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(54) **Title**: MHC MULTIMERS IN BORRELIA DIAGNOSTICS AND DISEASE

(57) **Abstract**: Novel compounds carrying ligands capable of binding to counter receptors on relevant target cells are disclosed. The compounds possess a number of advantageous features, rendering them very suitable for a wide range of applications, including use as detection systems, detection of relevant target cells as well as a number of other methods. In particular, novel MHC complexes comprising one or more MHC molecules containing one or more Borrelia derived peptides are disclosed. The possibility of presenting to the target cells a plurality of MHC-peptide complexes makes the MHC complexes according to the present invention an extremely powerful tool e.g. in the field of therapy and diagnosis. The invention generally relates to the sample-mounted use of MHC complexes and MHC multimers. Also comprised by the invention is the field of therapy and vaccine, including therapeutic/vaccine methods and therapeutic/vaccine compositions.

MHC MULTIMERS IN BORRELIA DIAGNOSTICS AND DISEASE

All patent and non-patent references cited in PA 2008 00295, PA 2008 01011 as well as in this application are hereby incorporated by reference in their entirety. PA 2008 00295 and PA 2008 01011 are hereby also incorporated herein by reference in its entirety.

FIELD OF INVENTION

The present invention relates to MHC-peptide complexes and uses thereof in the diagnosis, treatment and monitoring of treatment of a disease in an individual.

BACKGROUND OF INVENTION

Biochemical interactions between peptide epitope specific membrane molecules encoded by the Major Histocompatibility Complex (MHC, in humans HLA) and T-cell receptors (TCR) are required to elicit specific immune responses. This requires activation of T-cells by presentation to the T-cells of peptides against which a T-cell response should be raised. The peptides are presented to the T-cells by the MHC complexes.

The immune response

The immune response is divided into two parts termed the innate immune response and the adaptive immune response. Both responses work together to eliminate pathogens (antigens). Innate immunity is present at all times and is the first line of defense against invading pathogens. The immediate response by means of pre-existing elements, i.e. various proteins and phagocytic cells that recognize conserved features on the pathogens, is important in clearing and control of spreading of pathogens. If a pathogen is persistent in the body and thus only partially cleared by the actions of the innate immune system, the adaptive immune system initiate a response against the pathogen. The adaptive immune system is capable of eliciting a response against virtually any type of pathogen and is unlike the innate immune system capable of establishing immunological memory.

The adaptive response is highly specific to the particular pathogen that activated it but it is not so quickly launched as the innate when first encountering a pathogen.

However, due to the generation of memory cells, a fast and more efficient response is generated upon repeated exposure to the same pathogen. The adaptive response is carried out by two distinct sets of lymphocytes, the B cells producing antibodies leading to the humoral or antibody mediated immune response, and the T cells leading to the cell mediated immune response.

T cells express a clonotypic T cell receptor (TCR) on the surface. This receptor enable the T cell to recognize peptide antigens bound to major histocompatibility complex (MHC) molecules, called human leukocyte antigens (HLA) in man. Depending on the type of pathogen, being intracellular or extracellular, the antigenic peptides are bound to MHC class I or MHC class II, respectively. The two classes of MHC complexes are recognized by different subsets of T cells; Cytotoxic CD8+ T cells recognizing MHC class I and CD4+ helper cells recognizing MHC class II. In general, TCR recognition of MHC-peptide complexes result in T cell activation, clonal expansion and differentiation of the T cells into effector, memory and regulatory T cells.

B cells express a membrane bound form of immunoglobulin (Ig) called the B cell receptor (BCR). The BCR recognizes an epitope that is part of an intact three dimensional antigenic molecule. Upon BCR recognition of an antigen the BCR:antigen complex is internalized and fragments from the internalized antigen is presented in the context of MHC class II on the surface of the B cell to CD4+ helper T-cells (Th). The specific Th cell will then activate the B cell leading to differentiation into an antibody producing plasma cell.

A very important feature of the adaptive immune system is its ability to distinguish between self and non-self antigens, and preferably respond against non-self. If the immune system fails to discriminate between the two, specific immune responses against self-antigens are generated. These autoimmune reactions can lead to damage of self-tissue.

The adaptive immune response is initiated when antigens are taken up by professional antigen presenting cells such as dendritic cells, Macrophages, Langerhans cells and B-cells. These cells present peptide fragments, resulting from the degradation of proteins, in the context of MHC class II proteins (Major Histocompatibility Complex) to helper T cells. The T helper cells then mediate help to B-cells and antigen-specific cytotoxic T

cells, both of which have received primary activation signals via their BCR respective TCR. The help from the Th-cell is mediated by means of soluble mediators e.g. cytokines.

In general the interactions between the various cells of the cellular immune response is governed by receptor-ligand interactions directly between the cells and by production of various soluble reporter substances e.g. cytokines by activated cells.

MHC-peptide complexes

MHC complexes function as antigenic peptide receptors, collecting peptides inside the cell and transporting them to the cell surface, where the MHC-peptide complex can be recognized by T-lymphocytes. Two classes of classical MHC complexes exist, MHC class I and II. The most important difference between these two molecules lies in the protein source from which they obtain their associated peptides. MHC class I molecules present peptides derived from endogenous antigens degraded in the cytosol and are thus able to display fragments of viral proteins and unique proteins derived from cancerous cells. Almost all nucleated cells express MHC class I on their surface even though the expression level varies among different cell types. MHC class II molecules bind peptides derived from exogenous antigens. Exogenous proteins enter the cells by endocytosis or phagocytosis, and these proteins are degraded by proteases in acidified intracellular vesicles before presentation by MHC class II molecules. MHC class II molecules are only expressed on professional antigen presenting cells like B cells and macrophages.

The three-dimensional structure of MHC class I and II molecules are very similar but important differences exist. MHC class I molecules consist of two polypeptide chains, a heavy chain, α, spanning the membrane and a light chain, β2-microglobulin (β2m). The heavy chain is encoded in the gene complex termed the major histocompatibility complex (MHC), and its extracellular portion comprises three domains, α1, α2 and α3. The β2m chain is not encoded in the MHC gene and consists of a single domain, which together with the α3 domain of the heavy chain make up a folded structure that closely resembles that of the immunoglobulin. The α1 and α2 domains pair to form the peptide binding cleft, consisting of two segmented α helices lying on a sheet of eight β-strands. In humans as well as in mice three different types of MHC class I molecule exist. HLA-

A, B, C are found in humans while MHC class I molecules in mice are designated H-2K, H-2D and H-2L.

The MHC class II molecule is composed of two membrane spanning polypeptide chains, α and β, of similar size (about 30000 Da). Genes located in the major histocompatibility complex encode both chains. Each chain consists of two domains, where α1 and β1 forms a 9-pocket peptide-binding cleft, where pocket 1, 4, 6 and 9 are considered as major peptide binding pockets. The α2 and β2, like the α2 and β2m in the MHC class I molecules, have amino acid sequence and structural similarities to immunoglobulin constant domains. In contrast to MHC class I complexes, where the ends of the antigenic peptide is buried, peptide-ends in MHC class II complexes are not. HLA-DR, DQ and DP are the human class II molecules, H-2A, M and E are those of the mice.

A remarkable feature of MHC genes is their polymorphism accomplished by multiple alleles at each gene. The polygenic and polymorphic nature of MHC genes is reflected in the peptide-binding cleft so that different MHC complexes bind different sets of peptides. The variable amino acids in the peptide binding cleft form pockets where the amino acid side chains of the bound peptide can be buried. This permits a specific variant of MHC to bind some peptides better than others.

MHC multimers

Due to the short half-life of the peptide-MHC-T cell receptor ternary complex (typically between 10 and 25 seconds) it is difficult to label specific T cells with labelled MHC-peptide complexes, and like-wise, it is difficult to employ such monomers of MHC-peptide for therapeutic and vaccine purposes because of their weak binding. In order to circumvent this problem, MHC multimers have been developed. These are complexes that include multiple copies of MHC-peptide complexes, providing these complexes with an increased affinity and half-life of interaction, compared to that of the monomer MHC-peptide complex. The multiple copies of MHC-peptide complexes are attached, covalently or non-covalently, to a multimerization domain. Known examples of such MHC multimers include the following:

- MHC-dimers: Each MHC dimer contains two copies of MHC-peptide. IgG is used as multimerization domain, and one of the domains of the MHC protein is covalently linked to IgG.

- MHC-tetramers: Each MHC-tetramer contains four copies of MHC-peptide, each of which is biotinylated. The MHC complexes are held together in a complex by the streptavidin tetramer protein, providing a non-covalent linkage between a streptavidin monomer and the MHC protein. Tetramers are described in US patent 5,635,363.
- MHC pentamers: Five copies of MHC-peptide complexes are multimerised by a self-assembling coiled-coil domain, to form a MHC pentamer. MHC pentamers are described in the US patent 2004209295
- MHC dextramers: A large number of MHC-peptide complexes, typically more than ten, are attached to a dextran polymer. MHC-dextramers are described in the patent application WO 02/072631 A2.
- MHC streptamers: 8-12 MHC-peptide complexes attached to Streptactin. MHC streptamers are described in Knabel M et al. Reversibel MHC multimer staining for functional isolation of T-cell populations and effective adoptive transfer. Nature medicine 6. 631-637 (2002).

Use of MHC multimers in flow cytometry and related techniques

The concentration of antigen-specific T-cells in samples from e.g. peripheral blood can be very low. Flow cytometry and related methods offer the ability to analyze a large number of cells and simultaneously identify the few of interest. MHC multimers have turned out to be very valuable reagents for detection and characterization of antigen-specific T-cells in flow cytometer experiments. The relative amount of antigen-specific T cells in a sample can be determined and also the affinity of the binding of MHC multimer to the T-cell receptor can be determined.

The basic function of a flow cytometer is its ability to analyse and identify fluorochrome labelled entities in a liquid sample, by means of its excitation, using a light source such as a laser beam and the light emission from the bound fluorochrome.

MHC multimers is used as detections molecule for identification of antigen-specific T-cells in flow cytometry, by labelling the MHC multimer with a specific fluorochrome, which is detectable, by the flow cytometer used.

In order to facilitate the identification of a small amount of cells, the cells can be sub-categorized using antibodies or other fluorochrome labelled detections molecules directed against surface markers other than the TCR on the specific T-cells population. Antibodies or other fluorochrome labelled detections molecules can also be used to identify cells known not to be antigen-specific T-cells. Both kinds of detections

molecules are in the following referred to as gating reagents. Gating reagents, helps identify the "true" antigen-specific T cells bound by MHC multimers by identifying specific subpopulations in a sample, e.g. T cells and by excluding cells that for some reason bind MHC mulimers without being antigen-specific T-cells.

Other cytometry methods, e.g. fluorescence microscopy and IHC can like flow cytometry be employed in identification of antigen-specific T cells in a cell sample using MHC multimers.

Application of MHC multimers in immune monitoring, diagnostics, prognostics, therapy and vaccines

T cells are pivotal for mounting an adaptive immune response. It is therefore of importance to be able to measure the number of specific T cells when performing a monitoring of a given immune response, for example in connection with vaccine development, autologous cancer therapy, transplantation, infectious diseases, toxicity studies etc.

Accordingly, the present invention further provides powerful tools in the fields of vaccines, therapy and diagnosis. One objective of the present invention is to provide methods for anti-bacterial and anti-virus immunotherapy by generating antigen-specific T-cells capable of inactivating or eliminating undesirable target cells. Another objective is to isolate antigen-specific T-cells and culture these in the presence of co-stimulatory molecules. Ex vivo priming and expansion of T-cell populations allows the T-cells to be used in immunotherapy of various types of infectious diseases. A third objective of the present invention is to identify and label specific subsets of cells with relevance for the development or treatment of diseases.

SUMMARY OF INVENTION

Measurement of antigen-specific T cells during an immune response are important parameters in vaccine development, therapy and infectious diseases, inflammation, autoimmunity, toxicity studies etc. MHC multimers are crucial reagents in monitoring of antigen-specific T cells. The present invention describes novel methods to generate MHC multimers and methods to improve existing and new MHC multimers. The invention also describes improved methods for the use of MHC multimers in analysis of T cells in samples including diagnostic and prognostic methods. Furthermore the use of MHC multimers in therapy are described, e.g. anti-bacteria therapy.. The present

invention also relates to MHC multimers comprising one or more Borrelia peptides. In one preferred embodiment the present invention relates to a Borrelia vaccine. In a Borrelia vaccine the peptides bound in the peptide binding cleft of MHC are derived from antigenic borrelia proteins. In another preferred embodiment the present invention relates to diagnosis and monitoring of Borrelia infection using MHC multimers with Borrelia derived peptides bound in the peptide binding cleft of the MHC molecules.

DEFINITIONS

As used everywhere herein, the term"a", "an" or "the" is meant to be one or more, i. e. at least one.

“8 mers” are peptides consisting of 8 amino acids.
“9 mers” are peptides consisting of 9 amino acids.
“10 mers” are peptides consisting of 10 amino acids.
“11 mers” are peptides consisting of 11 amino acids.
“13 mers” are peptides consisting of 13 amino acids.
“14 mers” are peptides consisting of 14 amino acids.
“15 mers” are peptides consisting of 15 amino acids.
“16 mers” are peptides consisting of 16 amino acids.

As used everywhere herein, the term “Borrelia garini” also relates to “Borrelia garinii”.

An “amino acid residue” can be a natural or non-natural amino acid residue linked peptide bonds or bonds different from peptide bonds. The amino acid residues can be in D-configuration or L-configuration. An amino acid residue comprises an amino terminal part (NH_2) and a carboxy terminal part (COOH) separated by a central part comprising a carbon atom, or a chain of carbon atoms, at least one of which comprises at least one side chain or functional group. NH_2 refers to the amino group present at the amino terminal end of an amino acid or peptide, and COOH refers to the carboxy group present at the carboxy terminal end of an amino acid or peptide. The generic term amino acid comprises both natural and non-natural amino acids. Natural amino acids of standard nomenclature as listed in J. Biol. Chem., 243:3552-59 (1969) and adopted in 37 C.F.R., section 1.822(b)(2) belong to the group of amino acids listed in the table herein below. Non-natural amino acids are those not listed in the Table below. Examples of non-natural amino acids are those listed e.g. in 37 C.F.R. section

1.822(b)(4), all of which are incorporated herein by reference. Also, non-natural amino acid residues include, but are not limited to, modified amino acid residues, L-amino acid residues, and stereoisomers of D-amino acid residues.

Symbols		Amino acid
1-Letter	3-Letter	
Y	Tyr	tyrosine
G	Gly	glycine
F	Phe	phenylalanine
M	Met	methionine
A	Ala	alanine
S	Ser	serine
I	Ile	isoleucine
L	Leu	leucine
T	Thr	threonine
V	Val	valine
P	Pro	proline
K	Lys	lysine
H	His	histidine
Q	Gln	glutamine
E	Glu	glutamic acid
W	Trp	tryptophan
R	Arg	arginine
D	Asp	aspartic acid
N	Asn	asparagine
C	Cys	cysteine

Natural amino acids and their respective codes.

The terms "amino-terminal" and "carboxyl-terminal" are used herein to denote positions within polypeptides. Where the context allows, these terms are used with reference to a particular sequence or portion of a polypeptide to denote proximity or relative position. For example, a certain sequence positioned carboxyl-terminal to a reference sequence within a polypeptide is located proximal to the carboxyl terminus of the reference sequence, but is not necessarily at the carboxyl terminus of the complete polypeptide.

Adjuvant: adjuvants are drugs that have few or no pharmacological effects by themselves, but can increase the efficacy or potency of other drugs when given at the same time. In another embodiment, an adjuvant is an agent which, while not having any specific antigenic effect in itself, can stimulate the immune system, increasing the response to a vaccine.

Agonist: agonist as used herein is a substance that binds to a specific receptor and triggers a response in the cell. It mimics the action of an endogenous ligand that binds to the same receptor.

Anchor amino acid: Anchor amino acid is used interchangeably herein with anchor residue and is an amino acid of antigenic peptide having amino acid sidechains that bind into pockets lining the peptide-binding groove of MHC molecules thereby anchoring the peptide to the MHC molecule. Anchor residues being responsible for the main anchoring of peptide to MHC molecule are aclled primary anchor amino acids. Amino acids contributing to the binding of antigenic peptide to MHC molecule but in a lesser extend than primary anchor amino acids are called secondary anchor amino acids.

Anchor motif: The pattern of anchor residues in an antigenic peptide binding a certain MHC molecule. Peptides binding different MHC molecules have different anchor motifs defined by the patterns of anchor residues in the peptide sequence.

Anchor residue: Anchor residue is used interchangeably herein with anchor amino acid

Anchor position: The position of an anchor amino acid in antigenic peptide sequence. For MHC II the anchor positions is defined in the 9-mer core motif.

Antagonist: antagonist as used herein is a substance that binds to a specific receptor and blocks the response in the cell. It blocks the action of an endogenous ligand that binds to the same receptor.

Antibodies: As used herein, the term "antibody" means an isolated or recombinant binding agent that comprises the necessary variable region sequences to specifically bind an antigenic epitope. Therefore, an antibody is any form of antibody or fragment thereof that exhibits the desired biological activity, e.g., binding the specific target antigen. Antibodies can derive from multiple species. For example, antibodies include rodent (such as mouse and rat), rabbit, sheep, camel, and human antibodies. Antibodies can also include chimeric antibodies, which join variable regions from one species to constant regions from another species. Likewise, antibodies can be humanized, that is constructed by recombinant DNA technology to produce

immunoglobulins which have human framework regions from one species combined with complementarity determining regions (CDR's) from a another species' immunoglobulin. The antibody can be monoclonal or polyclonal. Antibodies can be divided into isotypes (IgA, IgG, IgM, IgD, IgE, IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM1, IgM2)

Antibodies: In another embodiment the term "antibody" refers to an intact antibody, or a fragment of an antibody that competes with the intact antibody for antigen binding. In certain embodiments, antibody fragments are produced by recombinant DNA techniques. In certain embodiments, antibody fragments are produced by enzymatic or chemical cleavage of intact antibodies. Exemplary antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, Fv, and scFv. Exemplary antibody fragments also include, but are not limited to, domain antibodies, nanobodies, minibodies ((scFv-C.sub.H3).sub.2), maxibodies ((scFv-C.sub.H2-C.sub.H3).sub.2), diabodies (noncovalent dimer of scFv).

Antigen presenting cell: An antigen-presenting cell (APC) as used herein is a cell that displays foreign antigen complexed with MHC on its surface.

Antigenic peptide: Used interchangeably with binding peptide. Any peptide molecule that is bound or able to bind into the binding groove of either MHC class 1 or MHC class 2 molecules.

Antigenic polypeptide: Polypeptide that contains one or more antigenic peptide sequences.

APC: Antigen presenting cell

Aptamer: the term aptamer as used herein is defined as oligonucleic acid or peptide molecules that bind a specific target molecule. Aptamers are usually created by selecting them from a large random sequence pool, but natural aptamers also exist. Aptamers can be divided into DNA amtamers, RNA aptamers and peptide aptamers.

Avidin: Avidin as used herein is a glycoprotein found in the egg white and tissues of birds, reptiles and amphibians. It contains four identical subunits having a combined

mass of 67,000-68,000 daltons. Each subunit consists of 128 amino acids and binds one molecule of biotin.

Biologically active molecule: A biologically active molecule is a molecule having itself a biological activity/effect or is able to induce a biological activity/effect when administered to a biological system. Biologically active molecules include adjuvants, immune targets (e.g. antigens), enzymes, regulators of receptor activity, receptor ligands, immune potentiators, drugs, toxins, cytotoxic molecules, co-receptors, proteins and peptides in general, sugar moieties, lipid groups, nucleic acids including siRNA, nanoparticles, small molecules.

Bioluminescent: Bioluminescence, as used herein, is the production and emission of light by a living organism as the result of a chemical reaction during which chemical energy is converted to light energy.

Biotin: Biotin, as used herein, is also known as vitamin H or B_7. Niotin has the chemical formula $C_{10}H_{16}N_2O_3S$.

Bispecific antibodies: The term bispecific antibodies as used herein is defined as antibodies that have binding specificities for at least two different antigens. The antibody can also be trispecific or multispecific.

Bispecific capture molecule: Molecule that have binding specificities for at least two different antigens. The molecule can also be trispecific or multispecific.

Carrier: A carrier as used herin can be any type of molecule that is directly or indirectly associated with the MHC peptide complex. In this invention, a carrier will typically refer to a functionalized polymer (e.g. dextran) that is capable of reacting with MHC-peptide complexes, thus covalently attaching the MHC-peptide complex to the carrier, or that is capable of reacting with scaffold molecules (e.g. streptavidin), thus covalently attaching streptavidin to the carrier; the streptavidin then may bind MHC-peptide complexes. Carrier and scaffold are used interchangeably herein where scaffold typically refers to smaller molecules of a multimerization domain and carrier typically refers to larger molecule and/or cell like structures.

Chelating chemical compound: Chelating chemical compound, as used herein, is the process of reversible bindingof a ligand to a metal ion, forming a metal complex.

Chemiluminescent: Chemiluminescence, as used herein, is the emission of light (luminescence) without emission of heat as the result of a chemical reaction.

Chromophore: A chromophore, as used herein, is the part of a visibly coloured molecule responsible for light absorption over a range of wavelengths thus giving rise to the colour. By extension the term can be applied to uv or ir absorbing parts of molecules.

Coiled-coil polypeptide: Used interchangeably with coiled-coil peptide and coiled-coil structure. The term coiled-coil polypeptide as used herein is a structural motif in proteins, in which 2-7 alpha-helices are coiled together like the strands of a rope

Complement protein: Protein of the complement system.

Counting beads: Beads countable in a flow cytometry experiment.

Covalent binding: The term covalent binding is used herein to describe a form of chemical bonding that is characterized by the sharing of pairs of electrons between atoms. Attraction-to-repulsion stability that forms between atoms when they share electrons is known as covalent bonding.

Crosslinking is the process of chemically joining two or more molecules by a covalent bond. Crosslinking reagents contain reactive ends to specific functional groups (primary amines, sulfhydryls, etc.) on proteins or other molecules.

CSF: Cerebrospinal fluid.

Diagnosis: The act or process of identifying or determining the nature and cause of a disease or injury through evaluation

Diabodies: The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH)

connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites.

Dendritic cell: The term dendritic cell as used herein is a type of immune cells. Their main function is to process antigen material and present it on the surface to other cells of the immune system, thus functioning as antigen-presenting cells.

Detection: In this invention detection means any method capable of measuringen one molecule bound to anoher molecule. The molecules are typically proteins but can be any type of molecule

Dextran: the term dextran as used herein is is a complex, branched polysaccharide made of many glucose molecules joined into chains of varying lengths. The straight chain consists of α1->6 glycosidic linkages between glucose molecules, while branches begin from α1->3 linkages (and in some cases, α1->2 and α1->4 linkages as well).

Direct detection of T cells: Direct detection of T cells is used herein interchangeably with direct detection of TCR and direct detection of T cell receptor. As used herein direct detection of T cells is detection directly of the binding interaction between a specific T cell receptor and a MHC multimer.

DNA: The term DNA (Deoxyribonucleic acid) duplex as used herein is a polymer of simple units called nucleotides, with a backbone made of sugars and phosphate atoms joined by ester bonds. Attached to each sugar is one of four types of molecules called bases.

DNA duplex: In living organisms, DNA does not usually exist as a single molecule, but instead as a tightly-associated pair of molecules. These two long strands entwine like vines, in the shape of a double helix.

Electrophilic: electrophile, as used herein, is a reagent attracted to electrons that participates in a chemical reaction by accepting an electron pair in order to bond to a nucleophile.

Enzyme label: enzyme labelling, as used herein, involves a detection method comprising a reaction catalysed by an enzyme.

Epitope-focused antibody: Antibodies also include epitope-focused antibodies, which have at least one minimal essential binding specificity determinant from a heavy chain or light chain CDR3 from a reference antibody, methods for making such epitope-focused antibodies are described in U.S. patent application Ser. No. 11/040,159, which is incorporated herein by reference in its entirety.

Flow cytomerty: The analysis of single cells using a flow cytometer.

Flow cytomter: Instrument that measures cell size, granularity and flourescence due to bound fluorescent marker molecules as single cells pass in a stream past photodectors. A flow cytomter carry out the measurements and/or sorting of individual cells.

Fluorescent: the term fluorescent as used herein is to have the ability to emit light of a certain wavelength when activated by light of another wavelength.

Fluorochromes: fluorochrome, as used herein, is any fluorescent compound used as a dye to mark e.g. protein with a fluorescent label.

Fluorophore: A fluorophore, as used herein, is a component of a molecule which causes a molecule to be fluorescent.

Folding: In this invention folding means in vitro or in vivo folding of proteins in a tertiery structure.

Fusion antibody: As used herein, the term "fusion antibody" refers to a molecule in which an antibody is fused to a non-antibody polypeptide at the N- or C-terminus of the antibody polypeptide.

Glycosylated: Glycosylation, as used herein, is the process or result of addition of saccharides to proteins and lipids.

Hapten: A residue on a molecule for which there is a specific molecule that can bind, e.g. an antibody.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells.

IgG: IgG as used herein is a monomeric immunoglobulin, built of two heavy chains and two light chains. Each molecule has two antigen binding sites.

Isolated antibody: The term "isolated" antibody as used herein is an antibody which has been identified and separated and/or recovered from a component of its natural environment.

Immunoconjugates: The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate). Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis(p-azidobenzoyl)hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene).

Immune monitoring: Immune monitoring of the present invention refers to testing of immune status in the diagnosis and therapy of diseases like but not limited to cancer, immunoproliferative and immunodeficiency disorders, autoimmune abnormalities, and infectious disease. It also refers to testing of immune status before, during and after vaccination and transplantation procedures.

Immune monitoring process: a serie of one or more immune monitoring analysis

Indirect detection of T cells: Indirect detection of T cells is used interchangeably herein with Indirect detection of TCR and indirect detection of T cell receptor. As used herein indirect detection of T cells is detection of the binding interaction between a specific T cell receptor and a MHC multimer by measurement of the effect of the binding interaction.

Ionophore: ionophore, as used herein, is a lipid-soluble molecule usually synthesized by microorganisms capable of transporting ions.

Label: Label herein is used interchangeable with labeling molecule. Label as described herein is an identifiable substance that is detectable in an assay and that can be attached to a molecule creating a labeled molecule. The behavior of the labeled molecule can then be studied.

Labelling: Labelling herein means attachment of a label to a molecule.

Lanthanide: lanthanide, as used herein, series comprises the 15 elements with atomic numbers 57 through 71, from lanthanum to lutetium.

Linker molecule: Linker molecule and linker is used interchangeable herein. A linker molecule is a molecule that covalently or non-covalently connects two or more molecules, thereby creating a larger complex consisting of all molecules including the linker molecule.

LDA: limiting dilution assay

Liposomes: The term liposomes as used herein is defined as a spherical vesicle with a membrane composed of a phospholipid and cholesterol bilayer. Liposomes, usually but not by definition, contain a core of aqueous solution; lipid spheres that contain no aqueous material are called micelles.

Immunoliposomes: The antibodies disclosed herein can also be formulated as immunoliposomes. Liposomes comprising the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA 82: 3688 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE).

Immuno profiling: Immuno profiling as used herein defines the profiling of an individual's antigen-specific T-cell repertoire

Marker: Marker is used interchangeably with marker molecule herein. A marker is molecule that specifically associates covalently or non-covalently with a molecule belonging to or associated with an entity.

MHC: Denotes the major histocompatibility complex.

MHC I is used interchangeably herein with MHC class I and denotes the major histocompatibility complex class I.

MHC II is used interchangeably herein with MHC class II and denotes the major histocompatibility complex class I.

MHC molecule: a MHC molecule as used everywhere herein is defined as any MHC class I molecule or MHC class II molecule as defined herein.

A "MHC Class I molecule" as used everywhere herein is used interchangeably with MHC I molecule and is defined as a molecule which comprises 1-3 subunits, including

a MHC I heavy chain, a MHC I heavy chain combined with a MHC I beta2microglobulin chain, a MHC I heavy chain combined with MHC I beta2microglobulin chain through a flexible linker, a MHC I heavy chain combined with an antigenic peptide, a MHC I heavy chain combined with an antigenic peptide through a linker, a MHC I heavy chain/ MHC I beta2microglobulin dimer combined with an antigenic peptide, and a MHC I heavy chain/ MHC I beta2microglobulin dimer combined with an antigenic peptide through a flexible linker to the heavy chain or beta2microglobulin. The MHC I molecule chains can be changed by substitution of single or by cohorts of native amino acids, or by inserts, or deletions to enhance or impair the functions attributed to said molecule.

MHC complex: MHC complex is herein used interchangeably with MHC-peptide complex, and defines any MHC I and/or MHC II molecule combined with antigenic peptide unless it is specified that the MHC complex is empty, i.e. is not complexed with antigenic peptide

MHC Class I like molecules (including non-classical MHC Class I molecules) include CD1d, HLA E, HLA G, HLA F, HLA H, MIC A, MIC B, ULBP-1, ULBP-2, and ULBP-3.

A “MHC Class II molecule” as used everywhere herein is used interchangeably with MHC II molecule and is defined as a molecule which comprises 2-3 subunits including a MHC II alpha-chain and a MHC II beta-chain (i.e. a MHC II alpha/beta-dimer), an MHC II alpha/beta dimer with an antigenic peptide, and an MHC II alpha/beta dimer combined with an antigenic peptide through a flexible linker to the MHC II alpha or MHC II beta chain, a MHC II alpha/beta dimer combined through an interaction by affinity tags e.g. jun-fos, a MHC II alpha/beta dimer combined through an interaction by affinity tags e.g. jun-fos and further combined with an antigenic peptide through a flexible linker to the MHC II alpha or MHC II beta chain. The MHC II molecule chains can be changed by substitution of single or by cohorts of native amino acids, or by inserts, or deletions to enhance or impair the functions attributed to said molecule. Under circumstances where the MHC II alpha-chain and MHC II beta-chain have been fused, to form one subunit, the “MHC Class II molecule” can comprise only 1 subunit or 2 subunits if antigenic peptide is also included.

MHC Class II like molecules (including non-classical MHC Class II molecules) include HLA DM, HLA DO, I-A beta2, and I-E beta2.

A “peptide free MHC Class I molecule” is used interchangeably herein with “peptide free MHC I molecule” and as used everywhere herein is meant to be a MHC Class I molecule as defined above with no peptide.

A “peptide free MHC Class II molecule” is used interchangeably herein with “peptide free MHC II molecule” and as used everywhere herein is meant to be a MHC Class II molecule as defined above with no peptide.

Such peptide free MHC Class I and II molecules are also called “empty” MHC Class I and II molecules.

The MHC molecule may suitably be a vertebrate MHC molecule such as a human, a mouse, a rat, a porcine, a bovine or an avian MHC molecule. Such MHC complexes from different species have different names. E.g. in humans, MHC complexes are denoted HLA. The person skilled in the art will readily know the name of the MHC complexes from various species.

In general, the term “MHC molecule” is intended to include all alleles. By way of example, in humans e.g. HLA A, HLA B, HLA C, HLA D, HLA E, HLA F, HLA G, HLA H, HLA DR, HLA DQ and HLA DP alleles are of interestshall be included, and in the mouse system, H-2 alleles are of interestshall be included. Likewise, in the rat system RT1-alleles, in the porcine system SLA-alleles, in the bovine system BoLA, in the avian system e.g. chicken–B alleles, are of interestshall be included.

“MHC complexes” and “MHC constructs” are used interchangeably herein.

By the terms “MHC complexes” and “MHC multimers” as used herein are meant such complexes and multimers thereof, which are capable of performing at least one of the functions attributed to said complex or multimer. The terms include both classical and non-classical MHC complexes. The meaning of “classical” and “non-classical” in connection with MHC complexes is well known to the person skilled in the art. Non-classical MHC complexes are subgroups of MHC-like complexes. The term “MHC complex” includes MHC Class I molecules, MHC Class II molecules, as well as MHC-like molecules (both Class I and Class II), including the subgroup non-classical MHC Class I and Class II molecules.

MHC multimer: The terms MHC multimer, MHC-multimer, MHCmer and MHC'mer herein are used interchangeably, to denote a complex comprising more than one MHC-peptide complexes, held together by covalent or non-covalent bonds.

Monoclonal antibodies: Monoclonal antibodies, as used herein, are antibodies that are identical because they were produced by one type of immune cell and are all clones of a single parent cell.

Monovalent antibodies: The antibodies in the present invention can be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking. In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

Multimerization domain: A multimerization domain is a molecule, a complex of molecules, or a solid support, to which one or more MHC or MHC-peptide complexes can be attached. A multimerization domain consist of one or more carriers and/or one or more scaffolds and may also contain one or more linkers connecting carrier to scaffold, carrier to carrier, scaffold to scaffold. The multimerization domain may also contain one or more linkers that can be used for attachment of MHC complexes and/or other molecules to the multimerization domain.
Multimerization domains thus include IgG, streptavidin, streptactin, micelles, cells, polymers, beads and other types of solid support, and small organic molecules carrying reactive groups or carrying chemical motifs that can bind MHC complexes and other molecules.

Nanobodies: Nanobodies as used herein is a type of antibodies derived from camels, and are much smaller than traditional antibodies.

Neutralizing antibodies: neutralizing antibodies as used herein is an antibody which, on mixture with the homologous infectious agent, reduces the infectious titer.

NMR: NMR (Nuclear magnetic resonance), as used herein, is a physical phenomenon based upon the quantum mechanical magnetic properties of an atom's nucleus. NMR refers to a family of scientific methods that exploit nuclear magnetic resonance to study molecules.

Non-covalent: The term noncovalent bond as used herein is a type of chemical bond that does not involve the sharing of pairs of electrons, but rather involves more dispersed variations of electromagnetic interactions.

Nucleic acid duplex: A nucleic acid is a complex, high-molecular-weight biochemical macromolecule composed of nucleotide chains that convey genetic information. The most common nucleic acids are deoxyribonucleic acid (DNA) and ribonucleic acid (RNA).

Nucleophilic: a nucleophile, as used herein, is a reagent that forms a chemical bond to its reaction partner (the electrophile) by donating both bonding electrons.

"One or more" as used everywhere herein is intended to include one and a plurality.

A “peptide free MHC Class I molecule” as used everywhere herein is meant to be a MHC Class I molecule as defined above with no peptide.

A “peptide free MHC Class II molecule” as used everywhere herein is meant to be a MHC Class II molecule as defined above with no peptide.

Such peptide free MHC Class I and II molecules are also called “empty” MHC Class I and II molecules.

Pegylated: pegylated, as used herein, is conjugation of Polyethylene glycol (PEG) to proteins.

Peptide or protein: Any molecule composed of at least two amino acids. Peptide normally refers to smaller molecules of up to around 30 amino acids and protein to larger molecules containing more amino acids.

Phosphorylated; phosphorylated, as used herein, is is the addition of a phosphate (PO_4) group to a protein molecule or a small molecule.

PNA: PNA (Peptide nucleic acid) as used herein is a chemical similar to DNA or RNA. PNA is not known to occur naturally in existing life on Earth but is artificially synthesized and used in some biological research and medical treatments.DNA and RNA have a deoxyribose and ribose sugar backbone, respectively, whereas PNA's backbone is composed of repeating N-(2-aminoethyl)-glycine units linked by peptide bonds. The various purine and pyrimidine bases are linked to the backbone by methylene carbonyl bonds. PNAs are depicted like peptides, with the N-terminus at the first (left) position and the C-terminus at the right.

"A plurality" as used everywhere herein should be interpreted as two or more.

This applies i.a. to the MHC peptide complex and the binding entity. When a plurality of MHC peptide complexes is attached to the multimerization domain, such as a scaffold or a carrier molecule, the number of MHC peptide complexes need only be limited by the capacity of the multimerization domain.

Polyclonal antibodies: a polyclonal antibody as used herein is an antibody that is derived from different B-cell lines. They are a mixture of immunoglobulin molecules secreted against a specific antigen, each recognising a different epitope.

Polymer: the tern polymer as used herein is defined as a compound composed of repeating structural units, or monomers, connected by covalent chemical bonds.

Polypeptide: Peptides are the family of short molecules formed from the linking, in a defined order, of various α-amino acids. The link between one amino acid residue and the next is an amide bond and is sometimes referred to as a peptide bond. Longer peptides are reffered to as proteins or polypeptide.

Polysaccharide: The term polysaccharide as used herein is defined as polymers made up of many monosaccharides joined together by glycosidic linkages.

Radicals: radicals, as used herein, are atomic or molecular species with unpaired electrons on an otherwise open shell configuration. These unpaired electrons are usually highly reactive, so radicals are likely to take part in chemical reactions.

Radioactivity: Radioactive decay is the process in which an unstable atomic nucleus loses energy by emitting radiation in the form of particles or electromagnetic waves.

RNA: RNA (Ribonucleic acid) as used herein is a nucleic acid polymer consisting of nucleotide monomers that plays several important roles in the processes that translate genetic information from deoxyribonucleic acid (DNA) into protein products.

RNA: RNA (Ribonucleic acid) as used herein is a nucleic acid polymer consisting of nucleotide monomers that plays several important roles in the processes that translate genetic information from deoxyribonucleic acid (DNA) into protein products

Scaffold: A scaffold is typically an organic molecule carrying reactive groups, capable of reacting with reactive groups on a MHC-peptide complex. Particularly small organic molecules of cyclic structure (e.g. functionalized cycloalkanes or functionalized aromatic ring structures) are termed scaffolds. Scaffold and carrier are used interchangeably herein where scaffold typically refers to smaller molecules of a multimerization domain and carrier typically refers to larger molecule and/or cell like structures.

Staining: In this invention staining means specific or unspecific labelling of cells by binding labeled molecules to defined proteins or other structures on the surface of cells or inside cells. The cells are either in suspension or part of a tissue. The labeled molecules can be MHC multimers, antibodies or similar molecules capable of binding specific structures on the surface of cells.

Streptavidin: Streptavidin as used herein is a tetrameric protein purified from the bacterium Streptomyces avidinii. Streptavidin is widely use in molecular biology through its extraordinarily strong affinity for biotin.

Sugar: Sugars as used herein include monosaccharides, disaccharides, trisaccharides and the oligosaccharides - comprising 1, 2, 3, and 4 or more monosaccharide units respectively.

Therapy: Treatment of illness or disability

Vaccine: A vaccine is an antigenic preparation used to establish immunity to a disease or illness and thereby protect or cure the body from a specific disease or illness. Vaccines are either prophylactic and prevent disease or therapeutic and treat disease. Vaccines may contain more than one type of antigen and is then called a combined vaccine.

Vaccination: The introduction of vaccine into the body of human or animals for the purpose of inducing immunity.

'B.L.' is an abbreviation for Bind level.

'Aff.' is an abbreviation for affinity.

DETAILED DESCRIPTION OF THE INVENTION

The present invention in one aspect refers to a MHC monomer comprising a-b-P, or a MHC multimer comprising $(a\text{-}b\text{-}P)_n$, wherein $n > 1$,

wherein a and b together form a functional MHC protein capable of binding the antigenic peptide P,

wherein (a-b-P) is the MHC-peptide complex formed when the antigenic peptide P binds to the functional MHC protein, and

wherein each MHC peptide complex of a MHC multimer is associated with one or more multimerization domains.

Another aspect of the present invention refers to an antigenic peptide P or an antigenic polypeptide featuring one or more anitgenic peptides P.

The antigenic peptide P is in one embodiment a Borrelia peptide such as e.g. a Borrelia burgdorferi B31 peptide, a Borreila afzelii PKo peptide or a Borrelia garinii PBi peptide.

MHC monomers and MHC multimers comprising one or more MHC peptide complexes of class 1 or class 2 MHC are covered by the present invention. Accordingly, the antigenic peptide P can have a length of e.g. 8, 9, 10, 11, 12, 13, 14, 15, 16, 16-20, or 20-30 amino acid residues.

Examples of the antigenic peptide P is provided herein below. In one embodiment, the antigenic peptide P can be selected from the group consisting of sequences disclosed in the "Sequence Listing" and annotated consecutively (using integers) starting with SEQ ID NO:1 and ending with SEQ ID NO:217791 or any fragment thereof.

In another aspect the present invention is directed to a composition comprising a plurality of MHC monomers and/or MHC multimers according to the present invention, wherein the MHC multimers are identical or different, and a carrier.

The present invention further relates to a method for detection of antigen-specific T cells, said method comprising the steps of 1) providing the MHC multimer described above, 2) providing a population of antigen-specific T cells, and 3) detecting antigen-specific T cells specific for the peptide P of the MHC multimer.

The present invention also relates to a method for detection of antigen-specific T cells, said method comprising the steps of 1) providing the antigenic peptid or antigenic polypeptide described above, 2) providing a population of antigen-specific T cells, and 3) detecting antigen-specific T cells specific for the antigenic peptide P in complex with MHC molecules.

In a further embodiment the present invention relates to a method for counting of antigen-specific T cells, said method comprising the steps of 1) providing the MHC multimer described above, 2) providing a population of antigen-specific T cells, and 3) counting antigen-specific T cells specific for the peptide P of the MHC multimer.

The present invention also relates to a method for sorting of antigen-specific T cells, said method comprising the steps of 1) providing the MHC multimer described above,

2) providing a population of antigen-specific T cells, and 3) sorting antigen-specific T cells specific for the peptide P of the MHC multimer.

In yet another embodiment the present invention relates to a method for isolation of antigen-specific T cells, said method comprising the steps of 1) providing the MHC multimer described above, 2) providing a population of antigen-specific T cells, and 3) isolating antigen-specific T cells specific for the peptide P of the MHC multimer.

In yet another aspect there is provided a kit comprising an antigenic peptide, an antigenic polypeptide, a MHC monomer or a MHC multimer according to the present invention, or a composition according to the present invention, and at least one additional component, such as a positive control and/or instructions for use.

In a still further aspect there is provided a method for immune monitoring one or more diseases comprising monitoring of antigen-specific T cells, said method comprising the steps of

i) providing the MHC monomer or MHC multimer or individual components thereof according to the present invention,
ii) providing a population of antigen-specific T cells or individual antigen-specific T cells, and
iii) measuring the number, activity or state and/or presence of antigen-specific of T cells specific for the peptide P of the said MHC monomer or MHC multimer, thereby immune monitoring said one or more diseases.

Or i) providing the antigenic peptide or antigenic polypeptide according to the present invention,
ii) providing a population of antigen-specific T cells or individual antigen-specific T cells, and providing antigen presenting cells expressing MHC molecules on their surface
iii) measuring the number, activity or state and/or presence of antigen-specific of T cells specific for the antigenic peptide P in complex with one or more MHC molecules displayed on the surface of the antigen presenting cell, thereby immune monitoring said one or more diseases.

In yet another aspect there is provided a method for diagnosing one or more diseases comprising immune monitoring of antigen-specific T cells, said method comprising the following steps: of

i) providing the MHC monomer or MHC multimer or individual components thereof according to the present invention, or individual components thereof,
ii) providing a population of antigen-specific T cells or individual antigen-specific T cells, and
iii) measuring the number, activity or state and/or presence of T cells specific for said MHC monomer or the peptide P of the MHC multimer, thereby diagnosing said one or more diseases.
Or
i) providing the antigenic peptide or antigenic polypeptide according to the present invention,
ii) providing a population of antigen-specific T cells or individual antigen-specific T cells, and providing antigen presenting cells expressing MHC molecules on their surface
iii) measuring the number, activity or state and/or presence of T cells specific for said antigenic peptide P in complex with one or more MHC molecules displayed on the surface of the antigen presenting cell, , thereby diagnosing said one or more diseases.

There is also provided a method for isolation of one or more antigen-specific T cells, said method comprising the steps of

i) providing the MHC monomer or MHC multimer or individual components thereof according to the present invention, or individual components thereof, and
ii) providing a population of antigen-specific T cells or individual antigen-specific T cells, and
iii) thereby isolating said T cells specific for the peptide P of the said MHC monomer or MHC multimer.

The present invention makes it possible to pursue different immune monitoring methods using the MHC monomers, MHC multimers, antigenic peptides or antigenic polypeptides according to the present invention. The immune monitoring methods

include e.g. flow cytometry, ELISPOT, LDA, Quantiferon and Quantiferon-like methods. Using the above-cited methods, the MHC monomers and/or the MHC multimers can be provided as a MHC peptide complex, or the antigenic peptide and the MHC monomer and/or multimer can be provided separately.

Accordingly, recognition of TCR's can be achieved by direct or indirect detection, e.g. by using one or more of the following methods:

ELISPOT technique using indirect detection, e.g. by adding the antigenic peptide optionally associated with a MHC monomer or MHC multimer, followed by measurement of INF-gamma secretion from a population of cells or from individual cells.

Another technique involves a Quantiferon-like detection assay, e.g. by using indirect detection, e.g. by adding the antigenic peptide optionally associated with a MHC monomer or MHC multimer, followed by measurement of INF-gamma secretion from a population of cells or from individual cells.

Flow cytometry offers another alternative for performing detection assays, e.g. by using direct detection (e.g. of MHC tetramers), e.g. by adding the antigenic peptide optionally associated with a MHC monomer or MHC multimer, followed by detection of a fluorescein label, thereby measuring the number of TCRs on specific T-cells.

Flow cytometry can also be used for indirect detection, e.g. by adding the antigenic peptide optionally associated with a MHC monomer or MHC multimer, followed by addition of a "cell-permeabilizing factor", and subsequent measurement of an intracellular component (e.g. INF-gamma mRNA), from individual cells or populations of cells.

By using the above-mentioned and other techniques, one can diagnose and/or monitor e.g. infectious diseases caused e.g. by mycobacetrium, Gram positive bacteria, Gram negative bacteria, Spirochetes, intracellular bacterium, extracelular bacterium, Borrelia, TB, CMV, HPV, Hepatitis, BK, fungal organisms and microorganisms. The diagnosis and/or monitoring of a particular disease can greatly aid in directing an optimal treatment of said disease in an individual.

In still further aspects of the present invention there is provided a method for performing a vaccination of an individual in need thereof, said method comprising the steps of

providing an antigenic peptide, an antigenic polypeptide, a MHC monomer or a MHC multimer, according to the present invention, or the individual components thereof, and

administering said antigenic peptide, antigenic polypeptide, MHC monomer or MHC multimer to said individual and obtaining a protective immune response, thereby performing a vaccination of the said individual.

In yet another embodiment there is provided a method for performing therapeutic treatment of an individual comprising the steps of

Providing the MHC multimer according to the present invention, or individual components thereof, and

Isolating or obtaining T-cells from a source, such as an individual or an ex-vivo library or cell bank, wherein said isolated or obtained T-cells are specific for said provided MHC multimer,

Optionally manipulating said T-cells, and

Introducing said isolated or obtianed T-cells into an individual to be subjected to a therapeutic treatment, wherein the individual can be the same individual or a different individual from the source individual.

There is also provided a method comprising one or more steps for minimizing undesired binding of the MHC multimer according to the present invention. This method is disclosed herein below in more detail.

In further aspects the present invention provides:

A method for performing a control experiment comprising the step of counting of particles comprising the MHC multimer according to the present invention.

A method for performing a control experiment comprising the step of sorting of particles comprising the MHC multimer according to the present invention.

A method for performing a control experiment comprising the step of performing flow cytometry analysis of particles comprising the MHC multimer according to the present invention.

A method for performing a control experiment comprising the step of performing a immunohistochemistry analysis comprising the MHC multimer according to the present invention.

A method for performing a control experiment comprising the step of performing a immunocytochemistry analysis comprising the MHC multimer according to the present invention.

A method for performing a control experiment comprising the step of performing an ELISA analysis comprising the MHC multimer according to the present invention.

In a still further aspect of the present invention there is provided a method for generating MHC multimers according to the present invention, said method comprising the steps of

i) providing one or more antigenic peptides P; and/or
ii) providing one or more functional MHC proteins,
iii) optionally providing one or more multimerization domains, and
iv) contacting the one or more peptides P and the one or more functional MHC proteins and the one or more multimerization domains simultaneously or sequentialy in any order, thereby obtaining MHC multimers according to the present invention.

The method can also be performed by initially providing one or more antigenic peptide(s) P and optionally one or more functional MHC proteins to generate a MHC-peptide complex (a-b-P); subsequently or simultaneusly providing one or more multimerisation domain(s); and reacting the one or more MHC-peptide complexes and the one or more multimerization domain(s) to generate a MHC multimer according to the present invention.

In one aspect, the present invention is directed to novel MHC complexes optionally comprising a multimerization domain preferably comprising a carrier molecule and/or a scaffold.

There is also provided a MHC multimer comprising 2 or more MHC-peptide complexes and a multimerization domain to which the 2 or more MHC-peptide complexes are associated. The MHC multimer can generally be formed by association of the 2 or more MHC-peptide complexes with the multimerization domain to which the 2 or more MHC-peptide complexes are capable of associating.

The multimerization domain can be a scaffold associated with one or more MHC-peptide complexes, or a carrier associated with one or more, preferably more than one, MHC-peptide complex(es), or a carrier associated with a plurality of scaffolds each associated with one or more MHC-peptide complexes, such as 2 MHC-peptide complexes, 3 MHC-peptide complexes, 4 MHC-peptide complexes, 5 MHC-peptide complexes or more than 5 MHC-peptide complexes. Accordingly, multimerization domain collectively refers to each and every of the above. It will be clear from the detailed description of the invention provided herein below when the multimerization domain refers to a scaffold or a carrier or a carrier comprising one or more scaffolds.

Generally, when a multimerization domain comprising a carrier and/or a scaffold is present, the MHC complexes can be associated with this domain either directly or via one or more binding entities. The association can be covalent or non-covalent.

Accordingly, there is provided in one embodiment a MHC complex comprising one or more entities $(a\text{-}b\text{-}P)_n$, wherein a and b together form a functional MHC protein capable of binding a peptide P, and wherein (a-b-P) is the MHC-peptide complex formed when the peptide P binds to the functional MHC protein, said MHC complex optionally further

comprising a multimerization domain comprising a carrier molecule and/or a scaffold. "MHC complex" refers to any MHC complex, including MHC monomers in the form of a single MHC-peptide complex and MHC multimers comprising a multimerization domain to which more than one MHC peptide complex is associated.

When the invention is directed to complexes comprising a MHC multimer, i.e. a plurality of MHC peptide complexes of the general composition $(a\text{-}b\text{-}P)_n$ associated with a multimerization domain, n is by definition more than 1, i.e. at least 2 or more. Accordingly, the term "MHC multimer" is used herein specifically to indicate that more than one MHC-peptide complex is associated with a multimerization domain, such as a scaffold or carrier or carrier comprising one or more scaffolds. Accordingly, a single MHC-peptide complex can be associated with a scaffold or a carrier or a carrier comprising a scaffold and a MHC-multimer comprising 2 or more MHC-peptide complexes can be formed by association of the individual MHC-peptide complexes with a scaffold or a carrier or a carrier comprising one or more scaffolds each associated with one or more MHC-peptide complexes.

When the MHC complex comprises a multimerization domain to which the n MHC-peptide complexes are associated, the association can be a covalent linkage so that each or at least some of the n MHC-peptide complexes is covalently linked to the multimerization domain, or the association can be a non-covalent association so that each or at least some of the n MHC-peptide complexes are non-covalently associated with the multimerization domain.

The MHC complexes of the invention may be provided in non-soluble or soluble form, depending on the intended application.

Effective methods to produce a variety of MHC complexes comprising highly polymorphic human HLA encoded proteins makes it possible to perform advanced analyses of complex immune responses, which may comprise a variety of peptide epitope specific T-cell clones.

