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(54) **METHOD OF MEASURING ADAPTIVE IMMUNITY**

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(57) **ABSTRACT**

A method of measuring immunocompetence is described. This method provides a means for assessing the effects of diseases or conditions that compromise the immune system and of therapies aimed to reconstitute it. This method is based on quantifying T-cell diversity by calculating the number of diverse T-cell receptor (TCR) beta chain variable regions from blood cells.

METHOD OF MEASURING ADAPTIVE IMMUNITY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. application Ser. No. 12/794,507, filed on Jun. 4, 2010, which claims the benefit of U.S. Provisional Application No. 61/220,344, filed on Jun. 25, 2009 and is hereby incorporated by reference in its entirety.

TECHNICAL FIELD

[0002] What is described is a method to measure the adaptive immunity of a patient by analyzing the diversity of T cell receptor genes or antibody genes using large scale sequencing of nucleic acid extracted from adaptive immune system cells.

BACKGROUND

[0003] Immunocompetence is the ability of the body to produce a normal immune response (i.e., antibody production and/or cell-mediated immunity) following exposure to a pathogen, which might be a live organism (such as a bacterium or fungus), a virus, or specific antigenic components isolated from a pathogen and introduced in a vaccine. Immunocompetence is the opposite of immunodeficiency or immuno-incompetent or immunocompromised. Several examples would be a newborn that does not yet have a fully functioning immune system but may have maternally transmitted antibody (immunodeficient); a late stage AIDS patient with a failed or failing immune system (immuno-incompetent); a transplant recipient taking medication so their body will not reject the donated organ (immunocompromised); age-related attenuation of T cell function in the elderly; or individuals exposed to radiation or chemotherapeutic drugs. There may be cases of overlap but these terms are all indicators of a dysfunctional immune system. In reference to lymphocytes, immunocompetence means that a B cell or T cell is mature and can recognize antigens and allow a person to mount an immune response.

[0004] Immunocompetence depends on the ability of the adaptive immune system to mount an immune response specific for any potential foreign antigens, using the highly polymorphic receptors encoded by B cells (immunoglobulins, Igs) and T cells (T cell receptors, TCRs).

[0005] Igs expressed by B cells are proteins consisting of four polypeptide chains, two heavy chains (H chains) and two light chains (L chains), forming an H_2L_2 structure. Each pair of H and L chains contains a hypervariable domain, consisting of a V_L and a V_H region, and a constant domain. The H chains of Igs are of several types, μ, δ, γ, α, and β. The diversity of Igs within an individual is mainly determined by the hypervariable domain. The V domain of H chains is created by the combinatorial joining of three types of germline gene segments, the V_H, D_H, and J_H segments. Hypervariable domain sequence diversity is further increased by independent addition and deletion of nucleotides at the V_H-D_H, D_H-J_H, and V_H-J_H junctions during the process of Ig gene rearrangement. In this respect, immunocompetence is reflected in the diversity of Igs.

[0006] TCRs expressed by αβ T cells are proteins consisting of two transmembrane polypeptide chains (α and β), expressed from the TCRA and TCRB genes, respectively. Similar TCR proteins are expressed in gamma-delta T cells, from the TCRD and TCRG loci. Each TCR peptide contains variable complementarity determining regions (CDRs), as well as framework regions (FRs) and a constant region. The sequence diversity of αβ T cells is largely determined by the amino acid sequence of the third complementarity-determining region (CDR3) loops of the α and β chain variable domains, which diversity is a result of recombination between variable (V_β), diversity (D_β), and joining (J_β) gene segments in the β chain locus, and between analogous V_α and J_α gene segments in the α chain locus, respectively. The existence of multiple such gene segments in the TCR α and β chain loci allows for a large number of distinct CDR3 sequences to be encoded. CDR3 sequence diversity is further increased by independent addition and deletion of nucleotides at the V_β-D_β, D_β-J_β, and V_α-J_α junctions during the process of TCR gene rearrangement. In this respect, immunocompetence is reflected in the diversity of TCRs.

[0007] There exists a long-felt need for methods of assessing or measuring the adaptive immune system of patients in a variety of settings, whether immunocompetence in the immunocompromised, or dysregulated adaptive immunity in autoimmune disease. A demand exists for methods of diagnosing a disease state or the effects of aging by assessing the immunocompetence of a patient. In the same way results of therapies that modify the immune system need to be monitored by assessing the immunocompetence of the patient while undergoing the treatment. Conversely, a demand exists for methods to monitor the adaptive immune system in the context of autoimmune disease flares and remissions, in order to monitor response to therapy, or the need to initiate prophylactic therapy pre-symptomatically.

SUMMARY

[0008] One aspect of the invention is composition comprising:

[0009] a multiplicity of V-segment primers, wherein each primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0010] a multiplicity of J-segment primers, wherein each primer comprises a sequence that is complementary to a J segment;

wherein the V segment and J-segment primers permit amplification of a TCR CDR3 region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules sufficient to quantify the diversity of the TCR genes. One embodiment of the invention is the composition, wherein each V-segment primer comprises a sequence that is complementary to a single Vβ segment, and each J segment primer comprises a sequence that is complementary to a Jβ segment, and wherein V segment and J-segment primers permit amplification of a TCRβ CDR3 region. Another embodiment is the composition, wherein each V-segment primer comprises a sequence that is complementary to a single functional Vα segment, and each J segment primer comprises a sequence that is complementary to a Jα segment, and wherein V segment and J-segment primers permit amplification of a TCRα CDR3 region.

[0011] Another embodiment of the invention is the composition, wherein the V segment primers hybridize with a conserved segment, and have similar annealing strength. Another embodiment is wherein the V segment primer is anchored at position −43 in the Vβ segment relative to the recombination signal sequence (RSS). Another embodiment is wherein the multiplicity of V segment primers consist of at least 45 primers specific to 45 different Vβ genes. Another embodiment is wherein the V segment primers have sequences that are selected from the group consisting of SEQ ID NOS:1-45. Another embodiment is wherein the V segment primers have sequences that are selected from the group consisting of SEQ ID NOS:58-102. Another embodiment is wherein there is a V segment primer for each Vβ segment.

[0012] Another embodiment of the invention is the composition, wherein the J segment primers hybridize with a conserved framework region element of the Jβ segment, and have similar annealing strength. The composition of claim **2**, wherein the multiplicity of J segment primers consist of at least thirteen primers specific to thirteen different Jβ genes. Another embodiment is The composition of claim **2**, wherein the J segment primers have sequences that are selected from the group consisting of SEQ ID NOS:46-57. Another embodiment is wherein the J segment primers have sequences that are selected from the group consisting of SEQ ID NOS:102-113. Another embodiment is wherein there is a J segment primer for each Jβ segment. Another embodiment is wherein all J segment primers anneal to the same conserved motif.

[0013] Another embodiment of the invention is the composition, wherein the amplified DNA molecule starts from said conserved motif and amplifies adequate sequence to diagnostically identify the J segment and includes the CDR3 junction and extends into the V segment. Another embodiment is wherein the amplified Jβ gene segments each have a unique four base tag at positions +11 through +14 downstream of the RSS site.

[0014] Another aspect of the invention is the composition further comprising a set of sequencing oligonucleotides, wherein the sequencing oligonucleotides hybridize to a regions within the amplified DNA molecules. An embodiment is wherein the sequencing oligonucleotides hybridize adjacent to a four base tag within the amplified Jβ gene segments at positions +11 through +14 downstream of the RSS site. Another embodiment is wherein the sequencing oligonucleotides are selected from the group consisting of SEQ ID NOS:58-70. Another embodiment is wherein the V-segment or J-segment are selected to contain a sequence error-correction by merger of closely related sequences. Another embodiment is the composition, further comprising a universal C segment primer for generating cDNA from mRNA.

[0015] Another aspect of the invention is a composition comprising:

[0016] a multiplicity of V segment primers, wherein each V segment primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0017] a multiplicity of J segment primers, wherein each J segment primer comprises a sequence that is complementary to a J segment;

[0018] wherein the V segment and J segment primers permit amplification of the TCRG CDR3 region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules sufficient to quantify the diversity of antibody heavy chain genes.

[0019] Another aspect of the invention is a composition comprising:

[0020] a multiplicity of V segment primers, wherein each V segment primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0021] a multiplicity of J segment primers, wherein each J segment primer comprises a sequence that is complementary to a J segment;

[0022] wherein the V segment and J segment primers permit amplification of antibody heavy chain (IGH) CDR3 region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules sufficient to quantify the diversity of antibody heavy chain genes.

[0023] Another aspect of the invention is a composition comprising:

[0024] a multiplicity of V segment primers, wherein each V segment primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0025] a multiplicity of J segment primers, wherein each J segment primer comprises a sequence that is complementary to a J segment;

[0026] wherein the V segment and J segment primers permit amplification of antibody light chain (IGL) V_L region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules sufficient to quantify the diversity of antibody light chain genes.

[0027] Another aspect of the invention is a method comprising:

[0028] selecting a multiplicity of V segment primers, wherein each V segment primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0029] selecting a multiplicity of J segment primers, wherein each J segment primer comprises a sequence that is complementary to a J segment;

[0030] combining the V segment and J segment primers with a sample of genomic DNA to permit amplification of a CDR3 region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules sufficient to quantify the diversity of the TCR genes.

[0031] One embodiment of the invention is the method wherein each V segment primer comprises a sequence that is complementary to a single functional Vβ segment, and each J segment primer comprises a sequence that is complementary to a Jβ segment; and wherein combining the V segment and J segment primers with a sample of genomic DNA permits amplification of a TCR CDR3 region by a multiplex polymerase chain reaction (PCR) and produces a multiplicity of amplified DNA molecules. Another embodiment is wherein each V segment primer comprises a sequence that is complementary to a single functional Vα segment, and each J segment primer comprises a sequence that is complementary to a Jα segment; and wherein combining the V segment and J segment primers with a sample of genomic DNA permits amplification of a TCR CDR3 region by a multiplex polymerase chain reaction (PCR) and produces a multiplicity of amplified DNA molecules.

[0032] Another embodiment of the invention is the method further comprising a step of sequencing the amplified DNA molecules. Another embodiment is wherein the sequencing step utilizes a set of sequencing oligonucleotides, that hybridize to regions within the amplified DNA molecules. Another embodiment is the method, further comprising a step of calculating the total diversity of TCRβ CDR3 sequences among the amplified DNA molecules. Another embodiment is wherein the method shows that the total diversity of a normal human subject is greater than $1*10^6$ sequences, greater than $2*10^6$ sequences, or greater than $3*10^6$ sequences.

[0033] Another aspect of the invention is a method of diagnosing immunodeficiency in a human patient, comprising measuring the diversity of TCR CDR3 sequences of the patient, and comparing the diversity of the subject to the diversity obtained from a normal subject. An embodiment of the invention is the method, wherein measuring the diversity of TCR sequences comprises the steps of:

[0034] selecting a multiplicity of V segment primers, wherein each V segment primer comprises a sequence that is complementary to a single functional V segment or a small family of V segments; and

[0035] selecting a multiplicity of J segment primers, wherein each J segment primer comprises a sequence that is complementary to a J segment;

[0036] combining the V segment and J segment primers with a sample of genomic DNA to permit amplification of a TCR CDR3 region by a multiplex polymerase chain reaction (PCR) to produce a multiplicity of amplified DNA molecules;

[0037] sequencing the amplified DNA molecules;

[0038] calculating the total diversity of TCR CDR3 sequences among the amplified DNA molecules.

[0039] An embodiment of the invention is the method, wherein comparing the diversity is determined by calculating using the following equation:

$$\begin{aligned}\Delta(t) &= \sum_x E(n_x)_{measurement1+2} - \sum_x E(n_x)_{measurement2} \\ &= S\int_0^\infty e^{-\lambda}(1-e^{-\lambda t})\,dG(\lambda)\end{aligned}$$

wherein $G(\lambda)$ is the empirical distribution function of the parameters $\lambda_1, \ldots, \lambda_S$, n_x is the number of clonotypes sequenced exactly x times, and

$$E(n_x) = S\int_0^\infty \left(\frac{e^{-\lambda}\lambda^x}{x!}\right)dG(\lambda).$$

[0040] Another embodiment of the invention is the method, wherein the diversity of at least two samples of genomic DNA are compared. Another embodiment is wherein one sample of genomic DNA is from a patient and the other sample is from a normal subject. Another embodiment is wherein one sample of genomic DNA is from a patient before a therapeutic treatment and the other sample is from the patient after treatment. Another embodiment is wherein the two samples of genomic DNA are from the same patient at different times during treatment. Another embodiment is wherein a disease is diagnosed based on the comparison of diversity among the samples of genomic DNA. Another embodiment is wherein the immunocompetence of a human patient is assessed by the comparison.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0041] The TCR and Ig genes can generate millions of distinct proteins via somatic mutation. Because of this diversity-generating mechanism, the hypervariable complementarity determining regions of these genes can encode sequences that can interact with millions of ligands, and these regions are linked to a constant region that can transmit a signal to the cell indicating binding of the protein's cognate ligand.

[0042] The adaptive immune system employs several strategies to generate a repertoire of T- and B-cell antigen receptors with sufficient diversity to recognize the universe of potential pathogens. In αβ and γδ T cells, which primarily recognize peptide antigens presented by MHC molecules, most of this receptor diversity is contained within the third complementarity-determining region (CDR3) of the T cell receptor (TCR) α and β chains (or γ and δ chains). Although it has been estimated that the adaptive immune system can generate up to 10^{18} distinct TCR αβ pairs, direct experimental assessment of TCR CDR3 diversity has not been possible.

[0043] What is described herein is a novel method of measuring TCR CDR3 diversity that is based on single molecule DNA sequencing, and use this approach to sequence the CDR3 regions in millions of rearranged TCRβ genes isolated from peripheral blood T cells of two healthy adults.

[0044] The ability of the adaptive immune system to mount an immune response specific for any of the vast number of potential foreign antigens to which an individual might be exposed relies on the highly polymorphic receptors encoded by B cells (immunoglobulins) and T cells (T cell receptors; TCRs). The TCRs expressed by αβ T cells, which primarily recognize peptide antigens presented by major histocompatibility complex (MHC) class I and II molecules, are heterodimeric proteins consisting of two transmembrane polypeptide chains (α and β), each containing one variable and one constant domain. The peptide specificity of αβ T cells is in large part determined by the amino acid sequence encoded in the third complementarity-determining region (CDR3) loops of the α and β chain variable domains. The CDR3 regions of the β and α chains are formed by recombination between noncontiguous variable (V_β), diversity (D_β), and joining (J_β) gene segments in the β chain locus, and between analogous V_α and J_α gene segments in the α chain locus, respectively. The existence of multiple such gene segments in the TCR α and β chain loci allows for a large number of distinct CDR3 sequences to be encoded. CDR3 sequence diversity is further increased by template-independent addition and deletion of nucleotides at the V_β-D_β, D_β-J_β, and V_α-J_α junctions during the process of TCR gene rearrangement.

[0045] Previous attempts to assess the diversity of receptors in the adult human αβ T cell repertoire relied on examining rearranged TCR α and β chain genes expressed in small, well-defined subsets of the repertoire, followed by extrapolation of the diversity present in these subsets to the entire repertoire, to estimate approximately 10^6 unique TCRβ chain CDR3 sequences per individual, with 10-20% of these unique TCRβ CDR3 sequences expressed by cells in the antigen-experienced $CD45RO^+$ compartment. The accuracy and precision of this estimate is severely limited by the need to extrapolate the diversity observed in hundreds of sequences to the entire repertoire, and it is possible that the actual number of unique TCRβ chain CDR3 sequences in the αβ T cell repertoire is significantly larger than 1×10^6.

[0046] Recent advances in high-throughput DNA sequencing technology have made possible significantly deeper sequencing than capillary-based technologies. A complex library of template molecules carrying universal PCR adapter sequences at each end is hybridized to a lawn of complementary oligonucleotides immobilized on a solid surface. Solid phase PCR is utilized to amplify the hybridized library, resulting in millions of template clusters on the surface, each comprising multiple (1,000) identical copies of a single DNA molecule from the original library. A 30-54 bp interval in the molecules in each cluster is sequenced using reversible dye-termination chemistry, to permit simultaneous sequencing from genomic DNA of the rearranged TCRβ chain CDR3 regions carried in millions of T cells. This approach enables direct sequencing of a significant fraction of the uniquely rearranged TCRβ CDR3 regions in populations of αβ T cells, which thereby permits estimation of the relative frequency of each CDR3 sequence in the population.

[0047] Accurate estimation of the diversity of TCRβ CDR3 sequences in the entire αβ T cell repertoire from the diversity measured in a finite sample of T cells requires an estimate of the number of CDR3 sequences present in the repertoire that were not observed in the sample. TCRβ chain CDR3 diversity in the entire αβ T cell repertoire were estimated using direct measurements of the number of unique TCRβ CDR3 sequences observed in blood samples containing millions of αβ T cells. The results herein identify a lower bound for TCRβ CDR3 diversity in the $CD4^+$ and $CD8^+$ T cell compartments that is several fold higher than previous estimates. In addition, the results herein demonstrat that there are at least 1.5×10^6 unique TCRβ CDR3 sequences in the $CD45RO^+$ compartment of antigen-experienced T-cells, a large proportion of which are present at low relative frequency. The existence of such a diverse population of TCRβ CDR3 sequences in antigen-experienced cells has not been previously demonstrated.

[0048] The diverse pool of TCRβ chains in each healthy individual is a sample from an estimated theoretical space of greater than 10^{11} possible sequences. However, the realized set of rearranged of TCRs is not evenly sampled from this theoretical space. Different Vβ's and Jβ's are found with over a thousand-fold frequency difference. Additionally, the insertion rates of nucleotides are strongly biased. This reduced space of realized TCRβ sequences leads to the possibility of shared β chains between people. With the sequence data generated by the methods described herein, the in vivo J usage, V usage, mono- and di-nucleotide biases, and position dependent amino acid usage can be computed. These biases significantly narrow the size of the sequence space from which TCRβ are selected, suggesting that different individuals share TCRβ chains with identical amino acid sequences. Results herein show that many thousands of such identical sequences are shared pairwise between individual human genomes.

[0049] The assay technology uses two pools of primers to provide for a highly multiplexed PCR reaction. The "forward" pool has a primer specific to each V segment in the gene (several primers targeting a highly conserved region are used, to simultaneously capture many V segments). The "reverse" pool primers anneal to a conserved sequence in the joining ("J") segment. The amplified segment pool includes adequate sequence to identify each J segment and also to allow for a J-segment-specific primer to anneal for resequencing. This enables direct observation of a large fraction of the somatic rearrangements present in an individual. This in turn enables rapid comparison of the TCR repertoire in individuals with an autoimmune disorder (or other target disease indication) against the TCR repertoire of controls.

[0050] The adaptive immune system can in theory generate an enormous diversity of T cell receptor CDR3 sequences—far more than are likely to be expressed in any one individual at any one time. Previous attempts to measure what fraction of this theoretical diversity is actually utilized in the adult αβ T cell repertoire, however, have not permitted accurate assessment of the diversity. What is described herein is the development of a novel approach to this question that is based on single molecule DNA sequencing and an analytic computational approach to estimation of repertoire diversity using diversity measurements in finite samples. The analysis demonstrated that the number of unique TCRβ CDR3 sequences in the adult repertoire significantly exceeds previous estimates based on exhaustive capillary sequencing of small segments of the repertoire. The TCRβ chain diversity in the $CD45RO^-$ population (enriched for naïve T cells) observed using the methods described herein is five-fold larger than previously reported. A major discovery is the number of unique TCRβ CDR3 sequences expressed in antigen-experienced $CD45RO^+$ T cells—the results herein show that this number is between 10 and 20 times larger than expected based on previous results of others. The frequency distribution of CDR3 sequences in $CD45RO^+$ cells suggests that the T cell repertoire contains a large number of clones with a small clone size.

[0051] The results herein show that the realized set of TCRβ chains are sampled non-uniformly from the huge potential space of sequences. In particular, the β chains sequences closer to germ line (few insertions and deletions at the V-D and D-J boundaries) appear to be created at a relatively high frequency. TCR sequences close to germ line are shared between different people because the germ line sequence for the V's, D's, and J's are shared, modulo a small number of polymorphisms, among the human population.

[0052] The T cell receptors expressed by mature αβ T cells are heterodimers whose two constituent chains are generated by independent rearrangement events of the TCR α and β chain variable loci. The α chain has less diversity than the β chain, so a higher fraction of α's are shared between individuals, and hundreds of exact TCR αβ receptors are shared between any pair of individuals.

Cells

[0053] B cells and T cells can be obtained from a variety of tissue samples including marrow, thymus, lymph glands, peripheral tissues and blood, but peripheral blood is most easily accessed. Peripheral blood samples are obtained by phlebotomy from subjects. Peripheral blood mononuclear cells (PBMC) are isolated by techniques known to those of skill in the art, e.g., by Ficoll-Hypaque® density gradient separation. Preferably, whole PBMCs are used for analysis. The B and/or T lymphocytes, instead, may be flow sorted into multiple compartments for each subject: e.g. $CD8^+$ $CD45RO^{+/-}$ and $CD4^+CD45RO^{+/-}$ using fluorescently labeled anti-human antibodies, e.g, CD4 FITC (clone M-T466, Miltenyi Biotec), CD8 PE (clone RPA-T8, BD Biosciences), CD45RO ECD (clone UCHL-1, Beckman Coulter), and CD45RO APC (clone UCHL-1, BD Biosciences). Staining of total PBMCs may be done with the appropriate combination of antibodies, followed by washing cells before analysis. Lymphocyte subsets can be isolated by FACS sorting, e.g., by a BD FACSAria™ cell-sorting system (BD Biosciences) and by analyzing results with FlowJo software (Treestar Inc.), and also by conceptually similar methods involving specific antibodies immobilized to surfaces or beads.

Nucleic Acid Extraction

[0054] Total genomic DNA is extracted from cells, e.g., by using the QIAamp® DNA blood Mini Kit (QIAGEN®). The approximate mass of a single haploid genome is 3 pg. Preferably, at least 100,000 to 200,000 cells are used for analysis of diversity, i.e., about 0.6 to 1.2 μg DNA from diploid T cells. Using PBMCs as a source, the number of T cells can be estimated to be about 30% of total cells.

[0055] Alternatively, total nucleic acid can be isolated from cells, including both genomic DNA and mRNA. If diversity is to be measured from mRNA in the nucleic acid extract, the mRNA must be converted to cDNA prior to measurement. This can readily be done by methods of one of ordinary skill.

DNA Amplification

[0056] A multiplex PCR system is used to amplify rearranged TCR loci from genomic DNA, preferably from a CDR3 region, more preferably from a TCRα, TCRγ or TCRδ CDR3 region, most preferably from a TCRβ CDR3 region.

[0057] In general, a multiplex PCR system may use at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25, preferably 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 39, most preferably 40, 41, 42, 43, 44, or 45 forward primers, in which each forward primer is specific to a sequence corresponding to one or more TRB V region segments shown in SEQ ID NOS:114-248; and at least 3, 4, 5, 6, or 7, preferably 8, 9, 10, 11, 12 or 13 reverse primers, in which each reverse primer is specific to a sequence corresponding to one or more TRB J region segments shown in SEQ ID NOS:249-261. Most preferably, there is a J segment primer for every J segment.

[0058] Preferably, the primers are designed not to cross an intron/exon boundary. The forward primers must preferably anneal to the V segments in a region of relatively strong sequence conservation between V segments so as to maximize the conservation of sequence among these primers. Accordingly, this minimizes the potential for differential annealing properties of each primer, and so that the amplified region between V and J primers contains sufficient TCR V sequence information to identify the specific V gene segment used.

[0059] Preferably, the J segment primers hybridize with a conserved element of the J segment, and have similar annealing strength. Most preferably, all J segment primers anneal to the same conserved framework region motif. The forward and reverse primers are both preferably modified at the 5' end with the universal forward primer sequence compatible with a DNA sequencer.

[0060] For example, a multiplex PCR system may use 45 forward primers (Table 1), each specific to a functional TCR Vβ segment, and thirteen reverse primers (Table 2), each specific to a TCR Jβ segment. Xn and Yn correspond to polynucleotides of lengths n and m, respectively, which would be specific to the single molecule sequencing technology being used to read out the assay.

TABLE 1

TCR-Vβ Forward primer sequences

TRBV gene segment(s)	SEQ ID NO:	Primer sequence*
TRBV2	1	**Xn**TCAAATTTCACTCTGAAGATCCGGTCCACAA
TRBV3-1	2	**Xn**GCTCACTTAAATCTTCACATCAATTCCCTGG
TRBV4-1	3	**Xn**CTTAAACCTTCACCTACACGCCCTGC
TRBV(4-2, 4-3)	4	**Xn**CTTATTCCTTCACCTACACACCCTGC
TRBV5-1	5	**Xn**GCTCTGAGATGAATGTGAGCACCTTG
TRBV5-3	6	**Xn**GCTCTGAGATGAATGTGAGTGCCTTG
TRBV(5-4, 5-5, 5-6, 5-7, 5-8)	7	**Xn**GCTCTGAGCTGAATGTGAACGCCTTG
TRBV6-1	8	**Xn**TCGCTCAGGCTGGAGTCGGCTG
TRBV(6-2, 6-3)	9	**Xn**GCTGGGGTTGGAGTCGGCTG
TRBV6-4	10	**Xn**CCCTCACGTTGGCGTCTGCTG
TRBV6-5	11	**Xn**GCTCAGGCTGCTGTCGGCTG
TRBV6-6	12	**Xn**CGCTCAGGCTGGAGTTGGCTG
TRBV6-7	13	**Xn**CCCCTCAAGCTGGAGTCAGCTG
TRBV6-8	14	**Xn**CACTCAGGCTGGTGTCGGCTG
TRBV6-9	15	**Xn**CGCTCAGGCTGGAGTCAGCTG
TRBV7-1	16	**Xn**CCACTCTGAAGTTCCAGCGCACAC
TRBV7-2	17	**Xn**CACTCTGACGATCCAGCGCACAC
TRBV7-3	18	**Xn**CTCTACTCTGAAGATCCAGCGCACAG
TRBV7-4	19	**Xn**CCACTCTGAAGATCCAGCGCACAG
TRBV7-6	20	**Xn**CACTCTGACGATCCAGCGCACAG
TRBV7-7	21	**Xn**CCACTCTGACGATTCAGCGCACAG
TRBV7-8	22	**Xn**CCACTCTGAAGATCCAGCGCACAC
TRBV7-9	23	**Xn**CACCTTGGAGATCCAGCGCACAG
TRBV9	24	**Xn**GCACTCTGAACTAAACCTGAGCTCTCTG
TRBV10-1	25	**Xn**CCCCTCACTCTGGAGTCTGCTG
TRBV10-2	26	**Xn**CCCCCTCACTCTGGAGTCAGCTA
TRBV10-3	27	**Xn**CCTCCTCACTCTGGAGTCCGCTA
TRBV(11-1, 11-3)	28	**Xn**CCACTCTCAAGATCCAGCCTGCAG
TRBV11-2	29	**Xn**CTCCACTCTCAAGATCCAGCCTGCAA
TRBV(12-3, 12-4, 12-5)	30	**Xn**CCACTCTGAAGATCCAGCCCTCAG
TRBV13	31	**Xn**CATTCTGAACTGAACATGAGCTCCTTGG
TRBV14	32	**Xn**CTACTCTGAAGGTGCAGCCTGCAG
TRBV15	33	**Xn**GATAACTTCCAATCCAGGAGGCCGAACA

TABLE 1-continued

TCR-Vβ Forward primer sequences

TRBV gene segment(s)	SEQ ID NO:	Primer sequence*
TRBV16	34	**Xn**CTGTAGCCTTGAGATCCAGGCTACGA
TRBV17	35	**Xn**CTTCCACGCTGAAGATCCATCCCG
TRBV18	36	**Xn**GCATCCTGAGGATCCAGCAGGTAG
TRBV19	37	**Xn**CCTCTCACTGTGACATCGGCCC
TRBV20-1	38	**Xn**CTTGTCCACTCTGACAGTGACCAGTG
TRBV23-1	39	**Xn**CAGCCTGGCAATCCTGTCCTCAG
TRBV24-1	40	**Xn**CTCCCTGTCCCTAGAGTCTGCCAT
TRBV25-1	41	**Xn**CCCTGACCCTGGAGTCTGCCA
TRBV27	42	**Xn**CCCTGATCCTGGAGTCGCCCA
TRBV28	43	**Xn**CTCCCTGATTCTGGAGTCCGCCA
TRBV29-1	44	**Xn**CTAACATTCTCAACTCTGACTGTGAGCAACA
TRBV30	45	**Xn**CGGCAGTTCATCCTGAGTTCTAAGAAGC

TABLE 2

TCR-Jβ Reverse Primer Sequences

TRBJ gene segment	SEQ ID NO:	Primer sequence*
TRBJ1-1	46	**Ym**TTACCTACAACTGTGAGTCTGGTGCCTTGTCCAAA
TRBJ1-2	47	**Ym**ACCTACAACGGTTAACCTGGTCCCCGAACCGAA
TRBJ1-3	48	**Ym**ACCTACAACAGTGAGCCAACTTCCCTCTCCAAA
TRBJ1-4	49	**Ym**CCAAGACAGAGAGCTGGGTTCCACTGCCAAA
TRBJ1-5	483	**Ym**ACCTAGGATGGAGAGTCGAGTCCCATCACCAAA
TRBJ1-6	50	**Ym**CTGTCACAGTGAGCCTGGTCCCGTTCCCAAA
TRBJ2-1	51	**Ym**CGGTGAGCCGTGTCCCTGGCCCGAA
TRBJ2-2	52	**Ym**CCAGTACGGTCAGCCTAGAGCCTTCTCCAAA
TRBJ2-3	53	**Ym**ACTGTCAGCCGGGTGCCTGGGCCAAA
TRBJ2-4	54	**Ym**AGAGCCGGGTCCCGGCGCCGAA
TRBJ2-5	55	**Ym**GGAGCCGCGTGCCTGGCCCGAA
TRBJ2-6	56	**Ym**GTCAGCCTGCTGCCGGCCCCGAA
TRBJ2-7	57	**Ym**GTGAGCCTGGTGCCCGGCCCGAA

[0061] The 45 forward PCR primers of Table 1 are complementary to each of the 48 functional Variable segments, and the thirteen reverse PCR primers of Table 2 are complementary to each of the functional joining (J) gene segments from the TRB locus (TRBJ). The TRB V region segments are identified in the Sequence Listing at SEQ ID NOS:114-248 and the TRB J region segments are at SEQ ID NOS:249-261. The primers have been designed such that adequate information is present within the amplified sequence to identify both the V and J genes uniquely (>40 base pairs of sequence upstream of the V gene recombination signal sequence (RSS), and >30 base pairs downstream of the J gene RSS). Alternative primers may be selected by one of ordinary skill from the V and J regions of the genes of each TCR subunit.

[0062] The forward primers are modified at the 5' end with the universal forward primer sequence compatible with the DNA sequencer (Xn of Table 1). Similarly, all of the reverse primers are modified with a universal reverse primer sequence (Ym of Table 2). One example of such universal primers is shown in Tables 3 and 4, for the Illumina GAIT single-end read sequencing system. The 45 TCR Vβ forward primers anneal to the Vβ segments in a region of relatively strong sequence conservation between Vβ segments so as to maximize the conservation of sequence among these primers.

