT	7	5611
DH_158	TGTAGCGGAGGAAGCTGTYHT	7	5612
DH_159	TGTAGCAGCACAAGCTGTYHT	7	5613
DH_160	NHCTGTGGAGGAGACTGTTHT	7	5614
DH_161	NHCGACTTCTGGAGCGGATHT	7	5615
DH_162	BHCGACAGCAGCGGATACTHT	7	5616
DH_163	VHATACTGTGGAGGAGACTGT	7	5617
DH_164	NHCTACTACGACAGCAGCGGATHT	8	5618
DH_165	NHCTACTACGGAAGCGGAAGCTHT	8	5619
DH_166	VBCTACTGTAGCAGCACAAGCTGT	8	5620
DH_167	VBCTACTGTAGCGGAGGAAGCTGT	8	5621
DH_168	NHCTACGACTTCTGGAGCGGATHT	8	5622
DH_169	NHCGACATACTAACAGGATACTHT	8	5623
DH_170	BHCTGTAGCGGAGGAAGCTGTTHT	8	5624
DH_171	BHCTGTAGCAGCACAAGCTGTTHT	8	5625
DH_172	VHATACTGTGGAGGAGACTGTTHT	8	5626
DH_173	NHCTACGACAGCAGCGGATACTHT	8	5627
DH_174	VNCTACTACGGAAGCGGAAGCTMT	8	5628
DH_175	NHCGACTTCTGGAGCGGATACTHT	8	5629
DH_176	VHACTAAGATACTTCGACTGGYWT	8	5630
DH_177	NHCTACTACGACAGCAGCGGATACTHT	9	5631
DH_178	VBCTACTGTAGCGGAGGAAGCTGTTHT	9	5632
DH_179	VBCTACTGTAGCAGCACAAGCTGTTHT	9	5633
DH_180	NHCTACGACTTCTGGAGCGGATACTHT	9	5634
DH_181	BHCTGTAGCGGAGGAAGCTGTTACTHT	9	5635
DH_182	NHCTACTACGACAGCAGCGGATACTACTHT	10	5636
DH_183	NHCTACGACTACGTATGGGGAAGCTACGCATHT	11	5637
DH_184	NHCTACGACTACGTATGGGGAAGCTACGCATACAHA	12	5638

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Table 28. Theoretical segment pool of unique DH polypeptide segments encoded by the degenerate oligonucleotides of Table 27.

Name	Sequence	Length	SEQ ID NO
PDH_0001	YE	2	n/a
PDH_0002	DD	2	n/a
PDH_0003	VD	2	n/a
PDH_0004	FD	2	n/a
PDH_0005	AE	2	n/a
PDH_0006	SD	2	n/a
PDH_0007	YD	2	n/a
PDH_0008	VE	2	n/a
PDH_0009	DE	2	n/a
PDH_0010	AD	2	n/a
PDH_0011	FE	2	n/a
PDH_0012	SE	2	n/a
PDH_0013	VG	2	n/a
PDH_0014	FW	2	n/a
PDH_0015	YG	2	n/a
PDH_0016	DW	2	n/a
PDH_0017	FG	2	n/a
PDH_0018	AW	2	n/a
PDH_0019	DG	2	n/a
PDH_0020	YW	2	n/a
PDH_0021	SG	2	n/a
PDH_0022	AG	2	n/a
PDH_0023	VW	2	n/a
PDH_0024	SW	2	n/a
PDH_0025	VP	2	n/a
PDH_0026	DH	2	n/a
PDH_0027	DP	2	n/a
PDH_0028	YP	2	n/a
PDH_0029	SH	2	n/a

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PDH_0030	VH	2	n/a
PDH_0031	FH	2	n/a
PDH_0032	YH	2	n/a
PDH_0033	FP	2	n/a
PDH_0034	AP	2	n/a
PDH_0035	SP	2	n/a
PDH_0036	AH	2	n/a
PDH_0037	YT	2	n/a
PDH_0038	DT	2	n/a
PDH_0039	AT	2	n/a
PDH_0040	ST	2	n/a
PDH_0041	FT	2	n/a
PDH_0042	VT	2	n/a
PDH_0043	AS	2	n/a
PDH_0044	AR	2	n/a
PDH_0045	DS	2	n/a
PDH_0046	GT	2	n/a
PDH_0047	GS	2	n/a
PDH_0048	GW	2	n/a
PDH_0049	GR	2	n/a
PDH_0050	DR	2	n/a
PDH_0051	PH	2	n/a
PDH_0052	RH	2	n/a
PDH_0053	PY	2	n/a
PDH_0054	GH	2	n/a
PDH_0055	GY	2	n/a
PDH_0056	RY	2	n/a
PDH_0057	HH	2	n/a
PDH_0058	HY	2	n/a
PDH_0059	DY	2	n/a
PDH_0060	AY	2	n/a
PDH_0061	AQ	2	n/a

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PDH_0062	FQ	2	n/a
PDH_0063	LE	2	n/a
PDH_0064	PE	2	n/a
PDH_0065	LQ	2	n/a
PDH_0066	PQ	2	n/a
PDH_0067	VQ	2	n/a
PDH_0068	SQ	2	n/a
PDH_0069	RK	2	n/a
PDH_0070	GK	2	n/a
PDH_0071	AK	2	n/a
PDH_0072	RQ	2	n/a
PDH_0073	GQ	2	n/a
PDH_0074	LK	2	n/a
PDH_0075	VK	2	n/a
PDH_0076	PK	2	n/a
PDH_0077	SK	2	n/a
PDH_0078	TK	2	n/a
PDH_0079	TQ	2	n/a
PDH_0080	GL	2	n/a
PDH_0081	GP	2	n/a
PDH_0082	GV	2	n/a
PDH_0083	EF	2	n/a
PDH_0084	GF	2	n/a
PDH_0085	EL	2	n/a
PDH_0086	EA	2	n/a
PDH_0087	ES	2	n/a
PDH_0088	EP	2	n/a
PDH_0089	GA	2	n/a
PDH_0090	EV	2	n/a
PDH_0091	GG	2	n/a
PDH_0092	EG	2	n/a
PDH_0093	EW	2	n/a

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PDH_0094	IE	2	n/a
PDH_0095	RE	2	n/a
PDH_0096	KE	2	n/a
PDH_0097	GD	2	n/a
PDH_0098	ID	2	n/a
PDH_0099	RD	2	n/a
PDH_0100	EE	2	n/a
PDH_0101	GE	2	n/a
PDH_0102	KD	2	n/a
PDH_0103	ED	2	n/a
PDH_0104	IG	2	n/a
PDH_0105	RG	2	n/a
PDH_0106	KG	2	n/a
PDH_0107	LD	2	n/a
PDH_0108	LH	2	n/a
PDH_0109	PD	2	n/a
PDH_0110	HD	2	n/a
PDH_0111	SY	2	n/a
PDH_0112	FY	2	n/a
PDH_0113	YY	2	n/a
PDH_0114	LY	2	n/a
PDH_0115	LT	2	n/a
PDH_0116	HP	2	n/a
PDH_0117	HT	2	n/a
PDH_0118	LP	2	n/a
PDH_0119	PT	2	n/a
PDH_0120	PP	2	n/a
PDH_0121	TE	2	n/a
PDH_0122	QE	2	n/a
PDH_0123	TD	2	n/a
PDH_0124	QD	2	n/a
PDH_0125	PG	2	n/a

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PDH_0126	LG	2	n/a
PDH_0127	TG	2	n/a
PDH_0128	QG	2	n/a
PDH_0129	QP	2	n/a
PDH_0130	QT	2	n/a
PDH_0131	KT	2	n/a
PDH_0132	KP	2	n/a
PDH_0133	IP	2	n/a
PDH_0134	TP	2	n/a
PDH_0135	TT	2	n/a
PDH_0136	IT	2	n/a
PDH_0137	IH	2	n/a
PDH_0138	IY	2	n/a
PDH_0139	TH	2	n/a
PDH_0140	TY	2	n/a
PDH_0141	RR	2	n/a
PDH_0142	QL	2	n/a
PDH_0143	QQ	2	n/a
PDH_0144	PL	2	n/a
PDH_0145	RP	2	n/a
PDH_0146	PR	2	n/a
PDH_0147	RL	2	n/a
PDH_0148	QR	2	n/a
PDH_0149	PM	2	n/a
PDH_0150	TM	2	n/a
PDH_0151	RT	2	n/a
PDH_0152	RM	2	n/a
PDH_0153	SM	2	n/a
PDH_0154	QA	2	n/a
PDH_0155	RA	2	n/a
PDH_0156	QS	2	n/a
PDH_0157	QV	2	n/a

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PDH_0158	RS	2	n/a
PDH_0159	QW	2	n/a
PDH_0160	RW	2	n/a
PDH_0161	RV	2	n/a
PDH_0162	WS	2	n/a
PDH_0163	WT	2	n/a
PDH_0164	IS	2	n/a
PDH_0165	WP	2	n/a
PDH_0166	SS	2	n/a
PDH_0167	WV	2	n/a
PDH_0168	WF	2	n/a
PDH_0169	RF	2	n/a
PDH_0170	WA	2	n/a
PDH_0171	WD	2	n/a
PDH_0172	WY	2	n/a
PDH_0173	WQ	2	n/a
PDH_0174	WE	2	n/a
PDH_0175	WH	2	n/a
PDH_0176	YK	2	n/a
PDH_0177	FK	2	n/a
PDH_0178	DK	2	n/a
PDH_0179	HK	2	n/a
PDH_0180	LW	2	n/a
PDH_0181	PW	2	n/a
PDH_0182	HW	2	n/a
PDH_0183	WI	2	n/a
PDH_0184	WG	2	n/a
PDH_0185	WL	2	n/a
PDH_0186	WR	2	n/a
PDH_0187	YS	2	n/a
PDH_0188	LS	2	n/a
PDH_0189	HS	2	n/a

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PDH_0190	FS	2	n/a
PDH_0191	PS	2	n/a
PDH_0192	VS	2	n/a
PDH_0193	GI	2	n/a
PDH_0194	HI	2	n/a
PDH_0195	RI	2	n/a
PDH_0196	DI	2	n/a
PDH_0197	TF	2	n/a
PDH_0198	TL	2	n/a
PDH_0199	TV	2	n/a
PDH_0200	TA	2	n/a
PDH_0201	PA	2	n/a
PDH_0202	HA	2	n/a
PDH_0203	DA	2	n/a
PDH_0204	AA	2	n/a
PDH_0205	MR	2	n/a
PDH_0206	MA	2	n/a
PDH_0207	MD	2	n/a
PDH_0208	MP	2	n/a
PDH_0209	MH	2	n/a
PDH_0210	MG	2	n/a
PDH_0211	VR	2	n/a
PDH_0212	ER	2	n/a
PDH_0213	LR	2	n/a
PDH_0214	VAL	3	n/a
PDH_0215	VAR	3	n/a
PDH_0216	VAI	3	n/a
PDH_0217	VAA	3	n/a
PDH_0218	VAT	3	n/a
PDH_0219	VAP	3	n/a
PDH_0220	VAV	3	n/a
PDH_0221	VAG	3	n/a

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PDH_0222	VAS	3	n/a
PDH_0223	VVL	3	n/a
PDH_0224	VEL	3	n/a
PDH_0225	REL	3	n/a
PDH_0226	TLL	3	n/a
PDH_0227	WEL	3	n/a
PDH_0228	RLL	3	n/a
PDH_0229	TQL	3	n/a
PDH_0230	RVL	3	n/a
PDH_0231	GLL	3	n/a
PDH_0232	TEL	3	n/a
PDH_0233	GVL	3	n/a
PDH_0234	LQL	3	n/a
PDH_0235	MEL	3	n/a
PDH_0236	SLL	3	n/a
PDH_0237	LVL	3	n/a
PDH_0238	MQL	3	n/a
PDH_0239	AVL	3	n/a
PDH_0240	AQL	3	n/a
PDH_0241	SQL	3	n/a
PDH_0242	GQL	3	n/a
PDH_0243	LEL	3	n/a
PDH_0244	TVL	3	n/a
PDH_0245	RQL	3	n/a
PDH_0246	LLL	3	n/a
PDH_0247	VQL	3	n/a
PDH_0248	ALL	3	n/a
PDH_0249	AEL	3	n/a
PDH_0250	WLL	3	n/a
PDH_0251	WVL	3	n/a
PDH_0252	SEL	3	n/a
PDH_0253	VLL	3	n/a

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PDH_0254	MVL	3	n/a
PDH_0255	GEL	3	n/a
PDH_0256	MLL	3	n/a
PDH_0257	SVL	3	n/a
PDH_0258	WQL	3	n/a
PDH_0259	ISG	3	n/a
PDH_0260	DSG	3	n/a
PDH_0261	VPG	3	n/a
PDH_0262	VSG	3	n/a
PDH_0263	GAG	3	n/a
PDH_0264	IPG	3	n/a
PDH_0265	APG	3	n/a
PDH_0266	TSG	3	n/a
PDH_0267	DPG	3	n/a
PDH_0268	LSG	3	n/a
PDH_0269	LAG	3	n/a
PDH_0270	NPG	3	n/a
PDH_0271	PAG	3	n/a
PDH_0272	SAG	3	n/a
PDH_0273	ASG	3	n/a
PDH_0274	RPG	3	n/a
PDH_0275	HPG	3	n/a
PDH_0276	GSG	3	n/a
PDH_0277	GPG	3	n/a
PDH_0278	IAG	3	n/a
PDH_0279	LPG	3	n/a
PDH_0280	AAG	3	n/a
PDH_0281	IPG	3	n/a
PDH_0282	PSG	3	n/a
PDH_0283	PPG	3	n/a
PDH_0284	SPG	3	n/a
PDH_0285	RAG	3	n/a

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PDH_0286	HAG	3	n/a
PDH_0287	SSG	3	n/a
PDH_0288	HSG	3	n/a
PDH_0289	RSG	3	n/a
PDH_0290	TAG	3	n/a
PDH_0291	DAG	3	n/a
PDH_0292	NAG	3	n/a
PDH_0293	NSG	3	n/a
PDH_0294	GTY	3	n/a
PDH_0295	ITY	3	n/a
PDH_0296	LTY	3	n/a
PDH_0297	ISY	3	n/a
PDH_0298	GAY	3	n/a
PDH_0299	LAY	3	n/a
PDH_0300	HSY	3	n/a
PDH_0301	AAY	3	n/a
PDH_0302	ASY	3	n/a
PDH_0303	TAY	3	n/a
PDH_0304	NAY	3	n/a
PDH_0305	HTY	3	n/a
PDH_0306	RTY	3	n/a
PDH_0307	PTY	3	n/a
PDH_0308	RAY	3	n/a
PDH_0309	ATY	3	n/a
PDH_0310	STY	3	n/a
PDH_0311	DSY	3	n/a
PDH_0312	GSY	3	n/a
PDH_0313	IAY	3	n/a
PDH_0314	PAY	3	n/a
PDH_0315	VTY	3	n/a
PDH_0316	PSY	3	n/a
PDH_0317	ITY	3	n/a

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PDH_0318	VAY	3	n/a
PDH_0319	NTY	3	n/a
PDH_0320	DAY	3	n/a
PDH_0321	TSY	3	n/a
PDH_0322	DTY	3	n/a
PDH_0323	RSY	3	n/a
PDH_0324	SSY	3	n/a
PDH_0325	NSY	3	n/a
PDH_0326	SAY	3	n/a
PDH_0327	HAY	3	n/a
PDH_0328	LSY	3	n/a
PDH_0329	VSY	3	n/a
PDH_0330	IVL	3	n/a
PDH_0331	KWL	3	n/a
PDH_0332	KVL	3	n/a
PDH_0333	PLL	3	n/a
PDH_0334	LGL	3	n/a
PDH_0335	QWL	3	n/a
PDH_0336	EGL	3	n/a
PDH_0337	EWL	3	n/a
PDH_0338	EVL	3	n/a
PDH_0339	QLL	3	n/a
PDH_0340	AGL	3	n/a
PDH_0341	VWL	3	n/a
PDH_0342	ELL	3	n/a
PDH_0343	KGL	3	n/a
PDH_0344	ILL	3	n/a
PDH_0345	IGL	3	n/a
PDH_0346	AWL	3	n/a
PDH_0347	LWL	3	n/a
PDH_0348	QGL	3	n/a
PDH_0349	PVL	3	n/a

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PDH_0350	VGL	3	n/a
PDH_0351	IWL	3	n/a
PDH_0352	KLL	3	n/a
PDH_0353	PGL	3	n/a
PDH_0354	PWL	3	n/a
PDH_0355	QVL	3	n/a
PDH_0356	TGL	3	n/a
PDH_0357	TWL	3	n/a
PDH_0358	PAD	3	n/a
PDH_0359	PAL	3	n/a
PDH_0360	PAA	3	n/a
PDH_0361	PAH	3	n/a
PDH_0362	PAP	3	n/a
PDH_0363	PAS	3	n/a
PDH_0364	PAF	3	n/a
PDH_0365	PAV	3	n/a
PDH_0366	IQL	3	n/a
PDH_0367	KRL	3	n/a
PDH_0368	PRL	3	n/a
PDH_0369	KQL	3	n/a
PDH_0370	QRL	3	n/a
PDH_0371	KEL	3	n/a
PDH_0372	EEL	3	n/a
PDH_0373	PEL	3	n/a
PDH_0374	VRL	3	n/a
PDH_0375	QEL	3	n/a
PDH_0376	LRL	3	n/a
PDH_0377	IEL	3	n/a
PDH_0378	QQL	3	n/a
PDH_0379	IRL	3	n/a
PDH_0380	EQL	3	n/a
PDH_0381	ERL	3	n/a

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PDH_0382	TRL	3	n/a
PDH_0383	ARL	3	n/a
PDH_0384	PQL	3	n/a
PDH_0385	HSS	3	n/a
PDH_0386	VST	3	n/a
PDH_0387	HSA	3	n/a
PDH_0388	YSG	3	n/a
PDH_0389	ASS	3	n/a
PDH_0390	HST	3	n/a
PDH_0391	VSS	3	n/a
PDH_0392	YSA	3	n/a
PDH_0393	DST	3	n/a
PDH_0394	PST	3	n/a
PDH_0395	AST	3	n/a
PDH_0396	FSS	3	n/a
PDH_0397	LST	3	n/a
PDH_0398	SST	3	n/a
PDH_0399	FST	3	n/a
PDH_0400	FSG	3	n/a
PDH_0401	SSS	3	n/a
PDH_0402	LSA	3	n/a
PDH_0403	LSS	3	n/a
PDH_0404	PSA	3	n/a
PDH_0405	DSA	3	n/a
PDH_0406	ASA	3	n/a
PDH_0407	SSA	3	n/a
PDH_0408	DSS	3	n/a
PDH_0409	PSS	3	n/a
PDH_0410	YSS	3	n/a
PDH_0411	FSA	3	n/a
PDH_0412	YST	3	n/a
PDH_0413	VSA	3	n/a

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PDH_0414	SGA	3	n/a
PDH_0415	AGD	3	n/a
PDH_0416	LGA	3	n/a
PDH_0417	SGY	3	n/a
PDH_0418	SGD	3	n/a
PDH_0419	FGY	3	n/a
PDH_0420	DGY	3	n/a
PDH_0421	LGS	3	n/a
PDH_0422	FGS	3	n/a
PDH_0423	DGS	3	n/a
PDH_0424	YGS	3	n/a
PDH_0425	YGA	3	n/a
PDH_0426	VGD	3	n/a
PDH_0427	PGS	3	n/a
PDH_0428	VGY	3	n/a
PDH_0429	VGS	3	n/a
PDH_0430	VGA	3	n/a
PDH_0431	LGD	3	n/a
PDH_0432	AGY	3	n/a
PDH_0433	LGY	3	n/a
PDH_0434	HGD	3	n/a
PDH_0435	HGA	3	n/a
PDH_0436	PGA	3	n/a
PDH_0437	YGD	3	n/a
PDH_0438	PGD	3	n/a
PDH_0439	YGY	3	n/a
PDH_0440	PGY	3	n/a
PDH_0441	SGS	3	n/a
PDH_0442	HGY	3	n/a
PDH_0443	FGD	3	n/a
PDH_0444	FGA	3	n/a
PDH_0445	AGS	3	n/a

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PDH_0446	DGD	3	n/a
PDH_0447	DGA	3	n/a
PDH_0448	HGS	3	n/a
PDH_0449	AGA	3	n/a
PDH_0450	SGV	3	n/a
PDH_0451	LGV	3	n/a
PDH_0452	AGG	3	n/a
PDH_0453	SGG	3	n/a
PDH_0454	DGV	3	n/a
PDH_0455	PGV	3	n/a
PDH_0456	HGV	3	n/a
PDH_0457	YGV	3	n/a
PDH_0458	LGG	3	n/a
PDH_0459	VGG	3	n/a
PDH_0460	VGV	3	n/a
PDH_0461	FGV	3	n/a
PDH_0462	PGG	3	n/a
PDH_0463	YGG	3	n/a
PDH_0464	HGG	3	n/a
PDH_0465	DGG	3	n/a
PDH_0466	AGV	3	n/a
PDH_0467	FGG	3	n/a
PDH_0468	HSD	3	n/a
PDH_0469	YSD	3	n/a
PDH_0470	ASD	3	n/a
PDH_0471	FSY	3	n/a
PDH_0472	FSD	3	n/a
PDH_0473	SSD	3	n/a
PDH_0474	VSD	3	n/a
PDH_0475	PSD	3	n/a
PDH_0476	LSD	3	n/a
PDH_0477	YSY	3	n/a

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PDH_0478	DSD	3	n/a
PDH_0479	SRL	3	n/a
PDH_0480	DQL	3	n/a
PDH_0481	FRL	3	n/a
PDH_0482	YRL	3	n/a
PDH_0483	HQL	3	n/a
PDH_0484	NQL	3	n/a
PDH_0485	NRL	3	n/a
PDH_0486	FQL	3	n/a
PDH_0487	DRL	3	n/a
PDH_0488	HRL	3	n/a
PDH_0489	YQL	3	n/a
PDH_0490	VSW	3	n/a
PDH_0491	PSW	3	n/a
PDH_0492	HSW	3	n/a
PDH_0493	NSW	3	n/a
PDH_0494	FSW	3	n/a
PDH_0495	ASW	3	n/a
PDH_0496	TSW	3	n/a
PDH_0497	LSW	3	n/a
PDH_0498	DSW	3	n/a
PDH_0499	ISW	3	n/a
PDH_0500	SSW	3	n/a
PDH_0501	YSW	3	n/a
PDH_0502	SGW	3	n/a
PDH_0503	FGW	3	n/a
PDH_0504	LGW	3	n/a
PDH_0505	AGW	3	n/a
PDH_0506	VGW	3	n/a
PDH_0507	YGW	3	n/a
PDH_0508	PGW	3	n/a
PDH_0509	DGW	3	n/a

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PDH_0510	HGW	3	n/a
PDH_0511	IGD	3	n/a
PDH_0512	GGA	3	n/a
PDH_0513	IGG	3	n/a
PDH_0514	GGD	3	n/a
PDH_0515	GGV	3	n/a
PDH_0516	RGD	3	n/a
PDH_0517	IGV	3	n/a
PDH_0518	RGV	3	n/a
PDH_0519	GGG	3	n/a
PDH_0520	IGA	3	n/a
PDH_0521	IGV	3	n/a
PDH_0522	RGG	3	n/a
PDH_0523	RGA	3	n/a
PDH_0524	TGD	3	n/a
PDH_0525	TGA	3	n/a
PDH_0526	TGG	3	n/a
PDH_0527	NSA	3	n/a
PDH_0528	NSD	3	n/a
PDH_0529	TSD	3	n/a
PDH_0530	TSA	3	n/a
PDH_0531	ISA	3	n/a
PDH_0532	ISD	3	n/a
PDH_0533	HYD	3	n/a
PDH_0534	HYG	3	n/a
PDH_0535	FYD	3	n/a
PDH_0536	FYG	3	n/a
PDH_0537	LYA	3	n/a
PDH_0538	LYD	3	n/a
PDH_0539	VYA	3	n/a
PDH_0540	VYD	3	n/a
PDH_0541	IYA	3	n/a

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PDH_0542	LYG	3	n/a
PDH_0543	DYD	3	n/a
PDH_0544	HYA	3	n/a
PDH_0545	TYD	3	n/a
PDH_0546	TYG	3	n/a
PDH_0547	YYA	3	n/a
PDH_0548	DYG	3	n/a
PDH_0549	YYD	3	n/a
PDH_0550	NYG	3	n/a
PDH_0551	NYD	3	n/a
PDH_0552	PYG	3	n/a
PDH_0553	YYG	3	n/a
PDH_0554	PYD	3	n/a
PDH_0555	NYA	3	n/a
PDH_0556	FYA	3	n/a
PDH_0557	PYA	3	n/a
PDH_0558	VYG	3	n/a
PDH_0559	AYD	3	n/a
PDH_0560	IYG	3	n/a
PDH_0561	AYA	3	n/a
PDH_0562	SYG	3	n/a
PDH_0563	IYD	3	n/a
PDH_0564	IYA	3	n/a
PDH_0565	AYG	3	n/a
PDH_0566	DYA	3	n/a
PDH_0567	SYD	3	n/a
PDH_0568	SYA	3	n/a
PDH_0569	TSE	3	n/a
PDH_0570	HSE	3	n/a
PDH_0571	YSE	3	n/a
PDH_0572	ASE	3	n/a
PDH_0573	NSE	3	n/a

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PDH_0574	FSE	3	n/a
PDH_0575	DSE	3	n/a
PDH_0576	ISE	3	n/a
PDH_0577	SSE	3	n/a
PDH_0578	VSE	3	n/a
PDH_0579	PSE	3	n/a
PDH_0580	LSE	3	n/a
PDH_0581	EWP	3	n/a
PDH_0582	PWP	3	n/a
PDH_0583	KWA	3	n/a
PDH_0584	IWP	3	n/a
PDH_0585	LWA	3	n/a
PDH_0586	LWV	3	n/a
PDH_0587	AWV	3	n/a
PDH_0588	AWA	3	n/a
PDH_0589	PWA	3	n/a
PDH_0590	QWP	3	n/a
PDH_0591	PWV	3	n/a
PDH_0592	TWV	3	n/a
PDH_0593	TWP	3	n/a
PDH_0594	QWA	3	n/a
PDH_0595	KWP	3	n/a
PDH_0596	QWV	3	n/a
PDH_0597	EWV	3	n/a
PDH_0598	VWA	3	n/a
PDH_0599	AWP	3	n/a
PDH_0600	VWV	3	n/a
PDH_0601	TWA	3	n/a
PDH_0602	EWA	3	n/a
PDH_0603	IWV	3	n/a
PDH_0604	VWP	3	n/a
PDH_0605	IWA	3	n/a

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PDH_0606	LWP	3	n/a
PDH_0607	KWV	3	n/a
PDH_0608	HDY	3	n/a
PDH_0609	IVY	3	n/a
PDH_0610	PVY	3	n/a
PDH_0611	AVY	3	n/a
PDH_0612	GVY	3	n/a
PDH_0613	LVY	3	n/a
PDH_0614	GDY	3	n/a
PDH_0615	ADY	3	n/a
PDH_0616	VVY	3	n/a
PDH_0617	NVY	3	n/a
PDH_0618	SDY	3	n/a
PDH_0619	RVY	3	n/a
PDH_0620	LDY	3	n/a
PDH_0621	HVY	3	n/a
PDH_0622	PDY	3	n/a
PDH_0623	RDY	3	n/a
PDH_0624	SVY	3	n/a
PDH_0625	IDY	3	n/a
PDH_0626	DDY	3	n/a
PDH_0627	NDY	3	n/a
PDH_0628	VDY	3	n/a
PDH_0629	DVY	3	n/a
PDH_0630	TVY	3	n/a
PDH_0631	TDY	3	n/a
PDH_0632	GKL	3	n/a
PDH_0633	GIL	3	n/a
PDH_0634	GRL	3	n/a
PDH_0635	GGL	3	n/a
PDH_0636	GAL	3	n/a
PDH_0637	GTL	3	n/a

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PDH_0638	LRG	3	n/a
PDH_0639	DTG	3	n/a
PDH_0640	ARG	3	n/a
PDH_0641	YIG	3	n/a
PDH_0642	IIG	3	n/a
PDH_0643	PIG	3	n/a
PDH_0644	DIG	3	n/a
PDH_0645	ATG	3	n/a
PDH_0646	STG	3	n/a
PDH_0647	HTG	3	n/a
PDH_0648	VRG	3	n/a
PDH_0649	YRG	3	n/a
PDH_0650	NIG	3	n/a
PDH_0651	VIG	3	n/a
PDH_0652	IRG	3	n/a
PDH_0653	LTG	3	n/a
PDH_0654	SRG	3	n/a
PDH_0655	VTG	3	n/a
PDH_0656	AIG	3	n/a
PDH_0657	IIG	3	n/a
PDH_0658	FTG	3	n/a
PDH_0659	HIG	3	n/a
PDH_0660	HRG	3	n/a
PDH_0661	PTG	3	n/a
PDH_0662	YTG	3	n/a
PDH_0663	PRG	3	n/a
PDH_0664	TIG	3	n/a
PDH_0665	DRG	3	n/a
PDH_0666	IRG	3	n/a
PDH_0667	FIG	3	n/a
PDH_0668	NTG	3	n/a
PDH_0669	FRG	3	n/a

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PDH_0670	LIG	3	n/a
PDH_0671	NRG	3	n/a
PDH_0672	TTG	3	n/a
PDH_0673	SIG	3	n/a
PDH_0674	EAG	3	n/a
PDH_0675	KAV	3	n/a
PDH_0676	IAD	3	n/a
PDH_0677	IAV	3	n/a
PDH_0678	KAD	3	n/a
PDH_0679	QAA	3	n/a
PDH_0680	LAA	3	n/a
PDH_0681	QAD	3	n/a
PDH_0682	AAD	3	n/a
PDH_0683	AAA	3	n/a
PDH_0684	LAD	3	n/a
PDH_0685	VAD	3	n/a
PDH_0686	TAA	3	n/a
PDH_0687	TAD	3	n/a
PDH_0688	TAV	3	n/a
PDH_0689	EAA	3	n/a
PDH_0690	AAV	3	n/a
PDH_0691	QAV	3	n/a
PDH_0692	EAV	3	n/a
PDH_0693	LAV	3	n/a
PDH_0694	QAG	3	n/a
PDH_0695	KAA	3	n/a
PDH_0696	IAA	3	n/a
PDH_0697	KAG	3	n/a
PDH_0698	EAD	3	n/a
PDH_0699	WVG	3	n/a
PDH_0700	VFG	3	n/a
PDH_0701	SFG	3	n/a

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PDH_0702	RFG	3	n/a
PDH_0703	WAG	3	n/a
PDH_0704	WFG	3	n/a
PDH_0705	SVG	3	n/a
PDH_0706	TVG	3	n/a
PDH_0707	GFG	3	n/a
PDH_0708	MVG	3	n/a
PDH_0709	MFG	3	n/a
PDH_0710	LVG	3	n/a
PDH_0711	WSG	3	n/a
PDH_0712	AFG	3	n/a
PDH_0713	MAG	3	n/a
PDH_0714	LFG	3	n/a
PDH_0715	MSG	3	n/a
PDH_0716	VVG	3	n/a
PDH_0717	RVG	3	n/a
PDH_0718	AVG	3	n/a
PDH_0719	GVG	3	n/a
PDH_0720	TFG	3	n/a
PDH_0721	DGI	3	n/a
PDH_0722	LGI	3	n/a
PDH_0723	SGI	3	n/a
PDH_0724	HGI	3	n/a
PDH_0725	PGI	3	n/a
PDH_0726	VGI	3	n/a
PDH_0727	YGI	3	n/a
PDH_0728	FGI	3	n/a
PDH_0729	AGI	3	n/a
PDH_0730	DVD	3	n/a
PDH_0731	FVA	3	n/a
PDH_0732	DVA	3	n/a
PDH_0733	YVD	3	n/a

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PDH_0734	YVA	3	n/a
PDH_0735	DVG	3	n/a
PDH_0736	EVG	3	n/a
PDH_0737	VVD	3	n/a
PDH_0738	HVD	3	n/a
PDH_0739	VVA	3	n/a
PDH_0740	IVA	3	n/a
PDH_0741	AVD	3	n/a
PDH_0742	YVG	3	n/a
PDH_0743	TVD	3	n/a
PDH_0744	FVG	3	n/a
PDH_0745	FVD	3	n/a
PDH_0746	TVA	3	n/a
PDH_0747	PVG	3	n/a
PDH_0748	PVA	3	n/a
PDH_0749	AVA	3	n/a
PDH_0750	PVD	3	n/a
PDH_0751	NVG	3	n/a
PDH_0752	IVD	3	n/a
PDH_0753	HVA	3	n/a
PDH_0754	SVA	3	n/a
PDH_0755	SVD	3	n/a
PDH_0756	IVG	3	n/a
PDH_0757	NVA	3	n/a
PDH_0758	LVD	3	n/a
PDH_0759	LVA	3	n/a
PDH_0760	NVD	3	n/a
PDH_0761	AYY	3	n/a
PDH_0762	LFY	3	n/a
PDH_0763	RFY	3	n/a
PDH_0764	IFY	3	n/a
PDH_0765	TYY	3	n/a

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PDH_0766	RYY	3	n/a
PDH_0767	PYY	3	n/a
PDH_0768	VYY	3	n/a
PDH_0769	SFY	3	n/a
PDH_0770	GYY	3	n/a
PDH_0771	GFY	3	n/a
PDH_0772	DFY	3	n/a
PDH_0773	VFY	3	n/a
PDH_0774	HYY	3	n/a
PDH_0775	SYY	3	n/a
PDH_0776	PFY	3	n/a
PDH_0777	LYY	3	n/a
PDH_0778	IYY	3	n/a
PDH_0779	TFY	3	n/a
PDH_0780	NFY	3	n/a
PDH_0781	HFY	3	n/a
PDH_0782	AFY	3	n/a
PDH_0783	DYY	3	n/a
PDH_0784	NYY	3	n/a
PDH_0785	VVV	3	n/a
PDH_0786	VVF	3	n/a
PDH_0787	VVP	3	n/a
PDH_0788	VVH	3	n/a
PDH_0789	VVS	3	n/a
PDH_0790	GDL	3	n/a
PDH_0791	SAL	3	n/a
PDH_0792	RAL	3	n/a
PDH_0793	RGL	3	n/a
PDH_0794	IAL	3	n/a
PDH_0795	LDL	3	n/a
PDH_0796	TDL	3	n/a
PDH_0797	ADL	3	n/a