One of the benefits of the MHC complexes of the present invention is that the MHC complexes overcome low intrinsic affinities of monomer ligands and counter receptors. The MHC complexes have a large variety of applications that include targeting of high

affinity receptors (e.g. hormone peptide receptors for insulin) on target cells. Taken together poly-ligand binding to target cells has numerous practical, clinical and scientifically uses.

Thus, the present invention provides MHC complexes which present mono-valent or multi-valent binding sites for MHC-peptide recognising cells, such as MHC complexes optionally comprising a multimerization domain, such as a scaffold or a carrier molecule, which multimerization domain have attached thereto, directly or indirectly via one or more linkers, covalently or non-covalently, one or more MHC peptide complexes. "One or more" as used herein is intended to include one as well as a plurality, such as at least 2. This applies i.a. to the MHC peptide complexes and to the binding entities of the multimerization domain. The scaffold or carrier molecule may thus have attached thereto a MHC peptide complex or a plurality of such MHC peptide complexes, and/or a linker or a plurality of linkers.

PRODUCT

In one embodiment of the present inevention the product is a MHC monomer or a MHC multimer as described above. As used in the description of this invention, the term "MHC multimers" will be used interchangeably with the terms MHC'mers and MHCmers, and will include any number, (larger than one) of MHC-peptide complexes, held together in a large complex by covalent or non-covalent interactions between a multimerization domain and one or more MHC-peptide complexes, and will also include the monomeric form of the MHC-peptide complex, i.e. a MHC-peptide complex that is not attached to a multimerization domain. The multimerization domain consists of one or more carriers and/or one or more scaffolds while the MHC-peptide complex consists of MHC molecule and antigenic peptide. MHC-peptide complexes may be attached to the multimerization domain through one or more linkers. A schematic representation of a MHC multimer is presented in figure 1.

In another embodiment of the present invention the product is antigenic peptide or antigenic polypeptide containing one or more antigenic peptide sequences. As used in the description of this invention the term antigenic peptide will be used interchangeably with the term binding peptide and refers to any peptide molecule that is bound or able to bind into the binding groove of either MHC class 1 or MHC class 2.

In the following the design and generation of antigenic peptides, antigenic polypeptides and the different components of MHC monomers and/or MHC multimers are described.

Design and generation of antigenic peptides

Antigenic peptides of the present invention may be used in processes of the present invention either as part of MHC monomers, MHC multimers or antigenic polypeptides or used themselves as a product. Antigenic polypeptide and antigenic peptide products will later in the process they are used for, bind MHC molecules and thereby generate MHC monomers and/or MHC multimers, e.g. when used as a vaccine the antigenic peptides may bind MHC molecules on cells inside the body or when used for an immune monitoring process antigenic peptides binds MHC molcules present in the sample they are applied to.
Therefore the features of and principles for design and generation of antigenic peptides used themselves as a product or used in MHC monormers, MHC multimers or in antigenic polypeptides are identical and will be described in more detail in the following.

MHC class 1 protein typically binds octa-, nona-, deca- or ondecamer (8-, 9-, 10,- 11-mer) peptides in their peptide binding groove. The individual MHC class 1 alleles have individual preferences for the peptide length within the given range. MHC class 2 proteins typically bind peptides with a total length of 13-18 amino acids, comprising a 9'-mer core motif containing the important amino acid anchor residues. However the total length is not strictly defined, as opposed to most MHC class 1 molecules.

For some of the MHC alleles the optimal peptide length and the preferences for specific amino acid residues in the so called anchor positions are known.

To identify high-afinity binding peptides derived from a specific protein for a given MHC allele it is necessary to systematically work through the amino acid sequence of the protein to identify the putative high-affinity binding peptides. Although a given peptide is a binder it is not necessarily a functional T-cell epitope. Functionality needs to be confirmed by a functional analysis e.g. ELISPOT, CTL killing assay or flow cytometry assay as described elsewhere herein.

The binding affinity of the peptide for the MHC molecules can for some MHC molecules be predicted in databases such as www.syfpeithi.de; http://www-

bimas.cit.nih.gov/molbio/hla_bind/; www.cbs.dtu.dk/services/NetMHC/; www.cbs.dtu.dk/services/NetMHCII/

Design of binding peptides

The first step in the design of binding peptides is obtaining the protein's amino acid sequence. In many cases the amino acid sequence of the protein from which antigenic peptides have to be identified from are known. However,when only the genomic DNA sequences are known, i.e. the reading frame and direction of transcription of the genes is unknown, the DNA sequence needs to be translated in all three reading frames in both directions leading to a total of six amino acid sequences for a given genome. From these amino acid sequences binding peptides can then be identified as described below. In organisms having intron/exon gene structure the present approach must be modified accordingly, to identify peptide sequence motifs that are derived by combination of amino acid sequences derived partly from two separate introns. cDNA sequences can be translated into the actual amino acid sequences to allow peptide identification. In cases where the protein sequence is known, these can directly be used to predict peptide epitopes.

Binding peptide sequences can be predicted from any protein sequence by either a total approach, generating binding peptide sequences for potentially any MHC allele, or by a directed approach, identifying a subset of binding peptides with certain preferred characteristics such as affinity for MHC protein, specificity for MHC protein, likelihood of being formed by proteolysis in the cell, and other important characteristics.

Design of MHC class 1 binding peptide sequence

Many parameters influence the design of the individual binding peptide, as well as the choice of the set of binding peptides to be used in a particular application. Important characteristics of the MHC-peptide complex are physical and chemical (e.g. proteolytic) stability. The relevance of these parameters must be considered for the production of the antigenic peptides, the antigenic polypeptides, the MHC-peptide complexes and the MHC multimers, as well as for their use in a given application. As an example, the stability of the MHC-peptide complex in assay buffer (e.g. PBS), in blood, or in the body can be very important for a particular application.

In the interaction of the MHC-peptide complex with the TCR, a number of additional characteristics must be considered, including binding affinity and specificity for the TCR, degree of cross-talk, undesired binding or interaction with other TCRs. Finally, a number of parameters must be considered for the interaction of MHC-peptide complexes, MHC multimers, antigenic peptides or antigenic polypeptides with the sample or individual it is being applied to. These include immunogenicity, allergenicity, as well as side effects resulting from un-desired interaction with "wrong" T cells, including cross-talk with e.g. autoimmune diseases and un-desired interaction with other cells than antigen-specific T cells.

For some applications, e.g. immuno profiling of an individual's immune response focused on one antigen, it is preferred that all possible binding peptides of that antigen are included in the application (i.e. the "total approach" for the design of binding peptides described below). For other applications, e.g vaccines it may be adequate to include a few or just one binding peptide for each of the HLA-alleles included in the application (i.e. the "directed approach" whereby only the most potent binding peptides can be included). Personalized diagnostics, therapeutics and vaccines will often fall in-between these two extremes, as it will only be necessary to include a few or just one binding peptide in e.g. a vaccine targeting a given individual, but the specific binding peptide may have to be picked from binding peptides designed by the total approach, and identified through the use of immuno profiling studies involving all possible binding peptides. The principles of immuno profiling is described elsewhere herein.

a) Total approach

The MHC class 1 binding peptide prediction is done as follows using the total approach. The actual protein sequence is split up into 8-, 9-, 10-, and 11-mer peptide sequences. This is performed by starting at amino acid position 1 identifying the first 8-mer; then move the start position by one amino acid identifying the second 8-mer; then move the start position by one amino acid, identifying the third 8-mer. This procedure continues by moving start position by one amino acid for each round of peptide identification. Generated peptides will be amino acid position 1-8, 2-9, 3-10 etc. This procedure can be carried out manually or by means of a software program (Figure 2). This procedure is then repeated in an identical fashion for 9-, 10 and 11-mers, respectively.

b) Directed approach

The directed approach identifies a preferred subset of binding peptides from the binding peptides generated in the total approach. This preferred subset is of particularly value in a given context.

One way to select subsets of antigenic peptides is to use consensus sequences to choose a set of relevant binding peptides able to bind the individual MHC allele and that will suit the "average" individual. Such consensus sequences often solely consider the affinity of the binding peptide for the MHC protein; in other words, a subset of binding peptides is identified where the designed binding peptides have a high probability of forming stable MHC-peptide complexes, but where it is uncertain whether this MHC-peptide complex is of high relevance in a population, and more uncertain whether this MHC-peptide complex is of high relevance in a given individual.

For class I MHC-alleles, the consensus sequence for a binding peptide is generally given by the formula

X1-X2-X3-X4-….-Xn,

where n equals 8, 9, 10, or 11, and where X represents one of the twenty naturally occurring amino acids, optionally modified as described elsewhere in this application. X1-Xn can be further defined. Thus certain positions in the consensus sequence are more likely to contribute to binding to a given MHC molecule than others.

Antigenic peptide-binding by MHC I is accomplished by interaction of specific amino acid side chains of the antigenic peptide with discrete pockets within the peptide-binding groove of the MHC molecule. The peptide-binding groove is formed by the α1 and α2 domains of the MHC I heavy chain and contains six pockets denoted A, B, C, D, E, F. For human HLA molecules the main binding energy associating antigenic peptide to MHC I is provided by interaction of amino acids in position 2 and at the c-terminus of the antigenic peptide with the B and F binding pockets of the MHC I molecule. The amino acids of the antigenic peptide being responsible for the main anchoring of the peptide to the MHC molecule are in the following called primary anchor amino acids and the motif they form for primary anchor motif. Other amino acid side chains of an antigenic peptide may also contribute to the anchoring of the antigenic peptide to the MHC molecule but to a lesser extent. Such amino acids are often referred to as secondary anchor amino acids and form a secondary anchor motif.

Different HLA alleles have different amino acids lining the various pockets of the peptide-binding groove enabling the various alleles to bind unique repertoires of

antigenic peptides with specific anchor amino acid motifs. Thus for a selected consensus sequence certain positions are the socalled anchor positions and the selection of useful amino acids for these positions is limited to those able to fit into the corresponding binding pockets in the HLA molecule. For example for peptides binding HLA-A*02, X2 and X9 are primary anchor positions docking into the B and F pocket of the HLA molecule respectively, and useful amino acids at these two positions in the binding peptide are preferable limited to leucine or methionine for X2 and to valine or leucine at postion X9. In contrast the primary anchor positions of peptides binding HLA-B*08 are X3, X5 and X9 and the corresponding preferred amino acids at these positions are lysine at position X3, lysine or arginine at position X5 and leucine at position X9.

However, the different HLA alleles can be grouped into clusters or supertypes where the alleles of the supertype share peptide-binding pocket similarities in that they are able to recognize the same type of antigenic peptide primary anchor motif. Therefore antigenic peptides can be selcted on their ability to bind a given HLA molecule or a given HLA supertype on the basis of their amino acid sequence, e.g. the identity of the primary anchor motif.

Antigenic peptide primary anchor motifs of special interest of the present invention are listed in table 6.

Table 6. HLA I supertype familie's and their antigenic peptide anchor motifs. Examples of usefull amino acids binding in pocket B and pocket F are shown as one letter code.

Supertype	**Anchor motif**				**Example of HLA allele's**
	B pocket specificity	*Example aa B pocket*	*F pocket specificity*	*Example aa F pocket*	
A01	Small and aliphatic	A,T, S, V, L, I, M, Q	Aromatic and large hydrophobic	F, W, Y, L, I, M	A*0101, A*2601, A*2602, A*2603, A*3002, A*3003, A*3004, A*3201
A01/A03	Small and aliphatic	A,T, S, V, L, I, M, Q	Aromatic and basic	Y, R, K	A*3001, A*3201, A*7401
A01/A24	Small, aliphatic and aromatic	A, S, T, V, L, I, M, Q, F, W, Y	Aromatic and large hydrophobic	F, W, Y, L, I, M	A*2902
A02	Small and aliphatic	A, T, S, V, L, I, M, Q	Aliphatic and small hydrophobic	L, I, V, M, Q, A	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206,

					A*0207, A*0214, A*0217, A*6802, A*6901
A03	Small and aliphatic	A, T, S, V, L, I, M, Q	Basic	R, H, K	A*0301, A*1101, A*3101, A*3301, A*3303, A*6601, A*6801, A*7401
A24	Aromatic and aliphatic	F, W, Y, L, I, V, M, Q	Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	A*2301, A*2402
B07	Proline	P	Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	B*0702, B*0703, B*0705, B*1508, B*3501, B*3503, B*4201, B*5101, B*5102, B*5103, B*5301, B*5401, B*5501, B*5502, B*5601, B*6701, B*7801
B08	Undefined		Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	B*0801, B*0802
B27	Basic	R, H, K	Aromatic, aliphatic, basic and hydrophbic	F, W, Y, L, I, V, M, Q, A, R, H, K	B*1402, B*1503, B*1509, B*1510, B*1518, B*2702, B*2703, B*2704, B*2705, B*2706, B*2707, B*2709, B*3801, B*3901, B*3902, B*3909, B*4801, B*7301
B44	Acidic	D, E	Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	B*1801, B*3701, B*4001, B*4002,B*4006, B*4402, B*4403, B*4501
B58	Small	A, S, T	Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	B*1516, B*1517, B*5701, B*5702, B*5801, B*5802
B62	Aliphatic	L, I, V, M, Q	Aromatic, aliphatic and hydrophbic	F, W, Y, L, I, V, M, Q, A	B*1501, B*1502, B*1512, B*1513, B*4501, B*4601, B*5201

Antigenic peptides able to bind a given MHC molecule do not necessarily have primary anchor amino acid residues compatible with both main anchoring pockets of the MHC molecule but may have one or no primary anchor amino acids suitable for binding the MHC molecule in question. However, having the preferred primary anchor motif for a

given MHC allele increases the affinity of the antigenic peptide for that given allele and thereby the likelihood of making a stable and usefull MHC-peptide molecule.

Therefore in one embodiment of the present invention antigenic peptides can be identified and selected on their ability to bind a given HLA or other MHC molecule based on what amino acids they have at primary anchor positions and/or secondary anchor positions.

Software programs are available that use neural networks or established binding preferences to predict the interaction of specific binding peptides with specific MHC class I alleles. Examples of such programs are www.syfpeithi.de; www.imtech.res.in/raghava/propred1/index.html; www.cbs.dtu.dk/services/NetMHC/.

Another usefull parameter for prediction and selection of usefull antigenic peptides are the probability of the binding peptide in question to be generated *in vivo* by the proteolytic machinery inside cells. For example for a given antigen the combined action of endosolic, cytosolic and membrane bound protease activities as well as the TAP1 and TAP2 transporter specificities can be taken into consideration. However, the proteolytic activitiy varies a lot among individuals, and for personalized diagnostics, treatment or vaccination it may be desirable to disregard these general proteolytic data. An example of a program predicting the ability of antigenic peptides to be processed is www.cbs.dtu.dk/services/NetCTL/.

Using the above descriped principles individual peptides or a subset of peptides able to bind one or more types of MHC molecules and make stable MHC-peptide complexes can be identified. The identified peptides can then be tested for biological relevance in functional assays such as interferon gamma release assays (e.g. ELISPOT), cytotoxicity assays (e.g. CTL killing assays) or using other methods as described in the section “Detection” elsewhere herein. Alternatively or complementary hereto the abillity of the identified antigenic peptides to bind selected MHC molecules may be determined in binding assays like Biacore measurement, compettion assays or other assays usefull for measurement of binding of peptide to MHC molecules, known by persons skilled in the art.

<u>Design of MHC class 2 binding peptide sequence.</u>

a) Total approach and b) directed approach

The approach to predict antigenic peptide binders for MHC class 2 can be done in a similar way as described for MHC class 1 binding peptide prediction above. The change is the different size of the antigenic peptides binding MHC II compared to MHC I. MHC II molecules bind antigenic peptides with a size of 12-24 amino acids or even longer peptides. From a given antigenic protein, MHC II molecules typically can bind sets of overlapping peptides that shares a common core sequence but differs in the overall peptide size and in positioning of the core sequence in the peptide. The core peptide sequence is typically 9 amino acids long but may also be shorter or longer. Usefull antigenic peptide sequences binding MHC II of the present invention are described by the central part of the peptide mainly the 9-mer core peptide. The core peptide sequence may be flanked with a few or several important amino acids, generating antigenic peptides with a length of 13-16 amino acids. In some cases the peptide may contain even more flanking residues resulting in binding peptides longer than 13-16 amino acids. Thus, antigenic peptides of special interest of the present invention are peptides consisting of or containing 9-mer core peptide sequences
The antigenic peptide sequences may be selected using the total approach as described for MHC I antigenic peptides elsewhere herein, e.g. using the software program shown in figure 2.

Alternatively a directed approach identifying a preferred subset of binding peptides from the binding peptides generated in the total approach can be used. As for MHC I one way to select subsets of antigenic peptides is to use consensus sequences to choose a set of relevant binding peptides able to bind the individual MHC allele and that will suit the “average” individual. Such consensus sequences often solely consider the affinity of the binding peptide for the MHC protein; in other words, a subset of binding peptides is identified where the designed binding peptides have a high probability of forming stable MHC-peptide complexes, but where it is uncertain whether this MHC-peptide complex is of high relevance in a population, and more uncertain whether this MHC-peptide complex is of high relevance in a given individual.
For class II MHC-alleles, the consensus sequence for the interacting **core** of a binding peptide is generally given by the formula

X1-X2-X3-X4-….-Xn,

where n equals 9, and where X represents one of the twenty naturally occurring amino acids, optionally modified as described elsewhere in this application.

X1-Xn can be further defined. Thus, certain positions in the consensus sequence are the socalled anchor positions and the selection of useful amino acids for these positions is limited to those able to fit into the corresponding binding pockets in the HLA molecule. For example HLA-DRB1*1501 have X1, X4 and X7 as primary anchor positions where preferred amino acids at the three positions are as follows, X1: leucine, valine and isoleucine, X4: phenylalanine, tyrosine or isoleucine, X7: isoleucine, leucine, valine, methionine or phenylalanine.

Therefore in one embodiment of the present invention antigenic peptides can be identified and selected on their ability to bind a given HLA or other MHC molecule based on what amino acids they have at various anchor positions.

In general, MHC II binding peptides have much more varied anchor positions than MHC I binding peptides and the number of usefull amino acids at each anchor position is much higher. For some MHC II alleles no really consensus sequence has been identified. In general position 1, 4, 6 and 9 of the 9-mer core motif of MHC II antigenic peptides are important for anchoring of the antigenic peptide to the MHC II molecule.

Table 7 shows examples of primary anchor positions and corresponding usefull amino acids for antigenic peptides binding various MHC II molecules.

Table 7. Examples of primary anchor positions and corresponding usefull amino acids shown as one letter code.

MHC II	1	2	3	4	5	6	7	8	9
DQ2	F, W, Y, I, L, V			D, E, L, V, I, H		P, D, E, H, P, A	D, E		F, W, Y, I, L, V, M
DQA1*0101/DQB1*0501	L				Y, F, W				
DQA1*0102/DQB1*0602						L, I, V			A, G, S, T
DR17 (DRB1*0301)	L, I, F, M, V			D		K, R, E, Q, N			Y, L, F
DR4 (DRB1*0401)	F, Y, W, I, L, V, M			P, W, I, L, V, A, D, E		N, S, T, Q, H, R	D, E, H, K, N, Q, R, S, T, Y, A, C,		E, H, K, N, Q, R, S, T, Y, A, C, I,

							I, L, M, V		L, M, V
DRB1*1101	W, Y, F			L, V, M, A, F, Y		R, K, H			A, G, S, P
DRB1*1301	I, V, F, L			Y, W, L, V, A, M		R, K			Y, F, A, S, T
DRB1*1302	Y, F, V, A, I			Y, W, L, V, A, M		R, K			Y, F, A, S, T

Another usefull parameter for prediction and selection of usefull antigenic peptides are the probability of the binding peptide in question to be generated *in vivo* or processed by the proteolytic machinery inside cells. However, like for MHC I, the proteolytic activitiy varies a lot among individuals, and for personalized diagnostics, treatment or vaccination it may be desirable to disregard these general proteolytic data.

Using the above descriped principles individual peptides or one or more subsets of peptides able to bind one or more types of MHC molecules and make stable MHC-peptide complexes can be identified. The identified peptides can then be tested for biological relevance in functional assays such as interferon gamma release assays, ELISPOT, CTL killing assays or using other methods as described in the section “Detection” elsewhere herein. Alternatively or complementary hereto the abillity of the identified antigenic peptides to bind selected MHC molecules may be determined in binding assays like Biacore measurement, compettion assays or other assays usefull for measurement of binding of peptide to MHC molecules, known by persons skilled in the art.

Peptide modifications

In addition to the binding peptides designed by the total approach and/or directed approach, homologous peptides and peptides that have been modified in the amino acid side chains or in the backbone can be used as binding peptides.

Homologous peptides

Homologues MHC peptide sequences may arise from the existence of multiple strongly homologous alleles, from small insertions, deletions, inversions or substitutions.If they are sufficiently homologous to peptides derived by the total approach, i.e. have an amino acid sequence identity greater than e.g. more than 90%, more than 80%, or more than 70%, or more than 60%, to one or two binding peptides derived by the total approach, they may be good candidates. Identity is often most important for the anchor residues.

A MHC binding peptide may be of split- or combinatorial epitope origin i.e. formed by linkage of peptide fragments derived from two different peptide fragments and/or proteins. Such peptides can be the result of either genetic recombination on the DNA level or due to peptide fragment association during the complex break down of proteins during protein turnover. Possibly it could also be the result of faulty reactions during protein synthesis i.e. caused by some kind of mixed RNA handling. A kind of combinatorial peptide epitope can also be seen if a portion of a longer peptide make a loop out leaving only the terminal parts of the peptide bound in the groove.

Uncommon, artificial and chemically modified amino acids.

Peptides having un-common amino acids, such as selenocysteine and pyrrolysine, may be bound in the MHC groove as well. Artificial amino acids e.g. having the isomeric D-form may also make up isomeric D-peptides that can bind in the binding groove of the MHC molecules. Bound peptides may also contain amino acids that are chemically modified or being linked to reactive groups that can be activated to induce changes in or disrupt the peptide. Example post-translational modifications are shown below. However, chemical modifications of amino acid side chains or the peptide backbone can also be performed.

Any of the modifications can be found individually or in combination at any position of the peptide, e.g. position 1, 2, 3, 4, 5, 6, etc. up to n.

Protein primary structure and posttranslational modifications	
N-terminus	Acetylation, Formylation, Pyroglutamate, Methylation, Glycation, Myristoylation (Gly), carbamylation
C-terminus	Amidation, Glycosyl phosphatidylinositol (GPI), O-methylation, Glypiation, Ubiquitination, Sumoylation
Lysine	Methylation, Acetylation, Acylation, Hydroxylation, Ubiquitination, SUMOylation, Desmosine formation, ADP-ribosylation, Deamination and Oxidation to aldehyde
Cysteine	Disulfide bond, Prenylation, Palmitoylation
Serine/Threonine	Phosphorylation, Glycosylation
Tyrosine	Phosphorylation, Sulfation, Porphyrin ring linkage, Flavin linkage GFP prosthetic group (Thr-Tyr-Gly sequence) formation, Lysine tyrosine quinone (LTQ) formation, Topaquinone (TPQ) formation
Asparagine	Deamidation, Glycosylation
Aspartate	Succinimide formation
Glutamine	Transglutamination
Glutamate	Carboxylation, Methylation, Polyglutamylation, Polyglycylation
Arginine	Citrullination, Methylation
Proline	Hydroxylation

Table 1 Post translational modification of peptides

Post translationally modified peptides

The amino acids of the antigenic peptides can also be modified in various ways dependent on the amino acid in question, or the modification can affect the amino- or carboxy-terminal end of the peptide. See table 1. Such peptide modifications are occuring naturally as the result of post tranlational processing of the parental protein. A

non-exhaustive description of the major post translational modifications is given below, divided into three main types.

a) Modification that adds a chemical moiety to the binding peptide.

acetylation, the addition of an acetyl group, usually at the N-terminus of the protein

alkylation, the addition of an alkyl group (e.g. methyl, ethyl). Methylation, the addition of a methyl group, usually at lysine or arginine residues is a type of alkylation. Demethylation involves the removal of a methyl-group.

amidation at C-terminus

biotinylation, acylation of conserved lysine residues with a biotin appendage

formylation

gamma-carboxylation dependent on Vitamin K

glutamylation, covalent linkage of glutamic acid residues to tubulin and some other proteins by means of tubulin polyglutamylase

glycosylation, the addition of a glycosyl group to either asparagine, hydroxylysine, serine, or threonine, resulting in a glycoprotein. Distinct from glycation, which is regarded as a nonenzymatic attachment of sugars.

glycylation, covalent linkage of one to more than 40 glycine residues to the tubulin C-terminal tail

heme moiety may be covalently attached

hydroxylation, is any chemical process that introduces one or more hydroxyl groups (-OH) into a compound (or radical) thereby oxidizing it. The principal residue to be hydroxylated is Proline. The hydroxilation occurs at the C^{γ} atom, forming hydroxyproline (Hyp). In some cases, proline may be hydroxylated instead on its C^{β} atom. Lysine may also be hydroxylated on its C^{δ} atom, forming hydroxylysine (Hyl).

iodination

isoprenylation, the addition of an isoprenoid group (e.g. farnesol and geranylgeraniol)

lipoylation, attachment of a lipoate functionality, as in prenylation, GPI anchor formation, myristoylation, farnesylation, geranylation

nucleotides or derivatives thereof may be covalently attached, as in ADP-ribosylation and flavin attachment

oxidation, lysine can be oxidized to aldehyde

pegylation, addition of poly-ethylen-glycol groups to a protein. Typical reactive amino acids include lysine, cysteine, histidine, arginine, aspartic acid, glutamic acid, serine, threonine, tyrosine. The N-terminal amino group and the C-terminal carboxylic acid can also be used

phosphatidylinositol may be covalently attached

phosphopantetheinylation, the addition of a 4'-phosphopantetheinyl moiety from coenzyme A, as in fatty acid, polyketide, non-ribosomal peptide and leucine biosynthesis

phosphorylation, the addition of a phosphate group, usually to serine, tyrosine, threonine or histidine

pyroglutamate formation as a result of N-terminal glutamine self-attack, resulting in formation of a cyclic pyroglutamate group.

racemization of proline by prolyl isomerase

tRNA-mediated addition of amino acids such as arginylation

sulfation, the addition of a sulfate group to a tyrosine.

Selenoylation (co-translational incorporation of selenium in selenoproteins)

b) Modification that adds protein or peptide.

ISGylation, the covalent linkage to the ISG15 protein (Interferon-Stimulated Gene 15)

SUMOylation, the covalent linkage to the SUMO protein (Small Ubiquitin-related MOdifier)

ubiquitination, the covalent linkage to the protein ubiquitin.

c) Modification that converts one or more amino acids to different amino acids.

citrullination, or deimination the conversion of arginine to citrulline

deamidation, the conversion of glutamine to glutamic acid or asparagine to aspartic acid

The peptide modifications can occur as modification of a single amino acid or more than one i.e. in combinations. Modifications can be present on any position within the peptide i.e. on position 1, 2, 3, 4, 5,etc. for the entire length of the peptide.

Sources of binding peptides

a) From natural sources

The binding peptides can be obtained from natural sources by enzymatic digestion or proteolysis of natural proteins or proteins derived by *in vitro* translation of mRNA. Binding peptides may also be eluted from the MHC binding groove.

b) From recombinant sources

1) as monomeric or multimeric peptide

Alternatively peptides can be produced recombinantly by transfected cells either as monomeric antigenic peptides or as multimeric (concatemeric) antigenic peptides. Optionally, the Multimeric antigenic peptides are cleaved to form monomeric antigenic peptides before binding to MHC protein.

2) as part of a bigger recombinant protein

Binding peptides may also constitute a part of a bigger recombinant protein e.g.consisting of,

2a) For MHC class 1 binding peptides,

Peptide-linker-β2m, β2m being full length or truncated;
Peptide-linker-MHC class 1 heavy chain, the heavy chain being full length or truncated. Most importantly the truncated class I heavy chain will consist of the extracellular part i.e the α1, α2, and α domains. The heavy chain fragment may also only contain the α1 and α2 domains, or α1 domain alone, or any fragment or full length β2m or heavy chain attached to a designer domain(s) or protein fragment(s).

2b) For MHC class 2 binding peptides the recombinant construction can consist of,
Peptide-linker-MHC class 2 α-chain, full length or truncated;
Peptide-linker-MHC class 2 β-chain, full length or truncated;
Peptide-linker-MHC class 2 α-chain-linker-MHC class 2 β-chain, both chains can be full length or truncated, truncation may involve, omission of α- and/or β-chain intermembrane domain, or omission of α- and/or β–chain intermembrane plus cytoplasmic domains. MHC class 2 part of the construction may consist of fused domains from NH2-terminal, MHC class 2 β1domain-MHC class 2 α1domain-constant α3 of MHC class 1, or alternatively of fused domains from NH2-terminal, MHC class 2 α1domain-MHC class 2 β1domain-constant α3 of MHC class 1. In both cases β2m will be associated non-covalently in the folded MHC complex. β2m can also be covalently associated in the folded MHC class 2 complex if the following constructs are used from NH2 terminal, MHC class 2 β1domain-MHC class 2 α1domain-constant α3 of MHC class 1-linker-β2m, or alternatively of fused domains from NH2-terminal, MHC class 2 α1domain-MHC class 2 β1domain-constant α3 of MHC class 1-linker-β2m; the construct may also consist of any of the above MHC class 2 constructs with added designer domain(s) or sequence(s).

c) From chemical synthesis
MHC binding peptide may also be chemically synthesized by solid phase or fluid phase synthesis, according to standard protocols.

Comprehensive collections of antigenic peptides, derived from one antigen, may be prepared by a modification of the solid phase synthesis protocol, as described in the following and exemplified in Example 24.

The protocol for the synthesis of the full-length antigen on solid support is modified by adding a partial cleavage step after each coupling of an amino acid. Thus, the starting point for the synthesis is a solid support to which has been attached a cleavable linker. Then the first amino acid X1 (corresponding to the C-terminal end of the antigen) is added and a coupling reaction performed. The solid support now carries the molecule "linker-X1". After washing, a fraction (e.g. 10%) of the cleavable linkers are now cleaved, to release into solution X1. The supernatant is transferred to a collection container. Additional solid support carrying a cleavable linker is added, e.g. corresponding to 10% of the initial amount of solid support.

Then the second amino acid X2 is added and coupled to X1 or the cleavable linker, to form on solid support the molecules "linker-X2" and "linker-X1-X2". After washing, a fraction (e.g. 10%) of the cleavable linker is cleaved, to release into solution X2 and X1-X2. The supernatant is collected into the collection container, which therefore now contains X1, X2, and X1-X2. Additional solid support carrying a cleavable linker is added, e.g. corresponding to 10% of the initial amount of solid support.

Then the third amino acid X3 is added and coupled to X2 or the cleavable linker, to form on solid support the molecules "linker-X3", "linker-X2-X3" and "linker-X1-X2-X3". After washing, a fraction (e.g. 10%) of the cleavable linker is cleaved, to release into solution X3, X2-X3 and X1-X2-X3. The supernatant is collected into the collection container, which therefore now contains X1, X2, X3, X1-X2, X2-X3 and X1-X2-X3. Additional solid support carrying a cleavable linker is added, e.g. corresponding to 10% of the initial amount of solid support.

This step-wise coupling and partial cleavage of the linker is continued until the N-terminal end of the antigen is reached. The collection container will now contain a large number of peptides of different length and sequence. In the present example where a 10% partial cleavage was employed, a large fraction of the peptides will be 8'-mers, 9'-mers, 10'-mers and 11'-mers, corresponding to class I antigenic peptides. As an example, for a 100 amino acid antigen the 8'-mers will consist of the sequences X1-X2-X3-X4-X5-X6-X7-X8, X2-X3-X4-X5-X6-X7-X8-X9, ….., X93-X94-X95-X96-X97-X98-X99-X100.

Optionally, after a number of coupling and cleavage steps or after each coupling and cleavage step, the used (inactivated) linkers on solid support can be regenerated, in order to maintain a high fraction of linkers available for synthesis. The collection of antigenic peptides can be used as a pool for e.g. the display by APCs to stimulate CTLs in ELISPOT assays, or the antigenic peptides may be mixed with one or more

MHC alleles, to form a large number of different MHC-peptide complexes which can e.g. be used to form a large number of different MHC multimers which can e.g. be used in flow cytometry experiments.

Sequences for use in MHC monomers, MHC multimers, antigenic polypepitdes and antigenic peptides

MHC Class I and MHC Class II molecules have different structures, as described above, and therefore have different restrictions on the size of the peptide which may be accommodated. In general, MHC Class I molecules will accommodate peptides of from about 8 amino acids in length to about 11 amino acids. MHC Class II molecules will in general accommodate peptides of from about 13 amino acids in length to about 16 amino acids.

Of special interest of the present invention is antigenic peptide sequences derived from proteins of Borrelia bacteria. In the following Borrelia bacteria and their genes and proteins are described in more detail.

Borrelia bacteria

The various species of Borrelia are known to humans in the form of Lyme disease and recurring fever, transmitted through tick or flea bite. The cycle of Borrelia through animals is related to the tick's life cycle. The tick has four stages in its two-year life cycle, egg, larva, nymph and adult. Between each stage the tick needs a blood meal in order to mature. The tick usually acquires the spirochaete during its larval stage, when it feeds on small animals such as rodents or birds. Usually the tick picks up Borrelia from the white-footed mouse, which is commonly infected. The tick then becomes the host for the spirochaete. The bacteria resides in the digestive tract of the host for its next nymph and adult stages during which it is passed on to other animals, and sometimes humans.

Borrelia species

Borrelia is a genus of bacteria of the spirochete class. It is a zoonotic, vector-borne disease transmitted primarily by ticks and some by lice, depending on the species. There are at least 37 known species of Borrelia. Different species of Borrelia results in different clinical symptoms. Of the 37 known species of Borrelia, 12 of these species are known to cause Lyme disease or borreliosis and are transmitted by ticks. The

major Borrelia species causing Lyme disease are Borrelia burgdorferi, Borrelia afzelii, Borrelia garinii and Borrelia valaisiana.

Other Borrelia species cause relapsing fever such as Borrelia recurrentis, caused by the human body louse. No animal reservoir of B. recurrentis exists. Lice that feed on infected humans acquire the Borrelia organisms that then multiply in the gut of the louse. When an infected louse feeds on an uninfected human, the organism gains access when the victim crushes the louse or scratches the area where the louse is feeding. B. recurrentis infects the person via mucous membranes and then invades the bloodstream.

Other tick-borne relapsing infections are acquired from other species, such as Borrelia hermsii or Borrelia Parkeri, which can be spread from rodents, and serve as a reservoir for the infection, via a tick vector. Borrelia hermsii and Borrelia recurrentis cause very similar diseases although the disease associated with Borrelia hermsii has more relapses and is responsible for more fatalities, while the disease caused by B. recurrentis has longer febrile and afebrile intervals and a longer incubation period.
The present invention relates in one embodiment to one or more antigenic peptides or one or more antigenic polypeptides or to MHC-peptide complexes or MHC multimers comprising one or more antigenic peptides comprising one or more sequences from one or more Borrelia species including the ones mentioned above.

Borrelia burgdorferi

In one preferered embodiment the invention relates to one or more antigenic peptides or antigenic polypeptides comprising one or more sequences from Borrelia burgdorferi such as Borrelia burgdorferi B31or to one or more MHC-peptide complexes or MHC multiemrs comprising one or more such antigenic peptides.
Borrelia burgdorferi is species of bacteria of the spirochete class of the genus Borrelia. B. burgdorferi is predominant in North America, but also exists in Europe, and is the agent of Lyme disease.

It is a zoonotic, vector-borne disease transmitted by ticks and is named after the researcher Willy Burgdorfer who first isolated the bacterium in 1982. B. burgdorferi is one of the few pathogenic bacteria that can survive without iron, having replaced all of its iron-sulphur cluster enzymes with enzymes that use manganese, thus avoiding the

problem many pathogenic bacteria face in acquiring iron. B. burgdorferi infections have been linked to non-Hodgkin lymphomas. The B. burgdorferi genome (B31 strain) contains 910,725 base pairs and 853 genes.

Borrelia afzelii

In one preferered embodiment the invention relates to one or more antigenic peptides or one or more antigenic polypeptides comprising one or more sequences from Borrelia afzelii such as borrelia afzelii Pko or one or more MHC-peptide complexes or one or more MHC multimers comprising one or more such antigenic peptides .

Borrelia afzelii is considered a new species of the Genus *Borrelia* and considered homologous to *Borrelia burgdorferi* with regard to phenotypic, genetic, and immunological characteristics. Diseases linked to this species of *Borrelia* are Lyme disease and Acrodermatitis chronica atrophicans (ACA). Better understanding of the structure and function of this pathogen will create better methods of treatment to people with the diseases it causes.

Borrelia garini

In one preferered embodiment the invention relates to one or more antigenic peptides or one or more antigenic polypeptides comprising one or more sequences from Borrelia garinii such as garinii PBi or to one or more MHC-peptide complexes or MHC multimers comprising one or more such antigenic peptides.

Borrelia garinii is one of two major strains found in Europe. It usually causes Lyme Disease symptoms of the neurological kind - such as extreme back- and leg-pains, meningitis and partial facial paralysis, Lyme arthritis due to *B garinii* may be associated in susceptible hosts with amoxicillin resistance or treatment resistance.

Other Borrelia species

In one preferred embodiment the present invention relates to or to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides is from Borrelia anserine, or to one or more MHC-peptide complexes or MHC multimers, compricing such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia barbouri, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from the Borrelia burgdorferi group such as burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia afzelii such as Borrelia afzelii ACA-1, Borrelia afzelii K78 and/or Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia andersonii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia bissettii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi (Lyme disease

spirochete),or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 118a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 156a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 29805,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 64b,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 72a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 80a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more Antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi 94a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi B31,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi Bol26,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi CA-11.2a, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi WI91-23, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia burgdorferi ZS7, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia californiensis, or to one or more

MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia garinii such as garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia garinii PBr, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia genomosp. 1, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia genomosp. 2,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia japonica,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia lusitaniae,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia spielmanii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia spielmanii A14S,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia tanukii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia turdi,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia valaisiana,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia valaisiana VS116,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Candidatus Borrelia texasensis,or to one or

more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. AA4Pool,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. AI-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. B31,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. BC-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA1133,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA1176,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA128,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA13,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA134,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA142,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA20,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA22,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA27,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA28,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA29,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA31,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA33,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA370,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA372,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA378,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA388,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA393,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA394,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA395,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA399,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA400,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA401,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA402,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA404,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA411,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA426,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA443,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA446,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA448,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA462,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA468,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA502,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA504,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA507,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA547,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA552,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CA8,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. D22,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. D35,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. FD-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. FL18,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. FL27,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. FL35,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. FL42,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HN6,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HN7,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HN8,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HNM13,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HNM14,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. HNM19,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. IA1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Ir-3519,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Ir-4721,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Ir-4812,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Ir-5215,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. LV5,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MI-2,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MI-5,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MI-6,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MI-8,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MI-9,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MOD-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MOD-5,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MOK-3a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MOS-1b,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. NE49,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. NE581,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PHaP,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PSigII,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SCGT-10,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SCGT-8a,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SCI-2,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SCW-30h,or to one or more

MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SI-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SI-10,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SM-1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. SV1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. W97F51,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Z41293,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. Z41493,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia coriaceae,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia crocidurae,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia duttonii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia duttonii Ly,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia hermsii,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia hermsii DAH,or to one or more

MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia hispanica,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia lonestari,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia miyamotoi,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia parkeri,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia persica,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia recurrentis,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia recurrentis A1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sinica,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia theileri,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia turcica,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia turicatae,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia turicatae 91E135,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 'Lake Gaillard',or to one or more

MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 000133,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 010298,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 10MT,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 5145,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 57Nsk,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 5MT,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. 6T04-2,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. BR,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. BR 2007,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. C5-N52,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CB-A1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CB-A11,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. CB-A3,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. EFL-S0100110,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. IK/23,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. IM/16,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. IM/19,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. KR1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. KR3,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. LB-2001,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. LB-M56,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. LB-W100,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. MK-N61,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. NR-N8,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. OkME1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PAnz,or to one or more MHC-

peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PJes,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PMai,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. PMew,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. R57,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. strain Spain,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. TA1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. TM,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. TM1,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the sequence of one or more antigenic peptides or antigenic polypeptides is from Borrelia sp. TM2,or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

Borrelia genome

All species of Borrelia have linear chromosomes ranging in size from 900,000 to 920,000 base pairs, with an accompaniment of circular and linear plasmids (some species contain up to 20 different plasmids). Between the linear chromosome and array of plasmids there is a high degree of redundancy in the genetic sequence. Although it has not been determined yet, it seems likely that the origin of replication of the main chromosome in species of Borrelia is almost exactly centered on the linear chromosome.

Some of the protein sequences from Borrelia burgdorferi, Borrelia garinii and Borrelia afzelii are homolog protein sequences. This means that the present invention in one embodiment relates to one or more antigenic peptides or antigenic polypeptides, wherein the one or more antigenic peptides or antigenic polypeptides are encoded by one or more of the Borrelia species Borrelia burgdorferi, Borrelia garinii and Borrelia afzelii, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In another embodiment the invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the one or more antigenic peptides or antigenic

polypeptides are encoded by Borrelia burgdorferi and not by Borrelia garinii or Borrelia afzelii, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In another embodiment the invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the one or more antigenic peptides or antigenic polypeptides are encoded by Borrelia garinii and not by Borrelia burgdorferi or Borrelia afzelii, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In another embodiment the invention relates to one or more antigenic peptides or antigenic polypeptides, wherein the one or more antigenic peptides or antigenic polypeptides are encoded by Borrelia afzelii and not by Borrelia garinii or Borrelia burgdorferi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

The present invention relates in one embodiment to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by a Borrelia genome and/or plasmid, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. The genomes and plasmids of Borrelia burgdoferi B31, Borrelia afzelii Pko and Borrelia garinii PBi are listed in Figure 26-29. The peptides can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the genome (NC_001318) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp5 (NC_000957) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp

17 (NC_001849) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp21 (NC_000955) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp25 (NC_001850) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28-1 (NC_001851) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28-2 (NC_001852) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28-3 (NC_001853) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28-4 (NC_001854) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp36 (NC_001855) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid

lp38 (NC_001856) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp56 (NC_000956) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp9 (NC_001904) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28-4 (NC_001854) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp26 (NC_001903) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-1 (NC_000948) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-3 (NC_000949) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-4 (NC_000950) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid

cp32-6 (NC_000951) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-7 (NC_000952) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-8 (NC_000953) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp32-9 (NC_000954) of Borrelia burgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the genome (NC_008277) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp25 (NC_008569) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp28 (NC_0085698) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp32 (NC_008567) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid

lp34 (NC_008566) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp60 (NC_008564) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp60-2 (NC_008565) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp27 (NC_008274) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp30 (NC_008273) of Borrelia afzelii PKo, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the genome (NC_006156) of Borrelia garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid lp54 (NC_006129) of Borrelia garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by the plasmid cp26 (NC_006128) of Borrelia garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides.

In another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a sequence encoded by variable plasmid

segments not finally assembled to whole plasmids of Borrelia garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. These variable plasmid segments not finally assembled to whole plasmids can in one preferred embodiment be selected from the group consisting of NT_108239, NT_108263, NT_108262, NT_108261 , NT_108260, NT_108259 , NT_108258, NT_108257 , NT_108256, NT_108255 , NT_108254, NT_108253 NT_108252, NT_108251, NT_108250, NT_108249, NT_108248, NT_108247, NT_108246, NT_108245 , NT_108244, NT_108243, NT_108242, NT_108241, NT_108240, NT_108238, NT_108237, NT_108236, NT_108235, NT_108234, NT_108233, NT_108232, NT_108231, NT_108230, NT_108229, NT_108228 and NT_108227.

In yet another embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides, optionally compriced in one or more MHC-peptide complexes or MHC multimers, where the antigenic peptides or antigenic polypeptides comprise a sequence encoded by a Borrelia genome and/or plasmid from one or more of the Borrelia species or subspecies: Borrelia anserina, Borrelia barbouri, Borrelia afzelii, Borrelia afzelii ACA-1, Borrelia afzelii K78, Borrelia afzelii PKo, Borrelia andersonii, Borrelia bissettii, Borrelia burgdorferi, Borrelia burgdorferi 118a, Borrelia burgdorferi 156a, Borrelia burgdorferi 29805, Borrelia burgdorferi 64b, Borrelia burgdorferi 72a, Borrelia burgdorferi 80a, Borrelia burgdorferi 94a, Borrelia burgdorferi B31, Borrelia burgdorferi Bol26, Borrelia burgdorferi CA-11.2a, Borrelia burgdorferi WI91-23, Borrelia burgdorferi ZS7, Borrelia californiensis, Borrelia garinii, Borrelia garinii PBi, Borrelia garinii PBr, Borrelia genomosp. 1, Borrelia genomosp. 2, Borrelia japonica, Borrelia lusitaniae, Borrelia spielmanii, Borrelia spielmanii A14S, Borrelia tanukii, Borrelia turdi, Borrelia valaisiana, Borrelia valaisiana VS116, Candidatus Borrelia texasensis, Borrelia sp. AA4Pool, Borrelia sp. Al-1, Borrelia sp. B31, Borrelia sp. BC-1, Borrelia sp. CA1133, Borrelia sp. CA1176, Borrelia sp. CA128, Borrelia sp. CA13, Borrelia sp. CA134, Borrelia sp. CA142, Borrelia sp. CA20, Borrelia sp. CA22, Borrelia sp. CA27, Borrelia sp. CA28, Borrelia sp. CA29, Borrelia sp. CA31, Borrelia sp. CA33, Borrelia sp. CA370, Borrelia sp. CA372, Borrelia sp. CA378, Borrelia sp. CA388, Borrelia sp. CA393, Borrelia sp. CA394, Borrelia sp. CA395, Borrelia sp. CA399, Borrelia sp. CA400, Borrelia sp. CA401, Borrelia sp. CA402, Borrelia sp. CA404, Borrelia sp. CA411, Borrelia sp. CA426, Borrelia sp. CA443, Borrelia sp. CA446, Borrelia sp. CA448, Borrelia sp. CA462, Borrelia sp. CA468, Borrelia sp. CA502,

Borrelia sp. CA504, Borrelia sp. CA507, Borrelia sp. CA547, Borrelia sp. CA552, Borrelia sp. CA8, Borrelia sp. D22, Borrelia sp. D35, Borrelia sp. FD-1, Borrelia sp. FL18, Borrelia sp. FL27, Borrelia sp. FL35, Borrelia sp. FL42, Borrelia sp. HN6, Borrelia sp. HN7, Borrelia sp. HN8, Borrelia sp. HNM13, Borrelia sp. HNM14, Borrelia sp. HNM19, Borrelia sp. IA1, Borrelia sp. Ir-3519, Borrelia sp. Ir-4721, Borrelia sp. Ir-4812, Borrelia sp. Ir-5215, Borrelia sp. LV5, Borrelia sp. MI-2, Borrelia sp. MI-5, Borrelia sp. MI-6, Borrelia sp. MI-8, Borrelia sp. MI-9, Borrelia sp. MOD-1, Borrelia sp. MOD-5, Borrelia sp. MOK-3a, Borrelia sp. MOS-1b, Borrelia sp. NE49, Borrelia sp. NE581, Borrelia sp. PHaP, Borrelia sp. PSigII, Borrelia sp. SCGT-10, Borrelia sp. SCGT-8a, Borrelia sp. SCI-2, Borrelia sp. SCW-30h, Borrelia sp. SI-1, Borrelia sp. SI-10, Borrelia sp. SM-1, Borrelia sp. SV1, Borrelia sp. W97F51, Borrelia sp. Z41293, Borrelia sp. Z41493, Borrelia coriaceae, Borrelia crocidurae, Borrelia duttonii, Borrelia duttonii Ly, Borrelia hermsii, Borrelia hermsii DAH, Borrelia hispanica, Borrelia lonestari, Borrelia miyamotoi, Borrelia parkeri, Borrelia persica, Borrelia recurrentis, Borrelia recurrentis A1, Borrelia sinica, Borrelia theileri, Borrelia turcica, Borrelia turicatae, Borrelia turicatae 91E135, Borrelia sp., Borrelia sp. 'Lake Gaillard', Borrelia sp. 000133, Borrelia sp. 010298, Borrelia sp. 10MT, Borrelia sp. 5145, Borrelia sp. 57Nsk, Borrelia sp. 5MT, Borrelia sp. 6T04-2, Borrelia sp. BR, Borrelia sp. BR 2007, Borrelia sp. C5-N52, Borrelia sp. CB-A1, Borrelia sp. CB-A11, Borrelia sp. CB-A3, Borrelia sp. EFL-S0100110, Borrelia sp. IK/23, Borrelia sp. IM/16, Borrelia sp. IM/19, Borrelia sp. KR1, Borrelia sp. KR3, Borrelia sp. LB-2001, Borrelia sp. LB-M56, Borrelia sp. LB-W100, Borrelia sp. MK-N61, Borrelia sp. NR-N8, Borrelia sp. OkME1, Borrelia sp. PAnz, Borrelia sp. PJes, Borrelia sp. PMai, Borrelia sp. PMew, Borrelia sp. R57, Borrelia sp. strain Spain, Borrelia sp. TA1, Borrelia sp. TM, Borrelia sp. TM1 and Borrelia sp. TM2. These peptides can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

Borrelia proteome

In another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a fragment of the sequence from one or more proteins from Borrelia bulgdorferi B31, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. The one or more proteins can be selected from the proteins listed in Figure 27 and Figure 38. These fagments can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

In another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a fragment of the sequence from one or more proteins from Borrelia afzelii Pko, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. The one or more proteins can be selected from the proteins listed in Figure 28 and Figure 38. These fagments can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

In another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a fragment of the sequence from one or more proteins from Borrelia garinii PBi, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. The one or more proteins can be selected from the proteins listed in Figure 29 and Figure 38. These fagments can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

In another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides comprising a fragment of the sequence from one or more proteins listed in figure 30 and Figure 38, or to one or more MHC-peptide complexes or MHC multimers, compricing one or more such antigenic peptides. These fagments can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

In yet another preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides or MHC-peptide complexes containing such antigenic peptides, where the antigenic peptides or antigenic polypeptides comprise a fragment of the sequence from one or more protein(s) from one or more of the Borrelia species or subspecies: Borrelia anserina, Borrelia barbouri, Borrelia afzelii, Borrelia afzelii ACA-1, Borrelia afzelii K78, Borrelia afzelii PKo, Borrelia andersonii, Borrelia bissettii, Borrelia burgdorferi, Borrelia burgdorferi 118a, Borrelia burgdorferi 156a, Borrelia burgdorferi 29805, Borrelia burgdorferi 64b, Borrelia burgdorferi 72a, Borrelia burgdorferi 80a, Borrelia burgdorferi 94a, Borrelia burgdorferi B31, Borrelia burgdorferi Bol26, Borrelia burgdorferi CA-11.2a, Borrelia burgdorferi WI91-23, Borrelia burgdorferi ZS7, Borrelia californiensis, Borrelia garinii, Borrelia garinii PBi, Borrelia

garinii PBr, Borrelia genomosp. 1, Borrelia genomosp. 2, Borrelia japonica, Borrelia lusitaniae, Borrelia spielmanii, Borrelia spielmanii A14S, Borrelia tanukii, Borrelia turdi, Borrelia valaisiana, Borrelia valaisiana VS116, Candidatus Borrelia texasensis, Borrelia sp. AA4Pool, Borrelia sp. AI-1, Borrelia sp. B31, Borrelia sp. BC-1, Borrelia sp. CA1133, Borrelia sp. CA1176, Borrelia sp. CA128, Borrelia sp. CA13, Borrelia sp. CA134, Borrelia sp. CA142, Borrelia sp. CA20, Borrelia sp. CA22, Borrelia sp. CA27, Borrelia sp. CA28, Borrelia sp. CA29, Borrelia sp. CA31, Borrelia sp. CA33, Borrelia sp. CA370, Borrelia sp. CA372, Borrelia sp. CA378, Borrelia sp. CA388, Borrelia sp. CA393, Borrelia sp. CA394, Borrelia sp. CA395, Borrelia sp. CA399, Borrelia sp. CA400, Borrelia sp. CA401, Borrelia sp. CA402, Borrelia sp. CA404, Borrelia sp. CA411, Borrelia sp. CA426, Borrelia sp. CA443, Borrelia sp. CA446, Borrelia sp. CA448, Borrelia sp. CA462, Borrelia sp. CA468, Borrelia sp. CA502, Borrelia sp. CA504, Borrelia sp. CA507, Borrelia sp. CA547, Borrelia sp. CA552, Borrelia sp. CA8, Borrelia sp. D22, Borrelia sp. D35, Borrelia sp. FD-1, Borrelia sp. FL18, Borrelia sp. FL27, Borrelia sp. FL35, Borrelia sp. FL42, Borrelia sp. HN6, Borrelia sp. HN7, Borrelia sp. HN8, Borrelia sp. HNM13, Borrelia sp. HNM14, Borrelia sp. HNM19, Borrelia sp. IA1, Borrelia sp. Ir-3519, Borrelia sp. Ir-4721, Borrelia sp. Ir-4812, Borrelia sp. Ir-5215, Borrelia sp. LV5, Borrelia sp. MI-2, Borrelia sp. MI-5, Borrelia sp. MI-6, Borrelia sp. MI-8, Borrelia sp. MI-9, Borrelia sp. MOD-1, Borrelia sp. MOD-5, Borrelia sp. MOK-3a, Borrelia sp. MOS-1b, Borrelia sp. NE49, Borrelia sp. NE581, Borrelia sp. PHaP, Borrelia sp. PSigII, Borrelia sp. SCGT-10, Borrelia sp. SCGT-8a, Borrelia sp. SCI-2, Borrelia sp. SCW-30h, Borrelia sp. SI-1, Borrelia sp. SI-10, Borrelia sp. SM-1, Borrelia sp. SV1, Borrelia sp. W97F51, Borrelia sp. Z41293, Borrelia sp. Z41493, Borrelia coriaceae, Borrelia crocidurae, Borrelia duttonii, Borrelia duttonii Ly, Borrelia hermsii, Borrelia hermsii DAH, Borrelia hispanica, Borrelia lonestari, Borrelia miyamotoi, Borrelia parkeri, Borrelia persica, Borrelia recurrentis, Borrelia recurrentis A1, Borrelia sinica, Borrelia theileri, Borrelia turcica, Borrelia turicatae, Borrelia turicatae 91E135, Borrelia sp., Borrelia sp. 'Lake Gaillard', Borrelia sp. 000133, Borrelia sp. 010298, Borrelia sp. 10MT, Borrelia sp. 5145, Borrelia sp. 57Nsk, Borrelia sp. 5MT, Borrelia sp. 6T04-2, Borrelia sp. BR, Borrelia sp. BR 2007, Borrelia sp. C5-N52, Borrelia sp. CB-A1, Borrelia sp. CB-A11, Borrelia sp. CB-A3, Borrelia sp. EFL-S0100110, Borrelia sp. IK/23, Borrelia sp. IM/16, Borrelia sp. IM/19, Borrelia sp. KR1, Borrelia sp. KR3, Borrelia sp. LB-2001, Borrelia sp. LB-M56, Borrelia sp. LB-W100, Borrelia sp. MK-N61, Borrelia sp. NR-N8, Borrelia sp. OkME1, Borrelia sp. PAnz, Borrelia sp. PJes, Borrelia sp. PMai, Borrelia sp. PMew, Borrelia sp. R57, Borrelia sp. strain Spain, Borrelia sp.