TABLE 3

TCR-Vβ Forward primer sequences

TRBV gene segment(s)	SEQ ID NO:	Primer sequence*
TRBV2	58	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**TCAAATTTCACTCTGAAGATCCGGTCCACAA
TRBV3-1	59	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTCACTTAAATCTTCACATCAATTCCCTGG
TRBV4-1	60	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTTAAACCTTCACCTACACGCCCTGC
TRBV(4-2, 4-3)	61	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTTATTCCTTCACCTACACACCCTGC
TRBV5-1	62	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTCTGAGATGAATGTGAGCACCTTG
TRBV5-3	63	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTCTGAGATGAATGTGAGTGCCTTG
TRBV(5-4, 5-5, 5-6,5-7,5-8)	64	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTCTGAGCTGAATGTGAACGCCTTG
TRBV6-1	65	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**TCGCTCAGGCTGGAGTCGGCTG

TABLE 3-continued

TCR-Vβ Forward primer sequences

TRBV gene segment(s)	SEQ ID NO:	Primer sequence*
TRBV(6-2, 6-3)	66	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTGGGGTTGGAGTCGGCTG
TRBV6-4	67	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCTCACGTTGGCGTCTGCTG
TRBV6-5	68	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCTCAGGCTGCTGTCGGCTG
TRBV6-6	69	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CGCTCAGGCTGGAGTTGGCTG
TRBV6-7	70	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCCTCAAGCTGGAGTCAGCTG
TRBV6-8	71	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CACTCAGGCTGGTGTCGGCTG
TRBV6-9	72	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CGCTCAGGCTGGAGTCAGCTG
TRBV7-1	73	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTGAAGTTCCAGCGCACAC
TRBV7-2	74	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CACTCTGACGATCCAGCGCACAC
TRBV7-3	75	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTCTACTCTGAAGATCCAGCGCACAG
TRBV7-4	76	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTGAAGATCCAGCGCACAG
TRBV7-6	77	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CACTCTGACGATCCAGCGCACAG
TRBV7-7	78	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTGACGATTCAGCGCACAG
TRBV7-8	79	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTGAAGATCCAGCGCACAC
TRBV7-9	80	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CACCTTGGAGATCCAGCGCACAG
TRBV9	81	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCACTCTGAACTAAACCTGAGCTCTCTG
TRBV10-1	82	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCCTCACTCTGGAGTCTGCTG
TRBV10-2	83	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCCCTCACTCTGGAGTCAGCTA
TRBV10-3	84	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCTCCTCACTCTGGAGTCCGCTA
TRBV(11-1,11-3)	85	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTCAAGATCCAGCCTGCAG
TRBV11-2	86	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTCCACTCTCAAGATCCAGCCTGCAA
TRBV(12-3, 12-4, 12-5)	87	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCACTCTGAAGATCCAGCCCTCAG
TRBV13	88	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CATTCTGAACTGAACATGAGCTCCTTGG
TRBV14	89	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTACTCTGAAGGTGCAGCCTGCAG
TRBV15	90	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GATAACTTCCAATCCAGGAGGCCGAACA
TRBV16	91	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTGTAGCCTTGAGATCCAGGCTACGA
TRBV17	92	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTTCCACGCTGAAGATCCATCCCG
TRBV18	93	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**GCATCCTGAGGATCCAGCAGGTAG
TRBV19	94	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCTCTCACTGTGACATCGGCCC
TRBV20-1	95	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTTGTCCACTCTGACAGTGACCAGTG
TRBV23-1	96	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CAGCCTGGCAATCCTGTCCTCAG
TRBV24-1	97	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTCCCTGTCCCTAGAGTCTGCCAT
TRBV25-1	98	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCTGACCCTGGAGTCTGCCA
TRBV27	99	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CCCTGATCCTGGAGTCGCCCA

TABLE 3-continued

TCR-Vβ Forward primer sequences

TRBV gene segment(s)	SEQ ID NO:	Primer sequence*
TRBV28	100	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTCCCTGATTCTGGAGTCCGCCA
TRBV29-1	101	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CTAACATTCTCAACTCTGACTGTGAGCAACA
TRBV30	102	**CAAGCAGAAGACGGCATACGAGCTCTTCCGATCT**CGGCAGTTCATCCTGAGTTCTAAGAAGC

TABLE 4

TCR-Jβ Reverse Primer Sequences

TRBJ gene segment	SEQ ID NO:	Primer sequence*
TRBJ1-1	103	**AATGATACGGCGACCACCGAGATCT**TTACCTACAACTGTGAGTCTGGTGCCTTGTCCAAA
TRBJ1-2	468	**AATGATACGGCGACCACCGAGATCT**ACCTACAACGGTTAACCTGGTCCCCGAACCGAA
TRBJ1-3	104	**AATGATACGGCGACCACCGAGATCT**ACCTACAACAGTGAGCCAACTTCCCTCTCCAAA
TRBJ1-4	105	**AATGATACGGCGACCACCGAGATCT**CCAAGACAGAGAGCTGGGTTCCACTGCCAAA
TRBJ1-5	484	**AATGATACGGCGACCACCGAGATCT**ACCTAGGATGGAGAGTCGAGTCCCATCACCAAA
TRBJ1-6	106	**AATGATACGGCGACCACCGAGATCT**CTGTCACAGTGAGCCTGGTCCCGTTCCCAAA
TRBJ2-1	107	**AATGATACGGCGACCACCGAGATCT**CGGTGAGCCGTGTCCCTGGCCCGAA
TRBJ2-2	108	**AATGATACGGCGACCACCGAGATCT**CCAGTACGGTCAGCCTAGAGCCTTCTCCAAA
TRBJ2-3	109	**AATGATACGGCGACCACCGAGATCT**ACTGTCAGCCGGGTGCCTGGGCCAAA
TRBJ2-4	110	**AATGATACGGCGACCACCGAGATCT**AGAGCCGGGTCCCGGCGCCGAA
TRBJ2-5	111	**AATGATACGGCGACCACCGAGATCT**GGAGCCGCGTGCCTGGCCCGAA
TRBJ2-6	112	**AATGATACGGCGACCACCGAGATCT**GTCAGCCTGCTGCCGGCCCCGAA
TRBJ2-7	113	**AATGATACGGCGACCACCGAGATCT**GTGAGCCTGGTGCCCGGCCCGAA

*bold sequence indicates universal R oligonucleotide for the sequence analysis

[0063] The total PCR product for a rearranged TCRβ CDR3 region using this system is expected to be approximately 200 bp long. Genomic templates are PCR amplified using a pool of the 45 TCR Vβ F primers (the "VF pool") and a pool of the twelve TCR Jβ R primers (the "JR pool"). For example, 50 μl PCR reactions may be used with 1.0 μM VF pool (22 nM for each unique TCR Vβ F primer), 1.0 μM JR pool (77 nM for each unique TCRBJR primer), 1× QIAGEN Multiple PCR master mix (QIAGEN part number 206145), 10% Q-solution (QIAGEN), and 16 ng/ul gDNA.

[0064] The IGH primer set was designed to try to accommodate the potential for somatic hypermutation within the rearranged IGH genes, as is observed after initial stimulation of naïve B cells. Consequently all primers were designed to be slightly longer than normal, and to anchor the 3' ends of each primer into highly conserved sequences of three or more nucleotides that should be resistant to both functional and non-functional somatic mutations.

[0065] The IGHJ reverse primers were designed to anchor the 3' end of each PCR primer on a highly conserved GGGG sequence motif within the IGHJ segments. These sequences are shown in Table 5. Underlined sequence are ten base pairs in from RSS that may be deleted. These were excluded from barcode design. Bold sequence is the reverse complement of the IGH J reverse PCR primers. Italicized sequence is the barcode for J identity (eight barcodes reveal six genes, and two alleles within genes). Further sequence within underlined segment may reveal additional allelic identities.

TABLE 5

IgH J segment	SEQ ID NO:	Sequence
>IGHJ4*01/1-48	452	ACTACTTTGA*CTA*CTG**GGGCCAAGGAACCCTGGTCACCGTCTCCTCAG**
>IGHJ4*03/1-48	453	GCTACTTTGA*CTA*CTG**GGGCCAAGGGACCCTGGTCACCGTCTCCTCAG**

TABLE 5-continued

IgH J segment	SEQ ID NO:	Sequence
>IGHJ4*02/1-48	454	ACTACTTTGA*CTA*CTG**GGGCCAGGGAACCCTGGTCACCGTCTCCTCAG**
>IGHJ3*01/1-50	455	TGATGCTTTTGA*TGT*CTG**GGGCCAAGGGACAATGGTCACCGTCTCTTCAG**
>IGHJ3*02/1-50	456	TGATGCTTTTGA*TAT*CTG**GGGCCAAGGGACAATGGTCACCGTCTCTTCAG**
>IGHJ6*01/1-63	457	ATTACTACTACTACTACGGTATGGA*CGT*CTG**GGGGCAAGGGACCACGGTCACCGTCTCCTCAG**
>IGHJ6*02/1-62	458	ATTACTACTACTACTACGGTATGGA*CGT*CTG**GGGCCAAGGGACCACGGTCACCGTCTCCTCAG**
>IGHJ6*04/1-63	459	ATTACTACTACTACTACGGTATGGA*CGT*CTG**GGGCAAAGGGACCACGGTCACCGTCTCCTCAG**
>IGHJ6*03/1-62	460	ATTACTACTACTACTACTACATGGA*CGT*CTGG**GGCAAAGGGACCACGGTCACCGTCTCCTCAG**
>IGHJ2*01/1-53	461	CTACTGGTACTTCGA*TCT*CTG**GGGCCGTGGCACCCTGGTCACTGTCTCCTCAG**
>IGHJ5*01/1-51	462	ACAACTGGTTCGA*CTC*CTG**GGGCCAAGGAACCCTGGTCACCGTCTCCTCAG**
>IGHJ5*02/1-51	463	ACAACTGGTTCGA*CCC*CTG**GGGCCAGGGAACCCTGGTCACCGTCTCCTCAG**
>IGHJ1*01/1-52	464	GCTGAATACTTCCA*GCA*CTG**GGGCCAGGGCACCCTGGTCACCGTCTCCTCAG**
>IGHJ2P*01/1-61	465	CTACAAGTGCTTGGAGCACTGGGGCAGGGCAGCCCGGACACCGTCTCCCTGGGAACGTCAG
>IGHJ1P*01/1-54	466	AAAGGTGCTGGGGGTCCCCTGAACCCGACCCGCCCTGAGACCGCAGCCACATCA
>IGHJ3P*01/1-52	467	CTTGCGGTTGGACTTCCCAGCCGACAGTGGTGGTCTGGCTTCTGAGGGGTCA

Sequences of the IGHJ reverse PCR primers are shown in Table 6.

TABLE 6

IgH J segment	SEQ ID NO:	sequence
>IGHJ4_1	421	TGAGGAGACGGTGACCAGGGTTCCTTGGCCC
>IGHJ4_3	422	TGAGGAGACGGTGACCAGGGTCCCTTGGCCC
>IGHJ4_2	423	TGAGGAGACGGTGACCAGGGTTCCCTGGCCC
>IGHJ3_12	424	CTGAAGAGACGGTGACCATTGTCCCTTGGCCC
>IGHJ6_1	425	CTGAGGAGACGGTGACCGTGGTCCCTTGCCCC
>IGHJ6_2	426	TGAGGAGACGGTGACCGTGGTCCCTTGGCCC
>IGHJ6_34	427	CTGAGGAGACGGTGACCGTGGTCCCTTTGCCC
>IGHJ2_1	428	CTGAGGAGACAGTGACCAGGGTGCCACGGCCC
>IGHJ5_1	429	CTGAGGAGACGGTGACCAGGGTTCCTTGGCCC
>IGHJ5_2	430	CTGAGGAGACGGTGACCAGGGTTCCCTGGCCC
>IGHJ1_1	431	CTGAGGAGACGGTGACCAGGGTGCCCTGGCCC

[0066] V primers were designed in a conserved in region of FR2 between the two conserved tryptophan (W) codons.

[0067] The primer sequences are anchored at the 3' end on a tryptophan codon for all IGHV families that conserve this codon. his allows for the last three nucleotides (tryptophan's TGG) to anchor on sequence that is expected to be resistant to somatic hypermutation, providing a 3' anchor of five out of six nucleotides for each primer. The upstream sequence is extended further than normal, and includes degenerate nucleotides to allow for mismatches induced by hypermutation (or between closely relate IGH V families) without dramatically changing the annealing characteristics of the primer, as shown in Table 7. The sequences of the V gene segments are SEQ ID NOS:262-420.

TABLE 7

IgH V segment	SEQ ID NO:	sequence
>IGHV1	443	TGGGTGCACCAGGTCCANGNACAAGGGCTTGAG TGG
>IGHV2	444	TGGGTGCGACAGGCTCGNGNACAACGCCTTGAG TGG
>IGHV3	445	TGGGTGCGCCAGATGCCNGNGAAAGGCCTGGAG TGG
>IGHV4	446	TGGGTCCGCCAGSCYCCNGNGAAGGGGCTGGAG TGG
>IGHV5	447	TGGGTCCGCCAGGCTCCNGNAAAGGGGCTGGAG TGG
>IGHV6	448	TGGGTCTGCCAGGCTCCNGNGAAGGGGCAGGAG TGG
>IGH7_3.25p	449	TGTGTCCGCCAGGCTCCAGGGAATGGGCTGGAG TTGG
>IGH8_3.54p	450	TCAGATTCCCAAGCTCCAGGGAAGGGGCTGGAG TGAG
>IGH9_3.63p	451	TGGGTCAATGAGACTCTAGGGAAGGGGCTGGA GGGAG

[0068] Thermal cycling conditions may follow methods of those skilled in the art. For example, using a PCR Express thermal cycler (Hybaid, Ashford, UK), the following cycling conditions may be used: 1 cycle at 95° C. for 15 minutes, 25 to 40 cycles at 94° C. for 30 seconds, 59° C. for 30 seconds and 72° C. for 1 minute, followed by one cycle at 72° C. for 10 minutes.

Sequencing

[0069] Sequencing is achieved using a set of sequencing oligonucleotides that hybridize to a defined region within the amplified DNA molecules.

[0070] Preferably, the amplified J gene segments each have a unique four base tag at positions +11 through +14 downstream from the RSS site. Accordingly, the sequencing oligonucleotides hybridize adjacent to a four base tag within the amplified Jβ gene segments at positions +11 through +14 downstream of the RSS site.

[0071] For example, sequencing oligonucleotides for TCRB may be designed to anneal to a consensus nucleotide motif observed just downstream of this "tag", so that the first four bases of a sequence read will uniquely identify the J segment (Table 8).

TABLE 8

Sequencing oligonucleotides

Sequencing oligo-nucleotide	SEQ ID NO:	Oligonucleotide sequence
Jseq 1-1	470	ACAACTGTGAGTCTGGTGCCTTGTCCAAAGAAA
Jseq 1-2	471	ACAACGGTTAACCTGGTCCCCGAACCGAAGGTG
Jseq 1-3	472	ACAACAGTGAGCCAACTTCCCTCTCCAAAATAT
Jseq 1-4	473	AAGACAGAGAGCTGGGTTCCACTGCCAAAAAAC
Jseq 1-5	474	AGGATGGAGAGTCGAGTCCCATCACCAAAATGC
Jseq 1-6	475	GTCACAGTGAGCCTGGTCCCGTTCCCAAAGTGG
Jseq 2-1	476	AGCACGGTGAGCCGTGTCCCTGGCCCGAAGAAC
Jseq 2-2	477	AGTACGGTCAGCCTAGAGCCTTCTCCAAAAAAC
Jseq 2-3	478	AGCACTGTCAGCCGGGTGCCTGGGCCAAAATAC
Jseq 2-4	479	AGCACTGAGAGCCGGGTCCCGGCGCCGAAGTAC
Jseq 2-5	480	AGCACCAGGAGCCGCGTGCCTGGCCCGAAGTAC
Jseq 2-6	481	AGCACGGTCAGCCTGCTGCCGGCCCCGAAAGTC
Jseq 2-7	482	GTGACCGTGAGCCTGGTGCCCGGCCCGAAGTAC

[0072] The information used to assign the J and V segment of a sequence read is entirely contained within the amplified sequence, and does not rely upon the identity of the PCR primers. These sequencing oligonucleotides were selected such that promiscuous priming of a sequencing reaction for one J segment by an oligonucleotide specific to another J segment would generate sequence data starting at exactly the same nucleotide as sequence data from the correct sequencing oligonucleotide. In this way, promiscuous annealing of the sequencing oligonucleotides did not impact the quality of the sequence data generated.

[0073] The average length of the CDR3 region, defined as the nucleotides between the second conserved cysteine of the V segment and the conserved phenylalanine of the J segment, is 35+/−3, so sequences starting from the Jβ segment tag will nearly always capture the complete V-D-J junction in a 50 base pair read.

[0074] TCR βJ gene segments are roughly 50 base pair in length. PCR primers that anneal and extend to mismatched sequences are referred to as promiscuous primers. The TCR Jβ Reverse PCR primers were designed to minimize overlap with the sequencing oligonucleotides to minimize promiscuous priming in the context of multiplex PCR. The 13 TCR Jβ reverse primers are anchored at the 3' end on the consensus splice site motif, with minimal overlap of the sequencing primers. The TCR Jβ primers provide consistent annealing temperature using the sequencer program under default parameters.

[0075] For the sequencing reaction, the IGHJ sequencing primers extend three nucleotides across the conserved CAG sequences as shown in Table 9.

TABLE 9

IgH J segment	SEQ ID NO:	sequence
>IGHJSEQ4_1	432	TGAGGAGACGGTGACCAGGGTTCCTTGGCCCCAG
>IGHJSEQ4_3	433	TGAGGAGACGGTGACCAGGGTCCCTTGGCCCCAG
>IGHJSEQ4_2	434	TGAGGAGACGGTGACCAGGGTTCCCTGGCCCCAG
>IGHJSEQ3_12	435	CTGAAGAGACGGTGACCATTGTCCCTTGGCCCCAG
>IGHJSEQ6_1	436	CTGAGGAGACGGTGACCGTGGTCCCTTGCCCCCAG
>IGHJSEQ6_2	437	TGAGGAGACGGTGACCGTGGTCCCTTGGCCCCAG
>IGHJSEQ6_34	438	CTGAGGAGACGGTGACCGTGGTCCCTTTGCCCCAG
>IGHJSEQ2_1	439	CTGAGGAGACAGTGACCAGGGTGCCACGGCCCCAG
>IGHJSEQ5_1	440	CTGAGGAGACGGTGACCAGGGTTCCTTGGCCCCAG
>IGHJSEQ5_2	441	CTGAGGAGACGGTGACCAGGGTTCCCTGGCCCCAG
>IGHJSEQ1_1	442	CTGAGGAGACGGTGACCAGGGTGCCCTGGCCCCAG

Processing Sequence Data

[0076] For rapid analysis of sequencing results, an algorithm can be developed by one of ordinary skill. A preferred method is as follows.

[0077] The use of a PCR step to amplify the TCRβ CDR3 regions prior to sequencing could potentially introduce a systematic bias in the inferred relative abundance of the sequences, due to differences in the efficiency of PCR amplification of CDR3 regions utilizing different Vβ and Jβ gene segments. Each cycle of PCR amplification potentially introduces a bias of average magnitude $1.5^{1/15}=1.027$. Thus, the 25 cycles of PCR introduces a total bias of average magnitude $1.027^{25}=1.95$ in the inferred relative abundance of distinct CDR3 region sequences.

[0078] Sequenced reads were filtered for those including CDR3 sequences. Sequencer data processing involves a series of steps to remove errors in the primary sequence of each read, and to compress the data. A complexity filter removes approximately 20% of the sequences that are misreads from the sequencer. Then, sequences were required to have a minimum of a six base match to both one of the thirteen TCRB J-regions and one of 54 V-regions. Applying the filter to the control lane containing phage sequence, on average only one sequence in 7-8 million passed these steps. Finally, a nearest neighbor algorithm was used to collapse the data into unique sequences by merging closely related sequences, in order to remove both PCR error and sequencing error.

[0079] Analyzing the data, the ratio of sequences in the PCR product must be derived working backward from the sequence data before estimating the true distribution of clonotypes in the blood. For each sequence observed a given number of times in the data herein, the probability that that sequence was sampled from a particular size PCR pool is estimated. Because the CDR3 regions sequenced are sampled randomly from a massive pool of PCR products, the number of observations for each sequence are drawn from Poisson distributions. The Poisson parameters are quantized according to the number of T cell genomes that provided the template for PCR. A simple Poisson mixture model both estimates these parameters and places a pairwise probability for each sequence being drawn from each distribution. This is an expectation maximization method which reconstructs the abundances of each sequence that was drawn from the blood.

[0080] To estimate diversity, the "unseen species" formula is employed. To apply this formula, unique adaptive immune receptors (e.g. TCRB) clonotypes takes the place of species. The mathematical solution provides that for a total number of TCRβ "species" or clonotypes, S, a sequencing experiment observes x_s copies of sequence s. For all of the unobserved clonotypes, x_s equals 0, and each TCR clonotype is "captured" in a blood draw according to a Poisson process with parameter λ_s. The number of T cell genomes sequenced in the first measurement 1, and in the second measurement. Since there are a large number of unique sequences, an integral will represent the sum. If G(λ) is the empirical distribution function of the parameters $\lambda_1, \ldots, \lambda_S$, and n_x is the number of clonotypes sequenced exactly x times, then the total number of clonotypes, i.e., the measurement of diversity E, is given by the following formula:

$$E(n_x) = S\int_0^\infty \left(\frac{e^{-\lambda}\lambda^x}{x!}\right) dG(\lambda).$$

[0081] For a given experiment, where T cells are sampled from some arbitrary source (e.g. a blood draw), the formula is used to estimate the total diversity of species in the entire source. The idea is that the sampled number of clonotypes at each size contains sufficient information to estimate the underlying distribution of clonotypes in the whole source. To derive the formula, the number of new species expected if the exact measurement was repeated was estimated. The limit of the formula as if repeating the measurements an infinite number of times. The result is the expect number of species in the total underlying source population. The value for Δ(t), the number of new clonotypes observed in a second measurement, should be determined, preferably using the following equation:

$$\Delta(t) = \sum_x E(n_x)_{msmt1+msmt2} - \sum_x E(n_x)_{msmt1}$$

-continued

$$= S\int_0^\infty e^{-\lambda}(1 - e^{-\lambda t})\, dG(\lambda)$$

in which msmt1 and msmt2 are the number of clonotypes from measurement 1 and 2, respectively. Taylor expansion of $1-e^{-\lambda t}$ gives $\Delta(t)=E(x_1)t-E(x_2)t^2+E(x_3)t^3- \ldots$, which can be approximated by replacing the expectations $E(n_x)$ with the observed numbers in the first measurement. Using in the numbers observed in the first measurement, this formula predicts that $1.6*10^5$ new unique sequences should be observed in the second measurement. The actual value of the second measurement was $1.8*10^5$ new TCRβ sequences, which implies that the prediction provided a valid lower bound on total diversity. An Euler's transformation was used to regularize Δ(t) to produce a lower bound for Δ(∞).

Using a Measurement of Diversity to Diagnose Disease

[0082] The measurement of diversity can be used to diagnose disease or the effects of a treatment, as follows. T cell and/or B cell receptor repertoires can be measured at various time points, e.g., after hematopoietic stem cell transplant (HSCT) treatment for leukemia. Both the change in diversity and the overall diversity of TCRB repertoire can be utilized to measure immunocompetence. A standard for the expected rate of immune reconstitution after transplant can be utilized. The rate of change in diversity between any two time points may be used to actively modify treatment. The overall diversity at a fixed time point is also an important measure, as this standard can be used to compare between different patients. In particular, the overall diversity is the measure that should correlate with the clinical definition of immune reconstitution. This information may be used to modify prophylactic drug regiments of antibiotics, antivirals, and antifungals, e.g., after HSCT.

[0083] The assessment of immune reconstitution after allogeneic hematopoietic cell transplantation can be determined by measuring changes in diversity. These techniques will also enhance the analysis of how lymphocyte diversity declines with age, as measured by analysis of T cell responses to vaccination. Further, the methods of the invention provide a means to evaluate investigational therapeutic agents (e.g., Interleukin-7 (IL-7)) that have a direct effect on the generation, growth, and development of αβ T cells. Moreover, application of these techniques to the study of thymic T cell populations will provide insight into the processes of both T cell receptor gene rearrangement as well as positive and negative selection of thymocytes.

[0084] A newborn that does not yet have a fully functioning immune system but may have maternally transmitted antibody is immunodeficient. A newborn is susceptible to a number of diseases until its immune system autonomously develops, and our measurement of the adaptive immune system may will likely prove useful with newborn patients.

[0085] Lymphocyte diversity can be assessed in other states of congenital or acquired immunodeficiency. An AIDS patient with a failed or failing immune system can be monitored to determine the stage of disease, and to measure a patient's response to therapies aimed to reconstitute immunocompetence.

[0086] Another application of the methods of the invention is to provide diagnostic measures for solid organ transplant recipients taking medication so their body will not reject the donated organ. Generally, these patients are under immunosuppressive therapies. Monitoring the immunocompetence of the host will assist before and after transplantation.

[0087] Individuals exposed to radiation or chemotherapeutic drugs are subject to bone marrow transplantations or otherwise require replenishment of T cell populations, along with associated immunocompetence. The methods of the invention provide a means for qualitatively and quantitatively assessing the bone marrow graft, or reconstitution of lymphocytes in the course of these treatments.

[0088] One manner of determining diversity is by comparing at least two samples of genomic DNA, preferably in which one sample of genomic DNA is from a patient and the other sample is from a normal subject, or alternatively, in which one sample of genomic DNA is from a patient before a therapeutic treatment and the other sample is from the patient after treatment, or in which the two samples of genomic DNA are from the same patient at different times during treatment. Another manner of diagnosis may be based on the comparison of diversity among the samples of genomic DNA, e.g., in which the immunocompetence of a human patient is assessed by the comparison.

Biomarkers

[0089] Shared TCR sequences between individuals represent a new class of potential biomarkers for a variety of diseases, including cancers, autoimmune diseases, and infectious diseases. These are the public T cells that have been reported for multiple human diseases. TCRs are useful as biomarkers because T cells are a result of clonal expansion, by which the immune system amplifies these biomarkers through rapid cell division. Following amplification, the TCRs are readily detected even if the target is small (e.g. an early stage tumor). TCRs are also useful as biomarkers because in many cases the T cells might additionally contribute to the disease causally and, therefore could constitute a drug target. T cells self interactions are thought to play a major role in several diseases associated with autoimmunity, e.g., multiple sclerosis, Type I diabetes, and rheumatoid arthritis.

EXAMPLES

Example 1

Sample Acquisition, PBMC Isolation, FACS Sorting and Genomic DNA Extraction

[0090] Peripheral blood samples from two healthy male donors aged 35 and 37 were obtained with written informed consent using forms approved by the Institutional Review Board of the Fred Hutchinson Cancer Research Center (FHCRC). Peripheral blood mononuclear cells (PBMC) were isolated by Ficoll-Hypaque® density gradient separation. The T-lymphocytes were flow sorted into four compartments for each subject: $CD8^+CD45RO^{+/-}$ and $CD4^+CD45RO^{+/-}$. For the characterization of lymphocytes the following conjugated anti-human antibodies were used: CD4 FITC (clone M-T466, Miltenyi Biotec), CD8 PE (clone RPA-T8, BD Biosciences), CD45RO ECD (clone UCHL-1, Beckman Coulter), and CD45RO APC (clone UCHL-1, BD Biosciences). Staining of total PBMCs was done with the appropriate combination of antibodies for 20 minutes at 4° C., and stained cells were washed once before analysis. Lymphocyte subsets were isolated by FACS sorting in the BD FACSAria™ cell-sorting system (BD Biosciences). Data were analyzed with FlowJo software (Treestar Inc.).

[0091] Total genomic DNA was extracted from sorted cells using the QIAamp® DNA blood Mini Kit (QIAGEN®). The approximate mass of a single haploid genome is 3 pg. In order to sample millions of rearranged TCRB in each T cell compartment, 6 to 27 micrograms of template DNA were obtained from each compartment (see Table 10).

TABLE 10

	CD8+/ CD45RO−	CD8+/ CD45RO+	CD4+/ CD45RO−	CD4+/ CD45RO+	Donor
cells ($\times 10^6$)	9.9	6.3	6.3	10	2
DNA (μg)	27	13	19	25	
PCR cycles	25	25	30	30	
clusters (K/tile)	29.3	27	102.3*	118.3*	
VJ sequences ($\times 10^6$)	3.0	2.0	4.4	4.2	
Cells	4.9	4.8	3.3	9	1
DNA	12	13	6.6	19	
PCR cycles	30	30	30	30	
Clusters	116.3	121	119.5	124.6	
VJ sequences	3.2	3.7	4.0	3.8	
Cells	NA	NA	NA	0.03	PCR Bias assessment
DNA	NA	NA	NA	0.015	
PCR cycles	NA	NA	NA	25 + 15	
clusters	NA	NA	NA	1.4/23.8	
VJ sequences	NA	NA	NA	1.6	

Example 2

Virtual T Cell Receptor β Chain Spectratyping

[0092] Virtual TCR β chain spectratyping was performed as follows. Complementary DNA was synthesized from RNA extracted from sorted T cell populations and used as template for multiplex PCR amplification of the rearranged TCR β chain CDR3 region. Each multiplex reaction contained a 6-FAM-labeled antisense primer specific for the TCR β chain constant region, and two to five TCR β chain variable (TRBV) gene-specific sense primers. All 23 functional Vβ families were studied. PCR reactions were carried out on a Hybaid PCR Express thermal cycler (Hybaid, Ashford, UK) under the following cycling conditions: 1 cycle at 95° C. for 6 minutes, 40 cycles at 94° C. for 30 seconds, 58° C. for 30 seconds, and 72° C. for 40 seconds, followed by 1 cycle at 72° C. for 10 minutes. Each reaction contained cDNA template, 500 μM dNTPs, 2 mM $MgCl_2$ and 1 unit of AmpliTaq Gold DNA polymerase (Perkin Elmer) in AmpliTaq Gold buffer, in a final volume of 20 μl. After completion, an aliquot of the PCR product was diluted 1:50 and analyzed using a DNA analyzer. The output of the DNA analyzer was converted to a distribution of fluorescence intensity vs. length by comparison with the fluorescence intensity trace of a reference sample containing known size standards.

Example 3

Multiplex PCR Amplification of TCRβ CDR3 Regions

[0093] The CDR3 junction region was defined operationally, as follows. The junction begins with the second conserved cysteine of the V-region and ends with the conserved phenylalanine of the J-region. Taking the reverse complements of the observed sequences and translating the flanking regions, the amino acids defining the junction boundaries were identified. The number of nucleotides between these boundaries determines the length and therefore the frame of the CDR3 region. In order to generate the template library for sequencing, a multiplex PCR system was selected to amplify rearranged TCRβ loci from genomic DNA. The multiplex PCR system uses 45 forward primers (Table 3), each specific to a functional TCR Vβ segment, and thirteen reverse primers (Table 4), each specific to a TCR Jβ segment. The primers were selected to provide that adequate information is present within the amplified sequence to identify both the V and J genes uniquely (>40 base pairs of sequence upstream of the V gene recombination signal sequence (RSS), and >30 base pairs downstream of the J gene RSS).

[0094] The forward primers are modified at the 5' end with the universal forward primer sequence compatible with the Illumina GA2 cluster station solid-phase PCR. Similarly, all of the reverse primers are modified with the GA2 universal reverse primer sequence. The 3' end of each forward primer is anchored at position −43 in the Vβ segment, relative to the recombination signal sequence (RSS), thereby providing a unique Vβ tag sequence within the amplified region. The thirteen reverse primers specific to each Jβ segment are anchored in the 3' intron, with the 3' end of each primer crossing the intron/exon junction. Thirteen sequencing primers complementary to the Jβ segments were designed that are complementary to the amplified portion of the Jβ segment, such that the first few bases of sequence generated will capture the unique Jβ tag sequence.