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PDH_0798	VDL	3	n/a
PDH_0799	IDL	3	n/a
PDH_0800	SDL	3	n/a
PDH_0801	TAL	3	n/a
PDH_0802	RDL	3	n/a
PDH_0803	AAL	3	n/a
PDH_0804	SGL	3	n/a
PDH_0805	PDL	3	n/a
PDH_0806	LAL	3	n/a
PDH_0807	AGE	3	n/a
PDH_0808	SGE	3	n/a
PDH_0809	HGE	3	n/a
PDH_0810	LGE	3	n/a
PDH_0811	VGE	3	n/a
PDH_0812	PGE	3	n/a
PDH_0813	YGE	3	n/a
PDH_0814	DGE	3	n/a
PDH_0815	FGE	3	n/a
PDH_0816	SDG	3	n/a
PDH_0817	NDG	3	n/a
PDH_0818	GDG	3	n/a
PDH_0819	HDG	3	n/a
PDH_0820	ADG	3	n/a
PDH_0821	TDG	3	n/a
PDH_0822	IDG	3	n/a
PDH_0823	DDG	3	n/a
PDH_0824	VDG	3	n/a
PDH_0825	RDG	3	n/a
PDH_0826	LDG	3	n/a
PDH_0827	PDG	3	n/a
PDH_0828	RHG	3	n/a
PDH_0829	RLG	3	n/a

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PDH_0830	RYG	3	n/a
PDH_0831	DLY	3	n/a
PDH_0832	IWY	3	n/a
PDH_0833	LWY	3	n/a
PDH_0834	ALY	3	n/a
PDH_0835	RWY	3	n/a
PDH_0836	SLY	3	n/a
PDH_0837	HLY	3	n/a
PDH_0838	ILY	3	n/a
PDH_0839	SWY	3	n/a
PDH_0840	GLY	3	n/a
PDH_0841	RLY	3	n/a
PDH_0842	DWY	3	n/a
PDH_0843	NLY	3	n/a
PDH_0844	VWY	3	n/a
PDH_0845	GWY	3	n/a
PDH_0846	AWY	3	n/a
PDH_0847	HWY	3	n/a
PDH_0848	PLY	3	n/a
PDH_0849	LLY	3	n/a
PDH_0850	TWY	3	n/a
PDH_0851	TLY	3	n/a
PDH_0852	NWY	3	n/a
PDH_0853	VLY	3	n/a
PDH_0854	PWY	3	n/a
PDH_0855	GSL	3	n/a
PDH_0856	ISL	3	n/a
PDH_0857	DWL	3	n/a
PDH_0858	SSL	3	n/a
PDH_0859	TSL	3	n/a
PDH_0860	VSL	3	n/a
PDH_0861	DSL	3	n/a

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PDH_0862	HWL	3	n/a
PDH_0863	ASL	3	n/a
PDH_0864	SWL	3	n/a
PDH_0865	NWL	3	n/a
PDH_0866	NLL	3	n/a
PDH_0867	DLL	3	n/a
PDH_0868	RSL	3	n/a
PDH_0869	PSL	3	n/a
PDH_0870	HLL	3	n/a
PDH_0871	GWL	3	n/a
PDH_0872	HSL	3	n/a
PDH_0873	NSL	3	n/a
PDH_0874	LSL	3	n/a
PDH_0875	RWL	3	n/a
PDH_0876	FDY	3	n/a
PDH_0877	YYY	3	n/a
PDH_0878	FYY	3	n/a
PDH_0879	YDY	3	n/a
PDH_0880	LIL	3	n/a
PDH_0881	LKL	3	n/a
PDH_0882	LTL	3	n/a
PDH_0883	YAG	3	n/a
PDH_0884	FPG	3	n/a
PDH_0885	YPG	3	n/a
PDH_0886	FAG	3	n/a
PDH_0887	FYH	3	n/a
PDH_0888	LYH	3	n/a
PDH_0889	IYH	3	n/a
PDH_0890	SYH	3	n/a
PDH_0891	TYH	3	n/a
PDH_0892	YYH	3	n/a
PDH_0893	NYH	3	n/a

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PDH_0894	PYH	3	n/a
PDH_0895	AYH	3	n/a
PDH_0896	VYH	3	n/a
PDH_0897	HYH	3	n/a
PDH_0898	DYH	3	n/a
PDH_0899	YTAM	4	5639
PDH_0900	HTAI	4	5640
PDH_0901	YTAS	4	5641
PDH_0902	YTAI	4	5642
PDH_0903	YTAR	4	5643
PDH_0904	PTAS	4	5644
PDH_0905	LTAM	4	5645
PDH_0906	DTAI	4	5646
PDH_0907	FTAS	4	5647
PDH_0908	FTAM	4	5648
PDH_0909	LTAS	4	5649
PDH_0910	ATAI	4	5650
PDH_0911	STAI	4	5651
PDH_0912	FTAR	4	5652
PDH_0913	DTAM	4	4420
PDH_0914	STAR	4	5653
PDH_0915	LTAR	4	5654
PDH_0916	FTAI	4	5655
PDH_0917	LTAI	4	5656
PDH_0918	STAM	4	5657
PDH_0919	ATAM	4	5658
PDH_0920	STAS	4	5659
PDH_0921	ATAR	4	5660
PDH_0922	HTAS	4	5661
PDH_0923	HTAM	4	5662
PDH_0924	VTAI	4	3907
PDH_0925	DTAR	4	5663

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PDH_0926	HTAR	4	5664
PDH_0927	ATAS	4	5665
PDH_0928	VTAM	4	5666
PDH_0929	PTAR	4	5667
PDH_0930	DTAS	4	5668
PDH_0931	VTAS	4	5669
PDH_0932	PTAM	4	5670
PDH_0933	VTAR	4	5671
PDH_0934	PTAI	4	5672
PDH_0935	LVAT	4	5673
PDH_0936	LAAT	4	5674
PDH_0937	MVAT	4	5675
PDH_0938	TGAT	4	5676
PDH_0939	AVAT	4	5677
PDH_0940	VAAT	4	3803
PDH_0941	PAAT	4	5678
PDH_0942	KGAT	4	5679
PDH_0943	EGAT	4	5680
PDH_0944	PVAT	4	5681
PDH_0945	AGAT	4	5682
PDH_0946	QAAT	4	5683
PDH_0947	AAAT	4	5684
PDH_0948	VVAT	4	5685
PDH_0949	VGAT	4	3756
PDH_0950	TVAT	4	5686
PDH_0951	EVAT	4	5687
PDH_0952	LGAT	4	5688
PDH_0953	KAAT	4	5689
PDH_0954	MGAT	4	5690
PDH_0955	PGAT	4	5691
PDH_0956	QVAT	4	5692
PDH_0957	KVAT	4	5693

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PDH_0958	EAAT	4	5694
PDH_0959	TAAT	4	5695
PDH_0960	MAAT	4	5696
PDH_0961	QGAT	4	5697
PDH_0962	RFGA	4	5698
PDH_0963	MFGE	4	5699
PDH_0964	MFGA	4	5700
PDH_0965	VFGG	4	5701
PDH_0966	RFGE	4	5702
PDH_0967	MFGV	4	5703
PDH_0968	VFGA	4	5704
PDH_0969	VFGE	4	5705
PDH_0970	VFGV	4	5706
PDH_0971	MFGG	4	5707
PDH_0972	LFGV	4	5708
PDH_0973	SFGE	4	5709
PDH_0974	SFGA	4	5710
PDH_0975	RFGG	4	5711
PDH_0976	SFGV	4	5712
PDH_0977	LFGA	4	5713
PDH_0978	SFGG	4	5714
PDH_0979	LFGG	4	5715
PDH_0980	LFGE	4	5716
PDH_0981	WFGE	4	3966
PDH_0982	WFGG	4	5717
PDH_0983	WFGV	4	5718
PDH_0984	WFGA	4	5719
PDH_0985	TFGG	4	4154
PDH_0986	TFGE	4	5720
PDH_0987	AFGV	4	5721
PDH_0988	AFGA	4	5722
PDH_0989	GFGV	4	5723

PDH_0990	GFGA	4	5724
PDH_0991	GFGG	4	5725
PDH_0992	IFGV	4	5726
PDH_0993	AFGE	4	5727
PDH_0994	IFGA	4	5728
PDH_0995	RFGV	4	5729
PDH_0996	AFGG	4	5730
PDH_0997	GFGE	4	5731
PDH_0998	AGDY	4	5732
PDH_0999	PGYY	4	5733
PDH_1000	VGAY	4	5734
PDH_1001	HGSY	4	5735
PDH_1002	SGSY	4	3763
PDH_1003	PGDY	4	5736
PDH_1004	LGDY	4	5737
PDH_1005	DGAY	4	5738
PDH_1006	FGDY	4	5739
PDH_1007	LGAY	4	5740
PDH_1008	DGYY	4	5741
PDH_1009	VGSY	4	5742
PDH_1010	YGAY	4	5743
PDH_1011	FGYY	4	5744
PDH_1012	DGDY	4	5745
PDH_1013	AGYY	4	5746
PDH_1014	YGSY	4	5747
PDH_1015	VGYY	4	5748
PDH_1016	AGAY	4	5749
PDH_1017	DGSY	4	5750
PDH_1018	HGDY	4	5751
PDH_1019	FGAY	4	5752
PDH_1020	HGYY	4	5753
PDH_1021	YGYY	4	5754

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PDH_1022	SGYY	4	4187
PDH_1023	SGAY	4	5755
PDH_1024	AGSY	4	5756
PDH_1025	HGAY	4	5757
PDH_1026	PGAY	4	5758
PDH_1027	PGSY	4	5759
PDH_1028	LGSY	4	5760
PDH_1029	VGDY	4	5761
PDH_1030	SGDY	4	5762
PDH_1031	LGYY	4	5763
PDH_1032	FGSY	4	5764
PDH_1033	YGDY	4	4350
PDH_1034	YSSV	4	5765
PDH_1035	YSSI	4	5766
PDH_1036	YSSS	4	4442
PDH_1037	YSSR	4	5767
PDH_1038	YSSP	4	5768
PDH_1039	YSSA	4	5769
PDH_1040	YSSL	4	5770
PDH_1041	YSSG	4	4462
PDH_1042	YSST	4	5771
PDH_1043	EVRG	4	5772
PDH_1044	PVRG	4	5773
PDH_1045	PVTG	4	5774
PDH_1046	EVAG	4	5775
PDH_1047	MVTG	4	5776
PDH_1048	MVGG	4	5777
PDH_1049	EVGG	4	3728
PDH_1050	QVRG	4	5778
PDH_1051	MVRG	4	4017
PDH_1052	QVGG	4	5779
PDH_1053	VVAG	4	5780

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PDH_1054	EVTG	4	5781
PDH_1055	VVRG	4	5782
PDH_1056	PVAG	4	5783
PDH_1057	LVAG	4	5784
PDH_1058	LVRG	4	5785
PDH_1059	QVTG	4	5786
PDH_1060	PVGG	4	5787
PDH_1061	AVGG	4	5788
PDH_1062	TVGG	4	5789
PDH_1063	KVGG	4	5790
PDH_1064	TVAG	4	5791
PDH_1065	AVTG	4	5792
PDH_1066	KVRG	4	5793
PDH_1067	LVTG	4	5794
PDH_1068	AVRG	4	5795
PDH_1069	LVGG	4	5796
PDH_1070	AVAG	4	4473
PDH_1071	QVAG	4	5797
PDH_1072	KVTG	4	5798
PDH_1073	TVTG	4	5799
PDH_1074	VVGG	4	5800
PDH_1075	KVAG	4	5801
PDH_1076	MVAG	4	5802
PDH_1077	VVTG	4	5803
PDH_1078	TVRG	4	5804
PDH_1079	SDGY	4	5805
PDH_1080	IDGF	4	5806
PDH_1081	ADGY	4	5807
PDH_1082	ADGS	4	5808
PDH_1083	RDGF	4	5809
PDH_1084	IDGS	4	5810
PDH_1085	GDGS	4	5811

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PDH_1086	LDGY	4	5812
PDH_1087	GDGY	4	5813
PDH_1088	IDGY	4	5814
PDH_1089	SDGS	4	5815
PDH_1090	SDGF	4	5816
PDH_1091	VDGF	4	5817
PDH_1092	GDGF	4	5818
PDH_1093	TDGY	4	5819
PDH_1094	RDGY	4	4410
PDH_1095	VDGY	4	5820
PDH_1096	TDGS	4	5821
PDH_1097	RDGS	4	5822
PDH_1098	LDGF	4	5823
PDH_1099	VDGS	4	5824
PDH_1100	ADGF	4	5825
PDH_1101	LDGS	4	5826
PDH_1102	PDGS	4	5827
PDH_1103	PDGF	4	5828
PDH_1104	PDGY	4	5829
PDH_1105	TDGF	4	5830
PDH_1106	NYGG	4	5831
PDH_1107	TYGD	4	5832
PDH_1108	LYGD	4	5833
PDH_1109	FYGG	4	5834
PDH_1110	SYGG	4	5835
PDH_1111	TYGG	4	5836
PDH_1112	LYGA	4	5837
PDH_1113	SYGA	4	5838
PDH_1114	LYGG	4	5839
PDH_1115	VYGD	4	5840
PDH_1116	SYGD	4	5841
PDH_1117	AYGG	4	5842

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PDH_1118	VYGG	4	5843
PDH_1119	HYGG	4	5844
PDH_1120	FYGA	4	5845
PDH_1121	NYGD	4	5846
PDH_1122	TYGA	4	5847
PDH_1123	FYGD	4	5848
PDH_1124	IYGD	4	5849
PDH_1125	DYGD	4	4349
PDH_1126	PYGD	4	5850
PDH_1127	DYGA	4	5851
PDH_1128	HYGA	4	5852
PDH_1129	PYGA	4	5853
PDH_1130	PYGG	4	5854
PDH_1131	HYGD	4	5855
PDH_1132	AYGA	4	5856
PDH_1133	VYGA	4	5857
PDH_1134	YYGD	4	5858
PDH_1135	AYGD	4	5859
PDH_1136	NYGA	4	5860
PDH_1137	YYGA	4	5861
PDH_1138	YYGG	4	5862
PDH_1139	IYGG	4	5863
PDH_1140	IYGA	4	5864
PDH_1141	DYGG	4	4357
PDH_1142	LMAT	4	5865
PDH_1143	VTAT	4	5866
PDH_1144	KMAT	4	5867
PDH_1145	QMAT	4	5868
PDH_1146	ETAT	4	5869
PDH_1147	TTAT	4	5870
PDH_1148	TMAT	4	5871
PDH_1149	PTAT	4	5872

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PDH_1150	VMAT	4	5873
PDH_1151	LTAT	4	5874
PDH_1152	KTAT	4	5875
PDH_1153	MMAT	4	5876
PDH_1154	ATAT	4	5877
PDH_1155	QTAT	4	5878
PDH_1156	PMAT	4	5879
PDH_1157	MTAT	4	5880
PDH_1158	EMAT	4	4402
PDH_1159	AMAT	4	5881
PDH_1160	TYSA	4	5882
PDH_1161	LYSS	4	5883
PDH_1162	LYST	4	5884
PDH_1163	QYSS	4	5885
PDH_1164	VYST	4	5886
PDH_1165	VYSS	4	5887
PDH_1166	AYSA	4	5888
PDH_1167	PYSG	4	5889
PDH_1168	PYST	4	5890
PDH_1169	VYSA	4	5891
PDH_1170	PYSS	4	5892
PDH_1171	VYSG	4	5893
PDH_1172	PYSA	4	5894
PDH_1173	KYST	4	5895
PDH_1174	QYST	4	5896
PDH_1175	TYSG	4	5897
PDH_1176	TYST	4	5898
PDH_1177	QYSA	4	5899
PDH_1178	AYSS	4	5900
PDH_1179	TYSS	4	5901
PDH_1180	IYSA	4	5902
PDH_1181	AYST	4	5903

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PDH_1182	IYSG	4	5904
PDH_1183	EYSS	4	4479
PDH_1184	KYSG	4	5905
PDH_1185	EYSA	4	5906
PDH_1186	LYSG	4	5907
PDH_1187	AYSG	4	5908
PDH_1188	EYSG	4	5909
PDH_1189	LYSA	4	5910
PDH_1190	QYSG	4	5911
PDH_1191	IYST	4	5912
PDH_1192	EYST	4	5913
PDH_1193	KYSS	4	5914
PDH_1194	IYSS	4	5915
PDH_1195	KYSA	4	5916
PDH_1196	QWLS	4	5917
PDH_1197	QWLL	4	5918
PDH_1198	QWLP	4	5919
PDH_1199	QWLD	4	5920
PDH_1200	QWLY	4	5921
PDH_1201	QWLA	4	5922
PDH_1202	QWLV	4	4475
PDH_1203	QWLH	4	5923
PDH_1204	QWLF	4	5924
PDH_1205	PVAD	4	5925
PDH_1206	PVAA	4	5926
PDH_1207	IVAA	4	5927
PDH_1208	EVAA	4	5928
PDH_1209	EVAV	4	5929
PDH_1210	VVAA	4	3802
PDH_1211	IVAD	4	5930
PDH_1212	EVAD	4	5931
PDH_1213	IVAG	4	5932

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PDH_1214	QVAD	4	5933
PDH_1215	AVAA	4	5934
PDH_1216	AVAV	4	5935
PDH_1217	AVAD	4	5936
PDH_1218	KVAA	4	5937
PDH_1219	QVAA	4	5938
PDH_1220	TVAV	4	5939
PDH_1221	LVAD	4	5940
PDH_1222	LVAA	4	5941
PDH_1223	IVAV	4	5942
PDH_1224	VVAD	4	5943
PDH_1225	VVAV	4	5944
PDH_1226	QVAV	4	5945
PDH_1227	PVAV	4	5946
PDH_1228	KVAV	4	5947
PDH_1229	LVAV	4	5948
PDH_1230	TVAD	4	5949
PDH_1231	KVAD	4	5950
PDH_1232	IVAA	4	5951
PDH_1233	STVA	4	5952
PDH_1234	STVK	4	5953
PDH_1235	RTVA	4	5954
PDH_1236	ITVT	4	5955
PDH_1237	PTVA	4	5956
PDH_1238	ATVT	4	5957
PDH_1239	ATVK	4	5958
PDH_1240	VTVK	4	5959
PDH_1241	TTVK	4	5960
PDH_1242	PTVE	4	5961
PDH_1243	VTVT	4	5962
PDH_1244	STVT	4	5963
PDH_1245	VTVE	4	5964

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PDH_1246	TTVT	4	4352
PDH_1247	LTVA	4	5965
PDH_1248	RTVT	4	5966
PDH_1249	LTVE	4	5967
PDH_1250	TTVE	4	5968
PDH_1251	RTVK	4	5969
PDH_1252	VTVA	4	5970
PDH_1253	STVE	4	5971
PDH_1254	ATVA	4	5972
PDH_1255	GTVE	4	5973
PDH_1256	GTVA	4	5974
PDH_1257	ITVE	4	5975
PDH_1258	PTVT	4	5976
PDH_1259	ITVA	4	5977
PDH_1260	ATVE	4	5978
PDH_1261	GTVK	4	5979
PDH_1262	LTVK	4	5980
PDH_1263	ITVK	4	5981
PDH_1264	RTVE	4	5982
PDH_1265	LTVT	4	5983
PDH_1266	TTVA	4	5984
PDH_1267	PTVK	4	5985
PDH_1268	GTVT	4	5986
PDH_1269	SSSA	4	5987
PDH_1270	SSSS	4	4480
PDH_1271	SSSL	4	5988
PDH_1272	SSSW	4	4443
PDH_1273	SSSR	4	5989
PDH_1274	SSSV	4	5990
PDH_1275	SSST	4	5991
PDH_1276	SSSM	4	5992
PDH_1277	SSSG	4	5993

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PDH_1278	LSYG	4	5994
PDH_1279	PYYG	4	5995
PDH_1280	ASYG	4	5996
PDH_1281	FYYG	4	5997
PDH_1282	DSYG	4	5998
PDH_1283	VYYG	4	5999
PDH_1284	IYYG	4	6000
PDH_1285	DYYG	4	6001
PDH_1286	HYYG	4	6002
PDH_1287	SYYG	4	6003
PDH_1288	YYYG	4	3989
PDH_1289	VSYG	4	6004
PDH_1290	NSYG	4	6005
PDH_1291	SSYG	4	6006
PDH_1292	FSYG	4	6007
PDH_1293	ISYG	4	6008
PDH_1294	TSYG	4	6009
PDH_1295	LYYG	4	6010
PDH_1296	PSYG	4	6011
PDH_1297	AYYG	4	6012
PDH_1298	YSYG	4	4433
PDH_1299	HSYG	4	6013
PDH_1300	NYYG	4	6014
PDH_1301	TYYG	4	6015
PDH_1302	FSWY	4	6016
PDH_1303	SSWF	4	6017
PDH_1304	DSWS	4	6018
PDH_1305	LSWS	4	6019
PDH_1306	DSWY	4	6020
PDH_1307	LSWF	4	6021
PDH_1308	LSWY	4	6022
PDH_1309	VSWS	4	6023

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PDH_1310	HSWY	4	6024
PDH_1311	SSWS	4	6025
PDH_1312	PSWS	4	6026
PDH_1313	SSWY	4	4444
PDH_1314	FSWF	4	6027
PDH_1315	FSWS	4	6028
PDH_1316	PSWF	4	6029
PDH_1317	VSWF	4	6030
PDH_1318	HSWF	4	6031
PDH_1319	VSWY	4	6032
PDH_1320	HSWS	4	6033
PDH_1321	DSWF	4	6034
PDH_1322	PSWY	4	6035
PDH_1323	ASWY	4	6036
PDH_1324	YSWS	4	6037
PDH_1325	ASWF	4	6038
PDH_1326	ASWS	4	6039
PDH_1327	YSWF	4	6040
PDH_1328	YSWY	4	6041
PDH_1329	IQLV	4	6042
PDH_1330	AQLG	4	6043
PDH_1331	IQLA	4	6044
PDH_1332	EQLV	4	6045
PDH_1333	AQLA	4	6046
PDH_1334	IQLG	4	6047
PDH_1335	KQLD	4	6048
PDH_1336	TQLV	4	6049
PDH_1337	QQLA	4	6050
PDH_1338	AQLD	4	6051
PDH_1339	IQLD	4	6052
PDH_1340	AQLV	4	6053
PDH_1341	KQLA	4	6054

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PDH_1342	KQLG	4	6055
PDH_1343	LQLD	4	6056
PDH_1344	LQLG	4	6057
PDH_1345	TQLA	4	6058
PDH_1346	VQLD	4	6059
PDH_1347	TQLD	4	6060
PDH_1348	VQLA	4	6061
PDH_1349	EQLD	4	6062
PDH_1350	VQLG	4	6063
PDH_1351	TQLG	4	6064
PDH_1352	PQLD	4	6065
PDH_1353	QQLV	4	4455
PDH_1354	QQLD	4	6066
PDH_1355	PQLA	4	6067
PDH_1356	PQLG	4	6068
PDH_1357	VQLV	4	6069
PDH_1358	QQLG	4	6070
PDH_1359	KQLV	4	6071
PDH_1360	LQLV	4	6072
PDH_1361	LQLA	4	6073
PDH_1362	EQLA	4	6074
PDH_1363	PQLV	4	6075
PDH_1364	EQLG	4	6076
PDH_1365	DGSA	4	6077
PDH_1366	DGSS	4	6078
PDH_1367	SGSA	4	6079
PDH_1368	DGSD	4	6080
PDH_1369	SGSD	4	6081
PDH_1370	PGSD	4	6082
PDH_1371	FGSS	4	6083
PDH_1372	HGSA	4	6084
PDH_1373	YGSS	4	6085

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PDH_1374	FGSA	4	6086
PDH_1375	FGSD	4	6087
PDH_1376	LGSA	4	6088
PDH_1377	LGSS	4	6089
PDH_1378	AGSD	4	6090
PDH_1379	VGSS	4	6091
PDH_1380	AGSS	4	6092
PDH_1381	HGSD	4	6093
PDH_1382	VGSA	4	6094
PDH_1383	YGSA	4	6095
PDH_1384	YGSD	4	6096
PDH_1385	AGSA	4	6097
PDH_1386	HGSS	4	6098
PDH_1387	VGSD	4	6099
PDH_1388	PGSA	4	6100
PDH_1389	PGSS	4	6101
PDH_1390	SGSS	4	6102
PDH_1391	LGSD	4	6103
PDH_1392	SGWY	4	4464
PDH_1393	PGWY	4	6104
PDH_1394	FGWY	4	6105
PDH_1395	YGWY	4	6106
PDH_1396	AGWY	4	6107
PDH_1397	VGWY	4	6108
PDH_1398	LGWY	4	6109
PDH_1399	DGWY	4	6110
PDH_1400	HGWY	4	6111
PDH_1401	PSGW	4	6112
PDH_1402	YSGW	4	6113
PDH_1403	FSGR	4	6114
PDH_1404	VSGG	4	6115
PDH_1405	NSGR	4	6116

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PDH_1406	DSGR	4	6117
PDH_1407	ASGR	4	6118
PDH_1408	FSGW	4	6119
PDH_1409	DSGW	4	6120
PDH_1410	VSGR	4	6121
PDH_1411	ISGW	4	6122
PDH_1412	LSGW	4	6123
PDH_1413	DSGG	4	3723
PDH_1414	HSGR	4	6124
PDH_1415	NSGW	4	6125
PDH_1416	HSGG	4	6126
PDH_1417	HSGW	4	6127
PDH_1418	ISGG	4	6128
PDH_1419	YSGR	4	6129
PDH_1420	ISGR	4	6130
PDH_1421	YSGG	4	6131
PDH_1422	NSGG	4	6132
PDH_1423	SSGW	4	4463
PDH_1424	VSGW	4	6133
PDH_1425	SSGR	4	6134
PDH_1426	LSGR	4	6135
PDH_1427	PSGR	4	6136
PDH_1428	FSGG	4	6137
PDH_1429	TSGR	4	6138
PDH_1430	TSGW	4	6139
PDH_1431	ASGG	4	6140
PDH_1432	LSGG	4	6141
PDH_1433	ASGW	4	6142
PDH_1434	PSGG	4	6143
PDH_1435	TSGG	4	6144
PDH_1436	SSGG	4	6145
PDH_1437	VGYD	4	6146

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PDH_1438	AGYD	4	6147
PDH_1439	DGYD	4	6148
PDH_1440	AGYA	4	6149
PDH_1441	DGYA	4	6150
PDH_1442	FGYA	4	6151
PDH_1443	FGYD	4	6152
PDH_1444	PGYA	4	6153
PDH_1445	DGYS	4	6154
PDH_1446	YGYA	4	6155
PDH_1447	FGYS	4	6156
PDH_1448	VGYA	4	6157
PDH_1449	PGYD	4	6158
PDH_1450	PGYS	4	6159
PDH_1451	VGYS	4	6160
PDH_1452	YGYD	4	6161
PDH_1453	HGYA	4	6162
PDH_1454	YGYS	4	6163
PDH_1455	HGYD	4	6164
PDH_1456	SGYS	4	6165
PDH_1457	LGYA	4	6166
PDH_1458	HGYS	4	6167
PDH_1459	LGYD	4	6168
PDH_1460	AGYS	4	6169
PDH_1461	LGYS	4	6170
PDH_1462	SGYD	4	4393
PDH_1463	SGYA	4	6171
PDH_1464	QVTA	4	6172
PDH_1465	PVTA	4	6173
PDH_1466	LVTT	4	6174
PDH_1467	PVTT	4	6175
PDH_1468	PVTE	4	6176
PDH_1469	QVTT	4	6177

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PDH_1470	AVTA	4	6178
PDH_1471	QVTK	4	6179
PDH_1472	IVTA	4	6180
PDH_1473	PVTK	4	6181
PDH_1474	LVTK	4	6182
PDH_1475	AVTE	4	6183
PDH_1476	LVTA	4	6184
PDH_1477	EVTA	4	6185
PDH_1478	LVTE	4	6186
PDH_1479	EVTE	4	6187
PDH_1480	IVTE	4	6188
PDH_1481	VVTA	4	3906
PDH_1482	TVTK	4	6189
PDH_1483	TVTT	4	4353
PDH_1484	IVTT	4	6190
PDH_1485	VVTE	4	6191
PDH_1486	IVTK	4	6192
PDH_1487	TVTE	4	6193
PDH_1488	AVTT	4	6194
PDH_1489	KVTA	4	6195
PDH_1490	KVTE	4	6196
PDH_1491	AVTK	4	6197
PDH_1492	EVTK	4	6198
PDH_1493	KVTK	4	6199
PDH_1494	VVTK	4	6200
PDH_1495	TVTA	4	6201
PDH_1496	QVTE	4	6202
PDH_1497	VVTT	4	6203
PDH_1498	EVTT	4	6204
PDH_1499	KVTT	4	6205
PDH_1500	AAAG	4	4453
PDH_1501	AAAS	4	6206

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PDH_1502	AAAL	4	6207
PDH_1503	AAAR	4	6208
PDH_1504	AAAI	4	6209
PDH_1505	AAAV	4	6210
PDH_1506	AAAP	4	6211
PDH_1507	AAAA	4	6212
PDH_1508	AIFG	4	6213
PDH_1509	ATFG	4	6214
PDH_1510	PTFG	4	6215
PDH_1511	TTFG	4	6216
PDH_1512	ITFG	4	4153
PDH_1513	RTFG	4	6217
PDH_1514	STFG	4	6218
PDH_1515	SIFG	4	6219
PDH_1516	LIFG	4	6220
PDH_1517	RIFG	4	6221
PDH_1518	TIFG	4	4291
PDH_1519	GIFG	4	6222
PDH_1520	IIFG	4	6223
PDH_1521	LTFG	4	6224
PDH_1522	VIFG	4	6225
PDH_1523	PIFG	4	6226
PDH_1524	GTFG	4	6227
PDH_1525	VTFG	4	6228
PDH_1526	VAAK	4	6229
PDH_1527	VAAL	4	6230
PDH_1528	VAAP	4	6231
PDH_1529	VAAQ	4	6232
PDH_1530	VAAA	4	6233
PDH_1531	VAAE	4	6234
PDH_1532	VAAV	4	6235
PDH_1533	VAAI	4	6236

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PDH_1534	YYYD	4	4182
PDH_1535	VYYA	4	6237
PDH_1536	AYYD	4	6238
PDH_1537	YYYA	4	6239
PDH_1538	PYYD	4	6240
PDH_1539	IYYD	4	6241
PDH_1540	VYYD	4	6242
PDH_1541	IYYA	4	6243
PDH_1542	TYYA	4	6244
PDH_1543	LYYD	4	6245
PDH_1544	DYYD	4	6246
PDH_1545	SYYD	4	6247
PDH_1546	LYYA	4	6248
PDH_1547	HYYA	4	6249
PDH_1548	DYYA	4	6250
PDH_1549	SYYA	4	6251
PDH_1550	FYYD	4	6252
PDH_1551	FYYA	4	6253
PDH_1552	PYYA	4	6254
PDH_1553	AYYA	4	6255
PDH_1554	HYYD	4	6256
PDH_1555	NYYA	4	6257
PDH_1556	TYYD	4	6258
PDH_1557	NYYD	4	6259
PDH_1558	GYGY	4	6260
PDH_1559	LYGY	4	6261
PDH_1560	SSGY	4	4186
PDH_1561	RYGY	4	6262
PDH_1562	TYGY	4	6263
PDH_1563	TSGY	4	6264
PDH_1564	VYGY	4	6265
PDH_1565	ISGY	4	6266

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PDH_1566	ASGY	4	6267
PDH_1567	PSGY	4	6268
PDH_1568	RSGY	4	6269
PDH_1569	GAGY	4	6270
PDH_1570	AAGY	4	6271
PDH_1571	LSGY	4	6272
PDH_1572	SYGY	4	4434
PDH_1573	VSGY	4	6273
PDH_1574	VAGY	4	6274
PDH_1575	TAGY	4	6275
PDH_1576	PAGY	4	6276
PDH_1577	SAGY	4	6277
PDH_1578	RAGY	4	6278
PDH_1579	IAGY	4	6279
PDH_1580	AYGY	4	6280
PDH_1581	PYGY	4	6281
PDH_1582	LAGY	4	6282
PDH_1583	IYGY	4	6283
PDH_1584	GSGY	4	6284
PDH_1585	LQLL	4	6285
PDH_1586	AQLW	4	6286
PDH_1587	TQLW	4	6287
PDH_1588	QQLL	4	6288
PDH_1589	IQLW	4	4427
PDH_1590	EQLL	4	6289
PDH_1591	QQLW	4	6290
PDH_1592	IQLL	4	6291
PDH_1593	EQLW	4	6292
PDH_1594	VQLW	4	6293
PDH_1595	KQLW	4	6294
PDH_1596	KQLL	4	6295
PDH_1597	PQLW	4	6296

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PDH_1598	VQLL	4	6297
PDH_1599	TQLL	4	6298
PDH_1600	PQLL	4	6299
PDH_1601	LQLW	4	6300
PDH_1602	AQLL	4	6301
PDH_1603	LGVA	4	6302
PDH_1604	LGGA	4	6303
PDH_1605	KGIA	4	6304
PDH_1606	KGSA	4	6305
PDH_1607	VGIA	4	6306
PDH_1608	KGGA	4	6307
PDH_1609	MGGA	4	6308
PDH_1610	TGGA	4	6309
PDH_1611	QGSA	4	6310
PDH_1612	QGIA	4	6311
PDH_1613	EGSA	4	6312
PDH_1614	PGVA	4	6313
PDH_1615	QGVA	4	6314
PDH_1616	EGIA	4	6315
PDH_1617	AGVA	4	6316
PDH_1618	MGVA	4	6317
PDH_1619	EGGA	4	3671
PDH_1620	PGIA	4	6318
PDH_1621	AGGA	4	6319
PDH_1622	VGGA	4	6320
PDH_1623	EGVA	4	6321
PDH_1624	PGGA	4	6322
PDH_1625	QGGA	4	6323
PDH_1626	AGIA	4	6324
PDH_1627	LGIA	4	6325
PDH_1628	MGIA	4	6326
PDH_1629	TGSA	4	6327