TA1, Borrelia sp. TM, Borrelia sp. TM1 and Borrelia sp. TM2. These peptides can e.g. be 8 mers, 9 mers, 10 mers, 11 mers, 12 mers, 13 mers, 14 mers, 15 mers or 16 mers.

Borrelia class I antigen peptide fragments

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigen peptide fragments themselves.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers.

In one preferred embodiment the present invention relates to one or more antigenic peptides or antigenic polypeptides being borrelia class I antigen peptide fragments, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigenic peptide fragments themselves, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers of a protein from or encoded by Borrelia burgdorferi such as Borrelia burgdorferi B31.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigenic peptide fragments themselves, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers of a protein from or encoded by Borrelia afzelii such as Borrelia afzelii PKo.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigenic peptide fragments themselves, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers of a protein from or encoded by Borrelia garinii such as Borrelia garinii PBi.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigenic peptide fragments themselves, wherein said peptide fragments are 8 mers, 9 mers, 10 mers and/or 11 mers of a protein from or encoded by Borrelia anserina, Borrelia barbouri, Borrelia afzelii, Borrelia afzelii ACA-1, Borrelia afzelii K78, Borrelia afzelii PKo, Borrelia andersonii, Borrelia bissettii, Borrelia burgdorferi, Borrelia burgdorferi 118a, Borrelia burgdorferi 156a, Borrelia burgdorferi 29805, Borrelia burgdorferi 64b, Borrelia burgdorferi 72a, Borrelia burgdorferi 80a, Borrelia burgdorferi 94a, Borrelia burgdorferi B31, Borrelia burgdorferi Bol26, Borrelia burgdorferi CA-11.2a, Borrelia burgdorferi WI91-23, Borrelia burgdorferi ZS7, Borrelia californiensis, Borrelia garinii, Borrelia garinii PBi, Borrelia garinii PBr, Borrelia genomosp. 1, Borrelia genomosp. 2, Borrelia japonica, Borrelia lusitaniae, Borrelia spielmanii, Borrelia spielmanii A14S, Borrelia tanukii, Borrelia turdi, Borrelia valaisiana, Borrelia valaisiana VS116, Candidatus Borrelia texasensis, Borrelia sp. AA4Pool, Borrelia sp. AI-1, Borrelia sp. B31, Borrelia sp. BC-1, Borrelia sp. CA1133, Borrelia sp. CA1176, Borrelia sp. CA128, Borrelia sp. CA13, Borrelia sp. CA134, Borrelia sp. CA142, Borrelia sp. CA20, Borrelia sp. CA22, Borrelia sp. CA27, Borrelia sp. CA28, Borrelia sp. CA29, Borrelia sp. CA31, Borrelia sp. CA33, Borrelia sp. CA370, Borrelia sp. CA372, Borrelia sp. CA378, Borrelia sp. CA388, Borrelia sp. CA393, Borrelia sp. CA394, Borrelia sp. CA395, Borrelia sp. CA399, Borrelia sp. CA400, Borrelia sp. CA401, Borrelia sp. CA402, Borrelia sp. CA404, Borrelia sp. CA411, Borrelia sp. CA426, Borrelia sp. CA443, Borrelia sp. CA446, Borrelia sp. CA448, Borrelia sp. CA462, Borrelia sp. CA468, Borrelia sp. CA502, Borrelia sp. CA504, Borrelia sp. CA507, Borrelia sp. CA547, Borrelia sp. CA552, Borrelia sp. CA8, Borrelia sp. D22, Borrelia sp. D35, Borrelia sp. FD-1, Borrelia sp. FL18, Borrelia sp. FL27, Borrelia sp. FL35, Borrelia sp. FL42, Borrelia sp. HN6, Borrelia sp. HN7, Borrelia sp. HN8, Borrelia sp. HNM13, Borrelia sp. HNM14, Borrelia sp. HNM19, Borrelia sp. IA1, Borrelia sp. Ir-3519, Borrelia sp. Ir-4721, Borrelia sp. Ir-4812, Borrelia sp. Ir-5215, Borrelia sp. LV5, Borrelia sp. MI-2, Borrelia sp. MI-5, Borrelia sp. MI-6, Borrelia sp. MI-8, Borrelia sp. MI-9, Borrelia sp. MOD-1, Borrelia sp. MOD-5, Borrelia sp. MOK-3a, Borrelia sp. MOS-1b, Borrelia sp. NE49, Borrelia sp. NE581, Borrelia sp. PHaP, Borrelia sp. PSigII, Borrelia sp. SCGT-10, Borrelia sp. SCGT-8a, Borrelia sp. SCI-2, Borrelia sp. SCW-30h, Borrelia sp. SI-1, Borrelia sp. SI-10, Borrelia sp. SM-1, Borrelia sp. SV1, Borrelia sp. W97F51, Borrelia sp. Z41293, Borrelia sp. Z41493, Borrelia coriaceae, Borrelia crocidurae, Borrelia duttonii, Borrelia duttonii Ly, Borrelia hermsii,

Borrelia hermsii DAH, Borrelia hispanica, Borrelia lonestari, Borrelia miyamotoi, Borrelia parkeri, Borrelia persica, Borrelia recurrentis, Borrelia recurrentis A1, Borrelia sinica, Borrelia theileri, Borrelia turcica, Borrelia turicatae, Borrelia turicatae 91E135, Borrelia sp., Borrelia sp. 'Lake Gaillard', Borrelia sp. 000133, Borrelia sp. 010298, Borrelia sp. 10MT, Borrelia sp. 5145, Borrelia sp. 57Nsk, Borrelia sp. 5MT, Borrelia sp. 6T04-2, Borrelia sp. BR, Borrelia sp. BR 2007, Borrelia sp. C5-N52, Borrelia sp. CB-A1, Borrelia sp. CB-A11, Borrelia sp. CB-A3, Borrelia sp. EFL-S0100110, Borrelia sp. IK/23, Borrelia sp. IM/16, Borrelia sp. IM/19, Borrelia sp. KR1, Borrelia sp. KR3, Borrelia sp. LB-2001, Borrelia sp. LB-M56, Borrelia sp. LB-W100, Borrelia sp. MK-N61, Borrelia sp. NR-N8, Borrelia sp. OkME1, Borrelia sp. PAnz, Borrelia sp. PJes, Borrelia sp. PMai, Borrelia sp. PMew, Borrelia sp. R57, Borrelia sp. strain Spain, Borrelia sp. TA1, Borrelia sp. TM, Borrelia sp. TM1 and/or Borrelia sp. TM2.

In another preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class I antigen peptide fragments or to the borrelia class I antigenic peptide fragments themselves, where the peptide fragments are selected from the peptides listed in Figure 31, Figure 32, Figure 39, Figure 40, Figure 41, Figure 42, Table A, Table B and Table C.

Borrelia class II antigen peptide fragments

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves, wherein said peptide fragments are 13 mers, 14 mers, 15 mers and/or 16 mers.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves, wherein said peptide fragments are 13 mers, 14 mers, 15 mers and/or 16 mers of a protein from or encoded by Borrelia burgdorferi such as Borrelia burgdorferi B31.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves, wherein said peptide fragments are 13 mers, 14 mers, 15 mers and/or 16 mers of a protein from or encoded by Borrelia afzelii such as Borrelia afzelii PKo.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves, wherein said peptide fragments are 13 mers, 14 mers, 15 mers and/or 16 mers of a protein from or encoded by Borrelia garinii such as Borrelia garinii PBi.

In one preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments, or to the borrelia class II antigen peptide fragments themselves, wherein said peptide fragments are 13 mers, 14 mers, 15 mers and/or 16 mers of a protein from or encoded by Borrelia anserina, Borrelia barbouri, Borrelia afzelii, Borrelia afzelii ACA-1, Borrelia afzelii K78, Borrelia afzelii PKo, Borrelia andersonii, Borrelia bissettii, Borrelia burgdorferi, Borrelia burgdorferi 118a, Borrelia burgdorferi 156a, Borrelia burgdorferi 29805, Borrelia burgdorferi 64b, Borrelia burgdorferi 72a, Borrelia burgdorferi 80a, Borrelia burgdorferi 94a, Borrelia burgdorferi B31, Borrelia burgdorferi Bol26, Borrelia burgdorferi CA-11.2a, Borrelia burgdorferi WI91-23, Borrelia burgdorferi ZS7, Borrelia californiensis, Borrelia garinii, Borrelia garinii PBi, Borrelia garinii PBr, Borrelia genomosp. 1, Borrelia genomosp. 2, Borrelia japonica, Borrelia lusitaniae, Borrelia spielmanii, Borrelia spielmanii A14S, Borrelia tanukii, Borrelia turdi, Borrelia valaisiana, Borrelia valaisiana VS116, Candidatus Borrelia texasensis, Borrelia sp. AA4Pool, Borrelia sp. AI-1, Borrelia sp. B31, Borrelia sp. BC-1, Borrelia sp. CA1133, Borrelia sp. CA1176, Borrelia sp. CA128, Borrelia sp. CA13, Borrelia sp. CA134, Borrelia sp. CA142, Borrelia sp. CA20, Borrelia sp. CA22, Borrelia sp. CA27, Borrelia sp. CA28, Borrelia sp. CA29, Borrelia sp. CA31, Borrelia sp. CA33, Borrelia sp. CA370, Borrelia sp. CA372, Borrelia sp. CA378, Borrelia sp. CA388, Borrelia sp. CA393, Borrelia sp. CA394, Borrelia sp. CA395, Borrelia sp. CA399, Borrelia sp. CA400, Borrelia sp. CA401, Borrelia sp. CA402, Borrelia sp. CA404, Borrelia sp. CA411, Borrelia sp. CA426, Borrelia sp. CA443, Borrelia sp. CA446, Borrelia sp. CA448, Borrelia sp. CA462, Borrelia sp. CA468, Borrelia sp. CA502, Borrelia sp. CA504,

Borrelia sp. CA507, Borrelia sp. CA547, Borrelia sp. CA552, Borrelia sp. CA8, Borrelia sp. D22, Borrelia sp. D35, Borrelia sp. FD-1, Borrelia sp. FL18, Borrelia sp. FL27, Borrelia sp. FL35, Borrelia sp. FL42, Borrelia sp. HN6, Borrelia sp. HN7, Borrelia sp. HN8, Borrelia sp. HNM13, Borrelia sp. HNM14, Borrelia sp. HNM19, Borrelia sp. IA1, Borrelia sp. Ir-3519, Borrelia sp. Ir-4721, Borrelia sp. Ir-4812, Borrelia sp. Ir-5215, Borrelia sp. LV5, Borrelia sp. MI-2, Borrelia sp. MI-5, Borrelia sp. MI-6, Borrelia sp. MI-8, Borrelia sp. MI-9, Borrelia sp. MOD-1, Borrelia sp. MOD-5, Borrelia sp. MOK-3a, Borrelia sp. MOS-1b, Borrelia sp. NE49, Borrelia sp. NE581, Borrelia sp. PHaP, Borrelia sp. PSigII, Borrelia sp. SCGT-10, Borrelia sp. SCGT-8a, Borrelia sp. SCI-2, Borrelia sp. SCW-30h, Borrelia sp. SI-1, Borrelia sp. SI-10, Borrelia sp. SM-1, Borrelia sp. SV1, Borrelia sp. W97F51, Borrelia sp. Z41293, Borrelia sp. Z41493, Borrelia coriaceae, Borrelia crocidurae, Borrelia duttonii, Borrelia duttonii Ly, Borrelia hermsii, Borrelia hermsii DAH, Borrelia hispanica, Borrelia lonestari, Borrelia miyamotoi, Borrelia parkeri, Borrelia persica, Borrelia recurrentis, Borrelia recurrentis A1, Borrelia sinica, Borrelia theileri, Borrelia turcica, Borrelia turicatae, Borrelia turicatae 91E135, Borrelia sp., Borrelia sp. 'Lake Gaillard', Borrelia sp. 000133, Borrelia sp. 010298, Borrelia sp. 10MT, Borrelia sp. 5145, Borrelia sp. 57Nsk, Borrelia sp. 5MT, Borrelia sp. 6T04-2, Borrelia sp. BR, Borrelia sp. BR 2007, Borrelia sp. C5-N52, Borrelia sp. CB-A1, Borrelia sp. CB-A11, Borrelia sp. CB-A3, Borrelia sp. EFL-S0100110, Borrelia sp. IK/23, Borrelia sp. IM/16, Borrelia sp. IM/19, Borrelia sp. KR1, Borrelia sp. KR3, Borrelia sp. LB-2001, Borrelia sp. LB-M56, Borrelia sp. LB-W100, Borrelia sp. MK-N61, Borrelia sp. NR-N8, Borrelia sp. OkME1, Borrelia sp. PAnz, Borrelia sp. PJes, Borrelia sp. PMai, Borrelia sp. PMew, Borrelia sp. R57, Borrelia sp. strain Spain, Borrelia sp. TA1, Borrelia sp. TM, Borrelia sp. TM1 and/or Borrelia sp. TM2.

In another preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments selected from the peptides listed in Figure 33, Figure 34, Figure 39, Figure 40, Figure 41, Figure 42, Table A, Table B and Table C.

In another preferred embodiment the present invention relates to one or more borrelia class II antigenic peptide fragments selected from the peptides listed in Figure 33, Figure 34, Figure 39, Figure 40, Figure 41, Figure 42, Table A, Table B and Table C.

Borrelia class II antigen peptide fragments comprising a conserved core peptide.

MHC class 2 proteins typically bind peptides with a total length of 13-18 amino acids, comprising a 9'-mer core motif containing the important amino acid anchor residues. However the total length is not strictly defined, as opposed to most MHC class 1 molecules.

The putative binding peptide sequences only describe the central part of the peptide including the 9-mer core motif; in other words, the peptide sequences shown represent the core of the binding peptide with a few important flanking amino acids, which in some cases may be of considerably length generating binding peptides longer than the 13-16 amino acids.

In another preferred embodiment the present invention relates to one or more MHC-peptide complexes or MHC multimers comprising one or more borrelia class II antigen peptide fragments comprising one or more of the 9 mer core peptides listed in Figure 34.

In another preferred embodiment the present invention relates to one or more borrelia class II antigen peptide fragments comprising one or more of the 9 mer core peptides listed in Figure 34.

The above mentioned 9 mer core peptides can be part of one or more 13 mers, 14 mers, 15 mers, 16 mers, 17 mers, 18 mers, 19 mers, 20 mers, 21 mers, 22 mers, 23,mers, 24 mers or 25 mer.

The 9 mer core peptides can have different positions in the 13 mers, 14 mers, 15 mers, 16 mers, 17 mers, 18 mers, 19 mers, 20 mers, 21 mers, 22 mers, 23,mers, 24 mers or 25 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 13 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 13 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 13 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 13 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 13 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 14 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 15 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 16 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 9 from the N-terminus of the 17 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 9 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 10 from the N-terminus of the 18 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 9 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 10 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 11 from the N-terminus of the 19 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 9 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 10 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 11 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 12 from the N-terminus of the 20 mer.

In one preferred embodiment the 9 mer starts at position 1 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 2 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 3 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 4 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 5 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 6 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 7 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 8 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 9 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 10 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 11 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 12 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 13 from the N-terminus of the 21 mer, 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 14 from the N-terminus of the 22 mer, 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 15 from the N-terminus of the 23 mer, 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 16 from the N-terminus of the 24 mer or 25 mer.

In one preferred embodiment the 9 mer starts at position 17 from the N-terminus of the 25 mer.

The amino acids surrounding the 9 mer core peptides in the 13 mers, 14 mers, 15 mers, 16 mers, 17 mers, 18 mers, 19 mers, 20 mers, 21 mers, 22 mers, 23 mers, 24 mers and/or 25 mers can be any amino acids.

Peptide fragments with amino acid substitutions

The present invention further relates to one or more antigenic Borrelia peptides that have one or more amino acid substitutions such as 1, 2, 3, 4, 5, 6, 7, or 8.

The present invention also relates to one or more MHC-peptide complexes or MHC multimers, wherein the one or more antigenic Borrelia peptides have one or more amino acid substitutions such as 1, 2, 3, 4, 5, 6, 7, or 8.

In one embodiment the one or more amino acid substitutions are within the amino acid anchor motif. In another embodiment the one or more amino acid substitutions are outside the amino acid anchor motif. In one embodiment the one or more amino acid substitutions are within the 9 mer core motif. In another embodiment the one or more amino acid substitutions are outside the 9 mer core motif.

In a preferred embodiment these amino acid substitutions comprise substitution with an "equivalent amino acid residue". An "equivalent amino acid residue" refers to an amino acid residue capable of replacing another amino acid residue in a polypeptide without substantially altering the structure and/or functionality of the polypeptide. Equivalent amino acids thus have similar properties such as bulkiness of the side-chain, side chain polarity (polar or non-polar), hydrophobicity (hydrophobic or hydrophilic), pH (acidic, neutral or basic) and side chain organization of carbon molecules (aromatic/aliphatic). As such, "equivalent amino acid residues" can be regarded as "conservative amino acid substitutions".

The classification of equivalent amino acids refers in one embodiment to the following classes: 1) HRK, 2) DENQ, 3) C, 4) STPAG, 5) MILV and 6) FYW.

Within the meaning of the term "equivivalent amino acid substitution" as applied herein, one amino acid may be substituted for another, in one embodiment, within the groups of amino acids indicated herein below:

Amino acids having polar side chains (Asp, Glu, Lys, Arg, His, Asn, Gln, Ser, Thr, Tyr, and Cys,)
Amino acids having non-polar side chains (Gly, Ala, Val, Leu, Ile, Phe, Trp, Pro, and Met)
Amino acids having aliphatic side chains (Gly, Ala Val, Leu, Ile)
Amino acids having cyclic side chains (Phe, Tyr, Trp, His, Pro)
Amino acids having aromatic side chains (Phe, Tyr, Trp)
Amino acids having acidic side chains (Asp, Glu)
Amino acids having basic side chains (Lys, Arg, His)
Amino acids having amide side chains (Asn, Gln)
Amino acids having hydroxy side chains (Ser, Thr)
Amino acids having sulphor-containing side chains (Cys, Met),
Neutral, weakly hydrophobic amino acids (Pro, Ala, Gly, Ser, Thr)
Hydrophilic, acidic amino acids (Gln, Asn, Glu, Asp), and
Hydrophobic amino acids (Leu, Ile, Val)

A Venn diagram is another method for grouping of amino acids according to their properties (Livingstone & Barton, *CABIOS*, **9**, 745-756, 1993). In another preferred

embodiment one or more amino acids may be substituted with another within the same Venn diagram group.

In another preferred embodiment these amino acid substitutions comprise substitution with a “non-equivalent amino acid residue”. Non-equivalent amino acid residues are amino acid residues with dissimilar properties to the properties of the amino acid they substitute according to the groupings described above.

In one preferred embodiment the amino acid substitutions increases the affinity of the peptide for the MHC molecule and thereby increase the stability of the MHC-peptide complex.

In another preferred embodiment the amino acid substitutions decreases the affinity of the peptide for the MHC molecule and thereby increase the stability of the MHC-peptide complex.

In one preferred embodiment the amino acid substitutions increases the overall affinity of one or more T-cell receptors for the MHC-peptide complex containing the modified antigenic peptide.

In another preferred embodiment the amino acid substitutions decreases the overall affinity of one or more T-cell receptors for the MHC-peptide complex containing the modified antigenic peptide.

Gene variants

The present invention further relates to one or more MHC-peptide complexes or MHC multimers, wherein the one or more antigenic Borrelia peptides are encoded by one or more gene variants.

The present invention also relates to one or more antigenic Borrelia peptides that are encoded by one or more gene variants.

The term "variant gene" refers to nucleic acid molecules that encode a polypeptide having an amino acid sequence that is a modification of the polypeptides according to the present invention. Such variants include naturally-occurring polymorphisms of

genes according to the present invention, as well as synthetic genes that contain conservative amino acid substitutions of the amino acid sequence of a polypeptide according to the present invention. Additional variant forms of genes are nucleic acid molecules that contain insertions or deletions of the nucleotide sequences described herein. A variant gene according to the present invention can be identified by determining whether the gene hybridizes with a nucleic acid molecule having the nucleotide sequence of a polypeptide according to the present invention, or its complement, under stringent conditions.

Antigenic peptides

The present invention relates in one embodiment to antigenic peptides derived from Borrelia antigens. The one or more antigenic peptides can in one embodiment comprise one or more fragments from one or more Borrelia antigens capable of interacting with one or more MHC class 1 molecules. The one or more antigenic peptides can in another embodiment comprise one or more fragments from one or more Borrelia antigens capable of interacting with one or more MHC class 2 molecules.

The antigenic peptides can be generated from any Borrelia antigen such as the Borrelia antigens listed in this application including the Borrelia antigens listed in figure 27, figure 28, figure 29, figure 30, figure 38 and figure 43.

MHC Class I and MHC Class II molecules have different structures, as described above, and therefore have different restrictions on the size of the peptide which may be accommodated. In general, MHC Class I molecules will accommodate peptides of from about 8 amino acids in length to about 11 amino acids. MHC Class II molecules will in general accommodate peptides of from about 13 amino acids in length to about 16 amino acids but may also accommodate longer peptides.

The antigenic peptides can in one embodiment be generated by computational prediction e.g. using NetMHC (www.cbs.dtu.dk/services/NetMHC/) or by selection of specific 8, 9, 10, 11, 13, 14, 15 or 16 amino acid sequences. Figure 31, figure 32, figure 33, figure 34, figure 36, figure 37, figure 39, figure 40, figure 41, figure 42, figure 43, figure 44, figure 45, table A, table B and table C comprise antigen peptides including Borrelia antigenic peptides.

The present invention relates to one or more antigenic peptides and/or one or more MHC multimers, MHC-peptide complexes and/or one or more antigenic polypeptides comprising one or more antigenic peptides such as the antigenic peptides listed in the figures and/or tables in this application (comprising SEQ ID NO 1 to SEQ ID NO 217791) and/or the antigenic peptides characterized by item 1 to 735 herein below.

The one or more antigenic peptides can in one embodiment comprise or consist of a fragment of one or more antigenic peptides listed in the figures and tables of this application (SEQ ID NO 1 to SEQ ID NO 217791) and/or the antigenic peptides characterized by item 1 to 735 herein below, such as a fragment consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 amino acids.
It is to be understood that said items are not meant to be limiting to the peptide according to the present invention in that said peptide may consist of more than said 8 to 16 amino acids, but at least comprising said 8 to 16 amino acids.

Thus, in another embodiment the antigenic peptide listed in figures and/or tables in this application (including SEQ ID NO 1 to SEQ ID NO 217791) and/or the antigenic peptides characterized by item 1 to 735 herein below can be a fragment or part of a larger antigenic polypeptide, wherein the larger antigenic polypeptide may be of a total length of 9, such as 10, for example 11, such as 12, for example 13, such as 14, for example 15, such as 16, for example 17, such as 18, for example 19, such as 20, for example 21, such as 22, for example 23, such as 24, for example 25, such as 26, for example 27, such as 28, for example 29, such as 30, for example 31, such as 32, for example 33, such as 34, for example 35, such as 36, for example 37, such as 38, for example 39, such as 40 amino acids, wherein 8 to 16 of said amino acids are defined in the items below. In another embodiment, the larger polypeptide may be of a total length of between 20 to 30, such as 30-40, for example 40-50, such as 50-60, for example 60-70, such as 70-80, for example 80-90, such as 90-100, for example 100-150, such as 150-200, for example 200-250, such as 250-300, for example 300-500, such as 500-1000, for example 1000-2000, such as 2000-3000, for example 3000-4000, such as 4000-5000, for example 5000-10,000, such as 10,000-20,000, for example 20,000-30,000, such as 30,000-40,000, for example 40,000-50,000, such as 50,000-75,000, for example 75,000-100,000, such as 100,000-250,000, for example 250,000-,500,000, such as 500,000-1,000,000 amino acids.

In one embodiment the antigenic peptides listed in the figures and/or tables of this application (SEQ ID NO 1 to SEQ ID NO 217791) are modified by one or more type(s) of post-translational modifications such as one or more of the post-translational modifications listed in the items (item 1 to 735) herein below. The same or different types of post-translational modification can occur on one or more amino acids in the antigenic peptide. Thus, in one embodiment, any one amino acid may be modified once, twice or three times with the same or different types of modifications. Furthermore, said identical and/or different modification may be present on 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18 of the amino acid residues of the peptide according to the present invention as defined in the items below. In addition, modifications may also be present on amino acid residues outside said 8 to 16 amino acids, in case the peptide is part of a larger protein.

Preferred Borrelia afzelii fragments of Osp C capable of interacting with one or more MHC class 1 and/or MHC class 2 molecules are listed in Table A.

Table A: Prediction of MHC class 1 and 2 Borrelia afzelii OspC peptide binders. Prediction of 8-, 9-, 10-, 11-, 13-, 14-, 15-, 16-mer peptides were generated using the program displayed in figure 2.

8 mers:

MKKNTLSA; KKNTLSAI; KNTLSAIL; NTLSAILM; TLSAILMT; LSAILMTL;
SAILMTLF; AILMTLFL; ILMTLFLF; LMTLFLFI; MTLFLFIS; TLFLFISC;
LFLFISCN; FLFISCNN; LFISCNNS; FISCNNSG; ISCNNSGK; SCNNSGKG;
CNNSGKGG; NNSGKGGD; NSGKGGDS; SGKGGDSA; GKGGDSAS; KGGDSAST;
GGDSASTN; GDSASTNP; DSASTNPA; SASTNPAD; ASTNPADE; STNPADES;
TNPADESA; NPADESAK; PADESAKG; ADESAKGP; DESAKGPN; ESAKGPNL;
SAKGPNLT; AKGPNLTE; KGPNLTEI; GPNLTEIS; PNLTEISK; NLTEISKK;
LTEISKKI; TEISKKIT; EISKKITD; ISKKITDS; SKKITDSN; KKITDSNA;
KITDSNAF; ITDSNAFV; TDSNAFVL; DSNAFVLA; SNAFVLAV; NAFVLAVK;
AFVLAVKE; FVLAVKEV; VLAVKEVE; LAVKEVET; AVKEVETL; VKEVETLV;
KEVETLVS; EVETLVSS; VETLVSSI; ETLVSSID; TLVSSIDE; LVSSIDEL;
VSSIDELA; SSIDELAN; SIDELANK; IDELANKA; DELANKAI; ELANKAIG;
LANKAIGK; ANKAIGKK; NKAIGKKI; KAIGKKIQ; AIGKKIQQ; IGKKIQQN;
GKKIQQNG; KKIQQNGL; KIQQNGLG; IQQNGLGA; QQNGLGAE; QNGLGAEA;
NGLGAEAN; GLGAEANR; LGAEANRN; GAEANRNE; AEANRNES; EANRNESL;
ANRNESLL; NRNESLLA; RNESLLAG; NESLLAGV; ESLLAGVH; SLLAGVHE;
LLAGVHEI; LAGVHEIS; AGVHEIST; GVHEISTL; VHEISTLI; HEISTLIT;
EISTLITE; ISTLITEK; STLITEKL; TLITEKLS; LITEKLSK; ITEKLSKL;
TEKLSKLK; EKLSKLKN; KLSKLKNS; LSKLKNSG; SKLKNSGE; KLKNSGEL;
LKNSGELK; KNSGELKA; NSGELKAK; SGELKAKI; GELKAKIE; ELKAKIED;
LKAKIEDA; KAKIEDAK; AKIEDAKK; KIEDAKKC; IEDAKKCS; EDAKKCSE;
DAKKCSEE; AKKCSEEF; KKCSEEFT; KCSEEFTN; CSEEFTNK; SEEFTNKL;
EEFTNKLR; EFTNKLRV; FTNKLRVS; TNKLRVSH; NKLRVSHA; KLRVSHAD;
LRVSHADL; RVSHADLG; VSHADLGK; SHADLGKQ; HADLGKQG; ADLGKQGV;
DLGKQGVN; LGKQGVND; GKQGVNDD; KQGVNDDD; QGVNDDDA; GVNDDDAK;
VNDDDAKK; NDDDAKKA; DDDAKKAI; DDAKKAIL; DAKKAILK; AKKAILKT;

KKAILKTN; KAILKTNA; AILKTNAD; ILKTNADK; LKTNADKT; KTNADKTK;
TNADKTKG; NADKTKGA; ADKTKGAE; DKTKGAEE; KTKGAEEL; TKGAEELG;
KGAEELGK; GAEELGKL; AEELGKLF; EELGKLFK; ELGKLFKS; LGKLFKSV;
GKLFKSVE; KLFKSVEG; LFKSVEGL; FKSVEGLV; KSVEGLVK; SVEGLVKA;
VEGLVKAA; EGLVKAAQ; GLVKAAQE; LVKAAQEA; VKAAQEAL; KAAQEALT;
AAQEALTN; AQEALTNS; QEALTNSV; EALTNSVK; ALTNSVKE; LTNSVKEL;
TNSVKELT; NSVKELTS; SVKELTSP; VKELTSPV; KELTSPVV; ELTSPVVA;
LTSPVVAE; TSPVVAES; SPVVAESP; PVVAESPK; VVAESPKK; VAESPKKP

9 mers:

MKKNTLSAI; KKNTLSAIL; KNTLSAILM; NTLSAILMT; TLSAILMTL; LSAILMTLF;
SAILMTLFL; AILMTLFLF; ILMTLFLFI; LMTLFLFIS; MTLFLFISC; TLFLFISCN;
LFLFISCNN; FLFISCNNS; LFISCNNSG; FISCNNSGK; ISCNNSGKG; SCNNSGKGG;
CNNSGKGGD; NNSGKGGDS; NSGKGGDSA; SGKGGDSAS; GKGGDSAST; KGGDSASTN;
GGDSASTNP; GDSASTNPA; DSASTNPAD; SASTNPADE; ASTNPADES; STNPADESA;
TNPADESAK; NPADESAKG; PADESAKGP; ADESAKGPN; DESAKGPNL; ESAKGPNLT;
SAKGPNLTE; AKGPNLTEI; KGPNLTEIS; GPNLTEISK; PNLTEISKK; NLTEISKKI;
LTEISKKIT; TEISKKITD; EISKKITDS; ISKKITDSN; SKKITDSNA; KKITDSNAF;
KITDSNAFV; ITDSNAFVL; TDSNAFVLA; DSNAFVLAV; SNAFVLAVK; NAFVLAVKE;
AFVLAVKEV; FVLAVKEVE; VLAVKEVET; LAVKEVETL; AVKEVETLV; VKEVETLVS;
KEVETLVSS; EVETLVSSI; VETLVSSID; ETLVSSIDE; TLVSSIDEL; LVSSIDELA;
VSSIDELAN; SSIDELANK; SIDELANKA; IDELANKAI; DELANKAIG; ELANKAIGK;
LANKAIGKK; ANKAIGKKI; NKAIGKKIQ; KAIGKKIQQ; AIGKKIQQN; IGKKIQQNG;
GKKIQQNGL; KKIQQNGLG; KIQQNGLGA; IQQNGLGAE; QQNGLGAEA; QNGLGAEAN;
NGLGAEANR; GLGAEANRN; LGAEANRNE; GAEANRNES; AEANRNESL; EANRNESLL;
ANRNESLLA; NRNESLLAG; RNESLLAGV; NESLLAGVH; ESLLAGVHE; SLLAGVHEI;
LLAGVHEIS; LAGVHEIST; AGVHEISTL; GVHEISTLI; VHEISTLIT; HEISTLITE;
EISTLITEK; ISTLITEKL; STLITEKLS; TLITEKLSK; LITEKLSKL; ITEKLSKLK;
TEKLSKLKN; EKLSKLKNS; KLSKLKNSG; LSKLKNSGE; SKLKNSGEL; KLKNSGELK;
LKNSGELKA; KNSGELKAK; NSGELKAKI; SGELKAKIE; GELKAKIED; ELKAKIEDA;
LKAKIEDAK; KAKIEDAKK; AKIEDAKKC; KIEDAKKCS; IEDAKKCSE; EDAKKCSEE;
DAKKCSEEF; AKKCSEEFT; KKCSEEFTN; KCSEEFTNK; CSEEFTNKL; SEEFTNKLR;
EEFTNKLRV; EFTNKLRVS; FTNKLRVSH; TNKLRVSHA; NKLRVSHAD; KLRVSHADL;
LRVSHADLG; RVSHADLGK; VSHADLGKQ; SHADLGKQG; HADLGKQGV; ADLGKQGVN;
DLGKQGVND; LGKQGVNDD; GKQGVNDDD; KQGVNDDDA; QGVNDDDAK; GVNDDDAKK;
VNDDDAKKA; NDDDAKKAI; DDDAKKAIL; DDAKKAILK; DAKKAILKT; AKKAILKTN;
KKAILKTNA; KAILKTNAD; AILKTNADK; ILKTNADKT; LKTNADKTK; KTNADKTKG;
TNADKTKGA; NADKTKGAE; ADKTKGAEE; DKTKGAEEL; KTKGAEELG; TKGAEELGK;
KGAEELGKL; GAEELGKLF; AEELGKLFK; EELGKLFKS; ELGKLFKSV; LGKLFKSVE;
GKLFKSVEG; KLFKSVEGL; LFKSVEGLV; FKSVEGLVK; KSVEGLVKA; SVEGLVKAA;
VEGLVKAAQ; EGLVKAAQE; GLVKAAQEA; LVKAAQEAL; VKAAQEALT; KAAQEALTN;
AAQEALTNS; AQEALTNSV; QEALTNSVK; EALTNSVKE; ALTNSVKEL; LTNSVKELT;
TNSVKELTS; NSVKELTSP; SVKELTSPV; VKELTSPVV; KELTSPVVA; ELTSPVVAE;
LTSPVVAES; TSPVVAESP; SPVVAESPK; PVVAESPKK; VVAESPKKP

10 mers:

MKKNTLSAIL; KKNTLSAILM; KNTLSAILMT; NTLSAILMTL; TLSAILMTLF;
LSAILMTLFL; SAILMTLFLF; AILMTLFLFI; ILMTLFLFIS; LMTLFLFISC;
MTLFLFISCN; TLFLFISCNN; LFLFISCNNS; FLFISCNNSG; LFISCNNSGK;
FISCNNSGKG; ISCNNSGKGG; SCNNSGKGGD; CNNSGKGGDS; NNSGKGGDSA;
NSGKGGDSAS; SGKGGDSAST; GKGGDSASTN; KGGDSASTNP; GGDSASTNPA;
GDSASTNPAD; DSASTNPADE; SASTNPADES; ASTNPADESA; STNPADESAK;
TNPADESAKG; NPADESAKGP; PADESAKGPN; ADESAKGPNL; DESAKGPNLT;
ESAKGPNLTE; SAKGPNLTEI; AKGPNLTEIS; KGPNLTEISK; GPNLTEISKK;
PNLTEISKKI; NLTEISKKIT; LTEISKKITD; TEISKKITDS; EISKKITDSN;
ISKKITDSNA; SKKITDSNAF; KKITDSNAFV; KITDSNAFVL; ITDSNAFVLA;
TDSNAFVLAV; DSNAFVLAVK; SNAFVLAVKE; NAFVLAVKEV; AFVLAVKEVE;

FVLAVKEVET; VLAVKEVETL; LAVKEVETLV; AVKEVETLVS; VKEVETLVSS;
KEVETLVSSI; EVETLVSSID; VETLVSSIDE; ETLVSSIDEL; TLVSSIDELA;
LVSSIDELAN; VSSIDELANK; SSIDELANKA; SIDELANKAI; IDELANKAIG;
DELANKAIGK; ELANKAIGKK; LANKAIGKKI; ANKAIGKKIQ; NKAIGKKIQQ;
KAIGKKIQQN; AIGKKIQQNG; IGKKIQQNGL; GKKIQQNGLG; KKIQQNGLGA;
KIQQNGLGAE; IQQNGLGAEA; QQNGLGAEAN; QNGLGAEANR; NGLGAEANRN;
GLGAEANRNE; LGAEANRNES; GAEANRNESL; AEANRNESLL; EANRNESLLA;
ANRNESLLAG; NRNESLLAGV; RNESLLAGVH; NESLLAGVHE; ESLLAGVHEI;
SLLAGVHEIS; LLAGVHEIST; LAGVHEISTL; AGVHEISTLI; GVHEISTLIT;
VHEISTLITE; HEISTLITEK; EISTLITEKL; ISTLITEKLS; STLITEKLSK;
TLITEKLSKL; LITEKLSKLK; ITEKLSKLKN; TEKLSKLKNS; EKLSKLKNSG;
KLSKLKNSGE; LSKLKNSGEL; SKLKNSGELK; KLKNSGELKA; LKNSGELKAK;
KNSGELKAKI; NSGELKAKIE; SGELKAKIED; GELKAKIEDA; ELKAKIEDAK;
LKAKIEDAKK; KAKIEDAKKC; AKIEDAKKCS; KIEDAKKCSE; IEDAKKCSEE;
EDAKKCSEEF; DAKKCSEEFT; AKKCSEEFTN; KKCSEEFTNK; KCSEEFTNKL;
CSEEFTNKLR; SEEFTNKLRV; EEFTNKLRVS; EFTNKLRVSH; FTNKLRVSHA;
TNKLRVSHAD; NKLRVSHADL; KLRVSHADLG; LRVSHADLGK; RVSHADLGKQ;
VSHADLGKQG; SHADLGKQGV; HADLGKQGVN; ADLGKQGVND; DLGKQGVNDD;
LGKQGVNDDD; GKQGVNDDDA; KQGVNDDDAK; QGVNDDDAKK; GVNDDDAKKA;
VNDDDAKKAI; NDDDAKKAIL; DDDAKKAILK; DDAKKAILKT; DAKKAILKTN;
AKKAILKTNA; KKAILKTNAD; KAILKTNADK; AILKTNADKT; ILKTNADKTK;
LKTNADKTKG; KTNADKTKGA; TNADKTKGAE; NADKTKGAEE; ADKTKGAEEL;
DKTKGAEELG; KTKGAEELGK; TKGAEELGKL; KGAEELGKLF; GAEELGKLFK;
AEELGKLFKS; EELGKLFKSV; ELGKLFKSVE; LGKLFKSVEG; GKLFKSVEGL;
KLFKSVEGLV; LFKSVEGLVK; FKSVEGLVKA; KSVEGLVKAA; SVEGLVKAAQ;
VEGLVKAAQE; EGLVKAAQEA; GLVKAAQEAL; LVKAAQEALT; VKAAQEALTN;
KAAQEALTNS; AAQEALTNSV; AQEALTNSVK; QEALTNSVKE; EALTNSVKEL;
ALTNSVKELT; LTNSVKELTS; TNSVKELTSP; NSVKELTSPV; SVKELTSPVV;
VKELTSPVVA; KELTSPVVAE; ELTSPVVAES; LTSPVVAESP; TSPVVAESPK;
SPVVAESPKK; PVVAESPKKP

11 mers:

MKKNTLSAILM; KKNTLSAILMT; KNTLSAILMTL; NTLSAILMTLF; TLSAILMTLFL;
LSAILMTLFLF; SAILMTLFLFI; AILMTLFLFIS; ILMTLFLFISC; LMTLFLFISCN;
MTLFLFISCNN; TLFLFISCNNS; LFLFISCNNSG; FLFISCNNSGK; LFISCNNSGKG;
FISCNNSGKGG; ISCNNSGKGGD; SCNNSGKGGDS; CNNSGKGGDSA; NNSGKGGDSAS;
NSGKGGDSAST; SGKGGDSASTN; GKGGDSASTNP; KGGDSASTNPA; GGDSASTNPAD;
GDSASTNPADE; DSASTNPADES; SASTNPADESA; ASTNPADESAK; STNPADESAKG;
TNPADESAKGP; NPADESAKGPN; PADESAKGPNL; ADESAKGPNLT; DESAKGPNLTE;
ESAKGPNLTEI; SAKGPNLTEIS; AKGPNLTEISK; KGPNLTEISKK; GPNLTEISKKI;
PNLTEISKKIT; NLTEISKKITD; LTEISKKITDS; TEISKKITDSN; EISKKITDSNA;
ISKKITDSNAF; SKKITDSNAFV; KKITDSNAFVL; KITDSNAFVLA; ITDSNAFVLAV;
TDSNAFVLAVK; DSNAFVLAVKE; SNAFVLAVKEV; NAFVLAVKEVE; AFVLAVKEVET;
FVLAVKEVETL; VLAVKEVETLV; LAVKEVETLVS; AVKEVETLVSS; VKEVETLVSSI;
KEVETLVSSID; EVETLVSSIDE; VETLVSSIDEL; ETLVSSIDELA; TLVSSIDELAN;
LVSSIDELANK; VSSIDELANKA; SSIDELANKAI; SIDELANKAIG; IDELANKAIGK;
DELANKAIGKK; ELANKAIGKKI; LANKAIGKKIQ; ANKAIGKKIQQ; NKAIGKKIQQN;
KAIGKKIQQNG; AIGKKIQQNGL; IGKKIQQNGLG; GKKIQQNGLGA; KKIQQNGLGAE;
KIQQNGLGAEA; IQQNGLGAEAN; QQNGLGAEANR; QNGLGAEANRN; NGLGAEANRNE;
GLGAEANRNES; LGAEANRNESL; GAEANRNESLL; AEANRNESLLA; EANRNESLLAG;
ANRNESLLAGV; NRNESLLAGVH; RNESLLAGVHE; NESLLAGVHEI; ESLLAGVHEIS;
SLLAGVHEIST; LLAGVHEISTL; LAGVHEISTLI; AGVHEISTLIT; GVHEISTLITE;
VHEISTLITEK; HEISTLITEKL; EISTLITEKLS; ISTLITEKLSK; STLITEKLSKL;
TLITEKLSKLK; LITEKLSKLKN; ITEKLSKLKNS; TEKLSKLKNSG; EKLSKLKNSGE;
KLSKLKNSGEL; LSKLKNSGELK; SKLKNSGELKA; KLKNSGELKAK; LKNSGELKAKI;
KNSGELKAKIE; NSGELKAKIED; SGELKAKIEDA; GELKAKIEDAK; ELKAKIEDAKK;
LKAKIEDAKKC; KAKIEDAKKCS; AKIEDAKKCSE; KIEDAKKCSEE; IEDAKKCSEEF;
EDAKKCSEEFT; DAKKCSEEFTN; AKKCSEEFTNK; KKCSEEFTNKL; KCSEEFTNKLR;

CSEEFTNKLRV; SEEFTNKLRVS; EEFTNKLRVSH; EFTNKLRVSHA; FTNKLRVSHAD; TNKLRVSHADL; NKLRVSHADLG; KLRVSHADLGK; LRVSHADLGKQ; RVSHADLGKQG; VSHADLGKQGV; SHADLGKQGVN; HADLGKQGVND; ADLGKQGVNDD; DLGKQGVNDDD; LGKQGVNDDDA; GKQGVNDDDAK; KQGVNDDDAKK; QGVNDDDAKKA; GVNDDDAKKAI; VNDDDAKKAIL; NDDDAKKAILK; DDDAKKAILKT; DDAKKAILKTN; DAKKAILKTNA; AKKAILKTNAD; KKAILKTNADK; KAILKTNADKT; AILKTNADKTK; ILKTNADKTKG; LKTNADKTKGA; KTNADKTKGAE; TNADKTKGAEE; NADKTKGAEEL; ADKTKGAEELG; DKTKGAEELGK; KTKGAEELGKL; TKGAEELGKLF; KGAEELGKLFK; GAEELGKLFKS; AEELGKLFKSV; EELGKLFKSVE; ELGKLFKSVEG; LGKLFKSVEGL; GKLFKSVEGLV; KLFKSVEGLVK; LFKSVEGLVKA; FKSVEGLVKAA; KSVEGLVKAAQ; SVEGLVKAAQE; VEGLVKAAQEA; EGLVKAAQEAL; GLVKAAQEALT; LVKAAQEALTN; VKAAQEALTNS; KAAQEALTNSV; AAQEALTNSVK; AQEALTNSVKE; QEALTNSVKEL; EALTNSVKELT; ALTNSVKELTS; LTNSVKELTSP; TNSVKELTSPV; NSVKELTSPVV; SVKELTSPVVA; VKELTSPVVAE; KELTSPVVAES; ELTSPVVAESP; LTSPVVAESPK; TSPVVAESPKK; SPVVAESPKKP;

13 mers:

MKKNTLSAILMTL; KKNTLSAILMTLF; KNTLSAILMTLFL; NTLSAILMTLFLF; TLSAILMTLFLFI; LSAILMTLFLFIS; SAILMTLFLFISC; AILMTLFLFISCN; ILMTLFLFISCNN; LMTLFLFISCNNS; MTLFLFISCNNSG; TLFLFISCNNSGK; LFLFISCNNSGKG; FLFISCNNSGKGG; LFISCNNSGKGGD; FISCNNSGKGGDS; ISCNNSGKGGDSA; SCNNSGKGGDSAS; CNNSGKGGDSAST; NNSGKGGDSASTN; NSGKGGDSASTNP; SGKGGDSASTNPA; GKGGDSASTNPAD; KGGDSASTNPADE; GGDSASTNPADES; GDSASTNPADESA; DSASTNPADESAK; SASTNPADESAKG; ASTNPADESAKGP; STNPADESAKGPN; TNPADESAKGPNL; NPADESAKGPNLT; PADESAKGPNLTE; ADESAKGPNLTEI; DESAKGPNLTEIS; ESAKGPNLTEISK; SAKGPNLTEISKK; AKGPNLTEISKKI; KGPNLTEISKKIT; GPNLTEISKKITD; PNLTEISKKITDS; NLTEISKKITDSN; LTEISKKITDSNA; TEISKKITDSNAF; EISKKITDSNAFV; ISKKITDSNAFVL; SKKITDSNAFVLA; KKITDSNAFVLAV; KITDSNAFVLAVK; ITDSNAFVLAVKE; TDSNAFVLAVKEV; DSNAFVLAVKEVE; SNAFVLAVKEVET; NAFVLAVKEVETL; AFVLAVKEVETLV; FVLAVKEVETLVS; VLAVKEVETLVSS; LAVKEVETLVSSI; AVKEVETLVSSID; VKEVETLVSSIDE; KEVETLVSSIDEL; EVETLVSSIDELA; VETLVSSIDELAN; ETLVSSIDELANK; TLVSSIDELANKA; LVSSIDELANKAI; VSSIDELANKAIG; SSIDELANKAIGK; SIDELANKAIGKK; IDELANKAIGKKI; DELANKAIGKKIQ; ELANKAIGKKIQQ; LANKAIGKKIQQN; ANKAIGKKIQQNG; NKAIGKKIQQNGL; KAIGKKIQQNGLG; AIGKKIQQNGLGA; IGKKIQQNGLGAE; GKKIQQNGLGAEA; KKIQQNGLGAEAN; KIQQNGLGAEANR; IQQNGLGAEANRN; QQNGLGAEANRNE; QNGLGAEANRNES; NGLGAEANRNESL; GLGAEANRNESLL; LGAEANRNESLLA; GAEANRNESLLAG; AEANRNESLLAGV; EANRNESLLAGVH; ANRNESLLAGVHE; NRNESLLAGVHEI; RNESLLAGVHEIS; NESLLAGVHEIST; ESLLAGVHEISTL; SLLAGVHEISTLI; LLAGVHEISTLIT; LAGVHEISTLITE; AGVHEISTLITEK; GVHEISTLITEKL; VHEISTLITEKLS; HEISTLITEKLSK; EISTLITEKLSKL; ISTLITEKLSKLK; STLITEKLSKLKN; TLITEKLSKLKNS; LITEKLSKLKNSG; ITEKLSKLKNSGE; TEKLSKLKNSGEL; EKLSKLKNSGELK; KLSKLKNSGELKA; LSKLKNSGELKAK; SKLKNSGELKAKI; KLKNSGELKAKIE; LKNSGELKAKIED; KNSGELKAKIEDA; NSGELKAKIEDAK; SGELKAKIEDAKK; GELKAKIEDAKKC; ELKAKIEDAKKCS; LKAKIEDAKKCSE; KAKIEDAKKCSEE; AKIEDAKKCSEEF; KIEDAKKCSEEFT; IEDAKKCSEEFTN; EDAKKCSEEFTNK; DAKKCSEEFTNKL; AKKCSEEFTNKLR; KKCSEEFTNKLRV; KCSEEFTNKLRVS; CSEEFTNKLRVSH; SEEFTNKLRVSHA; EEFTNKLRVSHAD; EFTNKLRVSHADL; FTNKLRVSHADLG; TNKLRVSHADLGK; NKLRVSHADLGKQ; KLRVSHADLGKQG; LRVSHADLGKQGV; RVSHADLGKQGVN; VSHADLGKQGVND; SHADLGKQGVNDD; HADLGKQGVNDDD; ADLGKQGVNDDDA; DLGKQGVNDDDAK; LGKQGVNDDDAKK; GKQGVNDDDAKKA; KQGVNDDDAKKAI; QGVNDDDAKKAIL; GVNDDDAKKAILK; VNDDDAKKAILKT; NDDDAKKAILKTN; DDDAKKAILKTNA; DDAKKAILKTNAD; DAKKAILKTNADK; AKKAILKTNADKT; KKAILKTNADKTK; KAILKTNADKTKG; AILKTNADKTKGA; ILKTNADKTKGAE; LKTNADKTKGAEE; KTNADKTKGAEEL; TNADKTKGAEELG; NADKTKGAEELGK;