[0095] On average J deletions were 4 bp +/−2.5 bp, which implies that J deletions greater than 10 nucleotides occur in less than 1% of sequences. The thirteen different TCR Jβ gene segments each had a unique four base tag at positions +11 through +14 downstream of the RSS site. Thus, sequencing oligonucleotides were designed to anneal to a consensus nucleotide motif observed just downstream of this "tag", so that the first four bases of a sequence read will uniquely identify the J segment (Table 5).

[0096] The information used to assign the J and V segment of a sequence read is entirely contained within the amplified sequence, and does not rely upon the identity of the PCR primers. These sequencing oligonucleotides were selected such that promiscuous priming of a sequencing reaction for one J segment by an oligonucleotide specific to another J segment would generate sequence data starting at exactly the same nucleotide as sequence data from the correct sequencing oligonucleotide. In this way, promiscuous annealing of the sequencing oligonucleotides did not impact the quality of the sequence data generated.

[0097] The average length of the CDR3 region, defined following convention as the nucleotides between the second conserved cysteine of the V segment and the conserved phenylalanine of the J segment, is 35+/−3, so sequences starting from the Jβ segment tag will nearly always capture the complete VNDNJ junction in a 50 bp read.

[0098] TCR βJ gene segments are roughly 50 bp in length. PCR primers that anneal and extend to mismatched sequences are referred to as promiscuous primers. Because of the risk of promiscuous priming in the context of multiplex PCR, especially in the context of a gene family, the TCR Jβ Reverse PCR primers were designed to minimize overlap with the sequencing oligonucleotides. Thus, the 13 TCR Jβ reverse primers are anchored at the 3' end on the consensus splice site motif, with minimal overlap of the sequencing primers. The TCR Jβ primers were designed for a consistent annealing temperature (58 degrees in 50 mM salt) using the OligoCalc program under default parameters (http://www.basic.northwestern.edu/biotools/oligocalc.html).

[0099] The 45 TCR Vβ forward primers were designed to anneal to the Vβ segments in a region of relatively strong sequence conservation between Vβ segments, for two express purposes. First, maximizing the conservation of sequence among these primers minimizes the potential for differential annealing properties of each primer. Second, the primers were chosen such that the amplified region between V and J primers will contain sufficient TCR Vβ sequence information to identify the specific Vβ gene segment used. This obviates the risk of erroneous TCR Vβ gene segment assignment, in the event of promiscuous priming by the TCR Vβ primers. TCR Vβ forward primers were designed for all known non-pseudogenes in the TCRβ locus.

[0100] The total PCR product for a successfully rearranged TCRβ CDR3 region using this system is expected to be approximately 200 bp long. Genomic templates were PCR amplified using an equimolar pool of the 45 TCR Vβ F primers (the "VF pool") and an equimolar pool of the thirteen TCR Jβ R primers (the "JR pool"). 50 μl PCR reactions were set up at 1.0 μM VF pool (22 nM for each unique TCR Vβ F primer), 1.0 μM JR pool (77 nM for each unique TCRBJR primer), 1× QIAGEN Multiple PCR master mix (QIAGEN part number 206145), 10% Q-solution (QIAGEN), and 16 ng/ul gDNA. The following thermal cycling conditions were used in a PCR Express thermal cycler (Hybaid, Ashford, UK) under the following cycling conditions: 1 cycle at 95° C. for 15 minutes, 25 to 40 cycles at 94° C. for 30 seconds, 59° C. for 30 seconds and 72° C. for 1 minute, followed by one cycle at 72° C. for 10 minutes. 12-20 wells of PCR were performed for each library, in order to sample hundreds of thousands to millions of rearranged TCRβ CDR3 loci.

Example 4

Pre-Processing of Sequence Data

[0101] Sequencer data processing involves a series of steps to remove errors in the primary sequence of each read, and to compress the data. First, a complexity filter removes approximately 20% of the sequences which are misreads from the sequencer. Then, sequences were required to have a minimum of a six base match to both one of the thirteen J-regions and one of 54 V-regions. Applying the filter to the control lane containing phage sequence, on average only one sequence in 7-8 million passed these steps without false positives. Finally, a nearest neighbor algorithm was used to collapse the data into unique sequences by merging closely related sequences, in order to remove both PCR error and sequencing error (see Table 10).

Example 5

Estimating Relative CDR3 Sequence Abundance in PCR Pools and Blood Samples

[0102] After collapsing the data, the underlying distribution of T-cell sequences in the blood reconstructing were derived from the sequence data. The procedure used three steps; 1) flow sorting T-cells drawn from peripheral blood, 2) PCR amplification, and 3) sequencing. Analyzing the data, the ratio of sequences in the PCR product must be derived working backward from the sequence data before estimating the true distribution of clonotypes in the blood.

[0103] For each sequence observed a given number of times in the data herein, the probability that that sequence was sampled from a particular size PCR pool is estimated. Because the CDR3 regions sequenced are sampled randomly from a massive pool of PCR products, the number of observations for each sequence are drawn from Poisson distributions. The Poisson parameters are quantized according to the number of T cell genomes that provided the template for PCR. A simple Poisson mixture model both estimates these parameters and places a pairwise probability for each sequence being drawn from each distribution. This is an expectation maximization method which reconstructs the abundances of each sequence that was drawn from the blood.

Example 6

Unseen Species Model for Estimation of True Diversity

[0104] A mixture model can reconstruct the frequency of each TCRβ CDR3 species drawn from the blood, but the larger question is how many unique CDR3 species were present in the donor? This is a fundamental question that needs to be answered as the available sample is limited in each donor, and will be more important in the future as these techniques are extrapolated to the smaller volumes of blood that can reasonably be drawn from patients undergoing treatment.

[0105] The mathematical solution provides that for a total number of TCRβ "species" or clonotypes, S, a sequencing experiment observes x_s copies of sequence s. For all of the unobserved clonotypes, x_s equals 0, and each TCR clonotype is "captured" in a blood draw according to a Poisson process with parameter λ_s. The number of T cell genomes sequenced in the first measurement 1, and in the second measurement. Since there are a large number of unique sequences, an integral will represent the sum. If G(λ) is the empirical distribution function of the parameters $\lambda_1, \ldots, \lambda_S$, and n_x is the number of clonotypes sequenced exactly x times, then

$$E(n_x) = S\int_0^\infty \left(\frac{e^{-\lambda}\lambda^x}{x!}\right) dG(\lambda).$$

[0106] The value Δ(t) is the number of new clonotypes observed in the second sequencing experiment.

$$\begin{aligned}\Delta(t) &= \sum_x E(n_x)_{exp1+exp2} - \sum_x E(n_x)_{exp1}\\ &= S\int_0^\infty e^{-\lambda}(1-e^{-\lambda t})\,dG(\lambda)\end{aligned}$$

[0107] Taylor expansion of $1-e^{-\lambda t}$ gives $\Delta(t)=E(x_1)t-E(x_2)t^2+E(x_3)t^3-\ldots$, which can be approximated by replacing the expectations $(E(n_x))$ with the observed numbers in the first measurement. Using in the numbers observed in the first measurement, this formula predicts that $1.6*10^5$ new unique sequences should be observed in the second measurement. The actual value of the second measurement was $1.8*10^5$ new TCRβ sequences, which implies that the prediction provided a valid lower bound on total diversity. An Euler's transformation was used to regularize Δ(t) to produce a lower bound for Δ(∞).

Example 7

Error Correction and Bias Assessment

[0108] Sequence error in the primary sequence data derives primarily from two sources: (1) nucleotide misincorporation that occurs during the amplification by PCR of TCRβ CDR3 template sequences, and (2) errors in base calls introduced during sequencing of the PCR-amplified library of CDR3 sequences. The large quantity of data allows us to implement a straightforward error correcting code to correct most of the errors in the primary sequence data that are attributable to these two sources. After error correction, the number of unique, in-frame CDR3 sequences and the number of observations of each unique sequence were tabulated for each of the four flow-sorted T cell populations from the two donors. The relative frequency distribution of CDR3 sequences in the four flow cytometrically-defined populations demonstrated that antigen-experienced $CD45RO^+$ populations contained significantly more unique CDR3 sequences with high relative frequency than the $CD45RO^-$ populations. Frequency histograms of TCRβ CDR3 sequences observed in four different T cell subsets distinguished by expression of CD4, CD8, and CD45RO and present in blood showed that ten unique sequences were each observed 200 times in the $CD4^+$ $CD45RO^+$ (antigen-experienced) T cell sample, which was more than twice as frequent as that observed in the $CD4^+$ $CD45RO^-$ populations.

[0109] The use of a PCR step to amplify the TCRβ CDR3 regions prior to sequencing could potentially introduce a systematic bias in the inferred relative abundance of the sequences, due to differences in the efficiency of PCR amplification of CDR3 regions utilizing different Vβ and Jβ gene segments. To estimate the magnitude of any such bias, the TCRβ CDR3 regions from a sample of approximately 30,000 unique $CD4^+CD45RO^+$ T lymphocyte genomes were amplified through 25 cycles of PCR, at which point the PCR product was split in half. Half was set aside, and the other half of the PCR product was amplified for an additional 15 cycles of PCR, for a total of 40 cycles of amplification. The PCR products amplified through 25 and 40 cycles were then sequenced and compared. Over 95% of the 25 cycle sequences were also found in the 40-cycle sample: a linear correlation is observed when comparing the frequency of sequences between these samples. For sequences observed a given number of times in the 25 cycle lane, a combination of PCR bias and sampling variance accounts for the variance around the mean of the number of observations at 40 cycles. Conservatively attributing the mean variation about the line (1.5-fold) entirely to PCR bias, each cycle of PCR amplification potentially introduces a bias of average magnitude $1.5^{1/15}=1.027$. Thus, the 25 cycles of PCR introduces a total bias of average magnitude $1.027^{25}=1.95$ in the inferred relative abundance of distinct CDR3 region sequences.

Example 8

Jβ Gene Segment Usage

[0110] The CDR3 region in each TCR β chain includes sequence derived from one of the thirteen J_β gene segments. Analysis of the CDR3 sequences in the four different T cell populations from the two donors demonstrated that the fraction of total sequences which incorporated sequences derived from the thirteen different J_β gene segments varied more than 20-fold. Jβ utilization among four different T flow cytometrically-defined T cells from a single donor is was relatively constant within a given donor. Moreover, the J_β usage patterns observed in two donors, which were inferred from analysis of genomic DNA from T cells sequenced using the GA, are qualitatively similar to those observed in T cells from umbilical cord blood and from healthy adult donors, both of which were inferred from analysis of cDNA from T cells sequenced using exhaustive capillary-based techniques.

Example 9

Nucleotide Insertion Bias

[0111] Much of the diversity at the CDR3 junctions in TCR α and β chains is created by non-templated nucleotide insertions by the enzyme Terminal Deoxynucloetidyl Transferase (TdT). However, in vivo, selection plays a significant role in shaping the TCR repertoire giving rise to unpredictability. The TdT nucleotide insertion frequencies, independent of selection, were calculated using out of frame TCR sequences. These sequences are non-functional rearrangements that are carried on one allele in T cells where the second allele has a functional rearrangement. The mono-nucleotide insertion bias of TdT favors C and G (Table 11).

TABLE 11

Mono-nucleotide bias in out of frame data

	A	C	G	T
Lane 1	0.24	0.294	0.247	0.216
Lane 2	0.247	0.284	0.256	0.211
Lane 3	0.25	0.27	0.268	0.209
Lane 4	0.255	0.293	0.24	0.21

[0112] Similar nucleotide frequencies are observed in the in frame sequences (Table 12).

TABLE 12

Mono-nucleotide bias in in-frame data

	A	C	G	T
Lane 1	0.21	0.285	0.275	0.228
Lane 2	0.216	0.281	0.266	0.235
Lane 3	0.222	0.266	0.288	0.221
Lane 4	0.206	0.294	0.228	0.27

[0113] The N regions from the out of frame TCR sequences were used to measure the di-nucleotide bias. To isolate the marginal contribution of a di-nucleotide bias, the di-nucleotide frequencies was divided by the mononucleotide frequencies of each of the two bases. The measure is

$$m = \frac{f(n_1 n_2)}{f(n_1)f(n_2)}.$$

[0114] The matrix for m is found in Table 13.

TABLE 13

Di-nucleotide odd ratios for out of frame data

	A	C	G	T
A	1.198	0.938	0.945	0.919
C	0.988	1.172	0.88	0.931
G	0.993	0.701	1.352	0.964
T	0.784	1.232	0.767	1.23

[0115] Many of the dinucleotides are under or over represented. As an example, the odds of finding a GG pair are very high. Since the codons GGN translate to glycine, many glycines are expected in the CDR3 regions.

Example 10

Amino Acid Distributions in the CDR3 Regions

[0116] The distribution of amino acids in the CDR3 regions of TCRβ chains are shaped by the germline sequences for V, D, and J regions, the insertion bias of TdT, and selection. The distribution of amino acids in this region for the four different T cell sub-compartments is very similar between different cell subtypes. Separating the sequences into β chains of fixed length, a position dependent distribution among amino acids, which are grouped by the six chemical properties: small, special, and large hydrophobic, neutral polar, acidic and basic. The distributions are virtually identical except for the CD8+ antigen experienced T cells, which have a higher proportion of acidic bases, particularly at position 5.

[0117] Of particular interest is the comparison between $CD8^+$ and $CD4^+$ TCR sequences as they bind to peptides presented by class I and class II HLA molecules, respectively. The $CD8^+$ antigen experienced T cells have a few positions with a higher proportion of acidic amino acids. This could be do binding with a basic residue found on HLA Class I molecules, but not on Class II.

Example 11

TCR β Chains with Identical Amino Acid Sequences Found in Different People

[0118] The TCR β chain sequences were translated to amino acids and then compared pairwise between the two donors. Many thousands of exact sequence matches were observed. For example, comparing the $CD4^+$ $CD45RO^-$ subcompartments, approximately 8,000 of the 250,000 unique amino acid sequences from donor 1 were exact matches to donor 2. Many of these matching sequences at the amino acid level have multiple nucleotide differences at third codon positions. Following the example mentioned above, 1,500/8,000 identical amino acid matches had >5 nucleotide mismatches. Between any two T cell sub-types, 4-5% of the unique TCRβ sequences were found to have identical amino acid matches.

[0119] Two possibilities were examined: that 1) selection during TCR development is producing these common sequences and 2) the large bias in nucleotide insertion frequency by TdT creates similar nucleotide sequences. The in-frame pairwise matches were compared to the out-of-frame pairwise matches (see Examples 1-4, above). Changing frames preserved all of the features of the genetic code and so the same number of matches should be found if the sequence bias was responsible for the entire observation. However, almost twice as many in-frame matches as out-of-frame matches were found, suggesting that selection at the protein level is playing a significant role.

[0120] To confirm this finding of thousands of identical TCR β chain amino acid sequences, two donors were compared with respect to the CD8$^+$ CD62L$^+$ CD45RA$^+$ (naïve-like) TCRs from a third donor, a 44 year old CMV$^+$ Caucasian female. Identical pairwise matches of many thousands of sequences at the amino acid level between the third donor and each of the original two donors were found. In contrast, 460 sequences were shared between all three donors. The large variation in total number of unique sequences between the donors is a product of the starting material and variations in loading onto the sequencer, and is not representative of a variation in true diversity in the blood of the donors.

Example 12

Higher Frequency Clonotypes are Closer to Germline

[0121] The variation in copy number between different sequences within every T cell sub-compartment ranged by a factor of over 10,000-fold. The only property that correlated with copy number was (the number of insertions plus the number of deletions), which inversely correlated. Results of the analysis showed that deletions play a smaller role than insertions in the inverse correlation with copy number.

[0122] Sequences with less insertions and deletions have receptor sequences closer to germ line. One possibility for the increased number of sequences closer to germ line is that they are the created multiple times during T cell development. Since germ line sequences are shared between people, shared TCRβ chains are likely created by TCRs with a small number of insertions and deletions.

Example 13

"Spectratype" Analysis of TCRβ CDR3 Sequences by V Gene Segment Utilization and CDR3 Length

[0123] TCR diversity has commonly been assessed using the technique of TCR spectratyping, an RT-PCR-based technique that does not assess TCR CDR3 diversity at the sequence level, but rather evaluates the diversity of TCRα or TCRβ CDR3 lengths expressed as mRNA in subsets of αβ T cells that use the same V_α or V_β gene segment. The spectratypes of polyclonal T cell populations with diverse repertoires of TCR CDR3 sequences, such as are seen in umbilical cord blood or in peripheral blood of healthy young adults typically contain CDR3 sequences of 8-10 different lengths that are multiples of three nucleotides, reflecting the selection for in-frame transcripts. Spectratyping also provides roughly quantitative information about the relative frequency of CDR3 sequences with each specific length. To assess whether direct sequencing of TCRβ CDR3 regions from T cell genomic DNA using the sequencer could faithfully capture all of the CDR3 length diversity that is identified by spectratyping, "virtual" TCRβ spectratypes (see Examples above) were generated from the sequence data and compared with TCRβ spectratypes generated using conventional PCR techniques. The virtual spectratypes contained all of the CDR3 length and relative frequency information present in the conventional spectratypes. Direct TCRβ CDR3 sequencing captures all of the TCR diversity information present in a conventional spectratype. A comparison of standard TCRβ spectratype data and calculated TCRβ CDR3 length distributions for sequences utilizing representative TCR Vβ gene segments and present in CD4$^+$CD45RO$^+$ cells from donor 1. Reducing the information contained in the sequence data to a frequency histogram of the unique CDR3 sequences with different lengths within each Vβ family readily reproduces all of the information contained in the spectratype data. In addition, the virtual spectratypes revealed the presence within each V_β family of rare CDR3 sequences with both very short and very long CDR3 lengths that were not detected by conventional PCR-based spectratyping.

Example 14

Estimation of Total CDR3 Sequence Diversity

[0124] After error correction, the number of unique CDR3 sequences observed in each lane of the sequencer flow cell routinely exceeded 1×10^5. Given that the PCR products sequenced in each lane were necessarily derived from a small fraction of the T cell genomes present in each of the two donors, the total number of unique TCRβ CDR3 sequences in the entire T cell repertoire of each individual is likely to be far higher. Estimating the number of unique sequences in the entire repertoire, therefore, requires an estimate of the number of additional unique CDR3 sequences that exist in the blood but were not observed in the sample. The estimation of total species diversity in a large, complex population using measurements of the species diversity present in a finite sample has historically been called the "unseen species problem" (see Examples above). The solution starts with determining the number of new species, or TCRβ CDR3 sequences, that are observed if the experiment is repeated, i.e., if the sequencing is repeated on an identical sample of peripheral blood T cells, e.g., an identically prepared library of TCRβ CDR3 PCR products in a different lane of the sequencer flow cell and counting the number of new CDR3 sequences. For CD8$^+$CD45RO$^-$ cells from donor 2, the predicted and observed number of new CDR3 sequences in a second lane are within 5% (see Examples above), suggesting that this analytic solution can, in fact, be used to estimate the total number of unique TCRβ CDR3 sequences in the entire repertoire.

[0125] The resulting estimates of the total number of unique TCRβ CDR3 sequences in the four flow cytometrically-defined T cell compartments are shown in Table 14.

TABLE 14

TCR repertoire diversity				
Donor	CD8	CD4	CD45RO	Diversity
1	+	−	+	$6.3*10^5$
	+	−	−	$1.24*10^6$
	−	+	+	$8.2*10^5$
	−	+	−	$1.28*10^6$
	Total T cell diversity			$3.97*10^6$
2	+	−	+	$4.4*10^5$
	+	−	−	$9.7*10^5$
	−	+	+	$8.7*10^5$
	−	+	−	$1.03*10^6$
	Total T cell diversity			$3.31*10^6$

[0126] Of note, the total TCRβ diversity in these populations is between 3-4 million unique sequences in the peripheral blood. Surprisingly, the CD45RO$^+$, or antigen-experienced, compartment constitutes approximately 1.5 million of these sequences. This is at least an order of magnitude larger than expected. This discrepancy is likely attributable to the large number of these sequences observed at low relative frequency, which could only be detected through deep sequencing. The estimated TCRβ CDR3 repertoire sizes of each compartment in the two donors are within 20% of each other.

[0127] The results herein demonstrate that the realized TCRβ receptor diversity is at least five-fold higher than previous estimates (~$4*10^6$ distinct CDR3 sequences), and, in particular, suggest far greater TCRβ diversity among CD45RO$^+$ antigen-experienced αβ T cells than has previously been reported (~$1.5*10^6$ distinct CDR3 sequences). However, bioinformatic analysis of the TCR sequence data shows strong biases in the mono- and di-nucleotide content, implying that the utilized TCR sequences are sampled from a distribution much smaller than the theoretical size. With the large diversity of TCRβ chains in each person sampled from a severely constrict space of sequences, overlap of the TCR sequence pools can be expected between each person. In fact, the results showed about 5% of CD8$^+$ naïve TCRβ chains with exact amino acid matches are shared between each pair of three different individuals. As the TCRα pool has been previously measured to be substantially smaller than the theoretical TCRβ diversity, these results show that hundreds to thousands of truly public αβ TCRs can be found.

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 6

ngctctgaga tgaatgtgag tgccttg                                          27


<210> SEQ ID NO 7
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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      TRBV(5-4, 5-5, 5-6, 5-7, 5-8) sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 7

ngctctgagc tgaatgtgaa cgccttg                                          27


<210> SEQ ID NO 8
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 8

ntcgctcagg ctggagtcgg ctg                                              23


<210> SEQ ID NO 9
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV(6-2, 6-3) sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 9

ngctggggtt ggagtcggct g                                                21


<210> SEQ ID NO 10
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-4 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 10

nccctcacgt tggcgtctgc tg                                               22
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<210> SEQ ID NO 11
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-5 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 11

ngctcaggct gctgtcggct g                                             21


<210> SEQ ID NO 12
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-6 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 12

ncgctcaggc tggagttggc tg                                            22


<210> SEQ ID NO 13
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-7 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 13

ncccctcaag ctggagtcag ctg                                           23


<210> SEQ ID NO 14
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-8 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 14

ncactcaggc tggtgtcggc tg                                              22


<210> SEQ ID NO 15
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-9 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 15

ncgctcaggc tggagtcagc tg                                              22


<210> SEQ ID NO 16
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 16

nccactctga agttccagcg cacac                                           25


<210> SEQ ID NO 17
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 17

ncactctgac gatccagcgc acac                                            24


<210> SEQ ID NO 18
<211> LENGTH: 27
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-3 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 18

nctctactct gaagatccag cgcacag                                          27


<210> SEQ ID NO 19
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-4 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 19

nccactctga agatccagcg cacag                                            25


<210> SEQ ID NO 20
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-6 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 20

ncactctgac gatccagcgc acag                                             24


<210> SEQ ID NO 21
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-7 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer
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<400> SEQUENCE: 21

nccactctga cgattcagcg cacag                                             25


<210> SEQ ID NO 22
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-8 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 22

nccactctga agatccagcg cacac                                             25


<210> SEQ ID NO 23
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-9 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 23

ncaccttgga gatccagcgc acag                                              24


<210> SEQ ID NO 24
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV9 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 24

ngcactctga actaaacctg agctctctg                                         29


<210> SEQ ID NO 25
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-1 sequence
<220> FEATURE:
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<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 25

ncccctcact ctggagtctg ctg                                              23


<210> SEQ ID NO 26
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 26

nccccctcac tctggagtca gcta                                             24


<210> SEQ ID NO 27
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-3 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 27

ncctcctcac tctggagtcc gcta                                             24


<210> SEQ ID NO 28
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV(11-1, 11-3) sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 28

nccactctca agatccagcc tgcag                                            25
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<210> SEQ ID NO 29
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV11-2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 29

nctccactct caagatccag cctgcaa                                      27


<210> SEQ ID NO 30
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV(12-3, 12-4, 12-5) sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 30

nccactctga agatccagcc ctcag                                        25


<210> SEQ ID NO 31
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV13 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 31

ncattctgaa ctgaacatga gctccttgg                                    29


<210> SEQ ID NO 32
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV14 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 32

nctactctga aggtgcagcc tgcag                                          25


<210> SEQ ID NO 33
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV15 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 33

ngataacttc caatccagga ggccgaaca                                      29


<210> SEQ ID NO 34
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV16 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 34

nctgtagcct tgagatccag gctacga                                        27


<210> SEQ ID NO 35
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV17 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 35

ncttccacgc tgaagatcca tcccg                                          25


<210> SEQ ID NO 36
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV18 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 36

ngcatcctga ggatccagca ggtag                                          25


<210> SEQ ID NO 37
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV19 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 37

ncctctcact gtgacatcgg ccc                                            23


<210> SEQ ID NO 38
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV20-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 38

ncttgtccac tctgacagtg accagtg                                        27


<210> SEQ ID NO 39
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV23-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 39
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ncagcctggc aatcctgtcc tcag                                         24


<210> SEQ ID NO 40
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV24-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 40

nctccctgtc cctagagtct gccat                                        25


<210> SEQ ID NO 41
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV25-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 41

nccctgaccc tggagtctgc ca                                           22


<210> SEQ ID NO 42
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV27 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 42

nccctgatcc tggagtcgcc ca                                           22


<210> SEQ ID NO 43
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV28 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
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<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 43

nctccctgat tctggagtcc gcca                                            24


<210> SEQ ID NO 44
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV29-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 44

nctaacattc tcaactctga ctgtgagcaa ca                                   32


<210> SEQ ID NO 45
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV30 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal forward primer

<400> SEQUENCE: 45

ncggcagttc atcctgagtt ctaagaagc                                       29


<210> SEQ ID NO 46
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 46

nttacctaca actgtgagtc tggtgccttg tccaaa                               36


<210> SEQ ID NO 47
<211> LENGTH: 34
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 47

nacctacaac ggttaacctg gtccccgaac cgaa                                34


<210> SEQ ID NO 48
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-3 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 48

nacctacaac agtgagccaa cttccctctc caaa                                34


<210> SEQ ID NO 49
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-4 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 49

nccaagacag agagctgggt tccactgcca aa                                  32


<210> SEQ ID NO 50
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-6 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer
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<400> SEQUENCE: 50

nctgtcacag tgagcctggt cccgttccca aa                                32


<210> SEQ ID NO 51
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 51

ncggtgagcc gtgtccctgg cccgaa                                       26


<210> SEQ ID NO 52
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 52

nccagtacgg tcagcctaga gccttctcca aa                                32


<210> SEQ ID NO 53
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-3 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 53

nactgtcagc cgggtgcctg ggccaaa                                      27


<210> SEQ ID NO 54
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-4 sequence
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<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 54

nagagccggg tcccggcgcc gaa                                              23


<210> SEQ ID NO 55
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-5 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 55

nggagccgcg tgcctggccc gaa                                              23


<210> SEQ ID NO 56
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-6 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 56

ngtcagcctg ctgccggccc cgaa                                             24


<210> SEQ ID NO 57
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-7 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 57

ngtgagcctg gtgcccggcc cgaa                                             24
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<210> SEQ ID NO 58
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV2 sequence

<400> SEQUENCE: 58

caagcagaag acggcatacg agctcttccg atcttcaaat ttcactctga agatccggtc 60

cacaa 65

<210> SEQ ID NO 59
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV3-1 sequence

<400> SEQUENCE: 59

caagcagaag acggcatacg agctcttccg atctgctcac ttaaatcttc acatcaattc 60

cctgg 65

<210> SEQ ID NO 60
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV4-1 sequence

<400> SEQUENCE: 60

caagcagaag acggcatacg agctcttccg atctcttaaa ccttcaccta cacgccctgc 60

<210> SEQ ID NO 61
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV(4-2, 4-3) sequence

<400> SEQUENCE: 61

caagcagaag acggcatacg agctcttccg atctcttatt ccttcaccta cacaccctgc 60

<210> SEQ ID NO 62
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-1 sequence

<400> SEQUENCE: 62

caagcagaag acggcatacg agctcttccg atctgctctg agatgaatgt gagcaccttg 60

<210> SEQ ID NO 63
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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TRBV5-3 sequence

<400> SEQUENCE: 63

caagcagaag acggcatacg agctcttccg atctgctctg agatgaatgt gagtgccttg 60

<210> SEQ ID NO 64
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV(5-4, 5-5, 5-6, 5-7, 5-8) sequence

<400> SEQUENCE: 64

caagcagaag acggcatacg agctcttccg atctgctctg agctgaatgt gaacgccttg 60

<210> SEQ ID NO 65
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-1 sequence

<400> SEQUENCE: 65

caagcagaag acggcatacg agctcttccg atcttcgctc aggctggagt cggctg 56

<210> SEQ ID NO 66
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV(6-2, 6-3) sequence

<400> SEQUENCE: 66

caagcagaag acggcatacg agctcttccg atctgctggg gttggagtcg gctg 54

<210> SEQ ID NO 67
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-4 sequence

<400> SEQUENCE: 67

caagcagaag acggcatacg agctcttccg atctccctca cgttggcgtc tgctg 55

<210> SEQ ID NO 68
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-5 sequence

<400> SEQUENCE: 68

caagcagaag acggcatacg agctcttccg atctgctcag gctgctgtcg gctg 54

<210> SEQ ID NO 69
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-6 sequence

<400> SEQUENCE: 69

caagcagaag acggcatacg agctcttccg atctcgctca ggctggagtt ggctg 55

<210> SEQ ID NO 70
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-7 sequence

<400> SEQUENCE: 70

caagcagaag acggcatacg agctcttccg atctcccctc aagctggagt cagctg 56

<210> SEQ ID NO 71
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-8 sequence

<400> SEQUENCE: 71

caagcagaag acggcatacg agctcttccg atctcactca ggctggtgtc ggctg 55

<210> SEQ ID NO 72
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-9 sequence

<400> SEQUENCE: 72

caagcagaag acggcatacg agctcttccg atctcgctca ggctggagtc agctg 55

<210> SEQ ID NO 73
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-1 sequence

<400> SEQUENCE: 73

caagcagaag acggcatacg agctcttccg atctccactc tgaagttcca gcgcacac 58

<210> SEQ ID NO 74
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-2 sequence

<400> SEQUENCE: 74

caagcagaag acggcatacg agctcttccg atctcactct gacgatccag cgcacac 57

<210> SEQ ID NO 75
<211> LENGTH: 60

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-3 sequence

<400> SEQUENCE: 75

caagcagaag acggcatacg agctcttccg atctctctac tctgaagatc cagcgcacag     60


<210> SEQ ID NO 76
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-4 sequence

<400> SEQUENCE: 76

caagcagaag acggcatacg agctcttccg atctccactc tgaagatcca gcgcacag       58


<210> SEQ ID NO 77
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-6 sequence

<400> SEQUENCE: 77

caagcagaag acggcatacg agctcttccg atctcactct gacgatccag cgcacag        57


<210> SEQ ID NO 78
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-7 sequence

<400> SEQUENCE: 78

caagcagaag acggcatacg agctcttccg atctccactc tgacgattca gcgcacag       58


<210> SEQ ID NO 79
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-8 sequence

<400> SEQUENCE: 79

caagcagaag acggcatacg agctcttccg atctccactc tgaagatcca gcgcacac       58


<210> SEQ ID NO 80
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-9 sequence

<400> SEQUENCE: 80

caagcagaag acggcatacg agctcttccg atctcacctt ggagatccag cgcacag        57
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<210> SEQ ID NO 81
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV9 sequence

<400> SEQUENCE: 81

caagcagaag acggcatacg agctcttccg atctgcactc tgaactaaac ctgagctctc     60

tg                                                                    62


<210> SEQ ID NO 82
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-1 sequence

<400> SEQUENCE: 82

caagcagaag acggcatacg agctcttccg atctcccctc actctggagt ctgctg         56


<210> SEQ ID NO 83
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-2 sequence