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PDH_1630	TGIA	4	6328
PDH_1631	MGSA	4	6329
PDH_1632	KGVA	4	6330
PDH_1633	TGVA	4	6331
PDH_1634	VGVA	4	6332
PDH_1635	PFGE	4	6333
PDH_1636	VVGE	4	6334
PDH_1637	ALGE	4	6335
PDH_1638	IFGE	4	6336
PDH_1639	PLGE	4	6337
PDH_1640	ILGE	4	6338
PDH_1641	PVGE	4	6339
PDH_1642	RVGE	4	6340
PDH_1643	LLGE	4	6341
PDH_1644	SVGE	4	6342
PDH_1645	GLGE	4	6343
PDH_1646	IVGE	4	6344
PDH_1647	RLGE	4	4068
PDH_1648	LVGE	4	6345
PDH_1649	SLGE	4	6346
PDH_1650	TLGE	4	6347
PDH_1651	VLGE	4	6348
PDH_1652	TVGE	4	6349
PDH_1653	GVGE	4	6350
PDH_1654	AVGE	4	6351
PDH_1655	PYSY	4	6352
PDH_1656	PYSD	4	6353
PDH_1657	DYSD	4	6354
PDH_1658	DYSA	4	6355
PDH_1659	SYSD	4	6356
PDH_1660	FYSY	4	6357
PDH_1661	VYSY	4	6358

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PDH_1662	FYSS	4	6359
PDH_1663	SYSS	4	6360
PDH_1664	YYSS	4	6361
PDH_1665	YYSY	4	6362
PDH_1666	AYSY	4	6363
PDH_1667	AYSD	4	6364
PDH_1668	HYSY	4	6365
PDH_1669	VYSD	4	6366
PDH_1670	FYSA	4	6367
PDH_1671	SYSY	4	6368
PDH_1672	SYSA	4	6369
PDH_1673	FYSD	4	6370
PDH_1674	YYSD	4	6371
PDH_1675	LYSY	4	6372
PDH_1676	YYSA	4	6373
PDH_1677	HYSS	4	6374
PDH_1678	DYSS	4	6375
PDH_1679	HYSA	4	6376
PDH_1680	DYSY	4	6377
PDH_1681	HYSD	4	6378
PDH_1682	LYSD	4	6379
PDH_1683	AVPA	4	6380
PDH_1684	AVRA	4	6381
PDH_1685	PVRA	4	6382
PDH_1686	PVPA	4	6383
PDH_1687	IVGA	4	3755
PDH_1688	EVPA	4	6384
PDH_1689	LVGA	4	6385
PDH_1690	IVRA	4	6386
PDH_1691	QVGA	4	6387
PDH_1692	IVPA	4	6388
PDH_1693	EVGA	4	6389

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PDH_1694	LVPA	4	6390
PDH_1695	QVPA	4	6391
PDH_1696	AVGA	4	6392
PDH_1697	QVRA	4	6393
PDH_1698	TVRA	4	6394
PDH_1699	KVGA	4	6395
PDH_1700	VVPA	4	3837
PDH_1701	VVGA	4	6396
PDH_1702	EVRA	4	6397
PDH_1703	LVRA	4	6398
PDH_1704	VVRA	4	6399
PDH_1705	PVGA	4	6400
PDH_1706	TVGA	4	6401
PDH_1707	KVRA	4	6402
PDH_1708	KVPA	4	6403
PDH_1709	TVPA	4	6404
PDH_1710	GRGV	4	6405
PDH_1711	SRGV	4	6406
PDH_1712	ILGV	4	6407
PDH_1713	AQGV	4	6408
PDH_1714	TQGV	4	6409
PDH_1715	VQGV	4	4062
PDH_1716	PQGV	4	6410
PDH_1717	SQGV	4	6411
PDH_1718	RRGV	4	6412
PDH_1719	PLGV	4	6413
PDH_1720	PRGV	4	6414
PDH_1721	IRGV	4	6415
PDH_1722	ALGV	4	6416
PDH_1723	VRGV	4	4018
PDH_1724	TRGV	4	6417
PDH_1725	TLGV	4	6418

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PDH_1726	GQGV	4	6419
PDH_1727	RQGV	4	6420
PDH_1728	ARGV	4	4812
PDH_1729	RLGV	4	6421
PDH_1730	LRGV	4	6422
PDH_1731	SLGV	4	6423
PDH_1732	VLGV	4	6424
PDH_1733	IQGV	4	6425
PDH_1734	LLGV	4	6426
PDH_1735	LQGV	4	6427
PDH_1736	GLGV	4	6428
PDH_1737	DSSW	4	6429
PDH_1738	DSSR	4	6430
PDH_1739	DSSV	4	6431
PDH_1740	DSST	4	6432
PDH_1741	DSSM	4	6433
PDH_1742	DSSG	4	4185
PDH_1743	DSSA	4	6434
PDH_1744	DSSS	4	6435
PDH_1745	DSSL	4	6436
PDH_1746	TGYS	4	6437
PDH_1747	SDYS	4	6438
PDH_1748	IAYS	4	6439
PDH_1749	VDYS	4	6440
PDH_1750	LDYS	4	6441
PDH_1751	PDYS	4	6442
PDH_1752	SAYS	4	6443
PDH_1753	TDYS	4	6444
PDH_1754	LAYS	4	6445
PDH_1755	GAYS	4	6446
PDH_1756	GDYS	4	6447
PDH_1757	VAYS	4	6448

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PDH_1758	RDYS	4	6449
PDH_1759	IDYS	4	6450
PDH_1760	RAYS	4	6451
PDH_1761	PAYS	4	6452
PDH_1762	ADYS	4	6453
PDH_1763	IAYS	4	6454
PDH_1764	IGYS	4	6455
PDH_1765	GGYS	4	6456
PDH_1766	RGYS	4	6457
PDH_1767	AAYS	4	6458
PDH_1768	LYGS	4	6459
PDH_1769	TYGS	4	6460
PDH_1770	DYGS	4	6461
PDH_1771	SYGS	4	6462
PDH_1772	FYGS	4	6463
PDH_1773	YYGS	4	3990
PDH_1774	NYGS	4	6464
PDH_1775	HYGS	4	6465
PDH_1776	VYGS	4	6466
PDH_1777	AYGS	4	6467
PDH_1778	PYGS	4	6468
PDH_1779	IYGS	4	6469
PDH_1780	YYYS	4	6470
PDH_1781	SYYS	4	6471
PDH_1782	YYYY	4	6472
PDH_1783	PYYF	4	6473
PDH_1784	FYYS	4	6474
PDH_1785	NYYS	4	6475
PDH_1786	NYYF	4	6476
PDH_1787	FYYF	4	6477
PDH_1788	FYYY	4	6478
PDH_1789	AYYY	4	6479

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PDH_1790	SYYY	4	6480
PDH_1791	DYYY	4	6481
PDH_1792	AYYS	4	6482
PDH_1793	IYYY	4	6483
PDH_1794	LYYY	4	6484
PDH_1795	DYYS	4	6485
PDH_1796	AYYF	4	6486
PDH_1797	PYYS	4	6487
PDH_1798	IYYS	4	6488
PDH_1799	YYYF	4	6489
PDH_1800	HYYS	4	6490
PDH_1801	PYYY	4	6491
PDH_1802	HYYF	4	6492
PDH_1803	HYYY	4	6493
PDH_1804	LYYS	4	6494
PDH_1805	VYYF	4	6495
PDH_1806	SYYF	4	6496
PDH_1807	IYYF	4	6497
PDH_1808	LYYF	4	6498
PDH_1809	DYYF	4	6499
PDH_1810	TYYS	4	6500
PDH_1811	NYYY	4	6501
PDH_1812	TYYF	4	6502
PDH_1813	TYYY	4	6503
PDH_1814	VYYS	4	6504
PDH_1815	VYYY	4	6505
PDH_1816	FSYS	4	6506
PDH_1817	VRYS	4	6507
PDH_1818	YSYS	4	6508
PDH_1819	LRYS	4	6509
PDH_1820	ARYS	4	6510
PDH_1821	FRYS	4	6511

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PDH_1822	SRYS	4	6512
PDH_1823	DSYS	4	6513
PDH_1824	LSYS	4	6514
PDH_1825	HRYS	4	6515
PDH_1826	PSYS	4	6516
PDH_1827	HSYS	4	6517
PDH_1828	ASYS	4	6518
PDH_1829	YRYS	4	6519
PDH_1830	SSYS	4	6520
PDH_1831	PRYS	4	6521
PDH_1832	VSYS	4	6522
PDH_1833	DRYS	4	6523
PDH_1834	TWFG	4	6524
PDH_1835	GWFG	4	6525
PDH_1836	RWFG	4	6526
PDH_1837	PWFG	4	6527
PDH_1838	LWFG	4	3965
PDH_1839	VWFG	4	6528
PDH_1840	SWFG	4	6529
PDH_1841	AWFG	4	6530
PDH_1842	IWFG	4	6531
PDH_1843	RYYY	4	6532
PDH_1844	RYYS	4	6533
PDH_1845	RYYF	4	6534
PDH_1846	GYYF	4	6535
PDH_1847	GYYS	4	6536
PDH_1848	GYYY	4	4188
PDH_1849	KFGG	4	6537
PDH_1850	ALGG	4	6538
PDH_1851	ILGG	4	6539
PDH_1852	EFGG	4	6540
PDH_1853	QFGG	4	6541

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PDH_1854	PLGG	4	6542
PDH_1855	VLGG	4	6543
PDH_1856	IVGG	4	6544
PDH_1857	LLGG	4	6545
PDH_1858	QLGG	4	6546
PDH_1859	KLGG	4	6547
PDH_1860	IFGG	4	6548
PDH_1861	ELGG	4	3713
PDH_1862	PFGG	4	6549
PDH_1863	TLGG	4	6550
PDH_1864	YMVRD	5	6551
PDH_1865	SMVRG	5	6552
PDH_1866	FMVRD	5	6553
PDH_1867	FMVRA	5	6554
PDH_1868	DMVRA	5	6555
PDH_1869	HMVRG	5	6556
PDH_1870	LMVRG	5	6557
PDH_1871	DMVRD	5	6558
PDH_1872	LMVRA	5	6559
PDH_1873	DMVRG	5	6560
PDH_1874	AMVRA	5	6561
PDH_1875	AMVRD	5	6562
PDH_1876	NMVRA	5	6563
PDH_1877	NMVRG	5	6564
PDH_1878	FMVRG	5	6565
PDH_1879	SMVRD	5	6566
PDH_1880	YMVRA	5	6567
PDH_1881	SMVRA	5	6568
PDH_1882	PMVRD	5	6569
PDH_1883	YMVRG	5	6570
PDH_1884	TMVRG	5	4010
PDH_1885	PMVRA	5	6571

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PDH_1886	PMVRG	5	6572
PDH_1887	VMVRA	5	6573
PDH_1888	NMVRD	5	6574
PDH_1889	VMVRG	5	6575
PDH_1890	IMVRD	5	6576
PDH_1891	VMVRD	5	6577
PDH_1892	IMVRA	5	6578
PDH_1893	AMVRG	5	6579
PDH_1894	LMVRD	5	6580
PDH_1895	HMVRD	5	6581
PDH_1896	HMVRA	5	6582
PDH_1897	IMVRD	5	6583
PDH_1898	IMVRA	5	6584
PDH_1899	IMVRG	5	6585
PDH_1900	AYGDF	5	6586
PDH_1901	VYGDS	5	6587
PDH_1902	DYGDY	5	4348
PDH_1903	NYGDF	5	6588
PDH_1904	DYGDS	5	6589
PDH_1905	HYGDS	5	6590
PDH_1906	HYGDY	5	6591
PDH_1907	IYGDS	5	6592
PDH_1908	LYGDS	5	6593
PDH_1909	LYGDF	5	6594
PDH_1910	AYGDY	5	6595
PDH_1911	AYGDS	5	6596
PDH_1912	SYGDS	5	6597
PDH_1913	SYGDY	5	6598
PDH_1914	NYGDS	5	6599
PDH_1915	HYGDF	5	6600
PDH_1916	FYGDS	5	6601
PDH_1917	IYGDF	5	6602

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PDH_1918	FYGDY	5	6603
PDH_1919	VYGDY	5	6604
PDH_1920	NYGDY	5	6605
PDH_1921	YYGDS	5	6606
PDH_1922	YYGDF	5	6607
PDH_1923	PYGDY	5	6608
PDH_1924	SYGDF	5	6609
PDH_1925	TYGDS	5	6610
PDH_1926	TYGDY	5	6611
PDH_1927	LYGDY	5	6612
PDH_1928	DYGDF	5	6613
PDH_1929	IYGDY	5	6614
PDH_1930	VYGDF	5	6615
PDH_1931	FYGDF	5	6616
PDH_1932	TYGDF	5	6617
PDH_1933	PYGDF	5	6618
PDH_1934	PYGDS	5	6619
PDH_1935	YYGDY	5	6620
PDH_1936	TYSYD	5	6621
PDH_1937	PYSYG	5	6622
PDH_1938	RYSYD	5	6623
PDH_1939	AYSYV	5	6624
PDH_1940	PYSYA	5	6625
PDH_1941	TYSYV	5	6626
PDH_1942	PYSYD	5	6627
PDH_1943	TYSYG	5	6628
PDH_1944	AYSYD	5	6629
PDH_1945	RYSYA	5	6630
PDH_1946	PYSYV	5	6631
PDH_1947	GYSYG	5	4430
PDH_1948	GYSYA	5	6632
PDH_1949	GYSYD	5	6633

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PDH_1950	GYSYV	5	6634
PDH_1951	LYSYG	5	6635
PDH_1952	SYSYV	5	6636
PDH_1953	LYSYA	5	6637
PDH_1954	LYSYD	5	6638
PDH_1955	RYSYV	5	6639
PDH_1956	IYSYD	5	6640
PDH_1957	VYSYV	5	6641
PDH_1958	IYSYG	5	6642
PDH_1959	IYSYA	5	6643
PDH_1960	IYSYV	5	6644
PDH_1961	RYSYG	5	6645
PDH_1962	VYSYA	5	6646
PDH_1963	AYSYA	5	6647
PDH_1964	SYSYA	5	6648
PDH_1965	VYSYG	5	6649
PDH_1966	AYSYG	5	6650
PDH_1967	VYSYD	5	6651
PDH_1968	TYSYA	5	6652
PDH_1969	SYSYD	5	6653
PDH_1970	SYSYG	5	6654
PDH_1971	LYSYV	5	6655
PDH_1972	GSGSS	5	6656
PDH_1973	GSGSF	5	6657
PDH_1974	ASGSS	5	6658
PDH_1975	RSGSY	5	6659
PDH_1976	NSGSY	5	6660
PDH_1977	NSGSS	5	6661
PDH_1978	TSGSS	5	6662
PDH_1979	RSGSS	5	6663
PDH_1980	SSGSY	5	6664
PDH_1981	VSGSF	5	6665

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PDH_1982	HSGSY	5	6666
PDH_1983	TSGSY	5	6667
PDH_1984	SSGSF	5	6668
PDH_1985	LSGSF	5	6669
PDH_1986	NSGSF	5	6670
PDH_1987	PSGSY	5	6671
PDH_1988	TSGSF	5	6672
PDH_1989	PSGSS	5	6673
PDH_1990	PSGSF	5	6674
PDH_1991	GSGSY	5	3987
PDH_1992	ISGSS	5	6675
PDH_1993	ISGSY	5	6676
PDH_1994	ASGSY	5	6677
PDH_1995	RSGSF	5	6678
PDH_1996	DSGSS	5	6679
PDH_1997	DSGSY	5	6680
PDH_1998	LSGSS	5	6681
PDH_1999	SSGSS	5	6682
PDH_2000	HSGSF	5	6683
PDH_2001	HSGSS	5	6684
PDH_2002	LSGSY	5	6685
PDH_2003	ASGSF	5	6686
PDH_2004	VSGSY	5	6687
PDH_2005	ISGSF	5	6688
PDH_2006	VSGSS	5	6689
PDH_2007	DSGSF	5	6690
PDH_2008	IFLES	5	6691
PDH_2009	IFLEL	5	6692
PDH_2010	RFLES	5	6693
PDH_2011	LFLEL	5	6694
PDH_2012	IFLES	5	6695
PDH_2013	GFLEW	5	6696

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PDH_2014	GFLES	5	6697
PDH_2015	TFLEW	5	6698
PDH_2016	TFLEL	5	6699
PDH_2017	VFLEW	5	6700
PDH_2018	SFLEL	5	6701
PDH_2019	VFLES	5	6702
PDH_2020	GFLEL	5	6703
PDH_2021	VFLEL	5	6704
PDH_2022	AFLEL	5	6705
PDH_2023	PFLES	5	6706
PDH_2024	SFLEW	5	6707
PDH_2025	AFLES	5	6708
PDH_2026	AFLEW	5	6709
PDH_2027	LFLEW	5	6710
PDH_2028	PFLEL	5	6711
PDH_2029	RFLEW	5	4231
PDH_2030	RFLEL	5	6712
PDH_2031	LFLES	5	6713
PDH_2032	PFLEW	5	6714
PDH_2033	SFLES	5	6715
PDH_2034	IFLEW	5	6716
PDH_2035	PGSYS	5	6717
PDH_2036	AGSYA	5	6718
PDH_2037	HGSYS	5	6719
PDH_2038	HGSYY	5	6720
PDH_2039	PGSYY	5	6721
PDH_2040	SGSYS	5	6722
PDH_2041	SGSYD	5	6723
PDH_2042	SGSYA	5	6724
PDH_2043	LGSYS	5	6725
PDH_2044	VGSYS	5	6726
PDH_2045	DGSYY	5	6727

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PDH_2046	FGSYS	5	6728
PDH_2047	FGSYY	5	6729
PDH_2048	HGSYD	5	6730
PDH_2049	LGSYA	5	6731
PDH_2050	HGSYA	5	6732
PDH_2051	LGSYD	5	6733
PDH_2052	DGSYS	5	6734
PDH_2053	VGSYD	5	6735
PDH_2054	VGSYY	5	6736
PDH_2055	AGSYY	5	6737
PDH_2056	YGSYS	5	6738
PDH_2057	AGSYS	5	6739
PDH_2058	AGSYD	5	6740
PDH_2059	VGSYA	5	6741
PDH_2060	DGSYD	5	6742
PDH_2061	FGSYD	5	6743
PDH_2062	DGSYA	5	6744
PDH_2063	YGSYA	5	6745
PDH_2064	FGSYA	5	6746
PDH_2065	YGSYD	5	6747
PDH_2066	LGSYY	5	6748
PDH_2067	SGSYY	5	3761
PDH_2068	PGSYA	5	6749
PDH_2069	PGSYD	5	6750
PDH_2070	YGSYY	5	6751
PDH_2071	FSGSF	5	6752
PDH_2072	FSGSY	5	6753
PDH_2073	YSGSF	5	6754
PDH_2074	YSGSS	5	6755
PDH_2075	FSGSS	5	6756
PDH_2076	YSGSY	5	3760
PDH_2077	ASSSW	5	6757

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PDH_2078	VSSSS	5	6758
PDH_2079	YSSSS	5	4478
PDH_2080	YSSSL	5	6759
PDH_2081	VSSSW	5	6760
PDH_2082	ASSSL	5	6761
PDH_2083	HSSSL	5	6762
PDH_2084	PSSSL	5	6763
PDH_2085	ASSSS	5	6764
PDH_2086	HSSSW	5	6765
PDH_2087	VSSSL	5	6766
PDH_2088	FSSSL	5	6767
PDH_2089	HSSSS	5	6768
PDH_2090	FSSSW	5	6769
PDH_2091	SSSSS	5	6770
PDH_2092	DSSSS	5	6771
PDH_2093	SSSSL	5	6772
PDH_2094	FSSSS	5	6773
PDH_2095	LSSSW	5	6774
PDH_2096	DSSSL	5	6775
PDH_2097	LSSSS	5	6776
PDH_2098	LSSSL	5	6777
PDH_2099	SSSSW	5	6778
PDH_2100	DSSSW	5	6779
PDH_2101	PSSSW	5	6780
PDH_2102	PSSSS	5	6781
PDH_2103	YSSSW	5	4439
PDH_2104	HSSGW	5	6782
PDH_2105	FSSGL	5	6783
PDH_2106	SSSGW	5	6784
PDH_2107	SSSGS	5	6785
PDH_2108	DSSGL	5	6786
PDH_2109	HSSGS	5	6787

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PDH_2110	FSSGW	5	6788
PDH_2111	ASSGW	5	6789
PDH_2112	DSSGW	5	6790
PDH_2113	DSSGS	5	6791
PDH_2114	ASSGL	5	6792
PDH_2115	LSSGL	5	6793
PDH_2116	FSSGS	5	6794
PDH_2117	ASSGS	5	6795
PDH_2118	PSSGS	5	6796
PDH_2119	LSSGW	5	6797
PDH_2120	LSSGS	5	6798
PDH_2121	YSSGL	5	6799
PDH_2122	VSSGS	5	6800
PDH_2123	PSSGW	5	6801
PDH_2124	PSSGL	5	6802
PDH_2125	VSSGL	5	6803
PDH_2126	VSSGW	5	6804
PDH_2127	YSSGW	5	4460
PDH_2128	SSSGL	5	6805
PDH_2129	HSSGL	5	6806
PDH_2130	YSSGS	5	6807
PDH_2131	VTVTT	5	6808
PDH_2132	RTVTT	5	6809
PDH_2133	LTVTK	5	6810
PDH_2134	ATVTK	5	6811
PDH_2135	GTVTT	5	6812
PDH_2136	VTVTK	5	6813
PDH_2137	LTVTR	5	6814
PDH_2138	ATVTT	5	6815
PDH_2139	RTVTR	5	6816
PDH_2140	VTVTR	5	6817
PDH_2141	TTVTK	5	6818

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PDH_2142	GTVTR	5	6819
PDH_2143	TTVTI	5	6820
PDH_2144	RTVTK	5	6821
PDH_2145	LTVTT	5	6822
PDH_2146	VTVTI	5	6823
PDH_2147	GTVTK	5	6824
PDH_2148	TTVTR	5	6825
PDH_2149	GTVTI	5	6826
PDH_2150	PTVTI	5	6827
PDH_2151	TTVTT	5	4351
PDH_2152	STVTT	5	6828
PDH_2153	STVTI	5	6829
PDH_2154	ITVTI	5	6830
PDH_2155	STVTK	5	6831
PDH_2156	STVTR	5	6832
PDH_2157	ATVTI	5	6833
PDH_2158	ITVTT	5	6834
PDH_2159	ITVTR	5	6835
PDH_2160	LTVTI	5	6836
PDH_2161	PTVTR	5	6837
PDH_2162	ATVTR	5	6838
PDH_2163	PTVTK	5	6839
PDH_2164	RTVTI	5	6840
PDH_2165	ITVTK	5	6841
PDH_2166	PTVTT	5	6842
PDH_2167	ASSSF	5	6843
PDH_2168	ASSSY	5	6844
PDH_2169	PSSSF	5	6845
PDH_2170	HSSSF	5	6846
PDH_2171	VSSSY	5	6847
PDH_2172	YSSSF	5	6848
PDH_2173	FSSSF	5	6849

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PDH_2174	HSSSY	5	6850
PDH_2175	VSSSF	5	6851
PDH_2176	SSSSY	5	6852
PDH_2177	SSSSF	5	6853
PDH_2178	LSSSY	5	6854
PDH_2179	DSSSY	5	6855
PDH_2180	FSSSY	5	6856
PDH_2181	PSSSY	5	6857
PDH_2182	YSSSY	5	6858
PDH_2183	DSSSF	5	6859
PDH_2184	LSSSF	5	6860
PDH_2185	FSGWF	5	6861
PDH_2186	FSGWS	5	6862
PDH_2187	ISGWY	5	6863
PDH_2188	FSGWY	5	6864
PDH_2189	ISGWS	5	6865
PDH_2190	PSGWS	5	6866
PDH_2191	DSGWF	5	6867
PDH_2192	PSGWY	5	6868
PDH_2193	PSGWF	5	6869
PDH_2194	TSGWY	5	6870
PDH_2195	ASGWF	5	6871
PDH_2196	LSGWF	5	6872
PDH_2197	ISGWF	5	6873
PDH_2198	SSGWY	5	4461
PDH_2199	SSGWS	5	6874
PDH_2200	SSGWF	5	6875
PDH_2201	NSGWS	5	6876
PDH_2202	NSGWY	5	6877
PDH_2203	NSGWF	5	6878
PDH_2204	VSGWS	5	6879
PDH_2205	VSGWY	5	6880

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PDH_2206	YSGWF	5	6881
PDH_2207	LSGWS	5	6882
PDH_2208	ASGWY	5	6883
PDH_2209	LSGWY	5	6884
PDH_2210	TSGWF	5	6885
PDH_2211	TSGWS	5	6886
PDH_2212	DSGWY	5	6887
PDH_2213	DSGWS	5	6888
PDH_2214	ASGWS	5	6889
PDH_2215	HSGWF	5	6890
PDH_2216	HSGWS	5	6891
PDH_2217	YSGWS	5	6892
PDH_2218	HSGWY	5	6893
PDH_2219	YSGWY	5	6894
PDH_2220	VSGWF	5	6895
PDH_2221	ISGYD	5	6896
PDH_2222	HSGYA	5	6897
PDH_2223	ISGYA	5	6898
PDH_2224	HSGYG	5	6899
PDH_2225	TSGYD	5	6900
PDH_2226	TSGYA	5	6901
PDH_2227	DSGYA	5	6902
PDH_2228	LSGYA	5	6903
PDH_2229	FSGYA	5	6904
PDH_2230	LSGYD	5	6905
PDH_2231	FSGYG	5	6906
PDH_2232	SSGYD	5	6907
PDH_2233	SSGYA	5	6908
PDH_2234	ISGYG	5	6909
PDH_2235	HSGYD	5	6910
PDH_2236	ASGYD	5	6911
PDH_2237	YSGYA	5	6912

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PDH_2238	YSGYD	5	4389
PDH_2239	VSGYA	5	6913
PDH_2240	VSGYG	5	6914
PDH_2241	SSGYG	5	6915
PDH_2242	DSGYD	5	6916
PDH_2243	DSGYG	5	6917
PDH_2244	FSGYD	5	6918
PDH_2245	LSGYG	5	6919
PDH_2246	TSGYG	5	6920
PDH_2247	NSGYA	5	6921
PDH_2248	NSGYG	5	6922
PDH_2249	NSGYD	5	6923
PDH_2250	PSGYA	5	6924
PDH_2251	PSGYG	5	6925
PDH_2252	PSGYD	5	6926
PDH_2253	ASGYG	5	6927
PDH_2254	VSGYD	5	6928
PDH_2255	ASGYA	5	6929
PDH_2256	YSGYG	5	6930
PDH_2257	FYYDS	5	6931
PDH_2258	YYYDT	5	6932
PDH_2259	DYYDS	5	6933
PDH_2260	AYYDS	5	6934
PDH_2261	AYYDT	5	6935
PDH_2262	DYYDI	5	6936
PDH_2263	VYYDI	5	6937
PDH_2264	FYYDT	5	6938
PDH_2265	LYYDI	5	6939
PDH_2266	PYYDI	5	6940
PDH_2267	HYYDI	5	6941
PDH_2268	IYYDI	5	6942
PDH_2269	LYYDS	5	6943

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PDH_2270	SYYDI	5	6944
PDH_2271	NYYDT	5	6945
PDH_2272	NYYDS	5	6946
PDH_2273	SYYDT	5	6947
PDH_2274	AYYDI	5	6948
PDH_2275	SYYDS	5	6949
PDH_2276	DYYDT	5	6950
PDH_2277	VYYDT	5	6951
PDH_2278	YYYDI	5	6952
PDH_2279	VYYDS	5	6953
PDH_2280	FYYDI	5	6954
PDH_2281	YYYDS	5	4176
PDH_2282	IYYDT	5	6955
PDH_2283	NYYDI	5	6956
PDH_2284	HYYDS	5	6957
PDH_2285	LYYDT	5	6958
PDH_2286	IYYDT	5	6959
PDH_2287	IYYDS	5	6960
PDH_2288	PYYDT	5	6961
PDH_2289	PYYDS	5	6962
PDH_2290	TYYDI	5	6963
PDH_2291	HYYDT	5	6964
PDH_2292	TYYDS	5	6965
PDH_2293	DSSGY	5	4179
PDH_2294	SSSGY	5	6966
PDH_2295	DSSGF	5	6967
PDH_2296	HSSGY	5	6968
PDH_2297	SSSGF	5	6969
PDH_2298	ASSGF	5	6970
PDH_2299	ASSGY	5	6971
PDH_2300	LSSGF	5	6972
PDH_2301	FSSGY	5	6973

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PDH_2302	FSSGF	5	6974
PDH_2303	YSSGF	5	6975
PDH_2304	PSSGY	5	6976
PDH_2305	VSSGY	5	6977
PDH_2306	LSSGY	5	6978
PDH_2307	ESSGF	5	6979
PDH_2308	PSSGF	5	6980
PDH_2309	VSSGF	5	6981
PDH_2310	YSSGY	5	6982
PDH_2311	QAARH	5	6983
PDH_2312	QAARP	5	6984
PDH_2313	TAARR	5	6985
PDH_2314	QAARL	5	6986
PDH_2315	KAARR	5	6987
PDH_2316	KAARP	5	6988
PDH_2317	KAARH	5	6989
PDH_2318	TAARH	5	6990
PDH_2319	IAARP	5	6991
PDH_2320	EAARL	5	6992
PDH_2321	EAARP	5	6993
PDH_2322	AAARL	5	6994
PDH_2323	LAARL	5	6995
PDH_2324	IAARL	5	6996
PDH_2325	IAARH	5	6997
PDH_2326	LAARR	5	6998
PDH_2327	LAARH	5	6999
PDH_2328	EAARH	5	7000
PDH_2329	IAARR	5	7001
PDH_2330	QAARR	5	7002
PDH_2331	IAARP	5	4483
PDH_2332	EAARR	5	7003
PDH_2333	KAARL	5	7004

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PDH_2334	PAARR	5	7005
PDH_2335	PAARP	5	7006
PDH_2336	PAARH	5	7007
PDH_2337	PAARL	5	7008
PDH_2338	VAARR	5	7009
PDH_2339	AAARH	5	7010
PDH_2340	VAARP	5	7011
PDH_2341	VAARH	5	7012
PDH_2342	AAARP	5	7013
PDH_2343	AAARR	5	7014
PDH_2344	TAARL	5	7015
PDH_2345	LAARP	5	7016
PDH_2346	VAARL	5	7017
PDH_2347	EYYYG	5	7018
PDH_2348	VYYYD	5	7019
PDH_2349	EYYYA	5	7020
PDH_2350	VYYYG	5	7021
PDH_2351	EYYYD	5	7022
PDH_2352	PYYYD	5	7023
PDH_2353	PYYYG	5	7024
PDH_2354	AYYYG	5	7025
PDH_2355	TYYYA	5	7026
PDH_2356	TYYYG	5	7027
PDH_2357	TYYYD	5	7028
PDH_2358	QYYYA	5	7029
PDH_2359	QYYYG	5	7030
PDH_2360	QYYYD	5	7031
PDH_2361	VYYYA	5	7032
PDH_2362	LYYYG	5	7033
PDH_2363	LYYYD	5	7034
PDH_2364	LYYYA	5	7035
PDH_2365	AYYYD	5	7036

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PDH_2366	AYYYA	5	7037
PDH_2367	PYYYA	5	7038
PDH_2368	MYYYD	5	7039
PDH_2369	KYYYD	5	7040
PDH_2370	KYYYG	5	7041
PDH_2371	MYYYA	5	7042
PDH_2372	KYYYA	5	7043
PDH_2373	MYYYG	5	7044
PDH_2374	LTMVR	5	7045
PDH_2375	RTMVQ	5	7046
PDH_2376	VTMVQ	5	7047
PDH_2377	TTMVR	5	7048
PDH_2378	LTMVQ	5	7049
PDH_2379	STMVQ	5	7050
PDH_2380	ATMVQ	5	7051
PDH_2381	PTMVR	5	7052
PDH_2382	RTMVR	5	7053
PDH_2383	ITMVQ	5	4055
PDH_2384	GTMVR	5	7054
PDH_2385	VTMVR	5	7055
PDH_2386	PTMVQ	5	7056
PDH_2387	ITMVR	5	4009
PDH_2388	ATMVR	5	7057
PDH_2389	STMVR	5	7058
PDH_2390	TTMVQ	5	7059
PDH_2391	GTMVQ	5	7060
PDH_2392	HMVQG	5	7061
PDH_2393	DMVQG	5	7062
PDH_2394	LMVQG	5	7063
PDH_2395	SMVQG	5	7064
PDH_2396	FMVQG	5	7065
PDH_2397	NMVQG	5	7066

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PDH_2398	VMVQG	5	7067
PDH_2399	IMVQG	5	4056
PDH_2400	PMVQG	5	7068
PDH_2401	YMVQG	5	7069
PDH_2402	AMVQG	5	7070
PDH_2403	IMVQG	5	7071
PDH_2404	PWGSY	5	7072
PDH_2405	TWGSY	5	7073
PDH_2406	SWGSY	5	7074
PDH_2407	HWGSY	5	7075
PDH_2408	LWGSY	5	7076
PDH_2409	DWGSY	5	7077
PDH_2410	FWGSY	5	7078
PDH_2411	AWGSY	5	7079
PDH_2412	YWGSY	5	7080
PDH_2413	IWGSY	5	7081
PDH_2414	NWGSY	5	7082
PDH_2415	VWGSY	5	4102
PDH_2416	FSSSWF	6	7083
PDH_2417	HSSSWS	6	7084
PDH_2418	VSSSWF	6	7085
PDH_2419	HSSSWY	6	7086
PDH_2420	VSSSWS	6	7087
PDH_2421	LSSSWY	6	7088
PDH_2422	VSSSWY	6	7089
PDH_2423	HSSSWF	6	7090
PDH_2424	ASSSWY	6	7091
PDH_2425	DSSSWS	6	7092
PDH_2426	PSSSWY	6	7093
PDH_2427	ASSSWS	6	7094
PDH_2428	DSSSWF	6	7095
PDH_2429	DSSSWY	6	7096