ADKTKGAEELGKL; DKTKGAEELGKLF; KTKGAEELGKLFK; TKGAEELGKLFKS;
KGAEELGKLFKSV; GAEELGKLFKSVE; AEELGKLFKSVEG; EELGKLFKSVEGL;
ELGKLFKSVEGLV; LGKLFKSVEGLVK; GKLFKSVEGLVKA; KLFKSVEGLVKAA;
LFKSVEGLVKAAQ; FKSVEGLVKAAQE; KSVEGLVKAAQEA; SVEGLVKAAQEAL;
VEGLVKAAQEALT; EGLVKAAQEALTN; GLVKAAQEALTNS; LVKAAQEALTNSV;
VKAAQEALTNSVK; KAAQEALTNSVKE; AAQEALTNSVKEL; AQEALTNSVKELT;
QEALTNSVKELTS; EALTNSVKELTSP; ALTNSVKELTSPV; LTNSVKELTSPVV;
TNSVKELTSPVVA; NSVKELTSPVVAE; SVKELTSPVVAES; VKELTSPVVAESP;
KELTSPVVAESPK; ELTSPVVAESPKK; LTSPVVAESPKKP

14 mers:

MKKNTLSAILMTLF; KKNTLSAILMTLFL; KNTLSAILMTLFLF; NTLSAILMTLFLFI;
TLSAILMTLFLFIS; LSAILMTLFLFISC; SAILMTLFLFISCN; AILMTLFLFISCNN;
ILMTLFLFISCNNS; LMTLFLFISCNNSG; MTLFLFISCNNSGK; TLFLFISCNNSGKG;
LFLFISCNNSGKGG; FLFISCNNSGKGGD; LFISCNNSGKGGDS; FISCNNSGKGGDSA;
ISCNNSGKGGDSAS; SCNNSGKGGDSAST; CNNSGKGGDSASTN; NNSGKGGDSASTNP;
NSGKGGDSASTNPA; SGKGGDSASTNPAD; GKGGDSASTNPADE; KGGDSASTNPADES;
GGDSASTNPADESA; GDSASTNPADESAK; DSASTNPADESAKG; SASTNPADESAKGP;
ASTNPADESAKGPN; STNPADESAKGPNL; TNPADESAKGPNLT; NPADESAKGPNLTE;
PADESAKGPNLTEI; ADESAKGPNLTEIS; DESAKGPNLTEISK; ESAKGPNLTEISKK;
SAKGPNLTEISKKI; AKGPNLTEISKKIT; KGPNLTEISKKITD; GPNLTEISKKITDS;
PNLTEISKKITDSN; NLTEISKKITDSNA; LTEISKKITDSNAF; TEISKKITDSNAFV;
EISKKITDSNAFVL; ISKKITDSNAFVLA; SKKITDSNAFVLAV; KKITDSNAFVLAVK;
KITDSNAFVLAVKE; ITDSNAFVLAVKEV; TDSNAFVLAVKEVE; DSNAFVLAVKEVET;
SNAFVLAVKEVETL; NAFVLAVKEVETLV; AFVLAVKEVETLVS; FVLAVKEVETLVSS;
VLAVKEVETLVSSI; LAVKEVETLVSSID; AVKEVETLVSSIDE; VKEVETLVSSIDEL;
KEVETLVSSIDELA; EVETLVSSIDELAN; VETLVSSIDELANK; ETLVSSIDELANKA;
TLVSSIDELANKAI; LVSSIDELANKAIG; VSSIDELANKAIGK; SSIDELANKAIGKK;
SIDELANKAIGKKI; IDELANKAIGKKIQ; DELANKAIGKKIQQ; ELANKAIGKKIQQN;
LANKAIGKKIQQNG; ANKAIGKKIQQNGL; NKAIGKKIQQNGLG; KAIGKKIQQNGLGA;
AIGKKIQQNGLGAE; IGKKIQQNGLGAEA; GKKIQQNGLGAEAN; KKIQQNGLGAEANR;
KIQQNGLGAEANRN; IQQNGLGAEANRNE; QQNGLGAEANRNES; QNGLGAEANRNESL;
NGLGAEANRNESLL; GLGAEANRNESLLA; LGAEANRNESLLAG; GAEANRNESLLAGV;
AEANRNESLLAGVH; EANRNESLLAGVHE; ANRNESLLAGVHEI; NRNESLLAGVHEIS;
RNESLLAGVHEIST; NESLLAGVHEISTL; ESLLAGVHEISTLI; SLLAGVHEISTLIT;
LLAGVHEISTLITE; LAGVHEISTLITEK; AGVHEISTLITEKL; GVHEISTLITEKLS;
VHEISTLITEKLSK; HEISTLITEKLSKL; EISTLITEKLSKLK; ISTLITEKLSKLKN;
STLITEKLSKLKNS; TLITEKLSKLKNSG; LITEKLSKLKNSGE; ITEKLSKLKNSGEL;
TEKLSKLKNSGELK; EKLSKLKNSGELKA; KLSKLKNSGELKAK; LSKLKNSGELKAKI;
SKLKNSGELKAKIE; KLKNSGELKAKIED; LKNSGELKAKIEDA; KNSGELKAKIEDAK;
NSGELKAKIEDAKK; SGELKAKIEDAKKC; GELKAKIEDAKKCS; ELKAKIEDAKKCSE;
LKAKIEDAKKCSEE; KAKIEDAKKCSEEF; AKIEDAKKCSEEFT; KIEDAKKCSEEFTN;
IEDAKKCSEEFTNK; EDAKKCSEEFTNKL; DAKKCSEEFTNKLR; AKKCSEEFTNKLRV;
KKCSEEFTNKLRVS; KCSEEFTNKLRVSH; CSEEFTNKLRVSHA; SEEFTNKLRVSHAD;
EEFTNKLRVSHADL; EFTNKLRVSHADLG; FTNKLRVSHADLGK; TNKLRVSHADLGKQ;
NKLRVSHADLGKQG; KLRVSHADLGKQGV; LRVSHADLGKQGVN; RVSHADLGKQGVND;
VSHADLGKQGVNDD; SHADLGKQGVNDDD; HADLGKQGVNDDDA; ADLGKQGVNDDDAK;
DLGKQGVNDDDAKK; LGKQGVNDDDAKKA; GKQGVNDDDAKKAI; KQGVNDDDAKKAIL;
QGVNDDDAKKAILK; GVNDDDAKKAILKT; VNDDDAKKAILKTN; NDDDAKKAILKTNA;
DDDAKKAILKTNAD; DDAKKAILKTNADK; DAKKAILKTNADKT; AKKAILKTNADKTK;
KKAILKTNADKTKG; KAILKTNADKTKGA; AILKTNADKTKGAE; ILKTNADKTKGAEE;
LKTNADKTKGAEEL; KTNADKTKGAEELG; TNADKTKGAEELGK; NADKTKGAEELGKL;
ADKTKGAEELGKLF; DKTKGAEELGKLFK; KTKGAEELGKLFKS; TKGAEELGKLFKSV;
KGAEELGKLFKSVE; GAEELGKLFKSVEG; AEELGKLFKSVEGL; EELGKLFKSVEGLV;
ELGKLFKSVEGLVK; LGKLFKSVEGLVKA; GKLFKSVEGLVKAA; KLFKSVEGLVKAAQ;
LFKSVEGLVKAAQE; FKSVEGLVKAAQEA; KSVEGLVKAAQEAL; SVEGLVKAAQEALT;
VEGLVKAAQEALTN; EGLVKAAQEALTNS; GLVKAAQEALTNSV; LVKAAQEALTNSVK;
VKAAQEALTNSVKE; KAAQEALTNSVKEL; AAQEALTNSVKELT; AQEALTNSVKELTS;
QEALTNSVKELTSP; EALTNSVKELTSPV; ALTNSVKELTSPVV; LTNSVKELTSPVVA;

TNSVKELTSPVVAE; NSVKELTSPVVAES; SVKELTSPVVAESP; VKELTSPVVAESPK; KELTSPVVAESPKK; ELTSPVVAESPKKP

15 mers:

MKKNTLSAILMTLFL; KKNTLSAILMTLFLF; KNTLSAILMTLFLFI; NTLSAILMTLFLFIS; TLSAILMTLFLFISC; LSAILMTLFLFISCN; SAILMTLFLFISCNN; AILMTLFLFISCNNS; ILMTLFLFISCNNSG; LMTLFLFISCNNSGK; MTLFLFISCNNSGKG; TLFLFISCNNSGKGG; LFLFISCNNSGKGGD; FLFISCNNSGKGGDS; LFISCNNSGKGGDSA; FISCNNSGKGGDSAS; ISCNNSGKGGDSAST; SCNNSGKGGDSASTN; CNNSGKGGDSASTNP; NNSGKGGDSASTNPA; NSGKGGDSASTNPAD; SGKGGDSASTNPADE; GKGGDSASTNPADES; KGGDSASTNPADESA; GGDSASTNPADESAK; GDSASTNPADESAKG; DSASTNPADESAKGP; SASTNPADESAKGPN; ASTNPADESAKGPNL; STNPADESAKGPNLT; TNPADESAKGPNLTE; NPADESAKGPNLTEI; PADESAKGPNLTEIS; ADESAKGPNLTEISK; DESAKGPNLTEISKK; ESAKGPNLTEISKKI; SAKGPNLTEISKKIT; AKGPNLTEISKKITD; KGPNLTEISKKITDS; GPNLTEISKKITDSN; PNLTEISKKITDSNA; NLTEISKKITDSNAF; LTEISKKITDSNAFV; TEISKKITDSNAFVL; EISKKITDSNAFVLA; ISKKITDSNAFVLAV; SKKITDSNAFVLAVK; KKITDSNAFVLAVKE; KITDSNAFVLAVKEV; ITDSNAFVLAVKEVE; TDSNAFVLAVKEVET; DSNAFVLAVKEVETL; SNAFVLAVKEVETLV; NAFVLAVKEVETLVS; AFVLAVKEVETLVSS; FVLAVKEVETLVSSI; VLAVKEVETLVSSID; LAVKEVETLVSSIDE; AVKEVETLVSSIDEL; VKEVETLVSSIDELA; KEVETLVSSIDELAN; EVETLVSSIDELANK; VETLVSSIDELANKA; ETLVSSIDELANKAI; TLVSSIDELANKAIG; LVSSIDELANKAIGK; VSSIDELANKAIGKK; SSIDELANKAIGKKI; SIDELANKAIGKKIQ; IDELANKAIGKKIQQ; DELANKAIGKKIQQN; ELANKAIGKKIQQNG; LANKAIGKKIQQNGL; ANKAIGKKIQQNGLG; NKAIGKKIQQNGLGA; KAIGKKIQQNGLGAE; AIGKKIQQNGLGAEA; IGKKIQQNGLGAEAN; GKKIQQNGLGAEANR; KKIQQNGLGAEANRN; KIQQNGLGAEANRNE; IQQNGLGAEANRNES; QQNGLGAEANRNESL; QNGLGAEANRNESLL; NGLGAEANRNESLLA; GLGAEANRNESLLAG; LGAEANRNESLLAGV; GAEANRNESLLAGVH; AEANRNESLLAGVHE; EANRNESLLAGVHEI; ANRNESLLAGVHEIS; NRNESLLAGVHEIST; RNESLLAGVHEISTL; NESLLAGVHEISTLI; ESLLAGVHEISTLIT; SLLAGVHEISTLITE; LLAGVHEISTLITEK; LAGVHEISTLITEKL; AGVHEISTLITEKLS; GVHEISTLITEKLSK; VHEISTLITEKLSKL; HEISTLITEKLSKLK; EISTLITEKLSKLKN; ISTLITEKLSKLKNS; STLITEKLSKLKNSG; TLITEKLSKLKNSGE; LITEKLSKLKNSGEL; ITEKLSKLKNSGELK; TEKLSKLKNSGELKA; EKLSKLKNSGELKAK; KLSKLKNSGELKAKI; LSKLKNSGELKAKIE; SKLKNSGELKAKIED; KLKNSGELKAKIEDA; LKNSGELKAKIEDAK; KNSGELKAKIEDAKK; NSGELKAKIEDAKKC; SGELKAKIEDAKKCS; GELKAKIEDAKKCSE; ELKAKIEDAKKCSEE; LKAKIEDAKKCSEEF; KAKIEDAKKCSEEFT; AKIEDAKKCSEEFTN; KIEDAKKCSEEFTNK; IEDAKKCSEEFTNKL; EDAKKCSEEFTNKLR; DAKKCSEEFTNKLRV; AKKCSEEFTNKLRVS; KKCSEEFTNKLRVSH; KCSEEFTNKLRVSHA; CSEEFTNKLRVSHAD; SEEFTNKLRVSHADL; EEFTNKLRVSHADLG; EFTNKLRVSHADLGK; FTNKLRVSHADLGKQ; TNKLRVSHADLGKQG; NKLRVSHADLGKQGV; KLRVSHADLGKQGVN; LRVSHADLGKQGVND; RVSHADLGKQGVNDD; VSHADLGKQGVNDDD; SHADLGKQGVNDDDA; HADLGKQGVNDDDAK; ADLGKQGVNDDDAKK; DLGKQGVNDDDAKKA; LGKQGVNDDDAKKAI; GKQGVNDDDAKKAIL; KQGVNDDDAKKAILK; QGVNDDDAKKAILKT; GVNDDDAKKAILKTN; VNDDDAKKAILKTNA; NDDDAKKAILKTNAD; DDDAKKAILKTNADK; DDAKKAILKTNADKT; DAKKAILKTNADKTK; AKKAILKTNADKTKG; KKAILKTNADKTKGA; KAILKTNADKTKGAE; AILKTNADKTKGAEE; ILKTNADKTKGAEEL; LKTNADKTKGAEELG; KTNADKTKGAEELGK; TNADKTKGAEELGKL; NADKTKGAEELGKLF; ADKTKGAEELGKLFK; DKTKGAEELGKLFKS; KTKGAEELGKLFKSV; TKGAEELGKLFKSVE; KGAEELGKLFKSVEG; GAEELGKLFKSVEGL; AEELGKLFKSVEGLV; EELGKLFKSVEGLVK; ELGKLFKSVEGLVKA; LGKLFKSVEGLVKAA; GKLFKSVEGLVKAAQ; KLFKSVEGLVKAAQE; LFKSVEGLVKAAQEA; FKSVEGLVKAAQEAL; KSVEGLVKAAQEALT; SVEGLVKAAQEALTN; VEGLVKAAQEALTNS; EGLVKAAQEALTNSV; GLVKAAQEALTNSVK; LVKAAQEALTNSVKE; VKAAQEALTNSVKEL; KAAQEALTNSVKELT; AAQEALTNSVKELTS; AQEALTNSVKELTSP; QEALTNSVKELTSPV; EALTNSVKELTSPVV; ALTNSVKELTSPVVA; LTNSVKELTSPVVAE; TNSVKELTSPVVAES; NSVKELTSPVVAESP; SVKELTSPVVAESPK; VKELTSPVVAESPKK; KELTSPVVAESPKKP

16 mers:

MKKNTLSAILMTLFLF; KKNTLSAILMTLFLFI; KNTLSAILMTLFLFIS; NTLSAILMTLFLFISC; TLSAILMTLFLFISCN; LSAILMTLFLFISCNN; SAILMTLFLFISCNNS; AILMTLFLFISCNNSG; ILMTLFLFISCNNSGK;

LMTLFLFISCNNSGKG; MTLFLFISCNNSGKGG; TLFLFISCNNSGKGGD;
LFLFISCNNSGKGGDS; FLFISCNNSGKGGDSA; LFISCNNSGKGGDSAS;
FISCNNSGKGGDSAST; ISCNNSGKGGDSASTN; SCNNSGKGGDSASTNP;
CNNSGKGGDSASTNPA; NNSGKGGDSASTNPAD; NSGKGGDSASTNPADE;
SGKGGDSASTNPADES; GKGGDSASTNPADESA; KGGDSASTNPADESAK;
GGDSASTNPADESAKG; GDSASTNPADESAKGP; DSASTNPADESAKGPN;
SASTNPADESAKGPNL; ASTNPADESAKGPNLT; STNPADESAKGPNLTE;
TNPADESAKGPNLTEI; NPADESAKGPNLTEIS; PADESAKGPNLTEISK;
ADESAKGPNLTEISKK; DESAKGPNLTEISKKI; ESAKGPNLTEISKKIT;
SAKGPNLTEISKKITD; AKGPNLTEISKKITDS; KGPNLTEISKKITDSN;
GPNLTEISKKITDSNA; PNLTEISKKITDSNAF; NLTEISKKITDSNAFV;
LTEISKKITDSNAFVL; TEISKKITDSNAFVLA; EISKKITDSNAFVLAV;
ISKKITDSNAFVLAVK; SKKITDSNAFVLAVKE; KKITDSNAFVLAVKEV;
KITDSNAFVLAVKEVE; ITDSNAFVLAVKEVET; TDSNAFVLAVKEVETL;
DSNAFVLAVKEVETLV; SNAFVLAVKEVETLVS; NAFVLAVKEVETLVSS;
AFVLAVKEVETLVSSI; FVLAVKEVETLVSSID; VLAVKEVETLVSSIDE;
LAVKEVETLVSSIDEL; AVKEVETLVSSIDELA; VKEVETLVSSIDELAN;
KEVETLVSSIDELANK; EVETLVSSIDELANKA; VETLVSSIDELANKAI;
ETLVSSIDELANKAIG; TLVSSIDELANKAIGK; LVSSIDELANKAIGKK;
VSSIDELANKAIGKKI; SSIDELANKAIGKKIQ; SIDELANKAIGKKIQQ;
IDELANKAIGKKIQQN; DELANKAIGKKIQQNG; ELANKAIGKKIQQNGL;
LANKAIGKKIQQNGLG; ANKAIGKKIQQNGLGA; NKAIGKKIQQNGLGAE;
KAIGKKIQQNGLGAEA; AIGKKIQQNGLGAEAN; IGKKIQQNGLGAEANR;
GKKIQQNGLGAEANRN; KKIQQNGLGAEANRNE; KIQQNGLGAEANRNES;
IQQNGLGAEANRNESL; QQNGLGAEANRNESLL; QNGLGAEANRNESLLA;
NGLGAEANRNESLLAG; GLGAEANRNESLLAGV; LGAEANRNESLLAGVH;
GAEANRNESLLAGVHE; AEANRNESLLAGVHEI; EANRNESLLAGVHEIS;
ANRNESLLAGVHEIST; NRNESLLAGVHEISTL; RNESLLAGVHEISTLI;
NESLLAGVHEISTLIT; ESLLAGVHEISTLITE; SLLAGVHEISTLITEK;
LLAGVHEISTLITEKL; LAGVHEISTLITEKLS; AGVHEISTLITEKLSK;
GVHEISTLITEKLSKL; VHEISTLITEKLSKLK; HEISTLITEKLSKLKN;
EISTLITEKLSKLKNS; ISTLITEKLSKLKNSG; STLITEKLSKLKNSGE;
TLITEKLSKLKNSGEL; LITEKLSKLKNSGELK; ITEKLSKLKNSGELKA;
TEKLSKLKNSGELKAK; EKLSKLKNSGELKAKI; KLSKLKNSGELKAKIE;
LSKLKNSGELKAKIED; SKLKNSGELKAKIEDA; KLKNSGELKAKIEDAK;
LKNSGELKAKIEDAKK; KNSGELKAKIEDAKKC; NSGELKAKIEDAKKCS;
SGELKAKIEDAKKCSE; GELKAKIEDAKKCSEE; ELKAKIEDAKKCSEEF;
LKAKIEDAKKCSEEFT; KAKIEDAKKCSEEFTN; AKIEDAKKCSEEFTNK;
KIEDAKKCSEEFTNKL; IEDAKKCSEEFTNKLR; EDAKKCSEEFTNKLRV;
DAKKCSEEFTNKLRVS; AKKCSEEFTNKLRVSH; KKCSEEFTNKLRVSHA;
KCSEEFTNKLRVSHAD; CSEEFTNKLRVSHADL; SEEFTNKLRVSHADLG;
EEFTNKLRVSHADLGK; EFTNKLRVSHADLGKQ; FTNKLRVSHADLGKQG;
TNKLRVSHADLGKQGV; NKLRVSHADLGKQGVN; KLRVSHADLGKQGVND;
LRVSHADLGKQGVNDD; RVSHADLGKQGVNDDD; VSHADLGKQGVNDDDA;
SHADLGKQGVNDDDAK; HADLGKQGVNDDDAKK; ADLGKQGVNDDDAKKA;
DLGKQGVNDDDAKKAI; LGKQGVNDDDAKKAIL; GKQGVNDDDAKKAILK;
KQGVNDDDAKKAILKT; QGVNDDDAKKAILKTN; GVNDDDAKKAILKTNA;
VNDDDAKKAILKTNAD; NDDDAKKAILKTNADK; DDDAKKAILKTNADKT;
DDAKKAILKTNADKTK; DAKKAILKTNADKTKG; AKKAILKTNADKTKGA;
KKAILKTNADKTKGAE; KAILKTNADKTKGAEE; AILKTNADKTKGAEEL;
ILKTNADKTKGAEELG; LKTNADKTKGAEELGK; KTNADKTKGAEELGKL;
TNADKTKGAEELGKLF; NADKTKGAEELGKLFK; ADKTKGAEELGKLFKS;
DKTKGAEELGKLFKSV; KTKGAEELGKLFKSVE; TKGAEELGKLFKSVEG;
KGAEELGKLFKSVEGL; GAEELGKLFKSVEGLV; AEELGKLFKSVEGLVK;
EELGKLFKSVEGLVKA; ELGKLFKSVEGLVKAA; LGKLFKSVEGLVKAAQ;
GKLFKSVEGLVKAAQE; KLFKSVEGLVKAAQEA; LFKSVEGLVKAAQEAL;
FKSVEGLVKAAQEALT; KSVEGLVKAAQEALTN; SVEGLVKAAQEALTNS;
VEGLVKAAQEALTNSV; EGLVKAAQEALTNSVK; GLVKAAQEALTNSVKE;
LVKAAQEALTNSVKEL; VKAAQEALTNSVKELT; KAAQEALTNSVKELTS;

AAQEALTNSVKELTSP; AQEALTNSVKELTSPV; QEALTNSVKELTSPVV; EALTNSVKELTSPVVA; ALTNSVKELTSPVVAE; LTNSVKELTSPVVAES; TNSVKELTSPVVAESP; NSVKELTSPVVAESPK; SVKELTSPVVAESPKK; VKELTSPVVAESPKKP

Preferred Borrelia burgdorferi fragments of Osp A capable of interacting with one or more MHC molecules are listed in Table B.

Table B: Prediction of Borrelia burgdorferi OspA protein specific MHC class 1, 8- , 9- ,10- , 11-mer peptide binders for 24 MHC class 1 alleles (see figure 10) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

CAA44492.1| Outer surface protein A [Borrelia burgdorferi] Seq9	HLA-A0101	
	HLA-A0201	YLLGIGLIL FTLEGTLAA KTSTLTISV FTKEDTITV ALIACKQNV LLGIGLILA SLEATVDKL ILKSGEITV KVTEGTVVL STLDEKNSV TLVSKKVTL GIGLILALI YLLGIGLILA TLDEKNSVSV ALDDSDTTQA LLGIGLILAL NILKSGEITV TLAADGKTTL VLKDFTLEGT YSLEATVDKL YLLGIGLILAL LVFTKEDTITV LLGIGLILALI ILALIACKQNV STLDEKNSVSV ALDDSDTTQAT VLKDFTLEGTL SLEATVDKLEL ILKSGEITVAL ALIACKQNVST TTLKVTEGTVV LAADGKTTLKV LIACKQNVSTL
	HLA-A0301	VVLSKNILK KTKNLVFTK LVSKKVTLK LILALIACK LTISVNSQK KAVEITTLK AADGKTTLK ISVNSQKTK

		RANGTRLEY SQTKFEIFK KSDGSGKAK TQATKKTGK MTELVSKEK TLVSKKVTLK TLTISVNSQK TVVLSKNILK GLILALIACK TLKELKNALK LSQTKFEIFK LAADGKTTLK VTEGTVVLSK KLELKGTSDK TTQATKKTGK GMTELVSKEK KYSLEATVDK KQNVSTLDEK TIADDLSQTK TISVNSQKTK KEDAKTLVSK GSGKAKEVLK KTIVRANGTR GTLEGEKTDK GKAVEITTLK GTRLEYTDIK VSKKVTLKDK IKSDGSGKAK TLAADGKTTLK STLTISVNSQK KTLVSKKVTLK KVTEGTVVLSK TTLKELKNALK LTISVNSQKTK GTVVLSKNILK FTKEDTITVQK IVRANGTRLEY TLKDKSSTEEK LVSKKVTLKDK KFNEKGETSEK LTIADDLSQTK SQKTKNLVFTK KSSTEEKFNEK ATKKTGKWDSK
	HLA- A1101	VVLSKNILK KTKNLVFTK SQTKFEIFK LTISVNSQK ATVDKLELK LILALIACK STEEKFNEK KAVEITTLK LVSKKVTLK MTELVSKEK AADGKTTLK SAGTNLEGK YSLEATVDK GSGTLEGEK TQATKKTGK

		RANGTRLEY IADDLSQTK ISVNSQKTK KSDGSGKAK GGMTELVSK TEGTVVLSK EITTLKELK TIVRANGTR TVVLSKNILK TTQATKKTGK TIADDLSQTK VTEGTVVLSK LSQTKFEIFK SSTEEKFNEK GLILALIACK KQNVSTLDEK TLTISVNSQK TLVSKKVTLK TISVNSQKTK LAADGKTTLK GMTELVSKEK TLKELKNALK KTIVRANGTR GSGKAKEVLK GTLEGEKTDK VSKKVTLKDK GTRLEYTDIK KLELKGTSDK DSAGTNLEGK STLTISVNSQK TTLKELKNALK KVTEGTVVLSK KTLVSKKVTLK GTVVLSKNILK LTIADDLSQTK TLAADGKTTLK AVEITTLKELK LTISVNSQKTK SQKTKNLVFTK KSSTEEKFNEK ATKKTGKWDSK TLKDKSSTEEK FTKEDTITVQK TLEGTLAADGK LVSKKVTLKDK MTELVSKEKDK DLSQTKFEIFK YTDIKSDGSGK LVSKEKDKDGK KFNEKGETSEK IGLILALIACK
	HLA- A2402	KYLLGIGLI KWDSKTSTL KYDSAGTNL KYLLGIGLIL KWDSKTSTLTI KYSLEATVDKL
	HLA- A2902	IVRANGTRLEY TIADDLSQTKF

	HLA-A6801	LTISVNSQK ETSEKTIVR MTELVSKEK EITTLKELK TIVRANGTR KAVEITTLK DAKTLVSKK KTKNLVFTK STEEKFNEK ATVDKLELK LVSKKVTLK SQTKFEIFK YSLEATVDK EGTLAADGK ISVNSQKTK LILALIACK DIKSDGSGK VVLSKNILK EDAKTLVSK DSDTTQATK SAGTNLEGK TVVLSKNILK TLTISVNSQK EATVDKLELK TIADDLSQTK DSAGTNLEGK TTQATKKTGK LAADGKTTLK KTIVRANGTR TISVNSQKTK TLVSKKVTLK SSTEEKFNEK TLKELKNALK LSQTKFEIFK VTEGTVVLSK EDAKTLVSKK DSDTTQATKK GLILALIACK
	HLA-B0702	IVRANGTRL KVTEGTVVL LAADGKTTL LPGGMTELV TVVLSKNIL KAVEITTLKEL
	HLA-B0801	TLKELKNAL ILKSGEITVAL YLLGIGLILAL TLKVTEGTVVL
	HLA-B1501	SQKTKNLVF RANGTRLEY YLLGIGLIL KVTEGTVVL TLKELKNAL KAKEVLKDF IVRANGTRL LGIGLILAL TLAADGKTTL IVRANGTRLEY YLLGIGLILAL

		VQKYDSAGTNL ILKSGEITVAL VSKEKDKDGKY VLKDFTLEGTL TLKVTEGTVVL VNSQKTKNLVF
	HLA-B2705	KKYLLGIGL VRANGTRLEY GKWDSKTSTL KKYLLGIGLIL
	HLA-B3501	LAADGKTTL RANGTRLEY FTLEGTLAA TVVLSKNIL VALDDSDTT YLLGIGLIL LPGGMTELV IADDLSQTKF LPGGMTELVS LKVTEGTVVL YSLEATVDKL YLLGIGLILAL NSVSVDLPGGM IVRANGTRLEY TIADDLSQTKF KAVEITTLKEL
	HLA-B4403	KEVLKDFTL GEITVALDD KEKDKDGKY KEDAKTLVS GEITVALDDS KEDTITVQKY GEITVALDDSD KEVLKDFTLEG
	HLA-B5101	LPGGMTELV
	HLA-B5701	TTQATKKTGKW

Preferred Borrelia garinii fragments of FlaB capable of interacting with one or more MHC molecules are listed in Table C.

Table C: Prediction of Borrelia garinii FlaB protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 10) using the http://www.cbs.dtu.dk/services/NetMHCII/ database. The MHC class 2 molecules for which no binders were found are not listed.

BAD18055.1 FlaB protein [Borrelia garinii] Seq15	HLA-A0101	NQDEAIAVNIY ELAVQSGNGTY
	HLA-A0201	SQASWTLRV QLTDEINRI AQAAQTAPV AIAVNIYAA SLAKIENAI

		AVNIYAANV AQYNQMHML TTVDANTSL SQGGVNSPV QTAPVQEGV NIYAANVANL NLNEVEKVLV VLVRMKELAV QLTDEINRIA NLFSGEGAQA IAVNIYAANV SLSGSQASWTL MLSNKSASQNV AIAVNIYAANV SQASWTLRVHV GMQPAKINTPA KVLVRMKELAV SLAKIENAIRM NLFSGEGAQAA
	HLA-A0301	NQMHMLSNK GSQASWTLR TVDANTSLAK YNQMHMLSNK LSGSQASWTLR TTVDANTSLAK LSNKSASQNVR
	HLA-A1101	NQMHMLSNK GSQASWTLR AVQSGNGTY TVDANTSLAK YNQMHMLSNK EVEKVLVRMK TTVDANTSLAK TTEGNLNEVEK TAEELGMQPAK TSLAKIENAIR QYNQMHMLSNK LSGSQASWTLR LSNKSASQNVR
	HLA-A2402	IYAANVANL YAANVANLF IYAANVANLF TYSDADRGSI IYAANVANLFS
	HLA-A2902	AVQSGNGTY YAANVANLF ELAVQSGNGTY EINRIADQAQY
	HLA-A6801	LAKIENAIR EGNLNEVEK YAANVANLF NGTYSDADR GSQASWTLR NQMHMLSNK TSKAINFIQ NKSASQNVR EVEKVLVRMK SLAKIENAIR

		TVDANTSLAK NTSKAINFIQ SGSQASWTLR TTVDANTSLA TTVDANTSLAK TTEGNLNEVEK EIEQLTDEINR LSNKSASQNVR TSLAKIENAIR EINRIADQAQY NLNEVEKVLVR LSGSQASWTLR TAEELGMQPAK QYNQMHMLSNK NIYAANVANLF QTAPVQEGVQQ
	HLA-B0702	SPVNVTTTV QPAKINTPA QPAPATAPS LVRMKELAV TPASLSGSQ APSQGGVNS APATAPSQG APVQEGVQQ TPASLSGSQA SPVNVTTTVD APSQGGVNSP QPAKINTPAS APSQGGVNSPV QPAKINTPASL APATAPSQGGV SPVNVTTTVDA TPASLSGSQAS
	HLA-B0801	KVLVRMKEL VEKVLVRMKEL
	HLA-B1501	YAANVANLF AVQSGNGTY AQAAQTAPV AQYNQMHML SQGGVNSPV SLSGSQASW SQASWTLRV IQIEIEQLT LAVQSGNGTY SQASWTLRVH SQNVRTAEEL VQQEGAQQPA INRIADQAQY AQAAQTAPVQ MQPAKINTPA ELAVQSGNGTY NIYAANVANLF NQDEAIAVNIY SLSGSQASWTL
	HLA-B2705	NRIADQAQY
	HLA-B3501	YAANVANLF QPAPATAPS SPVNVTTTV

		DEAIAVNIY TTVDANTSL LAVQSGNGT QPAKINTPA AVQSGNGTY QASWTLRVH IAVNIYAAN LAVQSGNGTY IADQAQYNQM QPAKINTPAS LAKIENAIRM QPAPATAPSQ YAANVANLFS TAEELGMQPA EAIAVNIYAA QAQYNQMHML TPASLSGSQA SPVNVTTTVD TPASLSGSQAS ELAVQSGNGTY NQDEAIAVNIY QPAKINTPASL IAVNIYAANVA NIYAANVANLF SPVNVTTTVDA EINRIADQAQY IADQAQYNQMH APSQGGVNSPV LAVQSGNGTYS
	HLA-B4403	EELGMQPAKI NEVEKVLVRM DEINRIADQA DEINRIADQAQ
	HLA-B5101	SPVNVTTTV APATAPSQGGV APSQGGVNSPV
	HLA-B5701	ASLSGSQASW

Choice of MHC allele for generation of MHC monomers and MHC multimers

More than 600 MHC alleles (class 1 and 2) are known in humans; for many of these, the peptide binding characteristics are known. Figure 3 presents an updated list of the HLA class 1 alleles. The frequency of the different HLA alleles varies considerably, also between different ethnic groups (Figure 4). Thus it is of outmost importance to carefully select the MHC alleles that corresponds to the population that one wish to study.

The combined choice of peptide, MHC and carrier.

Above it has been described how to generate binding peptides, and which MHC alleles are available. Below it is further described how one may modify the binding peptides in order to increase the stability, affinity, specificity and other features of the MHC-peptide complex or the MHC multimer. In the following it is described what characteristics of binding peptides and MHC alleles are important when using the MHC-peptide complex or MHC-multimer for different purposes.

A first preferred embodiment employs binding peptides of particularly high affinity for the MHC proteins. This may be done in order to increase the stability of the MHC-peptide complex. A higher affinity of the binding peptide for the MHC proteins may in some instances also result in increased rigidity of the MHC-peptide complex, which in turn often will result in higher affinity and/or specificity of the MHC-peptide complex for the T-cell receptor. A higher affinity and specificity will in turn have consequences for the immunogenicity and allergenicity, as well as possible side-effects of the MHC-peptide complex in e.g. the body.

Binding peptides of particularly high affinity for the MHC proteins may be identified by several means, including the following.

- Incubation of candidate binding peptides and MHC proteins, followed by analysis of the resulting complexes to identify those binding peptides that have most frequently been associated with MHC proteins. The binding peptides that have most frequently been associated with MHC proteins typically will represent high-affinity binding peptides. The identification of binding peptides with particularly high-affinity may involve enrichment of binding peptides, e.g. incubation of candidate peptides with immobilized MHC molecules, removal of non-binding peptides by e.g. washing, elution of binding peptides. This pool of peptides enriched for binding to the chosen MHC molecules may then be identified e.g. by mass spectrometry or HPLC and amino acid sequencing or the pool can be further enriched by another round of incubation with immobilized MHC.
- Candidate binding peptides may be compared to consensus sequences for the binding to a specific MHC allele. Thus, for a given class 1 allele, the consensus 8'mer sequence may be given by the sequence "X1-X2-X3-X4-X5-X6-X7-X8", where each of the X1-X8 amino acids can be chosen from a specific subset of amino acids, as described above.

Those binding peptides that correlate the best with the consensus sequence are expected to have particularly high affinity for the MHC allele in question.

- Based on a large data set of affinities of binding peptides for specific MHC alleles, software programs (often involving neural networks) have been developed that allow a relatively accurate prediction of the affinity of a given candidate binding peptide for a given MHC allele. By examining candidate binding peptides using such software programs, one can identify binding peptides of expected high-affinity for the MHC molecule.

A second prefered embodiment employs binding peptides with medium affinity for the MHC molecule. A medium affinity of the peptide for the MHC protein will often lead to lower physical and chemical stability of the MHC-peptide complex, which can be an advantage for certain applications. As an example, it is often desirable to administer a drug on a daily basis due to convenience. An MHC-peptide complex-based drug with high stability in the body would not allow this. In contrast a binding peptide with medium or low affinity for the MHC protein can be an advantage for such applications, since these functional MHC-peptide molecules will be cleared more rapidly from the body due to their lower stability.

For some applications where some level of cross-talk is desired, e.g. in applications where the target is a number of T cell clones that interact with a number of structurally related MHC-peptide complexes, e.g. MHC-peptide complexes containing binding peptides from different strains of a given species, a medium or low affinity of the binding peptide for the MHC protein can be an advantage. Thus, these MHC-peptide complexes are often more structurally flexible, allowing the MHC-peptide complexes to interact with several structurally related TCRs.

The affinity of a given peptide for a MHC protein, predicted by a software program or by its similarity to a consensus sequence, should only be considered a guideline to its real affinity. Moreover, the affinity can vary a lot depending on the conditions in the environment, e.g. the affinity in blood may be very different from the affinity in a biochemical assay. Further, in the context of a MHC multimer, the flexibility of the MHC-peptide complex can sometimes be an important parameter for overall avidity.

In summary, a lot of factors must be considered for the choice of binding peptides in a certain application. Some applications benefit from the use of all possible binding peptides for an antigen ("total approach"), other applications benefit from the selective choice of just a few binding peptides. Depending on the application, the affinity of the binding peptide for MHC protein is preferably high, medium, or low; the physical and/or chemical stability of the MHC-peptide complex is preferably high, medium or low; the binding peptide is preferably a very common or very rare epitope in a given population; etc.

It is obvious from the above preferred embodiments that most or all of the binding peptides generated by the total approach have important applications. In other words, in order to make relevant MHC multimers that suit the different applications with regard to e.g. personalized or general targeting, or with regard to affinity, avidity, specificity, immunogenicity, stimulatory efficiency, or stability, one must be able to choose from the whole set of binding peptides generated by the total approach

Loading of the peptide into the MHC multimer

Loading of the peptides into the MHCmer being either MHC class 1 or class 2 can be performed in a number of ways depending on the source of the peptide and the MHC, and depending on the application. MHC class 2 molecules can in principle be loaded with peptides in similar ways as MHC class 1. However, due to complex instability the most successful approach have been to make the complexes recombinant *in toto* in eukaryotic cells from a gene construct encoding the following form β chain-flexible linker-α chain-flexible linker-antigenic peptide.

The antigenic peptide may be added to the other peptide chain(s) at different times and in different forms, as follows.

a) Loading of antigenic peptide during MHC complex folding

a1) Antigenic peptide is added as a free peptide

MHC class I molecules are most often loaded with peptide during assembly in vitro by the individual components in a folding reaction i.e. consisting of purified recombinant heavy chain α with the purified recombinant β2 microglobulin and a peptide or a peptide mix.

a2) Antigenic peptide is part of a recombinant protein construct

Alternatively the peptide to be folded into the binding groove can be encoded together with e.g. the α heavy chain or fragment hereof by a gene construct having the structure, heavy chain-flexible linker- peptide. This recombinant molecule is then folded in vitro with β2-microglobulin.

b) Antigenic peptide replaces another antigenic peptide by an exchange reaction.

b1) Exchange reaction "in solution"

Loading of desired peptide can also be made by an in vitro exchange reaction where a peptide already in place in the binding groove are being exchanged by another peptide species.

b2) Exchange reaction "in situ"

Peptide exchange reactions can also take place when the parent molecule is attached to other molecules, structures, surfaces, artificial or natural membranes and nano-particles.

b3) Aided exchange reaction.

This method can be refined by making the parent construct with a peptide containing a meta-stable amino acid analog that is split by either light or chemically induction thereby leaving the parent structure free for access of the desired peptide in the binding groove.

b4) Display by in vivo loading

Loading of MHC class I and II molecules expressed on the cell surface with the desired peptides can be performed by an exchange reaction. Alternatively cells can be transfected by the peptides themselves or by the mother proteins that are then being processed leading to an *in vivo* analogous situation where the peptides are bound in the groove during the natural cause of MHC expression by the transfected cells. In the case of professional antigen presenting cells e.g. dendritic cells, macrophages, Langerhans cells, the proteins and peptides can be taken up by the cells themselves by phagocytosis and then bound to the MHC complexes the natural way and expressed on the cell surface in the correct MHC context.

Other features of product

In one preferred embodiment the MHC multimer is between 50,000 Da and 1,000,000 Da, such as from 50,000 Da to 980,000; for example from 50,000 Da to 960,000; such as from 50,000 Da to 940,000; for example from 50,000 Da to 920,000; such as from 50,000 Da to 900,000; for example from 50,000 Da to 880,000; such as from 50,000 Da to 860,000; for example from 50,000 Da to 840,000; such as from 50,000 Da to 820,000; for example from 50,000 Da to 800,000; such as from 50,000 Da to 780,000; for example from 50,000 Da to 760,000; such as from 50,000 Da to 740,000; for example from 50,000 Da to 720,000; such as from 50,000 Da to 700,000; for example from 50,000 Da to 680,000; such as from 50,000 Da to 660,000; for example from 50,000 Da to 640,000; such as from 50,000 Da to 620,000; for example from 50,000 Da to 600,000; such as from 50,000 Da to 580,000; for example from 50,000 Da to 560,000; such as from 50,000 Da to 540,000; for example from 50,000 Da to 520,000; such as from 50,000 Da to 500,000; for example from 50,000 Da to 480,000; such as from 50,000 Da to 460,000; for example from 50,000 Da to 440,000; such as from 50,000 Da to 420,000; for example from 50,000 Da to 400,000; such as from 50,000 Da to 380,000; for example from 50,000 Da to 360,000; such as from 50,000 Da to 340,000; for example from 50,000 Da to 320,000; such as from 50,000 Da to 300,000; for example from 50,000 Da to 280,000; such as from 50,000 Da to 260,000; for example from 50,000 Da to 240,000; such as from 50,000 Da to 220,000; for example from 50,000 Da to 200,000; such as from 50,000 Da to 180,000; for example from 50,000 Da to 160,000; such as from 50,000 Da to 140,000; for example from 50,000 Da to 120,000; such as from 50,000 Da to 100,000; for example from 50,000 Da to 80,000; such as from 50,000 Da to 60,000; such as from 100,000 Da to 980,000; for example from 100,000 Da to 960,000; such as from 100,000 Da to 940,000; for example from 100,000 Da to 920,000; such as from 100,000 Da to 900,000; for example from 100,000 Da to 880,000; such as from 100,000 Da to 860,000; for example from 100,000 Da to 840,000; such as from 100,000 Da to 820,000; for example from 100,000 Da to 800,000; such as from 100,000 Da to 780,000; for example from 100,000 Da to 760,000; such as from 100,000 Da to 740,000; for example from 100,000 Da to 720,000; such as from 100,000 Da to 700,000; for example from 100,000 Da to 680,000; such as from 100,000 Da to 660,000; for example from 100,000 Da to 640,000; such as from 100,000 Da to 620,000; for example from 100,000 Da to 600,000; such as from 100,000 Da to 580,000; for example from 100,000 Da to 560,000; such as from 100,000 Da to 540,000; for example from 100,000 Da to 520,000; such as from 100,000 Da to 500,000; for

example from 100,000 Da to 480,000; such as from 100,000 Da to 460,000; for example from 100,000 Da to 440,000; such as from 100,000 Da to 420,000; for example from 100,000 Da to 400,000; such as from 100,000 Da to 380,000; for example from 100,000 Da to 360,000; such as from 100,000 Da to 340,000; for example from 100,000 Da to 320,000; such as from 100,000 Da to 300,000; for example from 100,000 Da to 280,000; such as from 100,000 Da to 260,000; for example from 100,000 Da to 240,000; such as from 100,000 Da to 220,000; for example from 100,000 Da to 200,000; such as from 100,000 Da to 180,000; for example from 100,000 Da to 160,000; such as from 100,000 Da to 140,000; for example from 100,000 Da to 120,000; such as from 150,000 Da to 980,000; for example from 150,000 Da to 960,000; such as from 150,000 Da to 940,000; for example from 150,000 Da to 920,000; such as from 150,000 Da to 900,000; for example from 150,000 Da to 880,000; such as from 150,000 Da to 860,000; for example from 150,000 Da to 840,000; such as from 150,000 Da to 820,000; for example from 150,000 Da to 800,000; such as from 150,000 Da to 780,000; for example from 150,000 Da to 760,000; such as from 150,000 Da to 740,000; for example from 150,000 Da to 720,000; such as from 150,000 Da to 700,000; for example from 150,000 Da to 680,000; such as from 150,000 Da to 660,000; for example from 150,000 Da to 640,000; such as from 150,000 Da to 620,000; for example from 150,000 Da to 600,000; such as from 150,000 Da to 580,000; for example from 150,000 Da to 560,000; such as from 150,000 Da to 540,000; for example from 150,000 Da to 520,000; such as from 150,000 Da to 500,000; for example from 150,000 Da to 480,000; such as from 150,000 Da to 460,000; for example from 150,000 Da to 440,000; such as from 150,000 Da to 420,000; for example from 150,000 Da to 400,000; such as from 150,000 Da to 380,000; for example from 150,000 Da to 360,000; such as from 150,000 Da to 340,000; for example from 150,000 Da to 320,000; such as from 150,000 Da to 300,000; for example from 150,000 Da to 280,000; such as from 150,000 Da to 260,000; for example from 150,000 Da to 240,000; such as from 150,000 Da to 220,000; for example from 150,000 Da to 200,000; such as from 150,000 Da to 180,000; for example from 150,000 Da to 160,000.

In another preferred embodiment the MHC multimer is between 1,000,000 Da and 3,000,000 Da, such as from 1,000,000 Da to 2,800,000; for example from 1,000,000 Da to 2,600,000; such as from 1,000,000 Da to 2,400,000; for example from 1,000,000

Da to 2,200,000; such as from 1,000,000 Da to 2,000,000; for example from 1,000,000 Da to 1,800,000; such as from 1,000,000 Da to 1,600,000; for example from 1,000,000 Da to 1,400,000.

Above it was described how to design and produce the key components of the MHC multimers, i.e. the MHC-peptide complex. In the following it is described how to generate the MHC monomer or MHC multimer products of the present invention.

Number of MHC complexes pr multimer

A non-exhaustive list of possible MHC mono- and multimers illustrates the possibilities. 'n' indicates the number of MHC complexes comprised in the multimer:

a) n=1, Monomers

b) n=2, Dimers, multimerization can be based on IgG scaffold, streptavidin with two MHC's, coiled-coil dimerization e.g. Fos.Jun dimerization

c) n=3, Trimers, multimerization can be based on streptavidin as scaffold with three MHC's, TNFalpha-MHC hybrids, triplex DNA-MHC konjugates or other trimer structures

d) n=4, Tetramers, multimerization can be based on streptavidin with all four binding sites occupied by MHC molecules or based on dimeric IgA

e) n=5, Pentamers, multimerization can take place around a pentameric coil-coil structure

f) n=6, Hexamers

g) n=7, Heptamers

h) n=8-12, Octa- dodecamers, multimerization can take place using Streptactin

i) n=10, Decamers, multimerization can take place using IgM

j) 1<n<100, Dextramers, as multimerization domain polymers such as polypeptide, polysaccharides and Dextrans can be used.

k) 1<n<1000, Multimerization can make use of dendritic cells (DC), antigen-presenting cells (APC), micelles, liposomes, beads, surfaces e.g. microtiterplate, tubes, microarray devices, micro-fluidic systems

l) 1<n, n in billions or trillions or higher, multimerization take place on beads, and surfaces e.g. microtiterplate, tubes, microarray devices, micro-fluidic systems

MHC multimers thus include MHC-dimers, MHC-trimers, MHC-tetramers, MHC-pentamers, MHC-hexamers, as well as organic molecules, cells, membranes, polymers and particles that comprise two or more MHC-peptide complexes. Example organic molecule-based multimers include functionalized cyclic structures such as benzene rings where e.g. a benzene ring is functionalized and covalently linked to e.g. three MHC complexes; example cell-based MHC multimers include dendritic cells and antigen presenting cells (APCs); example membrane-based MHC multimers include liposomes and micelles carrying MHC-peptide complexes in their membranes; example polymer-based MHC multimers include MHC-dextramers (dextran to which a number of MHC-peptide complexes are covalently or non-covalently attached) and example particles include beads or other solid supports with MHC complexes immobilized on the surface. Obviously, any kind of multimerization domain can be used, including any kind of cell, polymer, protein or other molecular structure, or particles and solid supports.

MHC origin

Any of the three components of a MHC complex can be of any of the below mentioned origins. The list is non-exhaustive. A complete list would encompass all Chordate species. By origin is meant that the sequence is identical or highly homologous to a naturally occurring sequence of the specific species.

List of origins:

- Human
- Mouse
- Primate
    - Chimpansee
    - Gorilla
    - Orang Utan
- Monkey
    - Macaques
- Porcine (Swine/Pig)
- Bovine (Cattle/Antilopes)
- Equine (Horse)
- Camelides (Camels)
- Ruminants (Deears)
- Canine (Dog)

- Feline (Cat)
- Bird
    - Chicken
    - Turkey
- Fish
- Reptiles
- Amphibians

Generation of MHC multimers

Different approaches to the generation of various types of MHC multimers are described in US patent 5,635,363 (Altmann et al.), patent application WO 02/072631 A2 (Winther et al.), patent application WO 99/42597, US patent 2004209295, US patent 5,635,363, and is described elsewhere in the present patent application as well. In brief, MHC multimers can be generated by first expressing and purifying the individual protein components of the MHC protein, and then combining the MHC protein components and the peptide, to form the MHC-peptide complex. Then an appropriate number of MHC-peptide complexes are linked together by covalent or non-covalent bonds to a multimerization domain. This can be done by chemical reactions between reactive groups of the multimerization domain (e.g. vinyl sulfone functionalities on a dextran polymer) and reactive groups on the MHC protein (e.g. amino groups on the protein surface), or by non-covalent interaction between a part of the MHC protein (e.g. a biotinylated peptide component) and the multimerization domain (e.g. four binding sites for biotin on the strepavidin tetrameric protein). As an alternative, the MHC multimer can be formed by the non-covalent association of amino acid helices fused to one component of the MHC protein, to form a pentameric MHC multimer, held together by five helices in a coiled-coil structure making up the multimerization domain.