<400> SEQUENCE: 83

caagcagaag acggcatacg agctcttccg atctccccct cactctggag tcagcta        57


<210> SEQ ID NO 84
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV10-3 sequence

<400> SEQUENCE: 84

caagcagaag acggcatacg agctcttccg atctcctcct cactctggag tccgcta        57


<210> SEQ ID NO 85
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV(11-1, 11-3) sequence

<400> SEQUENCE: 85

caagcagaag acggcatacg agctcttccg atctccactc tcaagatcca gcctgcag       58


<210> SEQ ID NO 86
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV11-2 sequence

<400> SEQUENCE: 86
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caagcagaag acggcatacg agctcttccg atctctccac tctcaagatc cagcctgcaa     60


<210> SEQ ID NO 87
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV(12-3, 12-4, 12-5) sequence

<400> SEQUENCE: 87

caagcagaag acggcatacg agctcttccg atctccactc tgaagatcca gccctcag       58


<210> SEQ ID NO 88
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV13 sequence

<400> SEQUENCE: 88

caagcagaag acggcatacg agctcttccg atctcattct gaactgaaca tgagctcctt     60

gg                                                                    62


<210> SEQ ID NO 89
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV14 sequence

<400> SEQUENCE: 89

caagcagaag acggcatacg agctcttccg atctctactc tgaaggtgca gcctgcag       58


<210> SEQ ID NO 90
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV15 sequence

<400> SEQUENCE: 90

caagcagaag acggcatacg agctcttccg atctgataac ttccaatcca ggaggccgaa     60

ca                                                                    62


<210> SEQ ID NO 91
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV16 sequence

<400> SEQUENCE: 91

caagcagaag acggcatacg agctcttccg atctctgtag ccttgagatc caggctacga     60


<210> SEQ ID NO 92
<211> LENGTH: 58
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV17 sequence

<400> SEQUENCE: 92

caagcagaag acggcatacg agctcttccg atctcttcca cgctgaagat ccatcccg       58


<210> SEQ ID NO 93
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV18 sequence

<400> SEQUENCE: 93

caagcagaag acggcatacg agctcttccg atctgcatcc tgaggatcca gcaggtag       58


<210> SEQ ID NO 94
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV19 sequence

<400> SEQUENCE: 94

caagcagaag acggcatacg agctcttccg atctcctctc actgtgacat cggccc         56


<210> SEQ ID NO 95
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV20-1 sequence

<400> SEQUENCE: 95

caagcagaag acggcatacg agctcttccg atctcttgtc cactctgaca gtgaccagtg     60


<210> SEQ ID NO 96
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV23-1 sequence

<400> SEQUENCE: 96

caagcagaag acggcatacg agctcttccg atctcagcct ggcaatcctg tcctcag        57


<210> SEQ ID NO 97
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV24-1 sequence

<400> SEQUENCE: 97

caagcagaag acggcatacg agctcttccg atctctccct gtccctagag tctgccat       58


<210> SEQ ID NO 98
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<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV25-1 sequence

<400> SEQUENCE: 98

caagcagaag acggcatacg agctcttccg atctccctga ccctggagtc tgcca   55

<210> SEQ ID NO 99
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV27 sequence

<400> SEQUENCE: 99

caagcagaag acggcatacg agctcttccg atctccctga tcctggagtc gccca   55

<210> SEQ ID NO 100
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV28 sequence

<400> SEQUENCE: 100

caagcagaag acggcatacg agctcttccg atctctccct gattctggag tccgcca   57

<210> SEQ ID NO 101
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV29-1 sequence

<400> SEQUENCE: 101

caagcagaag acggcatacg agctcttccg atctctaaca ttctcaactc tgactgtgag   60

caaca   65

<210> SEQ ID NO 102
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV30 sequence

<400> SEQUENCE: 102

caagcagaag acggcatacg agctcttccg atctcggcag ttcatcctga gttctaagaa   60

gc   62

<210> SEQ ID NO 103
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-1 sequence

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<400> SEQUENCE: 103

aatgatacgg cgaccaccga gatctttacc tacaactgtg agtctggtgc cttgtccaaa     60


<210> SEQ ID NO 104
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-3 sequence

<400> SEQUENCE: 104

aatgatacgg cgaccaccga gatctaccta caacagtgag ccaacttccc tctccaaa       58


<210> SEQ ID NO 105
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-4 sequence

<400> SEQUENCE: 105

aatgatacgg cgaccaccga gatctccaag acagagagct gggttccact gccaaa         56


<210> SEQ ID NO 106
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-6 sequence

<400> SEQUENCE: 106

aatgatacgg cgaccaccga gatctctgtc acagtgagcc tggtcccgtt cccaaa         56


<210> SEQ ID NO 107
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-1 sequence

<400> SEQUENCE: 107

aatgatacgg cgaccaccga gatctcggtg agccgtgtcc ctggcccgaa                50


<210> SEQ ID NO 108
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ2-2 sequence

<400> SEQUENCE: 108

aatgatacgg cgaccaccga gatctccagt acggtcagcc tagagccttc tccaaa         56


<210> SEQ ID NO 109
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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TRBJ2-3 sequence

<400> SEQUENCE: 109

aatgatacgg cgaccaccga gatctactgt cagccgggtg cctgggccaa a 51

<210> SEQ ID NO 110
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBJ2-4 sequence

<400> SEQUENCE: 110

aatgatacgg cgaccaccga gatctagagc cgggtcccgg cgccgaa 47

<210> SEQ ID NO 111
<211> LENGTH: 47
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBJ2-5 sequence

<400> SEQUENCE: 111

aatgatacgg cgaccaccga gatctggagc cgcgtgcctg gcccgaa 47

<210> SEQ ID NO 112
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBJ2-6 sequence

<400> SEQUENCE: 112

aatgatacgg cgaccaccga gatctgtcag cctgctgccg gccccgaa 48

<210> SEQ ID NO 113
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBJ2-7 sequence

<400> SEQUENCE: 113

aatgatacgg cgaccaccga gatctgtgag cctggtgccc ggcccgaa 48

<210> SEQ ID NO 114
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV1*01 sequence

<400> SEQUENCE: 114

gatactggaa ttacccagac accaaaatac ctggtcacag caatggggag taaaaggaca 60

atgaaacgtg agcatctggg acatgattct atgtattggt acagacagaa agctaagaaa 120

tccctggagt tcatgtttta ctacaactgt aaggaattca ttgaaaacaa gactgtgcca 180

aatcacttca cacctgaatg ccctgacagc tctcgcttat accttcatgt ggtcgcactg 240

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cagcaagaag actcagctgc gtatctctgc accagcagcc aaga                   284


<210> SEQ ID NO 115
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV2*01 sequence

<400> SEQUENCE: 115

gaacctgaag tcacccagac tcccagccat caggtcacac agatgggaca ggaagtgatc     60

ttgcgctgtg tccccatctc taatcactta tacttctatt ggtacagaca aatcttgggg    120

cagaaagtcg agtttctggt ttccttttat aataatgaaa tctcagagaa gtctgaaata    180

ttcgatgatc aattctcagt tgaaaggcct gatggatcaa atttcactct gaagatccgg    240

tccacaaagc tggaggactc agccatgtac ttctgtgcca gcagtgaagc               290


<210> SEQ ID NO 116
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV2*03 sequence

<400> SEQUENCE: 116

gaacctgaag tcacccagac tcccagccat caggtcacac agatgggaca ggaagtgatc     60

ttgcgctgtg tccccatctc taatcactta tacttctatt ggtacagaca aatcttgggg    120

cagaaagtcg agtttctggt ttccttttat aataatgaaa tctcagagaa gtctgaaata    180

ttcgatgatc aattctcagt tgagaggcct gatggatcaa atttcactct gaagatccgg    240

tccacaaagc tggaggactc agccatgtac ttctgtgcca gcagtgaa                 288


<210> SEQ ID NO 117
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV3-1*01 sequence

<400> SEQUENCE: 117

gacacagctg tttcccagac tccaaaatac ctggtcacac agatgggaaa cgacaagtcc     60

attaaatgtg aacaaaatct gggccatgat actatgtatt ggtataaaca ggactctaag    120

aaatttctga agataatgtt tagctacaat aataaggagc tcattataaa tgaaacagtt    180

ccaaatcgct tctcacctaa atctccagac aaagctcact taaatcttca catcaattcc    240

ctggagcttg gtgactctgc tgtgtatttc tgtgccagca gccaaga                  287


<210> SEQ ID NO 118
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV3-1*02 sequence

<400> SEQUENCE: 118
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gacacagctg tttcccagac tccaaaatac ctggtcacac agatgggaaa cgacaagtcc 60

attaaatgtg aacaaaatct gggccatgat actatgtatt ggtataaaca ggactctaag 120

aaatttctga agataatgtt tagctacaat aacaaggaga tcattataaa tgaaacagtt 180

ccaaatcgat tctcacctaa atctccagac aaagctaaat taaatcttca catcaattcc 240

ctggagcttg gtgactctgc tgtgtatttc tgtgccagc 279

<210> SEQ ID NO 119
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV3-2*01 sequence

<400> SEQUENCE: 119

gacacagccg tttcccagac tccaaaatac ctggtcacac agatgggaaa aaaggagtct 60

cttaaatgag aacaaaatct gggccataat gctatgtatt ggtataaaca ggactctaag 120

aaatttctga agacaatgtt tatctacagt aacaaggagc caattttaaa tgaaacagtt 180

ccaaatcgct tctcacctga ctctccagac aaagctcatt taaatcttca catcaattcc 240

ctggagcttg gtgactctgc tgtgtatttc tgtgccagca gccaaga 287

<210> SEQ ID NO 120
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV3-2*02 sequence

<400> SEQUENCE: 120

gacacagccg tttcccagac tccaaaatac ctggtcacac agatgggaaa aaaggagtct 60

cttaaatgag aacaaaatct gggccataat gctatgtatt ggtataaaca ggactctaag 120

aaatttctga agacaatgtt tatctacagt aacaaggagc caattttaaa tgaaacagtt 180

ccaaatcgct tctcacctga ctctccagac aaagttcatt taaatcttca catcaattcc 240

ctggagcttg gtgactctgc tgtgtatttc tgtgccagca gccaaga 287

<210> SEQ ID NO 121
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV3-2*03 sequence

<400> SEQUENCE: 121

gacacagccg tttcccagac tccaaaatac ctggtcacac agacgggaaa aaaggagtct 60

cttaaatgag aacaaaatct gggccataat gctatgtatt ggtataaaca ggactctaag 120

aaatttctga agacaatgtt tatctacagt aacaaggagc caattttaaa tgaaacagtt 180

ccaaatcgct tctcacctga ctctccagac aaagttcatt taaatcttca catcaattcc 240

ctggagcttg gtgactctgc tgtgtatttc tgtgccagca gccaa 285

<210> SEQ ID NO 122

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<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV4-1*01 sequence

<400> SEQUENCE: 122

gacactgaag ttacccagac accaaaacac ctggtcatgg gaatgacaaa taagaagtct   60

ttgaaatgtg aacaacatat ggggcacagg gctatgtatt ggtacaagca gaaagctaag   120

aagccaccgg agctcatgtt tgtctacagc tatgagaaac tctctataaa tgaaagtgtg   180

ccaagtcgct tctcacctga atgccccaac agctctctct taaaccttca cctacacgcc   240

ctgcagccag aagactcagc cctgtatctc tgcgccagca gccaaga   287

<210> SEQ ID NO 123
<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV4-1*02 sequence

<400> SEQUENCE: 123

cacctggtca tgggaatgac aaataagaag tctttgaaat gtgaacaaca tatggggcac   60

agggcaatgt attggtacaa gcagaaagct aagaagccac cggagctcat gtttgtctac   120

agctatgaga aactctctat aaatgaaagt gtgccaagtc gcttctcacc tgaatgcccc   180

aacagctctc tcttaaacct tcacctacac gccctgcagc cagaagactc agccctgtat   240

ctctgcgcca gcagccaa   258

<210> SEQ ID NO 124
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV4-2*01 sequence

<400> SEQUENCE: 124

gaaacgggag ttacgcagac accaagacac ctggtcatgg gaatgacaaa taagaagtct   60

ttgaaatgtg aacaacatct ggggcataac gctatgtatt ggtacaagca aagtgctaag   120

aagccactgg agctcatgtt tgtctacaac tttaaagaac agactgaaaa caacagtgtg   180

ccaagtcgct tctcacctga atgccccaac agctctcact tattccttca cctacacacc   240

ctgcagccag aagactcggc cctgtatctc tgtgccagca gccaaga   287

<210> SEQ ID NO 125
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV4-2*02 sequence

<400> SEQUENCE: 125

gaaacgggag ttacgcagac accaagacac ctggtcatgg gaatgacaaa taagaagtct   60

ttgaaatgtg aacaacatct ggggcataac gctatgtatt ggtacaagca aagtgctaag   120

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aagccactgg agctcatgtt tgtctacaac tttaaagaac agactgaaaa caacagtgtg 180

ccaagtcgct tctcacctga atgccccaac agctctcact tatgccttca cctacacacc 240

ctgcagccag aagactcggc cctgtatctc tgtgccagca cc 282

<210> SEQ ID NO 126
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV4-3*01 sequence

<400> SEQUENCE: 126

gaaacgggag ttacgcagac accaagacac ctggtcatgg gaatgacaaa taagaagtct 60

ttgaaatgtg aacaacatct gggtcataac gctatgtatt ggtacaagca aagtgctaag 120

aagccactgg agctcatgtt tgtctacagt cttgaagaac gggttgaaaa caacagtgtg 180

ccaagtcgct tctcacctga atgccccaac agctctcact tattccttca cctacacacc 240

ctgcagccag aagactcggc cctgtatctc tgcgccagca gccaaga 287

<210> SEQ ID NO 127
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV4-3*02 sequence

<400> SEQUENCE: 127

gaaacgggag ttacgcagac accaagacac ctggtcatgg gaatgacaaa taagaagtct 60

ttgaaatgtg aacaacatct gggtcataac gctatgtatt ggtacaagca aagtgctaag 120

aagccactgg agctcatgtt tgtctacagt cttgaagaac gggttgaaaa caacagtgtg 180

ccaagtcgct tctcacctga atgccccaac agctctcact tatcccttca cctacacacc 240

ctgcagccag aagactcggc cctgtatctc tgcgccagca gc 282

<210> SEQ ID NO 128
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV4-3*03 sequence

<400> SEQUENCE: 128

gaaacgggag ttacgcagac accaagacac ctggtcatgg gaatgacaaa taagaagtct 60

ttgaaatgtg aacaacatct gggtcataac gctatgtatt ggtacaagca aagtgctaag 120

aagccactgg agctcatgtt tgtctacagt cttgaagaac gtgttgaaaa caacagtgtg 180

ccaagtcgct tctcacctga atgccccaac agctctcact tattccttca cctacacacc 240

ctgcagccag aagactcggc cctgtatctc tgcgccagca gc 282

<210> SEQ ID NO 129
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

TRBV4-3*04 sequence

<400> SEQUENCE: 129

aagaagtctt tgaaatgtga acaacatctg gggcataacg ctatgtattg gtacaagcaa 60

agtgctaaga agccactgga gctcatgttt gtctacagtc ttgaagaacg ggttgaaaac 120

aacagtgtgc caagtcgctt ctcacctgaa tgccccaaca gctctcactt attccttcac 180

ctacacaccc tgcagccaga agactcggcc ctgtatctct gcgccagcag c 231

<210> SEQ ID NO 130
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-1*01 sequence

<400> SEQUENCE: 130

aaggctggag tcactcaaac tccaagatat ctgatcaaaa cgagaggaca gcaagtgaca 60

ctgagctgct cccctatctc tgggcatagg agtgtatcct ggtaccaaca gaccccagga 120

cagggccttc agttcctctt tgaatacttc agtgagacac agagaaacaa aggaaacttc 180

cctggtcgat tctcagggcg ccagttctct aactctcgct ctgagatgaa tgtgagcacc 240

ttggagctgg gggactcggc cctttatctt tgcgccagca gcttgg 286

<210> SEQ ID NO 131
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-1*02 sequence

<400> SEQUENCE: 131

agggctgggg tcactcaaac tccaagacat ctgatcaaaa cgagaggaca gcaagtgaca 60

ctgggctgct cccctatctc tgggcatagg agtgtatcct ggtaccaaca gaccctagga 120

cagggccttc agttcctctt tgaatacttc agtgagacac agagaaacaa aggaaacttc 180

cttggtcgat tctcagggcg ccagttctct aactctcgct ctgagatgaa tgtgagcacc 240

ttggagctgg gggactcggc cctttatctt tgcgccagcg cttgc 285

<210> SEQ ID NO 132
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-3*01 sequence

<400> SEQUENCE: 132

gaggctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact 60

ctgagatgct ctcctatctc tgggcacagc agtgtgtcct ggtaccaaca ggccccgggt 120

caggggcccc agtttatctt tgaatatgct aatgagttaa ggagatcaga aggaaacttc 180

cctaatcgat tctcagggcg ccagttccat gactgttgct ctgagatgaa tgtgagtgcc 240

ttggagctgg gggactcggc cctgtatctc tgtgccagaa gcttgg 286

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<210> SEQ ID NO 133
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-3*02 sequence

<400> SEQUENCE: 133

gaggctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact   60

ctgagatgct ctcctatctc tgggcacagc agtgtgtcct ggtaccaaca ggccccgggt   120

caggggcccc agtttatctt tgaatatgct aatgagttaa ggagatcaga aggaaacttc   180

cctaatcgat tctcagggcg ccagttccat gactattgct ctgagatgaa tgtgagtgcc   240

ttggagctgg gggactcggc cctgtatctc tgtgccagaa gcttgg   286

<210> SEQ ID NO 134
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-4*01 sequence

<400> SEQUENCE: 134

gagactggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact   60

ctgagatgct cttctcagtc tgggcacaac actgtgtcct ggtaccaaca ggccctgggt   120

caggggcccc agtttatctt tcagtattat agggaggaag agaatggcag aggaaacttc   180

cctcctagat tctcaggtct ccagttccct aattatagct ctgagctgaa tgtgaacgcc   240

ttggagctgg acgactcggc cctgtatctc tgtgccagca gcttgg   286

<210> SEQ ID NO 135
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-4*02 sequence

<400> SEQUENCE: 135

gagactggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact   60

ctgagatgct cttctcagtc tgggcacaac actgtgtcct ggtaccaaca ggccctgggt   120

caggggcccc agtttatctt tcagtattat agggaggaag agaatggcag aggaaacttc   180

cctcctagat tctcaggtct ccagttccct aattataact ctgagctgaa tgtgaacgcc   240

ttggagctgg acgactcggc cctgtatctc tgtgccagca gc   282

<210> SEQ ID NO 136
<211> LENGTH: 234
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-4*03 sequence

<400> SEQUENCE: 136

cagcaagtga cactgagatg ctcttctcag tctgggcaca acactgtgtc ctggtaccaa   60

caggccctgg gtcaggggcc ccagtttatc tttcagtatt atagggagga agagaatggc   120

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agaggaaact tccctcctag attctcaggt ctccagttcc ctaattatag ctctgagctg    180

aatgtgaacg ccttggagct ggacgactcg gccctgtatc tctgtgccag cagc          234


<210> SEQ ID NO 137
<211> LENGTH: 192
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-4*04 sequence

<400> SEQUENCE: 137

actgtgtcct ggtaccaaca ggccctgggt caggggcccc agtttatctt tcagtattat     60

agggaggaag agaatggcag aggaaactcc cctcctagat tctcaggtct ccagttccct    120

aattatagct ctgagctgaa tgtgaacgcc ttggagctgg acgactcggc cctgtatctc    180

tgtgccagca gc                                                         192


<210> SEQ ID NO 138
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-5*01 sequence

<400> SEQUENCE: 138

gacgctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact     60

ctgagatgct ctcctatctc tgggcacaag agtgtgtcct ggtaccaaca ggtcctgggt    120

caggggcccc agtttatctt tcagtattat gagaaagaag agagaggaag aggaaacttc    180

cctgatcgat tctcagctcg ccagttccct aactatagct ctgagctgaa tgtgaacgcc    240

ttgttgctgg gggactcggc cctgtatctc tgtgccagca gcttgg                    286


<210> SEQ ID NO 139
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-5*02 sequence

<400> SEQUENCE: 139

gacgctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcacgtgact     60

ctgagatgct ctcctatctc tgggcacaag agtgtgtcct ggtaccaaca ggtcctgggt    120

caggggcccc agtttatctt tcagtattat gagaaagaag agagaggaag aggaaacttc    180

cctgatcgat tctcagctcg ccagttccct aactatagct ctgagctgaa tgtgaacgcc    240

ttgttgctgg gggactcggc cctgtatctc tgtgccagca gc                        282


<210> SEQ ID NO 140
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV5-5*03 sequence

<400> SEQUENCE: 140
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gacgctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact 60

ctgagatgct ctcctatctc tgagcacaag agtgtgtcct ggtaccaaca ggtcctgggt 120

caggggcccc agtttatctt tcagtattat gagaaagaag agagaggaag aggaaacttc 180

cctgatcgat tctcagctcg ccagttccct aactatagct ctgagctgaa tgtgaacgcc 240

ttgttgctgg gggactcggc cctgtatctc tgtgccagca gc 282

<210> SEQ ID NO 141
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-6*01 sequence

<400> SEQUENCE: 141

gacgctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcaagtgact 60

ctgagatgct ctcctaagtc tgggcatgac actgtgtcct ggtaccaaca ggccctgggt 120

caggggcccc agtttatctt tcagtattat gaggaggaag agagacagag aggcaacttc 180

cctgatcgat tctcaggtca ccagttccct aactatagct ctgagctgaa tgtgaacgcc 240

ttgttgctgg gggactcggc cctctatctc tgtgccagca gcttgg 286

<210> SEQ ID NO 142
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-7*01 sequence

<400> SEQUENCE: 142

gacgctggag tcacccaaag tcccacacac ctgatcaaaa cgagaggaca gcacgtgact 60

ctgagatgct ctcctatctc tgggcacacc agtgtgtcct cgtaccaaca ggccctgggt 120

caggggcccc agtttatctt tcagtattat gagaaagaag agagaggaag aggaaacttc 180

cctgatcaat tctcaggtca ccagttccct aactatagct ctgagctgaa tgtgaacgcc 240

ttgttgctag gggactcggc cctctatctc tgtgccagca gcttgg 286

<210> SEQ ID NO 143
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-8*01 sequence

<400> SEQUENCE: 143

gaggctggag tcacacaaag tcccacacac ctgatcaaaa cgagaggaca gcaagcgact 60

ctgagatgct ctcctatctc tgggcacacc agtgtgtact ggtaccaaca ggccctgggt 120

ctgggcctcc agttcctcct ttggtatgac gagggtgaag agagaaacag aggaaacttc 180

cctcctagat tttcaggtcg ccagttccct aattatagct ctgagctgaa tgtgaacgcc 240

ttggagctgg aggactcggc cctgtatctc tgtgccagca gcttgg 286

<210> SEQ ID NO 144

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<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV5-8*02 sequence

<400> SEQUENCE: 144

aggacagcaa gcgactctga gatgctctcc tatctctggg cacaccagtg tgtactggta 60

ccaacaggcc ctgggtctgg gcctccagct cctcctttgg tatgacgagg gtgaagagag 120

aaacagagga aacttccctc ctagattttc aggtcgccag ttccctaatt atagctctga 180

gctgaatgtg aacgccttgg agctggagga ctcggccctg tatctctgtg ccagcagc 238

<210> SEQ ID NO 145
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-1*01 sequence

<400> SEQUENCE: 145

aatgctggtg tcactcagac cccaaaattc caggtcctga agacaggaca gagcatgaca 60

ctgcagtgtg cccaggatat gaaccataac tccatgtact ggtatcgaca agacccaggc 120

atgggactga ggctgattta ttactcagct tctgagggta ccactgacaa aggagaagtc 180

cccaatggct acaatgtctc cagattaaac aaacgggagt tctcgctcag gctggagtcg 240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gtgaagc 287

<210> SEQ ID NO 146
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-2*01 sequence

<400> SEQUENCE: 146

aatgctggtg tcactcagac cccaaaattc cgggtcctga agacaggaca gagcatgaca 60

ctgctgtgtg cccaggatat gaaccatgaa tacatgtact ggtatcgaca agacccaggc 120

atggggctga ggctgattca ttactcagtt ggtgagggta caactgccaa aggagaggtc 180

cctgatggct acaatgtctc cagattaaaa aaacagaatt tcctgctggg gttggagtcg 240

gctgctccct cccaaacatc tgtgtacttc tgtgccagca gttactc 287

<210> SEQ ID NO 147
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-3*01 sequence

<400> SEQUENCE: 147

aatgctggtg tcactcagac cccaaaattc cgggtcctga agacaggaca gagcatgaca 60

ctgctgtgtg cccaggatat gaaccatgaa tacatgtact ggtatcgaca agacccaggc 120

atggggctga ggctgattca ttactcagtt ggtgagggta caactgccaa aggagaggtc 180

-continued

cctgatggct acaatgtctc cagattaaaa aaacagaatt tcctgctggg gttggagtcg 240

gctgctccct cccaaacatc tgtgtacttc tgtgccagca gttactc 287

<210> SEQ ID NO 148
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-4*01 sequence

<400> SEQUENCE: 148

attgctggga tcacccaggc accaacatct cagatcctgg cagcaggacg gcgcatgaca 60

ctgagatgta cccaggatat gagacataat gccatgtact ggtatagaca agatctagga 120

ctggggctaa ggctcatcca ttattcaaat actgcaggta ccactggcaa aggagaagtc 180

cctgatggtt atagtgtctc cagagcaaac acagatgatt tcccccctcac gttggcgtct 240

gctgtaccct ctcagacatc tgtgtacttc tgtgccagca gtgactc 287

<210> SEQ ID NO 149
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-4*02 sequence

<400> SEQUENCE: 149

actgctggga tcacccaggc accaacatct cagatcctgg cagcaggacg gagcatgaca 60

ctgagatgta cccaggatat gagacataat gccatgtact ggtatagaca agatctagga 120

ctggggctaa ggctcatcca ttattcaaat actgcaggta ccactggcaa aggagaagtc 180

cctgatggtt atagtgtctc cagagcaaac acagatgatt tcccccctcac gttggcgtct 240

gctgtaccct ctcagacatc tgtgtacttc tgtgccagca gtgactc 287

<210> SEQ ID NO 150
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-5*01 sequence

<400> SEQUENCE: 150

aatgctggtg tcactcagac cccaaaattc caggtcctga agacaggaca gagcatgaca 60

ctgcagtgtg cccaggatat gaaccatgaa tacatgtcct ggtatcgaca agacccaggc 120

atggggctga ggctgattca ttactcagtt ggtgctggta tcactgacca aggagaagtc 180

cccaatggct acaatgtctc cagatcaacc acagaggatt tcccgctcag gctgctgtcg 240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gttactc 287

<210> SEQ ID NO 151
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV6-6*01 sequence

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<400> SEQUENCE: 151

aatgctggtg tcactcagac cccaaaattc cgcatcctga agataggaca gagcatgaca     60

ctgcagtgta cccaggatat gaaccataac tacatgtact ggtatcgaca agacccaggc    120

atggggctga agctgattta ttattcagtt ggtgctggta tcactgataa aggagaagtc    180

ccgaatggct acaacgtctc cagatcaacc acagaggatt tcccgctcag gctggagttg    240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gttactc                 287


<210> SEQ ID NO 152
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-6*02 sequence

<400> SEQUENCE: 152

aatgctggtg tcactcagac cccaaaattc cgcatcctga agataggaca gagcatgaca     60

ctgcagtgtg cccaggatat gaaccataac tacatgtact ggtatcgaca agacccaggc    120

atggggctga agctgattta ttattcagtt ggtgctggta tcactgacaa aggagaagtc    180

ccgaatggct acaacgtctc cagatcaacc acagaggatt tcccgctcag gctggagttg    240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gt                      282


<210> SEQ ID NO 153
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-6*03 sequence

<400> SEQUENCE: 153

aatgctggtg tcactcagac cccaaaattc cgcatcctga agataggaca gagcatgaca     60

ctgcagtgtg cccaggatat gaaccataac tacatgtact ggtatcgaca agacccaggc    120

atggggctga agctgattta ttattcagtt ggtgctggta tcactgataa aggagaagtc    180

ccgaatggct acaacgtctc cagatcaacc acagaggatt tcccgctcag gctggagttg    240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gt                      282


<210> SEQ ID NO 154
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-6*04 sequence

<400> SEQUENCE: 154

aatgctggtg tcactcagac cccaaaattc cgcatcctga agataggaca gagcatgaca     60

ctgcagtgta cccaggatat gaaccatgaa tacatgtact ggtatcgaca agacccaggc    120

atggggctga agctgattta ttattcagtt ggtgctggta tcactgataa aggagaagtc    180

ccgaatggct acaatgtctc cagatcaacc acagaggatt tcccgctcag gctggagttg    240

gctgctccct cccagacatc tgtgtacttc tgtgccagca gtcga                   285
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<210> SEQ ID NO 155
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-6*05 sequence

<400> SEQUENCE: 155

aatgctggtg tcactcagac cccaaaattc cgcatcctga agataggaca gagcatgaca     60

ctgcagtgtg cccaggatat gaaccataac tacatgtact ggtatcgaca agacccaggc    120

atggggctga agctgattta ttattcagtt ggtgctggta tcactgacaa aggagaagtc    180

ccgaatggct acaacgtctc cagatcaacc acagaggatt tcccgctcag gctggagttg    240

gctgctgcct cccagacatc tgtgtacttc tgtgccagca gc                       282


<210> SEQ ID NO 156
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-7*01 sequence

<400> SEQUENCE: 156

aatgctggtg tcactcagac cccaaaattc cacgtcctga agacaggaca gagcatgact     60

ctgctgtgtg cccaggatat gaaccatgaa tacatgtatc ggtatcgaca agacccaggc    120

aaggggctga ggctgattta ctactcagtt gctgctgctc tcactgacaa aggagaagtt    180

cccaatggct acaatgtctc cagatcaaac acagaggatt tccccctcaa gctggagtca    240

gctgctccct ctcagacttc tgtttacttc tgtgccagca gttactc                  287


<210> SEQ ID NO 157
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-8*01 sequence

<400> SEQUENCE: 157

aatgctggtg tcactcagac cccaaaattc cacatcctga agacaggaca gagcatgaca     60

ctgcagtgtg cccaggatat gaaccatgga tacatgtcct ggtatcgaca agacccaggc    120

atggggctga gactgattta ctactcagct gctgctggta ctactgacaa agaagtcccc    180

aatggctaca atgtctctag attaaacaca gaggatttcc cactcaggct ggtgtcggct    240

gctccctccc agacatctgt gtacttgtgt gccagcagtt actc                     284


<210> SEQ ID NO 158
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV6-9*01 sequence

<400> SEQUENCE: 158

aatgctggtg tcactcagac cccaaaattc cacatcctga agacaggaca gagcatgaca     60

ctgcagtgtg cccaggatat gaaccatgga tacttgtcct ggtatcgaca agacccaggc    120
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atggggctga ggcgcattca ttactcagtt gctgctggta tcactgacaa aggagaagtc 180

cccgatggct acaatgtatc cagatcaaac acagaggatt tcccgctcag gctggagtca 240

gctgctccct cccagacatc tgtatacttc tgtgccagca gttattc 287

<210> SEQ ID NO 159
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-1*01 sequence