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PDH_2430	YSSSWS	6	7097
PDH_2431	YSSSWF	6	7098
PDH_2432	ASSSWF	6	7099
PDH_2433	LSSSWS	6	7100
PDH_2434	SSSSWS	6	7101
PDH_2435	YSSSWY	6	4437
PDH_2436	PSSSWS	6	7102
PDH_2437	SSSSWY	6	7103
PDH_2438	LSSSWF	6	7104
PDH_2439	PSSSWF	6	7105
PDH_2440	FSSSWS	6	7106
PDH_2441	SSSSWF	6	7107
PDH_2442	FSSSWY	6	7108
PDH_2443	AYYDST	6	7109
PDH_2444	AYYDSI	6	7110
PDH_2445	YYYDST	6	7111
PDH_2446	PYYDST	6	7112
PDH_2447	VYYDSS	6	7113
PDH_2448	NYYDSI	6	7114
PDH_2449	PYYDSS	6	7115
PDH_2450	YYYDSS	6	4171
PDH_2451	YYYDSI	6	7116
PDH_2452	VYYDST	6	7117
PDH_2453	VYYDSI	6	7118
PDH_2454	NYYDST	6	7119
PDH_2455	LYYDST	6	7120
PDH_2456	NYYDSS	6	7121
PDH_2457	SYYDSI	6	7122
PDH_2458	LYYDSS	6	7123
PDH_2459	SYYDST	6	7124
PDH_2460	LYYDSI	6	7125
PDH_2461	SYYDSS	6	7126

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PDH_2462	DYYDSI	6	7127
PDH_2463	DYYDST	6	7128
PDH_2464	DYYDSS	6	7129
PDH_2465	FYYDSS	6	7130
PDH_2466	TYYDSI	6	7131
PDH_2467	FYYDST	6	7132
PDH_2468	IYYDST	6	7133
PDH_2469	FYYDSI	6	7134
PDH_2470	IYYDSS	6	7135
PDH_2471	TYYDSS	6	7136
PDH_2472	TYYDST	6	7137
PDH_2473	HYYDSS	6	7138
PDH_2474	HYYDST	6	7139
PDH_2475	IYYDSI	6	7140
PDH_2476	HYYDSI	6	7141
PDH_2477	PYYDSI	6	7142
PDH_2478	AYYDSS	6	7143
PDH_2479	LYSGYA	6	7144
PDH_2480	GYSGYV	6	7145
PDH_2481	SYSGYD	6	7146
PDH_2482	LYSGYD	6	7147
PDH_2483	IYSGYV	6	7148
PDH_2484	SYSGYG	6	7149
PDH_2485	IYSGYG	6	7150
PDH_2486	SYSGYA	6	7151
PDH_2487	PYSGYG	6	7152
PDH_2488	VYSGYD	6	7153
PDH_2489	PYSGYA	6	7154
PDH_2490	VYSGYV	6	7155
PDH_2491	GYSGYG	6	7156
PDH_2492	VYSGYA	6	7157
PDH_2493	PYSGYV	6	7158

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PDH_2494	GYSGYA	6	7159
PDH_2495	IYSGYD	6	7160
PDH_2496	PYSGYD	6	7161
PDH_2497	RYSGYV	6	7162
PDH_2498	RYSGYA	6	7163
PDH_2499	RYSGYG	6	7164
PDH_2500	GYSGYD	6	4386
PDH_2501	IYSGYA	6	7165
PDH_2502	AYSGYA	6	7166
PDH_2503	RYSGYD	6	7167
PDH_2504	AYSGYG	6	7168
PDH_2505	AYSGYD	6	7169
PDH_2506	AYSGYV	6	7170
PDH_2507	VYSGYG	6	7171
PDH_2508	TYSGYV	6	7172
PDH_2509	TYSGYD	6	7173
PDH_2510	TYSGYA	6	7174
PDH_2511	TYSGYG	6	7175
PDH_2512	SYSGYV	6	7176
PDH_2513	LYSGYV	6	7177
PDH_2514	LYSGYG	6	7178
PDH_2515	SSSGWF	6	7179
PDH_2516	PSSGWY	6	7180
PDH_2517	FSSGWF	6	7181
PDH_2518	PSSGWS	6	7182
PDH_2519	FSSGWS	6	7183
PDH_2520	ASSGWY	6	7184
PDH_2521	FSSGWY	6	7185
PDH_2522	ASSGWS	6	7186
PDH_2523	SSSGWS	6	7187
PDH_2524	YSSGWY	6	4458
PDH_2525	SSSGWY	6	7188

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PDH_2526	HSSGWS	6	7189
PDH_2527	DSSGWS	6	7190
PDH_2528	YSSGWS	6	7191
PDH_2529	LSSGWF	6	7192
PDH_2530	HSSGWY	6	7193
PDH_2531	DSSGWF	6	7194
PDH_2532	DSSGWY	6	7195
PDH_2533	LSSGWY	6	7196
PDH_2534	HSSGWF	6	7197
PDH_2535	VSSGWS	6	7198
PDH_2536	LSSGWS	6	7199
PDH_2537	VSSGWY	6	7200
PDH_2538	VSSGWF	6	7201
PDH_2539	PSSGWF	6	7202
PDH_2540	ASSGWF	6	7203
PDH_2541	YSSGWF	6	7204
PDH_2542	IYYGSA	6	7205
PDH_2543	PYYGSG	6	7206
PDH_2544	PYYGSA	6	7207
PDH_2545	PYYGSD	6	7208
PDH_2546	VYYGSD	6	7209
PDH_2547	AYYGSA	6	7210
PDH_2548	VYYGSA	6	7211
PDH_2549	NYYGSA	6	7212
PDH_2550	YYYGSA	6	7213
PDH_2551	AYYGSD	6	7214
PDH_2552	NYYGSD	6	7215
PDH_2553	YYYGSD	6	7216
PDH_2554	FYYGSD	6	7217
PDH_2555	NYYGSG	6	7218
PDH_2556	YYYGSG	6	3979
PDH_2557	FYYGSA	6	7219

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PDH_2558	FYYGSG	6	7220
PDH_2559	AYYGSG	6	7221
PDH_2560	LYYGSG	6	7222
PDH_2561	DYYGSD	6	7223
PDH_2562	LYYGSA	6	7224
PDH_2563	IYYGSD	6	7225
PDH_2564	DYYGSG	6	7226
PDH_2565	DYYGSA	6	7227
PDH_2566	LYYGSD	6	7228
PDH_2567	HYYGSD	6	7229
PDH_2568	TYYGSA	6	7230
PDH_2569	TYYGSG	6	7231
PDH_2570	HYYGSA	6	7232
PDH_2571	SYYGSG	6	7233
PDH_2572	HYYGSG	6	7234
PDH_2573	SYYGSD	6	7235
PDH_2574	VYYGSG	6	7236
PDH_2575	SYYGSA	6	7237
PDH_2576	IYYGSG	6	7238
PDH_2577	IYYGSD	6	7239
PDH_2578	VSSGYS	6	7240
PDH_2579	VSSGYY	6	7241
PDH_2580	FSSGYY	6	7242
PDH_2581	ASSGYF	6	7243
PDH_2582	ASSGYS	6	7244
PDH_2583	FSSGYS	6	7245
PDH_2584	SSSGYY	6	7246
PDH_2585	ASSGYY	6	7247
PDH_2586	FSSGYF	6	7248
PDH_2587	HSSGYY	6	7249
PDH_2588	DSSGYY	6	4174
PDH_2589	HSSGYS	6	7250

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PDH_2590	SSSGYS	6	7251
PDH_2591	DSSGYS	6	7252
PDH_2592	DSSGYF	6	7253
PDH_2593	HSSGYF	6	7254
PDH_2594	PSSGYF	6	7255
PDH_2595	SSSGYF	6	7256
PDH_2596	YSSGYY	6	7257
PDH_2597	YSSGYF	6	7258
PDH_2598	YSSGYS	6	7259
PDH_2599	PSSGYS	6	7260
PDH_2600	PSSGYY	6	7261
PDH_2601	LSSGYY	6	7262
PDH_2602	LSSGYF	6	7263
PDH_2603	LSSGYS	6	7264
PDH_2604	VSSGYF	6	7265
PDH_2605	TYDSSD	6	7266
PDH_2606	YYDSSA	6	7267
PDH_2607	YYDSSG	6	4172
PDH_2608	LYDSSD	6	7268
PDH_2609	LYDSSA	6	7269
PDH_2610	PYDSSA	6	7270
PDH_2611	LYDSSG	6	7271
PDH_2612	PYDSSD	6	7272
PDH_2613	VYDSSD	6	7273
PDH_2614	HYDSSG	6	7274
PDH_2615	VYDSSG	6	7275
PDH_2616	VYDSSA	6	7276
PDH_2617	PYDSSG	6	7277
PDH_2618	SYDSSA	6	7278
PDH_2619	FYDSSG	6	7279
PDH_2620	NYDSSA	6	7280
PDH_2621	SYDSSG	6	7281

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PDH_2622	FYDSSA	6	7282
PDH_2623	NYDSSD	6	7283
PDH_2624	SYDSSD	6	7284
PDH_2625	FYDSSD	6	7285
PDH_2626	DYDSSG	6	7286
PDH_2627	AYDSSG	6	7287
PDH_2628	NYDSSG	6	7288
PDH_2629	IYDSSA	6	7289
PDH_2630	DYDSSD	6	7290
PDH_2631	IYDSSG	6	7291
PDH_2632	AYDSSD	6	7292
PDH_2633	DYDSSA	6	7293
PDH_2634	IYDSSD	6	7294
PDH_2635	HYDSSA	6	7295
PDH_2636	AYDSSA	6	7296
PDH_2637	HYDSSD	6	7297
PDH_2638	TYDSSG	6	7298
PDH_2639	TYDSSA	6	7299
PDH_2640	YYDSSD	6	7300
PDH_2641	TDFWSA	6	7301
PDH_2642	ADFWSG	6	7302
PDH_2643	PDFWSG	6	7303
PDH_2644	VDFWSD	6	7304
PDH_2645	TDFWSD	6	7305
PDH_2646	HDFWSA	6	7306
PDH_2647	HDFWSD	6	7307
PDH_2648	TDFWSG	6	7308
PDH_2649	LDFWSA	6	7309
PDH_2650	LDFWSG	6	7310
PDH_2651	HDFWSG	6	7311
PDH_2652	LDFWSD	6	7312
PDH_2653	FDFWSG	6	7313

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PDH_2654	DDFWSD	6	7314
PDH_2655	VDFWSA	6	7315
PDH_2656	SDFWSD	6	7316
PDH_2657	SDFWSG	6	7317
PDH_2658	NDFWSD	6	7318
PDH_2659	SDFWSA	6	7319
PDH_2660	NDFWSA	6	7320
PDH_2661	NDFWSG	6	7321
PDH_2662	VDFWSG	6	7322
PDH_2663	IDFWSD	6	7323
PDH_2664	IDFWSG	6	7324
PDH_2665	FDFWSA	6	7325
PDH_2666	ADFWSD	6	7326
PDH_2667	IDFWSA	6	7327
PDH_2668	FDFWSD	6	7328
PDH_2669	DDFWSG	6	7329
PDH_2670	ADFWSA	6	7330
PDH_2671	YDFWSA	6	7331
PDH_2672	PDFWSD	6	7332
PDH_2673	YDFWSG	6	4253
PDH_2674	DDFWSA	6	7333
PDH_2675	PDFWSA	6	7334
PDH_2676	YDFWSD	6	7335
PDH_2677	DDSSGY	6	7336
PDH_2678	LDSSGY	6	7337
PDH_2679	HDSSGS	6	7338
PDH_2680	DDSSGF	6	7339
PDH_2681	DDSSGS	6	7340
PDH_2682	LDSSGS	6	7341
PDH_2683	HDSSGY	6	7342
PDH_2684	SDSSGS	6	7343
PDH_2685	SDSSGF	6	7344

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PDH_2686	PDSSGS	6	7345
PDH_2687	SDSSGY	6	7346
PDH_2688	PDSSGY	6	7347
PDH_2689	ADSSGY	6	7348
PDH_2690	ADSSGS	6	7349
PDH_2691	ADSSGF	6	7350
PDH_2692	YDSSGF	6	7351
PDH_2693	VDSSGF	6	7352
PDH_2694	FDSSGF	6	7353
PDH_2695	VDSSGY	6	7354
PDH_2696	YDSSGY	6	4173
PDH_2697	FDSSGS	6	7355
PDH_2698	VDSSGS	6	7356
PDH_2699	YDSSGS	6	7357
PDH_2700	FDSSGY	6	7358
PDH_2701	LDSSGF	6	7359
PDH_2702	HDSSGF	6	7360
PDH_2703	PDSSGF	6	7361
PDH_2704	EYFDWS	6	7362
PDH_2705	QYFDWL	6	7363
PDH_2706	RYFDWF	6	7364
PDH_2707	AYFDWF	6	7365
PDH_2708	PYFDWF	6	7366
PDH_2709	PYFDWP	6	7367
PDH_2710	LYFDWP	6	7368
PDH_2711	EYFDWP	6	7369
PDH_2712	EYFDWL	6	7370
PDH_2713	RYFDWL	6	4305
PDH_2714	LYFDWL	6	7371
PDH_2715	PYFDWL	6	7372
PDH_2716	LYFDWS	6	7373
PDH_2717	QYFDWS	6	7374

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PDH_2718	QYFDWF	6	7375
PDH_2719	VYFDWF	6	7376
PDH_2720	RYFDWP	6	7377
PDH_2721	AYFDWP	6	7378
PDH_2722	LYFDWF	6	7379
PDH_2723	AYFDWL	6	7380
PDH_2724	GYFDWF	6	7381
PDH_2725	GYFDWS	6	7382
PDH_2726	VYFDWL	6	7383
PDH_2727	VYFDWS	6	7384
PDH_2728	VYFDWP	6	7385
PDH_2729	RYFDWS	6	7386
PDH_2730	PYFDWS	6	7387
PDH_2731	QYFDWP	6	7388
PDH_2732	EYFDWF	6	7389
PDH_2733	AYFDWS	6	7390
PDH_2734	GYFDWL	6	7391
PDH_2735	GYFDWP	6	7392
PDH_2736	CGSTSC	6	7393
PDH_2737	CSGTSC	6	7394
PDH_2738	CSSTSC	6	3814
PDH_2739	CGGTSC	6	7395
PDH_2740	PYYGSE	6	7396
PDH_2741	VYYGSE	6	7397
PDH_2742	AYYGSE	6	7398
PDH_2743	NYYGSE	6	7399
PDH_2744	FYYGSE	6	7400
PDH_2745	YYYGSE	6	7401
PDH_2746	DYYGSE	6	7402
PDH_2747	TYYGSE	6	7403
PDH_2748	HYYGSE	6	7404
PDH_2749	LYYGSE	6	7405

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PDH_2750	IYYGSE	6	7406
PDH_2751	SYYGSE	6	7407
PDH_2752	CSSGSC	6	7408
PDH_2753	CGGGSC	6	7409
PDH_2754	CGSGSC	6	7410
PDH_2755	CSGGSC	6	3775
PDH_2756	PFWSGS	6	7411
PDH_2757	DFWSGF	6	7412
PDH_2758	PFWSGY	6	7413
PDH_2759	AFWSGY	6	7414
PDH_2760	AFWSGS	6	7415
PDH_2761	AFWSGF	6	7416
PDH_2762	PFWSGF	6	7417
PDH_2763	VFWSGY	6	7418
PDH_2764	YFWSGF	6	7419
PDH_2765	IFWSGS	6	7420
PDH_2766	VFWSGF	6	7421
PDH_2767	VFWSGS	6	7422
PDH_2768	IFWSGF	6	7423
PDH_2769	IFWSGY	6	7424
PDH_2770	SFWSGF	6	7425
PDH_2771	YFWSGY	6	7426
PDH_2772	FFWSGS	6	7427
PDH_2773	YFWSGS	6	7428
PDH_2774	FFWSGY	6	7429
PDH_2775	LFWSGF	6	7430
PDH_2776	TFWSGF	6	7431
PDH_2777	NFWSGF	6	7432
PDH_2778	HFWSGF	6	7433
PDH_2779	NFWSGS	6	7434
PDH_2780	SFWSGS	6	7435
PDH_2781	IFWSGS	6	7436

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PDH_2782	NFWSGY	6	7437
PDH_2783	DFWSGY	6	4254
PDH_2784	LFWSGY	6	7438
PDH_2785	HFWSGS	6	7439
PDH_2786	SFWSGY	6	7440
PDH_2787	IFWSGY	6	7441
PDH_2788	DFWSGS	6	7442
PDH_2789	LFWSGS	6	7443
PDH_2790	HFWSGY	6	7444
PDH_2791	FFWSGF	6	7445
PDH_2792	DYYDSSG	7	7446
PDH_2793	SYYDSSG	7	7447
PDH_2794	IYYDSSG	7	7448
PDH_2795	HYYDSSG	7	7449
PDH_2796	SYYDSSA	7	7450
PDH_2797	SYYDSSD	7	7451
PDH_2798	IYYDSSA	7	7452
PDH_2799	AYYDSSA	7	7453
PDH_2800	IYYDSSD	7	7454
PDH_2801	AYYDSSD	7	7455
PDH_2802	HYYDSSD	7	7456
PDH_2803	VYYDSSD	7	7457
PDH_2804	HYYDSSA	7	7458
PDH_2805	AYYDSSG	7	7459
PDH_2806	VYYDSSA	7	7460
PDH_2807	LYYDSSG	7	7461
PDH_2808	VYYDSSG	7	7462
PDH_2809	LYYDSSD	7	7463
PDH_2810	FYYDSSG	7	7464
PDH_2811	LYYDSSA	7	7465
PDH_2812	FYYDSSD	7	7466
PDH_2813	IYYDSSG	7	7467

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PDH_2814	PYYDSSG	7	7468
PDH_2815	FYYDSSA	7	7469
PDH_2816	TYYDSSD	7	7470
PDH_2817	NYYDSSG	7	7471
PDH_2818	IYYDSSA	7	7472
PDH_2819	PYYDSSA	7	7473
PDH_2820	YYYDSSG	7	4167
PDH_2821	PYYDSSD	7	7474
PDH_2822	NYYDSSA	7	7475
PDH_2823	YYYDSSD	7	7476
PDH_2824	NYYDSSD	7	7477
PDH_2825	YYYDSSA	7	7478
PDH_2826	DYYDSSD	7	7479
PDH_2827	DYYDSSA	7	7480
PDH_2828	FDILTGF	7	7481
PDH_2829	FDILTGS	7	7482
PDH_2830	LDILTGY	7	7483
PDH_2831	YDILTGF	7	7484
PDH_2832	LDILTGS	7	7485
PDH_2833	SDILTGF	7	7486
PDH_2834	IDILTGS	7	7487
PDH_2835	PDILTGS	7	7488
PDH_2836	PDILTGF	7	7489
PDH_2837	IDILTGF	7	7490
PDH_2838	IDILTGY	7	7491
PDH_2839	PDILTGY	7	7492
PDH_2840	YDILTGY	7	4325
PDH_2841	DDILTGF	7	7493
PDH_2842	YDILTGS	7	7494
PDH_2843	HDILTGY	7	7495
PDH_2844	TDILTGF	7	7496
PDH_2845	VDILTGY	7	7497

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PDH_2846	LDILTGF	7	7498
PDH_2847	VDILTGS	7	7499
PDH_2848	HDILTGS	7	7500
PDH_2849	ADILTGS	7	7501
PDH_2850	HDILTGF	7	7502
PDH_2851	NDILTGS	7	7503
PDH_2852	NDILTGF	7	7504
PDH_2853	ADILTGY	7	7505
PDH_2854	VDILTGF	7	7506
PDH_2855	TDILTGY	7	7507
PDH_2856	ADILTGF	7	7508
PDH_2857	NDILTGY	7	7509
PDH_2858	TDILTGS	7	7510
PDH_2859	SDILTGS	7	7511
PDH_2860	DDILTGY	7	7512
PDH_2861	SDILTGY	7	7513
PDH_2862	DDILTGS	7	7514
PDH_2863	FDILTGY	7	7515
PDH_2864	SYDFWSA	7	7516
PDH_2865	FYDFWSG	7	7517
PDH_2866	IYDFWSD	7	7518
PDH_2867	LYDFWSD	7	7519
PDH_2868	AYDFWSD	7	7520
PDH_2869	IYDFWSA	7	7521
PDH_2870	PYDFWSD	7	7522
PDH_2871	AYDFWSA	7	7523
PDH_2872	SYDFWSG	7	7524
PDH_2873	FYDFWSA	7	7525
PDH_2874	PYDFWSA	7	7526
PDH_2875	YYDFWSG	7	4248
PDH_2876	FYDFWSD	7	7527
PDH_2877	IYDFWSG	7	7528

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PDH_2878	PYDFWSG	7	7529
PDH_2879	YYDFWSA	7	7530
PDH_2880	YYDFWSD	7	7531
PDH_2881	NYDFWSD	7	7532
PDH_2882	VYDFWSA	7	7533
PDH_2883	NYDFWSA	7	7534
PDH_2884	VYDFWSD	7	7535
PDH_2885	VYDFWSG	7	7536
PDH_2886	NYDFWSG	7	7537
PDH_2887	DYDFWSA	7	7538
PDH_2888	DYDFWSD	7	7539
PDH_2889	DYDFWSG	7	7540
PDH_2890	HYDFWSG	7	7541
PDH_2891	TYDFWSG	7	7542
PDH_2892	HYDFWSA	7	7543
PDH_2893	LYDFWSG	7	7544
PDH_2894	HYDFWSD	7	7545
PDH_2895	TYDFWSA	7	7546
PDH_2896	SYDFWSD	7	7547
PDH_2897	TYDFWSD	7	7548
PDH_2898	LYDFWSA	7	7549
PDH_2899	AYDFWSG	7	7550
PDH_2900	SCSSTSC	7	7551
PDH_2901	HCSSTSC	7	7552
PDH_2902	PCSSTSC	7	7553
PDH_2903	ACSSTSC	7	7554
PDH_2904	VCSSTSC	7	7555
PDH_2905	LCSSTSC	7	7556
PDH_2906	YCSSTSC	7	3812
PDH_2907	FCSSTSC	7	7557
PDH_2908	DCSSTSC	7	7558
PDH_2909	RYSSSWS	7	7559

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PDH_2910	VYSSSWY	7	7560
PDH_2911	GYSSSWY	7	4435
PDH_2912	VYSSSWS	7	7561
PDH_2913	TYSSSWY	7	7562
PDH_2914	TYSSSWF	7	7563
PDH_2915	TYSSSWS	7	7564
PDH_2916	GYSSSWF	7	7565
PDH_2917	LYSSSWF	7	7566
PDH_2918	AYSSSWS	7	7567
PDH_2919	SYSSSWF	7	7568
PDH_2920	WYSSSWS	7	7569
PDH_2921	WYSSSWF	7	7570
PDH_2922	MYSSSWS	7	7571
PDH_2923	SYSSSWS	7	7572
PDH_2924	LYSSSWY	7	7573
PDH_2925	AYSSSWY	7	7574
PDH_2926	AYSSSWF	7	7575
PDH_2927	LYSSSWS	7	7576
PDH_2928	WYSSSWY	7	7577
PDH_2929	VYSSSWF	7	7578
PDH_2930	SYSSSWY	7	7579
PDH_2931	RYSSSWF	7	7580
PDH_2932	MYSSSWF	7	7581
PDH_2933	RYSSSWY	7	7582
PDH_2934	MYSSSWY	7	7583
PDH_2935	GYSSSWS	7	7584
PDH_2936	IYDSSGY	7	7585
PDH_2937	PYDSSGS	7	7586
PDH_2938	VYDSSGF	7	7587
PDH_2939	PYDSSGY	7	7588
PDH_2940	NYDSSGS	7	7589
PDH_2941	LYDSSGY	7	7590

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PDH_2942	NYDSSGY	7	7591
PDH_2943	LYDSSGS	7	7592
PDH_2944	VYDSSGY	7	7593
PDH_2945	VYDSSGS	7	7594
PDH_2946	LYDSSGF	7	7595
PDH_2947	NYDSSGF	7	7596
PDH_2948	YYDSSGY	7	4168
PDH_2949	YYDSSGS	7	7597
PDH_2950	DYDSSGS	7	7598
PDH_2951	TYDSSGY	7	7599
PDH_2952	TYDSSGF	7	7600
PDH_2953	TYDSSGS	7	7601
PDH_2954	YYDSSGF	7	7602
PDH_2955	AYDSSGS	7	7603
PDH_2956	HYDSSGY	7	7604
PDH_2957	AYDSSGY	7	7605
PDH_2958	HYDSSGF	7	7606
PDH_2959	HYDSSGS	7	7607
PDH_2960	FYDSSGF	7	7608
PDH_2961	IYDSSGF	7	7609
PDH_2962	DYDSSGY	7	7610
PDH_2963	DYDSSGF	7	7611
PDH_2964	PYDSSGF	7	7612
PDH_2965	SYDSSGS	7	7613
PDH_2966	SYDSSGF	7	7614
PDH_2967	AYDSSGF	7	7615
PDH_2968	FYDSSGY	7	7616
PDH_2969	SYDSSGY	7	7617
PDH_2970	IYDSSGS	7	7618
PDH_2971	FYDSSGS	7	7619
PDH_2972	HYYGSGI	7	7620
PDH_2973	SYYGSGI	7	7621

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PDH_2974	AYYGSGT	7	7622
PDH_2975	DYYGSGI	7	7623
PDH_2976	VYYGSGT	7	7624
PDH_2977	AYYGSGS	7	7625
PDH_2978	VYYGSGI	7	7626
PDH_2979	VYYGSGS	7	7627
PDH_2980	HYYGSGS	7	7628
PDH_2981	LYYGSGS	7	7629
PDH_2982	HYYGSGT	7	7630
PDH_2983	LYYGSGT	7	7631
PDH_2984	PYYGSGS	7	7632
PDH_2985	SYYGSGS	7	7633
PDH_2986	NYYGSGS	7	7634
PDH_2987	IYYGSGS	7	7635
PDH_2988	DYYGSGT	7	7636
PDH_2989	PYYGSGI	7	7637
PDH_2990	PYYGSGT	7	7638
PDH_2991	SYYGSGT	7	7639
PDH_2992	FYYGSGS	7	7640
PDH_2993	YYYGSGS	7	3975
PDH_2994	NYYGSGT	7	7641
PDH_2995	IYYGSGT	7	7642
PDH_2996	DYYGSGS	7	7643
PDH_2997	TYYGSGS	7	7644
PDH_2998	FYYGSGT	7	7645
PDH_2999	YYYGSGT	7	7646
PDH_3000	TYYGSGT	7	7647
PDH_3001	YYYGSGI	7	7648
PDH_3002	FYYGSGI	7	7649
PDH_3003	AYYGSGI	7	7650
PDH_3004	TYYGSGI	7	7651
PDH_3005	IYYGSGI	7	7652

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PDH_3006	LYYGSGI	7	7653
PDH_3007	NYYGSGI	7	7654
PDH_3008	TYSSGWF	7	7655
PDH_3009	TYSSGWS	7	7656
PDH_3010	VYSSGWF	7	7657
PDH_3011	GYSSGWF	7	7658
PDH_3012	MYSSGWS	7	7659
PDH_3013	SYSSGWF	7	7660
PDH_3014	MYSSGWY	7	7661
PDH_3015	LYSSGWY	7	7662
PDH_3016	MYSSGWF	7	7663
PDH_3017	WYSSGWS	7	7664
PDH_3018	WYSSGWY	7	7665
PDH_3019	AYSSGWS	7	7666
PDH_3020	RYSSGWF	7	7667
PDH_3021	LYSSGWF	7	7668
PDH_3022	AYSSGWY	7	7669
PDH_3023	RYSSGWY	7	7670
PDH_3024	SYSSGWY	7	7671
PDH_3025	RYSSGWS	7	7672
PDH_3026	GYSSGWY	7	4456
PDH_3027	WYSSGWF	7	7673
PDH_3028	AYSSGWF	7	7674
PDH_3029	GYSSGWS	7	7675
PDH_3030	VYSSGWY	7	7676
PDH_3031	VYSSGWS	7	7677
PDH_3032	LYSSGWS	7	7678
PDH_3033	TYSSGWY	7	7679
PDH_3034	SYSSGWS	7	7680
PDH_3035	FCSGGSC	7	7681
PDH_3036	LCSGGSC	7	7682
PDH_3037	SCSGGSC	7	7683

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PDH_3038	YCSGGSC	7	3773
PDH_3039	DCSGGSC	7	7684
PDH_3040	HCSGGSC	7	7685
PDH_3041	PCSGGSC	7	7686
PDH_3042	ACSGGSC	7	7687
PDH_3043	VCSGGSC	7	7688
PDH_3044	CSGGSCH	7	7689
PDH_3045	CSGGSCL	7	7690
PDH_3046	CSGGSCS	7	7691
PDH_3047	CSGGSCY	7	3774
PDH_3048	CSGGSCP	7	7692
PDH_3049	CSGGSCF	7	7693
PDH_3050	CSSTSCY	7	3813
PDH_3051	CSSTSCL	7	7694
PDH_3052	CSSTSCF	7	7695
PDH_3053	CSSTSCH	7	7696
PDH_3054	CSSTSCS	7	7697
PDH_3055	CSSTSCP	7	7698
PDH_3056	ICGGDCF	7	7699
PDH_3057	VCGGDCS	7	7700
PDH_3058	DCGGDCF	7	7701
PDH_3059	SCGGDCF	7	7702
PDH_3060	NCGGDCY	7	7703
PDH_3061	VCGGDCY	7	7704
PDH_3062	SCGGDCS	7	7705
PDH_3063	NCGGDCS	7	7706
PDH_3064	HCGGDCF	7	7707
PDH_3065	LCGGDCS	7	7708
PDH_3066	LCGGDCY	7	7709
PDH_3067	ICGGDCY	7	7710
PDH_3068	LCGGDCF	7	7711
PDH_3069	ICGGDCS	7	7712

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PDH_3070	VCGGDCF	7	7713
PDH_3071	HCGGDCS	7	7714
PDH_3072	YCGGDCF	7	7715
PDH_3073	HCGGDCY	7	7716
PDH_3074	FCGGDCF	7	7717
PDH_3075	YCGGDCS	7	7718
PDH_3076	DCGGDCS	7	7719
PDH_3077	YCGGDCY	7	3866
PDH_3078	DCGGDCY	7	7720
PDH_3079	PCGGDCF	7	7721
PDH_3080	FCGGDCS	7	7722
PDH_3081	FCGGDCY	7	7723
PDH_3082	ACGGDCF	7	7724
PDH_3083	ACGGDCY	7	7725
PDH_3084	ACGGDCS	7	7726
PDH_3085	PCGGDCY	7	7727
PDH_3086	PCGGDCS	7	7728
PDH_3087	SCGGDCY	7	7729
PDH_3088	NCGGDCF	7	7730
PDH_3089	TCGGDCS	7	7731
PDH_3090	TCGGDCY	7	7732
PDH_3091	TCGGDCF	7	7733
PDH_3092	NDFWSGF	7	7734
PDH_3093	HDFWSGF	7	7735
PDH_3094	SDFWSGF	7	7736
PDH_3095	NDFWSGY	7	7737
PDH_3096	HDFWSGS	7	7738
PDH_3097	DDFWSGF	7	7739
PDH_3098	HDFWSGY	7	7740
PDH_3099	SDFWSGY	7	7741
PDH_3100	FDFWSGF	7	7742
PDH_3101	PDFWSGY	7	7743

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PDH_3102	IDFWSGF	7	7744
PDH_3103	SDFWSGS	7	7745
PDH_3104	PDFWSGS	7	7746
PDH_3105	TDFWSGF	7	7747
PDH_3106	LDFWSGS	7	7748
PDH_3107	DDFWSGY	7	7749
PDH_3108	LDFWSGY	7	7750
PDH_3109	FDFWSGS	7	7751
PDH_3110	ADFWSGF	7	7752
PDH_3111	FDFWSGY	7	7753
PDH_3112	TDFWSGS	7	7754
PDH_3113	PDFWSGF	7	7755
PDH_3114	VDFWSGF	7	7756
PDH_3115	TDFWSGY	7	7757
PDH_3116	IDFWSGY	7	7758
PDH_3117	DDFWSGS	7	7759
PDH_3118	YDFWSGS	7	7760
PDH_3119	YDFWSGF	7	7761
PDH_3120	IDFWSGS	7	7762
PDH_3121	NDFWSGS	7	7763
PDH_3122	YDFWSGY	7	4249
PDH_3123	LDFWSGF	7	7764
PDH_3124	ADFWSGY	7	7765
PDH_3125	VDFWSGS	7	7766
PDH_3126	ADFWSGS	7	7767
PDH_3127	VDFWSGY	7	7768
PDH_3128	YDSSGYS	7	7769
PDH_3129	VDSSGYF	7	7770
PDH_3130	VDSSGYS	7	7771
PDH_3131	ADSSGYS	7	7772
PDH_3132	HDSSGYF	7	7773
PDH_3133	ADSSGYY	7	7774

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PDH_3134	DDSSGYY	7	7775
PDH_3135	DDSSGYS	7	7776
PDH_3136	SDSSGYS	7	7777
PDH_3137	SDSSGYF	7	7778
PDH_3138	PDSSGYS	7	7779
PDH_3139	SDSSGYY	7	7780
PDH_3140	PDSSGYY	7	7781
PDH_3141	HDSSGYY	7	7782
PDH_3142	PDSSGYF	7	7783
PDH_3143	FDSSGYF	7	7784
PDH_3144	HDSSGYS	7	7785
PDH_3145	ADSSGYF	7	7786
PDH_3146	DDSSGYF	7	7787
PDH_3147	LDSSGYF	7	7788
PDH_3148	LDSSGYY	7	7789
PDH_3149	LDSSGYS	7	7790
PDH_3150	FDSSGYY	7	7791
PDH_3151	FDSSGYS	7	7792
PDH_3152	YDSSGYF	7	7793
PDH_3153	YDSSGYY	7	4169
PDH_3154	VDSSGYY	7	7794
PDH_3155	EYCGGDC	7	7795
PDH_3156	QYCGGDC	7	7796
PDH_3157	AYCGGDC	7	3865
PDH_3158	IYCGGDC	7	7797
PDH_3159	TYCGGDC	7	7798
PDH_3160	PYCGGDC	7	7799
PDH_3161	LYCGGDC	7	7800
PDH_3162	VYCGGDC	7	7801
PDH_3163	KYCGGDC	7	7802
PDH_3164	VYYDSSGF	8	7803
PDH_3165	IYYDSSGF	8	7804