Appropriate chemical reactions for the covalent coupling of MHC and the multimerization domain include nucleophilic substitution by activation of electrophiles (e.g. acylation such as amide formation, pyrazolone formation, isoxazolone formation; alkylation; vinylation; disulfide formation), addition to carbon-hetero multiple bonds (e.g. alkene formation by reaction of phosphonates with aldehydes or ketones; arylation; alkylation of arenes/hetarenes by reaction with alkyl boronates or enolethers),

nucleophilic substitution using activation of nucleophiles (e.g. condensations; alkylation of aliphatic halides or tosylates with enolethers or enamines), and cycloadditions.

Appropriate molecules, capable of providing non-covalent interactions between the multimerization domain and the MHC-peptide complex, involve the following molecule pairs and molecules: streptavidin/biotin, avidin/biotin, antibody/antigen, DNA/DNA, DNA/PNA, DNA/RNA, PNA/PNA, LNA/DNA, leucine zipper e.g. Fos/Jun, IgG dimeric protein, IgM multivalent protein, acid/base coiled-coil helices, chelate/metal ion-bound chelate, streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-transferase) glutathione affinity, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (*Canavalia ensiformis*) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity). Combinations of such binding entities are also comprised. In particular, when the MHC complex is tagged, the binding entity can be an “anti-tag”. By “anti-tag” is meant an antibody binding to the tag and any other molecule capable of binding to such tag.

Generation of components of MHC

When employing MHC multimers for diagnostic purposes, it is preferable to use a MHC allele that corresponds to the tissue type of the person or animal to be diagnosed. Once the MHC allele has been chosen, a peptide derived from the antigenic protein may be chosen. The choice will depend on factors such as known or expected binding affinity of the MHC protein and the various possible peptide fragments that may be derived from the full sequence of the antigenic peptide, and will depend on the expected or known binding affinity and specificity of the MHC-peptide complex for the TCR. Preferably, the affinity of the peptide for the MHC molecule, and the affinity and specificity of the MHC-peptide complex for the TCR, should be high.

Similar considerations apply to the choice of MHC allele and peptide for therapeutic and vaccine purposes. In addition, for some of these applications the effect of binding the MHC multimer to the TCR is also important. Thus, in these cases the effect on the T-cell's general state must be considered, e.g. it must be decided whether the desired end result is apoptosis or proliferation of the T-cell.

Likewise, it must be decided whether stability is important. For some applications low stability may be an advantage, e.g. when a short-term effect is desired; in other instances, a long-term effect is desired and MHC multimers of high stability is desired. Stabilities of the MHC protein and of the MHC-peptide complex may be modified as described elsewhere herein.

Finally, modifications to the protein structure may be advantageous for some diagnostics purposes, because of e.g. increased stability, while in for vaccine purposes modifications to the MHC protein structure may induce undesired allergenic responses.

Generation of protein chains of MHC

Generation of MHC class I heavy chain and β2-Microglobulin

MHC class I heavy chain (HC) and β2-mircroglobulin (β2m) can be obtained from a variety of sources.

a) Natural sources by means of purification from eukaryotic cells naturally expressing the MHC class 1 or β2m molecules in question.

b) The molecules can be obtained by recombinant means e.g. using.

a. *in vitro* translation of mRNA obtained from cells naturally expressing the MHC or β2m molecules in question

b. by expression and purification of HC and/or β2m gene transfected cells of mammalian, yeast, bacterial or other origin. This last method will normally be the method of choise.The genetic material used for transfection/transformation can be:

i. of natural origin isolated from cells, tissue or organisms

ii. of synthetical origin i.e. synthetic genes identical to the natural DNA sequence or it could be modified to introduce molecular changes or to ease recombinant expression.

The genetic material can encode all or only a fragment of β2m, all or only a fragment of MHC class 1 heavy chain. Of special interest are MHC class 1 heavy chain fragments consisting of, the complete chain minus the intramembrane domain, a chain consisting of only the extracellular α1 and α2 class 1 heavy chain domains, or any of the mentioned β2m and heavy chain fragments containing modified or added designer domain(s) or sequence(s).

Generation of MHC class 2 α- and β-chains

MHC class 2 α- and β-chains can be obtained from a variety of sources:

a) Natural sources by means of purification from eukaryotic cells naturally expressing the MHC class 2 molecules in question.

b) By recombinant means e.g. using:

a. *in vitro* translation of mRNA obtained from cells naturally expressing the MHC class 2 molecules in question

b. By purification from MHC class 2 gene transfected cells of mammalian, yeast, bacterial or other origin. This last method will normally be the method of choise.The genetic material used for transfection/transformation can be

i. of natural origin isolated from cells, tissue or organisms

ii. of synthetical origin i.e. synthetic genes identical to the natural DNA sequence or it could be modified to introduce molecular changes or to ease recombinant expression.

The genetic material can encode all or only a fragment of MHC class 2 α- and β-chains. Of special interest are MHC class 2 α- and β-chain fragments consisting of, the complete α- and β-chains minus the intramembrane domains of either or both chains; and α- and β-chains consisting of only the extracellular domains of either or both, i.e α1 plus α2 and β1 plus β2 domains, respectively.

The genetic material can be modified to encode the interesting MHC class 2 molecule fragments consisting of domains starting from the amino terminal in consecutive order, MHC class 2 β1 plus MHC class 2 α1 plus MHC class 1 α3 domains or in alternative order, MHC class 2 α1 plus MHC class 2 β1 plus MHC class 1 α3 domains.

Lastly, the gentic material can encode any of the above mentioned MHC class 2 α- and β-chain molecules or fragments containing modified or added designer domain(s) or sequence(s).

c) The MHC material may also be of exclusively synthetic origin manufactured by solid phase protein synthesis. Any of the above mentioned molecules can be made this way.

Modified MHC I or MHC II complexes

MHC I and MHC II complexes modified in any way as described above, can bind TCR. Modifications include mutations (substitutions, deletions or insertions of natural or non-natural amino acids, or any other organic molecule. The mutations are not limited to those that increase the stability of the MHC complex, and could be introduced anywhere in the MHC complex. One example of special interest is mutations introduced in the α3 subunit of MHC I heavy chain. The α3-subunit interacts with CD8 molecules on the surface of T cells. To minimize binding of MHC multimer to CD8 molecules on the surface of non-specific T cells, amino acids in α3 domain involved in the interaction with CD8 can be mutated. Such a mutation can result in altered or abrogated binding of MHC to CD8 molecules. Another example of special interest is mutations in areas of the β2-domain of MHC II molecules responsible for binding CD4 molecules.

Another embodiment is chemically modified MHC complexes where the chemical modification could be introduced anywhere in the complex, e.g. a MHC complex where the peptide in the peptide-binding cleft has a dinitrophenyl group attached.
Modified MHC complexes could also be MHC I or MHC II fusion proteins where the fusion protein is not necessarily more stable than the native protein. Of special interest is MHC complexes fused with genes encoding an amino acid sequence capable of being biotinylated with a Bir A enzyme (Schatz, P. J.,(1993), Biotechnology 11(10):1138-1143). This biotinylation sequence could be fused with the COOH-terminal of β2m or the heavy chain of MHC I molecules or the COOH-terminal of either the α-chain or β-chain of MHC II. Similarly, other sequences capable of being enzymatically or chemically modified can be fused to the NH_2 or COOH-terminal ends of the MHC complex.

Stabilization of empty MHC complexes and MHC-peptide complexes

Classical MHC complexes are in nature embedded in the membrane. A preferred embodiment includes multimers comprising a soluble form of MHC II or I where the transmembrane and cytosolic domains of the membrane-anchored MHC complexes are removed. The removal of the membrane-anchoring parts of the molecules can influence the stability of the MHC complexes. The stability of MHC complexes is an important parameter when generating and using MHC multimers.

MHC I complexes consist of a single membrane-anchored heavy chain that contains the complete peptide binding groove and is stable in the soluble form when complexed with β2m. The long-term stability is dependent on the binding of peptide in the peptide-binding groove. Without a peptide in the peptide binding groove the heavy chain and β2m tend to dissociate. Similarly, peptides with high affinity for binding in the peptide-binding groove will typically stabilize the soluble form of the MHC complex while peptides with low affinity for the peptide-binding groove will typically have a smaller stabilizing effect.

In contrast, MHC II complexes consist of two membrane-anchored chains of almost equal size. When not attached to the cell membrane the two chains tend to dissociate and are therefore not stable in the soluble form unless a high affinity peptide is bound in the peptide-binding groove or the two chains are held together in another way.

In nature MHC I molecules consist of a heavy chain combined with β2m, and a peptide of typically 8-11 amino acids. Herein, MHC I molecules also include molecules consisting of a heavy chain and β2m (empty MHC), or a heavy chain combined with a peptide or a truncated heavy chain comprising α1 and α2 subunits combined with a peptide, or a full-length or truncated heavy chain combined with a full-length or truncated β2m chain. These MHC I molecules can be produced in *E.coli* as recombinant proteins, purified and refolded *in vitro* (Garboczi et al., (1992), Proc. Natl. Acad. Sci. 89, 3429-33). Alternatively, insect cell systems or mammalian cell systems can be used. To produce stable MHC I complexes and thereby generate reliable MHC I multimers several strategies can be followed. Stabilization strategies for MHC I complexes are described in the following.

<u>Stabilization strategies for MHC I complexes</u>

- *Generation of covalent protein-fusions*

MHC I molecules can be stabilized by introduction of one or more linkers between the individual components of the MHC I complex. This could be a complex consisting of a heavy chain fused with β2m through a linker and a soluble peptide, a heavy chain fused to β2m through a linker, a heavy chain /β2m dimer covalently linked to a peptide through a linker to either heavy chain or β2m, and where there can or can not be a linker between the heavy chain and β2m, a heavy chain fused to a peptide through a linker, or the α1 and α2 subunits of the heavy chain fused to a peptide through a linker. In all of these example protein-fusions, each of the heavy chain, β2m and the peptide can be truncated.

The linker could be a flexible linker, e.g. made of glycine and serine and e.g. between 5-20 residues long. The linker could also be rigid with a defined structure, e.g. made of amino acids like glutamate, alanine, lysine, and leucine creating e.g. a more rigid structure.

In heavy chain-β2m fusion proteins the COOH terminus of β2m can be covalently linked to the NH_2 terminus of the heavy chain, or the NH_2 terminus of β2m can be linked to the COOH terminus of the heavy chain. The fusion-protein can also comprise a β2m domain, or a truncated β2m domain, inserted into the heavy chain, to form a fusion- protein of the form “heavy chain (first part)-β2m-heavy chain (last part)”.
Likewise, the fusion-protein can comprise a heavy chain domain, or a truncated heavy chain, inserted into the β2m chain, to form a fusion-protein of the form “β2m(first part)-heavy chain-β2m(last part)”.

In peptide-β2m fusion proteins the COOH terminus of the peptide is preferable linked to the NH_2 terminus of β2m but the peptide can also be linked to the COOH terminal of β2m via its NH_2 terminus. In heavy chain-peptide fusion proteins it is preferred to fuse the NH_2 terminus of the heavy chain to the COOH terminus of the peptide, but the fusion can also be between the COOH terminus of the heavy chain and the NH_2 terminus of the peptide. In heavy chain-β2m-peptide fusion proteins the NH_2 terminus of the heavy chain can be fused to the COOH terminus of β2m and the NH_2 terminus of β2m can be fused to the COOH terminus of the peptide.

- *Non-covalent stabilization by binding to an unnatural component*

Non-covalent binding of unnatural components to the MHC I complexes can lead to increased stability. The unnatural component can bind to both the heavy chain and the β2m, and in this way promote the assemble of the complex, and/or stabilize the formed complex. Alternatively, the unnatural component can bind to either β2m or heavy chain, and in this way stabilize the polypeptide in its correct conformation, and in this way increase the affinity of the heavy chain for β2m and/or peptide, or increase the affinity of β2m for peptide.

Here, unnatural components mean antibodies, peptides, aptamers or any other molecule with the ability to bind peptides stretches of the MHC complex. Antibody is here to be understood as truncated or full-length antibodies (of isotype IgG, IgM, IgA, IgE), Fab, scFv or bi-Fab fragments or diabodies.

An example of special interest is an antibody binding the MHC I molecule by interaction with the heavy chain as well as β2m. The antibody can be a bispecific antibody that binds with one arm to the heavy chain and the other arm to the β2m of the MHC complex. Alternatively the antibody can be monospecific, and bind at the interface between heavy chain and β2m.

Another example of special interest is an antibody binding the heavy chain but only when the heavy chain is correct folded. Correct folded is here a conformation where the MHC complex is able to bind and present peptide in such a way that a restricted T cell can recognize the MHC-peptide complex and be activated. This type of antibody can be an antibody like the one produced by the clone W6/32 (M0736 from Dako, Denmark) that recognizes a conformational epitope on intact human and some monkey MHC complexes containing β2m, heavy chain and peptide.

- *Generation of modified proteins or protein components*

One way to improve stability of a MHC I complex am to increase the affinity of the binding peptide for the MHC complex. This can be done by mutation/substitution of amino acids at relevant positions in the peptide, by chemical modifications of amino acids at relevant positions in the peptide or introduction by synthesis of non-natural amino acids at relevant positions in the peptide. Alternatively, mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions could be

introduced in the peptide binding cleft, i.e. in the binding pockets that accommodate peptide side chains responsible for anchoring the peptide to the peptide binding cleft. Moreover, reactive groups can be introduced into the antigenic peptide; before, during or upon binding of the peptide, the reactive groups can react with amino acid residues of the peptide binding cleft, thus covalently linking the peptide to the binding pocket.

Mutations/substitutions, chemical modifications, insertion of natural or non-natural amino acids or deletions could also be introduced in the heavy chain and/or β2m at positions outside the peptide-binding cleft. By example, it has been shown that substitution of XX with YY in position nn of human β_2m enhance the biochemical stability of MHC Class I molecule complexes and thus may lead to more efficient antigen presentation of subdominant peptide epitopes.

A preferred embodiment is removal of "unwanted cysteine residues" in the heavy chain by mutation, chemical modification, amino acid exchange or deletion. "Unwanted cysteine residues" is here to be understood as cysteines not involved in the correct folding of the final MHC I molecule. The presence of cysteine not directly involved in the formation of correctly folded MHC I molecules can lead to formation of intra molecular disulfide bridges resulting in a non correct folded MHC complex during *in vitro* refolding.

Another method for covalent stabilization of MHC I complex am to covalently attach a linker between two of the subunits of the MHC complex. This can be a linker between peptide and heavy chain or between heavy chain and beta2microglobulin.

<u>Stabilization strategies for MHC II complexes</u>

MHC II molecules as used herein are defined as classical MHC II molecule consisting of a α-chain and a β-chain combined with a peptide. It could also be a molecule only consisting of α-chain and β-chain (α/β dimer or empty MHC II), a truncated α-chain (e.g. α1 domain alone) combined with full-length β-chain either empty or loaded with a peptide, a truncated β-chain (e.g. β1 domain alone) combined with a full-length α-chain either empty or loaded with a peptide or a truncated α-chain combined with a truncated β-chain (e.g. α1 and β1 domain) either empty or loaded with a peptide.

In contrast to MHC I molecules MHC II molecules are not easily refolded *in vitro*. Only some MHC II alleles may be produced in *E.coli* followed by refolding *in vitro*.

Therefore preferred expression systems for production of MHC II molecules are eukaryotic systems where refolding after expression of protein is not necessary. Such expression systems could be stable Drosophila cell transfectants, baculovirus infected insect cells, CHO cells or other mammalian cell lines suitable for expression of proteins.

Stabilization of soluble MHC II molecules is even more important than for MHC I molecules since both α- and β-chain are participants in formation of the peptide binding groove and tend to dissociate when not embedded in the cell membrane.

- *Generation of covalent protein-fusions.*

MHC II complexes can be stabilized by introduction of one or more linkers between the individual components of the MHC II complex. This can be a α/β dimer with a linker between α-chain and β-chain; a α/β dimer covalently linked to the peptide via a linker to either the α-chain or β-chain; a α/β dimer, covalently linked by a linker between the α-chain and β-chain, and where the dimer is covalently linked to the peptide; a α/β dimer with a linker between α-chain and β-chain, where the dimer is combined with a peptide covalently linked to either α-chain or β-chain.

The linker can be a flexible linker, e.g. made of glycine and serine, and is typically between 5-20 residues long, but can be shorter or longer. The linker can also be more rigid with a more defined structure, e.g. made of amino acids like glutamate, alanine, lysine, and leucine.

The peptides can be linked to the NH_2- or COOH-terminus of either α-chain or β-chain. Of special interest are peptides linked to the NH_2-terminus of the β-chain via their COOH-terminus, since the linker required is shorter than if the peptide is linked to the COOH-terminus of the β-chain.

Linkage of α-chain to β-chain can be via the COOH-terminus of the β-chain to the NH_2-terminus of the α-chain or from the COOH-terminus of the α-chain to the NH_2-terminus of the β-chain.

In a three-molecule fusion protein consisting of α-chain, β-chain and peptide a preferred construct is where one linker connect the COOH-terminus of the β-chain with the NH_2-terminus of the α-chain and another linker connects the COOH-terminal of the peptide with the NH_2-terminal of the β-chain. Alternatively one linker joins the COOH-terminus of the α-chain with the NH_2-terminus of the β-chain and the second linker joins the NH_2-terminus of the peptide with the COOH-terminus of the β-chain. The three peptides of the MHC complex can further be linked as described above for the three peptides of the MHC complex, including internal fusion points for the proteins.

- *Non-covalent stabilization by binding ligand.*

Non-covalent binding of ligands to the MHC II complex can promote assembly of α- and β-chain by bridging the two chains, or by binding to either of the α- or β-chains, and in this way stabilize the conformation of α or β, that binds β or α, respectively, and/or that binds the peptide. Ligands here mean antibodies, peptides, aptamers or any other molecules with the ability to bind proteins.

A particular interesting example is an antibody binding the MHC complex distal to the interaction site with TCR, i.e. distal to the peptide-binding cleft. An antibody in this example can be any truncated or full length antibody of any isotype (e.g. IgG, IgM, IgA or IgE), a bi-Fab fragment or a diabody. The antibody could be bispecific with one arm binding to the α-chain and the other arm binding to the β-chain. Alternatively the antibody could be monospecific and directed to a sequence fused to the α-chain as well as to the β-chain.

Another example of interest is an antibody binding more central in the MHC II molecule, but still interacting with both α- and β-chain. Preferable the antibody binds a conformational epitope, thereby forcing the MHC molecule into a correct folded configuration. The antibody can be bispecific binding with one arm to the α-chain and the other arm to the β-chain. Alternatively the antibody is monospecific and binds to a surface of the complex that involves both the α- and β-chain, e.g. both the α2- and β2- domain or both the α1- and β1- domain.

The antibodies described above can be substituted with any other ligand that binds at the α-/β-chain interface, e.g. peptides and aptamers. The ligand can also bind

the peptide, although, in this case it is important that the ligand does not interfere with the interaction of the peptide or binding cleft with the TCR.

- *Non-covalent stabilization by induced multimerization.*

In nature the anchoring of the α- and β-chains in the cell membrane stabilizes the MHC II complexes considerably. As mentioned above, a similar concept for stabilization of the α/β-dimer was employed by attachment of the MHC II chains to the Fc regions of an antibody, leading to a stable α/β-dimer, where α and β are held together by the tight interactions between two Fc domains of an antibody. Other dimerization domains can be used as well.

In one other example of special interest MHC II molecules are incorporated into artificial membrane spheres like liposomes or lipospheres. MHC II molecules can be incorporated as monomers in the membrane or as dimers like the MHC II-antibody constructs describes above. In addition to stabilization of the MHC II complex an increased avidity is obtained. The stabilization of the dimer will in most cases also stabilize the trimeric MHC-peptide complex.

Induced multimerization can also be achieved by biotinylation of α- as well as β-chain and the two chains brought together by binding to streptavidin. Long flexible linkers such as extended glycine-serine tracts can be used to extend both chains, and the chains can be biotinylated at the end of such extended linkers. Then streptavidin can be used as a scaffold to bring the chains together in the presence of the peptide, while the flexible linkers still allow the chains to orientate properly.

- *Generation of modified proteins or protein components*

Stability of MHC II complexes can be increased by covalent modifications of the protein. One method is to increase the affinity of the peptide for the MHC complex. This can be done by exchange of the natural amino acids with other natural or non-natural amino acids at relevant positions in the peptide or by chemical modifications of amino acids at relevant positions in the peptide. Alternatively, mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions can be introduced in the peptide-binding cleft.

Mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions can alternatively be introduced in α- and/or β- chain at positions outside the peptide-binding cleft.

In this respect a preferred embodiment is to replace the hydrophobic transmembrane regions of α-chain and β-chain by leucine zipper dimerisation domains (e.g. Fos-Jun leucine zipper; acid-base coiled-coil structure) to promote assembly of α-chain and β-chain.

Another preferred embodiment is to introduce one or more cysteine residues by amino acid exchange at the COOH-terminal of both α-chain and β-chain, to create disulfide bridges between the two chains upon assembly of the MHC complex. Another embodiment is removal of "unwanted cysteine residues" in either of the chains by mutation, chemical modification, amino acid exchange or deletion. "Unwanted cysteine residues" is here to be understood as cysteines not involved in correct folding of the MHC II-peptide complex. The presence of cysteines not directly involved in the formation of correctly folded MHC II complexes can lead to formation of intra molecular disulfide bridges and incorrectly folded MHC complexes.

MHC II complexes can also be stabilized by chemically linking together the subunits and the peptide. That can be a linker between peptide and α-chain, between peptide and β-chain, between α-chain and β-chain, and combination thereof.

Such linkages can be introduced prior to folding by linking two of the complex constituents together, then folding this covalent hetero-dimer in the presence of the third constituent. An advantage of this method is that it only requires complex formation between two, rather than three species.

Another possibility is to allow all three constituents to fold, and then to introduce covalent cross-links on the folded MHC-complex, stabilizing the structure. An advantage of this method is that the two chains and the peptide will be correctly positioned relatively to each other when the cross linkages are introduced.

<u>Other stabilization of MHC I and/or MHC II complexes</u>

- *Stabilization with soluble additives.*

The stability of proteins in aqueous solution depends on the composition of the solution. Addition of salts, detergents organic solvent, polymers ect. can influence

the stability. Salts, detergents, organic solvent, polymers and any other soluble additives can be added to increase the stability of MHC complexes. Of special interest are additives that increase surface tension of the MHC molecule without binding the molecule. Examples are sucrose, mannose, glycine, betaine, alanine, glutamine, glutamic acid and ammoniumsulfate. Glycerol, mannitol and sorbitol are also included in this group even though they are able to bind polar regions.

Another group of additives of special interest are able to increase surface tension of the MHC molecule and simultaneously interact with charged groups in the protein. Examples are $MgSO_4$, NaCl, polyethylenglycol, 2-methyl-2,4-pentandiol and guanidiniumsulfate.

Correct formation of MHC complexes is dependent on binding of peptide in the peptide-binding cleft; the bound peptide appears to stabilize the complex in its correct conformation. Addition of molar excess of peptide will force the equilibrium towards correctly folded MHC-peptide complexes. Likewise is excess β2m also expected to drive the folding process in direction of correct folded MHC I complexes. Therefore peptide identical to the peptide bound in the peptide-binding cleft and/or β2m are included as stabilizing soluble additives.

Other additives of special interest for stabilization of MHC II molecules are BSA, fetal and bovine calf serum or individual protein components in serum with a protein stabilizing effect.

All of the above mentioned soluble additives can be added to any solution containing MHC complexes in order to increase the stability of the molecule. This can be during the refolding process, to the formed MHC complex, to the soluble MHC monomer, to a solution of MHC multimers comprising one or more MHC complexes or to solutions used during analysis of MHC specific T cells with MHC multimers.

Other additives of special interest for stabilization of MHC molecules are BSA, fetal and bovine calf serum or individual protein components in serum with a protein stabilizing effect.

- *Chemically modified MHC I and II complexes*

There are a number of amino acids that are particularly reactive towards chemical cross linkers. In the following, chemical reactions are described that are particularly preferable for the cross-linking or modification of MHC I or MHC II complexes.

The amino group at the N-terminal of both chains and of the peptide, as well as amino groups of lysine side chains, are nucleophilic and can be used in a number of chemical reactions, including nucleophilic substitution by activation of electrophiles (e.g. acylation such as amide formation, pyrazolone formation, isoxazolone formation; alkylation; vinylation; disulfide formation), addition to carbon-hetero multiple bonds (e.g. alkene formation by reaction of phosphonates with aldehydes or ketones; arylation; alkylation of arenes/hetarenes by reaction with alkyl boronates or enolethers), nucleophilic substitution using activation of nucleophiles (e.g. condensations; alkylation of aliphatic halides or tosylates with enolethers or enamines), and cycloadditions. Example reagents that can be used in a reaction with the amino groups are activated carboxylic acids such as NHS-ester, tetra and pentafluoro phenolic esters, anhydrides, acid chlorides and fluorides, to form stable amide bonds. Likewise, sulphonyl chlorides can react with these amino groups to form stable sulphone-amides. Iso-Cyanates can also react with amino groups to form stable ureas, and isothiocyanates can be used to introduce thio-urea linkages.

Aldehydes, such as formaldehyde and glutardialdehyde will react with amino groups to form shiff's bases, than can be further reduced to secondary amines. The guanidino group on the side chain of arginine will undergo similar reactions with the same type of reagents.

Another very useful amino acid is cysteine. The thiol on the side chain is readily alkylated by maleimides, vinyl sulphones and halides to form stable thioethers, and reaction with other thiols will give rise to disulphides.

Carboxylic acids at the C-terminal of both chains and peptide, as well as on the side chains of glutamic and aspartic acid, can also be used to introduce cross-links. They will require activation with reagents such as carbodiimides, and can then react with amino groups to give stable amides.

Thus, a large number of chemistries can be employed to form covalent cross-links. The crucial point is that the chemical reagents are bi-functional, being capable of reacting with two amino acid residues.

They can be either homo bi-functional, possessing two identical reactive moieties, such as glutardialdehyde or can be hetero bi-functional with two different reactive moieties, such as GMBS (MaleimidoButyryloxy-Succinimide ester).

Alternatively, two or more reagents can be used; i.e. GMBS can be used to introduce maleimides on the α-chain, and iminothiolane can be used to introduce thiols on the β-chain; the malemide and thiol can then form a thioether link between the two chains.

For the present invention some types of cross-links are particularly useful. The folded MHC-complex can be reacted with dextrans possessing a large number (up to many hundreds) of vinyl sulphones. These can react with lysine residues on both the α and β chains as well as with lysine residues on the peptide protruding from the binding site, effectively cross linking the entire MHC-complex. Such cross linking is indeed a favored reaction because as the first lysine residue reacts with the dextran, the MHC-complex becomes anchored to the dextran favoring further reactions between the MHC complex and the dextran multimerization domain. Another great advantage of this dextran chemistry is that it can be combined with fluorochrome labelling; i.e. the dextran is reacted both with one or several MHC-complexes and one or more fluorescent protein such as APC.

Another valuable approach is to combine the molecular biological tools described above with chemical cross linkers. As an example, one or more lysine residues can be inserted into the α-chain, juxtaposed with glutamic acids in the β-chain, where after the introduced amino groups and carboxylic acids are reacted by addition of carbodiimide. Such reactions are usually not very effective in water, unless as in this case, the groups are well positioned towards reaction. This implies that one avoids excessive reactions that could otherwise end up denaturing or changing the conformation of the MHC-complex.

Likewise a dextran multimerization domain can be cross-linked with appropriately modified MHC-complexes; i.e. one or both chains of the MHC complex can be

enriched with lysine residues, increasing reactivity towards the vinylsulphone dextran. The lysine's can be inserted at positions opposite the peptide binding cleft, orienting the MHC-complexes favorably for T-cell recognition.

Another valuable chemical tool is to use extended and flexible cross-linkers. An extended linker will allow the two chains to interact with little or no strain resulting from the linker that connects them, while keeping the chains in the vicinity of each other should the complex dissociate. An excess of peptide should further favor reformation of dissociated MHC-complex.

Other TCR binding molecules

MHC I and MHC II complexes bind to TCRs. However, other molecules also bind TCR. Some TCR-binding molecules are described in the following. MHC I and MHC II complexes binding to TCRs may be substituted with other molecules capable of binding TCR or molecules that have homology to the classical MHC molecules and therefore potentially could be TCR binding molecules. These other TCR binding or MHC like molecules include:

Non-classical MHC complexes and other MHC-like molecules

Non-classical MHC complexes include protein products of MHC Ib and MHC IIb genes. MHC Ib genes encode β2m-associated cell-surface molecules but show little polymorphism in contrast to classical MHC class I genes. Protein products of MHC class Ib genes include HLA-E, HLA-G, HLA-F, HLA-H, MIC A, MIC B, ULBP-1, ULBP-2, ULBP-3 in humans and H2-M, H2-Q, H2-T and Rae1 in mice.

Non-classical MHC II molecules (protein products of MHC IIb genes) include HLA–DM, HLA-DO in humans and H2-DM and H2-DO in mice that are involved in regulation of peptide loading into MHC II molecules.

Another MHC-like molecule of special interest is the MHC I-like molecule CD1. CD1 is similar to MHC I molecules in its organization of subunits and association with β2m but presents glycolipids and lipids instead of peptides.

Artificial molecules capable of binding specific TCRs

Of special interest are antibodies that bind TCRs. Antibodies herein include full length antibodies of isotype IgG, IgM, IgE, IgA and truncated versions of these, antibody fragments like Fab fragments and scFv. Antibodies also include antibodies of antibody fragments displayed on various supramolecular structures or solid supports, including filamentous phages, yeast, mammalian cells, fungi, artificial cells or micelles, and beads with various surface chemistries.

Peptide binding TCR

Another embodiment of special interest is peptides that bind TCRs. Peptides herein include peptides composed of natural, non-natural and/or chemically modified amino acids with a length of 8-20 amino acid. The peptides could also be longer than 20 amino acids or shorter than 8 amino acids. The peptides can or can not have a defined tertiary structure.

Aptamers

Aptamers are another preferred group of TCR ligands. Aptamers are herein understood as natural nucleic acids (e.g. RNA and DNA) or unnatural nucleic acids (e.g. PNA, LNA, morpholinos) capable of binding TCR. The aptamer molecules consist of natural or modified nucleotides in various lengths.

Other TCR-binding molecules can be ankyrin repeat proteins or other repeat proteins, Avimers, or small chemical molecules, as long as they are capable of binding TCR with a dissociation constant smaller than 10^{-3} M.

Verification of correctly folded MHC-peptide complexes

Quantitative ELISA and other techniques to quantify correctly folded MHC complexes

When producing MHC multimers, it is desirable to determine the degree of correctly folded MHC.

The fraction or amount of functional and/or correctly folded MHC can be tested in a number of different ways, including:

- Measurement of correctly folded MHC in a quantitative ELISA, e.g. where the MHC bind to immobilized molecules recognizing the correctly folded complex.

- Measurement of functional MHC in an assay where the total protein concentration is measured before functional MHC is captured, by binding to e.g. immobilized TCR, and the excess, non-bound protein are measured. If the dissociation constant for the interaction is known, the amount of total and the amount of non-bound protein can be determined. From these numbers, the fraction of functional MHC complex can be determined.
- Measurement of functional MHC complex by a non-denaturing gel-shift assay, where functional MHC complexes bind to TCR (or another molecule that recognize correctly folded MHC complex), and thereby shifts the TCR to another position in the gel.

Multimerization domain

A number of MHC complexes associate with a multimerization domain to form a MHC multimer. The size of the multimerization domain spans a wide range, from multimerisation domains based on small organic molecule scaffolds to large multimers based on a cellular structure or solid support. The multimerization domain may thus be based on different types of carriers or scaffolds, and likewise, the attachment of MHC complexes to the multimerization domain may involve covalent or non-covalent linkers. Characteristics of different kinds of multimerization domains are described below.

<u>Molecular weight of multimerization domain.</u>

- In one embodiment the multimerization domain(s) in the present invention is preferably less than 1,000 Da (small molecule scaffold). Examples include short peptides (e.g. comprising 10 amino acids), and various small molecule scaffolds (e.g. aromatic ring structures).
- In another embodiment the multimerization domain(s) is preferably between 1,000 Da and 10,000 Da (small molecule scaffold, small peptides, small polymers). Examples include polycyclic structures of both aliphatic and aromatic compounds, peptides comprising e.g. 10-100 amino acids, and other polymers such as dextran, polyethylenglycol, and polyureas.
- In another embodiment the multimerization domain(s) is between 10,000 Da and 100,000 Da (Small molecule scaffold, polymers e.g. dextran, streptavidin, IgG, pentamer structure). Examples include proteins and large polypeptides,

small molecule scaffolds such as steroids, dextran, dimeric streptavidin, and multi-subunit proteins such as used in Pentamers.

- In another embodiment the multimerization domain(s) is preferably between 100,000 Da and 1,000,000 Da (Small molecule scaffold, polymers e.g. dextran, streptavidin, IgG, pentamer structure). Typical examples include larger polymers such as dextran (used in e.g. Dextramers), and streptavidin tetramers.
- In another embodiment the multimerization domain(s) is preferably larger than 1,000,000 Da (Small molecule scaffold, polymers e.g. dextran, streptavidin, IgG, pentamer structure, cells, liposomes, artificial lipid bilayers, polystyrene beads and other beads. Most examples of this size involve cells or cell-based structures such as micelles and liposomes, as well as beads and other solid supports.

As mentioned elsewhere herein multimerisation domains can comprise carrier molecules, scaffolds or combinations of the two.

Type of multimerization domain.

In principle any kind of carrier or scaffold can be used as multimerization domain, including any kind of cell, polymer, protein or other molecular structure, or particles and solid supports. Below different types and specific examples of multimerization domains are listed.

- Cell. Cells can be used as carriers. Cells can be either alive and mitotic active, alive and mitotic inactive as a result of irradiation or chemically treatment, or the cells may be dead. The MHC expression may be natural (i.e. not stimulated) or may be induced/stimulated by e.g. Inf-γ. Of special interest are natural antigen presenting cells (APCs) such as dendritic cells, macrophages, Kupfer cells, Langerhans cells, B-cells and any MHC expressing cell either naturally expressing, being transfected or being a hybridoma.
- Cell-like structures. Cell-like carriers include membrane-based structures carrying MHC-peptide complexes in their membranes such as micelles, liposomes, and other structures of membranes, and phages such as filamentous phages.
- Solid support. Solid support includes beads, particulate matters and other surfaces. A preferred embodiment include beads (magnetic or non-magnetic beads) that carry electrophilic groups e.g. divinyl sulfone activated

polysaccharide, polystyrene beads that have been functionalized with tosyl-activated esters, magnetic polystyrene beads functionalized with tosyl-activated esters), and where MHC complexes may be covalently immobilized to these by reaction of nucleophiles comprised within the MHC complex with the electrophiles of the beads. Beads may be made of sepharose, sephacryl, polystyrene, agarose, polysaccharide, polycarbamate or any other kind of beads that can be suspended in aqueous buffer.

Another embodiment includes surfaces, i.e. solid supports and particles carrying immobilized MHC complexes on the surface. Of special interest are wells of a microtiter plate or other plate formats, reagent tubes, glass slides or other supports for use in microarray analysis, tubings or channels of micro fluidic chambers or devices, Biacore chips and beads

- Molecule. Multimerization domains may also be molecules or complexes of molecules held together by non-covalent bonds. The molecules constituting the multimerization domain can be small organic molecules or large polymers, and may be flexible linear molecules or rigid, globular structures such as e.g. proteins. Different kinds of molecules used in multimerization domains are described below.
    - Small organic molecules. Small organic molecules here includes steroids, peptides, linear or cyclic structures, and aromatic or aliphatic structures, and many others. The prototypical small organic scaffold is a functionalized benzene ring, i.e. a benzene ring functionalized with a number of reactive groups such as amines, to which a number of MHC molecules may be covalently linked. However, the types of reactive groups constituting the linker connecting the MHC complex and the multimerization domain, as well as the type of scaffold structure, can be chosen from a long list of chemical structures. A non-comprehensive list of scaffold structures are listed below.

      Typical scaffolds include aromatic structures, benzodiazepines, hydantoins, piperazines, indoles, furans, thiazoles, steroids, diketopiperazines, morpholines, tropanes, coumarines, qinolines, pyrroles, oxazoles, amino acid precursors, cyclic or aromatic ring structures, and many others.

      Typical carriers include linear and branched polymers such as peptides, polysaccharides, nucleic acids, and many others. Multimerization

domains based on small organic or polymer molecules thus include a wealth of different structures, including small compact molecules, linear structures, polymers, polypeptides, polyureas, polycarbamates, cyclic structures, natural compound derivatives, alpha-, beta-, gamma-, and omega-peptides, mono-, di- and tri-substituted peptides, L- and D-form peptides, cyclohexane- and cyclopentane-backbone modified beta-peptides, vinylogous polypeptides, glycopolypeptides, polyamides, vinylogous sulfonamide peptide, Polysulfonamide-conjugated peptide (i.e., having prosthetic groups), Polyesters, Polysaccharides such as dextran and aminodextran, polycarbamates, polycarbonates, polyureas, poly-peptidylphosphonates, Azatides, peptoids (oligo N-substituted glycines), Polyethers, ethoxyformacetal oligomers, poly-thioethers, polyethylene, glycols (PEG), polyethylenes, polydisulfides, polyarylene sulfides, Polynucleotides, PNAs, LNAs, Morpholinos, oligo pyrrolinone, polyoximes, Polyimines, Polyethyleneimine, Polyacetates, Polystyrenes, Polyacetylene, Polyvinyl, Lipids, Phospholipids, Glycolipids, polycycles, (aliphatic), polycycles (aromatic), polyheterocycles, Proteoglycan, Polysiloxanes, Polyisocyanides, Polyisocyanates, polymethacrylates, Monofunctional, Difunctional, Trifunctional and Oligofunctional open-chain hydrocarbons, Monofunctional, Difunctional, Trifunctional and Oligofunctional Nonaromat Carbocycles, Monocyclic, Bicyclic, Tricyclic and Polycyclic Hydrocarbons, Bridged Polycyclic Hydrocarbones, Monofunctional, Difunctional, Trifunctional and Oligofunctional Nonaromatic, Heterocycles, Monocyclic, Bicyclic, Tricyclic and Polycyclic Heterocycles, bridged Polycyclic Heterocycles, Monofunctional, Difunctional, Trifunctional and Oligofunctional Aromatic Carbocycles, Monocyclic, Bicyclic, Tricyclic and Polycyclic Aromatic Carbocycles, Monofunctional, Difunctional, Trifunctional and Oligofunctional Aromatic Hetero-cycles. Monocyclic, Bicyclic, Tricyclic and Polycyclic Heterocycles. Chelates, fullerenes, and any combination of the above and many others.

- Biological polymers. Biological molecules here include peptides, proteins (including antibodies, coiled-coil helices, streptavidin and many others), nucleic acids such as DNA and RNA, and polysaccharides such as dextran. The biological polymers may be reacted with MHC complexes (e.g. a number of MHC complexes chemically coupled to e.g.

the amino groups of a protein), or may be linked through e.g. DNA duplex formation between a carrier DNA molecule and a number of DNA oligonucleotides each coupled to a MHC complex. Another type of multimerization domain based on a biological polymer is the streptavidin-based tetramer, where a streptavidin binds up to four biotinylated MHC complexes, as described above (see Background of the invention).

- Self-assembling multimeric structures. Several examples of commercial MHC multimers exist where the multimer is formed through self-assembling. Thus, the Pentamers are formed through formation of a coiled-coil structure that holds together 5 MHC complexes in an apparently planar structure. In a similar way, the Streptamers are based on the Streptactin protein which oligomerizes to form a MHC multimer comprising several MHC complexes (see Background of the invention).

In the following, alternative ways to make MHC multimers based on a molecule multimerization domain are described. They involve one or more of the abovementoned types of multimerization domains.

MHC dextramers can be made by coupling MHC complexes to dextran via a streptavidin-biotin interaction. In principle, biotin-streptavdin can be replaced by any dimerization domain, where one half of the dimerization domain is coupled to the MHC-peptide complex and the other half is coupled to dextran. For example, an acidic helix (one half of a coiled-coil dimer) is coupled or fused to MHC, and a basic helix (other half of a coiled-coil dimmer) is coupled to dextran. Mixing the two results in MHC binding to dextran by forming the acid/base coiled-coil structure.

Antibodies can be used as scaffolds by using their capacity to bind to a carefully selected antigen found naturally or added as a tag to a part of the MHC molecule not involved in peptide binding. For example, IgG and IgE will be able to bind two MHC molecules, IgM having a pentameric structure will be able to bind 10 MHC molecules. The antibodies can be full-length or truncated; a standard antibody-fragment includes the Fab2 fragment.

Peptides involved in coiled-coil structures can act as scaffold by making stable dimeric, trimeric, tetrameric and pentameric interactions. Examples hereof are the Fos-Jun heterodimeric coiled coil, the E. coli homo-trimeric coiled-coil domain Lpp-56, the engineered Trp-zipper protein forming a discrete, stable, α-helical pentamer in water at physiological pH.

Further examples of suitable scaffolds, carriers and linkers are streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-tranferase), glutathione, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (*Canavalia ensiformis*) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity). Combinations of such binding entities are also comprised. Non-limiting examples are streptavidin-biotin and jun-fos. In particular, when the MHC molecule is tagged, the binding entity may be an “anti-tag”. By “anti-tag” is meant an antibody binding to the tag, or any other molecule capable of binding to such tag.

MHC complexes can be multimerized by other means than coupling or binding to a multimerization domain. Thus, the multimerization domain may be formed during the multimerization of MHCs. One such method is to extend the bound antigenic peptide with dimerization domains. One end of the antigenic peptide is extended with dimerization domain A (e.g. acidic helix, half of a coiled-coil dimer) and the other end is extended with dimerization domain B (e.g. basic helix, other half of a coiled-coil dimer). When MHC complexes are loaded/mixed with these extended peptides the following multimer structure will be formed: A-MHC-BA-MHC-BA-MHC-B etc. The antigenic peptides in the mixture can either be identical or a mixture of peptides with comparable extended dimerization domains. Alternatively both ends of a peptide are extended with the same dimerization domain A and another peptide (same amino acid sequence or a different amino acid sequence) is extended with dimerization domain B. When MHC and peptides are mixed the following structures are formed: A-MHC-AB-MHC-BA-

MHC-AB-MHC-B etc. Multimerization of MHC complexes by extension of peptides are restricted to MHC II molecules since the peptide binding groove of MHC I molecules is typically closed in both ends thereby limiting the size of peptide that can be embedded in the groove, and therefore preventing the peptide from extending out of the groove.

Another multimerization approach applicable to both MHC I and MHC II complexes is based on extension of N- and C-terminal of the MHC complex. For example the N-terminal of the MHC complex is extended with dimerization domain A and the C-terminal is extended with dimerization domain B. When MHC complexes are incubated together they pair with each other and form multimers like: A-MHC-BA-MHC-BA-MHC-BA-MHC-B etc. Alternatively the N-terminal and the C-terminal of a MHC complex are both extended with dimerization domain A and the N-terminal and C-terminal of another preparation of MHC complex (either the same or a different MHC) are extended with dimerization domain B. When these two types of MHC complexes are incubated together multimers will be formed: A-MHC-AB-MHC-BA-MHC-AB-MHC-B etc.

In all the above-described examples the extension can be either chemically coupled to the peptide/MHC complex or introduced as extension by gene fusion.
Dimerization domain AB can be any molecule pair able to bind to each other, such as acid/base coiled-coil helices, antibody-antigen, DNA-DNA, PNA-PNA, DNA-PNA, DNA-RNA, LNA-DNA, leucine zipper e.g. Fos/Jun, streptavidin-biotin and other molecule pairs as described elsewhere herein.

Linker molecules

A number of MHC complexes associate with a multimerization domain to form a MHC multimer. The attachment of MHC complexes to the multimerization domain may involve covalent or non-covalent linkers, and may involve small reactive groups as well as large protein-protein interactions.
The coupling of multimerization domains and MHC complexes involve the association of an entity X (attached to or part of the multimerization domain) and an entity Y (attached to or part of the MHC complex). Thus, the linker that connects the multimerization domain and the MHC complex comprises an XY portion.

- **Covalent linker**. The XY linkage can be covalent, in which case X and Y are reactive groups. In this case, X can be a nucleophilic group (such as $–NH_2$, -OH, -SH, $-NH-NH_2$), and Y an electrophilic group (such as CHO, COOH, CO) that react to form a covalent bond XY; or Y can be a nucleophilic group and X an electrophilic group that react to form a covalent bond XY. Other possibilities exist, e.g either of the reactive groups can be a radical, capable of reacting with the other reactive group. A number of reactive groups X and Y, and the bonds that are formed upon reaction of X and Y, are shown in figure 5.

  X and Y can be reactive groups naturally comprised within the multimerization domain and/or the MHC complex, or they can be artificially added reactive groups. Thus, linkers containing reactive groups can be linked to either of the multimerization domain and MHC complex; subsequently the introduced reactive group(s) can be used to covalently link the multimerization domain and MHC complex.

  Example natural reactive groups of MHC complexes include amino acid side chains comprising $-NH_2$, -OH, -SH, and -NH-. Example natural reactive groups of multimerization domains include hydroxyls of polysaccharides such as dextrans, but also include amino acid side chains comprising $-NH_2$, -OH, -SH, and -NH- of polypeptides, when the polypeptide is used as a multimerization domain. In some MHC multimers, one of the polypeptides of the MHC complex (i.e. the β2M, heavy chain or the antigenic peptide) is linked by a protein fusion to the multimerization domain. Thus, during the translation of the fusion protein, an acyl group (reactive group X or Y) and an amino group (reactive group Y or X) react to form an amide bond. Example MHC multimers where the bond between the multimerization domain and the MHC complex is covalent and results from reaction between natural reactive groups, include MHC-pentamers (described in US patent 2004209295) and MHC-dimers, where the linkage between multimerization domain and MHC complex is in both cases generated during the translation of the fusion protein.

  Example artificial reactive groups include reactive groups that are attached to the multimerization domain or MHC complex, through association of a linker molecule comprising the reactive group. The activation of dextran by reaction of the dextran hydroxyls with divinyl sulfone, introduces a reactive vinyl group that can react with e.g. amines of the MHC complex, to form an amine that now links the multimerization domain (the dextran polymer) and the MHC complex. An

alternative activation of the dextran multimerization domain involves a multistep reaction that results in the decoration of the dextran with maleimide groups, as described in the patent Siiman et al. US 6,387,622. In this approach, the amino groups of MHC complexes are converted to –SH groups, capable of reacting with the maleimide groups of the activated dextran. Thus, in the latter example, both the reactive group of the multimerization domain (the maleimide) and the reactive group of the MHC complex (the thiol) are artificially introduced.

Sometimes activating reagents are used in order to make the reactive groups more reactive. For example, acids such as glutamate or aspartate can be converted to activated esters by addition of e.g. carbodiimid and NHS or nitrophenol, or by converting the acid moiety to a tosyl-activated ester. The activated ester reacts efficiently with a nucleophile such as $–NH_2$, -SH, -OH, etc.

For the purpose of this invention, the multimerization domains (including small organic scaffold molecules, proteins, protein complexes, polymers, beads, liposomes, micelles, cells) that form a covalent bond with the MHC complexes can be divided into separate groups, depending on the nature of the reactive group that the multimerization domain contains. One group comprise multimerization domains that carry nucleophilic groups (e.g. $–NH_2$, -OH, -SH, -CN, $-NH-NH_2$), exemplified by polysaccharides, polypeptides containing e.g. lysine, serine, and cysteine; another group of multimerization domains carry electrophilic groups (e.g. –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides), exemplified by polypeptides containing e.g. glutamate and aspartate, or vinyl sulfone activated dextran; yet another group of multimerization domains carry radicals or conjugated double bonds.

The multimerization domains appropriate for this invention thus include those that contain any of the reactive groups shown in Figure 5 or that can react with other reactive groups to form the bonds shown in Figure 5.

Likewise, MHC complexes can be divided into separate groups, depending on the nature of the reactive group comprised within the MHC complex. One group comprise MHCs that carry nucleophilic groups (e.g. $–NH_2$, -OH, -SH, -CN, -NH-

NH_2), e.g. lysine, serine, and cysteine; another group of MHCs carry electrophilic groups (e.g. –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides), exemplified by e.g. glutamate and aspartate; yet another group of MHCs carry radicals or conjugated double bonds.

The reactive groups of the MHC complex are either carried by the amino acids of the MHC-peptide complex (and may be comprised by any of the peptides of the MHC-peptide complex, including the antigenic peptide), or alternatively, the reactive group of the MHC complex has been introduced by covalent or non-covalent attachment of a molecule containing the appropriate reactive group.

Preferred reactive groups in this regard include -CSO_2OH, phenylchloride, -SH, -SS, aldehydes, hydroxyls, isocyanate, thiols, amines, esters, thioesters, carboxylic acids, triple bonds, double bonds, ethers, acid chlorides, phosphates, imidazoles, halogenated aromatic rings, any precursors thereof, or any protected reactive groups, and many others. Example pairs of reactive groups, and the resulting bonds formed, are shown in figure 5.

Reactions that may be employed include acylation (formation of amide, pyrazolone, isoxazolone, pyrimidine, comarine, quinolinon, phthalhydrazide, diketopiperazine, benzodiazepinone, and hydantoin), alkylation, vinylation, disulfide formation, Wittig reaction, Horner-Wittig-Emmans reaction, arylation (formation of biaryl or vinylarene), condensation reactions, cycloadditions ((2+4), (3+2)), addition to carbon-carbon multiplebonds, cycloaddition to multiple bonds, addition to carbon-hetero multiple bonds, nucleophilic aromatic substitution, transition metal catalyzed reactions, and may involve formation of ethers, thioethers, secondary amines, tertiary amines, beta-hydroxy ethers, beta-hydroxy thioethers, beta-hydroxy amines, beta-amino ethers, amides, thioamides, oximes, sulfonamides, di- and tri-functional compounds, substituted aromatic compounds, vinyl substituted aromatic compounds, alkyn substituted aromatic compounds, biaryl compounds, hydrazines, hydroxylamine ethers, substituted cycloalkenes, substituted cyclodienes, substituted 1, 2, 3 triazoles, substituted cycloalkenes, beta-hydroxy ketones, beta-hydroxy aldehydes, vinyl ketones, vinyl aldehydes, substituted alkenes, substituted alkenes, substituted amines, and many others.

MHC dextramers can be made by covalent coupling of MHC complexes to the dextran backbone, e.g. by chemical coupling of MHC complexes to dextran backbones. The MHC complexes can be coupled through either heavy chain or β2-microglobulin if the MHC complexes are MHC I or through α-chain or β-chain if the MHC complexes are MHC II. MHC complexes can be coupled as folded complexes comprising heavy chain/beta2microglobulin or α-chain/β-chain or either combination together with peptide in the peptide-binding cleft. Alternatively either of the protein chains can be coupled to dextran and then folded in vitro together with the other chain of the MHC complex not coupled to dextran and together with peptide. Direct coupling of MHC complexes to dextran multimerization domain can be via an amino group or via a sulphide group. Either group can be a natural component of the MHC complex or attached to the MHC complex chemically. Alternatively, a cysteine may be introduced into the genes of either chain of the MHC complex.