<400> SEQUENCE: 159

ggtgctggag tctcccagtc cctgagacac aaggtagcaa agaagggaaa ggatgtagct 60

ctcagatatg atccaatttc aggtcataat gccctttatt ggtaccgaca gagcctgggg 120

cagggcctgg agtttccaat ttacttccaa ggcaaggatg cagcagacaa atcggggctt 180

ccccgtgatc ggttctctgc acagaggtct gagggatcca tctccactct gaagttccag 240

cgcacacagc agggggactt ggctgtgtat ctctgtgcca gcagctcagc 290

<210> SEQ ID NO 160
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-2*01 sequence

<400> SEQUENCE: 160

ggagctggag tctcccagtc ccccagtaac aaggtcacag agaagggaaa ggatgtagag 60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca gagcctgggg 120

cagggcctgg agtttttaat ttacttccaa ggcaacagtg caccagacaa atcagggctg 180

cccagtgatc gcttctctgc agagaggact gggggatccg tctccactct gacgatccag 240

cgcacacagc aggaggactc ggccgtgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 161
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-2*02 sequence

<400> SEQUENCE: 161

ggagctggag tctcccagtc ccccagtaac aaggtcacag agaagggaaa ggatgtagag 60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca gaggctgggg 120

cagggcctgg agtttttaat ttacttccaa ggcaacagtg caccagacaa atcagggctg 180

cccagtgatc gcttctctgc agagaggact ggggaatccg tctccactct gacgatccag 240

cgcacacagc aggaggactc ggccgtgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 162
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-2*03 sequence

<400> SEQUENCE: 162

ggagctggag tctcccagtc cccagtaac aaggtcacag agaagggaaa ggatgtagag     60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca gaggctgggg    120

cagggcctgg agtttttaat ttacttccaa ggcaacagtg caccagacaa atcagggctg    180

cccagtgatc gcttctctgc agagaggact ggggaatccg tctccactct gacgatccag    240

cgcacacagc aggaggactc ggccgtgtat ctctgtacca gcagcttagc               290


<210> SEQ ID NO 163
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-2*04 sequence

<400> SEQUENCE: 163

ggagctggag tttcccagtc cccagtaac aaggtcacag agaagggaaa ggatgtagag     60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca gagcctgggg    120

cagggcctgg agtttttaat ttacttccaa ggcaacagtg caccagacaa atcagggctg    180

cccagtgatc gcttctctgc agagaggact gggggatccg tctccactct gacgatccag    240

cgcacacagc aggaggactc ggccgtgtat ctctgtgcca gcagctta                 288


<210> SEQ ID NO 164
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-3*01 sequence

<400> SEQUENCE: 164

ggtgctggag tctcccagac cccagtaac aaggtcacag agaagggaaa atatgtagag     60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca aagcctgggg    120

cagggcccag agtttctaat ttacttccaa ggcacgggtg cggcagatga ctcagggctg    180

cccaacgatc ggttctttgc agtcaggcct gagggatccg tctctactct gaagatccag    240

cgcacagagc gggggactc agccgtgtat ctctgtgcca gcagcttaac               290


<210> SEQ ID NO 165
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-3*02 sequence

<400> SEQUENCE: 165

ggtgctggag tctcccagac cccagtaac aaggtcacag agaagggaaa agatgtagag     60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca aagcctgggg    120

cagggcccag agtttctaat ttacttccaa ggcacgggtg cggcagatga ctcagggctg    180

cccaaagatc ggttctttgc agtcaggcct gagggatccg tctctactct gaagatccag    240
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cgcacagagc agggggactc agccgtgtat ctccgtgcca gcagcttaac 290

<210> SEQ ID NO 166
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-3*03 sequence

<400> SEQUENCE: 166

ggtgctggag tctcccagac ccccagtaac aaggtcacag agaagggaaa agatgtagag 60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca aagcctgggg 120

cagggcccag agtttctaat ttacttccaa ggcacgggtg cggcagatga ctcagggctg 180

cccaaagatc ggttctttgc agtcaggcct gagggatccg tctctactct gaagatccag 240

cgcacagagc agggggactc agccgcgtat ctccgtgcca gcagctta 288

<210> SEQ ID NO 167
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-3*04 sequence

<400> SEQUENCE: 167

ggtgctggag tctcccagac ccccagtaac aaggtcacag agaagggaaa atatgtagag 60

ctcaggtgtg atccaatttc aggtcatact gccctttact ggtaccgaca aagcctgggg 120

cagggcccag agtttctaat ttacttccaa ggcacgggtg cggcagatga ctcagggctg 180

cccaacgatc ggttctttgc agtcaggcct gagggatccg tctctactct gaagatccag 240

cgcacagagc gggggactc tgccgtgtat ctctgtgcca gcagc 285

<210> SEQ ID NO 168
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-3*05 sequence

<400> SEQUENCE: 168

tgggagctca ggtgtgatcc aatttcaggt catactgccc tttactggta ccgacaaagc 60

ctggggcagg gcccagagct tctaatttac ttccaaggca cgggtgcggc agatgactca 120

gggctgccca acgatcggtt ctttgcagtc aggcctgagg gatccgtctc tactctgaag 180

atccagcgca cagagcgggg ggactcagcc gtgtatctct gtgccagcag c 231

<210> SEQ ID NO 169
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-4*01 sequence

<400> SEQUENCE: 169

ggtgctggag tctcccagtc cccaaggtac aaagtcgcaa agaggggacg ggatgtagct 60

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ctcaggtgtg attcaatttc gggtcatgta accctttatt ggtaccgaca gaccctgggg    120

cagggctcag aggttctgac ttactcccag agtgatgctc aacgagacaa atcagggcgg    180

cccagtggtc ggttctctgc agagaggcct gagagatccg tctccactct gaagatccag    240

cgcacagagc agggggactc agctgtgtat ctctgtgcca gcagcttagc              290


<210> SEQ ID NO 170
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-5*01 sequence

<400> SEQUENCE: 170

ggtgctggag tctcccagtc cccaaggtac gaagtcacac agaggggaca ggatgtagct     60

cccaggtgtg atccaatttc gggtcaggta accctttatt ggtaccgaca gaccctgggg    120

cagggccaag agtttctgac ttccttccag gatgaaactc aacaagataa atcagggctg    180

ctcagtgatc aattctccac agagaggtct gaggatcttt ctccacctga agatccagcg    240

cacagagcaa gggcgactcg gctgtgtatc tctgtgccag aagcttag                288


<210> SEQ ID NO 171
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-5*02 sequence

<400> SEQUENCE: 171

ggtgctggag tctcccagtc cccaaggtac gaagtcacac agaggggaca ggatgtagct     60

cccaggtgtg atccaatttc gggtcaggta accctttatt ggtaccgaca gaccctgggg    120

cagggccaag agtttctgac ttccttccag gatgaaactc aacaagataa atcagggctg    180

ctcagtgatc aattctccac agagaggtct gaggatcttt ctccacctga agatccagcg    240

cacagagcaa gggcgactcg gctgtgtatc tctgtgtcag aagcttagc               289


<210> SEQ ID NO 172
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-6*01 sequence

<400> SEQUENCE: 172

ggtgctggag tctcccagtc tcccaggtac aaagtcacaa agaggggaca ggatgtagct     60

ctcaggtgtg atccaatttc gggtcatgta tccctttatt ggtaccgaca ggccctgggg    120

cagggcccag agtttctgac ttacttcaat tatgaagccc aacaagacaa atcagggctg    180

cccaatgatc ggttctctgc agagaggcct gagggatcca tctccactct gacgatccag    240

cgcacagagc agcgggactc ggccatgtat cgctgtgcca gcagcttagc              290


<210> SEQ ID NO 173
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-6*02 sequence

<400> SEQUENCE: 173

ggtgctggag tctcccagtc tcccaggtac aaagtcacaa agaggggaca ggatgtagct 60

ctcaggtgtg atccaatctc gggtcatgta tccctttatt ggtaccgaca ggccctgggg 120

cagggcccag agtttctgac ttacttcaat tatgaagccc aacaagacaa atcagggctg 180

cccaatgatc ggttctctgc agagaggcct gagggatcca tctccactct gacgatccag 240

cgcacagagc agcgggactc ggccatgtat cgctgtgcca gcagc 285

<210> SEQ ID NO 174
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-7*01 sequence

<400> SEQUENCE: 174

ggtgctggag tctcccagtc tcccaggtac aaagtcacaa agaggggaca ggatgtaact 60

ctcaggtgtg atccaatttc gagtcatgca accctttatt ggtatcaaca ggccctgggg 120

cagggcccag agtttctgac ttacttcaat tatgaagctc aaccagacaa atcagggctg 180

cccagtgatc ggttctctgc agagaggcct gagggatcca tctccactct gacgattcag 240

cgcacagagc agcgggactc agccatgtat cgctgtgcca gcagcttagc 290

<210> SEQ ID NO 175
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-7*02 sequence

<400> SEQUENCE: 175

ggtgctggag tctcccagtc tcccaggtac aaagtcacaa agaggggaca ggatgtaact 60

ctcaggtgtg atccaatttc gagtcatgta accctttatt ggtatcaaca ggccctgggg 120

cagggcccag agtttctgac ttacttcaat tatgaagctc aaccagacaa atcagggctg 180

cccagtgatc ggttctctgc agagaggcct gagggatcca tctccactct gacgattcag 240

cgcacagagc agcgggactc agccatgtat cgctgtgcca gcagc 285

<210> SEQ ID NO 176
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-8*01 sequence

<400> SEQUENCE: 176

ggtgctggag tctcccagtc ccctaggtac aaagtcgcaa agagaggaca ggatgtagct 60

ctcaggtgtg atccaatttc gggtcatgta tcccttttt ggtaccaaca ggccctgggg 120

caggggccag agtttctgac ttatttccag aatgaagctc aactagacaa atcggggctg 180

cccagtgatc gcttctttgc agaaaggcct gagggatccg tctccactct gaagatccag 240

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cgcacacagc aggaggactc cgccgtgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 177
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-8*02 sequence

<400> SEQUENCE: 177

ggtgctggag tctcccagtc ccctaggtac aaagtcgcaa agagaggaca ggatgtagct 60

ctcaggtgtg atccaatttc gggtcatgta tccctttttt ggtaccaaca ggccctgggg 120

caggggccag agtttctgac ttatttccag aatgaagctc aactagacaa atcggggctg 180

cccagtgatc gcttctttgc agaaaggcct gagggatccg tctccactct gaagatccag 240

cgcacacaga aggaggactc cgccgtgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 178
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-8*03 sequence

<400> SEQUENCE: 178

ggtgctggag tctcccagtc ccctaggtac aaagtcgcaa agagaggaca ggatgtagct 60

ctcaggtgtg atccaatttc gggtcatgta tccctttttt ggtaccaaca ggccctcggg 120

caggggccag agtttctgac ttatttccag aatgaagctc aactagacaa atcggggctg 180

cccagtgatc gcttctttgc agaaaggcct gagggatccg tctccactct gaagatccag 240

cgcacacagc aggaggactc cgccgtgtat ctctgtgcca gcagccga 288

<210> SEQ ID NO 179
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-9*05 sequence

<400> SEQUENCE: 179

gatactggag tctcccagaa ccccagacac aagatcacaa agaggggaca gaatgtaact 60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaccctgggg 120

cagggcccag agtttctgac ttacttccag aatgaagctc aactagaaaa atcaaggctg 180

ctcagtgatc ggttctctgc agagaggcct aagggatctc tctccacctt ggagatccag 240

cgcacagagc agggggactc ggccatgtat ctctgtgcca gcaccaaa 288

<210> SEQ ID NO 180
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-9*06 sequence

<400> SEQUENCE: 180

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gatactggag tctcccagaa ccccagacac aagatcacaa agaggggaca gaatgtaact 60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaccctgggg 120

cagggcccag agtttctgac ttacttccag aatgaagctc aactagaaaa atcaaggctg 180

ctcagtgatc ggttctctgc agagaggcct aagggatctc tttccacctt ggagatccag 240

cgcacagagc aggggactc ggccatgtat ctctgtgcca gcacgttg 288

<210> SEQ ID NO 181
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-9*03 sequence

<400> SEQUENCE: 181

gatactggag tctcccagga ccccagacac aagatcacaa agaggggaca gaatgtaact 60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaccctgggg 120

cagggcccag agtttctgac ttacttccag aatgaagctc aactagaaaa atcaaggctg 180

ctcagtgatc ggttctctgc agagaggcct aagggatctt tctccacctt ggagatccag 240

cgcacagagc aggggactc ggccatgtat ctctgtgcca gcagc 285

<210> SEQ ID NO 182
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-9*01 sequence

<400> SEQUENCE: 182

gatactggag tctcccagaa ccccagacac aagatcacaa agaggggaca gaatgtaact 60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaccctgggg 120

cagggcccag agtttctgac ttacttccag aatgaagctc aactagaaaa atcaaggctg 180

ctcagtgatc ggttctctgc agagaggcct aagggatctt tctccacctt ggagatccag 240

cgcacagagc aggggactc ggccatgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 183
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV7-9*02 sequence

<400> SEQUENCE: 183

gatactggag tctcccagaa ccccagacac aacatcacaa agaggggaca gaatgtaact 60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaccctgggg 120

cagggcccag agtttctgac ttacttccag aatgaagctc aactagaaaa atcaaggctg 180

ctcagtgatc ggttctctgc agagaggcct aagggatctt tctccacctt ggagatccag 240

cgcacagagc aggggactc ggccatgtat ctctgtgcca gcagctta 288

<210> SEQ ID NO 184

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<211> LENGTH: 207
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-9*07 sequence

<400> SEQUENCE: 184

cacaaccgcc tttattggta ccgacagacc ctggggcagg gcccagagtt tctgacttac     60

ttccagaatg aagctcaact agaaaaatca aggctgctca gtgatcggtt ctctgcagag    120

aggcctaagg gatctttctc caccttggag atccagcgca cagaggaggg ggactcggcc    180

atgtatctct gtgccagcag cagcagt                                        207


<210> SEQ ID NO 185
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV7-9*04 sequence

<400> SEQUENCE: 185

atatctggag tctcccacaa ccccagacac aagatcacaa agaggggaca gaatgtaact     60

ttcaggtgtg atccaatttc tgaacacaac cgcctttatt ggtaccgaca gaaccctggg    120

cagggcccag agtttctgac ttacttccag aatgaagctc aactggaaaa atcagggctg    180

ctcagtgatc ggatctctgc agagaggcct aagggatctt tctccacctt ggagatccag    240

cgcacagagc agggggactc ggccatgtat ctctgtgcca gcagctct                 288


<210> SEQ ID NO 186
<211> LENGTH: 279
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV8-1*01 sequence

<400> SEQUENCE: 186

gaggcaggga tcagccagat accaagatat cacagacaca cagggaaaaa gatcatcctg     60

aaatatgctc agattaggaa ccattattca gtgttctgtt atcaataaga ccaagaatag    120

gggctgaggc tgatccatta ttcaggtagt attggcagca tgaccaaagg cggtgccaag    180

gaagggtaca atgtctctgg aaacaagctc aagcattttc cctcaaccct ggagtctact    240

agcaccagcc agacctctgt acctctgtgg cagtgcatc                          279


<210> SEQ ID NO 187
<211> LENGTH: 271
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV8-2*01 sequence

<400> SEQUENCE: 187

gatgctggga tcacccagat gccaagatat cacattgtac agaagaaaga gatgatcctg     60

gaatgtgctc aggttaggaa cagtgttctg atatcgacag gacccaagac gggggctgaa    120

gcttatccac tattcaggca gtggtcacag caggaccaaa gttgatgtca cagaggggta    180
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ctgtgtttct tgaaacaagc ttgagcattt ccccaatcct ggcatccacc agcaccagcc 240

agacctatct gtaccactgt ggcagcacat c 271

<210> SEQ ID NO 188
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV9*01 sequence

<400> SEQUENCE: 188

gattctggag tcacacaaac cccaaagcac ctgatcacag caactggaca gcgagtgacg 60

ctgagatgct cccctaggtc tggagacctc tctgtgtact ggtaccaaca gagcctggac 120

cagggcctcc agttcctcat tcagtattat aatggagaag agagagcaaa aggaaacatt 180

cttgaacgat tctccgcaca acagttccct gacttgcact ctgaactaaa cctgagctct 240

ctggagctgg gggactcagc tttgtatttc tgtgccagca gcgtag 286

<210> SEQ ID NO 189
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV9*03 sequence

<400> SEQUENCE: 189

gattctggag tcacacaaac cccaaagcac ctgatcacag caactggaca gcgagtgacg 60

ctgagatgct cccctaggtc tggagacctc tctgtgtact ggtaccaaca gagcctggac 120

cagggcctcc agttcctcat tcaatattat aatggagaag agagagcaaa aggaaacatt 180

cttgaacgat tctccgcaca acagttccct gacttgcact ctgaactaaa cctgagctct 240

ctggagctgg gggactcagc tttgtatttc tgtgccagca gc 282

<210> SEQ ID NO 190
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV9*02 sequence

<400> SEQUENCE: 190

gattctggag tcacacaaac cccaaagcac ctgatcacag caactggaca gcgagtgacg 60

ctgagatgct cccctaggtc tggagacctc tctgtgtact ggtaccaaca gagcctggac 120

cagggcctcc agttcctcat tcactattat aatggagaag agagagcaaa aggaaacatt 180

cttgaacgat tctccgcaca acagttccct gacttgcact ctgaactaaa cctgagctct 240

ctggagctgg gggactcagc tttgtatttc tgtgccagca gcgtag 286

<210> SEQ ID NO 191
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-1*01 sequence

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<400> SEQUENCE: 191

gatgctgaaa tcacccagag cccaagacac aagatcacag agacaggaag gcaggtgacc 60

ttggcgtgtc accagacttg gaaccacaac aatatgttct ggtatcgaca agacctggga 120

catgggctga ggctgatcca ttactcatat ggtgttcaag acactaacaa aggagaagtc 180

tcagatggct acagtgtctc tagatcaaac acagaggacc tccccctcac tctggagtct 240

gctgcctcct cccagacatc tgtatatttc tgcgccagca gtgagtc 287

<210> SEQ ID NO 192
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-1*02 sequence

<400> SEQUENCE: 192

gatgctgaaa tcacccagag cccaagacac aagatcacag agacaggaag gcaggtgacc 60

ttggcgtgtc accagacttg gaaccacaac aatatgttct ggtatcgaca agacctggga 120

catgggctga ggctgatcca ttactcatat ggtgttcacg acactaacaa aggagaagtc 180

tcagatggct acagtgtctc tagatcaaac acagaggacc tccccctcac tctggagtct 240

gctgcctcct cccagacatc tgtatatttc tgcgccagca gt 282

<210> SEQ ID NO 193
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-2*01 sequence

<400> SEQUENCE: 193

gatgctggaa tcacccagag cccaagatac aagatcacag agacaggaag gcaggtgacc 60

ttgatgtgtc accagacttg gagccacagc tatatgttct ggtatcgaca agacctggga 120

catgggctga ggctgatcta ttactcagca gctgctgata ttacagataa aggagaagtc 180

cccgatggct atgttgtctc cagatccaag acagagaatt tccccctcac tctggagtca 240

gctacccgct cccagacatc tgtgtatttc tgcgccagca gtgagtc 287

<210> SEQ ID NO 194
<211> LENGTH: 217
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-2*02 sequence

<400> SEQUENCE: 194

aaggcaggtg accttgatgt gtcaccagac ttggagccac agctatatgt tctggtatcg 60

acaagacctg ggacatgggc tgaggctgat ctattactca gcagctgctg atattacaga 120

taaaggagaa gtccccgatg gctacgttgt ctccagatcc aagacagaga atttccccct 180

cactctggag tcagctaccc gctcccagac atctgtg 217

<210> SEQ ID NO 195
<211> LENGTH: 273

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-3*03 sequence

<400> SEQUENCE: 195

gatgctggaa tcacccagag cccaagacac aaggtcacag agacaggaac accagtgact 60

ctgagatgtc accagactga gaaccaccgc tacatgtact ggtatcgaca agacccgggg 120

catgggctga ggctaatcca ttactcatat ggtgttaaag atactgacaa aggagaagtc 180

tcagatggct atagtgtctc tagatcaaag acagaggatt tcctcctcac tctggagtcc 240

gctaccagct cccagacatc tgtgtacttc tgt 273

<210> SEQ ID NO 196
<211> LENGTH: 273
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-3*04 sequence

<400> SEQUENCE: 196

gatgctggaa tcacccagag cccaagacac aaggtcacag agacaggaac accagtgact 60

ctgagatgtc accagactga gaaccaccgc tacatgtact ggtatcgaca agacccgggg 120

catgggctga ggctgatcca ttactcatat ggtgttaaag atactgacaa aggagaagtc 180

tcagatggct atagtgtctc tagatcaaag acagaggatt tcctcctcac tctggagtcc 240

gctaccagct cccagacatc tgtgtacttc tgt 273

<210> SEQ ID NO 197
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-3*01 sequence

<400> SEQUENCE: 197

gatgctggaa tcacccagag cccaagacac aaggtcacag agacaggaac accagtgact 60

ctgagatgtc accagactga gaaccaccgc tatatgtact ggtatcgaca agacccgggg 120

catgggctga ggctgatcca ttactcatat ggtgttaaag atactgacaa aggagaagtc 180

tcagatggct atagtgtctc tagatcaaag acagaggatt tcctcctcac tctggagtcc 240

gctaccagct cccagacatc tgtgtacttc tgtgccatca gtgagtc 287

<210> SEQ ID NO 198
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV10-3*02 sequence

<400> SEQUENCE: 198

gatgctggaa tcacccagag cccaagacac aaggtcacag agacaggaac accagtgact 60

ctgagatgtc atcagactga gaaccaccgc tatatgtact ggtatcgaca agacccgggg 120

catgggctga ggctgatcca ttactcatat ggtgttaaag atactgacaa aggagaagtc 180

-continued

tcagatggct atagtgtctc tagatcaaag acagaggatt tcctcctcac tctggagtcc 240

gctaccagct cccagacatc tgtgtacttc tgtgccatca gtgagtc 287

<210> SEQ ID NO 199
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-1*01 sequence

<400> SEQUENCE: 199

gaagctgaag ttgcccagtc ccccagatat aagattacag agaaaagcca ggctgtggct 60

ttttggtgtg atcctatttc tggccatgct accctttact ggtaccggca gatcctggga 120

cagggcccgg agcttctggt tcaatttcag gatgagagtg tagtagatga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccag 240

cctgcagagc ttggggactc ggccatgtat ctctgtgcca gcagcttagc 290

<210> SEQ ID NO 200
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-3*01 sequence

<400> SEQUENCE: 200

gaagctggag tggttcagtc tcccagatat aagattatag agaaaaaaca gcctgtggct 60

ttttggtgca atcctatttc tggccacaat accctttact ggtacctgca gaacttggga 120

cagggcccgg agcttctgat tcgatatgag aatgaggaag cagtagacga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccag 240

cctgcagagc ttggggactc ggccgtgtat ctctgtgcca gcagcttaga 290

<210> SEQ ID NO 201
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-3*02 sequence

<400> SEQUENCE: 201

gaagctggag tggttcagtc tcccagatat aagattatag agaaaaagca gcctgtggct 60

ttttggtgca atcctatttc tggccacaat accctttact ggtaccggca gaacttggga 120

cagggcccgg agcttctgat tcgatatgag aatgaggaag cagtagacga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccag 240

cctgcagagc ttggggactc ggccgtgtat ctctgtgcca gcagc 285

<210> SEQ ID NO 202
<211> LENGTH: 269
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-3*03 sequence

<400> SEQUENCE: 202

ggtctcccag atataagatt atagagaaga aacagcctgt ggctttttgg tgcaatccaa 60

tttctggcca caataccctt tactggtacc tgcagaactt gggacagggc ccggagcttc 120

tgattcgata tgagaatgag gaagcagtag acgattcaca gttgcctaag gatcgatttt 180

ctgcagagag gctcaaagga gtagactcca ctctcaagat ccagccagca gagcttgggg 240

actcggccat gtatctctgt gccagcagc 269

<210> SEQ ID NO 203
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-2*01 sequence

<400> SEQUENCE: 203

gaagctggag ttgcccagtc tcccagatat aagattatag agaaaaggca gagtgtggct 60

ttttggtgca atcctatatc tggccatgct accctttact ggtaccagca gatcctggga 120

cagggcccaa agcttctgat tcagtttcag aataacggtg tagtggatga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccag 240

cctgcaaagc ttgaggactc ggccgtgtat ctctgtgcca gcagcttaga 290

<210> SEQ ID NO 204
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-2*03 sequence

<400> SEQUENCE: 204

gaagctggag ttgcccagtc tcccagatat aagattatag agaaaaggca gagtgtggct 60

ttttggtgca atcctatatc tggccatgct accctttact ggtaccagca gatcctggga 120

cagggcccaa agcttctgat tcagtttcag aataacggtg tagtggatga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccaa 240

cctgcaaagc ttgaggactc ggccgtgtat ctctgtgcca gcagc 285

<210> SEQ ID NO 205
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV11-2*02 sequence

<400> SEQUENCE: 205

gaagctggag ttgcccagtc tcccagatat aagattatag agaaaaggca gagtgtggct 60

ttttggtgca atcctatatc tggccatgct accctttact ggtaccagca gatcctggga 120

cagggcccaa agcttctgat tcagtttcag aataacggtg tagtggatga ttcacagttg 180

cctaaggatc gattttctgc agagaggctc aaaggagtag actccactct caagatccag 240

cctgcaaagc ttgagaactc ggccgtgtat ctctgtgcca gcagt 285

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<210> SEQ ID NO 206
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV12-1*01 sequence

<400> SEQUENCE: 206

gatgctggtg ttatccagtc acccaggcac aaagtgacag agatgggaca atcagtaact   60

ctgagatgcg aaccaatttc aggccacaat gatcttctct ggtacagaca gacctttgtg   120

cagggactgg aattgctgaa ttacttctgc agctggaccc tcgtagatga ctcaggagtg   180

tccaaggatt gattctcagc acagatgcct gatgtatcat tctccactct gaggatccag   240

cccatggaac ccagggactt gggcctatat ttctgtgcca gcagctttgc   290

<210> SEQ ID NO 207
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV12-2*01 sequence

<400> SEQUENCE: 207

gatgctggca ttatccagtc acccaagcat gaggtgacag aaatgggaca aacagtgact   60

ctgagatgtg agccaatttt tggccacaat ttcctttttct ggtacagaga taccttcgtg   120

cagggactgg aattgctgag ttacttccgg agctgatcta ttatagataa tgcaggtatg   180

cccacagagc gattctcagc tgagaggcct gatggatcat tctctactct gaagatccag   240

cctgcagagc agggggactc ggccgtgtat gtctgtgcaa gtcgcttagc   290

<210> SEQ ID NO 208
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV12-4*01 sequence

<400> SEQUENCE: 208

gatgctggag ttatccagtc accccggcac gaggtgacag agatgggaca agaagtgact   60

ctgagatgta aaccaatttc aggacacgac taccttttct ggtacagaca gaccatgatg   120

cggggactgg agttgctcat ttactttaac aacaacgttc cgatagatga ttcagggatg   180

cccgaggatc gattctcagc taagatgcct aatgcatcat tctccactct gaagatccag   240

ccctcagaac ccagggactc agctgtgtac ttctgtgcca gcagtttagc   290

<210> SEQ ID NO 209
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV12-4*02 sequence

<400> SEQUENCE: 209

gatgctggag ttatccagtc accccggcac gaggtgacag agatgggaca agaagtgact   60

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ctgagatgta aaccaatttc aggacatgac taccttttct ggtacagaca gaccatgatg 120

cggggactgg agttgctcat ttactttaac aacaacgttc cgatagatga ttcagggatg 180

cccgaggatc gattctcagc taagatgcct aatgcatcat tctccactct gaggatccag 240

ccctcagaac ccagggactc agctgtgtac ttctgtgcca gcagttta 288

<210> SEQ ID NO 210
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV12-3*01 sequence

<400> SEQUENCE: 210

gatgctggag ttatccagtc accccgccat gaggtgacag agatgggaca agaagtgact 60

ctgagatgta aaccaatttc aggccacaac tcccttttct ggtacagaca gaccatgatg 120

cggggactgg agttgctcat ttactttaac aacaacgttc cgatagatga ttcagggatg 180

cccgaggatc gattctcagc taagatgcct aatgcatcat tctccactct gaagatccag 240

ccctcagaac ccagggactc agctgtgtac ttctgtgcca gcagtttagc 290

<210> SEQ ID NO 211
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV12-5*01 sequence

<400> SEQUENCE: 211

gatgctagag tcacccagac accaaggcac aaggtgacag agatgggaca agaagtaaca 60

atgagatgtc agccaatttt aggccacaat actgttttct ggtacagaca gaccatgatg 120

caaggactgg agttgctggc ttacttccgc aaccgggctc ctctagatga ttcggggatg 180

ccgaaggatc gattctcagc agagatgcct gatgcaactt tagccactct gaagatccag 240

ccctcagaac ccagggactc agctgtgtat ttttgtgcta gtggtttggt 290

<210> SEQ ID NO 212
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV13*01 sequence

<400> SEQUENCE: 212

gctgctggag tcatccagtc cccaagacat ctgatcaaag aaaagaggga aacagccact 60

ctgaaatgct atcctatccc tagacacgac actgtctact ggtaccagca gggtccaggt 120

caggaccccc agttcctcat ttcgttttat gaaaagatgc agagcgataa aggaagcatc 180

cctgatcgat tctcagctca acagttcagt gactatcatt ctgaactgaa catgagctcc 240

ttggagctgg gggactcagc cctgtacttc tgtgccagca gcttagg 287

<210> SEQ ID NO 213
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV13*02 sequence

<400> SEQUENCE: 213

gctgctggag tcatccagtc cccaagacat ctgatcagag aaaagaggga aacagccact   60

ctgaaatgct atcctatccc tagacacgac actgtctact ggtaccagca gggcccaggt   120

caggaccccc agttcttcat ttcgttttat gaaaagatgc agagcgataa aggaagcatc   180

cctgatcgat tctcagctca acagttcagt gactatcatt ctgaactgaa catgagctcc   240

ttggagctgg gggactcagc cctgtacttc tgtgccagca gc   282

<210> SEQ ID NO 214
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV14*01 sequence

<400> SEQUENCE: 214

gaagctggag ttactcagtt ccccagccac agcgtaatag agaagggcca gactgtgact   60

ctgagatgtg acccaatttc tggacatgat aatctttatt ggtatcgacg tgttatggga   120

aaagaaataa aatttctgtt acattttgtg aaagagtcta aacaggatga gtccggtatg   180

cccaacaatc gattcttagc tgaaaggact ggagggacgt attctactct gaaggtgcag   240

cctgcagaac tggaggattc tggagtttat ttctgtgcca gcagccaaga   290

<210> SEQ ID NO 215
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV14*02 sequence

<400> SEQUENCE: 215

gaagctggag ttactcagtt ccccagccac agcgtaatag agaagggcca gactgtgact   60

ctgagatgtg acccaatttc tggacatgat aatctttatt ggtatcgacg tgttatggga   120

aaagaaataa aatttctgtt acattttgtg aaagagtcta aacaggatga atccggtatg   180

cccaacaatc gattcttagc tgaaaggact ggagggacgt attctactct gaaggtgcag   240

cctgcagaac tggaggattc tggagtttat ttctgtgcca gcagc   285

<210> SEQ ID NO 216
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV15*01 sequence

<400> SEQUENCE: 216

gatgccatgg tcatccagaa cccaagatac caggttaccc agtttggaaa gccagtgacc   60

ctgagttgtt ctcagacttt gaaccataac gtcatgtact ggtaccagca gaagtcaagt   120

caggccccaa agctgctgtt ccactactat gacaaagatt ttaacaatga agcagacacc   180

cctgataact tccaatccag gaggccgaac acttctttct gctttcttga catccgctca   240

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ccaggcctgg gggacacagc catgtacctg tgtgccacca gcagaga                287