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PDH_3166	YYYDSSGY	8	4164
PDH_3167	PYYDSSGF	8	7805
PDH_3168	HYYDSSGF	8	7806
PDH_3169	HYYDSSGY	8	7807
PDH_3170	AYYDSSGF	8	7808
PDH_3171	HYYDSSGS	8	7809
PDH_3172	DYYDSSGY	8	7810
PDH_3173	DYYDSSGS	8	7811
PDH_3174	YYYDSSGS	8	7812
PDH_3175	SYYDSSGF	8	7813
PDH_3176	LYYDSSGF	8	7814
PDH_3177	NYYDSSGF	8	7815
PDH_3178	NYYDSSGY	8	7816
PDH_3179	IYYDSSGY	8	7817
PDH_3180	SYYDSSGS	8	7818
PDH_3181	AYYDSSGS	8	7819
PDH_3182	IYYDSSGS	8	7820
PDH_3183	AYYDSSGY	8	7821
PDH_3184	DYYDSSGF	8	7822
PDH_3185	SYYDSSGY	8	7823
PDH_3186	NYYDSSGS	8	7824
PDH_3187	LYYDSSGY	8	7825
PDH_3188	PYYDSSGS	8	7826
PDH_3189	LYYDSSGS	8	7827
PDH_3190	PYYDSSGY	8	7828
PDH_3191	TYYDSSGY	8	7829
PDH_3192	TYYDSSGS	8	7830
PDH_3193	FYYDSSGF	8	7831
PDH_3194	FYYDSSGY	8	7832
PDH_3195	FYYDSSGS	8	7833
PDH_3196	VYYDSSGS	8	7834
PDH_3197	TYYDSSGF	8	7835

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PDH_3198	YYYDSSGF	8	7836
PDH_3199	VYYDSSGY	8	7837
PDH_3200	TYYGSGSS	8	7838
PDH_3201	SYYGSGSY	8	7839
PDH_3202	SYYGSGSS	8	7840
PDH_3203	HYYGSGSF	8	7841
PDH_3204	PYYGSGSF	8	7842
PDH_3205	AYYGSGSS	8	7843
PDH_3206	AYYGSGSF	8	7844
PDH_3207	AYYGSGSY	8	7845
PDH_3208	YYYGSGSF	8	7846
PDH_3209	TYYGSGSY	8	7847
PDH_3210	YYYGSGSY	8	3972
PDH_3211	PYYGSGSS	8	7848
PDH_3212	PYYGSGSY	8	7849
PDH_3213	DYYGSGSY	8	7850
PDH_3214	VYYGSGSY	8	7851
PDH_3215	VYYGSGSF	8	7852
PDH_3216	YYYGSGSS	8	7853
PDH_3217	LYYGSGSF	8	7854
PDH_3218	LYYGSGSY	8	7855
PDH_3219	DYYGSGSS	8	7856
PDH_3220	VYYGSGSS	8	7857
PDH_3221	IYYGSGSS	8	7858
PDH_3222	FYYGSGSY	8	7859
PDH_3223	FYYGSGSS	8	7860
PDH_3224	LYYGSGSS	8	7861
PDH_3225	SYYGSGSF	8	7862
PDH_3226	IYYGSGSY	8	7863
PDH_3227	IYYGSGSF	8	7864
PDH_3228	FYYGSGSF	8	7865
PDH_3229	DYYGSGSF	8	7866

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PDH_3230	NYYGSGSS	8	7867
PDH_3231	NYYGSGSY	8	7868
PDH_3232	IYYGSGSF	8	7869
PDH_3233	HYYGSGSY	8	7870
PDH_3234	HYYGSGSS	8	7871
PDH_3235	NYYGSGSF	8	7872
PDH_3236	AYCSSTSC	8	7873
PDH_3237	PYCSSTSC	8	7874
PDH_3238	RYCSSTSC	8	7875
PDH_3239	IYCSSTSC	8	7876
PDH_3240	LYCSSTSC	8	7877
PDH_3241	VYCSSTSC	8	7878
PDH_3242	TYCSSTSC	8	7879
PDH_3243	SYCSSTSC	8	7880
PDH_3244	GYCSSTSC	8	3809
PDH_3245	IYCSGGSC	8	7881
PDH_3246	VYCSGGSC	8	7882
PDH_3247	LYCSGGSC	8	7883
PDH_3248	AYCSGGSC	8	7884
PDH_3249	TYCSGGSC	8	7885
PDH_3250	GYCSGGSC	8	3770
PDH_3251	RYCSGGSC	8	7886
PDH_3252	PYCSGGSC	8	7887
PDH_3253	SYCSGGSC	8	7888
PDH_3254	FYDFWSGY	8	7889
PDH_3255	AYDFWSGF	8	7890
PDH_3256	NYDFWSGF	8	7891
PDH_3257	IYDFWSGF	8	7892
PDH_3258	DYDFWSGS	8	7893
PDH_3259	DYDFWSGY	8	7894
PDH_3260	NYDFWSGY	8	7895
PDH_3261	VYDFWSGF	8	7896

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PDH_3262	VYDFWSGS	8	7897
PDH_3263	YYDFWSGF	8	7898
PDH_3264	PYDFWSGF	8	7899
PDH_3265	FYDFWSGS	8	7900
PDH_3266	HYDFWSGF	8	7901
PDH_3267	HYDFWSGY	8	7902
PDH_3268	YYDFWSGS	8	7903
PDH_3269	PYDFWSGY	8	7904
PDH_3270	PYDFWSGS	8	7905
PDH_3271	VYDFWSGY	8	7906
PDH_3272	SYDFWSGS	8	7907
PDH_3273	YYDFWSGY	8	4245
PDH_3274	LYDFWSGF	8	7908
PDH_3275	HYDFWSGS	8	7909
PDH_3276	SYDFWSGY	8	7910
PDH_3277	SYDFWSGF	8	7911
PDH_3278	LYDFWSGS	8	7912
PDH_3279	TYDFWSGF	8	7913
PDH_3280	LYDFWSGY	8	7914
PDH_3281	AYDFWSGY	8	7915
PDH_3282	AYDFWSGS	8	7916
PDH_3283	TYDFWSGS	8	7917
PDH_3284	IYDFWSGY	8	7918
PDH_3285	TYDFWSGY	8	7919
PDH_3286	NYDFWSGS	8	7920
PDH_3287	DYDFWSGF	8	7921
PDH_3288	IYDFWSGS	8	7922
PDH_3289	FYDFWSGF	8	7923
PDH_3290	HDILTGYS	8	7924
PDH_3291	PDILTGYY	8	7925
PDH_3292	PDILTGYF	8	7926
PDH_3293	TDILTGYS	8	7927

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PDH_3294	HDILTGYY	8	7928
PDH_3295	YDILTGYF	8	7929
PDH_3296	IDILTGYS	8	7930
PDH_3297	IDILTGYY	8	7931
PDH_3298	IDILTGYF	8	7932
PDH_3299	LDILTGYF	8	7933
PDH_3300	LDILTGYY	8	7934
PDH_3301	LDILTGYS	8	7935
PDH_3302	DDILTGYF	8	7936
PDH_3303	FDILTGYF	8	7937
PDH_3304	SDILTGYF	8	7938
PDH_3305	ADILTGYY	8	7939
PDH_3306	VDILTGYY	8	7940
PDH_3307	VDILTGYS	8	7941
PDH_3308	ADILTGYS	8	7942
PDH_3309	DDILTGYS	8	7943
PDH_3310	FDILTGYS	8	7944
PDH_3311	SDILTGYS	8	7945
PDH_3312	DDILTGYY	8	7946
PDH_3313	SDILTGYY	8	7947
PDH_3314	YDILTGYY	8	4322
PDH_3315	FDILTGYY	8	7948
PDH_3316	HDILTGYF	8	7949
PDH_3317	NDILTGYY	8	7950
PDH_3318	NDILTGYF	8	7951
PDH_3319	PDILTGYS	8	7952
PDH_3320	VDILTGYF	8	7953
PDH_3321	TDILTGYY	8	7954
PDH_3322	TDILTGYF	8	7955
PDH_3323	YDILTGYS	8	7956
PDH_3324	NDILTGYS	8	7957
PDH_3325	ADILTGYF	8	7958

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PDH_3326	SCSGGSCS	8	7959
PDH_3327	HCSGGSCF	8	7960
PDH_3328	DCSGGSCS	8	7961
PDH_3329	PCSGGSCF	8	7962
PDH_3330	PCSGGSCY	8	7963
PDH_3331	SCSGGSCY	8	7964
PDH_3332	PCSGGSCS	8	7965
PDH_3333	LCSGGSCY	8	7966
PDH_3334	ACSGGSCY	8	7967
PDH_3335	ACSGGSCS	8	7968
PDH_3336	ACSGGSCF	8	7969
PDH_3337	VCSGGSCY	8	7970
PDH_3338	VCSGGSCF	8	7971
PDH_3339	VCSGGSCS	8	7972
PDH_3340	YCSGGSCS	8	7973
PDH_3341	YCSGGSCF	8	7974
PDH_3342	DCSGGSCF	8	7975
PDH_3343	DCSGGSCY	8	7976
PDH_3344	FCSGGSCS	8	7977
PDH_3345	FCSGGSCY	8	7978
PDH_3346	FCSGGSCF	8	7979
PDH_3347	SCSGGSCF	8	7980
PDH_3348	YCSGGSCY	8	3771
PDH_3349	LCSGGSCF	8	7981
PDH_3350	LCSGGSCS	8	7982
PDH_3351	HCSGGSCS	8	7983
PDH_3352	HCSGGSCY	8	7984
PDH_3353	ACSSTSCY	8	7985
PDH_3354	YCSSTSCF	8	7986
PDH_3355	FCSSTSCY	8	7987
PDH_3356	PCSSTSCF	8	7988
PDH_3357	FCSSTSCS	8	7989

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PDH_3358	DCSSTSCF	8	7990
PDH_3359	VCSSTSCS	8	7991
PDH_3360	VCSSTSCF	8	7992
PDH_3361	LCSSTSCS	8	7993
PDH_3362	VCSSTSCY	8	7994
PDH_3363	ACSSTSCS	8	7995
PDH_3364	LCSSTSCY	8	7996
PDH_3365	LCSSTSCF	8	7997
PDH_3366	FCSSTSCF	8	7998
PDH_3367	HCSSTSCY	8	7999
PDH_3368	HCSSTSCS	8	8000
PDH_3369	HCSSTSCF	8	8001
PDH_3370	SCSSTSCF	8	8002
PDH_3371	SCSSTSCS	8	8003
PDH_3372	YCSSTSCS	8	8004
PDH_3373	DCSSTSCY	8	8005
PDH_3374	DCSSTSCS	8	8006
PDH_3375	SCSSTSCY	8	8007
PDH_3376	PCSSTSCS	8	8008
PDH_3377	ACSSTSCF	8	8009
PDH_3378	PCSSTSCY	8	8010
PDH_3379	YCSSTSCY	8	3810
PDH_3380	LYCGGDCS	8	8011
PDH_3381	EYCGGDCS	8	8012
PDH_3382	LYCGGDCY	8	8013
PDH_3383	VYCGGDCS	8	8014
PDH_3384	VYCGGDCY	8	8015
PDH_3385	AYCGGDCY	8	3863
PDH_3386	AYCGGDCF	8	8016
PDH_3387	EYCGGDCY	8	8017
PDH_3388	TYCGGDCF	8	8018
PDH_3389	LYCGGDCF	8	8019

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PDH_3390	AYCGGDCS	8	8020
PDH_3391	QYCGGDCF	8	8021
PDH_3392	QYCGGDCS	8	8022
PDH_3393	KYCGGDCF	8	8023
PDH_3394	KYCGGDCY	8	8024
PDH_3395	QYCGGDCY	8	8025
PDH_3396	KYCGGDCS	8	8026
PDH_3397	VYCGGDCF	8	8027
PDH_3398	IYCGGDCF	8	8028
PDH_3399	IYCGGDCY	8	8029
PDH_3400	IYCGGDCS	8	8030
PDH_3401	PYCGGDCS	8	8031
PDH_3402	PYCGGDCF	8	8032
PDH_3403	TYCGGDCY	8	8033
PDH_3404	EYCGGDCF	8	8034
PDH_3405	PYCGGDCY	8	8035
PDH_3406	TYCGGDCS	8	8036
PDH_3407	DYDSSGYS	8	8037
PDH_3408	YYDSSGYF	8	8038
PDH_3409	LYDSSGYS	8	8039
PDH_3410	AYDSSGYS	8	8040
PDH_3411	AYDSSGYY	8	8041
PDH_3412	NYDSSGYY	8	8042
PDH_3413	IYDSSGYS	8	8043
PDH_3414	FYDSSGYF	8	8044
PDH_3415	DYDSSGYY	8	8045
PDH_3416	YYDSSGYS	8	8046
PDH_3417	TYDSSGYY	8	8047
PDH_3418	TYDSSGYS	8	8048
PDH_3419	PYDSSGYF	8	8049
PDH_3420	IYDSSGYY	8	8050
PDH_3421	IYDSSGYF	8	8051

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PDH_3422	YYDSSGYY	8	4165
PDH_3423	NYDSSGYS	8	8052
PDH_3424	NYDSSGYF	8	8053
PDH_3425	VYDSSGYY	8	8054
PDH_3426	VYDSSGYF	8	8055
PDH_3427	FYDSSGYY	8	8056
PDH_3428	FYDSSGYS	8	8057
PDH_3429	SYDSSGYY	8	8058
PDH_3430	SYDSSGYS	8	8059
PDH_3431	PYDSSGYS	8	8060
PDH_3432	PYDSSGYY	8	8061
PDH_3433	LYDSSGYY	8	8062
PDH_3434	VYDSSGYS	8	8063
PDH_3435	SYDSSGYF	8	8064
PDH_3436	LYDSSGYF	8	8065
PDH_3437	HYDSSGYY	8	8066
PDH_3438	HYDSSGYS	8	8067
PDH_3439	TYDSSGYF	8	8068
PDH_3440	AYDSSGYF	8	8069
PDH_3441	DYDSSGYF	8	8070
PDH_3442	EYDSSGYF	8	8071
PDH_3443	RYYGSGSY	8	8072
PDH_3444	RYYGSGSS	8	8073
PDH_3445	GYYGSGSS	8	8074
PDH_3446	GYYGSGSY	8	8075
PDH_3447	FDFWSGYS	8	8076
PDH_3448	HDFWSGYF	8	8077
PDH_3449	FDFWSGYY	8	8078
PDH_3450	SDFWSGYS	8	8079
PDH_3451	SDFWSGYY	8	8080
PDH_3452	PDFWSGYS	8	8081
PDH_3453	HDFWSGYS	8	8082

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PDH_3454	IDFWSGYY	8	8083
PDH_3455	HDFWSGYY	8	8084
PDH_3456	NDFWSGYF	8	8085
PDH_3457	YDFWSGYS	8	8086
PDH_3458	IDFWSGYS	8	8087
PDH_3459	PDFWSGYY	8	8088
PDH_3460	SDFWSGYF	8	8089
PDH_3461	VDFWSGYS	8	8090
PDH_3462	IDFWSGYF	8	8091
PDH_3463	YDFWSGYY	8	4246
PDH_3464	YDFWSGYF	8	8092
PDH_3465	TDFWSGYY	8	8093
PDH_3466	DDFWSGYS	8	8094
PDH_3467	LDFWSGYS	8	8095
PDH_3468	DDFWSGYY	8	8096
PDH_3469	DDFWSGYF	8	8097
PDH_3470	VDFWSGYY	8	8098
PDH_3471	VDFWSGYF	8	8099
PDH_3472	NDFWSGYY	8	8100
PDH_3473	FDFWSGYF	8	8101
PDH_3474	NDFWSGYS	8	8102
PDH_3475	LDFWSGYY	8	8103
PDH_3476	ADFWSGYY	8	8104
PDH_3477	ADFWSGYS	8	8105
PDH_3478	TDFWSGYS	8	8106
PDH_3479	TDFWSGYF	8	8107
PDH_3480	ADFWSGYF	8	8108
PDH_3481	LDFWSGYF	8	8109
PDH_3482	PDFWSGYF	8	8110
PDH_3483	LLRYFDWY	8	8111
PDH_3484	QLRYFDWY	8	8112
PDH_3485	PLRYFDWL	8	8113

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PDH_3486	ILRYFDWF	8	8114
PDH_3487	ILRYFDWY	8	8115
PDH_3488	ALRYFDWL	8	8116
PDH_3489	QLRYFDWF	8	8117
PDH_3490	KLRYFDWL	8	8118
PDH_3491	TLRYFDWL	8	8119
PDH_3492	TLRYFDWH	8	8120
PDH_3493	ELRYFDWL	8	8121
PDH_3494	ELRYFDWH	8	8122
PDH_3495	PLRYFDWH	8	8123
PDH_3496	ELRYFDWY	8	8124
PDH_3497	ELRYFDWF	8	8125
PDH_3498	LLRYFDWL	8	8126
PDH_3499	VLRYFDWF	8	8127
PDH_3500	TLRYFDWF	8	8128
PDH_3501	ALRYFDWF	8	8129
PDH_3502	ILRYFDWH	8	8130
PDH_3503	QLRYFDWL	8	8131
PDH_3504	QLRYFDWH	8	8132
PDH_3505	VLRYFDWY	8	8133
PDH_3506	TLRYFDWY	8	8134
PDH_3507	ILRYFDWL	8	8135
PDH_3508	LLRYFDWH	8	8136
PDH_3509	VLRYFDWH	8	8137
PDH_3510	KLRYFDWY	8	8138
PDH_3511	KLRYFDWF	8	8139
PDH_3512	ALRYFDWH	8	8140
PDH_3513	ALRYFDWY	8	8141
PDH_3514	VLRYFDWL	8	4298
PDH_3515	KLRYFDWH	8	8142
PDH_3516	PLRYFDWY	8	8143
PDH_3517	PLRYFDWF	8	8144

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PDH_3518	LLRYFDWF	8	8145
PDH_3519	IYYDSSGYS	9	8146
PDH_3520	TYYDSSGYS	9	8147
PDH_3521	HYYDSSGYY	9	8148
PDH_3522	TYYDSSGYY	9	8149
PDH_3523	HYYDSSGYS	9	8150
PDH_3524	NYYDSSGYF	9	8151
PDH_3525	AYYDSSGYS	9	8152
PDH_3526	DYYDSSGYF	9	8153
PDH_3527	DYYDSSGYS	9	8154
PDH_3528	LYYDSSGYS	9	8155
PDH_3529	NYYDSSGYS	9	8156
PDH_3530	HYYDSSGYF	9	8157
PDH_3531	DYYDSSGYY	9	8158
PDH_3532	LYYDSSGYY	9	8159
PDH_3533	IYYDSSGYY	9	8160
PDH_3534	LYYDSSGYF	9	8161
PDH_3535	IYYDSSGYF	9	8162
PDH_3536	AYYDSSGYF	9	8163
PDH_3537	AYYDSSGYY	9	8164
PDH_3538	FYYDSSGYS	9	8165
PDH_3539	YYYDSSGYS	9	8166
PDH_3540	FYYDSSGYY	9	8167
PDH_3541	FYYDSSGYF	9	8168
PDH_3542	YYYDSSGYY	9	4162
PDH_3543	YYYDSSGYF	9	8169
PDH_3544	VYYDSSGYF	9	8170
PDH_3545	PYYDSSGYY	9	8171
PDH_3546	PYYDSSGYS	9	8172
PDH_3547	VYYDSSGYS	9	8173
PDH_3548	SYYDSSGYY	9	8174
PDH_3549	NYYDSSGYY	9	8175

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PDH_3550	VYYDSSGYY	9	8176
PDH_3551	SYYDSSGYS	9	8177
PDH_3552	SYYDSSGYF	9	8178
PDH_3553	TYYDSSGYF	9	8179
PDH_3554	PYYDSSGYF	9	8180
PDH_3555	PYCSGGSCF	9	8181
PDH_3556	TYCSGGSCF	9	8182
PDH_3557	IYCSGGSCF	9	8183
PDH_3558	VYCSGGSCS	9	8184
PDH_3559	TYCSGGSCY	9	8185
PDH_3560	VYCSGGSCF	9	8186
PDH_3561	TYCSGGSCS	9	8187
PDH_3562	GYCSGGSCS	9	8188
PDH_3563	IYCSGGSCS	9	8189
PDH_3564	GYCSGGSCY	9	3768
PDH_3565	IYCSGGSCY	9	8190
PDH_3566	VYCSGGSCY	9	8191
PDH_3567	AYCSGGSCF	9	8192
PDH_3568	GYCSGGSCF	9	8193
PDH_3569	LYCSGGSCF	9	8194
PDH_3570	RYCSGGSCF	9	8195
PDH_3571	LYCSGGSCS	9	8196
PDH_3572	RYCSGGSCY	9	8197
PDH_3573	AYCSGGSCS	9	8198
PDH_3574	SYCSGGSCY	9	8199
PDH_3575	SYCSGGSCF	9	8200
PDH_3576	AYCSGGSCY	9	8201
PDH_3577	SYCSGGSCS	9	8202
PDH_3578	PYCSGGSCS	9	8203
PDH_3579	LYCSGGSCY	9	8204
PDH_3580	RYCSGGSCS	9	8205
PDH_3581	PYCSGGSCY	9	8206

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PDH_3582	TYCSSTSCY	9	8207
PDH_3583	AYCSSTSCY	9	8208
PDH_3584	AYCSSTSCS	9	8209
PDH_3585	RYCSSTSCS	9	8210
PDH_3586	TYCSSTSCS	9	8211
PDH_3587	PYCSSTSCY	9	8212
PDH_3588	PYCSSTSCS	9	8213
PDH_3589	RYCSSTSCY	9	8214
PDH_3590	VYCSSTSCS	9	8215
PDH_3591	VYCSSTSCY	9	8216
PDH_3592	LYCSSTSCF	9	8217
PDH_3593	LYCSSTSCY	9	8218
PDH_3594	PYCSSTSCF	9	8219
PDH_3595	VYCSSTSCF	9	8220
PDH_3596	IYCSSTSCY	9	8221
PDH_3597	IYCSSTSCS	9	8222
PDH_3598	IYCSSTSCF	9	8223
PDH_3599	SYCSSTSCS	9	8224
PDH_3600	LYCSSTSCS	9	8225
PDH_3601	SYCSSTSCY	9	8226
PDH_3602	SYCSSTSCF	9	8227
PDH_3603	GYCSSTSCY	9	3807
PDH_3604	GYCSSTSCF	9	8228
PDH_3605	GYCSSTSCS	9	8229
PDH_3606	RYCSSTSCF	9	8230
PDH_3607	TYCSSTSCF	9	8231
PDH_3608	AYCSSTSCF	9	8232
PDH_3609	IYDFWSGYY	9	8233
PDH_3610	NYDFWSGYY	9	8234
PDH_3611	PYDFWSGYF	9	8235
PDH_3612	SYDFWSGYF	9	8236
PDH_3613	VYDFWSGYF	9	8237

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PDH_3614	VYDFWSGYY	9	8238
PDH_3615	HYDFWSGYY	9	8239
PDH_3616	HYDFWSGYF	9	8240
PDH_3617	HYDFWSGYS	9	8241
PDH_3618	IYDFWSGYS	9	8242
PDH_3619	NYDFWSGYS	9	8243
PDH_3620	AYDFWSGYS	9	8244
PDH_3621	SYDFWSGYS	9	8245
PDH_3622	PYDFWSGYS	9	8246
PDH_3623	AYDFWSGYY	9	8247
PDH_3624	SYDFWSGYY	9	8248
PDH_3625	PYDFWSGYY	9	8249
PDH_3626	FYDFWSGYY	9	8250
PDH_3627	FYDFWSGYF	9	8251
PDH_3628	DYDFWSGYS	9	8252
PDH_3629	FYDFWSGYS	9	8253
PDH_3630	DYDFWSGYF	9	8254
PDH_3631	LYDFWSGYY	9	8255
PDH_3632	AYDFWSGYF	9	8256
PDH_3633	LYDFWSGYS	9	8257
PDH_3634	DYDFWSGYY	9	8258
PDH_3635	LYDFWSGYF	9	8259
PDH_3636	YYDFWSGYY	9	4243
PDH_3637	TYDFWSGYY	9	8260
PDH_3638	TYDFWSGYF	9	8261
PDH_3639	YYDFWSGYS	9	8262
PDH_3640	YYDFWSGYF	9	8263
PDH_3641	TYDFWSGYS	9	8264
PDH_3642	VYDFWSGYS	9	8265
PDH_3643	NYDFWSGYF	9	8266
PDH_3644	IYDFWSGYF	9	8267
PDH_3645	FCSGGSCYS	9	8268

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PDH_3646	LCSGGSCYS	9	8269
PDH_3647	VCSGGSCYS	9	8270
PDH_3648	ACSGGSCYS	9	8271
PDH_3649	ACSGGSCYY	9	8272
PDH_3650	FCSGGSCYY	9	8273
PDH_3651	LCSGGSCYF	9	8274
PDH_3652	LCSGGSCYY	9	8275
PDH_3653	VCSGGSCYY	9	8276
PDH_3654	YCSGGSCYS	9	3769
PDH_3655	PCSGGSCYS	9	8277
PDH_3656	PCSGGSCYY	9	8278
PDH_3657	PCSGGSCYF	9	8279
PDH_3658	YCSGGSCYF	9	8280
PDH_3659	YCSGGSCYY	9	8281
PDH_3660	SCSGGSCYY	9	8282
PDH_3661	HCSGGSCYF	9	8283
PDH_3662	DCSGGSCYY	9	8284
PDH_3663	SCSGGSCYF	9	8285
PDH_3664	DCSGGSCYS	9	8286
PDH_3665	HCSGGSCYS	9	8287
PDH_3666	SCSGGSCYS	9	8288
PDH_3667	FCSGGSCYF	9	8289
PDH_3668	ACSGGSCYF	9	8290
PDH_3669	DCSGGSCYF	9	8291
PDH_3670	HCSGGSCYY	9	8292
PDH_3671	VCSGGSCYF	9	8293
PDH_3672	FYYDSSGYYY	10	8294
PDH_3673	YYYDSSGYYF	10	8295
PDH_3674	PYYDSSGYYY	10	8296
PDH_3675	VYYDSSGYYS	10	8297
PDH_3676	PYYDSSGYYS	10	8298
PDH_3677	FYYDSSGYYS	10	8299

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PDH_3678	NYYDSSGYYY	10	8300
PDH_3679	NYYDSSGYYS	10	8301
PDH_3680	DYYDSSGYYS	10	8302
PDH_3681	HYYDSSGYYF	10	8303
PDH_3682	DYYDSSGYYY	10	8304
PDH_3683	NYYDSSGYYF	10	8305
PDH_3684	HYYDSSGYYY	10	8306
PDH_3685	LYYDSSGYYF	10	8307
PDH_3686	IYYDSSGYYS	10	8308
PDH_3687	YYYDSSGYYS	10	8309
PDH_3688	IYYDSSGYYF	10	8310
PDH_3689	YYYDSSGYYY	10	4161
PDH_3690	HYYDSSGYYS	10	8311
PDH_3691	TYYDSSGYYS	10	8312
PDH_3692	IYYDSSGYYY	10	8313
PDH_3693	TYYDSSGYYF	10	8314
PDH_3694	LYYDSSGYYS	10	8315
PDH_3695	TYYDSSGYYY	10	8316
PDH_3696	LYYDSSGYYY	10	8317
PDH_3697	AYYDSSGYYF	10	8318
PDH_3698	FYYDSSGYYF	10	8319
PDH_3699	AYYDSSGYYY	10	8320
PDH_3700	VYYDSSGYYY	10	8321
PDH_3701	SYYDSSGYYF	10	8322
PDH_3702	PYYDSSGYYF	10	8323
PDH_3703	SYYDSSGYYY	10	8324
PDH_3704	AYYDSSGYYS	10	8325
PDH_3705	DYYDSSGYYF	10	8326
PDH_3706	SYYDSSGYYS	10	8327
PDH_3707	VYYDSSGYYF	10	8328
PDH_3708	IYDYVWGSYAS	11	8329
PDH_3709	AYDYVWGSYAS	11	8330

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PDH_3710	IYDYVWGSYAY	11	8331
PDH_3711	NYDYVWGSYAY	11	8332
PDH_3712	NYDYVWGSYAS	11	8333
PDH_3713	YYDYVWGSYAF	11	8334
PDH_3714	DYDYVWGSYAF	11	8335
PDH_3715	SYDYVWGSYAY	11	8336
PDH_3716	DYDYVWGSYAS	11	8337
PDH_3717	DYDYVWGSYAY	11	8338
PDH_3718	FYDYVWGSYAS	11	8339
PDH_3719	NYDYVWGSYAF	11	8340
PDH_3720	YYDYVWGSYAS	11	8341
PDH_3721	FYDYVWGSYAY	11	8342
PDH_3722	SYDYVWGSYAS	11	8343
PDH_3723	PYDYVWGSYAF	11	8344
PDH_3724	TYDYVWGSYAY	11	8345
PDH_3725	VYDYVWGSYAY	11	8346
PDH_3726	SYDYVWGSYAF	11	8347
PDH_3727	FYDYVWGSYAF	11	8348
PDH_3728	HYDYVWGSYAS	11	8349
PDH_3729	VYDYVWGSYAS	11	8350
PDH_3730	VYDYVWGSYAF	11	8351
PDH_3731	YYDYVWGSYAY	11	4071
PDH_3732	AYDYVWGSYAY	11	8352
PDH_3733	LYDYVWGSYAS	11	8353
PDH_3734	TYDYVWGSYAF	11	8354
PDH_3735	AYDYVWGSYAF	11	8355
PDH_3736	HYDYVWGSYAY	11	8356
PDH_3737	TYDYVWGSYAS	11	8357
PDH_3738	LYDYVWGSYAF	11	8358
PDH_3739	PYDYVWGSYAY	11	8359
PDH_3740	PYDYVWGSYAS	11	8360
PDH_3741	HYDYVWGSYAF	11	8361

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PDH_3742	LYDYVWGSYAY	11	8362
PDH_3743	IYDYVWGSYAF	11	8363
PDH_3744	NYDYVWGSYAYT	12	8364
PDH_3745	NYDYVWGSYAYI	12	8365
PDH_3746	IYDYVWGSYAYI	12	8366
PDH_3747	YYDYVWGSYAYK	12	8367
PDH_3748	NYDYVWGSYAYK	12	8368
PDH_3749	YYDYVWGSYAYT	12	4070
PDH_3750	PYDYVWGSYAYT	12	8369
PDH_3751	DYDYVWGSYAYI	12	8370
PDH_3752	PYDYVWGSYAYK	12	8371
PDH_3753	FYDYVWGSYAYI	12	8372
PDH_3754	VYDYVWGSYAYT	12	8373
PDH_3755	DYDYVWGSYAYK	12	8374
PDH_3756	IYDYVWGSYAYT	12	8375
PDH_3757	IYDYVWGSYAYK	12	8376
PDH_3758	LYDYVWGSYAYI	12	8377
PDH_3759	HYDYVWGSYAYK	12	8378
PDH_3760	TYDYVWGSYAYI	12	8379
PDH_3761	HYDYVWGSYAYT	12	8380
PDH_3762	AYDYVWGSYAYT	12	8381
PDH_3763	AYDYVWGSYAYK	12	8382
PDH_3764	AYDYVWGSYAYI	12	8383
PDH_3765	TYDYVWGSYAYK	12	8384
PDH_3766	DYDYVWGSYAYT	12	8385
PDH_3767	VYDYVWGSYAYK	12	8386
PDH_3768	TYDYVWGSYAYT	12	8387
PDH_3769	FYDYVWGSYAYK	12	8388
PDH_3770	LYDYVWGSYAYK	12	8389
PDH_3771	VYDYVWGSYAYI	12	8390
PDH_3772	LYDYVWGSYAYT	12	8391
PDH_3773	PYDYVWGSYAYI	12	8392

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PDH_3774	FYDYVWGSYAYT	12	8393
PDH_3775	YYDYVWGSYAYI	12	8394
PDH_3776	SYDYVWGSYAYI	12	8395
PDH_3777	HYDYVWGSYAYI	12	8396
PDH_3778	SYDYVWGSYAYT	12	8397
PDH_3779	SYDYVWGSYAYK	12	8398

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Table 29. Theoretical segment pool of oligonucleotide sequences encoding N2 segments of Example 14.