Another way to covalently link MHC complexes to dextran multimerization domains is to use the antigenic peptide as a linker between MHC and dextran. Linker containing antigenic peptide at one end is coupled to dextran. Antigenic peptide here means a peptide able to bind MHC complexes in the peptide-binding cleft. As an example, 10 or more antigenic peptides may be coupled to one dextran molecule. When MHC complexes are added to such peptide-dextran construct the MHC complexes will bind the antigenic peptides and thereby MHC-peptide complexes are displayed around the dextran multimerization domain. The antigenic peptides can be identical or different from each other. Similarly MHC complexes can be either identical or different from each other as long as they are capable of binding one or more of the peptides on the dextran multimerization domain.

- **Non-covalent linker.** The linker that connects the multimerization domain and the MHC complex comprises an XY portion. Above different kinds of covalent linkages XY were described. However, the XY linkage can also be non-covalent.
  Non-covalent XY linkages can comprise natural dimerization pairs such as antigen-antibody pairs, DNA-DNA interactions, or can include natural

interactions between small molecules and proteins, e.g. between biotin and streptavidin. Artificial XY examples include XY pairs such as His_6 tag (X) interacting with Ni-NTA (Y) and PNA-PNA interations.

Protein-protein interactions. The non-covalent linker may comprise a complex of two or more polypeptides or proteins, held together by non-covalent interactions. Example polypeptides and proteins belonging to this group include Fos/Jun, Acid/Base coiled coil structure, antibody/antigen (where the antigen is a peptide), and many others.

A preferred embodiment involving non-covalent interactions between polypeptides and/or proteins are represented by the Pentamer structure described in US patent 2004209295.

Another preferred embodiment involves the use of antibodies, with affinity for the surface of MHC opposite to the peptide-binding groove. Thus, an anti-MHC antibody, with its two binding site, will bind two MHC complexes and in this way generate a bivalent MHC multimer. In addition, the antibody can stabilize the MHC complex through the binding interactions. This is particularly relevant for MHC class II complexes, as these are less stable than class I MHC complexes.

Polynucleotide-polynucleotide interactions. The non-covalent linker may comprise nucleotides that interact non-covalently. Example interactions include PNA/PNA, DNA/DNA, RNA/RNA, LNA/DNA, and any other nucleic acid duplex structure, and any combination of such natural and unnatural polynucleotides such as DNA/PNA, RNA/DNA, and PNA/LNA.

Protein-small molecule interactions. The non-covalent linker may comprise a macromolecule (e.g. protein, polynucleotide) and a small molecule ligand of the macromolecule. The interaction may be natural (i.e., found in Nature, such as the Streptavidin/biotin interaction) or non-natural (e.g. His-tag peptide/Ni-NTA interaction). Example interactions include Streptavidin/biotin and anti-biotin antibody/biotin.

Combinations – non-covalent linker molecules. Other combinations of proteins, polynucleotides, small organic molecules, and other molecules, may be used to link the MHC to the multimerization domain. These other combinations include protein-DNA interactions (e.g. DNA binding protein such as the gene regulatory protein CRP interacting with its DNA recognition sequence), RNA aptamer-protein interactions (e.g. RNA aptamer specific for growth hormone interacting with growth hormone)

Synthetic molecule-synthetic molecule interaction. The non-covalent linker may comprise a complex of two or more organic molecules, held together by non-covalent interactions. Example interactions are two chelate molecules binding to the same metal ion (e.g. EDTA-Ni^{++}-NTA), or a short polyhistidine peptide (e.g. His_6) bound to NTA-Ni^{++}.

In another preferred embodiment the multimerization domain is a bead. The bead is covalently or non-covalently coated with MHC multimers or single MHC complexes, through non-cleavable or cleavable linkers. As an example, the bead can be coated with streptavidin monomers, which in turn are associated with biotinylated MHC complexes; or the bead can be coated with streptavidin tetramers, each of which are associated with 0, 1, 2, 3, or 4 biotinylated MHC complexes; or the bead can be coated with MHC-dextramers where e.g. the reactive groups of the MHC-dextramer (e.g. the divinyl sulfone-activated dextran backbone) has reacted with nucleophilic groups on the bead, to form a covalent linkage between the dextran of the dextramer and the beads.

In another preferred embodiment, the MHC multimers described above (e.g. where the multimerization domain is a bead) further contains a flexible or rigid, and water soluble, linker that allows for the immobilized MHC complexes to interact efficiently with cells, such as T-cells with affinity for the MHC complexes. In yet another embodiment, the linker is cleavable, allowing for release of the MHC complexes from the bead. If T-cells have been immobilized, by binding to the MHC complexes, the T-cells can very gently be released by cleavage of this cleavable linker. Appropriate cleavable linkers are shown in Figure 6. Most preferably, the linker is cleaved at physiological conditions, allowing for the integrity of the isolated cells.

Further examples of linker molecules that may be employed in the present invention include Calmodulin-binding peptide (CBP), 6xHIS, Protein A, Protein G, biotin, Avidine, Streptavidine, Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, GST tagged proteins, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope.

The list of dimerization- and multimerization domains, described elsewhere in this document, define alternative non-covalent linkers between the multimerization domain and the MHC complex.

The abovementioned dimerization- and multimerization domains represent specific binding interactions. Another type of non-covalent interactions involves the non-specific adsorption of e.g. proteins onto surfaces. As an example, the non-covalent adsorption of proteins onto glass beads represents this class of XY interactions. Likewise, the interaction of MHC complexes (comprising full-length polypeptide chains, including the transmembrane portion) with the cell membrane of for example dendritic cells is an example of a non-covalent, primarily non-specific XY interaction.

In some of the abovementioned embodiments, several multimerization domains (e.g. streptavidin tetramers bound to biotinylated MHC complexes) are linked to another multimerization domain (e.g. the bead). For the purpose of this invention we shall call both the smaller and the bigger multimerization domain, as well as the combined multimerization domain, for multimerization domain.

Additional features of MHC multimer, antigenic peptide or antigenic polypeptide product

Additional components may be coupled to carrier or added as individual components not coupled to carrier.

Attachment of biologically active molecules to MHC multimers

Engagement of MHC complex to the specific T cell receptor leads to a signaling cascade in the T cell. However, T-cells normally respond to a single signal stimulus by going into apoptosis. T cells needs a second signal in order to become activated and

start development into a specific activation state e.g. become an active cytotoxic T cell, helper T cell or regulatory T cell.

It is to be understood that the MHC multimer of the invention may further comprise one or more additional substituents. The definition of the terms “one or more”, “a plurality”, “a”, “an”, and “the” also apply here. Such biologically active molecules may be attached to the construct in order to affect the characteristics of the constructs, e.g. with respect to binding properties, effects, MHC molecule specificities, solubility, stability, or detectability. For instance, spacing could be provided between the MHC complexes, one or both chromophores of a Fluorescence Resonance Energy Transfer (FRET) donor/acceptor pair could be inserted, functional groups could be attached, or groups having a biological activity could be attached.

MHC multimers can be covalently or non-covalently associated with various molecules: having adjuvant effects; being immune targets e.g. antigens; having biological activity e.g. enzymes, regulators of receptor activity, receptor ligands, immune potentiators, drugs, toxins, co-receptors, proteins and peptides in general; sugar moieties; lipid groups; nucleic acids including siRNA; nano particles; small molecules. In the following these molecules are collectively called biologically active molecules. Such molecules can be attached to the MHC multimer using the same principles as those described for attachment of MHC complexes to multimerisation domains as described elsewhere herein. In brief, attachment can be done by chemical reactions between reactive groups on the biologically active molecule and reactive groups of the multimerisation domain and/or between reactive groups on the biologically active molecule and reactive groups of the MHC-peptide complex. Alternatively, attachment is done by non-covalent interaction between part of the multimerisation domain and part of the biological active molecule or between part of the MHC-peptide complex and part of the biological active molecule. In both covalent and non-covalent attachment of the biologically molecule to the multimerisation domain a linker molecule can connect the two. The linker molecule can be covalent or non-covalent attached to both molecules. Examples of linker molecules are described elsewhere herein. Some of the MHCmer structures better allows these kind of modifications than others.
Biological active molecules can be attached repetitively aiding to recognition by and stimulation of the innate immune system via Toll or other receptors.

MHC multimers carrying one or more additional groups can be used as therapeutic or vaccine reagents.

In particular, the biologically active molecule may be selected from:

- proteins such as MHC Class I-like proteins like MIC A, MIC B, CD1d, HLA E, HLA F, HLA G, HLA H, ULBP-1, ULBP-2, and ULBP-3,

- co-stimulatory molecules such as CD2, CD3, CD4, CD5, CD8, CD9, CD27, CD28, CD30, CD69, CD134 (OX40), CD137 (4-1BB), CD147, CDw150 (SLAM), CD152 (CTLA-4), CD153 (CD30L), CD40L (CD154), NKG2D, ICOS, HVEM, HLA Class II, PD-1, Fas (CD95), FasL expressed on T and/or NK cells, CD40, CD48, CD58, CD70, CD72, B7.1 (CD80), B7.2 (CD86), B7RP-1, B7-H3, PD-L1, PD-L2, CD134L, CD137L, ICOSL, LIGHT expressed on APC and/or tumour cells,

- cell modulating molecules such as CD16, NKp30, NKp44, NKp46, NKp80, 2B4, KIR, LIR, CD94/NKG2A, CD94/NKG2C expressed on NK cells, IFN-alpha, IFN-beta, IFN-gamma, IL-1, IL-2, IL-3, IL-4, IL-6, IL-7, IL-8, IL-10, IL-11, IL-12, IL-15, CSFs (colony-stimulating factors), vitamin D3, IL-2 toxins, cyclosporin, FK-506, rapamycin, TGF-beta, clotrimazole, nitrendipine, and charybdotoxin,

- accessory molecules such as LFA-1, CD11a/18, CD54 (ICAM-1), CD106 (VCAM), and CD49a,b,c,d,e,f/CD29 (VLA-4),

- adhesion molecules such as ICAM-1, ICAM-2, GlyCAM-1, CD34, anti-LFA-1, anti-CD44, anti-beta7, chemokines, CXCR4, CCR5, anti-selectin L, anti-selectin E, and anti-selectin P,

- toxic molecules selected from toxins, enzymes, antibodies, radioisotopes, chemiluminescent substances, bioluminescent substances, polymers, metal particles, and haptens, such as cyclophosphamide, methrotrexate, Azathioprine, mizoribine, 15-deoxuspergualin, neomycin, staurosporine, genestein, herbimycin A, Pseudomonas exotoxin A, saporin, Rituxan, Ricin, gemtuzumab ozogamicin, Shiga toxin, heavy metals like inorganic and organic

mercurials, and FN18-CRM9, radioisotopes such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor, and haptens such as DNP, and digoxiginin,

and combinations of any of the foregoing, as well as antibodies (monoclonal, polyclonal, and recombinant) to the foregoing, where relevant. Antibody derivatives or fragments thereof may also be used.

Biological active molecules as described above may also be attached to antigenic peptide products or antigenic polypeptide products using same principles for attachment.

DESIGN AND GENERATION OF PRODUCT TO BE USED FOR IMMUNE MONITORING, DIAGNOSIS, THERAPY OR VACCINATION

The product of the present invention may be used for immune monitoring, diagnosis, therapy and/or vaccination. The generation of product may follow some or all of the following general steps.

1. Design of antigenic peptides
2. Choise of MHC allele
3. Generation of product
4. Validation and optimization of product

Production of a MHC multimer, antigenic peptide or antigenic polypeptide diagnostic or immune monitoring reagent may follow some or all of the following steps.

1. Identify disease of interest. Most relevant diseases in this regard are infectious-, auto immune-related diseases.
2. Identify relevant protein antigen(s). This may be individual proteins, a group of proteins from a given tissue or subgroups of proteins from an organism.
3. Identify the protein sequence. Amino acid sequences can be directly found in databases or deduced from gene- or mRNA sequence e.g. using the following link http://www.ncbi.nlm.nih.gov/Genbank/index.html. If not in databases relevant proteins or genes encoding relevant proteins may be isolated and sequenced. In some cases only DNA sequences will be available without

knowing which part of the sequence is protein coding. Then the DNA sequence is translated into amino acid sequence in all reading frames.

4. Choose MHC allele(s). Decide on needed MHC allele population coverage. If a broad coverage of a given population is needed (i.e. when a generally applicable reagents are sought) the most frequently expressed MHC alleles by the population of interest may be chosen e.g. using the database http://www.allelefrequencies.net/test/default1.asp or http://epitope.liai.org:8080/tools/population/iedb_input.
In case of personalized medicine the patient is tissue typed (HLA type) and then MHC alleles may be selected according to that.
5. Run the general peptide epitope generator program described elsewhere herein on all selected amino acid sequences from step 3, thereby generating all possible epitopes of defined length (8'-, 9'-, 10'-,11'-, 13'-, 14'-, 15' and/or 16'-mers). This procedure is particularly useful when the amino acid sequence is derived from a DNA sequence not knowing the protein encoding areas.
6. If searching for broadly applicable epitope sequences, a good alternative to step 5 is to run the "intelligent" peptide epitope prediction programs on the selected amino acid sequences of step 3 using the selected MHC alleles from step 4 e.g. using epitope prediction programs like http://www.syfpeithi.de/, http://www.cbs.dtu.dk/services/NetMHC/, and http://www.cbs.dtu.dk/services/NetMHCII/.
This step can also be used supplementary to step 5 by running selected or all epitopes from the general peptide epitope generator program through one or more of the intelligent peptide epitope prediction programs.
7. If searching for broadly applicable epitope sequences, one may choose to select the epitopes with highest binding score, or the most likely proteolytic products of the species in question for the chosen MHC alleles and run them through the BLAST program (http://www.ncbi.nlm.nih.gov/blast/Blast.cgi) to validate the uniqueness of the peptides. If the peptide sequences are present in other species, evaluate the potential risk of disease states caused by the non-relevant species in relation to causing false positive results. If considered being a potential problem for evaluating the future analysis outcome, leave out the peptide. Preferably, choose unique peptide sequences only present in the selected protein.

8. Produce selected peptides as described elsewhere herein, e.g. by standard organic synthesis, and optionally test for binding to the desired MHC alleles by e.g *in vitro* folding, peptide exchange of already preloaded MHC complexes or another method able to test for peptide binding to MHC I or II molecules.
9. Generate desired MHC multimer by covalently or non-covalently attaching MHC-peptide complex(es) to multimerization domain, and optionally attach a fluorophore to the MHC multimer, as described elsewhere herein. Optionally, test efficacy in detecting specific T-cells using e.g. the methods described in the section "Detection".

The MHC multimer reagents may be used in a diagnostic procedure or kit for testing patient and control samples e.g. by flow cytometry, immune histochemistry, Elispot or other methods as described herein.

In some applications it is desirable to identify epitopes that covers several species and/or strains. E.g. the protein Bap A from Borrelia bacteria is very heterologous among Borrelia strains meaning that the amino acid sequence of this protein isolated from Borrelia different Borrelia isolates are varies. In such cases the amino acid sequence from several starins can be aligned e.g. using protein alignment programs (e.g. Vector NTI from Invitrogen) and a homologous sequence for all strains can be identified. This homologous sequence can be run through the general peptide epitope generator program and/or the "intelligent" peptide epitope prediction programs as described above to identify epitopes able to bind selected MHC alleles. The identified epitope may not nescessarily have 100% homology to amino acid stretches in any of the proteins selected for alignment. The selected epitopes can be used for generation of MHC multimer diagnostic, immune monitoring or therapeutic reagents.

Production of a MHC multimer vaccine or therapeutic reagent may follow some or all of the following steps.

1. As step 1 - 8 above for diagnostic reagent.
9. Select additional molecules (e.g. biologically active molecules, toxins) to attach to the MHC multimer as described elsewhere herein. The additional molecules can have different functionalities as e.g. adjuvants, specific activators, toxins etc.

10. Test the therapeutic reagent following general guidelines
11. Use for therapy

PROCESSES INVOLVING MHC MULTIMERS, ANTIGENIC PEPTIDES AND/OR ANTIGENIC POLYPEPTIDES.

The present invention relates to methods for detecting the presence of MHC-peptide recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer
Binding indicates the presence of MHC-peptide recognising cells.
or
(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with an antigenic peptide or antigenic polypepitde, and
(c) determining any binding of the MHC multimer generatede as a consequence of addition of antigenic peptide or antigenic polypeptide.
Binding indicates the presence of MHC-peptide recognising cells.

Such methods are a powerful tool in diagnosing various diseases. Establishing a diagnosis is important in several ways. A diagnosis provides information about the disease, thus the patient can be offered a suitable treatment regime. Also, establishing a more specific diagnosis may give important information about a subtype of a disease for which a particular treatment will be beneficial (i.e. various subtypes of diseases may involve display of different peptides which are recognised by MHC-peptide recognising cells, and thus treatment can be targeted effectively against a particular subtype). In this way, it may also be possible to gain information about aberrant cells, which emerge through the progress of the disease or condition, or to investigate whether and how T-cell specificity is affected. The binding of the MHC multimer makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC multimers displaying the peptide.

The present invention also relates to methods for monitoring MHC-peptide recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, thereby monitoring MHC-peptide recognising cells.
Or
(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with an antigenic peptide or antigenic polypeptide as defined above, and
(c) determining any binding of the MHC multimer generated as a consequence of contacting sample with antigenic peptide or antigenic polypeptide, thereby monitoring MHC-peptide recognising cells.

Such methods are a powerful tool in monitoring the progress of a disease, e.g. to closely follow the effect of a treatment. The method can i.a. be used to manage or control the disease in a better way, to ensure the patient receives the optimum treatment regime, to adjust the treatment, to confirm remission or recurrence, and to ensure the patient is not treated with a medicament which does not cure or alleviate the disease. In this way, it may also be possible to monitor aberrant cells, which emerge through the progress of the disease or condition, or to investigate whether and how T-cell specificity is affected during treatment. The binding of the MHC multimer makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC multimers displaying the peptide.

The present invention also relates to methods for establishing a prognosis of a disease involving MHC-peptide recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, thereby establishing a prognosis of a disease involving MHC-peptide recognising cells.
Or
(a) providing a sample suspected of comprising MHC-peptide recognising cells,

(b) contacting the sample with an antigenic peptide or antigenic polypeptide as defined above, and
(c) determining any binding of the MHC multimer generated as a consequence of contacting sample with antigenic peptide or antigenic polypeptide, thereby establishing a prognosis of a disease involving MHC-peptide recognising cells.

Such methods are a valuable tool in order to manage diseases, i.a. to ensure the patient is not treated without effect, to ensure the disease is treated in the optimum way, and to predict the chances of survival or cure. In this way, it may also be possible to gain information about aberrant cells, which emerge through the progress of the disease or condition, or to investigate whether and how T-cell specificity is affected, thereby being able to establish a prognosis. The binding of the MHC multimer makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC-peptide complexs displaying the peptide.

The present invention also relates to methods for determining the status of a disease involving MHC-peptide recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, thereby determining the status of a disease involving MHC-peptide recognising cells.
Or
(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with an antigenic peptide or antigenic polypeptide as defined above, and
(c) determining any binding of the MHC multimer generated as a consequence of contacting sample with antigenic peptide or antigenic polypeptide, thereby establishing a prognosis of a disease involving MHC-peptide recognising cells.

Such methods are a valuable tool in managing and controlling various diseases. A disease could, e.g. change from one stage to another, and thus it is important to be able to determine the disease status. In this way, it may also be possible to gain information about aberrant cells which emerge through the progress of the disease or

condition, or to investigate whether and how T-cell specificity is affected, thereby determining the status of a disease or condition. The binding of the MHC-peptide complex makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC-peptide complexs displaying the peptide.

The present invention also relates to methods for the diagnosis of a disease involving MHC-peptide recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, thereby diagnosing a disease involving MHC-peptide recognising cells.
Or
(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with an antigenic peptide or antigenic polypeptide as defined above, and
(c) determining any binding of the MHC multimer generated as a consequence of contacting sample with antigenic peptide or antigenic polypeptide, thereby establishing a prognosis of a disease involving MHC-peptide recognising cells.

Such diagnostic methods are a powerful tool in the diagnosis of various diseases. Establishing a diagnosis is important in several ways. A diagnosis gives information about the disease, thus the patient can be offered a suitable treatment regime. Also, establishing a more specific diagnosis may give important information about a subtype of a disease for which a particular treatment will be beneficial (i.e. various subtypes of diseases may involve display of different peptides which are recognised by MHC-peptide recognising cells, and thus treatment can be targeted effectively against a particular subtype). Valuable information may also be obtained about aberrant cells emerging through the progress of the disease or condition as well as whether and how T-cell specificity is affected. The binding of the MHC multimer makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC multimers displaying the peptide.

The present invention also relates to methods of correlating cellular morphology with the presence of MHC-peptide recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, thereby correlating the binding of the MHC-peptide multimer with the cellular morphology.

Such methods are especially valuable as applied in the field of histochemical methods, as the binding pattern and distribution of the MHC multimers can be observed directly. In such methods, the sample is treated so as to preserve the morphology of the individual cells of the sample. The information gained is important i.a. in diagnostic procedures as sites affected can be observed directly.

The present invention also relates to methods for determining the effectiveness of a medicament against a disease involving MHC-peptide recognising cells comprising the steps of

(a) providing a sample from a subject receiving treatment with a medicament,
(b) contacting the sample with a MHC multimer as defined herein, and
(c) determining any binding of the MHC multimer, thereby determining the effectiveness of the medicament.
Or
(a) providing a sample from a subject receiving treatment with a medicament,
(b) contacting the sample with an antigenic peptide or antigenic polypeptide as defined herein, and
(c) determining any binding of the MHC multimer generated as a consequence of contacting sample with antigenic peptide, thereby determining the effectiveness of the medicament.

Such methods are a valuable tool in several ways. The methods may be used to determine whether a treatment is effectively combating the disease. The method may also provide information about aberrant cells which emerge through the progress of the disease or condition as well as whether and how T-cell specificity is affected, thereby providing information of the effectiveness of a medicament in question. The binding of

the MHC multimer makes possible these options, since the binding is indicative for the presence of the MHC-peptide recognising cells in the sample, and accordingly the presence of MHC multimers displaying the peptide.

The present invention also relates to methods for manipulating MHC-peptide recognising cells populations comprising the steps of

(a) providing a sample comprising MHC-peptide recognising cells,
(b) contacting the sample with a MHC multimer immobilised onto a solid support as defined above,
(c) isolating the relevant MHC-peptide recognising cells, and
(d) expanding such cells to a clinically relevant number, with or without further manipulation.

Such ex vivo methods are a powerful tool to generate antigen-specific, long-lived human effector T-cell populations that, when re-introduced to the subject, enable killing of target cells and has a great potential for use in immunotherapy applications against various types of cancer and infectious diseases.

As used everywhere herein, the term “MHC-peptide recognising cells” are intended to mean such which are able to recognise and bind to MHC multimers. The intended meaning of “MHC multimers” is given above. Such MHC-peptide recognising cells may also be called MHC-peptide recognising cell clones, target cells, target MHC-peptide recognising cells, target MHC molecule recognising cells, MHC molecule receptors, MHC receptors, MHC peptide specific receptors, or peptide-specific cells. The term “MHC-peptide recognising cells” is intended to include all subsets of normal, abnormal and defect cells, which recognise and bind to the MHC molecule. Actually, it is the receptor on the MHC-peptide recognising cell that binds to the MHC molecule.

As described above, in diseases and various conditions, peptides are displayed by means of MHC multimers, which are recognised by the immune system, and cells targeting such MHC multimers are produced (MHC-peptide recognising cells). Thus, the presence of such MHC protein recognising cells is a direct indication of the presence of MHC multimers displaying the peptides recognised by the MHC protein

recognising cells. The peptides displayed are indicative and may involved in various diseases and conditions.

For instance, such MHC-peptide recognising cells may be involved in diseases of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft versus host and host versus graft) origin.

The MHC multimers, antigenic polypeptides and antigenic peptides of the present invention have numerous uses and are a valuable and powerful tools e.g. in the fields of therapy, diagnosis, prognosis, monitoring, stratification, and determining the status of diseases or conditions. Thus, the MHC multimers, antigenic polypeptides and/or antigenic peptides may be applied in the various methods involving the detection of MHC-peptide recognising cells.

Furthermore, the present invention relates to compositions comprising the MHC multimers, antigenic polypeptides and/or antigenic peptides in a solubilising medium. The present invention also relates to compositions comprising the MHC multimers, antigenic polypeptides and/or antigenic peptides immobilised onto a solid or semi-solid support.

The MHC multimers, antigenic polypeptides and/or antigenic peptides can be used in a number of applications, including analyses such as flow cytometry, immunohistochemistry (IHC), and ELISA-like analyses, and can be used for diagnostic, prognostic or therapeutic purposes including autologous cancer therapy or vaccines such as HIV vaccine or cancer vaccine.

The MHC multimers are very suitable as detection systems. Thus, the present invention relates to the use of the MHC multimers as defined herein as detection systems.

In another aspect, the present invention relates to the general use of antigenic, antigenic polypeptides peptides, MHC-peptide complexes and multimers of such MHC-peptide complexes in various methods. These methods include therapeutic methods, diagnostic methods, prognostic methods, methods for determining the progress and status of a disease or condition, and methods for the stratification of a patient.

The MHC multimers, antigenic polypeptides and/or antigenic peptides of the present invention are also of value in testing the expected efficacy of medicaments against or for the treatment of various diseases. Thus, the present invention relates to methods of testing the effect of medicaments or treatments, the methods comprising detecting the binding of the MHC multimers to MHC-peptide recognising cells and establishing the effectiveness of the medicament or the treatment in question based on the specificity of the MHC-peptide recognising cells.

As mentioned above, the present invention also relates generally to the field of therapy. Thus, the present invention relates per se to the antigenic peptides, antigenic polypeptides and/or the MHC multimer as defined herein for use as medicaments, and to the antigenic peptides, antigenic polypeptides and the MHC multimers for use in in vivo and ex vivo therapy.

The present invention relates to therapeutic compositions comprising as active ingredients the MHC multimers, antigenic polypeptides and/or the antigenic peptides as defined herein.

An important aspect of the present invention is therapeutic compositions comprising as active ingredients effective amounts of MHC-peptide recognising cells obtained using the MHC multimers as defined herein to isolate relevant MHC-peptide recognising cells, and expanding such cells to a clinically relevant number.

The present invention further relates to methods for treating, preventing or alleviating diseases, methods for inducing anergy of cells, as well as to methods for up-regulating, down-regulating, modulating, stimulating, inhibiting, restoring, enhancing and/or otherwise manipulating immune responses.

The invention also relates to methods for obtaining MHC-peptide recognising cells by using the MHC multimers as described herein.

Also encompassed by the present invention are methods for preparing the therapeutic compositions of the invention.

The present invention is also directed to generating MHC multimers for detecting and analysing receptors on MHC-peptide recognising cells, such as epitope specific T-cell clones or other immune competent effector cells.

It is a further object of the present invention to provide new and powerful strategies for the development of curative vaccines. This in turn will improve the possibilities for directed and efficient immune manipulations against diseases caused by tumour genesis or infection by pathogenic agent like viruses and bacteria. HIV is an important example. The ability to generate and optionally attach recombinant MHC multimers to multimerization domains, such as scaffolds and/or carrier molecules, will enable the development of a novel analytical and therapeutical tool for monitoring immune responses and contribute to a rational platform for novel therapy and "vaccine" applications.

Therapeutic compositions (e.g. "therapeutical vaccines") that stimulate specific T-cell proliferation by peptide-specific stimulation is indeed a possibility within the present invention. Thus, quantitative analysis and ligand-based detection of specific T-cells that proliferate by the peptide specific stimulation should be performed simultaneously to monitoring the generated response.

Application of MHC multimer, antigenic peptides and antigenic polypeptides in immune monitoring, diagnostics, therapy, vaccine

MHC multimers, antigenic polypeptides and antigenic peptides as described herein can be used to identify and isolate specific T cells in a wide array of applications. In principle all kind of samples possessing T cells can be analyzed using MHC multimers, antigenic peptides and/or antigenic polypeptides creating one or more MHC multimers in sample.

MHC multimers detect antigen-specific T cells of the various T cell subsets. T cells are pivotal for mounting an adaptive immune response. It is therefore of importance to be able to measure the number of specific T cells when performing a monitoring of a given immune response. Typically, the adaptive immune response is monitored by measuring the specific antibody response, which is only one of the effector arms of the immune system. This can lead to miss-interpretation of the actual clinical immune status.

In many cases intruders of the organism can hide away inside the cells, which can not provoke a humoral response. In other cases, e.g. in the case of certain viruses the intruder mutates fast, particularly in the genes encoding the proteins that are targets for the humoral response. Examples include the influenza and HIV viruses. The high rate of mutagenesis renders the humoral response unable to cope with the infection. In these cases the immune system relies on the cellular immune response. When developing vaccines against such targets one needs to provoke the cellular response in order to get an efficient vaccine.

MHC multimers, antigenic peptides and/or antigenic polypeptides compricing antigenic peptides can be used for monitoring immune responses elicited by vaccines.
One preferred embodiment of the present invention is monitoring the effect of vaccines against infectious disease, e.g. vaccines against Lyme Borreliosis. Lyme Borreliosis is a dangerous, multisystem and multiorgan disease caused by infection with the bacterial spirochete Borrelia Burgdorferi senso lato and therefore the possibilities of prophylaxis are of great importance. Many Borrelia vaccines aim at eliciting an antibody response, but since the Borrelia bacteria have proven to be able to go inside cells a vaccine eliciting a cellular cytotoxic response is desirable. MHC multimers can be used to monitor the effectiveness of such a vaccine, where MHC multimers are any MHC multimer that can be added to a sample or one or more MHC multimers generated in sample by addition of antigenic peptide or antigenic polypeptide.
MHC multimers, antigenic peptides and/or antigenic polypeptides themself can also be valuable as a Borrelia vaccine in order to elicit a cellular immune response.
In one embodiment of the present invention MHC multimers having many MHC molecules attached to the multimerisation domain are used as vaccine. Such MHC multimers are able to bind several TCR simultaneously thereby crosslinking the receptors resulting in activation of the T cell in question. Example MHC multimers usefull as vaccine are MHC dextramers where many MHC molecules are coupled to dextran. In principle any MHC multimer as described elsewhere herein that are able to bind several TCR's simultaneously can be used.
In another embodiment of the present invention antigenic peptides and/or antigenic polypeptides are used as a vaccine eliciting a T cell responses directed against the peptide(s). Following administration of such vaccine antigenic peptides and/or antigenic polypeptides are taken up by antigen presenting cells, processed inside cell and displayed as MHC-peptide complexes on the surface of the antigen presenting cells

thereby generating cell-based MHC multimers in sample. Such antigen presenting cells displaying antigenic peptide by MHC molecules may then bind TCR on antigen specific T cells and elicit a specific T cell immune response against the antigenic peptides.

In a Borrelia vaccine the antigenic peptides used as vaccine themselves, comprised in antigenic polypeptides or bound in the peptide binding cleft of MHC molecules in MHC multimers are derived from antigenic borrelia proteins. In vaccines against other infectious agents peptides derived from antigenic proteins of the relevant pathogen are used.

To further enhance the MHC-peptide specific stimulation of the T cell bound, T cell stimulatory molecules can be coupled to the multimerisation domain together with MHC or may be added as soluble adjuvant together with the MHC multimer, antigenic peptide and/or antigenic polypeptide. Example T cell stimulatory molecules include but are not limited to IL-2, CD80 (B7.1), CD86 (B7.2), anti-CD28 antibody, CD40, CD37ligand (4-1BBL), IL-6, IL-15,IL-21, IFN-γ, IFN-α, IFN-β, CD27 ligand, CD30 ligand, IL-23, IL-1α and IL-1β.

One or more T cell stimulatory molecules may be added together with or coupled to MHC multimer, antigenic peptide and/or antigenic polypeptide. Likewise other adjuvants or molecules enhancing or otherwise affecting the cellular, humoral or innate immune response may be coupled to or added together with the MHC multimer, antigenic peptide and/or antigenic polypeptide vaccine.

The number of antigen-specific cytotoxic T cells can be used as surrogate markers for the overall wellness of the immune system. The immune system can be compromised severely by natural causes such as HIV infections or big traumas or by immuno suppressive therapy in relation to transplantation. The efficacy of an anti HIV treatment can be evaluated by studying the number of common antigen-specific cytotoxic T cells, specific against for example Cytomegalovirus (CMV) and Epstein- Barr virus. In this case the measured T cells can be conceived as surrogate markers. The treatment can then be corrected accordingly and a prognosis can be made.

A similar situation is found for patients undergoing transplantation as they are severely immune compromised due to pharmaceutical immune suppression to avoid organ rejection. The suppression can lead to outbreak of opportunistic infections caused by reactivation of otherwise dormant viruses residing in the transplanted patients or the

grafts. This can be the case for CMV and EBV viruses. Therefore measurement of the number of virus specific T cells can be used to give a prognosis for the outcome of the transplantation and adjustment of the immune suppressive treatment. Similarly, the BK virus has been implied as a causative reagent for kidney rejection. Therefore measurement of BK-virus specific T cells can have prognostic value.
Measurement of borrelia bacteria specific T cells or T cells specific for other latent bacterial infcetions can also have a prognostic value.

MHC multimers, antigenic peptide and/or antigenic polypeptide can be of importance in diagnosis of infections caused by bacteria, virus and parasites that hide away inside cells. Serum titers can be very low and direct measurement of the disease-causing organisms by PCR can be very difficult because the host cells are not identified or are inaccessible. Other clinical symptoms of a chronical infection can be unrecognizable in an otherwise healthy individuals, even though such persons still are disease-carriers and at risk of becoming spontaneously ill if being compromised by other diseases or stress.
MHC multimers, antigenic peptide and/or antigenic polypeptide can be of importance in diagnosis of infections caused by bacteria, virus and parasites especially those hiding inside cells. Clinical symptoms of a chronic infection can be unrecognizable in otherwise healthy individuals, even though such persons still are disease-carriers and at risk of becoming spontaneously ill if being compromised by other diseases or stress. In some acute infections the clinical symptoms are similar to clinical symptoms of completely unrelated diseases and therefore diagnosis of the disease is difficult based on clinical symptoms alone. Many infectious agents can be detected directly eg by measurement in serum. However, serum titers of the infectious agent can for other infectious agents be very low and therefore hard to measure. For intracellular pathogens direct measurement of the disease-causing organisms by e.g. PCR can be very difficult because the host cells are not identified or are inaccessible. Instead of detecting the infectious agent directly the immune response elicited by the infections agent may be measured.
Infections caused by extracellular bacteria and parasites often mediate a humoral immune response that can be monitored by measuring the specific antibody response. An alternative to measure antibodies could be measurement of CD4+ T cells which are important for establishing a humoral response.

Likewise infections caused by virus, intracellular bacteria or other infectious agents able to go inside cells can be detected by measurement of CD8+ T cells specific for the infectious agent.

An example of an infectious disease where MHC multimers, antigenic peptide and/or antigenic polypeptide could be usefull is in diagnosis of Borreliosis also called Lyme disease caused by Borrelia bacteria. Borrelia bacteria are very difficult to detect directly due to low serum titers and their ability to stay inside cells of unknown origin. Clinical symptoms caused by infection with borrelia bacteria depend on the type of bacteria and are similar to clinical symptoms of other diseases. Borrelia specific CD4+ and CD8+ T cells can be measured in serum, cerebrospinal fluid and/or joint fluid from infected individuals. The presence of a Borrelia infection can be measured using MHC multimers able to detect Borrelia specific T cells in liquid samples, preferably blood, from patients suspected to have borreliosis. Such MHC multimers may be added directly to sample or alternatively antigenic peptide and/or antigenic polypeptide may be added to sample and then cell-based MHC multimer generated in sample as described elsewhere herein.

Other bacterial infections where MHC multimers could be usefull for diagnosis is infections caused by intracellular bacteria like Brucella, Bartonella, Mycobacterium, Listeria, Rickettsia, Chlamydia and Salmonella.

MHC multimers can in principle be applied to diagnosis of any infection caused by an infectious agent eliciting a cellular immune response by measurement of antigen-specific T cells or changes in the amount antigen-specific T cells in the circulation.

Antigen-specific T helper cells and regulatory T cells have been implicated in the development of autoimmune disorders. In most cases the timing of events leading to autoimmune disease is unknown and the exact role of the immune cells not clear. Use of MHC multimers to study these diseases will lead to greater understanding of the disease-causing scenario and make provisions for development of therapies and vaccines for these diseases.

Therapeutic use of MHC multimers, antigenic peptide and/or antigenic polypeptide is possible, either directly or as part of therapeutic vaccines. In therapies involving T cells, e.g. treatment with *in vitro* amplified antigen-specific effector T cells, the T cells often do not home effectively to the correct target sites but ends up in undesired parts of the body. If the molecules responsible for interaction with the correct homing receptor can

be identified these can be added to the MHC multimer making a dual, triple or multiple molecular structure that are able to aid the antigen-specific T cells home to the correct target, as the MHC multimer will bind to the specific T cell and the additional molecules will mediate binding to the target cells.

In a preferable embodiment, MHC multimers bound to other functional molecules are employed to directly block, regulate or kill the targeted cells.

In a preferable embodiment, MHC multimers bound to other functional molecules are employed to directly block, regulate or kill these cells.

In another aspect of the present invention modulation of regulatory T cells could be part of a treatment. In diseases where the function of regulatory T cells is understood it may be possible to directly block, regulate or kill these regulatory cells by means of MHC multimers that besides MHC-peptide complexes also features other functional molecules. The MHC multimers specifically recognize the target regulatory T cells and direct the action of the other functional molecules to this target T cell.

Diseases

MHC multimers, antigenic peptides and/or antigenic polypeptides can be used in immune monitoring, diagnostics, prognostics, therapy and vaccines for many different diseases, including but not limited to the diseases listed in the following.

a) **Infectious diseases caused by virus** such as,
Adenovirus (subgropus A-F), BK-virus, CMV (Cytomegalo virus, HHV-5), EBV (Epstein Barr Virus, HHV-4), HBV (Hepatitis B Virus), HCV (Hepatitis C virus), HHV-6a and b (Human Herpes Virus-6a and b), HHV-7, HHV-8, HSV-1 (Herpes simplex virus-1, HHV-1), HSV-2 (HHV-2), JC-virus, SV-40 (Simian virus 40), VZV (Varizella-Zoster-Virus, HHV-3), Parvovirus B19, Haemophilus influenza, HIV-1 (Human immunodeficiency Virus-1), HTLV-1 (Human T-lymphotrophic virus-1), HPV (Human Papillomavirus giving rise to clinical manifestions such as Hepatitis, AIDS, Measles, Pox, Chicken pox, Rubella, Herpes and others.

b) **Infectious diseases** *caused by bacteria such as,*
Gram positive bacteria, gram negative bacteria, intracellular bacterium, extracellular bacterium, Mycobacterium tuberculosis, Mycobacterium bovis, Mycobacterium avium

subsp. Paratuberculosis, Borrelia burgdorferi, Borrelia Garinii, Borrelia Afzelii, other spirochetes, Helicobacter pylori, Streptococcus pneumoniae, Listeria monocytogenes, Histoplasma capsulatum, Bartonella henselae, Bartonella quintana giving rise to clinical manifestations such as Tuberculosis, Pneumonia, Stomach ulcers, Paratuberculosis and others.

c) **Infectious diseases** *caused by fungus such as,*
Aspergillus fumigatus, Candida albicans, Cryptococcus neoformans, Pneumocystis carinii giving rise to clinical manifestations such as skin-, nail-, and mucosal infections, Meningitis, Sepsis and others.

d) Parasitic diseases caused by parasites such as,
Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae, Schistosoma mansoni, Schistosoma japonicum, Schistosoma haematobium, Trypanosoma cruzi, Trypanosoma rhodesiense, Trypanosoma gambiense, Leishmania donovani, and Leishmania tropica.

e) Allergic diseases caused by allergens such as,
Birch, Hazel, Elm, Ragweed, Wormwood, Grass, Mould, Dust Mite giving rise to clinical manifestations such as Asthma.

f) Transplantation-related diseases caused by
reactions to minor histocompatibility antigens such as HA-1, HA-8, USP9Y, SMCY, TPR-protein, HB-1Y and other antigens in relation to**,** Graft-versus-host-related disease, allo- or xenogene reactions i.e. graft-versus-host and host-versus-graft disease.

g) Cancerous diseases associated with antigens such as
Survivin, Survivin-2B, Livin/ML-IAP, Bcl-2, Mcl-1, Bcl-X(L), Mucin-1, NY-ESO-1, Telomerase, CEA, MART-1, HER-2/neu, bcr-abl, PSA, PSCA, Tyrosinase, p53, hTRT, Leukocyte Proteinase-3, hTRT, gp100, MAGE antigens, GASC, JMJD2C, JARD2 (JMJ), JHDM3a, WT-1,CA 9, Protein kinases, where the cancerous diseases include malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostatic cancer, pancreatic cancer, brain cancer, head and

neck cancer, leukemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer.

h) Autoimmune and inflammatory diseases, associated with antigens such as GAD64, Collagen, human cartilage glycoprotein 39, β-amyloid, Aβ42, APP, Presenilin 1, where the autoimmune and inflammatory diseases include Diabetes type 1, Rheumatoid arthritis, Alzheimer, chronic inflammatory bowel disease, Crohn's disease, ulcerative colitis uterosa, Multiple Sclerosis, Psoriasis

Approaches to the analysis or treatment of diseases

For each application of a MHC multimer, antigenic peptide or antigenic polypeptide, a number of choices must be made. These include:

A. Disease (to be e.g. treated, prevented, diagnosed, monitored).
B. Application (e.g. analyze by flow cytometry, isolate specific cells, induce an immune response)
C. Label (e.g. should the MHC multimer be labelled with a fluorophore or a chromophore)
D. Biologically active molecule (e.g. should a biologically active molecule such as an interleukin be added or chemically linked to the complex)
E. Peptide sequence (e.g. decide on the sequence of one or more antigenic peptide to be complexed with MHC, encoded in antigenic polypeptide or used as product itself)
F. MHC (e.g. use a MHC allele that does not interfere with the patient's immune system in an undesired way. This step is directly relevant for use of MHC multimers but also indirectly applicable when using antigenic peptide or polypeptide since these will following addition to assay/individual bind MHC molecules in sample/individual generating MHC multimer in sample/individual as described elsewhere herein).

A number of diseases A_1-A_n, relevant in connection with MHC multimers, antigenic peptide or antigenic polypeptide, have been described herein; a number of applications B_1-B_n, relevant in connection with MHC multimers, antigenic peptide or antigenic polypeptide, have been described herein; a number of Labels C_1-C_n, relevant in connection with MHC multimers, have been described herein; a number of biologically active molecules D_1-D_n, relevant in connection with MHC multimers antigenic peptide

or antigenic polypeptide, have been described herein; a number of peptide sequences E_1-E_n, relevant in connection with MHC multimers, antigenic peptide or antigenic polypeptide, have been described herein; and a number of MHC molecules F_1-F_n, relevant in connection with MHC multimers, have been described herein.

Thus, each approach involves a choice to be made regarding all or some of the parameters A-F. A given application and the choices it involves can thus be described as follows:

Ai x Bi x Ci x Di x Ei x Fi

Where i specifies a number between 1 and n. n is different for different choices A, B, C, D, E, or F. Consequently, the present invention describes a large number of approaches to the diagnosis, monitoring, prognosis, therapeutic or vaccine treatment of diseases. The total number of approaches, as defined by these parameters, are

n(A) x n(B) x n(C) x n(D) x n(E) x n(F),

where n(A) describes the number of different diseases A described herein, n(B) describes the number of different applications B described herein, etc.

Detection

Diagnostic procedures, immune monitoring and some therapeutic processes of the present invention all involve identification and/or enumeration and/or isolation of antigen-specific T cells. Identification and enumeration of antigen-specific T cells may be done in a number of ways, and several assays are currently employed to provide this information.

In the following it is described how MHC multimers, antigenic peptides and/or antigenic polypeptides as described in the present invention can be used to detect specific T cell receptors (TCRs) and thereby antigen-specific T cells in a variety of methods and assays. In the present invention detection includes detection of the presence of antigen-specific TCR/ T cells in a sample, detection of and isolation of cells or entities with antigen-specific TCR from a sample and detection and enrichment of cells or entities with antigen-specific TCR in a sample.

The sample may be a biological sample including solid tissue, solid tissue section and fluid samples such as, but not limited to, whole blood, serum, plasma, nasal secretions, sputum, urine, sweat, saliva, transdermal exudates, pharyngeal exudates, bronchoalveolar lavage, tracheal aspirations, cerebrospinal fluid, synovial fluid, fluid from joints, vitreous fluid, vaginal or urethral secretions, seemen, or the like. Herein, disaggregated cellular tissues such as, for example, hair, skin, synovial tissue, tissue biopsies and nail scrapings are also considered as biological samples.

Many of the assays and methods described in the present inevntion are particularly useful for assaying T-cells in blood samples. Blood samples includes but is not limited to whole blood samples or blood processed to remove erythrocytes and platelets (e.g., by Ficoll density centrifugation or other such methods known to one of skill in the art) and the remaining PBMC sample, which includes the T-cells of interest, as well as B-cells, macrophages and dendritic cells, is used directly. Also included are blood samples processed in other ways e.g. isolating various subsets of blood cells by selecting or deselecting cells or entities in blood.

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In order to be able to detect specific T cells by MHC multimers, labels and marker molecules can be used.

Marker molecules

Marker molecules are molecules or complexes of molecules that bind to other molecules. Marker molecules thus may bind to molecules on entities, including the desired entities as well as undesired entities. Labeling molecules are molecules that may be detected in a certain analysis, i.e. the labeling molecules provide a signal detectable by the used method. Marker molecules, linked to labeling molecules, constitute detection molecules. Likewise labeling molecules linked to MHC multimers also constitute detection molecules but in contrast to detection molecules made up of marker and lebelling molecule labeled MHC multimers are specific for TCR.
Sometimes a marker molecule in itself provides a detectable signal, wherefore attachment to a labeling molecule is not necessary.
Marker molecules are typically antibodies or antibodyfragments but can also be aptamers, proteins, peptides, small organic molecules, natural compounds (e.g. steroids), non-peptide polymers, or any other molecules that specifically and efficiently bind to other molecules are also marker molecules.

Labelling molecules

Labelling molecules are molecules that can be detected in a certain analysis, i.e. the labelling molecules provide a signal detectable by the used method. The amount of labelling molecules can be quantified.

The labelling molecule is preferably such which is directly or indirectly detectable.

The labelling molecule may be any labelling molecule suitable for direct or indirect detection. By the term “direct” is meant that the labelling molecule can be detected per se without the need for a secondary molecule, i.e. is a “primary” labelling molecule. By the term “indirect” is meant that the labelling molecule can be detected by using one or more “secondary” molecules, i.e. the detection is performed by the detection of the binding of the secondary molecule(s) to the primary molecule.

The labelling molecule may further be attached via a suitable linker. Linkers suitable for attachment to labelling molecules would be readily known by the person skilled in the art and as described elsewhere herein for attachment of MHC molecules to multimerisation domains.

Examples of such suitable labelling compounds are fluorescent labels, enzyme labels, radioisotopes, chemiluminescent labels, bioluminescent labels, polymers, metal particles, haptens, antibodies, and dyes.

The labelling compound may suitably be selected:

from fluorescent labels such as 5-(and 6)-carboxyfluorescein, 5- or 6-carboxy-fluorescein, 6-(fluorescein)-5-(and 6)-carboxamido hexanoic acid, fluorescein isothio-cyanate (FITC), rhodamine, tetramethylrhodamine, and dyes such as Cy2, Cy3, and Cy5, optionally substituted coumarin including AMCA, PerCP, phycobiliproteins including R-phycoerythrin (RPE) and allophycoerythrin (APC), Texas Red, Princeston Red, Green fluorescent protein (GFP) and analogues thereof, and conjugates of R-phycoerythrin or allophycoerythrin and e.g. Cy5 or Texas Red, and inorganic fluorescent labels based on semiconductor nanocrystals (like quantum dot and Qdot™ nanocrystals), and time-resolved fluorescent labels based on lanthanides like Eu3+ and Sm3+,

from haptens such as DNP, biotin, and digoxiginin,

from enzymic labels such as horse radish peroxidase (HRP), alkaline phosphatase (AP), beta-galactosidase (GAL), glucose-6-phosphate dehydrogenase, beta-N-acetyl-glucosaminidase, ß-glucuronidase, invertase, Xanthine Oxidase, firefly luciferase and glucose oxidase (GO),

from luminiscence labels such as luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines, and

from radioactivity labels such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor.

Radioactive labels may in particular be interesting in connection with labelling of the peptides harboured by the MHC multimers.

Different principles of labelling and detection exist, based on the specific property of the labelling molecule. Examples of different types of labelling are emission of radioactive radiation (radionuclide, isotopes), absorption of light (e.g. dyes, chromophores), emission of light after excitation (fluorescence from fluorochromes), NMR (nuclear magnetic resonance form paramagnetic molecules) and reflection of light (scatter from e.g. such as gold-, plastic- or glass –beads/particles of various sizes and shapes). Alternatively, the labelling molecules can have an enzymatic activity, by which they catalyze a reaction between chemicals in the near environment of the labelling molecules, producing a signal, which include production of light (chemi-luminescence), precipitation of chromophor dyes, or precipitates that can be detected by an additional layer of detection molecules. The enzymatic product can deposit at the location of the enzyme or, in a cell based analysis system, react with the membrane of the cell or diffuse into the cell to which it is attached. Examples of labelling molecules and associated detection principles are shown in table 2 below.

Table 2: Examples of labelling molecules and associated detection principles.

Labelling substance	Effect	Assay-principle
Fluorochromes	emission of light having a specific spectra	¤Photometry, Microscopy, spectroscopy PMT, photographic film, CCD's (Color-Capture Device or Charge-coupled device).
Radionuclide	irradiation, α, ß or gamma rays	Scintillation counting, GM-tube, photographic film, excitation of phosphor-imager screen
Enzyme; HRP,(horse reddish peroxidase), peroxidases in general	catalysis of H_2O_2 reduction using luminol as Oxygen acceptor, resulting in oxidized luminal + light	¤Photometry, Microscopy, spectroscopy PMT, photographic film, CCD's (Colour-Capture Device or Charge-coupled device), Secondary label linked antibody
	catalysis of H_2O_2 reduction using a soluble dye, or molecule containing a hapten, such as a biotin residue as Oxygen acceptor, resulting in precipitation. The habten can be recognized by a detection molecule.	
Particles; gold, polystyrene beads, pollen and other particles	Change of scatter, reflection and transparency of the associated entity	Microscopy, cytometry, electron microscopy PMT's, light detecting devices, flowcytometry scatter
AP (Alkaline Phosphatase)	Catalyze a chemical conversion of a non-detectable to a precipitated detectable molecule, such as a dye or a hapten	¤Photometry, Microscopy, spectroscopy Secondary label linked antibody
Ionophores or chelating chemical compounds binding to specific ions, e.g. Ca^{2+}	Change in absorption and emission spectrums when binding. Change in intensity	¤Photometry, Cytometry, spectroscopy
Lanthanides	Fluorescence	¤photometry, cytometry, spectroscopy
	Phosphorescence	
	Paramagnetic	NMR (Nuclear magnetic resonance)
DNA fluorescing stains	Propidium iodide Hoechst stain DAPI AMC DraQ5™ Acridine orange 7-AAD	¤Photometry, cytometry, spectroscopy

¤Photometry; is to be understood as any method that can be applied to detect the intensity, analyze the wavelength spectra, and or measure the accumulation of light derived form a source emitting light of one or multiple wavelength or spectra.

Labelling molecules can be used to label MHC multimers as well as other reagents used together with MHC multimers, e.g. antibodies, aptamers or other proteins or molecules able to bind specific structures in another protein, in sugars, in DNA or in other molecules. In the following molecules able to bind a specific structure in another molecule are named a marker.