<210> SEQ ID NO 217
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV15*03 sequence

<400> SEQUENCE: 217

gatgccatgg tcatccagaa cccaagatac cgggttaccc agtttggaaa gccagtgacc     60

ctgagttgtt ctcagacttt gaaccataac gtcatgtact ggtaccagca gaagtcaagt    120

caggccccaa agctgctgtt ccactactat aacaaagatt ttaacaatga agcagacacc    180

cctgataact tccaatccag gaggccgaac acttctttct gctttctaga catccgctca    240

ccaggcctgg gggacgcagc catgtaccag tgtgccacca gc                       282


<210> SEQ ID NO 218
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV15*02 sequence

<400> SEQUENCE: 218

gatgccatgg tcatccagaa cccaagatac caggttaccc agtttggaaa gccagtgacc     60

ctgagttgtt ctcagacttt gaaccataac gtcatgtact ggtaccagca gaagtcaagt    120

caggccccaa agctgctgtt ccactactat gacaaagatt ttaacaatga agcagacacc    180

cctgataact tccaatccag gaggccgaac acttctttct gctttcttga catccgctca    240

ccaggcctgg gggacgcagc catgtacctg tgtgccacca gc                       282


<210> SEQ ID NO 219
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV16*01 sequence

<400> SEQUENCE: 219

ggtgaagaag tcgcccagac tccaaaacat cttgtcagag gggaaggaca gaaagcaaaa     60

ttatattgtg ccccaataaa aggacacagt tatgtttttt ggtaccaaca ggtcctgaaa    120

aacgagttca agttcttgat ttccttccag aatgaaaatg tctttgatga aacaggtatg    180

cccaaggaaa gattttcagc taagtgcctc ccaaattcac cctgtagcct tgagatccag    240

gctacgaagc ttgaggattc agcagtgtat ttttgtgcca gcagccaatc               290


<210> SEQ ID NO 220
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV16*02 sequence

<400> SEQUENCE: 220
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ggtgaagaag tcgcccagac tccaaaacat cttgtcagag gggaaggaca gaaagcaaaa 60

ttatattgtg ccccaataaa aggacacagt taggtttttt ggtaccaaca ggtcctgaaa 120

aacgagttca agttcttgat ttccttccag aatgaaaatg tctttgatga aacaggtatg 180

cccaaggaaa gattttcagc taagtgcctc ccaaattcac cctgtagcct tgagatccag 240

gctacgaagc ttgaggattc agcagtgtat ttttgtgcca gcagccaatc 290

<210> SEQ ID NO 221
<211> LENGTH: 285
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV16*03 sequence

<400> SEQUENCE: 221

ggtgaagaag tcgcccagac tccaaaacat cttgtcagag gggaaggaca gaaagcaaaa 60

ttatattgtg ccccaataaa aggacacagt tatgtttttt ggtaccaaca ggtcctgaaa 120

aacgagttca agttcttggt ttccttccag aatgaaaatg tctttgatga aacaggtatg 180

cccaaggaaa gattttcagc taagtgcctc ccaaattcac cctgtagcct tgagatccag 240

gctacgaagc ttgaggattc agcagtgtat ttttgtgcca gcagc 285

<210> SEQ ID NO 222
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV17*01 sequence

<400> SEQUENCE: 222

gagcctggag tcagccagac cccccagacac aaggtcacca acatgggaca ggaggtgatt 60

ctgaggtgcg atccatcttc tggtcacatg tttgttcact ggtaccgaca gaatctgagg 120

caagaaatga agttgctgat ttccttccag taccaaaaca ttgcagttga ttcagggatg 180

cccaaggaac gattcacagc tgaaagacct aacggaacgt cttccacgct gaagatccat 240

cccgcagagc cgagggactc agccgtgtat ctctacagta gcggtgg 287

<210> SEQ ID NO 223
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV18*01 sequence

<400> SEQUENCE: 223

aatgccggcg tcatgcagaa cccaagacac ctggtcagga ggaggggaca ggaggcaaga 60

ctgagatgca gcccaatgaa aggacacagt catgtttact ggtatcggca gctcccagag 120

gaaggtctga aattcatggt ttatctccag aaagaaaata tcatagatga gtcaggaatg 180

ccaaaggaac gattttctgc tgaatttccc aaagagggcc ccagcatcct gaggatccag 240

caggtagtgc gaggagattc ggcagcttat ttctgtgcca gctcaccacc 290

<210> SEQ ID NO 224

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<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV19*01 sequence

<400> SEQUENCE: 224

gatggtggaa tcactcagtc cccaaagtac ctgttcagaa aggaaggaca gaatgtgacc 60

ctgagttgtg aacagaattt gaaccacgat gccatgtact ggtaccgaca ggacccaggg 120

caagggctga gattgatcta ctactcacag atagtaaatg actttcagaa aggagatata 180

gctgaagggt acagcgtctc tcgggagaag aaggaatcct ttcctctcac tgtgacatcg 240

gcccaaaaga acccgacagc tttctatctc tgtgccagta gtataga 287

<210> SEQ ID NO 225
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV19*02 sequence

<400> SEQUENCE: 225

gatggtggaa tcactcagtc cccaaagtac ctgttcagaa aggaaggaca gaatgtgacc 60

ctgagttgtg aacagaattt gaaccacgat gccatgtact ggtaccgaca ggtcccaggg 120

caagggctga gattgatcta ctactcacac atagtaaatg actttcagaa aggagatata 180

gctgaagggt acagcgtctc tcgggagaag aaggaatcct ttcctctcac tgtgacatcg 240

gcccaaaaga acccgacagc tttctatctc tgtgccagta gtataga 287

<210> SEQ ID NO 226
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV19*03 sequence

<400> SEQUENCE: 226

gatggtggaa tcactcagtc cccaaagtac ctgttcagaa aggaaggaca gaatgtgacc 60

ctgagttgtg aacagaattt gaaccacgat gccatgtact ggtaccgaca ggacccaggg 120

caagggctga gattgatcta ctactcacac atagtaaatg actttcagaa aggagatata 180

gctgaagggt acagcgtctc tcgggagaag aaggaatcct ttcctctcac tgtgacatcg 240

gcccaaaaga acccgacagc tttctatctc tgtgccagta gc 282

<210> SEQ ID NO 227
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV20-1*05 sequence

<400> SEQUENCE: 227

ggtgctgtcg tctctcaaca tccgagcagg gttatctgta agagtggaac ctctgtgaag 60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg 120

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aaaaagagtc tcatgctgat ggcaacttcc aatgagggct ccaaggccac atacgagcaa 180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca 240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgctag a 291

<210> SEQ ID NO 228
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV20-1*07 sequence

<400> SEQUENCE: 228

ggtgctgtcg tctctcaaca tccgagcagg gttatctgta agagtggaac ctctgtgaag 60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg 120

aaaaagagtc tcatgcagat cgcaacttcc aatgagggct ccaaggccac atacgagcaa 180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca 240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgctag a 291

<210> SEQ ID NO 229
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV20-1*04 sequence

<400> SEQUENCE: 229

ggtgctgtcg tctctcaaca tccgagcagg gttatctgta agagtggaac ctctgtgaag 60

atcgagtgcc gttccttgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg 120

aaaaagagtc tcatgctgat ggcaacttcc aatgagggct ccaaggccac atacgagcaa 180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca 240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgctag t 291

<210> SEQ ID NO 230
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV20-1*06 sequence

<400> SEQUENCE: 230

ggtgctgtcg tctctcaaca tccgagtagg gttatctgta agagtggaac ctctgtgaag 60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg 120

aaaaagagtc tcatgctgat ggcaacttcc aatgagggct ccaaggccac atacgagcaa 180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca 240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgct 288

<210> SEQ ID NO 231
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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      TRBV20-1*02 sequence

<400> SEQUENCE: 231

ggtgctgtcg tctctcaaca tccgagcagg gttatctgta agagtggaac ctctgtgaag     60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg    120

aaacagagtc tcatgctgat ggcaacttcc aatgagggct ccaaggccac atacgagcaa    180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca    240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgct                 288


<210> SEQ ID NO 232
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV20-1*01 sequence

<400> SEQUENCE: 232

ggtgctgtcg tctctcaaca tccgagctgg gttatctgta agagtggaac ctctgtgaag     60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg    120

aaacagagtc tcatgctgat ggcaacttcc aatgagggct ccaaggccac atacgagcaa    180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca    240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgctag aga           293


<210> SEQ ID NO 233
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV20-1*03 sequence

<400> SEQUENCE: 233

ggtgctgtcg tctctcaaca tccgagctgg gttatctgta agagtggaac ctctgtgaag     60

atcgagtgcc gttccctgga ctttcaggcc acaactatgt tttggtatcg tcagttcccg    120

aaacagagtc tcatgctgat ggcaacttcc aatgagggct gcaaggccac atacgagcaa    180

ggcgtcgaga aggacaagtt tctcatcaac catgcaagcc tgaccttgtc cactctgaca    240

gtgaccagtg cccatcctga agacagcagc ttctacatct gcagtgct                 288


<210> SEQ ID NO 234
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBV21-1*01 sequence

<400> SEQUENCE: 234

gacaccaagg tcacccagag acctagactt ctggtcaaag caagtgaaca gaaagcaaag     60

atggattgtg ttcctataaa agcacatagt tatgtttact ggtatcgtaa gaagctggaa    120

gaagagctca agtttttggt ttactttcag aatgaagaac ttattcagaa agcagaaata    180

atcaatgagc gatttttagc ccaatgctcc aaaaactcat cctgtacctt ggagatccag    240

tccacggagt caggggacac agcactgtat ttctgtgcca gcagcaaagc               290
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<210> SEQ ID NO 235
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV22-1*01 sequence

<400> SEQUENCE: 235

gatgctgaca tctatcagat gccattccag ctcactgggg ctggatggga tgtgactctg 60

gagtggaaac ggaatttgag acacaatgac atgtactgct actggtactg gcaggaccca 120

aagcaaaatc tgagactgat ctattactca agggttgaaa aggatattca gagaggagat 180

ctaactgaag gctacgtgtc tgccaagagg agaaggggct atttcttctc agggtgaagt 240

tggcccacac cagccaaaca gctttgtact tctgtcctgg gagcgcac 288

<210> SEQ ID NO 236
<211> LENGTH: 290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV23-1*01 sequence

<400> SEQUENCE: 236

catgccaaag tcacacagac tccaggacat ttggtcaaag gaaaaggaca gaaaacaaag 60

atggattgta cccccgaaaa aggacatact tttgtttatt ggtatcaaca gaatcagaat 120

aaagagttta tgcttttgat ttcctttcag aatgaacaag ttcttcaaga aacggagatg 180

cacaagaagc gattctcatc tcaatgcccc aagaacgcac cctgcagcct ggcaatcctg 240

tcctcagaac cgggagacac ggcactgtat ctctgcgcca gcagtcaatc 290

<210> SEQ ID NO 237
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV24-1*01 sequence

<400> SEQUENCE: 237

gatgctgatg ttacccagac cccaaggaat aggatcacaa agacaggaaa gaggattatg 60

ctggaatgtt ctcagactaa gggtcatgat agaatgtact ggtatcgaca agacccagga 120

ctgggcctac ggttgatcta ttactccttt gatgtcaaag atataaacaa aggagagatc 180

tctgatggat acagtgtctc tcgacaggca caggctaaat tctccctgtc cctagagtct 240

gccatcccca accagacagc tctttacttc tgtgccacca gtgatttg 288

<210> SEQ ID NO 238
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV25-1*01 sequence

<400> SEQUENCE: 238

gaagctgaca tctaccagac cccaagatac cttgttatag ggacaggaaa gaagatcact 60

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ctggaatgtt ctcaaaccat gggccatgac aaaatgtact ggtatcaaca agatccagga 120

atggaactac acctcatcca ctattcctat ggagttaatt ccacagagaa gggagatctt 180

tcctctgagt caacagtctc cagaataagg acggagcatt ttcccctgac cctggagtct 240

gccaggccct cacatacctc tcagtacctc tgtgccagca gtgaata 287

<210> SEQ ID NO 239
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV26*01 sequence

<400> SEQUENCE: 239

gatgctgtag ttacacaatt cccaagacac agaatcattg ggacaggaaa ggaattcatt 60

ctacagtgtt cccagaatat gaatcatgtt acaatgtact ggtatcgaca ggacccagga 120

cttggactga agctggtcta ttattcacct ggcactggga gcactgaaaa aggagatatc 180

tctgaggggt atcatgtttc ttgaaatact atagcatctt ttcccctgac cctgaagtct 240

gccagcacca accagacatc tgtgtatctc tatgccagca gttcatc 287

<210> SEQ ID NO 240
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV27*01 sequence

<400> SEQUENCE: 240

gaagcccaag tgacccagaa cccaagatac ctcatcacag tgactggaaa gaagttaaca 60

gtgacttgtt ctcagaatat gaaccatgag tatatgtcct ggtatcgaca agacccaggg 120

ctgggcttaa ggcagatcta ctattcaatg aatgttgagg tgactgataa gggagatgtt 180

cctgaagggt acaaagtctc tcgaaaagag aagaggaatt tcccccctgat cctggagtcg 240

cccagcccca accagacctc tctgtacttc tgtgccagca gtttatc 287

<210> SEQ ID NO 241
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV28*01 sequence

<400> SEQUENCE: 241

gatgtgaaag taacccagag ctcgagatat ctagtcaaaa ggacgggaga gaaagttttt 60

ctggaatgtg tccaggatat ggaccatgaa aatatgttct ggtatcgaca agacccaggt 120

ctggggctac ggctgatcta tttctcatat gatgttaaaa tgaaagaaaa aggagatatt 180

cctgaggggt acagtgtctc tagagagaag aaggagcgct tctccctgat tctggagtcc 240

gccagcacca accagacatc tatgtacctc tgtgccagca gtttatg 287

<210> SEQ ID NO 242
<211> LENGTH: 290
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV29-1*01 sequence

<400> SEQUENCE: 242

agtgctgtca tctctcaaaa gccaagcagg gatatctgtc aacgtggaac ctccctgacg 60

atccagtgtc aagtcgatag ccaagtcacc atgatgttct ggtaccgtca gcaacctgga 120

cagagcctga cactgatcgc aactgcaaat cagggctctg aggccacata tgagagtgga 180

tttgtcattg acaagtttcc catcagccgc ccaaacctaa cattctcaac tctgactgtg 240

agcaacatga gccctgaaga cagcagcata tatctctgca gcgttgaaga 290

<210> SEQ ID NO 243
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV29-1*02 sequence

<400> SEQUENCE: 243

agtgctgtca tctctcaaaa gccaagcagg gatatctgtc aacgtggaac ctccctgacg 60

atccagtgtc aagtcgatag ccaagtcacc atgatgttct ggtaccgtca gcaacctgga 120

cagagcctga cactgatcgc aactgcaaat cagggctctg aggccacata tgagagtgga 180

tttgtcattg acaagtttcc catcagccgc ccaaacctaa cattctcaag tctgactgtg 240

agcaacatga gccctgaaga cagcagcata tatctctgca gcgttgaa 288

<210> SEQ ID NO 244
<211> LENGTH: 231
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV29-1*03 sequence

<400> SEQUENCE: 244

acgatccagt gtcaagtcga tagccaagtc accatgatat tctggtaccg tcagcaacct 60

ggacagagcc tgacactgat cgcaactgca aatcagggct ctgaggccac atatgagagt 120

ggatttgtca ttgacaagtt tcccatcagc cgcccaaacc taacattctc aactctgact 180

gtgagcaaca tgagccctga agacagcagc atatatctct gcagcgcggg c 231

<210> SEQ ID NO 245
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV30*02 sequence

<400> SEQUENCE: 245

tctcagacta ttcatcaatg gccagcgacc ctggtgcagc ctgtgggcag cccgctctct 60

ctggagtgca ctgtggaggg aacatcaaac cccaacctat actggtaccg acaggctgca 120

ggcaggggcc tccagctgct cttctactcc gttggtattg gccagatcag ctctgaggtg 180

ccccagaatc tctcagcctc cagaccccag gaccggcagt tcatcctgag ttctaagaag 240

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ctcctcctca gtgactctgg cttctatctc tgtgcctgga gtgt 284

<210> SEQ ID NO 246
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV30*05 sequence

<400> SEQUENCE: 246

tctcagacta ttcatcaatg gccagcgacc ctggtgcagc ctgtgggcag cccgctctcc 60

ctggagtgca ctgtggaggg aacatcaaac cccaacctat actggtaccg acaggctgca 120

ggacggggcc tccagctgct cttctactcc gttggtattg gccagatcag ctctgaggtg 180

ccccagaatc tctcagcctc cagaccccag gaccggcagt tcatcctgag ttctaagaag 240

ctccttctca gtgactctgg cttctatctc tgtgcctggg ga 282

<210> SEQ ID NO 247
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV30*01 sequence

<400> SEQUENCE: 247

tctcagacta ttcatcaatg gccagcgacc ctggtgcagc ctgtgggcag cccgctctct 60

ctggagtgca ctgtggaggg aacatcaaac cccaacctat actggtaccg acaggctgca 120

ggcaggggcc tccagctgct cttctactcc gttggtattg gccagatcag ctctgaggtg 180

ccccagaatc tctcagcctc cagaccccag gaccggcagt tcatcctgag ttctaagaag 240

ctccttctca gtgactctgg cttctatctc tgtgcctgga gtgt 284

<210> SEQ ID NO 248
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV30*04 sequence

<400> SEQUENCE: 248

actattcatc aatggccagc gaccctggtg cagcctgtgg gcagcccgct ctctctggag 60

tgcactgtgg agggaacatc aaaccccaac ctatactggt accgacaggc tgcaggcagg 120

ggcctccagc tgctcttcta ctccattggt attgaccaga tcagctctga ggtgccccag 180

aatctctcag cctccagacc ccaggaccgg cagttcattc tgagttctaa gaagctcctc 240

ctcagtgact ctggcttcta tctctgtgcc tggagt 276

<210> SEQ ID NO 249
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ1S1 sequence

<400> SEQUENCE: 249

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ttgaaaaagg aacctaggac cctgtggatg gactctgtca ttctccatgg tcctaaaaag 60

caaaagtcaa agtgttcttc tgtgtaatac ccataaagca caggaggaga tttcttagct 120

cactgtcctc catcctagcc agggccctct cccctctcta tgccttcaat gtgattttca 180

ccttgacccc tgtcactgtg tgaacactga agctttcttt ggacaaggca ccagactcac 240

agttgtaggt aagacatttt tcaggttctt ttgcagatcc gtcacaggga aaagtgggtc 300

cacagtgtcc cttttagagt ggctatattc ttatgtgcta actatggcta caccttcggt 360

tcggggacca ggttaaccgt tgtaggtaag gctgggggtc tctaggaggg gtgcgatgag 420

ggaggactct gtcctgggaa atgtcaaa 448

<210> SEQ ID NO 250
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ1S2 sequence

<400> SEQUENCE: 250

gccagggccc tctcccctct ctatgccttc aatgtgattt tcaccttgac ccctgtcact 60

gtgtgaacac tgaagctttc tttggacaag gcaccagact cacagttgta ggtaagacat 120

ttttcaggtt cttttgcaga tccgtcacag ggaaaagtgg gtccacagtg tcccttttag 180

agtggctata ttcttatgtg ctaactatgg ctacaccttc ggttcgggga ccaggttaac 240

cgttgtaggt aaggctgggg gtctctagga ggggtgcgat gagggaggac tctgtcctgg 300

gaaatgtcaa agagaacaga gatcccagct cccggagcca gactgaggga gacgtcatgt 360

catgtcccgg gattgagttc aggggaggct ccctgtgagg gcgaatccac ccaggcttcc 420

cagaggctct gagcagtcac agctgagc 448

<210> SEQ ID NO 251
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ1S3 sequence

<400> SEQUENCE: 251

gattttatag gaggccactc tgtgtctctt tttgtcacct gcctgagtct tgggcaagct 60

ctggaaggga acacagagta ctggaagcag agctgctgtc cctgtgaggg aagagttccc 120

atgaactccc aacctctgcc tgaatcccag ctgtgctcag cagagactgg ggggttttga 180

agtggccctg ggaggctgtg ctctggaaac accatatatt ttggagaggg aagttggctc 240

actgttgtag gtgagtaagt caaggctgga cagctgggaa cttgcaaaaa ggggctggaa 300

tccagacgga gcctttgtct ctagtgctta ggtgaaagtg tatttttgtc aggaaggcct 360

atgaggcaga tgaggagggg atagcctccc tctcctctcg actattttgt agactgcctg 420

tgccaagtta ggttccccta ctgagagatg 450

<210> SEQ ID NO 252
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ1S4 sequence

<400> SEQUENCE: 252

cagaagaggg aacttggggg atcacacggg gcctaattgg tctgctgacc accgcatttt     60

gggttgtacc attgtctacc cctctaccca ccagggttaa aattctacta aggaacagga    120

gaggacctgg caggtggact tggggaggca ggagtggaag gcagcaggtc gcggttttcc    180

ttccagtctt taatgttgtg caactaatga aaaactgttt tttggcagtg gaacccagct    240

ctctgtcttg ggtatgtaaa agacttcttt cgggatagtg tatcataagg tcggagttcc    300

aggaggaccc cttgcgggag ggcagaaact gagaacacag ccaagaaaag ctcataaaat    360

gtgggtcagt ggagtgtgtg gtggggcccc aagagttctg tgtgtaagca gcttctggaa    420

ggaagggccc acaccagctc ctctggggtt t                                   451


<210> SEQ ID NO 253
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ1S5 sequence

<400> SEQUENCE: 253

gatagtgtat cataaggtcg gagttccagg aggacccctt gcgggagggc agaaactgag     60

aacacagcca agaaaagctc ataaaatgtg ggtcagtgga gtgtgtggtg gggccccaag    120

agttctgtgt gtaagcagct tctggaagga agggcccaca ccagctcctc tggggtttgc    180

cacactcatg atgcactgtg tagcaatcag ccccagcatt ttggtgatgg gactcgactc    240

tccatcctag gtaagttgca gaatcagggt ggtatggcca ttgtcccttg aaggcagagt    300

tctctgcttc tcctcccggt gctggtgagg cagattgagt aaaatctctt accccatggg    360

gtaagagctg tgcctgtgcc tgcgttccct ttggtgtgtc ttggttgact cctctatttc    420

tcttctctaa gtcttcagtc cataatctgc                                     450


<210> SEQ ID NO 254
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ1S6 sequence

<400> SEQUENCE: 254

atggctctgc ctctcctaag cctcttcctc ttgcgcctta tgctgcacag tatgcttagg     60

ccttttttcct aacagaatcc ctttggtcca gagccatgaa tccaggcaga gaaaggcagc    120

catcctgctg tcagggagct aagacttgcc ctctgactgg agatcgccgg gtgggtttta    180

tctaagcctc tgcagctgtg ctcctataat tcacccctcc actttgggaa cgggaccagg    240

ctcactgtga caggtatggg ggctccactc ttgactcggg ggtgcctggg tttgactgca    300

atgatcagtt gctgggaagg gaattgagtg taagaacgga ggtcagggtc acccccttctt    360

acctggagca ctgtgccctc tcctcccctc cctggagctc ttccagcttg ttgctctgct    420

gtgttgcctg cagttcctca gctgtagagc tcc                                 453
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<210> SEQ ID NO 255
<211> LENGTH: 449
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ2S1 sequence

<400> SEQUENCE: 255

aatccactgt gttgtccccc agccaagtgg attctcctct gcaaattggt ggtggcctca     60

tgcaagatcc agttaccgtg tccagctaac tcgagacagg aaaagatagg ctcaggaaag    120

agaggaaggg tgtgccctct gtctgtgcta agggaggtgg ggaaggagaa ggaattctgg    180

gcagcccctt cccactgtgc tcctacaatg agcagttctt cgggccaggg acacggctca    240

ccgtgctagg taagaagggg gctccaggtg ggagagaggg tgagcagccc agcctgcacg    300

accccagaac cctgttctta ggggagtgga cactgggcaa tccagggccc tcctcgaggg    360

aagcggggtt tgcgccaggg tccccagggc tgtgcgaaca ccggggagct gtttttgga    420

gaaggctcta ggctgaccgt actgggtaa                                       449


<210> SEQ ID NO 256
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ2S2 sequence

<400> SEQUENCE: 256

ctgtgctcct acaatgagca gttcttcggg ccagggacac ggctcaccgt gctaggtaag     60

aagggggctc caggtgggag agagggtgag cagcccagcc tgcacgaccc cagaaccctg    120

ttcttagggg agtggacact gggcaatcca gggccctcct cgagggaagc ggggtttgcg    180

ccagggtccc cagggctgtg cgaacaccgg ggagctgttt tttggagaag gctctaggct    240

gaccgtactg ggtaaggagg cggttggggc tccggagagc tccgagaggg cgggatgggc    300

agaggtaagc agctgcccca ctctgagagg ggctgtgctg agaggcgctg ctgggcgtct    360

gggcggagga ctcctggttc tgggtgctgg gagagcgatg gggctctcag cggtgggaag    420

gacccgagct gagtctggga cagcagagcg g                                   451


<210> SEQ ID NO 257
<211> LENGTH: 449
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TCRBJ2S3 sequence

<400> SEQUENCE: 257

gggcgggatg ggcagaggta agcagctgcc ccactctgag aggggctgtg ctgagaggcg     60

ctgctgggcg tctgggcgga ggactcctgg ttctgggtgc tgggagagcg atggggctct    120

cagcggtggg aaggacccga gctgagtctg ggacagcaga gcgggcagca ccggttttg    180

tcctgggcct ccaggctgtg agcacagata cgcagtattt tggcccaggc acccggctga    240

cagtgctcgg taagcggggg ctcccgctga agccccggaa ctggggaggg ggcgccccgg    300

gacgccgggg gcgtcgcagg gccagtttct gtgccgcgtc tcggggctgt gagccaaaaa    360
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cattcagtac ttcggcgccg ggacccggct ctcagtgctg ggtaagctgg ggccgccggg 420

ggaccgggga cgagactgcg ctcgggttt 449

<210> SEQ ID NO 258
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ2S4 sequence

<400> SEQUENCE: 258

gacagcagag cgggcagcac cggtttttgt cctgggcctc caggctgtga gcacagatac 60

gcagtatttt ggcccaggca cccggctgac agtgctcggt aagcgggggc tcccgctgaa 120

gccccggaac tggggagggg gcgccccggg acgccggggg cgtcgcaggg ccagtttctg 180

tgccgcgtct cggggctgtg agccaaaaac attcagtact tcggcgccgg gacccggctc 240

tcagtgctgg gtaagctggg gccgccgggg gaccggggac gagactgcgc tcgggttttt 300

gtgcggggct cgggggccgt gaccaagaga cccagtactt cgggccaggc acgcggctcc 360

tggtgctcgg tgagcgcggg ctgctggggc gcgggcgcgg gcggcttggg tctggttttt 420

gcggggagtc cccgggctgt gctctggggc 450

<210> SEQ ID NO 259
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ2S5 sequence

<400> SEQUENCE: 259

ccccggaact ggggaggggg cgccccggga cgccgggggc gtcgcagggc cagtttctgt 60

gccgcgtctc ggggctgtga gccaaaaaca ttcagtactt cggcgccggg acccggctct 120

cagtgctggg taagctgggg ccgccggggg accggggacg agactgcgct cgggtttttg 180

tgcggggctc gggggccgtg accaagagac ccagtacttc gggccaggca cgcggctcct 240

ggtgctcggt gagcgcgggc tgctggggcg cgggcgcggg cggcttgggt ctggtttttg 300

cggggagtcc ccgggctgtg ctctggggcc aacgtcctga ctttcggggc cggcagcagg 360

ctgaccgtgc tgggtgagtt ttcgcgggac cacccgggcg gcgggattca ggtggaaggc 420

ggcggctgct tcgcggcacc cggtccgg 448

<210> SEQ ID NO 260
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ2S6 sequence

<400> SEQUENCE: 260

cagtgctggg taagctgggg ccgccggggg accggggacg agactgcgct cgggtttttg 60

tgcggggctc gggggccgtg accaagagac ccagtacttc gggccaggca cgcggctcct 120

ggtgctcggt gagcgcgggc tgctggggcg cgggcgcggg cggcttgggt ctggtttttg 180

cggggagtcc ccgggctgtg ctctggggcc aacgtcctga ctttcggggc cggcagcagg 240

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ctgaccgtgc tgggtgagtt ttcgcgggac cacccgggcg gcgggattca ggtggaaggc 300

ggcggctgct tcgcggcacc cggtccggcc ctgtgctggg agacctgggc tgggtcccca 360

gggtgggcag gagctcgggg agccttagag gtttgcatgc gggggtgcac ctccgtgctc 420

ctacgagcag tacttcgggc cgggcaccag gct 453

<210> SEQ ID NO 261
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TCRBJ2S7 sequence

<400> SEQUENCE: 261

tgactttcgg ggccggcagc aggctgaccg tgctgggtga gttttcgcgg gaccacccgg 60

gcggcgggat tcaggtggaa ggcggcggct gcttcgcggc acccggtccg gccctgtgct 120

gggagacctg ggctgggtcc ccagggtggg caggagctcg gggagcctta gaggtttgca 180

tgcgggggtg cacctccgtg ctcctacgag cagtacttcg ggccgggcac caggctcacg 240

gtcacaggtg agattcgggc gtctccccac cttccagccc ctcggtcccc ggagtcggag 300

ggtggaccgg agctggagga gctgggtgtc cggggtcagc tctgcaaggt cacctccccg 360

ctcctgggga aagactgggg aagagggagg gggtggggag gtgctcagag tccggaaagc 420

tgagcagagg gcgaggccac ttttaat 447

<210> SEQ ID NO 262
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-46*02 sequence

<400> SEQUENCE: 262

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcaac agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 263
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1/OR15-5*01 sequence

<400> SEQUENCE: 263

agaagcctgg ggcctcagtg aaggtctcct gcaaggcttc tggatacacc ttcaccagct 60

actgtatgca ctgggtgcac caggtccatg cacaagggct tgagtggatg ggattggtgt 120

gccctagtga tggcagcaca agctatgcac agaagttcca ggccagagtc accataacca 180

gggacacatc catgagcaca gcctacatgg agctaagcag tctgagatct gaggacacgg 240

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ccatgtatta ctgtgtgaga 260

<210> SEQ ID NO 264
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1/OR15-5*03 sequence

<400> SEQUENCE: 264

caggtacagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc aactactgta tgcactgggt gcgccaggtc 120

catgcacaag ggcttgagtg gatgggattg gtgtgcccta gtgatggcag cacaagctat 180

gcacaaaagt tccaggccag agtcaccata accagggaca catccatgag cacagcctac 240

atggagctaa gcagtctgag atctgaggac acggccatgt attactgtgt gaga 294

<210> SEQ ID NO 265
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1/OR15-9*01 sequence

<400> SEQUENCE: 265

caggtacagc tgatgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaggatc 60

tcctgcaagg cttctggata caccttcacc agctactgta tgcactgggt gtgccaggcc 120

catgcacaag ggcttgagtg gatgggattg gtgtgcccta gtgatggcag cacaagctat 180

gcacagaagt tccagggcag agtcaccata accagggaca catccatggg cacagcctac 240

atggagctaa gcagcctgag atctgaggac acggccatgt attactgtgt gagaga 296

<210> SEQ ID NO 266
<211> LENGTH: 260
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-c*01 sequence

<400> SEQUENCE: 266

ggaagtctgg ggcctcagtg aaagtctcct gtagtttttc tgggtttacc atcaccagct 60

acggtataca ttgggtgcaa cagtcccctg gacaagggct tgagtggatg ggatggatca 120

accctggcaa tggtagccca agctatgcca agaagtttca gggcagattc accatgacca 180

gggacatgtc cacaaccaca gcctacacag acctgagcag cctgacatct gaggacatgg 240

ctgtgtatta ctatgcaaga 260

<210> SEQ ID NO 267
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-NL1*01 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (136)..(136)