Name	Degenerate Oligo	Peptide Length		SEQ ID NO
N2_000		0	Not degenerate	n/a
N2_001	GCT	1	Not degenerate	n/a
N2_002	GAT	1	Not degenerate	n/a
N2_003	GAG	1	Not degenerate	n/a
N2_004	TTT	1	Not degenerate	n/a
N2_005	GGC	1	Not degenerate	n/a
N2_006	CAT	1	Not degenerate	n/a
N2_007	ATC	1	Not degenerate	n/a
N2_008	AAA	1	Not degenerate	n/a
N2_009	TTG	1	Not degenerate	n/a
N2_010	ATG	1	Not degenerate	n/a
N2_011	CCT	1	Not degenerate	n/a
N2_012	CAA	1	Not degenerate	n/a
N2_013	AGG	1	Not degenerate	n/a
N2_014	TCA	1	Not degenerate	n/a
N2_015	ACC	1	Not degenerate	n/a
N2_016	GTT	1	Not degenerate	n/a
N2_017	TGG	1	Not degenerate	n/a
N2_018	TAC	1	Not degenerate	n/a
N2_019	GMCKHT	2		n/a
N2_020	GMCSVT	2		n/a
N2_021	GMCSHT	2		n/a
N2_022	GMCSVG	2		n/a
N2_023	GMTDYT	2		n/a
N2_024	KHCGAS	2		n/a
N2_025	KHCGRC	2		n/a
N2_026	KHCGWG	2		n/a
N2_027	KHTTTM	2		n/a
N2_028	KHTTYC	2		n/a
N2_029	KHTTWC	2		n/a

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N2_030	KHCRGA	2		n/a
N2_031	KHCKGG	2		n/a
N2_032	KHCCWC	2		n/a
N2_033	KHCCMT	2		n/a
N2_034	KHCMCA	2		n/a
N2_035	GVCSWG	2		n/a
N2_036	GVCMKC	2		n/a
N2_037	GVCWSG	2		n/a
N2_038	SVCYAC	2		n/a
N2_039	GNAAHA	2		n/a
N2_040	BYCSAG	2		n/a
N2_041	RBAAWA	2		n/a
N2_042	RBAAYA	2		n/a
N2_043	SBAMAA	2		n/a
N2_044	VSCMAA	2		n/a
N2_045	GRARVG	2		n/a
N2_046	GRADYT	2		n/a
N2_047	GRABYT	2		n/a
N2_048	GRAKBG	2		n/a
N2_049	RDAGMT	2		n/a
N2_050	RDAGAK	2		n/a
N2_051	RDAGRT	2		n/a
N2_052	RDAGWG	2		n/a
N2_053	RDARGG	2		n/a
N2_054	RDACYA	2		n/a
N2_055	SDACSA	2		n/a
N2_056	VWACYA	2		n/a
N2_057	VWATYA	2		n/a
N2_058	VWAASA	2		n/a
N2_059	YHCGMC	2		n/a
N2_060	YHCGMG	2		n/a
N2_061	YHCGST	2		n/a

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N2_062	YHCSCG	2		n/a
N2_063	YHCKCG	2		n/a
N2_064	YHCSAC	2		n/a
N2_065	YHCKAC	2		n/a
N2_066	YHCRGA	2		n/a
N2_067	YHCCWC	2		n/a
N2_068	YHCMCA	2		n/a
N2_069	WTCYHT	2		n/a
N2_070	HYCGWG	2		n/a
N2_071	HYCTTM	2		n/a
N2_072	HYCAGM	2		n/a
N2_073	HYCTMC	2		n/a
N2_074	VKCTWT	2		n/a
N2_075	CNCVGC	2		n/a
N2_076	MHAGAK	2		n/a
N2_077	MHAGRC	2		n/a
N2_078	MHAGWG	2		n/a
N2_079	MHAMCA	2		n/a
N2_080	ANAGBT	2		n/a
N2_081	MBCYAC	2		n/a
N2_082	MBCAWA	2		n/a
N2_083	MHGGKA	2		n/a
N2_084	CNABTT	2		n/a
N2_085	CVACNA	2		n/a
N2_086	CVAYSG	2		n/a
N2_087	MSCAHG	2		n/a
N2_088	CRAKBG	2		n/a
N2_089	WSGHCA	2		n/a
N2_090	WGGKHC	2		n/a
N2_091	MBCATR	2		n/a
N2_092	AYABSG	2		n/a
N2_093	VYCAWG	2		n/a

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N2_094	BGGSAK	2		n/a
N2_095	AHGRYT	2		n/a
N2_096	BWCAMA	2		n/a
N2_097	BHCTGG	2		n/a
N2_098	TGGBHC	2		n/a
N2_099	TGGVBT	2		n/a
N2_100	NHCGCAGCC	3		n/a
N2_101	BHCGGAATG	3		n/a
N2_102	BHCGGAGGA	3		n/a
N2_103	BHCGGAGTA	3		n/a
N2_104	VNCGCAGGA	3		n/a
N2_105	VBCGGAGCC	3		n/a
N2_106	VBCGGAGGA	3		n/a
N2_107	VBCGGACTA	3		n/a
N2_108	VBCGGAAGG	3		n/a
N2_109	VBCGGAAGC	3		n/a
N2_110	VBCGGAGTA	3		n/a
N2_111	VNCCTTGGA	3		n/a
N2_112	VNCCCAGGA	3		n/a
N2_113	VNCCCACCA	3		n/a
N2_114	VNCAGAGGA	3		n/a
N2_115	VNCAGCGGA	3		n/a
N2_116	VBCACAGGA	3		n/a
N2_117	VNCGTAGGA	3		n/a
N2_118	BHCGGACAC	3		n/a
N2_119	NHCAAACAA	3		n/a
N2_120	NHCAAAAGA	3		n/a
N2_121	BHCACACAA	3		n/a
N2_122	VNCTTTGAG	3		n/a
N2_123	VNCCCACTA	3		n/a
N2_124	VNCCCATAC	3		n/a
N2_125	BHCGGAGAG	3		n/a

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N2_126	BHCGGACTA	3		n/a
N2_127	BHCGGATGG	3		n/a
N2_128	BHCGGATAC	3		n/a
N2_129	NHCAGAGGA	3		n/a
N2_130	NHCAGCGAG	3		n/a
N2_131	NHCAGCTGG	3		n/a
N2_132	VHAGGAGGA	3		n/a
N2_133	BHCGGAAGG	3		n/a
N2_134	NHCCAAGGA	3		n/a
N2_135	BHCACAGCT	3		n/a
N2_136	GGABHCGGATAC	4		8399
N2_137	AGABHCGGATAC	4		8400
N2_138	AGCBHCGGATAC	4		8401
N2_139	CCABHCGGATAC	4		8402
N2_140	GGTAGAVHGTAC	4		8403
N2_141	AGGAGAVHGTAC	4		8404
N2_142	GGABHCGGATGG	4		8405
N2_143	GGABHCGGACTA	4		8406
N2_144	GGABHCACAGCT	4		8407
N2_145	GGABHCACACAA	4		8408

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Table 30. Theoretical segment pool of unique N2 polypeptide segments encoded by the oligonucleotides of Table 29.

Name	Sequence	Length	SEQ ID NO
PN2_000		0	#N/A
PN2_001	A	1	#N/A
PN2_002	D	1	#N/A
PN2_003	E	1	#N/A
PN2_004	F	1	#N/A
PN2_005	G	1	#N/A
PN2_006	H	1	#N/A
PN2_007	I	1	#N/A
PN2_008	K	1	#N/A
PN2_009	L	1	#N/A
PN2_010	M	1	#N/A
PN2_011	P	1	#N/A
PN2_012	Q	1	#N/A
PN2_013	R	1	#N/A
PN2_014	S	1	#N/A
PN2_015	T	1	#N/A
PN2_016	V	1	#N/A
PN2_017	W	1	#N/A
PN2_018	Y	1	#N/A
PN2_019	GW	2	#N/A
PN2_020	GV	2	#N/A
PN2_021	GT	2	#N/A
PN2_022	GS	2	#N/A
PN2_023	GR	2	#N/A
PN2_024	GQ	2	#N/A
PN2_025	GP	2	#N/A
PN2_026	GY	2	#N/A
PN2_027	GG	2	#N/A
PN2_028	GF	2	#N/A

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PN2_029	GE	2	#N/A
PN2_030	GD	2	#N/A
PN2_031	GA	2	#N/A
PN2_032	GL	2	#N/A
PN2_033	GK	2	#N/A
PN2_034	GI	2	#N/A
PN2_035	GH	2	#N/A
PN2_036	MG	2	#N/A
PN2_037	MA	2	#N/A
PN2_038	MI	2	#N/A
PN2_039	MT	2	#N/A
PN2_040	MV	2	#N/A
PN2_041	FP	2	#N/A
PN2_042	FQ	2	#N/A
PN2_043	FR	2	#N/A
PN2_044	FS	2	#N/A
PN2_045	FT	2	#N/A
PN2_046	FV	2	#N/A
PN2_047	FW	2	#N/A
PN2_048	FY	2	#N/A
PN2_049	FA	2	#N/A
PN2_050	FD	2	#N/A
PN2_051	FE	2	#N/A
PN2_052	FF	2	#N/A
PN2_053	FG	2	#N/A
PN2_054	FH	2	#N/A
PN2_055	FK	2	#N/A
PN2_056	FL	2	#N/A
PN2_057	SY	2	#N/A
PN2_058	SS	2	#N/A
PN2_059	SR	2	#N/A
PN2_060	SQ	2	#N/A

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PN2_061	SP	2	#N/A
PN2_062	SW	2	#N/A
PN2_063	SV	2	#N/A
PN2_064	ST	2	#N/A
PN2_065	SK	2	#N/A
PN2_066	SI	2	#N/A
PN2_067	SH	2	#N/A
PN2_068	SM	2	#N/A
PN2_069	SL	2	#N/A
PN2_070	SA	2	#N/A
PN2_071	SG	2	#N/A
PN2_072	SF	2	#N/A
PN2_073	SE	2	#N/A
PN2_074	SD	2	#N/A
PN2_075	YH	2	#N/A
PN2_076	YK	2	#N/A
PN2_077	YL	2	#N/A
PN2_078	YA	2	#N/A
PN2_079	YE	2	#N/A
PN2_080	YD	2	#N/A
PN2_081	YG	2	#N/A
PN2_082	YF	2	#N/A
PN2_083	YY	2	#N/A
PN2_084	YP	2	#N/A
PN2_085	YS	2	#N/A
PN2_086	YR	2	#N/A
PN2_087	YT	2	#N/A
PN2_088	YW	2	#N/A
PN2_089	YV	2	#N/A
PN2_090	LF	2	#N/A
PN2_091	LD	2	#N/A
PN2_092	LE	2	#N/A

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PN2_093	LL	2	#N/A
PN2_094	LM	2	#N/A
PN2_095	LK	2	#N/A
PN2_096	LH	2	#N/A
PN2_097	LI	2	#N/A
PN2_098	LW	2	#N/A
PN2_099	LT	2	#N/A
PN2_100	LR	2	#N/A
PN2_101	LS	2	#N/A
PN2_102	LP	2	#N/A
PN2_103	LQ	2	#N/A
PN2_104	LY	2	#N/A
PN2_105	LG	2	#N/A
PN2_106	LA	2	#N/A
PN2_107	RT	2	#N/A
PN2_108	RV	2	#N/A
PN2_109	RW	2	#N/A
PN2_110	RP	2	#N/A
PN2_111	RQ	2	#N/A
PN2_112	RR	2	#N/A
PN2_113	RS	2	#N/A
PN2_114	RY	2	#N/A
PN2_115	RD	2	#N/A
PN2_116	RE	2	#N/A
PN2_117	RF	2	#N/A
PN2_118	RG	2	#N/A
PN2_119	RA	2	#N/A
PN2_120	RL	2	#N/A
PN2_121	RM	2	#N/A
PN2_122	RH	2	#N/A
PN2_123	RI	2	#N/A
PN2_124	RK	2	#N/A

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PN2_125	LV	2	#N/A
PN2_126	IP	2	#N/A
PN2_127	EL	2	#N/A
PN2_128	VK	2	#N/A
PN2_129	EI	2	#N/A
PN2_130	EK	2	#N/A
PN2_131	EE	2	#N/A
PN2_132	ED	2	#N/A
PN2_133	EG	2	#N/A
PN2_134	EF	2	#N/A
PN2_135	EA	2	#N/A
PN2_136	IT	2	#N/A
PN2_137	ET	2	#N/A
PN2_138	EW	2	#N/A
PN2_139	EV	2	#N/A
PN2_140	EP	2	#N/A
PN2_141	ES	2	#N/A
PN2_142	ER	2	#N/A
PN2_143	II	2	#N/A
PN2_144	IH	2	#N/A
PN2_145	VR	2	#N/A
PN2_146	VT	2	#N/A
PN2_147	KA	2	#N/A
PN2_148	KG	2	#N/A
PN2_149	KE	2	#N/A
PN2_150	KD	2	#N/A
PN2_151	KI	2	#N/A
PN2_152	KL	2	#N/A
PN2_153	KS	2	#N/A
PN2_154	KR	2	#N/A
PN2_155	KP	2	#N/A
PN2_156	KV	2	#N/A

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PN2_157	KT	2	#N/A
PN2_158	DK	2	#N/A
PN2_159	DH	2	#N/A
PN2_160	DI	2	#N/A
PN2_161	DF	2	#N/A
PN2_162	DG	2	#N/A
PN2_163	DD	2	#N/A
PN2_164	DE	2	#N/A
PN2_165	DA	2	#N/A
PN2_166	DY	2	#N/A
PN2_167	DV	2	#N/A
PN2_168	DW	2	#N/A
PN2_169	DT	2	#N/A
PN2_170	DR	2	#N/A
PN2_171	DS	2	#N/A
PN2_172	DP	2	#N/A
PN2_173	DQ	2	#N/A
PN2_174	QQ	2	#N/A
PN2_175	QP	2	#N/A
PN2_176	QS	2	#N/A
PN2_177	QR	2	#N/A
PN2_178	QT	2	#N/A
PN2_179	QW	2	#N/A
PN2_180	QA	2	#N/A
PN2_181	QE	2	#N/A
PN2_182	QD	2	#N/A
PN2_183	QG	2	#N/A
PN2_184	QF	2	#N/A
PN2_185	QL	2	#N/A
PN2_186	WG	2	#N/A
PN2_187	WF	2	#N/A
PN2_188	WE	2	#N/A

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PN2_189	WD	2	#N/A
PN2_190	WA	2	#N/A
PN2_191	WL	2	#N/A
PN2_192	WI	2	#N/A
PN2_193	WH	2	#N/A
PN2_194	WV	2	#N/A
PN2_195	WT	2	#N/A
PN2_196	WS	2	#N/A
PN2_197	WR	2	#N/A
PN2_198	WQ	2	#N/A
PN2_199	WP	2	#N/A
PN2_200	WY	2	#N/A
PN2_201	PR	2	#N/A
PN2_202	PS	2	#N/A
PN2_203	PP	2	#N/A
PN2_204	PQ	2	#N/A
PN2_205	PV	2	#N/A
PN2_206	PW	2	#N/A
PN2_207	PT	2	#N/A
PN2_208	PY	2	#N/A
PN2_209	PA	2	#N/A
PN2_210	PF	2	#N/A
PN2_211	PG	2	#N/A
PN2_212	PD	2	#N/A
PN2_213	PE	2	#N/A
PN2_214	PK	2	#N/A
PN2_215	PH	2	#N/A
PN2_216	PI	2	#N/A
PN2_217	PL	2	#N/A
PN2_218	PM	2	#N/A
PN2_219	DL	2	#N/A
PN2_220	IY	2	#N/A

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PN2_221	VA	2	#N/A
PN2_222	VD	2	#N/A
PN2_223	VE	2	#N/A
PN2_224	VF	2	#N/A
PN2_225	VG	2	#N/A
PN2_226	VH	2	#N/A
PN2_227	VI	2	#N/A
PN2_228	IS	2	#N/A
PN2_229	IR	2	#N/A
PN2_230	VL	2	#N/A
PN2_231	VM	2	#N/A
PN2_232	IW	2	#N/A
PN2_233	IV	2	#N/A
PN2_234	VP	2	#N/A
PN2_235	VQ	2	#N/A
PN2_236	IK	2	#N/A
PN2_237	VS	2	#N/A
PN2_238	IM	2	#N/A
PN2_239	IL	2	#N/A
PN2_240	VV	2	#N/A
PN2_241	VW	2	#N/A
PN2_242	IA	2	#N/A
PN2_243	VY	2	#N/A
PN2_244	IE	2	#N/A
PN2_245	ID	2	#N/A
PN2_246	IG	2	#N/A
PN2_247	IF	2	#N/A
PN2_248	TQ	2	#N/A
PN2_249	TF	2	#N/A
PN2_250	HY	2	#N/A
PN2_251	HR	2	#N/A
PN2_252	HS	2	#N/A

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PN2_253	HP	2	#N/A
PN2_254	HW	2	#N/A
PN2_255	HT	2	#N/A
PN2_256	HK	2	#N/A
PN2_257	HH	2	#N/A
PN2_258	HL	2	#N/A
PN2_259	HA	2	#N/A
PN2_260	HG	2	#N/A
PN2_261	HD	2	#N/A
PN2_262	HE	2	#N/A
PN2_263	QV	2	#N/A
PN2_264	TY	2	#N/A
PN2_265	TV	2	#N/A
PN2_266	TW	2	#N/A
PN2_267	TT	2	#N/A
PN2_268	TR	2	#N/A
PN2_269	TS	2	#N/A
PN2_270	TP	2	#N/A
PN2_271	TL	2	#N/A
PN2_272	TM	2	#N/A
PN2_273	TK	2	#N/A
PN2_274	TH	2	#N/A
PN2_275	TI	2	#N/A
PN2_276	TG	2	#N/A
PN2_277	TD	2	#N/A
PN2_278	TE	2	#N/A
PN2_279	TA	2	#N/A
PN2_280	AA	2	#N/A
PN2_281	AE	2	#N/A
PN2_282	AD	2	#N/A
PN2_283	AG	2	#N/A
PN2_284	AF	2	#N/A

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PN2_285	AI	2	#N/A
PN2_286	AH	2	#N/A
PN2_287	AK	2	#N/A
PN2_288	AM	2	#N/A
PN2_289	AL	2	#N/A
PN2_290	AQ	2	#N/A
PN2_291	AP	2	#N/A
PN2_292	AS	2	#N/A
PN2_293	AR	2	#N/A
PN2_294	AT	2	#N/A
PN2_295	AW	2	#N/A
PN2_296	AV	2	#N/A
PN2_297	AY	2	#N/A
PN2_298	AGM	3	#N/A
PN2_299	AGL	3	#N/A
PN2_300	AGH	3	#N/A
PN2_301	AGG	3	#N/A
PN2_302	AGE	3	#N/A
PN2_303	AGA	3	#N/A
PN2_304	TQG	3	#N/A
PN2_305	AGY	3	#N/A
PN2_306	AGW	3	#N/A
PN2_307	AGV	3	#N/A
PN2_308	AGS	3	#N/A
PN2_309	AGR	3	#N/A
PN2_310	SPY	3	#N/A
PN2_311	SPP	3	#N/A
PN2_312	TAG	3	#N/A
PN2_313	SPL	3	#N/A
PN2_314	TAA	3	#N/A
PN2_315	SPG	3	#N/A
PN2_316	VAA	3	#N/A

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PN2_317	VAG	3	#N/A
PN2_318	NPL	3	#N/A
PN2_319	PAA	3	#N/A
PN2_320	NPG	3	#N/A
PN2_321	LAG	3	#N/A
PN2_322	LAA	3	#N/A
PN2_323	NPY	3	#N/A
PN2_324	ALG	3	#N/A
PN2_325	RLG	3	#N/A
PN2_326	TSG	3	#N/A
PN2_327	DTA	3	#N/A
PN2_328	PAG	3	#N/A
PN2_329	QGG	3	#N/A
PN2_330	DLG	3	#N/A
PN2_331	DTQ	3	#N/A
PN2_332	LSG	3	#N/A
PN2_333	LSE	3	#N/A
PN2_334	PGR	3	#N/A
PN2_335	VLG	3	#N/A
PN2_336	LSW	3	#N/A
PN2_337	AFE	3	#N/A
PN2_338	TTG	3	#N/A
PN2_339	FTQ	3	#N/A
PN2_340	IGV	3	#N/A
PN2_341	NFE	3	#N/A
PN2_342	IGS	3	#N/A
PN2_343	IGR	3	#N/A
PN2_344	PGS	3	#N/A
PN2_345	IGG	3	#N/A
PN2_346	GRG	3	#N/A
PN2_347	IGA	3	#N/A
PN2_348	DSG	3	#N/A

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PN2_349	IGL	3	#N/A
PN2_350	HLG	3	#N/A
PN2_351	HPP	3	#N/A
PN2_352	AKQ	3	#N/A
PN2_353	GLG	3	#N/A
PN2_354	LFE	3	#N/A
PN2_355	GGV	3	#N/A
PN2_356	GGS	3	#N/A
PN2_357	GGR	3	#N/A
PN2_358	GGG	3	#N/A
PN2_359	GGA	3	#N/A
PN2_360	GGL	3	#N/A
PN2_361	YTA	3	#N/A
PN2_362	LTQ	3	#N/A
PN2_363	FQG	3	#N/A
PN2_364	LVG	3	#N/A
PN2_365	LTA	3	#N/A
PN2_366	LTG	3	#N/A
PN2_367	DPY	3	#N/A
PN2_368	DFE	3	#N/A
PN2_369	DPG	3	#N/A
PN2_370	HTA	3	#N/A
PN2_371	DPP	3	#N/A
PN2_372	PGG	3	#N/A
PN2_373	VPP	3	#N/A
PN2_374	PGA	3	#N/A
PN2_375	VPY	3	#N/A
PN2_376	PGV	3	#N/A
PN2_377	VPL	3	#N/A
PN2_378	STG	3	#N/A
PN2_379	STA	3	#N/A
PN2_380	HGV	3	#N/A

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PN2_381	HGW	3	#N/A
PN2_382	HGR	3	#N/A
PN2_383	HGL	3	#N/A
PN2_384	HGM	3	#N/A
PN2_385	STQ	3	#N/A
PN2_386	HGH	3	#N/A
PN2_387	HGG	3	#N/A
PN2_388	DSW	3	#N/A
PN2_389	HGE	3	#N/A
PN2_390	TFE	3	#N/A
PN2_391	PGY	3	#N/A
PN2_392	PGL	3	#N/A
PN2_393	PGM	3	#N/A
PN2_394	DKR	3	#N/A
PN2_395	DKQ	3	#N/A
PN2_396	VFE	3	#N/A
PN2_397	PRG	3	#N/A
PN2_398	PGH	3	#N/A
PN2_399	PPL	3	#N/A
PN2_400	EGG	3	#N/A
PN2_401	RAG	3	#N/A
PN2_402	SAA	3	#N/A
PN2_403	FGW	3	#N/A
PN2_404	SAG	3	#N/A
PN2_405	FGR	3	#N/A
PN2_406	FGH	3	#N/A
PN2_407	FGG	3	#N/A
PN2_408	TPG	3	#N/A
PN2_409	LPY	3	#N/A
PN2_410	TPL	3	#N/A
PN2_411	LPP	3	#N/A
PN2_412	LPL	3	#N/A

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PN2_413	TPP	3	#N/A
PN2_414	LPG	3	#N/A
PN2_415	HRG	3	#N/A
PN2_416	TPY	3	#N/A
PN2_417	APY	3	#N/A
PN2_418	IPG	3	#N/A
PN2_419	APP	3	#N/A
PN2_420	PQG	3	#N/A
PN2_421	IPL	3	#N/A
PN2_422	IPP	3	#N/A
PN2_423	APL	3	#N/A
PN2_424	SFE	3	#N/A
PN2_425	APG	3	#N/A
PN2_426	YSE	3	#N/A
PN2_427	IFE	3	#N/A
PN2_428	YSW	3	#N/A
PN2_429	PKR	3	#N/A
PN2_430	RTG	3	#N/A
PN2_431	PKQ	3	#N/A
PN2_432	HGY	3	#N/A
PN2_433	TKR	3	#N/A
PN2_434	NLG	3	#N/A
PN2_435	VKR	3	#N/A
PN2_436	RFE	3	#N/A
PN2_437	SSW	3	#N/A
PN2_438	NPP	3	#N/A
PN2_439	SSE	3	#N/A
PN2_440	SSG	3	#N/A
PN2_441	YGR	3	#N/A
PN2_442	ATG	3	#N/A
PN2_443	ATA	3	#N/A
PN2_444	HPL	3	#N/A

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PN2_445	ISW	3	#N/A
PN2_446	ATQ	3	#N/A
PN2_447	ISG	3	#N/A
PN2_448	ISE	3	#N/A
PN2_449	DGR	3	#N/A
PN2_450	ASW	3	#N/A
PN2_451	DGG	3	#N/A
PN2_452	DGE	3	#N/A
PN2_453	EPG	3	#N/A
PN2_454	DGH	3	#N/A
PN2_455	DGL	3	#N/A
PN2_456	DGM	3	#N/A
PN2_457	LKQ	3	#N/A
PN2_458	DGV	3	#N/A
PN2_459	DGW	3	#N/A
PN2_460	PVG	3	#N/A
PN2_461	ASG	3	#N/A
PN2_462	IRG	3	#N/A
PN2_463	VTA	3	#N/A
PN2_464	TSE	3	#N/A
PN2_465	FRG	3	#N/A
PN2_466	ASE	3	#N/A
PN2_467	VTG	3	#N/A
PN2_468	GTG	3	#N/A
PN2_469	LGW	3	#N/A
PN2_470	VTQ	3	#N/A
PN2_471	TLG	3	#N/A
PN2_472	YAA	3	#N/A
PN2_473	DGY	3	#N/A
PN2_474	ITG	3	#N/A
PN2_475	HVG	3	#N/A
PN2_476	RPP	3	#N/A

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PN2_477	AAG	3	#N/A
PN2_478	RSG	3	#N/A
PN2_479	AAA	3	#N/A
PN2_480	TGR	3	#N/A
PN2_481	TGS	3	#N/A
PN2_482	TGV	3	#N/A
PN2_483	RPY	3	#N/A
PN2_484	TGA	3	#N/A
PN2_485	TGG	3	#N/A
PN2_486	RPG	3	#N/A
PN2_487	RPL	3	#N/A
PN2_488	TGL	3	#N/A
PN2_489	FKQ	3	#N/A
PN2_490	FKR	3	#N/A
PN2_491	SLG	3	#N/A
PN2_492	LGM	3	#N/A
PN2_493	LGA	3	#N/A
PN2_494	NRG	3	#N/A
PN2_495	LGG	3	#N/A
PN2_496	LGE	3	#N/A
PN2_497	LGY	3	#N/A
PN2_498	LGR	3	#N/A
PN2_499	LGS	3	#N/A
PN2_500	LGV	3	#N/A
PN2_501	GFE	3	#N/A
PN2_502	LQG	3	#N/A
PN2_503	HSG	3	#N/A
PN2_504	HSE	3	#N/A
PN2_505	HSW	3	#N/A
PN2_506	DPL	3	#N/A
PN2_507	GPL	3	#N/A
PN2_508	HAA	3	#N/A

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PN2_509	IAG	3	#N/A
PN2_510	GPG	3	#N/A
PN2_511	IAA	3	#N/A
PN2_512	EAG	3	#N/A
PN2_513	DQG	3	#N/A
PN2_514	GPY	3	#N/A
PN2_515	GPP	3	#N/A
PN2_516	VQG	3	#N/A
PN2_517	RGR	3	#N/A
PN2_518	RGS	3	#N/A
PN2_519	SKQ	3	#N/A
PN2_520	RGV	3	#N/A
PN2_521	SKR	3	#N/A
PN2_522	RGA	3	#N/A
PN2_523	RGG	3	#N/A
PN2_524	RGL	3	#N/A
PN2_525	VGL	3	#N/A
PN2_526	VGM	3	#N/A
PN2_527	VGH	3	#N/A
PN2_528	FGY	3	#N/A
PN2_529	VGE	3	#N/A
PN2_530	VGG	3	#N/A
PN2_531	VGA	3	#N/A
PN2_532	YKR	3	#N/A
PN2_533	YKQ	3	#N/A
PN2_534	VGY	3	#N/A
PN2_535	VGV	3	#N/A
PN2_536	VGW	3	#N/A
PN2_537	VGR	3	#N/A
PN2_538	VGS	3	#N/A
PN2_539	FTA	3	#N/A
PN2_540	PSG	3	#N/A

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PN2_541	PSE	3	#N/A
PN2_542	NVG	3	#N/A
PN2_543	FGV	3	#N/A
PN2_544	FGL	3	#N/A
PN2_545	ILG	3	#N/A
PN2_546	PGW	3	#N/A
PN2_547	FSE	3	#N/A
PN2_548	DVG	3	#N/A
PN2_549	FSW	3	#N/A
PN2_550	IKR	3	#N/A
PN2_551	IKQ	3	#N/A
PN2_552	DSE	3	#N/A
PN2_553	FGM	3	#N/A
PN2_554	VRG	3	#N/A
PN2_555	NKQ	3	#N/A
PN2_556	TVG	3	#N/A
PN2_557	NQG	3	#N/A
PN2_558	SRG	3	#N/A
PN2_559	YRG	3	#N/A
PN2_560	FGE	3	#N/A
PN2_561	PLG	3	#N/A
PN2_562	PPG	3	#N/A
PN2_563	NSE	3	#N/A
PN2_564	NSG	3	#N/A
PN2_565	PPP	3	#N/A
PN2_566	GAG	3	#N/A
PN2_567	PPY	3	#N/A
PN2_568	FAA	3	#N/A
PN2_569	NSW	3	#N/A
PN2_570	HPY	3	#N/A
PN2_571	PSW	3	#N/A
PN2_572	ARG	3	#N/A

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PN2_573	SGS	3	#N/A
PN2_574	NAA	3	#N/A
PN2_575	NAG	3	#N/A
PN2_576	SGW	3	#N/A
PN2_577	GSG	3	#N/A
PN2_578	DRG	3	#N/A
PN2_579	RVG	3	#N/A
PN2_580	HKR	3	#N/A
PN2_581	HKQ	3	#N/A
PN2_582	AQG	3	#N/A
PN2_583	VPG	3	#N/A
PN2_584	AKR	3	#N/A
PN2_585	VVG	3	#N/A
PN2_586	SGL	3	#N/A
PN2_587	VKQ	3	#N/A
PN2_588	SVG	3	#N/A
PN2_589	SQG	3	#N/A
PN2_590	LKR	3	#N/A
PN2_591	PTG	3	#N/A
PN2_592	PGE	3	#N/A
PN2_593	PTA	3	#N/A
PN2_594	LLG	3	#N/A
PN2_595	PTQ	3	#N/A
PN2_596	TRG	3	#N/A
PN2_597	GVG	3	#N/A
PN2_598	IVG	3	#N/A
PN2_599	LRG	3	#N/A
PN2_600	HTQ	3	#N/A
PN2_601	AVG	3	#N/A
PN2_602	IPY	3	#N/A
PN2_603	YQG	3	#N/A
PN2_604	HFE	3	#N/A

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PN2_605	RRG	3	#N/A
PN2_606	LGH	3	#N/A
PN2_607	LGL	3	#N/A
PN2_608	TSW	3	#N/A
PN2_609	TKQ	3	#N/A
PN2_610	IQG	3	#N/A
PN2_611	HQG	3	#N/A
PN2_612	SGY	3	#N/A
PN2_613	DAG	3	#N/A
PN2_614	DAA	3	#N/A
PN2_615	SGR	3	#N/A
PN2_616	SGV	3	#N/A
PN2_617	SGH	3	#N/A
PN2_618	SGM	3	#N/A
PN2_619	SGA	3	#N/A
PN2_620	SGE	3	#N/A
PN2_621	SGG	3	#N/A
PN2_622	YTQ	3	#N/A
PN2_623	YGG	3	#N/A
PN2_624	YGE	3	#N/A
PN2_625	PFE	3	#N/A
PN2_626	VSW	3	#N/A
PN2_627	YGM	3	#N/A
PN2_628	YGL	3	#N/A
PN2_629	YGH	3	#N/A
PN2_630	YGW	3	#N/A
PN2_631	YGV	3	#N/A
PN2_632	NKR	3	#N/A
PN2_633	VSE	3	#N/A
PN2_634	KGG	3	#N/A
PN2_635	VSG	3	#N/A
PN2_636	YGY	3	#N/A

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PN2_637	RPGY	4	8409
PN2_638	SAGY	4	6277
PN2_639	PSGY	4	6268
PN2_640	RFGY	4	8410
PN2_641	RLGY	4	8411
PN2_642	PYGY	4	6281
PN2_643	GREY	4	8412
PN2_644	GRKY	4	8413
PN2_645	GHGW	4	8414
PN2_646	RVGY	4	8415
PN2_647	GLGL	4	8416
PN2_648	GHGY	4	8417
PN2_649	RDGY	4	4410
PN2_650	RRVY	4	8418
PN2_651	GLGW	4	8419
PN2_652	GHGL	4	8420
PN2_653	GLGY	4	8421
PN2_654	PVGY	4	8422
PN2_655	GPGY	4	8423
PN2_656	GPGW	4	8424
PN2_657	PDGY	4	5829
PN2_658	GPGL	4	8425
PN2_659	GVTA	4	8426
PN2_660	GRLY	4	8427
PN2_661	RRAY	4	8428
PN2_662	GHTQ	4	8429
PN2_663	GVGL	4	8430
PN2_664	SYGY	4	4434
PN2_665	RRQY	4	8431
PN2_666	GATQ	4	8432
PN2_667	PFGY	4	8433
PN2_668	GVGY	4	8434

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PN2_669	GVGW	4	8435
PN2_670	RAGY	4	6278
PN2_671	GATA	4	8436
PN2_672	RYGY	4	6262
PN2_673	GRAY	4	8437
PN2_674	GRMY	4	8438
PN2_675	GRTY	4	8439
PN2_676	PPGY	4	8440
PN2_677	RRPY	4	8441
PN2_678	RHGY	4	8442
PN2_679	GDGY	4	5813
PN2_680	SVGY	4	8443
PN2_681	GVTQ	4	8444
PN2_682	GDGW	4	8445
PN2_683	GRQY	4	8446
PN2_684	GDGL	4	8447
PN2_685	SHGY	4	8448
PN2_686	GSGY	4	6284
PN2_687	GFGY	4	8449
PN2_688	GFGW	4	8450
PN2_689	GSGW	4	8451
PN2_690	GFGL	4	8452
PN2_691	GSGL	4	8453
PN2_692	RRLY	4	8454
PN2_693	GFTA	4	8455
PN2_694	PLGY	4	8456
PN2_695	GYTQ	4	8457
PN2_696	GLTQ	4	8458
PN2_697	GHTA	4	8459
PN2_698	PHGY	4	8460
PN2_699	GFTQ	4	8461
PN2_700	GRVY	4	8462

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PN2_701	GYTA	4	8463
PN2_702	GLTA	4	8464
PN2_703	PAGY	4	6276
PN2_704	RRKY	4	8465
PN2_705	SSGY	4	4186
PN2_706	GPTQ	4	8466
PN2_707	SDGY	4	5805
PN2_708	GPTA	4	8467
PN2_709	GDTQ	4	8468
PN2_710	GAGW	4	8469
PN2_711	GAGY	4	6270
PN2_712	GDTA	4	8470
PN2_713	SFGY	4	8471
PN2_714	GAGL	4	8472
PN2_715	GSTQ	4	8473
PN2_716	GRPY	4	8474
PN2_717	SLGY	4	8475
PN2_718	GSTA	4	8476
PN2_719	GYGL	4	8477
PN2_720	RSGY	4	6269
PN2_721	RREY	4	8478
PN2_722	SPGY	4	8479
PN2_723	GYGY	4	6260
PN2_724	RRTY	4	8480
PN2_725	GYGW	4	8481
PN2_726	RRMY	4	8482

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Table 31. Theoretical segment pool of oligonucleotides encoding JH segments of Example 15.