Labelling molecules can be attached to a given MHC multimer or any other protein marker by covalent linkage as described for attachment of MHC multimers to multimerization domains elsewhere herein. The attachment can be directly between reactive groups in the labelling molecule and reactive groups in the marker molecule or the attachment can be through a linker covalently attached to labelling molecule and marker, both as described elsewhere herein. When labelling MHC multimers the label can be attached either to the MHC complex (heavy chain, β2m or peptide) or to the multimerization domain.

In particular,

one or more labelling molecules may be attached to the carrier molecule, or
one or more labelling molecules may be attached to one or more of the scaffolds, or
one or more labelling compounds may be attached to one or more of the MHC complexes, or one or more labelling compounds may be attached to the carrier molecule and/or one or more of the scaffolds and/or one or more of the MHC complexes, or one or more labelling compounds may be attached to the peptide harboured by the MHC molecule.

A single labelling molecule on a marker does not always generate sufficient signal intensity. The signal intensity can be improved by assembling single label molecules into large multi-labelling compounds, containing two or more label molecule residues. Generation of multi-label compounds can be achived by covalent or non-covalent, association of labelling molecules with a major structural molecule. Examples of such structures are synthetic or natural polymers (e.g. dextramers), proteins (e.g. streptavidin), or polymers. The labelling molecules in a multi-labelling compound can all be of the same type or can be a mixture of different labelling molecules.

In some applications, it may be advantageous to apply different MHC complexs, either as a combination or in individual steps. Such different MHC multimers can be

differently labelled (i.e. by labelling with different labelling compounds) enabling visualisation of different target MHC-peptide recognising cells. Thus, if several different MHC multimers with different labelling compounds are present, it is possible simultaneously to identify more than one specific receptor, if each of the MHC multimers presents a different peptide.

Detection principles, such as listed in Table 2, can be applied to flow cytometry, stationary cytometry, and batch-based analysis. Most batch–based approaches can use any of the labelling substances depending on the purpose of the assay. Flow cytometry primarily employs fluorescence, whereas stationary cytometry primarily employs light absorption, e.g. dyes or chromophore deposit from enzymatic activity. In the following section, principles involving fluorescence detection will be exemplified for flow cytometry, and principles involving chromophore detection will be exemplified in the context of stationary cytometry. However, the labelling molecules can be applied to any of the analyses described in this invention.

Labelling molecules of particular utility in Flow Cytometry:

In flowcytometry the typical label is detected by its fluorescence. Most often a positive detection is based on the presents of light from a single fluorochrome, but in other techniques the signal is detected by a shift in wavelength of emitted light; as in FRET based techniques, where the exited fluorochrome transfer its energy to an adjacent bound fluorochrome that emits light, or when using Ca^{2+} chelating fluorescent props, which change the emission (and absorption) spectra upon binding to calcium. Preferably labelling molecules employed in flowcytometry are illustrated in Table 3 and 4 and described in the following.

Simple fluorescent labels:

- Fluor dyes, Pacific Blue™, Pacific Orange™, Cascade Yellow™,
- AlexaFluor®(AF);
    - AF405, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750, AF800
- Quantum Dot based dyes, QDot® Nanocrystals (Invitrogen, MolecularProbs)

- Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800

- DyLight™ Dyes (Pierce) (DL);
  - DL549, DL649, DL680, DL800
- Fluorescein (Flu) or any derivate of that, ex. FITC
- Cy-Dyes
  - Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7
- Fluorescent Proteins;
  - RPE, PerCp, APC
  - Green fluorescent proteins;
    - GFP and GFP-derived mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine, mStrawberry, mCherry
- Tandem dyes:
  - RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed
  - APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5
- Ionophors; ion chelating fluorescent props
  - Props that change wavelength when binding a specific ion, such as Calcium
    Props that change intensity when binding to a specific ion, such as Calcium
- Combinations of fluorochromes on the same marker. Thus, the marker is not identified by a single fluorochrome but by a code of identification being a specific combination of fluorochromes, as well as inter related ratio of intensities.
  Example: Antibody Ab1 and Ab2, are conjugated to both. FITC and BP but Ab1 have 1 FITC to 1 BP whereas Ab2 have 2 FITC to 1 BP. Each antibodymay then be identified individually by the relative intensity of each fluorochrome. Any

such combinations of n fluorochromes with m different ratios can be generated.

Table 3: Examples of preferable fluorochromes

Fluorofor / Fluorochrome	Excitation nm	Emission nm
2-(4'-maleimidylanilino)naphthalene-6-sulfonic acid, sodium salt	322	417
5-((((2-iodoacetyl)amino)ethyl)amino) naphthalene-1-sulfonic acid	336	490
Pyrene-1-butanoic acid	340	376
AlexaFluor 350 (7-amino-6-sulfonic acid-4-methyl coumarin-3-acetic acid)	346	442
AMCA (7-amino-4-methyl coumarin-3-acetic acid)	353	442
7-hydroxy-4-methyl coumarin-3-acetic acid	360	455
Marina Blue (6,8-difluoro-7-hydroxy-4-methyl coumarin-3-acetic acid)	362	459
7-dimethylamino-coumarin-4-acetic acid	370	459
Fluorescamin-N-butyl amine adduct	380	464
7-hydroxy-coumarine-3-carboxylic acid	386	448
CascadeBlue (pyrene-trisulphonic acid acetyl azide)	396	410
Cascade Yellow	409	558
Pacific Blue (6,8 difluoro-7-hydroxy coumarin-3-carboxylic acid)	416	451
7-diethylamino-coumarin-3-carboxylic acid	420	468
N-(((4-azidobenzoyl)amino)ethyl)- 4-amino-3,6-disulfo-1,8-naphthalimide, dipotassium salt	426	534
Alexa Fluor 430	434	539
3-perylenedodecanoic acid	440	448
8-hydroxypyrene-1,3,6-trisulfonic acid, trisodium salt	454	511
12-(N-(7-nitrobenz-2-oxa-1,3- diazol-4-yl)amino)dodecanoic acid	467	536
N,N'-dimethyl-N- (iodoacetyl)-N'-(7-nitrobenz-2- oxa-1,3-diazol-4-yl)ethylenediamine	478	541
Oregon Green 488 (difluoro carboxy fluorescein)	488	518
5-iodoacetamidofluorescein	492	515
Propidium iodide-DNA adduct	493	636
Carboxy fluorescein	495	519

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Table 4: Examples of preferable fluorochrome families

Fluorochrome family	Example fluorochrome
AlexaFluor®(AF)	AF®350, AF405, AF430, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750, AF800
Quantum Dot (Qdot®) based dyes	Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800
DyLight™ Dyes (DL)	DL549, DL649, DL680, DL800
Small fluorescing dyes	FITC, Pacific Blue™, Pacific Orange™, Cascade Yellow™, Marina blue™, DSred, DSred-2, 7-AAD, TO-Pro-3,
Cy-Dyes	Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7
Phycobili Proteins:	R-Phycoerythrin (RPE), PerCP, Allophycocyanin (APC), B-Phycoerythrin, C-Phycocyanin
Fluorescent Proteins	(E)GFP and GFP ((enhanced) green fluorescent protein) derived mutant proteins; BFP, CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine, mStrawberry, mCherry
Tandem dyes with RPE	RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed
Tandem dyes with APC	APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5
Calcium dyes	Indo-1-Ca2+ Indo-2-Ca2+

Preferably labelling molecules employed in stationary cytometry and IHC

- Enzymatic labelling, as exemplified in Table 5:
    - Horse radish peroxidase; reduces peroxides (H_2O_2),and the signal is generated by the Oxygen acceptor when being oxidized.
        - Precipitating dyes; Dyes that when they arereduced they are soluble, and precipitate when oxidized, generating a coloured deposit at the site of the reaction.
        - Precipitating agent, carrying a chemical residue, a hapten, for second layer binding of marker molecules, for amplification of the primary signal.
        - Luminol reaction, generating a light signal at the site of reaction.
    - Other enzymes, such as Alkaline Phosphatase, capable of converting a chemical compound from a non-detectable molecule to a precipitated

detectable molecule, which can be coloured, or carries a hapten as described above.

- Fluorescent labels, as exemplified in Table 3 and 4; as those described for Flow cytometry are likewise important for used in stationary cytometry, such as in fluorescent microscopy.

Table 5: Examples of preferable labels for stationary cytometry

Label	Enzyme substrate, Oxygen acceptor Chromogen / precipitating agent	Precipitate or Residue, hapten* for secondary detection layer	Binding partner to hapten
HRP	diaminobenzidine (DAB)	Colored precipitate	-
HRP	3-amino-9-ethyl-carbazole (AEC+)	Colored precipitate	-
AP	Fast red dye	Red precipitate	-
HRP	biotinyl tyramide	Exposed Biotin residue	Streptavidin, avidine
HRP	fluorescein tyramide	Exposed Fluorescein residue	Anti-Fluorecein Antibody
“Enzyme"	Substrate that when reacted precipitate	Primary label; being a dye, chemiluminescence’s, or exposure of a hapten	Secondary label in case the primary label is a hapten

Detection methods and principles

MHC multimers can be used to detect T-cell receptors (TCR) e.g. T-cells carrying specific TCR. For example, the MHC multimers can be labelled with fluorophores and used in flow cytometer, the MHC multimers can be labelled with chromophores, in order to specifically stain specific T-cells carrying TCRs that specifically bind the MHC multimer in question in e.g. sections of solid tissues using IHC.

ELISA and ELISA-like analyses can be performed with MHC multimers that are labelled with e.g. chromophores, fluorophores or enzymes.

MHC multimers can be used in a wide range os other methods using various principles. In the following methods and principles using MHC multimers for detection of TCR are outlined.

Detection of TCRs with MHC multimers may be direct or indirect.

Direct detection

Direct detection of TCRs is detection directly of the binding interaction between the specific T cell receptor and the MHC multimer. The MHC multimer may be generated and then added to sample or alternatively MHC multimers are generated in sample by addition of antigenic peptide and MHC molecules attached to multimerization domain to sample.

Direct detection includes detection of TCR when TCR is attached to lipid bilayer (e.g. T cells), when TCR is attached to or in a solid medium or when TCR is in solution.

Direct detection of TCR attached to lipid bilayer

One type of TCRs to detect and measure are TCRs attached to lipid bilayer including but not limited to naturally occurring T cells (from blood, spleen, lymphnode, brain or any other tissue containing T cells), TCR transfected cells, T cell hybridomas, TCRs embedded in liposomes or any other membrane structure. In the following methods for direct detection of entities of TCRs attached to lipid bilayer will be described and any entity consisting of TCR attached to lipid bilayer will be referred to as T cells.

T cells can be directly detected either when in a fluid solution or when immobilized to a solid support.

Direct detection of T cells in fluid sample.

T cells can be detected in fluid samples using the methods described below including but not limited to detection of T cells in culture media, in buffers, in water or in other liquids and also suspensions of disrupted tissues e.g. homogenized tissue resuspended in the fluids described above. T cells in fluid samples can be detected individually or detected as populations of T cells. In the following different methods for direct detction of T cells in fluid samples are described.

Direct detection of individual T cells

- *Direct detection of individual T cells using flow cytometry.*

  An example of direct detection of individual T cells by flow cytometry is measurement of antigen specific T cells using MHC multimers like Tetramers, Pentamers, Dextramers or similar types of reagents.

Briefly, a suspension of T cells are added MHC multimers, the sample washed and then the amount of MHC multimer bound to each cell are measured. Bound MHC multimers may be labelled directly or measured through addition and binding of labelled marker molecules. The sample is analyzed using a flow cytometer, able to detect and count individual cells passing in a stream through a laser beam. For identification of specific T cells using MHC multimers, cells are stained with fluorescently labeled MHC multimer by incubating cells with fluorochrome labelled MHC multimer and then forcing the cells with a large volume of liquid through a nozzle creating a stream of spaced cells. Each cell passes through a laser beam and any fluorochrome bound to the cell is excited and thereby fluoresces. Sensitive photomultipliers detect emitted fluorescence, providing information about the amount of MHC multimer bound to the cell. By this method MHC multimers can be used to identify specific T cell populations in liquid samples such as blood, CSF, synovial fluid, cell cultures or any other liquid sample containing T cells..

When analyzing blood samples whole blood can be used with or without lysis of red blood cells. Alternatively lymphocytes can be purified from blood before flow cytometry analysis e.g. using a standard procedure like a Ficoll-Hypaque gradient. Another possibility is to isolate lymphocytes, subgroups of lymphocytes, T cells or subgroups of T cells from the blood sample for example by affinity purification like binding to antibody coated surfaces, followed by elution of bound cells. This purified lymphocyte or T cell population can then be used for flow cytometry analysis together with MHC multimers.

Instead of actively isolating T cells or subgroups of lymphocytes unwanted cells like B cells, NK cells or any other unwanted cells or substances can be removed prior to the analysis. One way to do this is by affinity purification e.g. using columns or beads or other surfaces coated with antibodies specific for the unwanted cells. Alternatively, specific antibodies recognizing the unwanted cells can be added to the blood sample together with complement proteins, thereby killing cells recognized by the antibodies.

Various gating reagents can be included in the analysis. Gating reagents here means labeled antibodies or other labeled marker molecules identifying subsets of cells by binding to unique surface proteins. Preferred gating reagents when using MHC multimers are antibodies or other marker molecules directed against CD3, CD4, and CD8 identifying major subsets of T cells. Other preferred gating

reagents are antibodies or marker molecules specifically binding CD14, CD15, CD19, CD25, CD56, CD27, CD28, CD45, CD45RA, CD45RO, CCR7, CCR5, CD62L, Foxp3, CD95, CD127, CD7, CD57, CD154 or other specific proteins or molecules unique for different lymphocytes of the immune system.

Following labelling with MHC multimers and before analysis on a flow cytometer stained cells can be treated with a fixation reagent e.g. formaldehyde to cross-link bound MHC multimer to the cell surface. Stained cells can also be analyzed directly without fixation.

The number of cells in a sample can vary. When the target cells are rare, it is preferable to analyze large amounts of cells. In contrast, fewer cells are required when looking at T cell lines or samples containing many cells of the target cell type.

The flow cytometer can be equipped to separate and collect particular types of cells. This is called cell sorting. MHC multimers in combination with sorting on a flowcytometer can be used to isolate specific T cell populations. Isolated specific T cell populations can then be further manipulated as described elsewhere herein, e.g. expanded *in vitro*. This can be useful in autologous cancer therapy.

Amounts of MHC-peptide specific T cells in a blood sample can be determined by flow cytometry by calculating the amount of MHC multimer labeled cells in a given volumen of sample with a given cell density and then back calculate. Exact enumeration of specific T cells is better achieved by incubating sample with MHC multimers (and optionally gating reagents) together with an exact amount of counting beads followed by flow cytometry analysis. Counting beads is here to be understood as any fluorescent bead with a size that can be visualized in a sample containing T cells by flow cytometry. The beads could e.g. be made of polystyrene with a size of about 1-10 μm. They could also be made of agarose, polyacrylamide, silica, or any other material, and have any size between 0,1 μm and 100 μm. The counting beads are used as reference population to measure the exact volume of analyzed sample. The sample are analyzed on a flow cytometer and the amount of MHC-specific T cell detected can then be correlated with the amount of counting beads in the same volume

of the sample and an exact number of MHC-peptide specific T cells determined using the following equation:

Concentration of MHC-specific T-cell in sample = (number of MHC-peptide specific T cells counted/number of counting beads counted) x concentration of counting beads in sample

Alternatively MHC multimers are added to one tube (below denoted tube 1) together with sample and counting beads are added to a separate tube (below denoted tube 2) containing the same sample but no MHC multimers. To both tubes one or more gating reagents are added able to identify other cell subsets in sample e.g. CD3+, CD4+, CD8+, CD19+, CD56+ cells. The exact amount of one of the cell subsets for which gating reagents are included are then calculated from the tube containing counting beads. For example if CD8+ cells are measured in both tubes the following equation can be used to determine the exact concentration of CD8+ cells in the sample:

(((number of CD8+ cells counted (tube 2)) / (number of counting beads counted (tube 2))) x (concentration of counting beads in sample) = exact concentration of CD8+ cells in sample

The exact concentration of CD8+ cells in sample are then used to determine the exact concentration of MHC-specific T cells in sample using the equation:

(Calculated exact concentration of CD8+ cells in sample (calculated from tube 2)) x (MHC-specific T cells counted as percentage of CD8+ events counted in sample (tube 1)) = concentration of MHC-specific T-cell in sample

- *Direct detection of individual T cells in fluid sample by microscopy*

A suspension of T cells are added MHC multimers, the sample washed and then the amount of MHC multimer bound to each cell are measured. Bound MHC multimers may be labelled directly or labelled through addition of labelled marker molecules. The sample is then spread out on a slide or similar in a thin layer able to distinguish individual cells and labelled cells identified using a microscope. Depending on the type of label different types of microscopes may

be used, e.g. if fluorescent labels are used a fluorescent microscope is used for the analysis. For example MHC multimers can be labeled with a flourochrome or bound MHC multimer detected with a fluorescent antibody. Cells with bound fluorescent MHC multimers can then be visualized using an immunofluorescence microscope or a confocal fluorescence microscope.

Direct detection of populations of T cells

- Cell suspensions are added labeled MHC multimer, samples are washed and then total signal from label are measured. The MHC multimers may be labeled themselves or detected through a labeled marker molecule.

- Cell suspensions are added labeled MHC multimer, samples are washed and then signal from label are amplified and then total signal from label and/or amplifier are measured.

Direct detection of immobilized T cells.

T cells may be immobilized and then detected directly. Immobilization can be on solid support, in solid tissue or in fixator (e.g. paraffin, a sugar matrix or another medium fixing the T cells).

Direct detection of T cells immobilized on solid support.

In a number of applications, it may be advantageous to immobilize the T cell onto a solid or semi-solid support. Such support may be any which is suited for immobilisation, separation etc. Non-limiting examples include particles, beads, biodegradable particles, sheets, gels, filters, membranes (e. g. nylon membranes), fibres, capillaries, needles, microtitre strips, tubes, plates or wells, combs, pipette tips, micro arrays, chips, slides, or indeed any solid surface material. The solid or semi-solid support may be labelled, if this is desired. The support may also have scattering properties or sizes, which enable discrimination among supports of the same nature, e.g. particles of different sizes or scattering properties, colour or intensities.

Conveniently the support may be made of glass, silica, latex, plastic or any polymeric material. The support may also be made from a biodegradable material.

Generally speaking, the nature of the support is not critical and a variety of materials may be used. The surface of support may be hydrophobic or hydrophilic.

Preferred are materials presenting a high surface area for binding of the T cells. Such supports may for example be porous or particulate e.g. particles, beads, fibres, webs, sinters or sieves. Particulate materials like particles and beads are generally preferred due to their greater binding capacity. Particularly polymeric beads and particles may be of interest.

Conveniently, a particulate support (e.g. beads or particles) may be substantially spherical. The size of the particulate support is not critical, but it may for example have a diameter of at least 1 µm and preferably at least 2 µm, and have a maximum diameter of preferably not more than 10 µm and more preferably not more than 6 µm. For example, particulate supports having diameters of 2.8 µm and 4.5 µm will work well.

An example of a particulate support is monodisperse particles, i.e. such which are substantially uniform in size (e. g. size having a diameter standard deviation of less than 5%). Such have the advantage that they provide very uniform reproducibility of reaction. Monodisperse particles, e.g. made of a polymeric material, produced by the technique described in US 4,336,173 (ref. 25) are especially suitable.

Non-magnetic polymer beads may also be applicable. Such are available from a wide range of manufactures, e.g. Dynal Particles AS, Qiagen, Amersham Biosciences, Serotec, Seradyne, Merck, Nippon Paint, Chemagen, Promega, Prolabo, Polysciences, Agowa, and Bangs Laboratories.

Another example of a suitable support is magnetic beads or particles. The term "magnetic" as used everywhere herein is intended to mean that the support is capable of having a magnetic moment imparted to it when placed in a magnetic field, and thus is displaceable under the action of that magnetic field. In other words, a support comprising magnetic beads or particles may readily be removed by magnetic aggregation, which provides a quick, simple and efficient way of separating out the beads or particles from a solution. Magnetic beads and particles may suitably be paramagnetic or superparamagnetic. Superparamagnetic beads and particles are e.g.

described in EP 0 106 873 (Sintef, ref. 26). Magnetic beads and particles are available from several manufacturers, e.g. Dynal Biotech ASA (Oslo, Norway, previously Dynal AS, e.g. Dynabeads®).

The support may suitably have a functionalised surface. Different types of functionalisation include making the surface of the support positively or negatively charged, or hydrophilic or hydrophobic. This applies in particular to beads and particles. Various methods therefore are e.g. described in US 4,336,173 (ref. 25), US 4,459,378 (ref. 27) and US 4,654,267 (ref. 28).

Immobilized T cells may be detected in several ways including:

- *Direct detection of T cells directly immobilized on solid support.*
  T cells may be directly immobilized on solid support e.g. by non-specific adhesion. Then MHC multimers are added to the immobilized T cells thereby allowing specific T cells to bind the MHC multimers. Bound MHC multimer may be measured through label directly attached to the multimer or through labeled marker molecules. Individual T cells may be detected if the method for analysis is able to distinguish individual labelled cells, e.g. cells are immobilized in a monolayer on a cell culture well or a glass slide. Following staining with labelled multimer a digital picture is taken and labelled cells identified and counted. Alternatively a population of T cells is detected by measurement of total signal from all labelled T cells, e.g. cells are plated to wells of a microtiter plate, stained with labelled MHC multimer and total signal from each well are measured.

- *Direct detection of T cells immobilized on solid support through linker molecule*
  T cells can also be immobilized to solid support through a linker molecule. The linker molecule can be an antibody specific for the T cell, a MHC multimer, or any molecule capable of binding T cells. In any case the linker may be attached directly to the solid support, to the solid support through another linker, or the linker molecule may be embedded in a matrix, e.g. a sugar matrix.
  Then MHC multimers are added to the immobilized T cells thereby allowing specific T cells to bind the MHC multimers. Bound MHC multimer may be measured through label directly attached to the multimer or through labeled

marker molecules. Individual T cells may be detected if the method for analysis is able to distinguish individual labelled cells, e.g. a digital picture is taken and labelled cells identified and counted.

By using a specific MHC multimer both for the immobilization of the T-cells and for the labelling of immobilized cells (e.g. by labelling immobilized cells with chromophore- or fluorophore-labelled MHC multimer), a very high analytical specificity may be achieved because of the low background noise that results.

Alternatively a population of T cells is detected by measurement of total signal from all labeled T cells.

- *Immuno profiling: Phenotyping T cell sample using MHC multimer beads or arrays.*

Different MHC multimers are immobilized to different beads with different characteristics (e.g. different size, different fluorophores or different fluorescence intensities) where each kind of bead has a specific type of MHC multimer molecule immobilized. The immobilization may be direct or through a linker molecule as described above. The amount of bound T cells to a specific population of beads can be analyzed, thereby phenotyping the sample. The TCR on the T cell is defined by the MHC multimer and hence the bead to which it binds.

Likewise, MHC multimers can be immobilized in an array, e.g. on a glass plate or pin array so that the position in the array specifies the identity of the MHC multimer. Again, the immobilization may be direct or through a linker molecule as described above. After addition of T cells, the amount of bound T cells at a specified position in the array can be determined by addition of a label or labelled marker that binds to cells in general, or that binds specifically to the cells of interest. For example, the cells may be generally labelled by the addition of a labelled molecule that binds to all kinds of cells, or specific cell types, e.g. CD4+ T-cells, may be labelled with anti-CD4 antibodies that are labelled with e.g. a chromophore or fluorophore. Either of these approaches allow a phenotyping of the sample. An example for the use of immuno profiling is given below.

- Profiling of an individual's disease-specific T-cell repertoire.
  Mass profiling of the T-cells of an individual may be done by first immobilizing specific MHC multimers (e.g. 10-10^6 different MHC multimers, each comprising a specific MHC-peptide combination) in an array (e.g. a glass plate), adding e.g. a blood sample from the individual, and then after washing the unbound cells off, label the immobilized cells. Positions in the array of particularly high staining indicate MHC-peptide combinations that recognize specific T-cells of particularly high abundance or affinity. Thus, an immuno profiling of the individual with regard to the tested MHC-peptide combinations is achieved. A similar profiling of an individuals disease may be made using MHC multimers immobilized to different beads as described above.

Whether the profiling is performed using beads or arrays, the profiling may entail a number of diseases, a specific disease, a set of specific antigens implicated in one or more diseases, or a specific antigen (e.g. implicated in a specific disease or set of diseases).
In a preferred embodiment, an individual's immuno profile for a particular antigen is obtained. Thus, peptides corresponding to all possible 8'-, 9'- 10'- and 11'-mer peptide sequences derived from the peptide antigen sequence are generated, for example by standard organic synthesis or combinatorial chemistry, and the corresponding MHC multimers are produced, using one or more of the class I MHC-alleles of the individual in question. Further, peptides of e.g. 13, 14, 15, 16 and upto 25 amino acids length may be generated, for example by organic synthesis or combinatorial chemistry, corresponding to all 13', 14', 15', 16' and upto 25'-mers of the antigen, and the corresponding class II MHC multimers are produced, using one or more of the class II MHC-alleles of the individual in question. For a complete profiling for this particular antigen, all of the HLA-alleles of the individual in question should be used for the generation of the array; i.e., if the HLA class I haplotype of the individual is HLA-A*02, HLA-A*03, HLA-B*08 and HLA-B*07, all these HLA class I alleles should be combined with every tested peptide and similarly for all HLA class II alleles of the given individual.
Based on the profile, a personalized drug, -vaccine or -diagnostic test may be produced.

The principle described above may also be employed to distinguish between the immune response raised against a disease (e.g. an infection with a bacterium or the formation of a tumour), and the immune response raised against a vaccine for the same disease (in the example, a vaccine against the bacterium or the tumour). Most vaccines consists of subcomponents of the pathogen /tumour they are directed against and/or are designed to elicit an immune response different from the natural occuring immune response i.e. the T cell epitopes of the two immune reponses differs. Thus, by establishing the immuno profile, using a comprehensive array (i.e. an array that comprises all possible epitopes from one or more antigen(s)) or a subset of these epitopes, it is possible to deduce whether the immune response has been generated against the disease or the vaccine, or against both the disease and the vaccine. If the vaccine raises a response against a particular epitope or a particular set of epitopes, the corresponding positions in the array will give rise to high signals (compared to the remaining positions). Similarly a natural generated immune response will be directed against other and/or more particular epitopes and therefore give rise to high signals in other positions and/or more positions in the array. When an individual is vaccinated the immuno profile will reflect the effect of the vaccination on the immune response, and even if the individual has encountered the disease before and has generated a general immune response towards this disease, it will still be possible to deduce from the profiling whether this individual also has generated a specific response against the vaccine.

In another preferred embodiment, an individual's immuno profile for a set of antigens implicated in a specific disease is obtained. A subset of epitopes from a number of antigens is used. Thus, this is not a comprehensive profiling of this individual with regard to these antigens, but careful selection of the epitopes used may ensure that the profiling data can be used afterwards to choose between e.g. a limited set of vaccines available, or the data can be used to evaluate the immune response of the individual following an infection, where the epitopes used have been selected in order to avoid interference from related infectious diseases.

As above, a personalized drug, -vaccine or -diagnostic test may be produced. based on the information obtained from the immuno profiling.

In yet another preferred embodiment, the array comprising all possible 8'-, 9'-10'- and 11'-mer peptide sequences derived from a given peptide antigen, and all 13, 14, 15 and 16'-mers of the same antigen, are synthesized and assembled in MHC multimers, and immobilized in an array. Then, the ability of the individual peptide to form a complex with MHC is tested. As an example, one may add labelled W6/32 antibody, an antibody that binds correctly folded MHC I heavy chain, when this heavy chain is assembled together with antigenic peptide and beta2microglobulin, and which therefore can be used to detect formation of MHC-peptide complex, as binding of W6/32 antibody is usually considered a strong indication that the MHC-peptide complex has been formed. The ability of different peptides to enter into a MHC-peptide complex may also be promoted by the addition to the array of T-cells. Specific T-cells will drive the formation of the corresponding specific MHC-peptide complexes. Thus, after addition of T-cells to the array, the MHC-peptide complex integrity can be examined by addition of the labelled W6/32 antibody or other antibodies specific for correct conformation. Positions on the array that have strong signals indicate that the peptide that was added to MHC and immobilized at this position, was capable of forming the MHC-peptide complex in the presence of specific T-cells. Alternatively, the binding of the specific T-cells to the corresponding MHC-peptide complexes may be detected directly through a labbelled antibody specific for the T cell.

Direct detection of immobilized T cells followed by sorting

Specific T cells or specific T cell subsets can be isolated from a sample containing other T cells, T cell subsets and/or other cells by immobilization of the wanted specific T cells in sample to solid support as described above followed by washing and elution. For example, MHC multimers are immobilized to a support e.g. beads, immunotubes, wells of a microtiterplate, CD, mircrochip or similar as decribed elsewhere herein, then a suspension of T cells (the sample) are added allowing specific T cells to bind MHC multimer molecules. Following washing bound T cells are recovered/eluted (e.g. using acid or competition with one or more competitor molecules) and counted.

Specific T-cells can e.g.be isolated through the use of bead-based MHC multimers. Bead-based MHC multimers are beads whereto monomer MHC-peptide complexes or MHC multimers are immobilized.

The isolated T cells can following elution optionally be manipulated further before final use. For example the isolated cells can be activated (to differentiate or proliferate), they can undergo induced apoptosis, or undesired cells of the isolated cell population can be removed. Then, the manipulated cell population can be re-introduced into the patient from which the sample originate, or can be introduced into another patient.

A typical cell sorting experiment, based on bead-based MHC multimers, would follow some of the steps of the general procedure outlined in general terms in the following:

Acquire the sample, e.g. a cell sample from the blood or bone marrow of a cancer patient.

Block the sample with a protein solution, e.g. BSA or skim milk.

Block the beads coated with MHC complexes or MHC multimers, with BSA or skim milk.

Mix MHC-coated beads and the cell sample, and incubate.

Wash the beads with washing buffer, to remove unbound cells and non-specifically bound cells.

Isolate the immobilized cells, by either cleavage of the linker that connects MHC complex/MHC multimer and bead; or alternatively, release the cells by a change in pH, salt-concentration addition of competitive binding molecule or the like. Preferably, the cells are released under conditions that do not disrupt the integrity of the cells.

Manipulate the isolated cells (e.g. induce apoptosis, proliferation or differentiation)

Direct detection of T cells in solid tissue.

- *Direct detection of T cells in solid tissue in vitro.*

  Example direct detection of T cells in solid tissue *in vitro* include but is not limited til Immunohsitochemistry (IHC). IHC is here referred to as the detection of antigens in solid tissue by antibodies or other marker molecules labelled with a labelling molecule as described elsewhere herein.

  For *in vitro* methods of the present invention solid tissue includes tissue, tissue biopsies, frozen tissue or tissue biopsies, paraffin embedded tissue or tissue biopsies and sections of either of the above mentioned. In a preferred method of this invention sections of fixed or frozen tissues are incubated with MHC multimer, allowing MHC multimer to bind to specific T cells in the tissue section.

The MHC multimer may be labeled directly or through a labeled marker molecule. As an example, the MHC multimer can be labeled with a tag that can be recognized by e.g. a secondary antibody, optionally labeled with HRP or another label. The bound MHC multimer is then detected by its fluorescence or absorbance (for fluorophore or chromophore), or by addition of an enzyme-labeled antibody directed against this tag, or another component of the MHC multimer (e.g. one of the protein chains, a label on the multimerization domain). The enzyme can be Horse Raddish Peroxidase (HRP) or Alkaline Phosphatase (AP), both of which convert a colorless substrate into a colored reaction product *in situ.* This colored deposit identifies the binding site of the MHC multimer, and can be visualized under a light microscope. The MHC multimer can also be directly labeled with e.g. HRP or AP, and used in IHC without an additional antibody.

The tissue sections may derive from blocks of tissue or tissue biopsies embedded in paraffin, and tissue sections from this paraffin-tissue block fixed in formalin before staining. This procedure may influence the structure of the TCR in the fixed T cells and thereby influence the ability to recognize specific MHC complexes. In this case, the native structure of TCR needs to be at least partly preserved in the fixed tissue. Fixation of tissue therefore should be gentle. Alternatively, the staining is performed on frozen tissue sections, and the fixation is done after MHC multimer staining.

- *Direct detection of T cells in solid tissue in vivo*

For in vivo detection of T cells labeled MHC multimers are injected in to the body of the individual to be investigated. The MHC multimers may be labeled with e.g. a paramagnetic isotope. Using a magnetic resonance imaging (MRI) scanner or electron spin resonance (ESR) scanner MHC multimer binding T cells can then be measured and localized. In general, any conventional method for diagnostic imaging visualization can be utilized. Usually gamma and positron emitting radioisotopes are used for camera and paramagnetic isotopes for MRI.

The methods described above for direct detection of TCR embedded in lipid bilayers collectively called T cells using MHC multimers also applies to detection of TCR in solution and detection of TCR attached to or in a solid medium. Though detection of individual TCRs may not be possible when TCR is in solution.

Indirect detection of TCR

Indirect detection of TCR is primarily usefull for detection of TCRs embedded in lipid bilayer, preferably natural occurring T cells, T cell hybridomas or transfected T cells. MHC multimers used for the indirect detection may be generated and then added to sample. Alternatively MHC multimers are generated in sample by addition of antigenic peptide and/or antigenic polypeptide to sample and optionally also addition of MHC molecules, components of MHC molecules or MHC molecules coupled to carrier. For example when antigenic peptide and/or antigenic polypeptide is added to a sample containing antigen presenting cells, the antigenic peptide and/or antigenic polypeptide are taken up by antigen presenting cells in sample, processed inside cells and displayed on their surface by binding MHC molecules, or the antigenic peptides added are bound directly to MHC molecules displayed on the surface of antigen presenting cells by exchange with peptide already present in the peptide binding cleft of the MHC molecules.

In indirect detection, the number or activity of T cells are measured, by detection of events that are the result of TCR-MHC-peptide complex interaction. Interaction between MHC multimer and T cell may stimulate the T cell resulting in activation of T cells, in cell division and proliferation of T cell populations or alternatively result in inactivation of T cells. All these mechanism can be measured using various detection methods.

Indirect detection of T cells by measurement of activation.

MHC multimers, e.g. antigen presenting cells, can stimulate T cells resulting in activation of the stimulated T cells. Activation of T cell can be detected by measurement of production of specific soluble factor from the stimulated T cell, e.g. production of cytokines like INFγ and IL2. Stimulation of T cells can also be detected by measurement of changes in expression of specific surface receptors, or by measurement of T cell effector functions.

Measurement of activation of T cells involves the following steps:

a) Antigenic peptide is added to a sample of T cells containing antigen presenting cells, preferably a suspension of cells e.g. blood. The antigenic peptide have to be able to bind MHC I or MHC II molecules of one or more antigen presenting cells in the sample thereby generating one or more cell based MHC multimer(s) in sample. Alternatively, antigenic polypeptide protein or protein fragment containing one or

more antigenic peptides sequences is added to such sampe. The protein/protein fragmentsantigenic polypeptide is then taken up by antigen presenting cells in sample, processed into antigenic peptides and presented by MHC I or MHC II molecules on the surface of antigen presenting cells thereby creating cell based MHC multimers in the sample. Several different antigenic peptides or antigenic proteins polypeptides may be added to the sample. The peptide-loaded antigen presenting cells (the cell based MHC multimers) can then stimulate specific T cells in sample, and thereby induce the production of soluble factor, up- or down-regulation of surface receptors, or mediate other changes in the T cell, e.g. enhancing effector functions.

Alternatively, one or more MHC multimer(s) containing one or more antigenic peptide(s) are added to a sample containing T cells, preferably a suspension of cells, to stimulate MHC multimer specific T cells in sample and thereby induce production of soluble factor, up- or down-regulation of surface receptor and/or other changes in the T cell.

Following addition of antigenic peptide, antigenic proteinantigenic polypeptide or MHC multimer to sample, a second soluble factor, e.g. cytokine and/or growth factor(s) may optionally be added to facilitate continued activation and expansion of antigen-specific T cells

b) Detection of the presence of produced soluble factor, the presence/ absence of surface receptor or detection of effector function.

Correlate the measured result with presence of T cells. The measured signal/response indicates the presence of specific T cells that have been stimulated with particular MHC multimer. The signal/response of a T lymphocyte population is a measure of the overall response in sample.

The frequency of specific T cells able to respond to a given MHC multimer can be determined by including a limiting-dilution culture in the assay also called a Limiting dilution assay.

The limiting-dilution culture method involves the following steps:

i. Sample of T cells in suspension are plated into culture wells at increasing dilutions.

ii. Antigen presenting cells are provided into the sample if not already in sample and then antigenic peptide or protein polypeptide containing one or

more antigenic peptide sequence(s) is added to the sample as described above thereby creating cell based MHC multimers in sample able to stimulate antigen-specific T cells in the sample. Alternatively, already generated MHC multimers are added to sample to stimulate specific T cells.

Optionally growth factors, cytokines or other factors helping T cells to proliferate are added.

iii. Cells are allowed to grow and proliferate (½- several days). Each well that initially contained a specific T cell will make a response to the MHC multimer and divide.

iv. Wells are tested for a specific response e.g. production of soluble factors, cell proliferation, cytotoxicity or other effector functions.

The assay is replicated with different numbers of T cells in the sample, and each well that originally contained a specific T cell will make a response to the MHC multimer. The frequency of specific T cells in the sample equals the reciprocal of the number of cells added to each well when 37% of the wells are negative, because due to Poisson distrubtion each well then on average contained one specific T cell at the beginning of the culture.

Optionally step i) and ii) from above maybe reversed, e.g. adding sample containing T cells in various dilutions to wells or containers containing MHC multimer, antigenic peptide, antigenic peptide + antigen presenting cells, antigenic polypeptide or antigenic polypeptide+ antigen presenting cells or MHC multimer..

In the following various methods to measure production of specific soluble factor, expression of surface receptors, effector functions or proliferation is described.

Indirect detection of T cells by measurement of production of soluble factors.

Indirect detection of T cells by measurement of secreted soluble factors.

Secreted soluble factors can be measured directly in fluid suspension or the soluble factor captured by immobilization on solid support and then detected or an effect of the secreted soluble factor can be detected.

Examples of such detection methods are interferon gamma release assays (IGRA's) like Quantiferon, enzyme-linked immunospot (ELISPOT) and cytokine flow cytometry

(CFC), where INF-γ released from antigen stimulated T cells are measured. Principles of the various and alternative assays are described in more details below.

- *Indirect detection of T cells by measurement of secreted soluble factor directly in fluid sample.*

  A sample of T cells are added MHC multimer or antigenic peptideMHC multimer and/or antigenic peptide and/or antigenic polypeptide as described above to induce production and secretion of soluble factors from antigen-specific T cells. The secreted soluble factors can be measured directly in the supernatant using e.g. mass spectrometry.

- *Indirect detection of T cells by capture of secreted soluble factor on solid support.*

  A sample of T cells are added MHC multimer and/or, antigenic peptide and/or antigenic proteinantigenic polypeptide as described above to induce production and secretion of soluble factors from antigen-specific T cells. Secreted soluble factors in the supernatant are then immobilized on a solid support either directly or through a linker as described for immobilization of T cells elsewhere herein. Then immobilized soluble factors can be detected using labeled marker molecules.

Soluble factors secreted from **individual** T cells can be detected using ELISPOT assays or related techniques. The principle is capturing of the secreted soluble factors locally by marker molecules, e.g antibodies specific for the soluble factor. Soluble factor recognised by marker molecules are immobilised on a solid support together with T cells and soluble factors secreted by individual T cells are thereby captured in the proximity of each T cell. Bound soluble factor can then be measured using labelled marker molecules specific for the captured soluble factor. The number of T cells that has given rise to labelled spots on solid support can then be enumerated and these spots indicate the presence of specific T cells that have been stimulated with particular MHC multimer and/or antigenic peptide and/or antigenic polypeptide.

Soluble factors secreted from **a population** of T cells are detected by capture and detection of soluble factor secreted from the entire population of specific T cells. In this case soluble factor do not have to be captured locally close to each T cell but the secreted soluble factors my be captured and detected in the same well or container as where the T cells are, or supernatant containing secreted soluble factor transferred to another solid support with marker molecules for capture e.g. beads or wells of ELISA plate. An example of such an assay is QuantiFERON or QuantiFERON like assays measuring secretion of INF-γ from antigen stimulated T cells.

- *Indirect detection of T cells immobilized to solid support in a defined pattern.* Different MHC multimers, or MHC-peptide complexes are immobilized to a support to form a spatial array in a defined pattern, where the position specifies the identity of the MHC multimer/MHC-peptide complex immobilized at this position. Marker molecules able to bind T cell secreted soluble factors are co-spotted together with MHC multimer/MHC-peptide complex. Such marker molecules can e.g. be antibodies specific for cytokines like INFγ or IL-2. The immobilization may be direct or through a linker molecule as described above. Then a suspension of labeled T cells are added or passed over the array of MHC multimers/MHC-peptide complexes and specific T cells will bind to the immobilized MHC multimers/MHC-peptide complexes and upon binding be stimulated to secrete soluble factors e.g. cytokines like INFγ ord IL-2. Soluble factors secreted by individual T cells are then captured in the proximity of each T cell and bound soluble factor can be measured using labelled marker molecule specific for the soluble factor. The number and position of different specific T cells that has given rise to labelled spots on solid support can then be identified and enumerated. In this way T cells bound to defined areas of the support are analyzed, thereby, phenotyping the sample. Each individual T cell is defined by the TCR it expose and depending on these TCRs each entity will bind to different types of MHC multimers/MHC-peptide complexes immobilized at defined positions on the solid support.
  Alternatively to MHC multimers or MHC-peptide comlexes antigenic peptides or antigenic polypeptides can be immobilized to a support to form a spatial array in a defined pattern, where the position specifies the identity of the antigenic peptide/antigenic polypeptide immobilized. As described above marker

molecules able to bind T cell secreted soluble factors are co-spotted together with antigenic peptide/antigenic polypeptide. Before or together with addition of the suspension of T cells, MHC molecules, components of MHC molecules or MHC molecules attached to carrier are added to the array thereby generating MHC multimers. Then antigen specific T cells in sample are detected as described above.

- *Indirect detection of T cells by measurement of secreted soluble factor on surface of T cell*

An alternative way to detect secretion of soluble factor from individual cells is to use soluble factor capture on the surface of the T cell secreting the soluble factor. This can be done by using a bispecific capture molecule able to bind a component on the surface of the T cell with one part of the capture molecule and bind the secreted soluble factor by another part of the capture molecule. Example useful capture molecules are bispecific antibodies in which two different heavy- and light chain pairs from different antibodies are combined in one antibody resulting in an antibody molecule with the two antigen-binding sites recognizing different ligands.

Activated T cells in a sample can then be detected by adding the bispecific capture molecules to the sample. These molecules will then bind all T cells with on part of the molecule. T cells secreting soluble factor (due to activation) will then capture the secreted soluble factor on their surface by the soluble factor binding part of the capture molecule. Bound soluble factor can then be detected by addition of a labelled marker molecule specific for the soluble factor in question.

- *Indirect detection of T cells by measurement of effect of secreted soluble factor.*

Secreted soluble factors can be measured and quantified indirectly by measurement of the effect of the soluble factor on other cell systems. Briefly, a sample of T cells are added MHC multimer or antigenic peptideMHC multimer and/or antigenic peptide and/or antigenic polypeptide as described above to induce secretion of soluble factors from antigen-specific T cells. The supernatant containing secreted soluble factor are transferred to another cell system and the effect measured. The soluble factor may induce proliferation,

secretion of other soluble factors, expression/downregulation of receptors, or the soluble factor may have cytotoxic effects on these other cells,. All effects can be measured as described elsewhere herein.

Indirect detection of T cells by measurement of produced soluble factors intracellularly

Production of soluble factors can be measured intracellularly using flow cytometry. Often cytokines are measured and the method is therefore referred to as cytokine flow cytometry (CFC). The principles are described below.

Soluble factor production by stimulated T cells can also be measured intracellular by e.g. flow cytometry. This can be done using block of secretion of soluble factor (e.g. by monensin), permeabilization of cell (by e.g. saponine) followed by immunofluorescent staining. The method involves the following steps: 1) Stimulation of T cells e.g. by binding specific MHC multimers: The MHC multimers may be generated and added to sample containing T cells or antigenic peptid or protein polypeptide containing antigenic peptide sequences can be added to sample and MHC multimers generated in sample as described elsewhere herein. An example of usefull MHC multimers for stimulation of specific T cells is antigen presenting cells displaying MHC molrecules containing antigenic peptide. A reagent able to block extracellular secretion of cytokine is added during stimulation, e.g. monensin that interrupt intracellular transport processes leading to accumulation of produced soluble factor, e.g. cytokine in the Golgi complex. Other soluble factors may be added to the T cell sample during stimulation to enhance activation and/or expansion .This other soluble factor can be cytokine and or growth factors. 2) addition of one or more labelled marker molecules able to detect special surface receptors (e.g. marker molecules able to bind CD8, CD4, CD3, CD27, CD28, CD2). 3) Fixation of cell membrane using mild fixator followed by permeabilization of cell membrane e.g. by saponine. 4) Addition of labelled marker specific for the produced soluble factor to be determined, e.g. INFγ, IL-2, IL-4, IL-10. 5) Measurement of labelled cells using a flow cytometer.

An alternative to this procedure is to trap secreted soluble factors on the surface of the secreting T cell as described elsewhere herein or as described by Manz, R. et al., Proc. Natl. Acad. Sci. USA 92:1921 (1995).

Indirect detection of T cells by measurement of expression of receptors

Activation of T cells can be detected by measurement of expression and/or down regulation of specific surface receptors. The method includes the following steps. A

sample of T cells are added MHC multimer, antigenic peptide or protein containng antigenic peptide as described elsewhere hereinantigenic polypeptide to stimulate T cell and thereby induce expression or downregulation of specific surface receptors on antigen-specific T cells.These receptors include but are not limited to CD28, CD27, CCR7, CD45RO, CD45RA, IL2-receptor, CD62L, CCR5. Their expression level can be detected by addition of labelled marker specific for the desired receptor and then measure the amount of labelt cells using flow cytometry, microscopy, immobilization of activated T cell on solid support or any other method like those decribed for direct detection of TCR.

Indirect detection of T cells by measurement of effector function

Activation of T cells can be detected indirectly by measurement of effector functions. A sample of T cells are added MHC multimer, antigenic peptide or antigenic polypeptide protein containing antigenic peptide as described elsewhere herein to stimulate T cell and thereby induce one or more effector functions of the antigen-specific T cells. The one or more effector function(s) are then measured. For example activation of antigen-specific CD8 positive T cells can be determined by measurement of killing of target cells, i.e. cells displaying specific MHC-peptide complexes recognized by the activated antigen-specific CD8 positive T cell. This method is often referred to as cytotoxicity assays or CTL killing assays and involves the following steps:

1) Sample containing antigen-specific CD8 positive cells are stimulated by addition of MHC multimer, antigenic peptide or antigenic polypeptideprotein containing antigenic peptide as described elsewhere herein. 2) Another sampe containing live target cells displaying MHC I molecules containing specific antigenic peptide are added labelled molecules that can be taken up by live cells but that are not spontaneously released by the target cells following uptake e.g. radioactive labelled compounds. 3) Stimulated and activated T cells from step 1 are then added to target cells of step 2. target cells displaying the MHC complexes containing specific antigenic peptide(s) are then killed releasing labelled compound from the target cells and the presence of this labelled compound may be detected in the supernatant of mixtures of target and cytoxic cells. Alternatively, amount of labelled compound in cells that are not killed by the CD8 positive T cells are measured, by removing labelled compound released by killed target cells followed by measurement of label inside remaining cells either directly or by release of the labelled compund from these remaining cells.

Indirect detection of T cells by measurement of proliferation

T cells can be stimulated to proliferate upon binding specific MHC multimers. Proliferation of T cells can be measured several ways including but not limited to:

- Detection of mRNA

  Proliferation of T cells can be detected by measurement of mRNA inside cell.Cell division and proliferation requires production of new protein in each cell which as an initial step requires production of mRNA encoding the proteins to be synthesized.

  A sample of T cells are added MHC multimer or antigenic peptideMHC multimer and/or antigenic peptide and/or antigenic polypeptide as described above to induce proliferation of antigen-specific T cells. Detection of levels of mRNA inside the proliferating T cells can be done by quantitative PCR and indirectly measure activation of a T cell population as a result of interaction with MHC multimer. An example is measurement of cytokine mRNA by in sity hybridization.

- Detection of incorporation of thymidine

  The proliferative capacity of T cells in response to stimulation by MHC multimer can be determined by a radioactive assay based on incorporation of [^{3}H]thymidine ([^{3}H]TdR) into newly generated DNA followed by measurement of radioactive signal.

- Detection of incorporation of BrdU

  T cell proliferation can also be detected by of incorporation of bromo-2′-deoxyuridine (BrdU) followed by measurement of incorporated BrdU using a labeled anti-BrdU antibody in an ELISA based analysis.

Viability of cells may be measured by measurement ATP in a cell culture.

Indirect detection of T cells by measurement of inactivation

Not all MHC multimers will lead to activation of the T cells they bind. Under certain circumstances some MHC multimers may rather inactivate the T cells they bind to.

Indirect detection of T cells by measurement of effect of blockade of TCR

Inactivation of T cells by MHC multimers may be measured be measuring the effect of blocking TCR on antigen-specific T cells. MHC multimers, e.g. MHC-peptide complexes coupled to IgG scaffold can block the TCR of an antigen-specific T cell by binding the TCR, thereby prevent the blocked T cell receptor interacting with e.g. antigen presenting cells. Blockade of TCRs of a T cell can be detected in any of the above described medthods for detection of TCR by addition of an unlabeled blocking MHC multimer together with the labelled MHC multimer and then measuring the effect of the blockade on the readout.

Indirect detection of T cells by measurement of induction of apoptosis

Inactivation of T cells by MHC multimers may be measured be measuring apoptosis of the antigen-specific T cell. Binding of some MHC multimers to specific T cells may lead to induction of apoptosis. Inactivation of T cells by binding MHC multimer may therefore be detected by measuring apoptosis in the T cell population. Methods to measure apoptosis in T cells include but are not limited to measurement of the following:

- DNA fragmentation
- Alterations in membrane asymmetry (phosphatidylserine translocation)
- Activation of apoptotic caspases
- Release of cytochrome C and AIF from mitochondria into the cytoplasm

Positive control experiments for the use of MHC multimers in flow cytometry and related techniques

When performing flow cytometry experiments, or when using similar technologies, it is important to include appropriate positive and negative controls. In addition to establishing proper conditions for the experiments, positive and negative control reagents can also be used to evaluate the quality (e.g. specificity and affinity) and stability (e.g. shelf life) of produced MHC multimers.

The quality and stability of a given MHC multimer can be tested in a number of different ways, including:

- Measurement of specific MHC multimer binding to beads, other types of solid support, or micelles and liposomes, to which TCR's have been immobilized. Other kinds of molecules that recognize specifically the MHC-peptide complex can be immobilized and used as well. Depending on the nature of the solid support or membrane structure to which the TCR is immobilized, the TCR can be full-length (i.e. comprise the intracellular- and intra-membrane domains), or can be truncated (e.g. only comprise the extracellular domains). Likewise, the TCR can be recombinant, and can be chemically or enzymatically modified.
- Measurement of MHC multimer binding to beads, other types of solid support, or micelles and liposomes, to which aptamers, antibodies or other kinds of molecules that recognize correctly folded MHC-peptide complexes have been immobilized.
- Measurement of specific MHC multimer binding to specific cell lines (e.g. T-cell lines) displaying MHC multimer-binding molecules, e.g. displaying TCRs with appropriate specificity and affinity for the MHC multimer in question.
- Measurement of specific MHC multimer binding to cells in blood samples, preparations of purified lymphocytes (HPBMCs), or other bodily fluids that contain cells carrying receptor molecules specific for the MHC multimer in question.
- Measurement of specific MHC multimer binding to soluble TCRs, aptamers, antibodies, or other soluble MHC-peptide complex-binding molecules, by density-gradient centrifugation (e.g. in CsCl) or by size exclusion chromatography, PAGE or other type of chromatographic method.