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<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (253)..(253)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 267

caggttcagc tgttgcagcc tggggtccag gtgaagaagc ctgggtcctc agtgaaggtc     60

tcctgctagg cttccagata caccttcacc aaatacttta cacggtgggt gtgacaaagc    120

cctggacaag ggcatnagtg gatgggatga atcaaccctt acaacgataa cacacactac    180

gcacagacgt tctggggcag agtcaccatt accagtgaca ggtccatgag cacagcctac    240

atggagctga gcngcctgag atccgaagac atggtcgtgt attactgtgt gagaga        296


<210> SEQ ID NO 268
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-58*01 sequence

<400> SEQUENCE: 268

caaatgcagc tggtgcagtc tgggcctgag gtgaagaagc ctgggacctc agtgaaggtc     60

tcctgcaagg cttctggatt cacctttact agctctgctg tgcagtgggt gcgacaggct    120

cgtggacaac gccttgagtg gataggatgg atcgtcgttg gcagtggtaa cacaaactac    180

gcacagaagt tccaggaaag agtcaccatt accagggaca tgtccacaag cacagcctac    240

atggagctga gcagcctgag atccgaggac acggccgtgt attactgtgc ggcaga        296


<210> SEQ ID NO 269
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-58*02 sequence

<400> SEQUENCE: 269

caaatgcagc tggtgcagtc tgggcctgag gtgaagaagc ctgggacctc agtgaaggtc     60

tcctgcaagg cttctggatt cacctttact agctctgcta tgcagtgggt gcgacaggct    120

cgtggacaac gccttgagtg gataggatgg atcgtcgttg gcagtggtaa cacaaactac    180

gcacagaagt tccaggaaag agtcaccatt accagggaca tgtccacaag cacagcctac    240

atggagctga gcagcctgag atccgaggac acggccgtgt attactgtgc ggcaga        296


<210> SEQ ID NO 270
<211> LENGTH: 275
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*03 sequence

<400> SEQUENCE: 270

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac    180
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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgatgac acggc                               275


<210> SEQ ID NO 271
<211> LENGTH: 233
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*07 sequence

<400> SEQUENCE: 271

agaagcctgg gtcctcggtg aaggtctcct gcaaggcttc tggaggcacc ttcagcagct     60

atgctatcag ctgggtgcga caggcccctg gacaagggct tgagtggatg ggaaggatca    120

tccctatctt tggtacagca aactacgcac agaagttcca gggcagagtc acgattaccg    180

cggacgaatc cacgagcaca gcctacatgg agctgagcag cctgagatct gag           233


<210> SEQ ID NO 272
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*12 sequence

<400> SEQUENCE: 272

caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac    180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga        296


<210> SEQ ID NO 273
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*05 sequence

<400> SEQUENCE: 273

caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac    180

gcacagaagt tccagggcag agtcacgatt accacggacg aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga          294


<210> SEQ ID NO 274
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*13 sequence

<400> SEQUENCE: 274
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caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 275
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-69*01 sequence

<400> SEQUENCE: 275

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 276
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-69*06 sequence

<400> SEQUENCE: 276

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 277
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-69*02 sequence

<400> SEQUENCE: 277

caggtccagc tggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaga 294

<210> SEQ ID NO 278

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<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*08 sequence

<400> SEQUENCE: 278

caggtccagc tggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatacta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtac agcaaactac    180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga        296


<210> SEQ ID NO 279
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*04 sequence

<400> SEQUENCE: 279

caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac    180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga        296


<210> SEQ ID NO 280
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*11 sequence

<400> SEQUENCE: 280

caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120

cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtac agcaaactac    180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac    240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga        296


<210> SEQ ID NO 281
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV1-69*09 sequence

<400> SEQUENCE: 281

caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc     60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc    120
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cctggacaag ggcttgagtg gatgggaagg atcatcccta tccttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 282
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-69*10 sequence

<400> SEQUENCE: 282

caggtccagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtc 60

tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggg atcatcccta tccttggtat agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 283
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-f*01 sequence

<400> SEQUENCE: 283

gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggata caccttcacc gactactaca tgcactgggt gcaacaggcc 120

cctggaaaag ggcttgagtg gatgggactt gttgatcctg aagatggtga aacaatatac 180

gcagagaagt tccagggcag agtcaccata accgcggaca cgtctacaga cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aaca 294

<210> SEQ ID NO 284
<211> LENGTH: 233
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-f*02 sequence

<400> SEQUENCE: 284

agaagcctgg ggctacagtg aaaatctcct gcaaggtttc tggatacacc ttcaccgact 60

actacatgca ctgggtgcaa caggcccctg gaaaagggct tgagtggatg ggacttgttg 120

atcctgaaga tggtgaaaca atatatgcag agaagttcca gggcagagtc accataaccg 180

cggacacgtc tacagacaca gcctacatgg agctgagcag cctgagatct gag 233

<210> SEQ ID NO 285
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV1-24*01 sequence

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<400> SEQUENCE: 285

caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg tttccggata caccctcact gaattatcca tgcactgggt gcgacaggct 120

cctggaaaag ggcttgagtg gatgggaggt tttgatcctg aagatggtga aacaatctac 180

gcacagaagt tccagggcag agtcaccatg accgaggaca catctacaga cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc aacaga 296

<210> SEQ ID NO 286
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV7-4-1*01 sequence

<400> SEQUENCE: 286

caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agctatgcta tgaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacacca acactgggaa cccaacgtat 180

gcccagggct tcacaggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatct gcagcctaaa ggctgaggac actgccgtgt attactgtgc gaga 294

<210> SEQ ID NO 287
<211> LENGTH: 274
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV7-4-1*03 sequence

<400> SEQUENCE: 287

caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agctatgcta tgaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacacca acactgggaa cccaacgtat 180

gcccagggct tcacaggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcacgctaaa ggctgaggac actg 274

<210> SEQ ID NO 288
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV7-4-1*02 sequence

<400> SEQUENCE: 288

caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggata caccttcact agctatgcta tgaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacacca acactgggaa cccaacgtat 180

gcccagggct tcacaggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240

ctgcagatca gcagcctaaa ggctgaggac actgccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 289
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV7-81*01 sequence

<400> SEQUENCE: 289

caggtgcagc tggtgcagtc tggccatgag gtgaagcagc ctggggcctc agtgaaggtc   60

tcctgcaagg cttctggtta cagtttcacc acctatggta tgaattgggt gccacaggcc   120

cctggacaag ggcttgagtg gatgggatgg ttcaacacct acactgggaa cccaacatat   180

gcccagggct tcacaggacg gtttgtcttc tccatggaca cctctgccag cacagcatac   240

ctgcagatca gcagcctaaa ggctgaggac atggccatgt attactgtgc gagata   296

<210> SEQ ID NO 290
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV7-40*03 sequence

<400> SEQUENCE: 290

ctgcagctgg tgcagtctgg gcctgaggtg aagaagcctg gggcctcagt gaaggtctcc   60

tataagtctt ctggttacac cttcaccatc tatggtatga attgggtatg atagacccct   120

ggacagggct ttgagtggat gtgatggatc atcacctaca ctgggaaccc aacgtatacc   180

cacggcttca caggatggtt tgtcttctcc atggacacgt ctgtcagcac ggcgtgtctt   240

cagatcagca gcctaaaggc tgaggacacg gccgagtatt actgtgcga   289

<210> SEQ ID NO 291
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV5-51*01 sequence

<400> SEQUENCE: 291

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc   60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg   120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac   180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac   240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaca   296

<210> SEQ ID NO 292
<211> LENGTH: 245
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV5-51*05 sequence

<400> SEQUENCE: 292

aaaagcccgg ggagtctctg aagatctcct gtaagggttc tggatacagc tttaccagct   60

actggatcgg ctgggtgcgc cagatgccca ggaaaggcct ggagtggatg gggatcatct   120

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atcctggtga ctctgatacc agatacagcc cgtccttcca aggccaggtc accatctcag 180

ccgacaagtc catcagcacc gcctacctgc agtggagcag cctgaaggcc tcggacaccg 240

ccatg 245

<210> SEQ ID NO 293
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-51*02 sequence

<400> SEQUENCE: 293

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga ccggctgggt gcgccagatg 120

cccgggaaag gcttggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaca 296

<210> SEQ ID NO 294
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-51*03 sequence

<400> SEQUENCE: 294

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaga 294

<210> SEQ ID NO 295
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-51*04 sequence

<400> SEQUENCE: 295

gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc cgggggagtc tctgaagatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agcccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaga 294

<210> SEQ ID NO 296
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-a*01 sequence

<400> SEQUENCE: 296

gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcagctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggagg attgatccta gtgactctta taccaactac 180

agcccgtcct tccaaggcca cgtcaccatc tcagctgaca agtccatcag cactgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaga 294

<210> SEQ ID NO 297
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-a*03 sequence

<400> SEQUENCE: 297

gaagtgcagc tggtgcagtc cggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcagctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggagg attgatccta gtgactctta taccaactac 180

agcccgtcct tccaaggcca cgtcaccatc tcagctgaca agtccatcag cactgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaga 294

<210> SEQ ID NO 298
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-a*04 sequence

<400> SEQUENCE: 298

gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcagctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggagg attgatccta gtgactctta taccaactac 180

agcccgtcct tccaaggcca ggtcaccatc tcagctgaca agtccatcag cactgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gaga 294

<210> SEQ ID NO 299
<211> LENGTH: 295
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-a*02 sequence

<400> SEQUENCE: 299

gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggata cagctttacc agctactgga tcagctgggt gcgccagatg 120

cccgggaaag gcttggagtg gatggggagg attgatccta gtgactctta taccaactac 180

agcccgtcct tccaaggcca cgtcaccatc tcagctgaca agtccatcag cactgcctac 240

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ctgcagtgga gcagcctgaa ggctcggaca ccgccatgta ttactgtgcg agaca 295

<210> SEQ ID NO 300
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV5-78*01 sequence

<400> SEQUENCE: 300

gaggtgcagc tgttgcagtc tgcagcagag gtgaaaagac ccggggagtc tctgaggatc 60

tcctgtaaga cttctggata cagctttacc agctactgga tccactgggt gcgccagatg 120

cccgggaaag aactggagtg gatggggagc atctatcctg ggaactctga taccagatac 180

agcccatcct tccaaggcca cgtcaccatc tcagccgaca gctccagcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac gccgccatgt attattgtgt gaga 294

<210> SEQ ID NO 301
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-11*01 sequence

<400> SEQUENCE: 301

caggtgcagc tggtggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagggaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gagaga 296

<210> SEQ ID NO 302
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-11*03 sequence

<400> SEQUENCE: 302

caggtgcagc tgttggagtc tgggggaggc ttggtcaagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtagtagtta cacaaactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaga 294

<210> SEQ ID NO 303
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-21*01 sequence

<400> SEQUENCE: 303

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gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtagtta catatactac 180

gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 304
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-21*02 sequence

<400> SEQUENCE: 304

gaggtgcaac tggtggagtc tgggggaggc ctggtcaagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtagtta catatactac 180

gcagactcag tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 305
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-48*01 sequence

<400> SEQUENCE: 305

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtagtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 306
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-48*02 sequence

<400> SEQUENCE: 306

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatagca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtagtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agacgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 307
<211> LENGTH: 293

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-h*01 sequence

<400> SEQUENCE: 307

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtaccat atactacgca 180

gactctgtga agggccgatt caccatctcc agagacaacg ccaagaactc actgtatctg 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aga 293

<210> SEQ ID NO 308
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-h*02 sequence

<400> SEQUENCE: 308

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gactactaca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtagta gtagtaccat atactacgca 180

gactctgtga agggccgatt caccatctcc agagacaacg ccaagaactc actgtatctg 240

caaatgaaca gcctgagagc cgaggacacg gctgtttatt actgtgcgag aga 293

<210> SEQ ID NO 309
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-48*03 sequence

<400> SEQUENCE: 309

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agttatgaaa tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtagtac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgttt attactgtgc gagaga 296

<210> SEQ ID NO 310
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-8*01 sequence

<400> SEQUENCE: 310

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactg 60

tcctgtccag cctctggatt caccttcagt aaccactaca tgagctgggt ccgccaggct 120

ccagggaagg gactggagtg ggtttcatac attagtggtg atagtggtta cacaaactac 180

```
gcagactctg tgaagggccg attcaccatc tccagggaca acgccaataa ctcaccgtat    240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgt ga            292


<210> SEQ ID NO 311
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3/OR16-9*01 sequence

<400> SEQUENCE: 311

gaggtgcagc tggtggagtc tggaggaggc ttggtacagc ctgggggggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt aaccactaca cgagctgggt ccgccaggct    120

ccagggaagg gactggagtg ggtttcatac agtagtggta atagtggtta cacaaactac    180

gcagactctg tgaaaggccg attcaccatc tccagggaca acgccaagaa ctcactgtat    240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgt ga            292


<210> SEQ ID NO 312
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-13*01 sequence

<400> SEQUENCE: 312

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctacgaca tgcactgggt ccgccaagct    120

acaggaaaag gtctggagtg ggtctcagct attggtactg ctggtgacac atactatcca    180

ggctccgtga agggccgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt    240

caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag aga           293


<210> SEQ ID NO 313
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-13*03 sequence

<400> SEQUENCE: 313

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc     60

tcctgtgcag cctgtggatt caccttcagt agctacgaca tgcactgggt ccgccaagct    120

acaggaaaag gtctggagtg ggtctcagct attggtactg ctggtgacac atactatcca    180

ggctccgtga agggccaatt caccatctcc agagaaaatg ccaagaactc cttgtatctt    240

caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag a             291


<210> SEQ ID NO 314
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-13*02 sequence
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<400> SEQUENCE: 314

gaggtgcatc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactacgaca tgcactgggt ccgccaagct 120

acaggaaaag gtctggagtg ggtctcagcc aatggtactg ctggtgacac atactatcca 180

ggctccgtga aggggcgatt caccatctcc agagaaaatg ccaagaactc cttgtatctt 240

caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag aga 293

<210> SEQ ID NO 315
<211> LENGTH: 123
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-47*02 sequence

<400> SEQUENCE: 315

atactatgca gactccgtga tgggccgatt caccatctcc agagacaacg ccaagaagtc 60

cttgtatctt caaatgaaca gcctgatagc tgaggacatg gctgtgtatt attgtgcaag 120

aga 123

<210> SEQ ID NO 316
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-47*03 sequence

<400> SEQUENCE: 316

gaggatcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagaccc 60

tcctgtgcag cctctggatt cgccttcagt agctatgttc tgcactgggt tcgccgggct 120

ccagggaagg gtccggagtg ggtatcagct attggtactg gtggtgatac atactatgca 180

gactccgtga tgggccgatt caccatctcc agagacaacg ccaagaagtc cttgtatctc 240

aaatgaacag cctgatagct gaggacatgg ctgtgtatta tg 282

<210> SEQ ID NO 317
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-47*01 sequence

<400> SEQUENCE: 317

gaggatcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgcgaccc 60

tcctgtgcag cctctggatt cgccttcagt agctatgctc tgcactgggt tcgccgggct 120

ccagggaagg gtctggagtg ggtatcagct attggtactg gtggtgatac atactatgca 180

gactccgtga tgggccgatt caccatctcc agagacaacg ccaagaagtc cttgtatctt 240

catatgaaca gcctgatagc tgaggacatg gctgtgtatt attgtgcaag a 291

<210> SEQ ID NO 318
<211> LENGTH: 291
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3/OR16-10*01 sequence

<400> SEQUENCE: 318

gaggttcagc tggtgcagtc tgggggaggc ttggtacatc ctgggggtc cctgagactc     60

tcctgtgcag gctctggatt caccttcagt agctatgcta tgcactgggt tcgccaggct    120

ccaggaaaag gtctggagtg ggtatcagct attggtactg gtggtggcac atactatgca    180

gactccgtga agggccgatt caccatctcc agagacaatg ccaagaactc cttgtatctt    240

caaatgaaca gcctgagagc cgaggacatg gctgtgtatt actgtgcaag a             291


<210> SEQ ID NO 319
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3/OR16-10*02 sequence

<400> SEQUENCE: 319

gaggttcagc tggtgcagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc     60

tcctgtgcag gctctggatt caccttcagt agctatgcta tgcactgggt tcgccaggct    120

ccaggaaaag gtctggagtg ggtatcagct attggtactg gtggtggcac atactatgca    180

gactccgtga agggccgatt caccatctcc agagacaatg ccaagaactc cttgtatctt    240

caaatgaaca gcctgagagc cgaggacatg gctgtgtatt actgtgcaag a             291


<210> SEQ ID NO 320
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-62*01 sequence

<400> SEQUENCE: 320

gaggtgcagc tggtggagtc tggggaaggc ttggtccagc ctgggggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctctgcta tgcactgggt ccgccaggct    120

ccaagaaagg gtttgtagtg ggtctcagtt attagtacaa gtggtgatac cgtactctac    180

acagactctg tgaagggccg attcaccatc tccagagaca atgcccagaa ttcactgtct    240

ctgcaaatga acagcctgag agccgagggc acagttgtgt actactgtgt gaaaga        296


<210> SEQ ID NO 321
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-64*01 sequence

<400> SEQUENCE: 321

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct    120

ccagggaagg gactggaata tgtttcagct attagtagta atgggggtag cacatattat    180
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gcaaactctg tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatgg gcagcctgag agctgaggac atggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 322
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-64*02 sequence

<400> SEQUENCE: 322

gaggtgcagc tggtggagtc tggggaaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccagggaagg gactggaata tgtttcagct attagtagta atgggggtag cacatattat 180

gcagactctg tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240

cttcaaatgg gcagcctgag agctgaggac atggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 323
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-64*03 sequence

<400> SEQUENCE: 323

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgttcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccagggaagg gactggaata tgtttcagct attagtagta atgggggtag cacatactac 180

gcagactcag tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240

gtccaaatga gcagtctgag agctgaggac acggctgtgt attactgtgt gaaaga 296

<210> SEQ ID NO 324
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-64*05 sequence

<400> SEQUENCE: 324

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgttcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccagggaagg gactggaata tgtttcagct attagtagta atgggggtag cacatactac 180

gcagactcag tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240

gttcaaatga gcagtctgag agctgaggac acggctgtgt attactgtgt gaaaga 296

<210> SEQ ID NO 325
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-64*04 sequence

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<400> SEQUENCE: 325

caggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgttcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccagggaagg gactggaata tgtttcagct attagtagta atgggggtag cacatactac 180

gcagactcag tgaagggcag attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 326
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-16*01 sequence

<400> SEQUENCE: 326

gaggtacaac tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggc ccgcaaggct 120

ccaggaaagg ggctggagtg ggtatcgggt gttagttgga atggcagtag gacgcactat 180

gtggactccg tgaagcgccg attcatcatc tccagagaca attccaggaa ctccctgtat 240

ctgcaaaaga acagacggag agccgaggac atggctgtgt attactgtgt gagaaa 296

<210> SEQ ID NO 327
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-16*02 sequence

<400> SEQUENCE: 327

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggc ccgcaaggct 120

ccaggaaagg ggctggagtg ggtatcgggt gttagttgga atggcagtag gacgcactat 180

gtggactccg tgaagcgccg attcatcatc tccagagaca attccaggaa ctccctgtat 240

ctgcaaaaga acagacggag agccgaggac atggctgtgt attactgtgt gagaaa 296

<210> SEQ ID NO 328
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-15*02 sequence

<400> SEQUENCE: 328

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagacac 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggt cctctaggct 120

ccaggaaagg ggctggagtg ggtctcgggt attagttgga atggcggtaa gacgcactat 180

gtggactccg tgaagggcca atttaccatc tccagagaca attccagcaa gtccctgtat 240

ctgcaaaaga acagacagag agccaaagac atggccgtgt attactgtgt gaga 294

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<210> SEQ ID NO 329
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-16*01 sequence

<400> SEQUENCE: 329

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagacac 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggt cctctaggct 120

ccaggaaagg ggctggagtg ggtctcggat attagttgga atggcggtaa gacgcactat 180

gtggactccg tgaagggcca atttaccatc tccagagaca attccagcaa gtccctgtat 240

ctgcaaaaga acagacagag agccaaggac atggccgtgt attactgtgt gaga 294

<210> SEQ ID NO 330
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-15*01 sequence

<400> SEQUENCE: 330

gaagtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctgtatt caccttcagt aacagtgaca taaactgggt cctctaggct 120

ccaggaaagg ggctggagtg ggtctcgggt attagttgga atggcggtaa gacgcactat 180

gtggactccg tgaagggcca attttccatc tccagagaca attccagcaa gtccctgtat 240

ctgcaaaaga acagacagag agccaaggac atggccgtgt attactgtgt gagaaa 296

<210> SEQ ID NO 331
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-19*01 sequence

<400> SEQUENCE: 331

acagtgcagc tggtggagtc tgggggaggc ttggtagagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggt ccgccaggct 120

ccaggaaagg ggctggagtg ggtatcgggt gttagttgga atggcagtag gacgcactat 180

gcagactctg tgaagggccg attcatcatc tccagagaca attccaggaa cttcctgtat 240

cagcaaatga acagcctgag gcccgaggac atggctgtgt attactgtgt gagaaa 296

<210> SEQ ID NO 332
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-35*01 sequence

<400> SEQUENCE: 332

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggatc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aacagtgaca tgaactgggt ccatcaggct 120 ccaggaaagg ggctggagtg ggtatcgggt gttagttgga atggcagtag gacgcactat 180

gcagactctg tgaagggccg attcatcatc tccagagaca attccaggaa caccctgtat 240

ctgcaaacga atagcctgag ggccgaggac acggctgtgt attactgtgt gagaaa 296

<210> SEQ ID NO 333
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-43*01 sequence

<400> SEQUENCE: 333

gaagtgcagc tggtggagtc tgggggagtc gtggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccgtcaagct 120

ccggggaagg gtctggagtg ggtctctctt attagttggg atggtggtag cacatactat 180

gcagactctg tgaagggccg attcaccatc tccagagaca acagcaaaaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac accgccttgt attactgtgc aaaagata 298

<210> SEQ ID NO 334
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-43*02 sequence

<400> SEQUENCE: 334

gaagtgcagc tggtggagtc tgggggaggc gtggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgtcaagct 120

ccagggaagg gtctggagtg ggtctctctt attagtgggg atggtggtag cacatactat 180

gcagactctg tgaagggccg attcaccatc tccagagaca acagcaaaaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac accgccttgt attactgtgc aaaa 294

<210> SEQ ID NO 335
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-9*01 sequence

<400> SEQUENCE: 335

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagata 298

<210> SEQ ID NO 336
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-20*01 sequence

<400> SEQUENCE: 336

gaggtgcagc tggtggagtc tgggggaggt gtggtacggc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatggca tgagctgggt ccgccaagct 120

ccagggaagg ggctggagtg ggtctctggt attaattgga atggtggtag cacaggttat 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agccgaggac acggccttgt atcactgtgc gagaga 296

<210> SEQ ID NO 337
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-74*01 sequence

<400> SEQUENCE: 337

gaggtgcagc tggtggagtc cgggggaggc ttagttcagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggtgtg ggtctcacgt attaatagtg atgggagtag cacaagctac 180

gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacgctgtat 240

ctgcaaatga acagtctgag agccgaggac acggctgtgt attactgtgc aagaga 296

<210> SEQ ID NO 338
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-74*02 sequence

<400> SEQUENCE: 338

gaggtgcagc tggtggagtc tgggggaggc ttagttcagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggtgtg ggtctcacgt attaatagtg atgggagtag cacaagctac 180

gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacgctgtat 240

ctgcaaatga acagtctgag agccgaggac acggctgtgt attactgtgc aaga 294

<210> SEQ ID NO 339
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-74*03 sequence

<400> SEQUENCE: 339

gaggtgcagc tggtggagtc cgggggaggc ttagttcagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggtgtg ggtctcacgt attaatagtg atgggagtag cacaacgtac 180

gcggactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacgctgtat 240

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ctgcaaatga acagtctgag agccgaggac acggctgtgt attactgtgc aagaga 296

<210> SEQ ID NO 340
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-13*01 sequence

<400> SEQUENCE: 340

gaggtgcagc tggtggagtc tgggggaggc ttagtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgcactgggt ccgccaagct 120

ccagggaagg ggctggtgtg ggtctcacgt attaatagtg atgggagtag cacaagctac 180

gcagactcca tgaagggcca attcaccatc tccagagaca atgctaagaa cacgctgtat 240

ctgcaaatga acagtctgag agctgaggac atggctgtgt attactgtac taga 294

<210> SEQ ID NO 341
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-14*01 sequence

<400> SEQUENCE: 341

gaggtgcagc tggaggagtc tgggggaggc ttagtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctactgga tgcactgggt ccgccaatct 120

ccagggaagg ggctggtgtg agtctcacgt attaatagtg atgggagtag cacaagctac 180

gcagactcct tgaagggcca attcaccatc tccagagaca atgctaagaa cacgctgtat 240

ctgcaaatga acagtctgag agctgaggac atggctgtgt attactgtac taga 294

<210> SEQ ID NO 342
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*01 sequence

<400> SEQUENCE: 342

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 343
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*08 sequence

<400> SEQUENCE: 343

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caggtgcagc tggtggactc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctgcatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaga   294

<210> SEQ ID NO 344
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*17 sequence

<400> SEQUENCE: 344

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccgggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 345
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*11 sequence

<400> SEQUENCE: 345

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cgtctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 346
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*10 sequence

<400> SEQUENCE: 346

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 347
<211> LENGTH: 296

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*16 sequence

<400> SEQUENCE: 347

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggcc    120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac    180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat    240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga        296


<210> SEQ ID NO 348
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*15 sequence

<400> SEQUENCE: 348

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct    120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac    180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat    240

ctgcaaatga gcagcctgag agctgaggac acggctgtgt attactgtgc gagaga        296


<210> SEQ ID NO 349
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*07 sequence

<400> SEQUENCE: 349

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct    120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac    180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat    240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga        296


<210> SEQ ID NO 350
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*04 sequence

<400> SEQUENCE: 350

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc     60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct    120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac    180
```

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 351
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*09 sequence

<400> SEQUENCE: 351

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcgccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 352
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*14 sequence

<400> SEQUENCE: 352

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

cttcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 353
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30-3*01 sequence

<400> SEQUENCE: 353

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaga   294

<210> SEQ ID NO 354
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30-3*02 sequence

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<400> SEQUENCE: 354

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatgcta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagcaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaga 296

<210> SEQ ID NO 355
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*03 sequence

<400> SEQUENCE: 355

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 356
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*18 sequence

<400> SEQUENCE: 356

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaga 296

<210> SEQ ID NO 357
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*06 sequence

<400> SEQUENCE: 357

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga 296

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<210> SEQ ID NO 358
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*12 sequence

<400> SEQUENCE: 358

caggtgcagc tggtggagtc tgggggggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct   120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 359
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*19 sequence

<400> SEQUENCE: 359

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 360
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-33*05 sequence

<400> SEQUENCE: 360

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct   120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat   180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga   296

<210> SEQ ID NO 361
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-30*05 sequence

<400> SEQUENCE: 361

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc   60

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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgagggc acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 362
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*13 sequence

<400> SEQUENCE: 362

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa caggctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 363
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-33*01 sequence

<400> SEQUENCE: 363

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 364
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-33*04 sequence

<400> SEQUENCE: 364

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctagagtg ggtggcagtt atatggtatg acggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 365
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-33*02 sequence

<400> SEQUENCE: 365

caggtacagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180

gcagactccg cgaagggccg attcaccatc tccagagaca attccacgaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 366
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-33*03 sequence

<400> SEQUENCE: 366

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaaaga 296

<210> SEQ ID NO 367
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-30*02 sequence

<400> SEQUENCE: 367

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggggggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcattt atacggtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaga 296

<210> SEQ ID NO 368
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-52*01 sequence

<400> SEQUENCE: 368

gaggtgcagc tggtggagtc tgggtgaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctcctgga tgcactgggt ctgccaggct 120

ccggagaagg ggctggagtg ggtggccgac ataaagtgtg acggaagtga gaaatactat 180

gtagactctg tgaagggccg attgaccatc tccagagaca atgccaagaa ctccctctat 240

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ctgcaagtga acagcctgag agctgaggac atgaccgtgt attactgtgt gagagg 296

<210> SEQ ID NO 369
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-52*02 sequence

<400> SEQUENCE: 369

gaggtgcagc tggtggagtc tgggtgaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctcctgga tgcactgggt ctgccaggct 120

ccggagaagg ggcaggagtg ggtggccgac ataaagtgtg acggaagtga gaaatactat 180

gtagactctg tgaagggccg attgaccatc tccagagaca atgccaagaa ctccctctat 240

ctgcaagtga acagcctgag agctgaggac atgaccgtgt attactgtgt gaga 294

<210> SEQ ID NO 370
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-52*03 sequence

<400> SEQUENCE: 370

gaggtgcagc tggtcgagtc tgggtgaggc ttggtacagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctcctgga tgcactgggt ctgccaggct 120

ccggagaagg ggctggagtg ggtggccgac ataaagtgtg acggaagtga gaaatactat 180

gtagactctg tgaagggccg attgaccatc tccagagaca atgccaagaa ctccctctat 240

ctgcaagtga acagcctgag agctgaggac atgaccgtgt attactgtgt gaga 294

<210> SEQ ID NO 371
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-7*01 sequence

<400> SEQUENCE: 371

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga 296

<210> SEQ ID NO 372
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-7*02 sequence

<400> SEQUENCE: 372

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gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagt agctattgga tgagctgggt ccgccaggct   120

ccagggaaag ggctggagtg ggtggccaac ataaagcaag atggaagtga gaaatactat   180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctcactgtat   240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gaga   294

<210> SEQ ID NO 373
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-23*01 sequence

<400> SEQUENCE: 373

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga   296

<210> SEQ ID NO 374
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-23*04 sequence

<400> SEQUENCE: 374

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga   296

<210> SEQ ID NO 375
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-23*02 sequence

<400> SEQUENCE: 375

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct   120

ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac   180

ggagactccg tgaagggccg gttcaccatc tcaagagaca attccaagaa cacgctgtat   240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga   296

<210> SEQ ID NO 376

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<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-23*03 sequence

<400> SEQUENCE: 376

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc     60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagtag cacatactat    180

gcagactccg tgaagggccg gttcaccatc tccagagata attccaagaa cacgctgtat    240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaa          294


<210> SEQ ID NO 377
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-23*05 sequence

<400> SEQUENCE: 377

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc     60

tcctgtgcag cctctggatt cacctttagc agctatgcca tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtctcagct atttatagca gtggtagtag cacatactat    180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat    240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaa          294


<210> SEQ ID NO 378
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-53*01 sequence

<400> SEQUENCE: 378

gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctggggggtc cctgagactc     60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca    180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt    240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag aga           293


<210> SEQ ID NO 379
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-53*02 sequence

<400> SEQUENCE: 379

gaggtgcagc tggtggagac tggaggaggc ttgatccagc ctggggggtc cctgagactc     60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct    120
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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca    180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt    240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag a             291


<210> SEQ ID NO 380
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-66*03 sequence

<400> SEQUENCE: 380

gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctggggggtc cctgagactc     60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtctcagtt atttatagct gtggtagcac atactacgca    180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt    240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag aga           293