Name	Degenerate Oligo	Peptide Length	Degenerate	SEQ ID NO
JH4_001	TGGGGACAGGGTACATTGGTCACCGTCTCCTCA	0		8483
JH1_002	CATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8484
JH1_003	ATTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8485
JH1_004	TACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8486
JH1_005	CCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8487
JH1_006	GTCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8488
JH1_007	GATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8489
JH1_008	TTCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8490
JH1_009	AATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8491
JH1_010	AGTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8492
JH1_011	ACTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8493
JH1_200	GCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	1		8494
JH4_013	GATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8495
JH4_016	GCTTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8496
JH4_017	TTCTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8497
JH4_018	GGCTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8498
JH4_019	CATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8499
JH4_023	AGTTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8500
JH4_024	GTTTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8501
JH4_025	TACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2		8502
JH4_022	CSATACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2	YES	8503
JH3_012	RACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	2	YES	8504
JH5_014	RACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2	YES	8505
JH3_015	RACGTATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	2	YES	8506
JH4_021	AMCTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2	YES	8507
JH4_020	MTATACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	2	YES	8508
JH4_029	TTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8509
JH4_030	ATTGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8510
JH4_031	GTGGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8511

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JH4_032	TTAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8512
JH4_033	TCCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8513
JH4_034	CACGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8514
JH4_035	AGAGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8515
JH4_036	CCAGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8516
JH4_037	AACGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8517
JH4_038	ACTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8518
JH4_039	GATGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8519
JH4_040	GGTGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8520
JH4_041	GCAGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8521
JH4_042	TACGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8522
JH5_043	TTCGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3		8523
JH6_044	ATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	3		8524
JH1_026	TTMCAACACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3	YES	8525
JH3_046	STAGACGTATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	3	YES	8526
JH3_028	TTMGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	3	YES	8527
JH2_027	TTMGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	3	YES	8528
JH5_045	TYAGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	3	YES	8529
JH3_049	GCCTTTGATATTTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	4		8530
JH4_051	TACTTTGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8531
JH4_052	AATTTCGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8532
JH4_053	GACTTCGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8533
JH4_054	CATTTCGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8534
JH4_055	TTCTTTGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8535
JH4_056	TCTTTTGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8536
JH4_057	AGATTCGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8537
JH4_058	TTGTTCGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8538
JH4_059	CCCTTCGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8539
JH4_060	ATTTTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8540
JH4_061	ACCTTTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8541
JH4_062	GGATTCGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8542
JH4_063	GTTTTCGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8543

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JH4_064	GCTTTTGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8544
JH5_065	TGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4		8545
JH6_068	GGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	4		8546
JH6_070	YCAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	4	YES	8547
JH6_069	KACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	4	YES	8548
JH3_198	STATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	4	YES	8549
JH2_048	KACTTCGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	4	YES	8550
JH1_047	KACTTCCAACACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4	YES	8551
JH5_067	GSATTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4	YES	8552
JH3_050	YCATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	4	YES	8553
JH5_066	AGMTTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	4	YES	8554
JH2_072	TGGTACTTCGACTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	5		8555
JH3_075	GACGCATTTGATATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8556
JH3_076	TACGCATTTGATATTTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8557
JH3_077	CACGCATTCGACATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8558
JH3_078	TTCGCATTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8559
JH3_079	TCAGCTTTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8560
JH3_080	AGAGCCTTCGATATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8561
JH3_081	TTAGCCTTCGATATCTGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8562
JH3_082	GGAGCCTTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5		8563
JH4_086	GACTATTTTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8564
JH4_087	TATTACTTTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8565
JH4_088	CACTATTTCGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8566
JH4_089	TTCTATTTTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8567
JH4_090	AGTTATTTTGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8568
JH4_091	AGATACTTTGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8569
JH4_092	TTATATTTCGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8570
JH4_093	CCCTACTTTGACTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8571
JH4_095	GGATATTTCGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8572
JH4_096	GTTTACTTTGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8573
JH4_097	GCTTACTTTGATTATTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8574
JH4_098	AACTACTTCGATTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8575

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JH5_099	AATTGGTTCGATCCTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8576
JH5_100	GATTGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8577
JH5_101	TATTGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8578
JH5_102	CACTGGTTCGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8579
JH5_103	TTCTGGTTTGACCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8580
JH5_104	TCTTGGTTTGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8581
JH5_105	AGATGGTTTGATCCTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8582
JH5_107	GGTTGGTTCGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8583
JH5_109	GCTTGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5		8584
JH6_110	TACGGTATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	5		8585
JH6_112	GATGGGATGGATGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	5		8586
JH3_084	SCAGCATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5	YES	8587
JH5_106	MCATGGTTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5	YES	8588
JH2_073	RGCTACTTCGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	5	YES	8589
JH4_094	AYATACTTCGACTACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5	YES	8590
JH5_108	RTATGGTTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5	YES	8591
JH6_113	CWCGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	5	YES	8592
JH6_114	KCAGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	5	YES	8593
JH3_083	RTAGCATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5	YES	8594
JH1_071	RAGTACTTCCAACACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	5	YES	8595
JH3_085	AMCGCATTCGACATATGGGGTCAGGGTACAATGGTCACCGTCTCCTCA	5	YES	8596
JH2_074	CKATACTTCGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	5	YES	8597
JH6_111	KACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	5	YES	8598
JH2_116	TACTGGTACTTCGATTTGTGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	6		8599
JH2_117	GATTGGTACTTCGATTTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	6		8600
JH5_120	GATAATTGGTTCGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8601
JH5_121	TATAACTGGTTCGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8602
JH5_122	CACAATTGGTTCGACCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8603
JH5_123	TTCAATTGGTTTGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8604
JH5_124	AGCAACTGGTTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8605
JH5_125	AGAAACTGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8606
JH5_126	TTAAATTGGTTCGACCCTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8607

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JH5_127	CCCAATTGGTTTGATCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8608
JH5_128	ATAAATTGGTTCGACCCTTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8609
JH5_129	ACTAACTGGTTTGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8610
JH5_130	GGTAACTGGTTTGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8611
JH5_131	GTGAACTGGTTTGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8612
JH5_132	GCCAACTGGTTCGATCCCTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8613
JH5_133	AACAATTGGTTCGACCCATGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6		8614
JH6_134	TACTACGGCATGGATGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8615
JH6_136	GATTATGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8616
JH6_137	TTCTACGGTATGGATGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8617
JH6_138	CATTACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8618
JH6_139	TTGTACGGAATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8619
JH6_140	AACTATGGCATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6		8620
JH2_118	CWCTGGTACTTCGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	6	YES	8621
JH6_141	SCATACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6	YES	8622
JH1_115	SCAGAATACTTCCAACACTGGGGACAGGGTACATTGGTCACCGTCTCCTCA	6	YES	8623
JH6_135	KACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	6	YES	8624
JH6_199	GKATACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6	YES	8625
JH6_142	AKCTACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6	YES	8626
JH2_119	ARCTGGTACTTCGACCTATGGGGGAGAGGTACCTTGGTCACCGTCTCCTCA	6	YES	8627
JH6_143	ASATACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	6	YES	8628
JH6_144	TATTACTATGGTATGGATGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	7		8629
JH6_145	TATTACTATTATATGGATGTTTGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	7		8630
JH6_146	GATTACTACGGCATGGATGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	7		8631
JH6_148	AACTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	7		8632
JH6_147	CWCTACTACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	7	YES	8633
JH6_150	RACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	7	YES	8634
JH6_149	YCATACTACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	7	YES	8635
JH6_151	TATTACTACTACGGAATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8636
JH6_152	AATTATTATTACGGCATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8637
JH6_153	GATTACTATTACGGTATGGATGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8638
JH6_154	CACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8639

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JH6_155	TTCTATTATTATGGTATGGATGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8640
JH6_156	TCTTACTACTATGGGATGGACGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8641
JH6_157	AGATATTACTACGGCATGGATGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8642
JH6_158	TTATACTACTATGGGATGGATGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8643
JH6_159	CCTTACTACTATGGCATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8644
JH6_160	ACCTATTACTATGGTATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8645
JH6_161	GGATACTACTATGGGATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8646
JH6_163	GCCTACTATTATGGCATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8		8647
JH6_164	TACTACTATTATTATATGGACGTTTGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	8		8648
JH6_165	AACTACTACTACTATATGGATGTTTGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	8		8649
JH6_166	GATTATTATTACTATATGGACGTCTGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	8		8650
JH6_162	RTATACTACTACGGAATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	8	YES	8651
JH6_168	RGCTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	8	YES	8652
JH6_167	CMCTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	8	YES	8653
JH6_169	TATTACTATTATTACGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8654
JH6_170	AATTATTATTATTATGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8655
JH6_171	GACTATTACTATTATGGAATGGATGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8656
JH6_172	CATTATTATTATTACGGAATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8657
JH6_173	TTCTATTACTATTATGGCATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8658
JH6_174	AGCTACTACTATTATGGTATGGACGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8659
JH6_175	AGATATTACTACTATGGCATGGATGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8660
JH6_176	TTATACTACTATTACGGCATGGATGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8661
JH6_177	CCCTATTATTACTACGGAATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8662
JH6_178	ATCTATTACTATTATGGCATGGATGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8663
JH6_179	ACCTATTACTACTATGGCATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8664
JH6_180	GGCTACTATTACTATGGGATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8665
JH6_181	GTCTACTATTATTATGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8666
JH6_182	GCTTACTATTACTACGGCATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	9		8667
JH6_183	GATTATTATTATTACTATGGTATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8668
JH6_184	TACTATTACTACTATTATGGCATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8669
JH6_185	CACTACTACTATTATTATGGGATGGACGTATGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8670
JH6_186	TTCTATTATTATTATTACGGAATGGACGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8671

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JH6_187	AGCTACTATTACTACTATGGGATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8672
JH6_188	AGATATTACTATTACTATGGTATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8673
JH6_189	TTGTACTATTACTATTATGGAATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8674
JH6_190	CCTTACTATTATTATTATGGGATGGATGTCTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8675
JH6_191	ATATATTACTATTACTACGGGATGGATGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8676
JH6_192	ACCTACTATTATTATTACGGGATGGACGTTTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8677
JH6_193	GGTTACTATTATTACTACGGGATGGACGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8678
JH6_194	GTGTATTACTATTACTACGGGATGGACGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8679
JH6_195	GCCTATTACTACTACTATGGGATGGATGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8680
JH6_196	AATTATTATTACTATTACGGTATGGACGTGTGGGGCCAGGGAACAACTGTCACCGTCTCCTCA	10		8681
JH6_197	KACTACTACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCACCGTCTCCTCA	10	YES	8682

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Table 32. Theoretical segment pool of unique H3-JH polypeptide segments encoded by the oligonucleotides of Table 31.

Name	Sequence	Length	SEQ ID NO
PJH4_001		0	n/a
PJH1_002	H	1	n/a
PJH1_003	I	1	n/a
PJH1_004	Y	1	n/a
PJH1_005	P	1	n/a
PJH1_006	V	1	n/a
PJH1_007	D	1	n/a
PJH1_008	F	1	n/a
PJH1_009	N	1	n/a
PJH1_010	S	1	n/a
PJH1_011	T	1	n/a
PJH1_200	A	1	n/a
PJH4_013	DY	2	n/a
PJH4_016	AY	2	n/a
PJH4_017	FY	2	n/a
PJH4_018	GY	2	n/a
PJH4_019	HY	2	n/a
PJH4_023	SY	2	n/a
PJH4_024	VY	2	n/a
PJH4_025	YY	2	n/a
PJH3_012A	NI	2	n/a
PJH3_012B	DI	2	n/a
PJH3_015A	NV	2	n/a
PJH3_015B	DV	2	n/a
PJH4_020A	LY	2	n/a
PJH4_020B	IY	2	n/a
PJH4_021A	NY	2	n/a
PJH4_021B	TY	2	n/a
PJH4_022A	PY	2	n/a

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PJH4_022B	RY	2	n/a
PJH5_014A	NP	2	n/a
PJH5_014B	DP	2	n/a
PJH4_029	FDY	3	n/a
PJH4_030	IDY	3	n/a
PJH4_031	VDY	3	n/a
PJH4_032	LDY	3	n/a
PJH4_033	SDY	3	n/a
PJH4_034	HDY	3	n/a
PJH4_035	RDY	3	n/a
PJH4_036	PDY	3	n/a
PJH4_037	NDY	3	n/a
PJH4_038	TDY	3	n/a
PJH4_039	DDY	3	n/a
PJH4_040	GDY	3	n/a
PJH4_041	ADY	3	n/a
PJH4_042	YDY	3	n/a
PJH5_043	FDP	3	n/a
PJH6_044	MDV	3	n/a
PJH1_026A	LQH	3	n/a
PJH1_026B	FQH	3	n/a
PJH2_027A	FDL	3	n/a
PJH2_027B	LDL	3	n/a
PJH3_028A	FDI	3	n/a
PJH3_028B	LDI	3	n/a
PJH3_046A	VDV	3	n/a
PJH3_046B	LDV	3	n/a
PJH5_045A	LDP	3	n/a
PJH5_045B	SDP	3	n/a
PJH3_049	AFDI	4	4539
PJH4_051	YFDY	4	4567
PJH4_052	NFDY	4	4580

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PJH4_053	DFDY	4	4581
PJH4_054	HFDY	4	4582
PJH4_055	FFDY	4	4583
PJH4_056	SFDY	4	4584
PJH4_057	RFDY	4	4585
PJH4_058	LFDY	4	4586
PJH4_059	PFDY	4	4587
PJH4_060	IFDY	4	4588
PJH4_061	TFDY	4	4589
PJH4_062	GFDY	4	4590
PJH4_063	VFDY	4	4591
PJH4_064	AFDY	4	4592
PJH5_065	WFDP	4	4596
PJH6_068	GMDV	4	4641
PJH1_047A	YFQH	4	4489
PJH1_047B	DFQH	4	4514
PJH2_048A	DFDL	4	4537
PJH2_048B	YFDL	4	4529
PJH3_050A	PFDI	4	4554
PJH3_050B	SFDI	4	4553
PJH3_198A	VFDI	4	4563
PJH3_198B	LFDI	4	4558
PJH5_066A	RFDP	4	4622
PJH5_066B	SFDP	4	4625
PJH5_067A	GFDP	4	4623
PJH5_067B	AFDP	4	4633
PJH6_069A	YMDV	4	4687
PJH6_069B	DMDV	4	8683
PJH6_070A	PMDV	4	8684
PJH6_070B	SMDV	4	8685
PJH2_072	WYFDL	5	4528
PJH3_075	DAFDI	5	4538

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PJH3_076	YAFDI	5	4540
PJH3_077	HAFDI	5	4541
PJH3_078	FAFDI	5	4542
PJH3_079	SAFDI	5	4543
PJH3_080	RAFDI	5	4544
PJH3_081	LAFDI	5	4545
PJH3_082	GAFDI	5	4549
PJH4_086	DYFDY	5	4566
PJH4_087	YYFDY	5	4568
PJH4_088	HYFDY	5	4569
PJH4_089	FYFDY	5	4570
PJH4_090	SYFDY	5	4571
PJH4_091	RYFDY	5	4572
PJH4_092	LYFDY	5	4573
PJH4_093	PYFDY	5	4574
PJH4_095	GYFDY	5	4577
PJH4_096	VYFDY	5	4578
PJH4_097	AYFDY	5	4579
PJH4_098	NYFDY	5	4593
PJH5_099	NWFDP	5	4595
PJH5_100	DWFDP	5	4609
PJH5_101	YWFDP	5	4610
PJH5_102	HWFDP	5	4611
PJH5_103	FWFDP	5	4612
PJH5_104	SWFDP	5	4613
PJH5_105	RWFDP	5	4614
PJH5_107	GWFDP	5	4619
PJH5_109	AWFDP	5	4621
PJH6_110	YGMDV	5	4640
PJH6_112	DGMDV	5	8686
PJH1_071A	EYFQH	5	4488
PJH1_071B	KYFQH	5	4502

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PJH2_073A	SYFDL	5	8687
PJH2_073B	GYFDL	5	4533
PJH2_074A	RYFDL	5	4534
PJH2_074B	LYFDL	5	8688
PJH3_083A	IAFDI	5	4547
PJH3_083B	VAFDI	5	4550
PJH3_084A	PAFDI	5	4546
PJH3_084B	AAFDI	5	4551
PJH3_085A	NAFDI	5	4565
PJH3_085B	TAFDI	5	4548
PJH4_094A	IYFDY	5	4575
PJH4_094B	TYFDY	5	4576
PJH5_106A	PWFDP	5	4616
PJH5_106B	TWFDP	5	4618
PJH5_108A	IWFDP	5	4617
PJH5_108B	VWFDP	5	4620
PJH6_111A	YYMDV	5	4686
PJH6_111B	DYMDV	5	8689
PJH6_113A	HGMDV	5	8690
PJH6_113B	LGMDV	5	8691
PJH6_114A	SGMDV	5	8692
PJH6_114B	AGMDV	5	8693
PJH2_116	YWYFDL	6	4527
PJH2_117	DWYFDL	6	4530
PJH5_120	DNWFDP	6	4594
PJH5_121	YNWFDP	6	4597
PJH5_122	HNWFDP	6	4598
PJH5_123	FNWFDP	6	4599
PJH5_124	SNWFDP	6	4600
PJH5_125	RNWFDP	6	4601
PJH5_126	LNWFDP	6	4602
PJH5_127	PNWFDP	6	4603

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PJH5_128	INWFDP	6	4604
PJH5_129	TNWFDP	6	4605
PJH5_130	GNWFDP	6	4606
PJH5_131	VNWFDP	6	4607
PJH5_132	ANWFDP	6	4608
PJH5_133	NNWFDP	6	4634
PJH6_134	YYGMDV	6	4639
PJH6_136	DYGMDV	6	8694
PJH6_137	FYGMDV	6	8695
PJH6_138	HYGMDV	6	8696
PJH6_139	LYGMDV	6	8697
PJH6_140	NYGMDV	6	8698
PJH1_115A	AEYFQH	6	4526
PJH1_115B	PEYFQH	6	4491
PJH2_118A	LWYFDL	6	8699
PJH2_118B	HWYFDL	6	4531
PJH2_119A	NWYFDL	6	4532
PJH2_119B	SWYFDL	6	8700
PJH6_135A	DYYMDV	6	8701
PJH6_135B	YYYMDV	6	4685
PJH6_141A	AYGMDV	6	8702
PJH6_141B	PYGMDV	6	8703
PJH6_142A	SYGMDV	6	8704
PJH6_142B	IYGMDV	6	8705
PJH6_143A	TYGMDV	6	8706
PJH6_143B	RYGMDV	6	8707
PJH6_199A	GYGMDV	6	8708
PJH6_199B	VYGMDV	6	8709
PJH6_144	YYYGMDV	7	4638
PJH6_145	YYYYMDV	7	4684
PJH6_146	DYYGMDV	7	8710
PJH6_148	NYYGMDV	7	8711

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PJH6_147A	LYYGMDV	7	8712
PJH6_147B	HYYGMDV	7	8713
PJH6_149A	SYYGMDV	7	8714
PJH6_149B	PYYGMDV	7	8715
PJH6_150A	NYYYMDV	7	8716
PJH6_150B	DYYYMDV	7	8717
PJH6_151	YYYYGMDV	8	4637
PJH6_152	NYYYGMDV	8	4667
PJH6_153	DYYYGMDV	8	4668
PJH6_154	HYYYGMDV	8	4669
PJH6_155	FYYYGMDV	8	4670
PJH6_156	SYYYGMDV	8	4671
PJH6_157	RYYYGMDV	8	4672
PJH6_158	LYYYGMDV	8	4673
PJH6_159	PYYYGMDV	8	4674
PJH6_160	TYYYGMDV	8	4676
PJH6_161	GYYYGMDV	8	4677
PJH6_163	AYYYGMDV	8	4679
PJH6_164	YYYYYMDV	8	4683
PJH6_165	NYYYYMDV	8	4713
PJH6_166	DYYYYMDV	8	4714
PJH6_162A	VYYYGMDV	8	4678
PJH6_162B	IYYYGMDV	8	4675
PJH6_167A	HYYYYMDV	8	4715
PJH6_167B	PYYYYMDV	8	4720
PJH6_168A	SYYYYMDV	8	4717
PJH6_168B	GYYYYMDV	8	4723
PJH6_169	YYYYYGMDV	9	4636
PJH6_170	NYYYYGMDV	9	4654
PJH6_171	DYYYYGMDV	9	4655
PJH6_172	HYYYYGMDV	9	4656
PJH6_173	FYYYYGMDV	9	4657

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PJH6_174	SYYYYGMDV	9	4658
PJH6_175	RYYYYGMDV	9	4659
PJH6_176	LYYYYGMDV	9	4660
PJH6_177	PYYYYGMDV	9	4661
PJH6_178	IYYYYGMDV	9	4662
PJH6_179	TYYYYGMDV	9	4663
PJH6_180	GYYYYGMDV	9	4664
PJH6_181	VYYYYGMDV	9	4665
PJH6_182	AYYYYGMDV	9	4666
PJH6_183	DYYYYYGMDV	10	4635
PJH6_184	YYYYYYGMDV	10	4642
PJH6_185	HYYYYYGMDV	10	4643
PJH6_186	FYYYYYGMDV	10	4644
PJH6_187	SYYYYYGMDV	10	4645
PJH6_188	RYYYYYGMDV	10	4646
PJH6_189	LYYYYYGMDV	10	4647
PJH6_190	PYYYYYGMDV	10	4648
PJH6_191	IYYYYYGMDV	10	4649
PJH6_192	TYYYYYGMDV	10	4650
PJH6_193	GYYYYYGMDV	10	4651
PJH6_194	VYYYYYGMDV	10	4652
PJH6_195	AYYYYYGMDV	10	4653
PJH6_196	NYYYYYGMDV	10	4680
PJH6_197A	DYYYYYYMDV	10	4681
PJH6_197B	YYYYYYYMDV	10	4688

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

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APPENDIX A

GI NUMBERS OF 3,571 SEQUENCES IN THE HEALTHY PREIMMUNE SET (HPS)

Date Reçue/Date Received 2020-07-15

33628
37745
37747
37749
37751
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264183
297147
306949
306951
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483348
483350
510999
547164
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587254
587266
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What is claimed:

1. A library of synthetic polynucleotides encoding light chain variable regions, wherein the light chain variable regions are selected from the group consisting of:

    (a) a VK1-05 sequence varied at one or more of positions 4, 49, and 46;

    (b) a VK1-12 sequence varied at one or more of positions 4, 49, 46, and 66;

    (c) a VK1-33 sequence varied at one or more of positions 4, 49, and 66;

    (d) a VK1-39 sequence varied at one or more of positions 4, 49, and 46;

    (e) a VK2-28 sequence varied at one or more of positions 2, 4, 46, and 49;

    (f) a VK3-11 sequence varied at one or more of positions 2, 4, 36, and 49;

    (g) a VK3-15 sequence varied at one or more of positions 2, 4, 48, and 49;

    (h) a VK3-20 sequence varied at one or more of positions 2, 4, 48, and 49; and

    (i) a VK4-1 sequence varied at one or more of positions 4, 46, 49, and 66.

2. The library of claim 1, wherein the library comprises polynucleotides encoding light chain variable regions that comprise polypeptide sequences at least 80%, 90%, or 95% identical to two or more of the light chain polypeptide sequences provided in Table 3.

3. The library of claim 1, wherein the light chain variable regions comprise the polypeptide sequences provided in Table 3.

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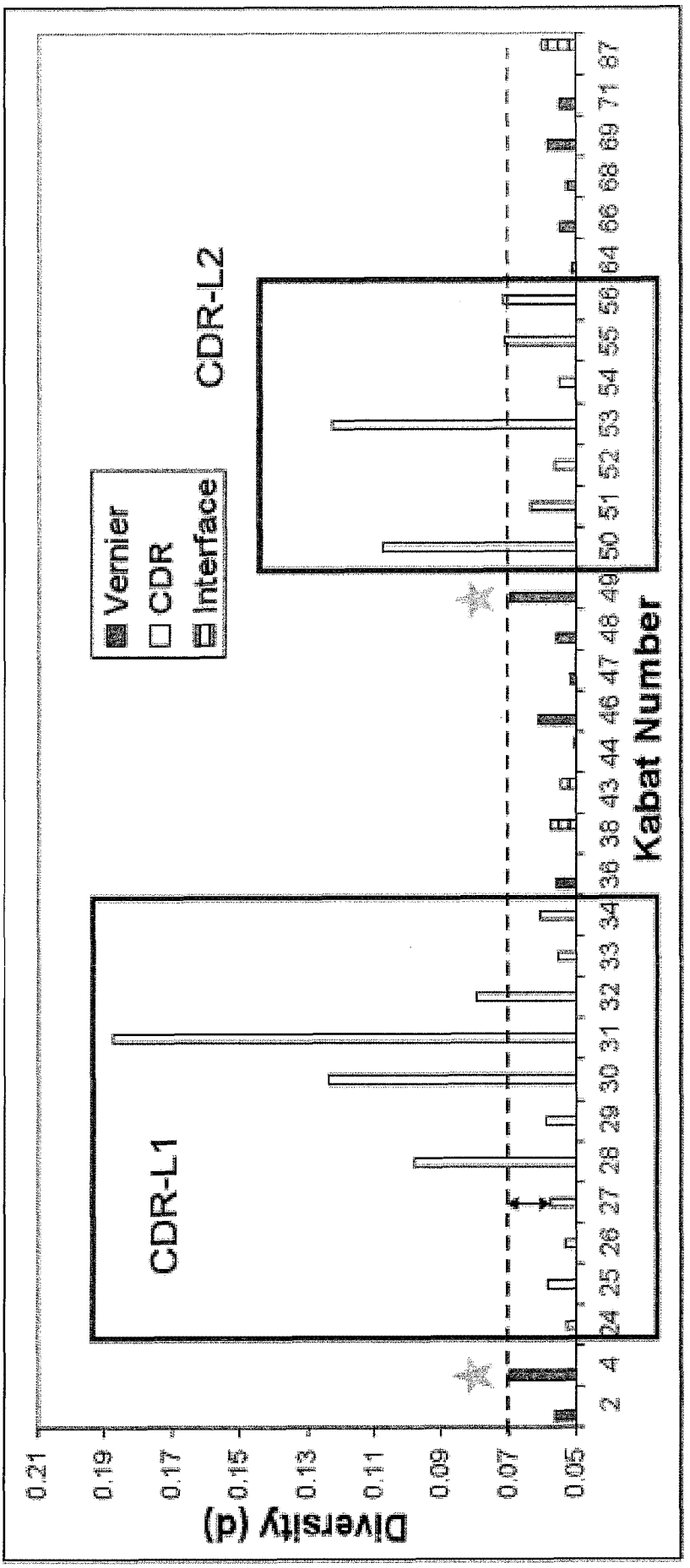
FIGURE 1



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Date Reçue/Date Received 2020-07-15

FIGURE 2

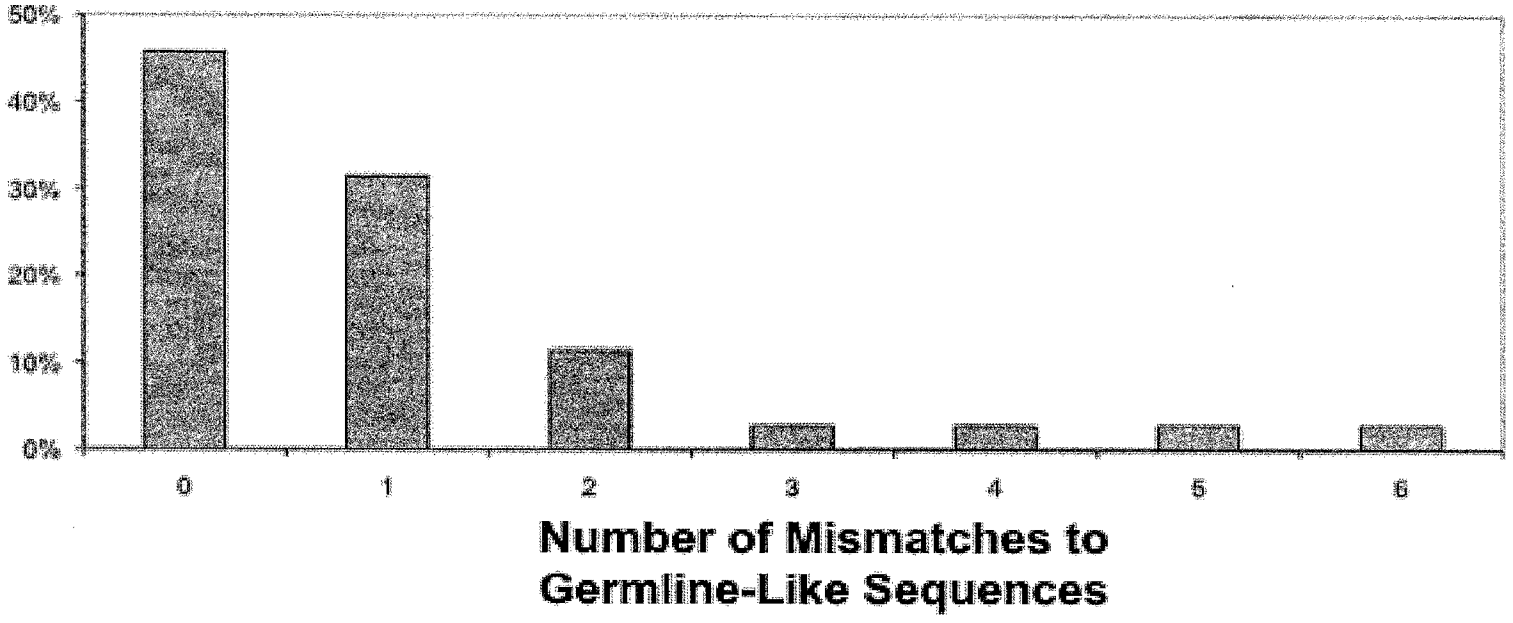

FIGURE 3

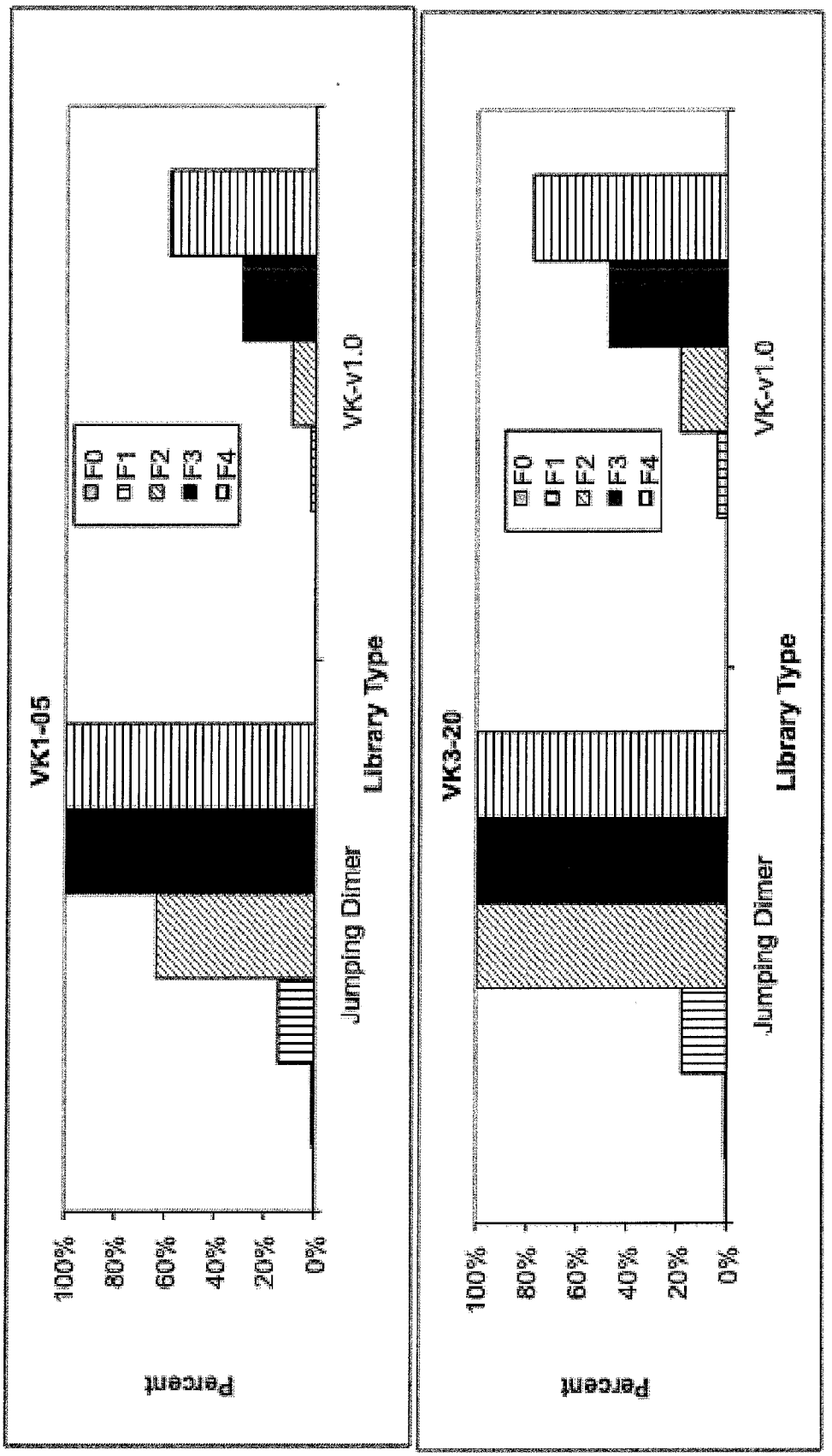
VK1-05
VK3-20
F0
F1
F2
F3
F4
100%
80%
60%
40%
20%
0%
Percent
Jumping Dimer
VK-v1.0
Library Type

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FIGURE 4

IGHJ3-02	-	**AT**GCTTTTGATATCT...TCTTCAG
IGHJ3-02-1	Mutate 5' doublet	**NN**TGCTTTTGATATCT...TCTTCAG
IGHJ3-02-2	Delete 5' codon	GCTTTTGATATCT...TCTTCAG
IGHJ3-02-3	Mutate 5' doublet	**NN**TTTTGATATCT...TCTTCAG
IGHJ3-02-4	Delete 5' codon	TTTGATATCT...TCTTCAG
IGHJ3-02-5	Mutate 5' doublet	**NN**TGATATCT...TCTTCAG