<210> SEQ ID NO 381
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-53*03 sequence

<400> SEQUENCE: 381

gaggtgcagc tggtggagtc tggaggaggc ttgatccagc ctggggggtc cctgagactc     60

tcctgtgcag cctctgggtt caccgtcagt agcaactaca tgagctgggt ccgccagcct    120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca    180

gactctgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt    240

caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgctag gga           293


<210> SEQ ID NO 382
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-66*01 sequence

<400> SEQUENCE: 382

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc     60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca    180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt    240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aga           293


<210> SEQ ID NO 383
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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IGHV3-66*04 sequence

<400> SEQUENCE: 383

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aca 293

<210> SEQ ID NO 384
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-66*02 sequence

<400> SEQUENCE: 384

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaactaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atactacgca 180

gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag a 291

<210> SEQ ID NO 385
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-38*01 sequence

<400> SEQUENCE: 385

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctagggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaatgaga tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtggtg gtagcacata ctacgcagac 180

tccaggaagg gcagattcac catctccaga gacaattcca agaacacgct gtatcttcaa 240

atgaacaacc tgagagctga gggcacggcc gcgtattact gtgccagata ta 292

<210> SEQ ID NO 386
<211> LENGTH: 292
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-38*02 sequence

<400> SEQUENCE: 386

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctagggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaatgaga tgagctggat ccgccaggct 120

ccagggaagg ggctggagtg ggtctcatcc attagtggtg gtagcacata ctacgcagac 180

tccaggaagg gcagattcac catctccaga gacaattcca agaacacgct gtatcttcaa 240

atgaacaacc tgagagctga gggcacggcc gtgtattact gtgccagata ta 292

<210> SEQ ID NO 387
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-d*01 sequence

<400> SEQUENCE: 387

gaggtgcagc tggtggagtc tcggggagtc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccgtcagt agcaatgaga tgagctgggt ccgccaggct 120

ccagggaagg gtctggagtg ggtctcatcc attagtggtg gtagcacata ctacgcagac 180

tccaggaagg gcagattcac catctccaga gacaattcca agaacacgct gcatcttcaa 240

atgaacagcc tgagagctga ggacacggct gtgtattact gtaagaaa 288

<210> SEQ ID NO 388
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR16-12*01 sequence

<400> SEQUENCE: 388

gaggtgcagc tggtagagtc tgggagaggc ttggcccagc ctgggggta cctaaaactc 60

tccggtgcag cctctggatt caccgtcggt agctggtaca tgagctggat ccaccaggct 120

ccagggaagg gtctggagtg ggtctcatac attagtagta gtggttgtag cacaaactac 180

gcagactctg tgaagggcag attcaccatc tccacagaca actcaaagaa cacgctctac 240

ctgcaaatga acagcctgag agtggaggac acggccgtgt attactgtgc aaga 294

<210> SEQ ID NO 389
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*01 sequence

<400> SEQUENCE: 389

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 390
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*02 sequence

<400> SEQUENCE: 390

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gaggtgcagc tggtggagtc tgggggagcc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 391
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*04 sequence

<400> SEQUENCE: 391

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attgaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 392
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*05 sequence

<400> SEQUENCE: 392

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag tctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 393
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*06 sequence

<400> SEQUENCE: 393

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggtc ccttagactc 60

tcctgtgcag cctctggatt cactttcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcggccgt attaaaagca aaactgatgg tgggacaaca 180

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aactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 394
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*07 sequence

<400> SEQUENCE: 394

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctggggggtc ccttagactc 60

tcctgtgcag cctctggttt cactttcagt aacgcctgga tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcggccgt attaaaagca aaactgatgg tgggacaaca 180

gactacgctg cacccgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 395
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*03 sequence

<400> SEQUENCE: 395

gaggtgcagc tggtggagtc tgccggagcc ttggtacagc ctggggggtc ccttagactc 60

tcctgtgcag cctctggatt cacttgcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca aagctaatgg tgggacaaca 180

gactacgctg cacctgtgaa aggcagattc accatctcaa gagttgattc aaaaaacacg 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtaccaca 300

ga 302

<210> SEQ ID NO 396
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-15*08 sequence

<400> SEQUENCE: 396

gaggtgcagc tggtggagtc tgcgggaggc ttggtacagc ctggggggtc ccttagactc 60

tcctgtgcag cctctggatt cacttgcagt aacgcctgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggctgt attaaaagca aagctaatgg tgggacaaca 180

gactacgctg cacctgtgaa aggcagattc accatctcaa gagatgattc aaaaaacacg 240

ctgtatctgc aaatgatcag cctgaaaacc gaggacacgg ccgtgtatta ctgtaccaca 300

gg 302

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<210> SEQ ID NO 397
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-72*01 sequence

<400> SEQUENCE: 397

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gaccactaca tggactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt actagaaaca aagctaacag ttacaccaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc aaagaactca 240

ctgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300

ga 302

<210> SEQ ID NO 398
<211> LENGTH: 165
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-72*02 sequence

<400> SEQUENCE: 398

accttcagtg accactacat ggactgggtc cgccaggctc cagggaaggg gctggagtgg 60

gttggccgta ctagaaacaa agctaacagc tacaccacag aatacgccgc gtctgtgaaa 120

ggcagattca ccatctcaag agatgattca aagaactcac tgtat 165

<210> SEQ ID NO 399
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR15-7*01 sequence

<400> SEQUENCE: 399

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggttc tctgagactc 60

tcatgtgcag cctctggatt caccttcagt gaccactaca tgagctgggt ccgccaggct 120

caagggaaag ggctagagtt ggtaggttta ataagaaaca aagctaacag ttacacgaca 180

gaatatgctg cgtctgtgaa aggcagactt accatctcaa gagaggattc aaagaacacg 240

atgtatctgc aaatgagcaa cctgaaaacc gaggacttgg ccgtgtatta ctgtgctaga 300

<210> SEQ ID NO 400
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR15-7*03 sequence

<400> SEQUENCE: 400

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggttc tctgagactc 60

tcatgtgcag cctctggatt caccttcagt gaccactaca tgagctgggt ccgccaggct 120

caagggaaag ggctagagtt ggtaggttta ataagaaaca aagctaacag ttacacgaca 180

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gaatatgctg cgtctgtgaa aggcagactt accatctcaa gagaggattc aaagaacacg 240

ctgtatctgc aaatgagcag cctgaaaacc gaggacttgg ccgtgtatta ctgtgctaga 300

<210> SEQ ID NO 401
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3/OR15-7*02 sequence

<400> SEQUENCE: 401

gaggtgcagc tgttggagtc tgggggaggc ttggtccagc ctggggggttc tctgagactc 60

tcatgtgctg cctctggatt caccttcagt gaccactaca tgagctgggt ccgccaggct 120

caagggaaag ggctagagtt ggtaggttta ataagaaaca aagctaacag ttacacgaca 180

gaatatgctg cgtctgtgaa aggcagactt accatctcaa gagaggattc aaagaacacg 240

ctgtatctgc aaatgagcag cctgaaaacc gaggacttgg ccgtgtatta ctgtgctaga 300

<210> SEQ ID NO 402
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-73*01 sequence

<400> SEQUENCE: 402

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgaaactc 60

tcctgtgcag cctctgggtt caccttcagt ggctctgcta tgcactgggt ccgccaggct 120

tccgggaaag ggctggagtg ggttggccgt attagaagca aagctaacag ttacgcgaca 180

gcatatgctg cgtcggtgaa aggcaggttc accatctcca gagatgattc aaagaacacg 240

gcgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtactaga 300

ca 302

<210> SEQ ID NO 403
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-73*02 sequence

<400> SEQUENCE: 403

gaggtgcagc tggtggagtc cgggggaggc ttggtccagc ctgggggggtc cctgaaactc 60

tcctgtgcag cctctgggtt caccttcagt ggctctgcta tgcactgggt ccgccaggct 120

tccgggaaag ggctggagtg ggttggccgt attagaagca aagctaacag ttacgcgaca 180

gcatatgctg cgtcggtgaa aggcaggttc accatctcca gagatgattc aaagaacacg 240

gcgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtactaga 300

ca 302

<210> SEQ ID NO 404
<211> LENGTH: 302
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-22*01 sequence

<400> SEQUENCE: 404

gaggtgcatc tggtggagtc tgggggagcc ttggtacagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt tactactaca tgagcggggt ccgccaggct   120

cccgggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca   180

gaatagacca cgtctgtgaa aggcagattc acaatctcaa gagatgattc caaaagcatc   240

acctatctgc aaatgaagag cctgaaaacc gaggacacgg ccgtgtatta ctgttccaga   300

ga   302

<210> SEQ ID NO 405
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-22*02 sequence

<400> SEQUENCE: 405

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt tactactaca tgagcggggt ccgccaggct   120

cccgggaagg ggctggaatg ggtaggtttc attagaaaca aagctaatgg tgggacaaca   180

gaatagacca cgtctgtgaa aggcagattc acaatctcaa gagatgattc caaaagcatc   240

acctatctgc aaatgaagag cctgaaaacc gaggacacgg ccgtgtatta ctgttccaga   300

ga   302

<210> SEQ ID NO 406
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-71*01 sequence

<400> SEQUENCE: 406

gaggtgcagc tggtggagtc cgggggaggc ttggtccagc ctggggggtc cctgagactc   60

tcctgtgcag cctctggatt caccttcagt gactactaca tgagctgggt ccgccaggct   120

cccgggaagg ggctggagtg ggtaggtttc attagaaaca aagctaatgg tgggacaaca   180

gaatagacca cgtctgtgaa aggcagattc acaatctcaa gagatgattc caaaagcatc   240

acctatctgc aaatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga   300

ga   302

<210> SEQ ID NO 407
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-49*03 sequence

<400> SEQUENCE: 407

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

tcctgtacag cttctggatt cacctttggt gattatgcta tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga 300

ga 302

<210> SEQ ID NO 408
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-49*05 sequence

<400> SEQUENCE: 408

gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc cagggcggtc cctgagactc 60

tcctgtacag cttctggatt cacctttggt gattatgcta tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga 300

ga 302

<210> SEQ ID NO 409
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
HV3-49*01 sequence

<400> SEQUENCE: 409

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

tcctgtacag cttctggatt cacctttggt gattatgcta tgagctggtt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180

gaatacaccg cgtctgtgaa aggcagattc accatctcaa gagatggttc caaaagcatc 240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga 300

ga 302

<210> SEQ ID NO 410
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-49*04 sequence

<400> SEQUENCE: 410

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60

tcctgtacag cttctggatt cacctttggt gattatgcta tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca 180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc 240

```
gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga    300

ga                                                                   302


<210> SEQ ID NO 411
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-49*02 sequence

<400> SEQUENCE: 411

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggccgtc cctgagactc     60

tcctgtacag cttctggatt cacctttggg tattatccta tgagctgggt ccgccaggct    120

ccagggaagg ggctggagtg ggtaggtttc attagaagca aagcttatgg tgggacaaca    180

gaatacgccg cgtctgtgaa aggcagattc accatctcaa gagatgattc caaaagcatc    240

gcctatctgc aaatgaacag cctgaaaacc gaggacacag ccgtgtatta ctgtactaga    300

ga                                                                   302


<210> SEQ ID NO 412
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-25*01 sequence

<400> SEQUENCE: 412

gagatgcagc tggtggagtc tgggggaggc ttgcaaaagc ctgcgtggtc cccgagactc     60

tcctgtgcag cctctcaatt caccttcagt agctactaca tgaactgtgt ccgccaggct    120

ccagggaatg ggctggagtt ggtttgacaa gttaatccta atgggggtag cacatacctc    180

atagactccg gtaaggaccg attcaatacc tccagagata acgccaagaa cacacttcat    240

ctgcaaatga acagcctgaa aaccgaggac acggccctct attagtgtac cagaga        296


<210> SEQ ID NO 413
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      IGHV3-25*02 sequence

<400> SEQUENCE: 413

gagatgcagc tggtggagtc tgggggaggc ttggcaaagc ctgcgtggtc cccgagactc     60

tcctgtgcag cctctcaatt caccttcagt agctactaca tgaactgtgt ccgccaggct    120

ccagggaatg ggctggagtt ggtttgacaa gttaatccta atgggggtag cacatacctc    180

atagactccg gtaaggaccg attcaatacc tccagagata acgccaagaa cacacttcat    240

ctgcaaatga acagcctgaa aaccgaggac acggccctct attagtgtac cagaga        296


<210> SEQ ID NO 414
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-25*03 sequence

<400> SEQUENCE: 414

gagatgcagc tggtggagtc tgggggaggc ttggcaaagc ctgcgtggtc cccgagactc 60

tcctgtgcag cctctcaatt caccttcagt agctactaca tgaactgtgt ccgccaggct 120

ccagggaatg ggctggagtt ggttggacaa gttaatccta atgggggtag cacatacctc 180

atagactccg gtaaggaccg attcaatacc tccagagata acgccaagaa cacacttcat 240

ctgcaaatga acagcctgaa aaccgaggac acggccctgt attagtgtac caga 294

<210> SEQ ID NO 415
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-63*01 sequence

<400> SEQUENCE: 415

gaggtggagc tgatagagtc catagagggc ctgagacaac ttgggaagtt cctgagactc 60

tcctgtgtag cctctggatt caccttcagt agctactgaa tgagctgggt caatgagact 120

ctagggaagg ggctggaggg agtaatagat gtaaaatatg atggaagtca gatataccat 180

gcagactctg tgaagggcag attcaccatc tccaaagaca atgctaagaa ctcaccgtat 240

ctccaaacga acagtctgag agctgaggac atgaccatgc atggctgtac ataaggtt 298

<210> SEQ ID NO 416
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-63*02 sequence

<400> SEQUENCE: 416

gaggtggagc tgatagagtc catagagggc ctgagacaac ttgggaagtt cctgagactc 60

tcctgtgtag cctctggatt caccttcagt agctactgaa tgagctgggt caatgagact 120

ctagggaagg ggctggaggg agtaatagat gtaaaatatg atggaagtca gatataccat 180

gcagactctg tgaagggcag attcaccatc tccaaagaca atgctaagaa ctcaccgtat 240

ctgcaaacga acagtctgag agctgaggac atgaccatgc atggctgtac ataa 294

<210> SEQ ID NO 417
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-32*01 sequence

<400> SEQUENCE: 417

gaggtggagc tgatagagtc catagaggac ctgagacaac ctgggaagtt cctgagactc 60

tcctgtgtag cctctagatt cgccttcagt agcttctgaa tgagccgagt tcaccagtct 120

ccaggcaagg ggctggagtg agtaatagat ataaaagatg atggaagtca gatacaccat 180

gcagactctg tgaagggcag attctccatc tccaaagaca atgctaagaa ctctctgtat 240 ctgcaaatga acactcagag agctgaggac gtggccgtgt atggctatac ataaggtc 298

<210> SEQ ID NO 418
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-54*01 sequence

<400> SEQUENCE: 418

gaggtacagc tggtggagtc tgaagaaaac caaagacaac ttgggggatc cctgagactc 60

tcctgtgcag actctggatt aaccttcagt agctactgaa tgagctcaga ttcccaagct 120

ccagggaagg ggctggagtg agtagtagat atatagtagg atagaagtca gctatgttat 180

gcacaatctg tgaagagcag attcaccatc tccaaagaaa atgccaagaa ctcactctgt 240

ttgcaaatga acagtctgag agcagagggc acggccgtgt attactgtat gtgagy 296

<210> SEQ ID NO 419
<211> LENGTH: 296
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-54*04 sequence

<400> SEQUENCE: 419

gaggtacagc tggtggagtc tgaagaaaac caaagacaac ttgggggatc cctgagactc 60

tcctgtgcag actctggatt aaccttcagt agctactgaa tgagctcaga ttcccaggct 120

ccagggaagg ggctggagtg agtagtagat atatagtagg atagaagtca gctatgttat 180

gcacaatctg tgaagagcag attcaccatc tccaaagaaa atgccaagaa ctcactctgt 240

ttgcaaatga acagtctgag agcagagggc acggccgtgt attactgtat gtgagt 296

<210> SEQ ID NO 420
<211> LENGTH: 207
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IGHV3-54*02 sequence

<400> SEQUENCE: 420

tagctactga atgagctcag attcccaggc tccagggaag gggctggagt gagtagtaga 60

tatatagtac gatagaagtc agatatgtta tgcacaatct gtgaagagca gattcaccat 120

ctccaaagaa aatgccaaga actcactccg tttgcaaatg aacagtctga gagcagaggg 180

cacggccgtg tattactgta tgtgagg 207

<210> SEQ ID NO 421
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJ4_1 sequence

<400> SEQUENCE: 421

tgaggagacg gtgaccaggg ttccttggcc c 31

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<210> SEQ ID NO 422
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ4_3 sequence

<400> SEQUENCE: 422

tgaggagacg gtgaccaggg tcccttggcc c                                    31


<210> SEQ ID NO 423
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ4_2 sequence

<400> SEQUENCE: 423

tgaggagacg gtgaccaggg ttccctggcc c                                    31


<210> SEQ ID NO 424
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ3_12 sequence

<400> SEQUENCE: 424

ctgaagagac ggtgaccatt gtcccttggc cc                                   32


<210> SEQ ID NO 425
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6_1 sequence

<400> SEQUENCE: 425

ctgaggagac ggtgaccgtg gtcccttgcc cc                                   32


<210> SEQ ID NO 426
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6_2 sequence

<400> SEQUENCE: 426

tgaggagacg gtgaccgtgg tcccttggcc c                                    31


<210> SEQ ID NO 427
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6_34 sequence

<400> SEQUENCE: 427
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ctgaggagac ggtgaccgtg gtccctttgc cc                                32


<210> SEQ ID NO 428
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ2_1 sequence

<400> SEQUENCE: 428

ctgaggagac agtgaccagg gtgccacggc cc                                32


<210> SEQ ID NO 429
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ5_1 sequence

<400> SEQUENCE: 429

ctgaggagac ggtgaccagg gttccttggc cc                                32


<210> SEQ ID NO 430
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ5_2 sequence

<400> SEQUENCE: 430

ctgaggagac ggtgaccagg gttccctggc cc                                32


<210> SEQ ID NO 431
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ1_1 sequence

<400> SEQUENCE: 431

ctgaggagac ggtgaccagg gtgccctggc cc                                32


<210> SEQ ID NO 432
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJSEQ4_1 sequence

<400> SEQUENCE: 432

tgaggagacg gtgaccaggg ttccttggcc ccag                              34


<210> SEQ ID NO 433
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJSEQ4_3 sequence
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<400> SEQUENCE: 433

tgaggagacg gtgaccaggg tcccttggcc ccag 34

<210> SEQ ID NO 434
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ4_2 sequence

<400> SEQUENCE: 434

tgaggagacg gtgaccaggg ttccctggcc ccag 34

<210> SEQ ID NO 435
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ3_12 sequence

<400> SEQUENCE: 435

ctgaagagac ggtgaccatt gtcccttggc cccag 35

<210> SEQ ID NO 436
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ6_1 sequence

<400> SEQUENCE: 436

ctgaggagac ggtgaccgtg gtcccttgcc cccag 35

<210> SEQ ID NO 437
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ6_2 sequence

<400> SEQUENCE: 437

tgaggagacg gtgaccgtgg tcccttggcc ccag 34

<210> SEQ ID NO 438
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ6_34 sequence

<400> SEQUENCE: 438

ctgaggagac ggtgaccgtg gtccctttgc cccag 35

<210> SEQ ID NO 439
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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>IGHJSEQ2_1 sequence

<400> SEQUENCE: 439

ctgaggagac agtgaccagg gtgccacggc cccag 35

<210> SEQ ID NO 440
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ5_1 sequence

<400> SEQUENCE: 440

ctgaggagac ggtgaccagg gttccttggc cccag 35

<210> SEQ ID NO 441
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ5_2 sequence

<400> SEQUENCE: 441

ctgaggagac ggtgaccagg gttccctggc cccag 35

<210> SEQ ID NO 442
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJSEQ1_1 sequence

<400> SEQUENCE: 442

ctgaggagac ggtgaccagg gtgccctggc cccag 35

<210> SEQ ID NO 443
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHV1 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 443

tgggtgcacc aggtccangn acaagggctt gagtgg 36

<210> SEQ ID NO 444
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHV2 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base

<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 444

tgggtgcgac aggctcgngn acaacgcctt gagtgg 36

<210> SEQ ID NO 445
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHV3 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 445

tgggtgcgcc agatgccngn gaaaggcctg gagtgg 36

<210> SEQ ID NO 446
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHV4 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 446

tgggtccgcc agscyccngn gaaggggctg gagtgg 36

<210> SEQ ID NO 447
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHV5 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 447

tgggtccgcc aggctccngn aaaggggctg gagtgg 36

<210> SEQ ID NO 448

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<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHV6 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: a, c, g or t

<400> SEQUENCE: 448

tgggtctgcc aggctccngn gaaggggcag gagtgg                            36


<210> SEQ ID NO 449
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGH7_3.25p sequence

<400> SEQUENCE: 449

tgtgtccgcc aggctccagg gaatgggctg gagttgg                           37


<210> SEQ ID NO 450
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGH8_3.54p sequence

<400> SEQUENCE: 450

tcagattccc aagctccagg gaaggggctg gagtgag                           37


<210> SEQ ID NO 451
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGH9_3.63p sequence

<400> SEQUENCE: 451

tgggtcaatg agactctagg gaaggggctg gagggag                           37


<210> SEQ ID NO 452
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ4*01/1-48 sequence

<400> SEQUENCE: 452

actactttga ctactggggc caaggaaccc tggtcaccgt ctcctcag               48


<210> SEQ ID NO 453
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ4*03/1-48 sequence

<400> SEQUENCE: 453

gctactttga ctactggggc caagggaccc tggtcaccgt ctcctcag                48


<210> SEQ ID NO 454
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ4*02/1-48 sequence

<400> SEQUENCE: 454

actactttga ctactggggc cagggaaccc tggtcaccgt ctcctcag                48


<210> SEQ ID NO 455
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ3*01/1-50 sequence

<400> SEQUENCE: 455

tgatgctttt gatgtctggg gccaagggac aatggtcacc gtctcttcag              50


<210> SEQ ID NO 456
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ3*02/1-50 sequence

<400> SEQUENCE: 456

tgatgctttt gatatctggg gccaagggac aatggtcacc gtctcttcag              50


<210> SEQ ID NO 457
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6*01/1-63 sequence

<400> SEQUENCE: 457

attactacta ctactacggt atggacgtct gggggcaagg gaccacggtc accgtctcct    60

cag                                                                  63


<210> SEQ ID NO 458
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6*02/1-62 sequence

<400> SEQUENCE: 458

attactacta ctactacggt atggacgtct ggggccaagg gaccacggtc accgtctcct    60

cag                                                                  63
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<210> SEQ ID NO 459
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6*04/1-63 sequence

<400> SEQUENCE: 459

attactacta ctactacggt atggacgtct ggggcaaagg gaccacggtc accgtctcct   60

cag   63

<210> SEQ ID NO 460
<211> LENGTH: 63
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ6*03/1-62 sequence

<400> SEQUENCE: 460

attactacta ctactactac atggacgtct ggggcaaagg gaccacggtc accgtctcct   60

cag   63

<210> SEQ ID NO 461
<211> LENGTH: 53
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ2*01/1-53 sequence

<400> SEQUENCE: 461

ctactggtac ttcgatctct ggggccgtgg caccctggtc actgtctcct cag   53

<210> SEQ ID NO 462
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ5*01/1-51 sequence

<400> SEQUENCE: 462

acaactggtt cgactcctgg ggccaaggaa ccctggtcac cgtctcctca g   51

<210> SEQ ID NO 463
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      >IGHJ5*02/1-51 sequence

<400> SEQUENCE: 463

acaactggtt cgacccctgg ggccagggaa ccctggtcac cgtctcctca g   51

<210> SEQ ID NO 464
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJ1*01/1-52 sequence

<400> SEQUENCE: 464

gctgaatact tccagcactg gggccagggc accctggtca ccgtctcctc ag 52

<210> SEQ ID NO 465
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJ2P*01/1-61 sequence

<400> SEQUENCE: 465

ctacaagtgc ttggagcact ggggcagggc agcccggaca ccgtctccct gggaacgtca 60

g 61

<210> SEQ ID NO 466
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJ1P*01/1-54 sequence

<400> SEQUENCE: 466

aaaggtgctg gggtcccct gaacccgacc cgccctgaga ccgcagccac atca 54

<210> SEQ ID NO 467
<211> LENGTH: 52
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
>IGHJ3P*01/1-52 sequence

<400> SEQUENCE: 467

cttgcggttg gacttcccag ccgacagtgg tggtctggct tctgaggggt ca 52

<210> SEQ ID NO 468
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBJ1-2 sequence

<400> SEQUENCE: 468

aatgatacgg cgaccaccga gatctaccta caacggttaa cctggtcccc gaaccgaa 58

<210> SEQ ID NO 469
<211> LENGTH: 284
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
TRBV2*02 sequence

<400> SEQUENCE: 469

gaacctgaag tcacccagac tcccagccat caggtcacac agatgggaca ggaagtgatc 60

ttgcactgtg tccccatctc taatcactta tacttctatt ggtacagaca aatcttgggg 120

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cagaaagtcg agtttctggt ttccttttat aataatgaaa tctcagagaa gtctgaaata    180

ttcgatgatc aattctcagt tgaaaggcct gatggatcaa atttcactct gaagatccgg    240

tccacaaagc tggaggactc agccatgtac ttctgtgcca gcag                     284


<210> SEQ ID NO 470
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-1 sequence

<400> SEQUENCE: 470

acaactgtga gtctggtgcc ttgtccaaag aaa                                  33


<210> SEQ ID NO 471
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-2 sequence

<400> SEQUENCE: 471

acaacggtta acctggtccc cgaaccgaag gtg                                  33


<210> SEQ ID NO 472
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-3 sequence

<400> SEQUENCE: 472

acaacagtga gccaacttcc ctctccaaaa tat                                  33


<210> SEQ ID NO 473
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-4 sequence

<400> SEQUENCE: 473

aagacagaga gctgggttcc actgccaaaa aac                                  33


<210> SEQ ID NO 474
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-5 sequence

<400> SEQUENCE: 474

aggatggaga gtcgagtccc atcaccaaaa tgc                                  33


<210> SEQ ID NO 475
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 1-6 sequence

<400> SEQUENCE: 475

gtcacagtga gcctggtccc gttcccaaag tgg                                  33


<210> SEQ ID NO 476
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-1 sequence

<400> SEQUENCE: 476

agcacggtga gccgtgtccc tggcccgaag aac                                  33


<210> SEQ ID NO 477
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-2 sequence

<400> SEQUENCE: 477

agtacggtca gcctagagcc ttctccaaaa aac                                  33


<210> SEQ ID NO 478
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-3 sequence

<400> SEQUENCE: 478

agcactgtca gccgggtgcc tgggccaaaa tac                                  33


<210> SEQ ID NO 479
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-4 sequence

<400> SEQUENCE: 479

agcactgaga gccgggtccc ggcgccgaag tac                                  33


<210> SEQ ID NO 480
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-5 sequence

<400> SEQUENCE: 480

agcaccagga gccgcgtgcc tggcccgaag tac                                  33


<210> SEQ ID NO 481
<211> LENGTH: 33
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-6 sequence

<400> SEQUENCE: 481

agcacggtca gcctgctgcc ggccccgaaa gtc                                33


<210> SEQ ID NO 482
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      Jseq 2-7 sequence

<400> SEQUENCE: 482

gtgaccgtga gcctggtgcc cggcccgaag tac                                33


<210> SEQ ID NO 483
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-5 sequence
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: a, c, g or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5' end modified with universal reverse primer

<400> SEQUENCE: 483

nacctaggat ggagagtcga gtcccatcac caaa                               34


<210> SEQ ID NO 484
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      TRBJ1-5 sequence

<400> SEQUENCE: 484

aatgatacgg cgaccaccga gatctaccta ggatggagag tcgagtccca tcaccaaa     58
```

What is claimed:

1. A method, comprising:

contacting a sample comprising genomic DNA from mammalian lymphoid cells with a plurality of distinct V-segment primers and at least 3 distinct J-segment primers,

wherein said plurality of distinct V-segment primers are each capable of specifically hybridizing to at least one immunoglobulin (Ig) V-region gene segment, wherein each V-segment primer hybridizes to a V-region gene sequence that is outside a first region where untemplated deletions occur during Ig gene rearrangement, wherein said first region of said V-region gene segment is adjacent to and 5' to a V-recombination signal sequence (V-RSS) of said V-region gene segment, wherein each V-segment primer hybridizes with the 3' end of said V-segment primer closer to the RSS than the 5' end of said V-segment primer and is positioned with the 3' end of said V-segment primer at least 10 nucleotides upstream from said V-RSS;

wherein said at least 3 distinct J-segment primers are each capable of specifically hybridizing to at least one Ig J-region gene segment, wherein each J-segment primer hybridizes to a J-region gene sequence that is outside a second region where untemplated deletions occur during Ig gene rearrangement, wherein said second region of said J-region gene segment is adjacent to and 3' to a J-recombination signal sequence (J-RSS) of said J-region gene segment, wherein said J-segment primer hybridizes with the 3' end of said J-region primer closer to said J-RSS than the 5' end of said J-segment primer and is positioned with the 3' end of the J-segment primer at least 10 nucleotides downstream from the J-RSS;

amplifying in a single multiplex PCR reaction said genomic DNA with said plurality of distinct V-segment primers and said at least 3 distinct J-segment primers to produce at least 10^4 distinct rearranged DNA amplicons representing the diversity of Ig genes in said sample; and

sequencing each of said at least 10^4 distinct rearranged DNA amplicons using high-throughput sequencing.

2. The method of claim **1**, further comprising quantifying the full diversity of rearranged Ig genes in said sample using sequencing data of said at least 10^4 distinct rearranged DNA amplicons.

3. The method of claim **1**, wherein amplifying produces at least 10^5 distinct rearranged DNA amplicons.

4. The method of claim **1**, wherein amplifying produces at least 10^6 distinct rearranged DNA amplicons.

5. The method of claim **1**, wherein sequencing comprises using a plurality of sequencing oligonucleotides that hybridize to a defined region of said distinct rearranged DNA amplicons.

6. The method of claim **5**, wherein said sequencing oligonucleotides are selected from the group consisting of SEQ ID NOs:432-442.

7. The method of claim **5**, wherein said sequencing oligonucleotides hybridize adjacent to a unique nucleotide base tag within a J gene segment of said distinct rearranged DNA amplicons.

8. The method of claim **1**, wherein said plurality of V-segment primers have similar annealing temperatures.

9. The method of claim **1**, wherein said at least 3 distinct J-segment primers have similar annealing temperatures.

10. The method of claim **1**, wherein said each of said distinct rearranged DNA amplicons spans a V-D-J or V-J junction.

11. The method of claim **1**, wherein said Ig V-region gene segment comprises an IGH V gene segment, an IGL V gene segment, or an IGK V gene segment.

12. The method of claim **1**, wherein said Ig J-region gene segment comprises an IGH J gene segment, an IGL J gene segment, or an IGK V gene segment.

13. The method of claim **1**, further comprising contacting said sample with 3 to 45 distinct V-segment primers.

14. The method of claim **1**, further comprising contacting said sample with 3 to 13 distinct J-segment primers.

15. The method of claim **1**, wherein each of said plurality of distinct V-segment primers do not cross an intron/exon boundary.

16. The method of claim **1**, wherein each of said at least 3 distinct J-segment primers do not cross an intron/exon boundary.

17. The method of claim **1**, wherein each of said at least 3 distinct J segment primers hybridize to a conserved element of the J-region gene segment.

18. The method of claim **1**, wherein each of said at least 3 distinct J-segment primers specifically hybridizes to a different Ig J-region gene segment.

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