IGHJ1-01	-	GCTGAATACTTCCAG...TCCTCAG
IGHJ1-01-1	Mutate 5' doublet	**NN**TGAATACTTCCAG...TCCTCAG
IGHJ1-01-2	Delete 5' codon	GAATACTTCCAG...TCCTCAG
IGHJ1-01-3	Mutate 5' doublet	**NN**ATACTTCCAG...TCCTCAG
IGHJ1-01-4	Delete 5' codon	TACTTCCAG...TCCTCAG
IGHJ1-01-5	Mutate 5' doublet	**NN**CTTCCAG...TCCTCAG

IGHJ2-01	-	**C**TACTGGTACTTCGA...TCCTCAG
IGHJ2-01-1	Mutate 5' doublet	**NN**ACTGGTACTTCGA...TCCTCAG
IGHJ2-01-2	Delete 5' codon	CTGGTACTTCGA...TCCTCAG
IGHJ2-01-3	Mutate 5' doublet	**NN**GGTACTTCGA...TCCTCAG
IGHJ2-01-4	Delete 5' codon	GTACTTCGA...TCCTCAG
IGHJ2-01-5	Mutate 5' doublet	**NN**ACTTCGA...TCCTCAG

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FIGURE 5

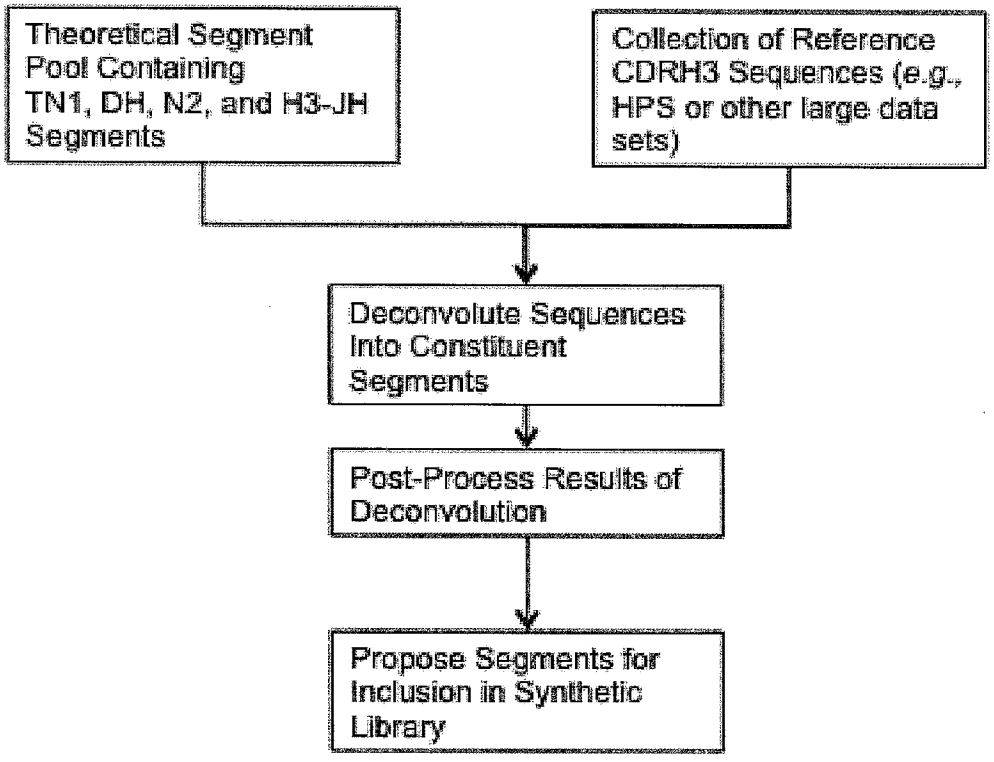

FIGURE 6

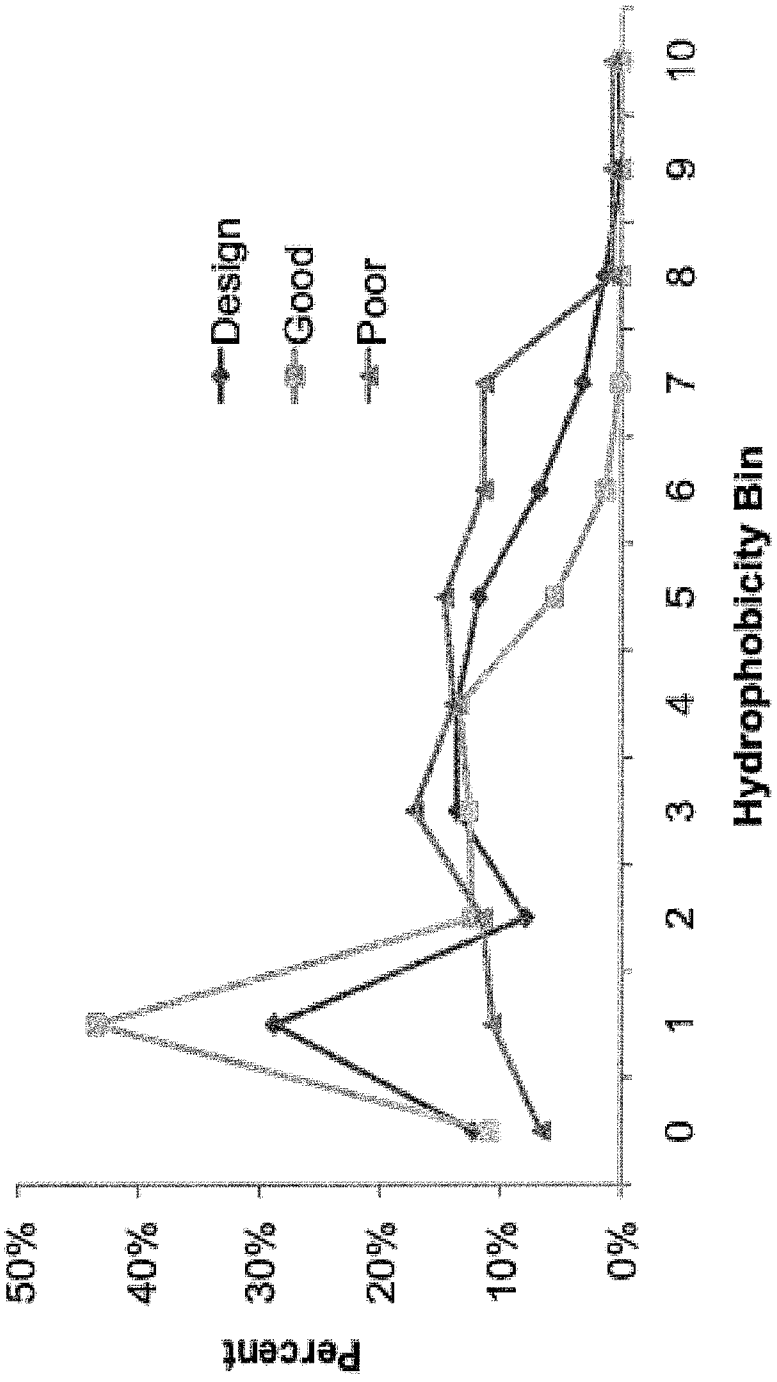

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FIGURE 7

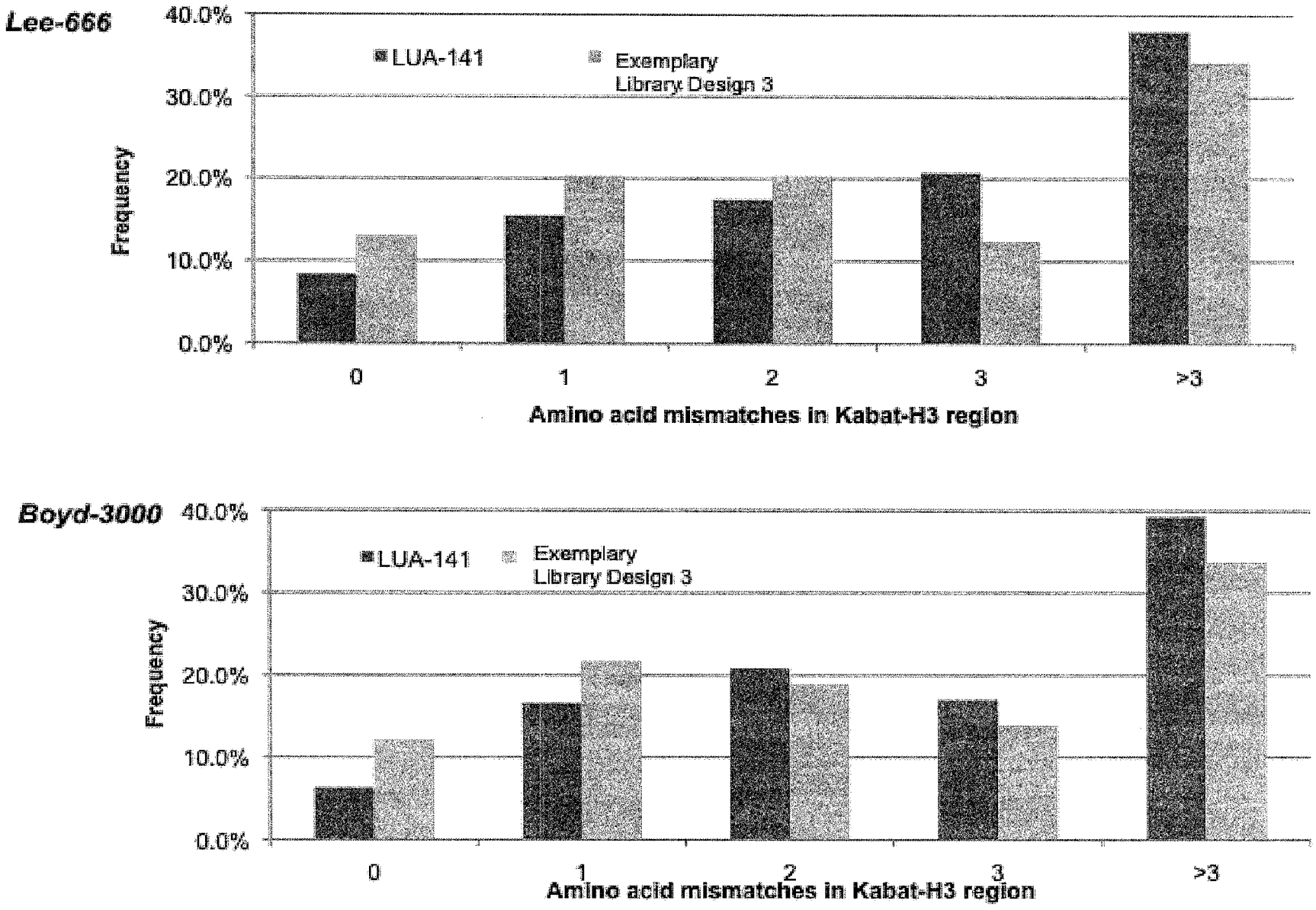

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FIGURE 8

Based on a set of CDRH3 sequences derived from 55 clinically relevant human mAbs

Amino acid mismatches in Kabat-H3 region	LUA-141	Exemplary Library Design 3 (EDLD-3)	Extended Diversity Library Design (EDLD)
0	4	7	25
1	16	27	15
2	19	5	9
3-or-more	16	16	6
Total	55	55	55

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FIGURE 9

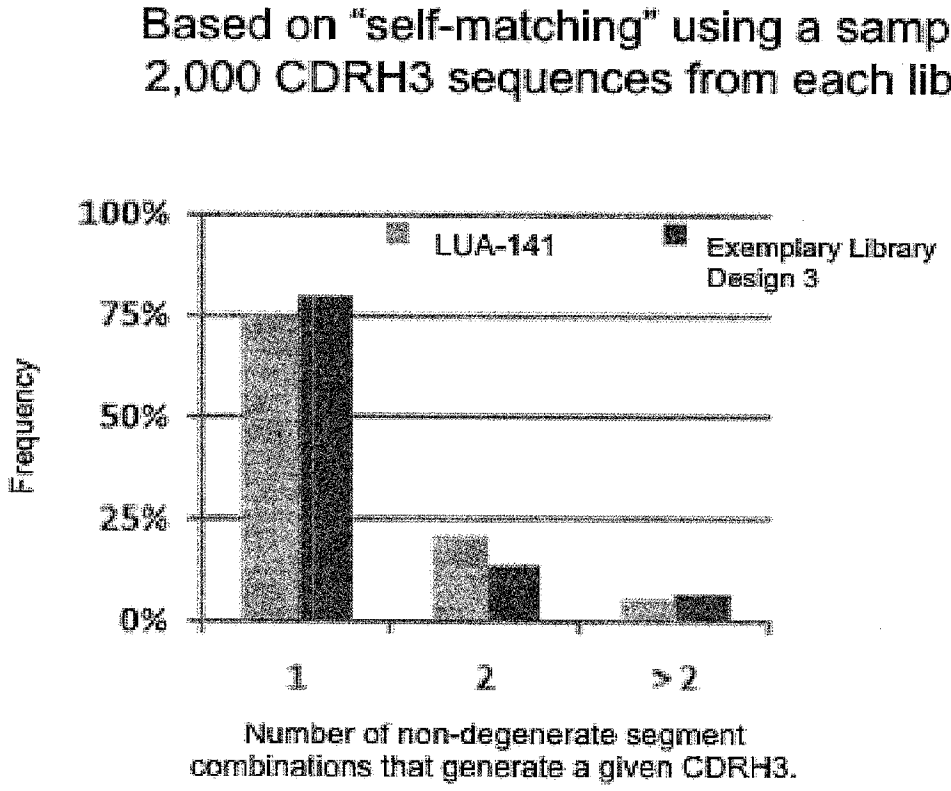

FIGURE 10

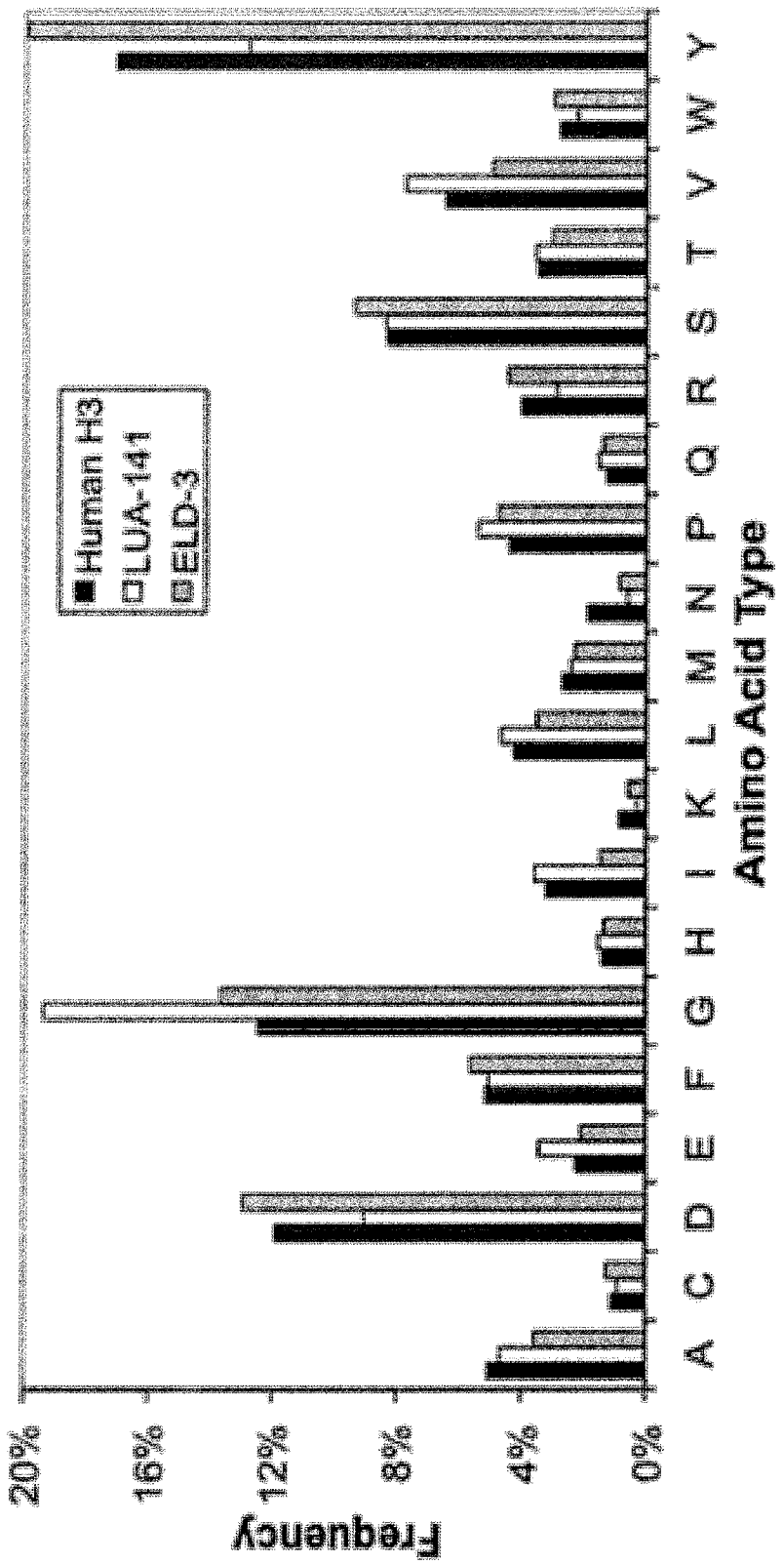
Human H3
LUA-141
ELD-3
Frequency
20%
16%
12%
8%
4%
0%
A C D E F G H I K L M N P Q R S T V W Y
Amino Acid Type

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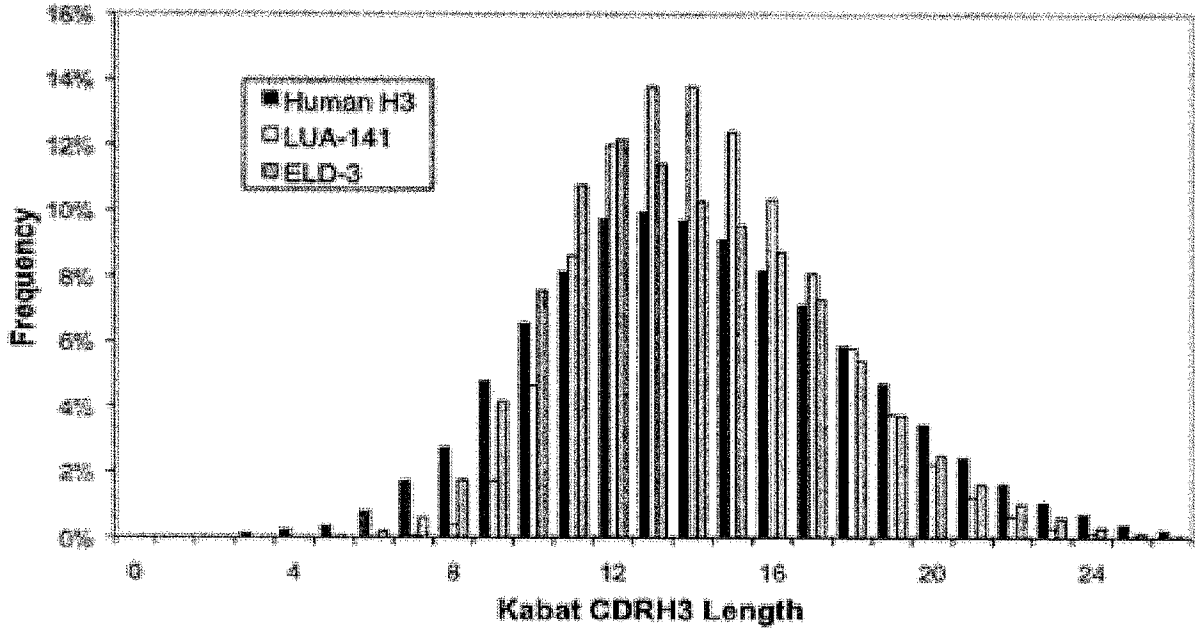
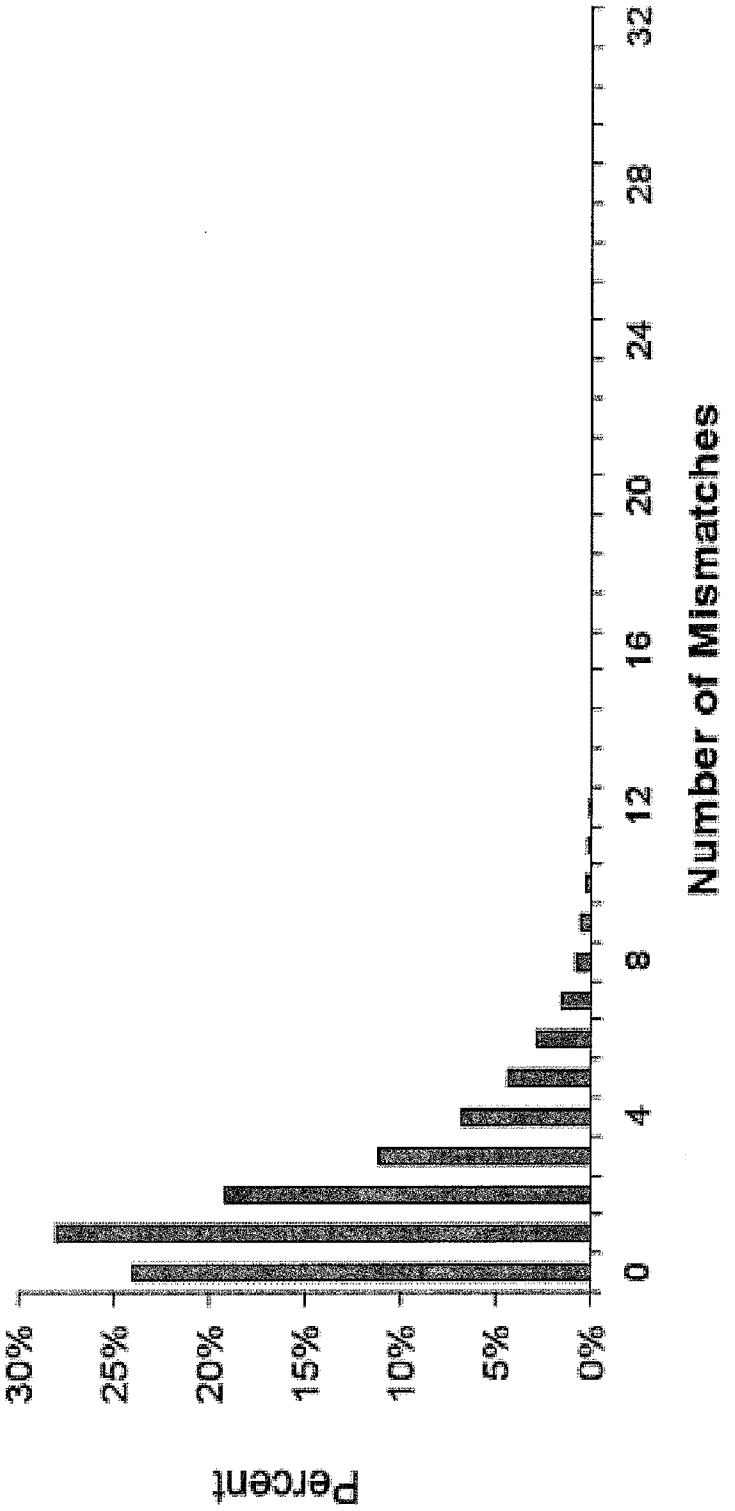
FIGURE 11



Library	LUA-141	Exemplary Library Design 3	Human H3
Average	14.37	13.94	13.99
Stdev	2.82	3.35	3.55
Shortest	5	2	2
Longest	26	28	35

FIGURE 12



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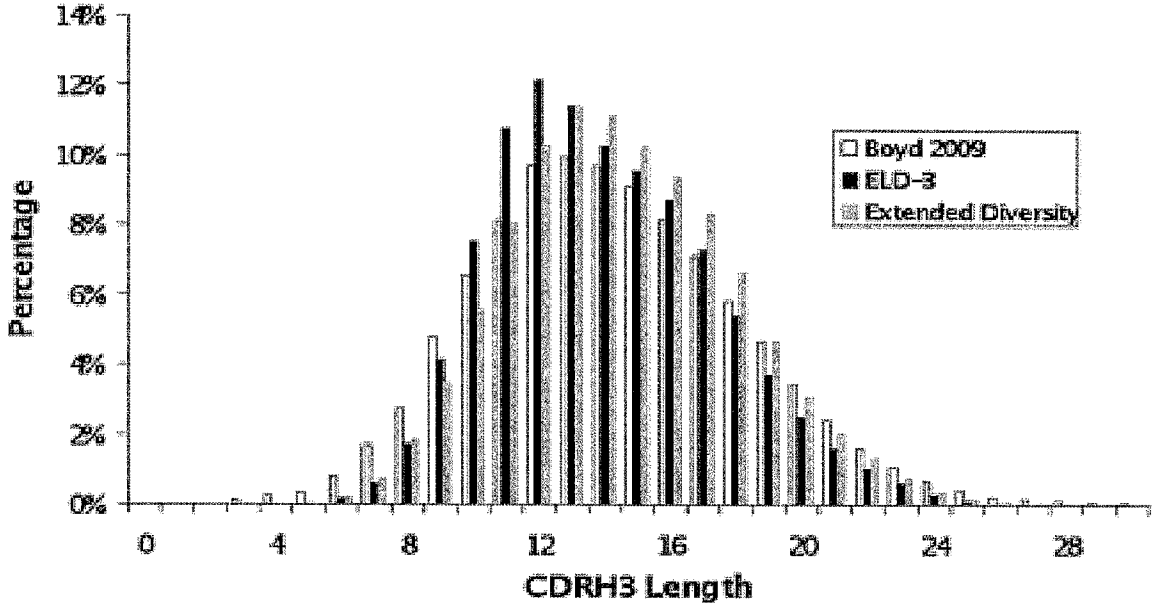
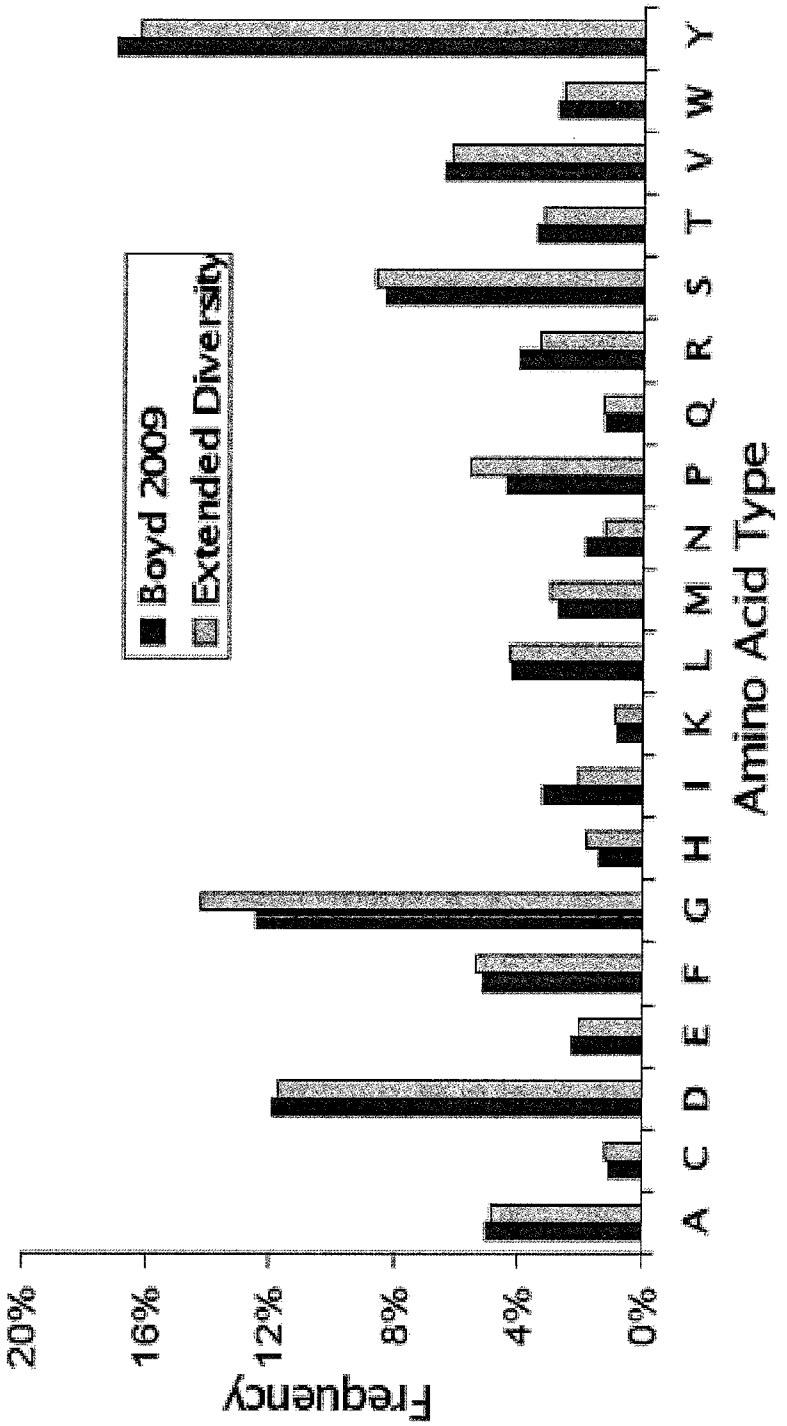
Date Reçue/Date Received 2020-07-15

FIGURE 13



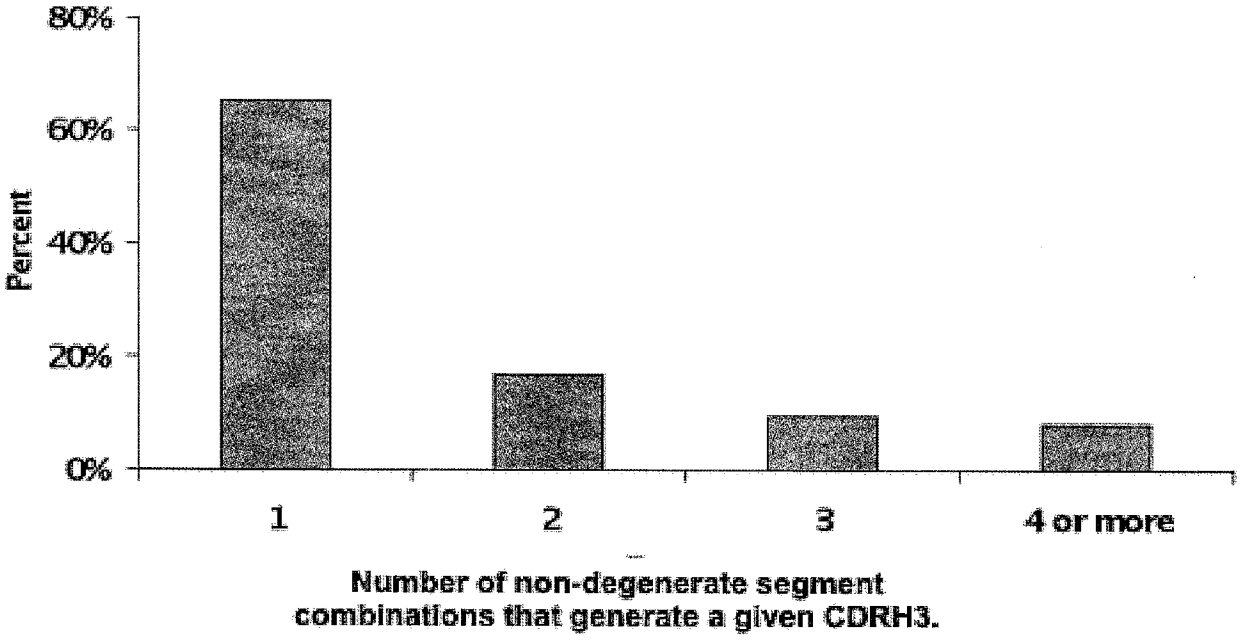
Set:	Boyd	ELD-3	Extended Diversity
r2-to-Boyd	1.00	0.986	0.990
Mean	14.27	13.99	14.47
Standard Deviation	4.02	3.35	3.47
Shortest	1	2	2
Longest	39	28	30

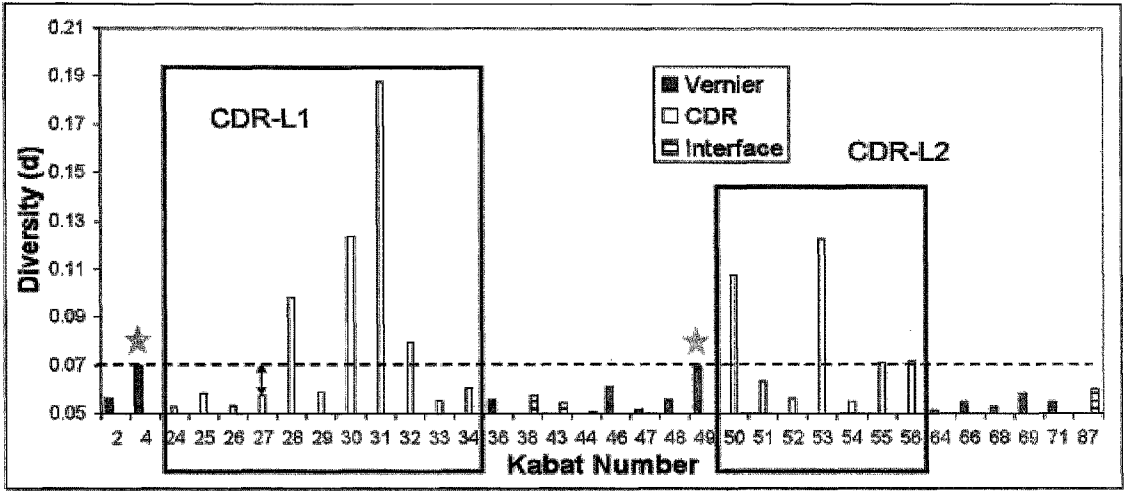
FIGURE 14


Boyd 2009
Extended Diversity
Frequency
20%
16%
12%
8%
4%
0%
A C D E F G H I K L M N P Q R S T V W Y
Amino Acid Type

Date Reçue/Date Received 2020-07-15

FIGURE 15




0.21
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0.11
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0.05
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CDR-L1
CDR-L2
Vernier
CDR
Interface
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Kabat Number