Measurement of specific MHC binding to TCRs, aptamers, antibodies, streptavidin, or other MHC-peptide complex-binding molecules immobilized on a solid surface (e.g. a microtiter plate). The degree of MHC multimer binding can be visualized with a secondary component that binds the MHC multimer, e.g. a biotinylated fluorophore in cases where the MHC multimer contains streptavidin proteins, not fully loaded with biotin. Alternatively, the secondary component is unlabelled, and a labelled second component-specific compound is employed (e.g. EnVision System, Dako) for visualization. This solid surface can be beads, immunotubes, microtiterplates act. The principle for purification are basically the same I.e. T cells are added to the solid with

immobilized MHC'mer, non-binding T cells are washed away and MHC-peptide specific T cells can be retrieved by elution with mild acid or a competitive binding reagent.

- Measurement of specific MHC multimer binding to TCRs, aptamers, antibodies, streptavidin, or other MHC-peptide complex-binding molecules immobilized on a solid surface (e.g. a microtiter plate) visualized with a secondary component specific to MHC multimer (e.g. TCRs, aptamers, antibodies, streptavidin, or other MHC-peptide binding complex-binding molecules). Alternatively the secondary receptor is unlabelled, and a labelled second receptor-specific compound is employed (e.g. EnVision System, Dako) before visualization.

In the above mentioned approaches, positive control reagents include MHC multimers comprising correctly folded MHC, complexed with an appropriate peptide that allows the MHC multimer to interact specifically and efficiently with its cognate TCR. Negative control reagents include empty MHC multimers, or correctly folded MHC multimers complexed with so-called nonsense peptides that support a correct conformation of the MHC-peptide complex, but that do not efficiently bind TCRs through the peptide-binding site of the MHC complex.

Negative control reagents and negative control experiments for the use of MHC multimers in flow cytometry and related techniques

Experiments with MHC multimers require a negative control in order to determine background staining with MHC multimer. Background staining can be due to unwanted binding of any of the individual components of the MHC multimer, e.g., MHC complex or individual components of the MHC complex, multimerization domain or label molecules. The unwanted binding can be to any surface or intracellular protein or other cellular structure of any cell in the test sample, e.g. undesired binding to B cells, NK cells or T cells. Unwanted binding to certain cells or certain components on cells can normally be corrected for during the analysis, by staining with antibodies that bind to unique surface markers of these specific cells, and thus identifies these as false positives, or alternatively, that bind to other components of the target cells, and thus identifies these cells as true positives. A negative control reagent can be used in any experiment involving MHC multimers, e.g. flow cytometry analysis, other cytometric

methods, immunohistochemistry (IHC) and ELISA. Negative control reagents include the following:

- MHC complexes or MHC multimers comprising MHC complexes carrying nonsense peptides. A nonsense peptide is here to be understood as a peptide that binds the MHC protein efficiently, but that does not support binding of the resultant MHC-peptide complex to the desired TCR. An example nonsense peptide is a peptide with an amino acid sequence different from the linear sequence of any peptide derived from any known protein. When choosing an appropriate nonsense peptide the following points are taken into consideration. The peptide should ideally have appropriate amino acids at relevant positions that can anchor the peptide to the peptide-binding groove of the MHC. The remaining amino acids should ideally be chosen in such a way that possible binding to TCR (through interactions with the peptide or peptide-binding site of MHC) are minimized. The peptide should ideally be soluble in water to make proper folding with MHC alpha chain and β2m possible in aqueous buffer. The length of the peptide should ideally match the type and allele of MHC complex. The final peptide sequence should ideally be taken through a blast search or similar analysis, to ensure that it is not identical with any peptide sequence found in any known naturally occurring proteins.

- MHC complexes or MHC multimers comprising MHC complexes carrying a chemically modified peptide in the peptide-binding groove. The modification should ideally allow proper conformation of the MHC-peptide structure, yet should not allow efficient interaction of the peptide or peptide-binding site of MHC with the TCR.

- MHC complexes or MHC multimers comprising MHC complexes carrying a naturally occurring peptide different from the peptide used for analysis of specific T cells in the sample. When choosing the appropriate natural peptide the following should be taken into consideration. The peptide in complex with the MHC protein should ideally not be likely to bind a TCR of any T cell in the sample with such an affinity that it can be detected with the applied analysis method. The peptide should ideally be soluble in water to make proper folding with MHC alpha chain and β2m possible in aqueous buffer. The length of the peptide should match the type and allele of MHC complex.

- Empty MHC complexes or MHC multimers comprising empty MHC complexes, meaning any correctly folded MHC complex without a peptide in the peptide-binding groove.

- MHC heavy chain or MHC multimers comprising MHC heavy chain, where MHC heavy chain should be understood as full-length MHC I or MHC II heavy chain or any truncated version of MHC I or MHC II heavy chain. The MHC heavy chains can be either folded or unfolded. Of special interest is MHC I alpha chains containing the α3 domain that binds CD8 molecules on cytotoxic T cells. Another embodiment of special interest is MHC II β chains containing the β2 domain that binds CD4 on the surface of helper T cells.

- Beta2microglobulin or subunits of beta2microglobulin, or MHC multimers comprising Beta2microglobulin or subunits of beta2microglobulin, folded or unfolded.

- MHC-like complexes or MHC multimers comprising MHC-like complexes, folded or unfolded. An example could be CD1 molecules that are able to bind peptides in a peptide-binding groove that can be recognized by T cells (Russano et al. (2007). CD1-restricted recognition of exogenous and self-lipid antigens by duodenal gammadelta+ T lymphocytes. J Immunol. 178(6):3620-6)

- Multimerization domains without MHC or MHC-like molecules, e.g. dextran, streptavidin, IgG, coiled-coil-domain liposomes.

- Labels, e.g. FITC, PE, APC, pacific blue, cascade yellow, or any other label listed elsewhere herein.

Negative controls 1-4 can provide information about potentially undesired binding of the MHC multimer, through interaction of a surface of the MHC-peptide complex different from the peptide-binding groove and its surroundings. Negative control 5 and 6 can provide information about binding through interactions through the MHC I or MHC II proteins (in the absence of peptide). Negative control 7 can provide information about binding through surfaces of the MHC complex that is not unique to the MHC complex.

Negative controls 8 and 9 provide information about pontential undesired interactions between non-MHC-peptide complex components of the MHC multimer and cell constituents.

Minimization of undesired binding of the MHC multimer

Identification of MHC-peptide specific T cells can give rise to background signals due to unwanted binding to cells that do not carry TCRs. This undesired binding can result from binding to cells or other material, by various components of the MHC multimer, e.g. the dextran in a MHC dextramer construct, the labelling molecule (e.g. FITC), or surface regions of the MHC-peptide complex that do not include the peptide and the peptide-binding cleft.

MHC-peptide complexes bind to specific T cells through interaction with at least two receptors in the cell membrane of the T-cell. These two receptors are the T-cell receptor (TCR) and CD8 for MHC I-peptide complexes and TCR and CD4 receptor protein for MHC II-peptide complexes. Therefore, a particularly interesting example of undesired binding of a MHC multimer is its binding to the CD8 or CD4 molecules of T cells that do not carry a TCR specific for the actual MHC-peptide complex. The interaction of CD8 or CD4 molecules with the MHC is not very strong; however, because of the avidity gained from the binding of several MHC complexes of a MHC multimer, the interaction between the MHC multimer and several CD8 or CD4 receptors potentially can result in undesired but efficient binding of the MHC multimer to these T cells. In an analytical experiment this would give rise to an unwanted background signal; in a cell sorting experiment undesired cells might become isolated. Other particular interesting examples of undesired binding is binding to lymphoid cells different from T cells, e.g. NK-cells, B-cells, monocytes, dendritic cells, and granulocytes like eosinophils, neutrophils and basophiles.

Apart from the MHC complex, other components in the MHC multimer can give rise to unspecific binding. Of special interest are the multimerization domain, multimerization domain molecules, and labelling molecules.

One way to overcome the problem with unwanted binding is to include negative controls in the experiment and subtract this signal from signals derived from the analyzed sample, as described elsewhere in the invention.

Alternatively, unwanted binding could be minimized or eliminated during the experiment. Methods to minimize or eliminate background signals include:

- Mutations in areas of the MHC complex responsible for binding to unwanted cells can be introduced. Mutations here mean substitution, insertion, or deletion of natural or non-natural amino acids. Sub-domains in the MHC complex can be responsible for unwanted binding of the MHC multimer to cells without a TCR specific for the MHC-peptide complex contained in the MHC multimer. One example of special interest is a small region in the α3-domain of the α-chain of MHC I molecules that is responsible for binding to CD8 on all cytotoxic T cells. Mutations in this area can alter or completely abolish the interaction between CD8 on cytotoxic T cells and MHC multimer (Neveu et al. (2006) Int Immunol. 18, 1139-45). Similarly a sub domain in the β2 domain of the β-chain of MHC II molecules is responsible for binding CD4 molecules on all CD4 positive T cells. Mutations in this sub domain can alter or completely abolish the interaction between MHC II and CD4.
  Another embodiment is to mutate other areas of MHC I /MHC II complexes that are involved in interactions with T cell surface receptors different from TCR, CD8 and CD4, or that bind surface receptors on B cells, NK cells, Eosiniophils, Neutrophils, Basophiles, Dendritic cells or monocytes.

- Chemical alterations in areas of the MHC complex responsible for binding to unwanted cells can be employed in order to minimize unwanted binding of MHC multimer to irrelevant cells. Chemical alteration here means any chemical modification of one or more amino acids. Regions in MHC complexes that are of special interest are as mentioned above the α3 domain of the α-chain in MHC I molecules and β2 domains in the β-chain of MHC II molecules. Other regions in MHC I /MHC II molecules that can be chemically modified to decrease the extent of undesired binding are regions involved in interaction with T cell surface receptors different from TCR, CD8 and CD4, or that bind surface receptors on B cells, NK cells, Eosiniophils, Neutrophils, Basophiles, Dendritic cells or monocytes.

- Another method to minimize undesired binding involves the addition of one or more components of a MHC multimer, predicted to be responsible for the unwanted binding. The added component is not labeled, or carries a label different from the label of the MHC multimer used for analysis. Of special interest is addition of MHC

multimers that contain nonsense peptides, i.e. peptides that interact efficiently with the MHC protein, but that expectably do not support specific binding of the MHC multimer to the TCR in question. Another example of interest is addition of soluble MHC complexes not coupled to a multimerization domain, and with or without peptide bound in the peptide binding cleft. In another embodiment, individual components of the MHC complex can be added to the sample, e.g. I α-chain or subunits of MHC I α-chain either folded or unfolded, beta2microglobulin or subunits thereof either folded or unfolded, α/β-chain of MHC II or subunits thereof either folded or unfolded. Any of the above mentioned individual components can also be attached to a multimerization domain identical or different from the one used in the MHC multimer employed in the analysis.
Of special interest is also addition of multimerization domain similar or identical to the multimerization domain used in the MHC multimer or individual components of the multimerization domain.

- Reagents able to identify specific cell types either by selection or exclusion can be included in the analysis to help identify the population of T cells of interest, and in this way deselect the signal arising from binding of the MHC multimer to undesired cells.
Of special interest is the use of appropriate gating reagents in flow cytometry experiments. Thus, fluorescent antibodies directed against specific surface markers can be used for identification of specific subpopulations of cells, and in this way help to deselect signals resulting from MHC multimers binding to undesired cells. Gating reagents of special interest that helps identify the subset of T cells of interest when using MHC I multimers are reagents binding to CD3 and CD8 identifying all cytotoxic T cells. These reagents are preferably antibodies but can be any labeled molecule capable of binding CD3 or CD8. Gating reagents directed against CD3 and CD8 are preferably used together. As they stain overlapping cell populations they are preferably labeled with distinct fluorochromes. However, they can also be used individually in separate samples. In experiments with MHC II multimers reagents binding to CD3 and CD4 identifying T helper cells can be used. These reagents are preferably antibodies but can be any labeled molecule capable of binding CD3 or CD4. Gating reagents directed against CD3 and CD4 are preferable used together. As they stain overlapping cell populations they are preferably labeled with distinct fluorochromes. However, they can also be used individually in separate samples.

Other gating reagents of special interest in experiments with any MHC multimer, are reagents binding to the cell surface markers CD2, CD27, CD28, CD45RA, CD45RO, CD62L and CCR7. These surface markers are unique to T cells in various differentiation states. Co staining with either of these reagents or combinations thereof together with MHC multimers helps to select MHC multimer binding T cells expressing a correct TCR. These reagents can also be combined with reagents directed against CD3, CD4 and/or CD8.

Another flow cytometric method of special interest to remove signals from MHC multimer stained cells not expressing the specific TCR, is to introduce an exclusion gate. Antibodies or other reagents specific for surface markers unique to the unwanted cells are labeled with a fluorochrome and added to the test sample together with the MHC multimer. The number of antibodies or surface marker specific reagents are not limited to one but can be two, three, four, five, six, seven, eight, nine, ten or more individual reagents recognizing different surface markers, all of which are unique to the unwanted cells. During or after collection of data all events representing cells labeled with these antibodies are dumped in the same gate and removed from the dataset. This is possible because all the antibodies/reagents that bind to the wrong cells are labeled with the same fluorochrome.

Reagents of special interest that exclude irrelevant cells include reagents against CD45 expressed on red blood cells, CD19 expressed on B cells, CD56 expressed on NK cells, CD4 expressed on T helper cells and CD8 expressed on cytotoxic T cells, CD14 expressed on monocytes and CD15 expressed on granulocytes and monocytes.

Vaccine treatment

For the purpose of making vaccines it can be desirable to employ MHC multimers that comprise a polymer such as dextran, or that are cell-based (e.g. specialized dendritic cells such as described by Banchereau and Palucka, Nature Reviews, Immunology, 2005, vol. 5, p. 296-306).

- Preventive vaccination leading to prophylaxis/sterile immunity by inducing memory in the immune system may be obtained by immunizing/vaccinating an individual or animal with MHC alone, or with MHC in combination with other molecules as mentioned elsewhere in the patent.
    - Vaccine antigens can be administered alone
    - Vaccine can be administered in combination with adjuvant(s).

- Adjuvant can be mixed with vaccine component or administered alone, simultaneously or in any order.
- Adjuvant can be administered by the same route as the other vaccine components

- o Vaccine administered more than once may change composition from 1st administration to the 2nd, 3rd, etc.
- o Vaccine administered more than once can be administered by alternating routes
- o Vaccine components can be administered alone or in combinations by the same route or by alternating/mixed routes
- o Vaccine can be administered by the following routes
  - Cutaneously
  - Subcutaneously (SC)
  - Intramuscular (IM)
  - Intravenous (IV)
  - Per-oral (PO)
  - Inter peritoneally
  - Pulmonally
  - Vaginally
  - Rectally
  -

- Therapeutic vaccination i.e. vaccination “teaching” the immune system to fight an existing infection or disease, may be obtained by immunizing/vaccinating an individual or animal with MHC alone, or with MHC in combination with other molecules as mentioned elsewhere in the patent.
  - o Vaccine antigens can be administered alone
  - o Vaccine can be administered in combination with adjuvant(s).
    - Adjuvant can be mixed with vaccine component or administered alone, simultaneously or in any order.
    - Adjuvant can be administered by the same route as the other vaccine components
  - o Vaccine administered more than once may change composition from 1st administration to the 2nd, 3rd, etc.

- o Vaccine administered more than once can be administered by alternating routes
- o Vaccine components can be administered alone or in combinations by the same route or by alternating/mixed routes
- o Vaccine can be administered by the following routes
  - Cutaneously
  - Subcutaneously (SC)
  - Intramuscular (IM)
  - Intravenous (IV)
  - Per-oral (PO)
  - Inter peritoneally
  - Pulmonally
  - Vaginally
  - Rectally

Therapeutic treatment

- Therapeutic treatment includes the use of MHC molecules alone or in any molecular combination mentioned elsewhere in the patent application for the purpose of treating a disease in any state. Treatment may be in the form of
  - o Per-orally intake
    - Pills
    - Capsules
  - o Injections
    - Systemic
    - Local
  - o Jet-infusion (micro-drops, micro-spheres, micro-beads) through skin
  - o Drinking solution, suspension or gel
  - o Inhalation
  - o Nose-drops
  - o Eye-drops
  - o Ear-drops
  - o Skin application as ointment, gel or creme
  - o Vaginal application as ointment, gel, crème or washing

- o Gastro-Intestinal flushing
- o Rectal washings or by use of suppositories

- Treatment can be performed as
  - o Single intake, injection, application, washing
  - o Multiple intake, injection, application, washing
    - On single day basis
    - Over prolonged time as days, month, years

- Treatment dose and regimen can be modified during the course

The variation in peptide epitope usage among individuals must be considered when developing personalized medicine based on antigenic peptides and/or MHC complexes.

The immune system is very complex. Each individual has a very large repertoire of specific T cells (on the order of 10^6-10^9 different T cell specificities, differing in the identity of the T cell receptor), which again is only a small subset of the total T cell repertoire of a population of individuals. It is estimated that the Caucasian population represents a T cell diversity of 10^{10}-10^{12}.

The T cell receptor recognizes MHC peptide complexes, embedded in the cell membrane. Each individual has between 3 and 6 MHC I alleles and 3 and 8 MHC II alleles. Each of these MHC alleles forms complexes with short antigenic peptides generated by proteolytic degradation and prematurely terminated protein synthesis. Individuals of a population differ in their pattern of peptide degradation. The MHC allele diversity described above combined with this variation among individuals' proteolytic metabolism further enhances the variation among different individuals' immune responses. As a result, each individual has its own characteristic immune response profile, comprising its unique set of alleles and peptide combinations.

This is important when designing an antigenic peptide-based or a MHC multimer-based immune monitoring reagent or immunotherapeutic agent. If an agent is sought that should be generally applicable to the majority of individuals in a population, one should try to identify peptide epitopes and MHC alleles that are common to the majority of individuals of a population. As described elsewhere in this application, such peptide

epitopes can be identified through computerized search algorithms and/or experimental testing of a large set of individuals.

This approach will be advantageous in many cases, but because of the variability among immune response profiles of different individuals, is likely to be inefficient in certain individuals, because of these individuals' non-average profile. In these latter cases one may have to turn to personalized medicine. In the case of immune monitoring and immunotherapy, this may involve testing a large number of different epitopes from a given antigen, in order to find peptide epitopes that apllies to the given individual.

When considering the patient population as a whole,a large fraction of the epitopes that theoretically may be generated from a given antigen, for use as a free antigenic peptide agent or to be included in a MHC I or MHC II multimer reagent, are therefore of relevance in personalized medicine. For the individual patient only a small fraction of these will be efficient; and in order to make generally applicable diagnostics, vaccines or therapeutics, even less epitopes are of relevance. Only in the case where one wants to generate a therapeutic agent or diagnostic reagent that is applicable to the majority of individuals of a population can the large majority of epitope sequences be said to be irrelevant, and those identified by computerized search algorithms and experimental testing be said to be the only epitopes of value. For the odd individual with the odd immune response these disregarded peptide epitopes may be the epitopes that provide an efficient diagnostic reagent or cures that individual from a deadly disease.
In conclusion, a large fraction of the theoretical epitopes that can be generated from an antigen are of great practical value for use in personalized diagnostics, vaccines and therapeutics.

ITEMS

1. A peptide of between 8 to 16 consecutive amino acids, comprising at least 8 of amino acid number X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16}
2. The peptide according to item 1, wherein X_1 is alanine
3. The peptide according to item 1, wherein X_1 is arginine
4. The peptide according to item 1, wherein X_1 is asparagine

5. The peptide according to item 1, wherein X_1 is aspartic acid
6. The peptide according to item 1, wherein X_1 is cysteine
7. The peptide according to item 1, wherein X_1 is glutamic acid
8. The peptide according to item 1, wherein X_1 is glutamine
9. The peptide according to item 1, wherein X_1 is glycine
10. The peptide according to item 1, wherein X_1 is histidine
11. The peptide according to item 1, wherein X_1 is isoleucine
12. The peptide according to item 1, wherein X_1 is leucine
13. The peptide according to item 1, wherein X_1 is lysine
14. The peptide according to item 1, wherein X_1 is methionine
15. The peptide according to item 1, wherein X_1 is phenylalanine
16. The peptide according to item 1, wherein X_1 is proline
17. The peptide according to item 1, wherein X_1 is serine
18. The peptide according to item 1, wherein X_1 is threonine
19. The peptide according to item 1, wherein X_1 is tryptophan
20. The peptide according to item 1, wherein X_1 is tyrosine
21. The peptide according to item 1, wherein X_1 is valine
22. The peptide according to item 1, wherein X_2 is alanine
23. The peptide according to item 1, wherein X_2 is arginine
24. The peptide according to item 1, wherein X_2 is asparagine
25. The peptide according to item 1, wherein X_2 is aspartic acid
26. The peptide according to item 1, wherein X_2 is cysteine
27. The peptide according to item 1, wherein X_2 is glutamic acid
28. The peptide according to item 1, wherein X_2 is glutamine
29. The peptide according to item 1, wherein X_2 is glycine
30. The peptide according to item 1, wherein X_2 is histidine
31. The peptide according to item 1, wherein X_2 is isoleucine
32. The peptide according to item 1, wherein X_2 is leucine
33. The peptide according to item 1, wherein X_2 is lysine
34. The peptide according to item 1, wherein X_2 is methionine
35. The peptide according to item 1, wherein X_2 is phenylalanine
36. The peptide according to item 1, wherein X_2 is proline
37. The peptide according to item 1, wherein X_2 is serine
38. The peptide according to item 1, wherein X_2 is threonine
39. The peptide according to item 1, wherein X_2 is tryptophan

40. The peptide according to item 1, wherein X_2 is tyrosine
41. The peptide according to item 1, wherein X_2 is valine
42. The peptide according to item 1, wherein X_3 is alanine
43. The peptide according to item 1, wherein X_3 is arginine
44. The peptide according to item 1, wherein X_3 is asparagine
45. The peptide according to item 1, wherein X_3 is aspartic acid
46. The peptide according to item 1, wherein X_3 is cysteine
47. The peptide according to item 1, wherein X_3 is glutamic acid
48. The peptide according to item 1, wherein X_3 is glutamine
49. The peptide according to item 1, wherein X_3 is glycine
50. The peptide according to item 1, wherein X_3 is histidine
51. The peptide according to item 1, wherein X_3 is isoleucine
52. The peptide according to item 1, wherein X_3 is leucine
53. The peptide according to item 1, wherein X_3 is lysine
54. The peptide according to item 1, wherein X_3 is methionine
55. The peptide according to item 1, wherein X_3 is phenylalanine
56. The peptide according to item 1, wherein X_3 is proline
57. The peptide according to item 1, wherein X_3 is serine
58. The peptide according to item 1, wherein X_3 is threonine
59. The peptide according to item 1, wherein X_3 is tryptophan
60. The peptide according to item 1, wherein X_3 is tyrosine
61. The peptide according to item 1, wherein X_3 is valine
62. The peptide according to item 1, wherein X_4 is alanine
63. The peptide according to item 1, wherein X_4 is arginine
64. The peptide according to item 1, wherein X_4 is asparagine
65. The peptide according to item 1, wherein X_4 is aspartic acid
66. The peptide according to item 1, wherein X_4 is cysteine
67. The peptide according to item 1, wherein X_4 is glutamic acid
68. The peptide according to item 1, wherein X_4 is glutamine
69. The peptide according to item 1, wherein X_4 is glycine
70. The peptide according to item 1, wherein X_4 is histidine
71. The peptide according to item 1, wherein X_4 is isoleucine
72. The peptide according to item 1, wherein X_4 is leucine
73. The peptide according to item 1, wherein X_4 is lysine
74. The peptide according to item 1, wherein X_4 is methionine

75. The peptide according to item 1, wherein X_4 is phenylalanine
76. The peptide according to item 1, wherein X_4 is proline
77. The peptide according to item 1, wherein X_4 is serine
78. The peptide according to item 1, wherein X_4 is threonine
79. The peptide according to item 1, wherein X_4 is tryptophan
80. The peptide according to item 1, wherein X_4 is tyrosine
81. The peptide according to item 1, wherein X_4 is valine
82. The peptide according to item 1, wherein X_5 is alanine
83. The peptide according to item 1, wherein X_5 is arginine
84. The peptide according to item 1, wherein X_5 is asparagine
85. The peptide according to item 1, wherein X_5 is aspartic acid
86. The peptide according to item 1, wherein X_5 is cysteine
87. The peptide according to item 1, wherein X_5 is glutamic acid
88. The peptide according to item 1, wherein X_5 is glutamine
89. The peptide according to item 1, wherein X_5 is glycine
90. The peptide according to item 1, wherein X_5 is histidine
91. The peptide according to item 1, wherein X_5 is isoleucine
92. The peptide according to item 1, wherein X_5 is leucine
93. The peptide according to item 1, wherein X_5 is lysine
94. The peptide according to item 1, wherein X_5 is methionine
95. The peptide according to item 1, wherein X_5 is phenylalanine
96. The peptide according to item 1, wherein X_5 is proline
97. The peptide according to item 1, wherein X_5 is serine
98. The peptide according to item 1, wherein X_5 is threonine
99. The peptide according to item 1, wherein X_5 is tryptophan
100. The peptide according to item 1, wherein X_5 is tyrosine
101. The peptide according to item 1, wherein X_5 is valine
102. The peptide according to item 1, wherein X_6 is alanine
103. The peptide according to item 1, wherein X_6 is arginine
104. The peptide according to item 1, wherein X_6 is asparagine
105. The peptide according to item 1, wherein X_6 is aspartic acid
106. The peptide according to item 1, wherein X_6 is cysteine
107. The peptide according to item 1, wherein X_6 is glutamic acid
108. The peptide according to item 1, wherein X_6 is glutamine
109. The peptide according to item 1, wherein X_6 is glycine

110. The peptide according to item 1, wherein X_6 is histidine
111. The peptide according to item 1, wherein X_6 is isoleucine
112. The peptide according to item 1, wherein X_6 is leucine
113. The peptide according to item 1, wherein X_6 is lysine
114. The peptide according to item 1, wherein X_6 is methionine
115. The peptide according to item 1, wherein X_6 is phenylalanine
116. The peptide according to item 1, wherein X_6 is proline
117. The peptide according to item 1, wherein X_6 is serine
118. The peptide according to item 1, wherein X_6 is threonine
119. The peptide according to item 1, wherein X_6 is tryptophan
120. The peptide according to item 1, wherein X_6 is tyrosine
121. The peptide according to item 1, wherein X_6 is valine
122. The peptide according to item 1, wherein X_7 is alanine
123. The peptide according to item 1, wherein X_7 is arginine
124. The peptide according to item 1, wherein X_7 is asparagine
125. The peptide according to item 1, wherein X_7 is aspartic acid
126. The peptide according to item 1, wherein X_7 is cysteine
127. The peptide according to item 1, wherein X_7 is glutamic acid
128. The peptide according to item 1, wherein X_7 is glutamine
129. The peptide according to item 1, wherein X_7 is glycine
130. The peptide according to item 1, wherein X_7 is histidine
131. The peptide according to item 1, wherein X_7 is isoleucine
132. The peptide according to item 1, wherein X_7 is leucine
133. The peptide according to item 1, wherein X_7 is lysine
134. The peptide according to item 1, wherein X_7 is methionine
135. The peptide according to item 1, wherein X_7 is phenylalanine
136. The peptide according to item 1, wherein X_7 is proline
137. The peptide according to item 1, wherein X_7 is serine
138. The peptide according to item 1, wherein X_7 is threonine
139. The peptide according to item 1, wherein X_7 is tryptophan
140. The peptide according to item 1, wherein X_7 is tyrosine
141. The peptide according to item 1, wherein X_7 is valine
142. The peptide according to item 1, wherein X_8 is alanine
143. The peptide according to item 1, wherein X_8 is arginine
144. The peptide according to item 1, wherein X_8 is asparagine

145. The peptide according to item 1, wherein X_8 is aspartic acid
146. The peptide according to item 1, wherein X_8 is cysteine
147. The peptide according to item 1, wherein X_8 is glutamic acid
148. The peptide according to item 1, wherein X_8 is glutamine
149. The peptide according to item 1, wherein X_8 is glycine
150. The peptide according to item 1, wherein X_8 is an histidine
151. The peptide according to item 1, wherein X_8 is isoleucine
152. The peptide according to item 1, wherein X_8 is leucine
153. The peptide according to item 1, wherein X_8 is lysine
154. The peptide according to item 1, wherein X_8 is methionine
155. The peptide according to item 1, wherein X_8 is phenylalanine
156. The peptide according to item 1, wherein X_8 is proline
157. The peptide according to item 1, wherein X_8 is serine
158. The peptide according to item 1, wherein X_8 is threonine
159. The peptide according to item 1, wherein X_8 is tryptophan
160. The peptide according to item 1, wherein X_8 is tyrosine
161. The peptide according to item 1, wherein X_8 is valine
162. The peptide according to item 1, wherein X_9 is alanine
163. The peptide according to item 1, wherein X_9 is arginine
164. The peptide according to item 1, wherein X_9 is asparagine
165. The peptide according to item 1, wherein X_9 is aspartic acid
166. The peptide according to item 1, wherein X_9 is cysteine
167. The peptide according to item 1, wherein X_9 is glutamic acid
168. The peptide according to item 1, wherein X_9 is glutamine
169. The peptide according to item 1, wherein X_9 is glycine
170. The peptide according to item 1, wherein X_9 is an histidine
171. The peptide according to item 1, wherein X_9 is isoleucine
172. The peptide according to item 1, wherein X_9 is leucine
173. The peptide according to item 1, wherein X_9 is lysine
174. The peptide according to item 1, wherein X_9 is methionine
175. The peptide according to item 1, wherein X_9 is phenylalanine
176. The peptide according to item 1, wherein X_9 is proline
177. The peptide according to item 1, wherein X_9 is serine
178. The peptide according to item 1, wherein X_9 is threonine
179. The peptide according to item 1, wherein X_9 is tryptophan

180. The peptide according to item 1, wherein X_9 is tyrosine
181. The peptide according to item 1, wherein X_9 is valine
182. The peptide according to item 1, wherein X_9 is alanine
183. The peptide according to item 1, wherein X_9 is arginine
184. The peptide according to item 1, wherein X_9 is asparagine
185. The peptide according to item 1, wherein X_9 is aspartic acid
186. The peptide according to item 1, wherein X_9 is cysteine
187. The peptide according to item 1, wherein X_9 is glutamic acid
188. The peptide according to item 1, wherein X_9 is glutamine
189. The peptide according to item 1, wherein X_9 is glycine
190. The peptide according to item 1, wherein X_9 is an histidine
191. The peptide according to item 1, wherein X_9 is isoleucine
192. The peptide according to item 1, wherein X_9 is leucine
193. The peptide according to item 1, wherein X_9 is lysine
194. The peptide according to item 1, wherein X_9 is methionine
195. The peptide according to item 1, wherein X_9 is phenylalanine
196. The peptide according to item 1, wherein X_9 is proline
197. The peptide according to item 1, wherein X_9 is serine
198. The peptide according to item 1, wherein X_9 is threonine
199. The peptide according to item 1, wherein X_9 is tryptophan
200. The peptide according to item 1, wherein X_9 is tyrosine
201. The peptide according to item 1, wherein X_9 is valine
202. The peptide according to item 1, wherein X_{10} is alanine
203. The peptide according to item 1, wherein X_{10} is arginine
204. The peptide according to item 1, wherein X_{10} is asparagine
205. The peptide according to item 1, wherein X_{10} is aspartic acid
206. The peptide according to item 1, wherein X_{10} is cysteine
207. The peptide according to item 1, wherein X_{10} is glutamic acid
208. The peptide according to item 1, wherein X_{10} is glutamine
209. The peptide according to item 1, wherein X_{10} is glycine
210. The peptide according to item 1, wherein X_{10} is an histidine
211. The peptide according to item 1, wherein X_{10} is isoleucine
212. The peptide according to item 1, wherein X_{10} is leucine
213. The peptide according to item 1, wherein X_{10} is lysine
214. The peptide according to item 1, wherein X_{10} is methionine

215. The peptide according to item 1, wherein X_{10} is phenylalanine
216. The peptide according to item 1, wherein X_{10} is proline
217. The peptide according to item 1, wherein X_{10} is serine
218. The peptide according to item 1, wherein X_{10} is threonine
219. The peptide according to item 1, wherein X_{10} is tryptophan
220. The peptide according to item 1, wherein X_{10} is tyrosine
221. The peptide according to item 1, wherein X_{10} is valine
222. The peptide according to item 1, wherein X_{11} is alanine
223. The peptide according to item 1, wherein X_{11} is arginine
224. The peptide according to item 1, wherein X_{11} is asparagine
225. The peptide according to item 1, wherein X_{11} is aspartic acid
226. The peptide according to item 1, wherein X_{11} is cysteine
227. The peptide according to item 1, wherein X_{11} is glutamic acid
228. The peptide according to item 1, wherein X_{11} is glutamine
229. The peptide according to item 1, wherein X_{11} is glycine
230. The peptide according to item 1, wherein X_{11} is an histidine
231. The peptide according to item 1, wherein X_{11} is isoleucine
232. The peptide according to item 1, wherein X_{11} is leucine
233. The peptide according to item 1, wherein X_{11} is lysine
234. The peptide according to item 1, wherein X_{11} is methionine
235. The peptide according to item 1, wherein X_{11} is phenylalanine
236. The peptide according to item 1, wherein X_{11} is proline
237. The peptide according to item 1, wherein X_{11} is serine
238. The peptide according to item 1, wherein X_{11} is threonine
239. The peptide according to item 1, wherein X_{11} is tryptophan
240. The peptide according to item 1, wherein X_{11} is tyrosine
241. The peptide according to item 1, wherein X_{11} is valine

242. The peptide according to item 1, wherein X_{12} is alanine
243. The peptide according to item 1, wherein X_{12} is arginine
244. The peptide according to item 1, wherein X_{12} is asparagine
245. The peptide according to item 1, wherein X_{12} is aspartic acid
246. The peptide according to item 1, wherein X_{12} is cysteine
247. The peptide according to item 1, wherein X_{12} is glutamic acid
248. The peptide according to item 1, wherein X_{12} is glutamine

249. The peptide according to item 1, wherein X_{12} is glycine
250. The peptide according to item 1, wherein X_{12} is histidine
251. The peptide according to item 1, wherein X_{12} is isoleucine
252. The peptide according to item 1, wherein X_{12} is leucine
253. The peptide according to item 1, wherein X_{12} is lysine
254. The peptide according to item 1, wherein X_{12} is methionine
255. The peptide according to item 1, wherein X_{12} is phenylalanine
256. The peptide according to item 1, wherein X_{12} is proline
257. The peptide according to item 1, wherein X_{12} is serine
258. The peptide according to item 1, wherein X_{12} is threonine
259. The peptide according to item 1, wherein X_{12} is tryptophan
260. The peptide according to item 1, wherein X_{12} is tyrosine
261. The peptide according to item 1, wherein X_{12} is valine
262. The peptide according to item 1, wherein X_{13} is alanine
263. The peptide according to item 1, wherein X_{13} is arginine
264. The peptide according to item 1, wherein X_{13} is asparagine
265. The peptide according to item 1, wherein X_{13} is aspartic acid
266. The peptide according to item 1, wherein X_{13} is cysteine
267. The peptide according to item 1, wherein X_{13} is glutamic acid
268. The peptide according to item 1, wherein X_{13} is glutamine
269. The peptide according to item 1, wherein X_{13} is glycine
270. The peptide according to item 1, wherein X_{13} is histidine
271. The peptide according to item 1, wherein X_{13} is isoleucine
272. The peptide according to item 1, wherein X_{13} is leucine
273. The peptide according to item 1, wherein X_{13} is lysine
274. The peptide according to item 1, wherein X_{13} is methionine
275. The peptide according to item 1, wherein X_{13} is phenylalanine
276. The peptide according to item 1, wherein X_{13} is proline
277. The peptide according to item 1, wherein X_{13} is serine
278. The peptide according to item 1, wherein X_{13} is threonine
279. The peptide according to item 1, wherein X_{13} is tryptophan
280. The peptide according to item 1, wherein X_{13} is tyrosine
281. The peptide according to item 1, wherein X_{13} is valine
282. The peptide according to item 1, wherein X_{14} is alanine
283. The peptide according to item 1, wherein X_{14} is arginine

284. The peptide according to item 1, wherein X_{14} is asparagine
285. The peptide according to item 1, wherein X_{14} is aspartic acid
286. The peptide according to item 1, wherein X_{14} is cysteine
287. The peptide according to item 1, wherein X_{14} is glutamic acid
288. The peptide according to item 1, wherein X_{14} is glutamine
289. The peptide according to item 1, wherein X_{14} is glycine
290. The peptide according to item 1, wherein X_{14} is histidine
291. The peptide according to item 1, wherein X_{14} is isoleucine
292. The peptide according to item 1, wherein X_{14} is leucine
293. The peptide according to item 1, wherein X_{14} is lysine
294. The peptide according to item 1, wherein X_{14} is methionine
295. The peptide according to item 1, wherein X_{14} is phenylalanine
296. The peptide according to item 1, wherein X_{14} is proline
297. The peptide according to item 1, wherein X_{14} is serine
298. The peptide according to item 1, wherein X_{14} is threonine
299. The peptide according to item 1, wherein X_{14} is tryptophan
300. The peptide according to item 1, wherein X_{14} is tyrosine
301. The peptide according to item 1, wherein X_{14} is valine
302. The peptide according to item 1, wherein X_{15} is alanine
303. The peptide according to item 1, wherein X_{15} is arginine
304. The peptide according to item 1, wherein X_{15} is asparagine
305. The peptide according to item 1, wherein X_{15} is aspartic acid
306. The peptide according to item 1, wherein X_{15} is cysteine
307. The peptide according to item 1, wherein X_{15} is glutamic acid
308. The peptide according to item 1, wherein X_{15} is glutamine
309. The peptide according to item 1, wherein X_{15} is glycine
310. The peptide according to item 1, wherein X_{15} is histidine
311. The peptide according to item 1, wherein X_{15} is isoleucine
312. The peptide according to item 1, wherein X_{15} is leucine
313. The peptide according to item 1, wherein X_{15} is lysine
314. The peptide according to item 1, wherein X_{15} is methionine
315. The peptide according to item 1, wherein X_{15} is phenylalanine
316. The peptide according to item 1, wherein X_{15} is proline
317. The peptide according to item 1, wherein X_{15} is serine
318. The peptide according to item 1, wherein X_{15} is threonine

319. The peptide according to item 1, wherein X_{15} is tryptophan
320. The peptide according to item 1, wherein X_{15} is tyrosine
321. The peptide according to item 1, wherein X_{15} is valine
322. The peptide according to item 1, wherein X_{16} is alanine
323. The peptide according to item 1, wherein X_{16} is arginine
324. The peptide according to item 1, wherein X_{16} is asparagine
325. The peptide according to item 1, wherein X_{16} is aspartic acid
326. The peptide according to item 1, wherein X_{16} is cysteine
327. The peptide according to item 1, wherein X_{16} is glutamic acid
328. The peptide according to item 1, wherein X_{16} is glutamine
329. The peptide according to item 1, wherein X_{16} is glycine
330. The peptide according to item 1, wherein X_{16} is histidine
331. The peptide according to item 1, wherein X_{16} is isoleucine
332. The peptide according to item 1, wherein X_{16} is leucine
333. The peptide according to item 1, wherein X_{16} is lysine
334. The peptide according to item 1, wherein X_{16} is methionine
335. The peptide according to item 1, wherein X_{16} is phenylalanine
336. The peptide according to item 1, wherein X_{16} is proline
337. The peptide according to item 1, wherein X_{16} is serine
338. The peptide according to item 1, wherein X_{16} is threonine
339. The peptide according to item 1, wherein X_{16} is tryptophan
340. The peptide according to item 1, wherein X_{16} is tyrosine
341. The peptide according to item 1, wherein X_{16} is valine
342. The peptide according to any of items 2, 22, 42, 62, 82, 102, 122, 142, 162, 182, 202, 222, 242, 262, 282, 302 or 322, wherein the alanine is D-alanine
343. The peptide according to any of items 2, 22, 42, 62, 82, 102, 122, 142, 162, 182, 202, 222, 242, 262, 282, 302 or 322, wherein the alanine is L-alanine
344. The peptide according to any of items 3, 23, 43, 63, 83, 103, 123, 143, 163, 183, 203, 223, 243, 263, 283, 303 or 323, wherein the arginine is D-arginine
345. The peptide according to any of items 3, 23, 43, 63, 83, 103, 123, 143, 163, 183, 203, 223, 243, 263, 283, 303 or 323, wherein the arginine is L-arginine

346. The peptide according to any of items 4, 24, 44, 64, 84, 104, 124, 144, 164, 184, 204, 224, 244, 264, 284, 304 or 324, wherein the asparagine is D-asparagine

347. The peptide according to any of items 4, 24, 44, 64, 84, 104, 124, 144, 164, 184, 204, 224, 244, 264, 284, 304 or 324, wherein the asparagine is L-asparagine

348. The peptide according to any of items 5, 25, 45, 65, 85, 105, 125, 145, 165, 185, 205, 225, 245, 265, 285, 305 or 325, wherein the aspartic acid is D-aspartic acid

349. The peptide according to any of items 5, 25, 45, 65, 85, 105, 125, 145, 165, 185, 205, 225, 245, 265, 285, 305 or 325, wherein the aspartic acid is L-aspartic acid

350. The peptide according to any of items 6, 26, 46, 66, 86, 106, 126, 146, 166, 186, 206, 226, 246, 266, 286, 306 or 326, wherein the cysteine is D-cysteine

351. The peptide according to any of items 6, 26, 46, 66, 86, 106, 126, 146, 166, 186, 206, 226, 246, 266, 286, 306 or 326, wherein the cysteine is L-cysteine

352. The peptide according to any of items 7, 27, 47, 67, 87, 107, 127, 147, 167, 187, 207, 227, 247, 267, 287, 307 or 327, wherein the glutamic acid is D-glutamic acid

353. The peptide according to any of items 7, 27, 47, 67, 87, 107, 127, 147, 167, 187, 207, 227, 247, 267, 287, 307 or 327, wherein the glutamic acid is L-glutamic acid

354. The peptide according to any of items 8, 28, 48, 68, 88, 108, 128, 148, 168, 188, 208, 228, 248, 268, 288, 308 or 328, wherein the glutamine is D-glutamine

355. The peptide according to any of items 8, 28, 48, 68, 88, 108, 128, 148, 168, 188, 208, 228, 248, 268, 288, 308 or 328, wherein the glutamine is L-glutamine

356. The peptide according to any of items 9, 29, 49, 69, 89, 109, 129, 149, 169, 189, 209, 229, 249, 269, 289, 309 or 329, wherein the glycine is D-glycine

357. The peptide according to any of items 9, 29, 49, 69, 89, 109, 129, 149, 169, 189, 209, 229, 249, 269, 289, 309 or 329, wherein the glycine is L-glycine

358. The peptide according to any of items 10, 30, 50, 70, 90, 110, 130, 150, 170, 190, 210, 230, 250, 270, 290, 310 or 330, wherein the histidine is D-histidine

359. The peptide according to any of items 10, 30, 50, 70, 90, 110, 130, 150, 170, 190, 210, 230, 250, 270, 290, 310 or 330, wherein the histidine is L-histidine

360. The peptide according to any of items 11, 31, 51, 71, 91, 111, 131, 151, 171, 191, 211, 231, 251, 271, 291, 311 or 331, wherein the isoleucine is D-isoleucine

361. The peptide according to any of items 11, 31, 51, 71, 91, 111, 131, 151, 171, 191, 211, 231, 251, 271, 291, 311 or 331, wherein the isoleucine is L-isoleucine

362. The peptide according to any of items 12, 32, 52, 72, 92, 112, 132, 152, 172, 192, 212, 232, 252, 272, 292, 312 or 332, wherein the leucine is D-leucine

363. The peptide according to any of items 12, 32, 52, 72, 92, 112, 132, 152, 172, 192, 212, 232, 252, 272, 292, 312 or 332, wherein the leucine is L-leucine

364. The peptide according to any of items 13, 33, 53, 73, 93, 113, 133, 153, 173, 193, 213, 233, 253, 273, 293, 313 or 333, wherein the lysine is D-lysine

365. The peptide according to any of items 13, 33, 53, 73, 93, 113, 133, 153, 173, 193, 213, 233, 253, 273, 293, 313 or 333, wherein the lysine is L-lysine

366. The peptide according to any of items 14, 34, 54, 74, 94, 114, 134, 154, 174, 194, 214, 234, 254, 274, 294, 314 or 334, wherein the methionine is D-methionine

367. The peptide according to any of items 14, 34, 54, 74, 94, 114, 134, 154, 174, 194, 214, 234, 254, 274, 294, 314 or 334, wherein the methionine is L-methionine

368. The peptide according to any of items 15, 35, 55, 75, 95, 115, 135, 155, 175, 195, 215, 235, 255, 275, 295, 315 or 335, wherein the phenylalanine is D-phenylalanine

369. The peptide according to any of items 15, 35, 55, 75, 95, 115, 135, 155, 175, 195, 215, 235, 255, 275, 295, 315 or 335, wherein the phenylalanine is L-phenylalanine

370. The peptide according to any of items 16, 36, 56, 76, 96, 116, 136, 156, 176, 196, 216, 236, 256, 276, 296, 316 or 336, wherein the proline is D-proline

371. The peptide according to any of items 16, 36, 56, 76, 96, 116, 136, 156, 176, 196, 216, 236, 256, 276, 296, 316 or 336, wherein the proline is L-proline

372. The peptide according to any of items 17, 37, 57, 77, 97, 117, 137, 157, 177, 197, 217, 237, 257, 277, 297, 317 or 337, wherein the serine is D-serine

373. The peptide according to any of items 17, 37, 57, 77, 97, 117, 137, 157, 177, 197, 217, 237, 257, 277, 297, 317 or 337, wherein the serine is L-serine

374. The peptide according to any of items 18, 38, 58, 78, 98, 118, 138, 158, 178, 198, 218, 238, 258, 278, 298, 318 or 338, wherein the threonine is D-threonine

375. The peptide according to any of items 18, 38, 58, 78, 98, 118, 138, 158, 178, 198, 218, 238, 258, 278, 298, 318 or 338, wherein the threonine is L-threonine

376. The peptide according to any of items 19, 39, 59, 79, 99, 119, 139, 159, 179, 199, 219, 239, 259, 279, 299, 319 or 339, wherein the tryptophan is D-tryptophan

377. The peptide according to any of items 19, 39, 59, 79, 99, 119, 139, 159, 179, 199, 219, 239, 259, 279, 299, 319 or 339, wherein the tryptophan is L-tryptophan

378. The peptide according to any of items 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320 or 340, wherein the tyrosine is D-tyrosine

379. The peptide according to any of items 20, 40, 60, 80, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320 or 340, wherein the tyrosine is L-tyrosine

380. The peptide according to any of items 21, 41, 61, 81, 101, 121, 141, 161, 181, 201, 221, 241, 261, 281, 301, 321 or 341, wherein the valine is D-valine

381. The peptide according to any of items 21, 41, 61, 81, 101, 121, 141, 161, 181, 201, 221, 241, 261, 281, 301, 321 or 341, wherein the valine is L-valine

382. The peptide according to item 1 to 381, wherein one or more of said amino acid residues are modified, such as post-translationally modified or co-translationally modified

383. The peptide according to item 382, wherein said modification is acetylation of one or more amino acid residues

384. The peptide according to item 382, wherein said modification is phosphorylation of one or more amino acid residues

385. The peptide according to item 382, wherein said modification is glycosylation of one or more amino acid residues

386. The peptide according to item 382, wherein said modification is non-enzymatic glycosylation (or glycation) of one or more amino acid residues

387. The peptide according to item 382, wherein said modification is methylation of one or more amino acid residues

388. The peptide according to item 382, wherein said modification is amidation of one or more amino acid residues

389. The peptide according to item 382, wherein said modification is deamidation of one or more amino acid residues

390. The peptide according to item 382, wherein said modification is succinimide formation of one or more amino acid residues

391. The peptide according to item 382, wherein said modification is biotinylation of one or more amino acid residues

392. The peptide according to item 382, wherein said modification is formylation of one or more amino acid residues

393. The peptide according to item 382, wherein said modification is carboxylation of one or more amino acid residues

394. The peptide according to item 382, wherein said modification is carbamylation of one or more amino acid residues

395. The peptide according to item 382, wherein said modification is hydroxylation of one or more amino acid residues

396. The peptide according to item 382, wherein said modification is iodination of one or more amino acid residues

397. The peptide according to item 382, wherein said modification is isoprenylation (or prenylation or lipidation or lipoylation) of one or more amino acid residues

398. The peptide according to item 382, wherein said modification is GPI (glycosyl phosphatidylinositol) anchor formation of one or more amino acid residues

399. The peptide according to item 382, wherein said modification is myristoylation of one or more amino acid residues

400. The peptide according to item 382, wherein said modification is farnesylation of one or more amino acid residues

401. The peptide according to item 382, wherein said modification is geranylgeranylation of one or more amino acid residues

402. The peptide according to item 382, wherein said modification is covalent attachment of nucleotides or derivates thereof to one or more amino acid residues

403. The peptide according to item 382, wherein said modification is ADP-ribosylation of one or more amino acid residues

404. The peptide according to item 382, wherein said modification is flavin attachment to one or more amino acid residues

405. The peptide according to item 382, wherein said modification is oxidation of one or more amino acid residues

406. The peptide according to item 382, wherein said modification is oxidative deamination of one or more amino acid residues

407. The peptide according to item 382, wherein said modification is deamination of one or more amino acid residues

408. The peptide according to item 382, wherein said modification is palmitoylation of one or more amino acid residues

409. The peptide according to item 382, wherein said modification is pegylation of one or more amino acid residues

410. The peptide according to item 382, wherein said modification is attachment of phosphatidyl-inositol of one or more amino acid residues

411. The peptide according to item 382, wherein said modification is phosphopantetheinylation of one or more amino acid residues

412. The peptide according to item 382, wherein said modification is polysialylation of one or more amino acid residues

413. The peptide according to item 382, wherein said modification is sulfation of one or more amino acid residues

414. The peptide according to item 382, wherein said modification is selenoylation of one or more amino acid residues

415. The peptide according to item 382, wherein said modification is arginylation of one or more amino acid residues

416. The peptide according to item 382, wherein said modification is glutamylation or polyglutamylation of one or more amino acid residues

417. The peptide according to item 382, wherein said modification is glycylation or polyglycylation of one or more amino acid residues

418. The peptide according to item 382, wherein said modification is acylation (or alkanoylation) of one or more amino acid residues

419. The peptide according to item 382, wherein said modification is Methylidene-imidazolone (MIO) formation of one or more amino acid residues

420. The peptide according to item 382, wherein said modification is p-Hydroxybenzylidene-imidazolone formation of one or more amino acid residues

421. The peptide according to item 382, wherein said modification is Lysine tyrosyl quinone (LTQ) formation of one or more amino acid residues

422. The peptide according to item 382, wherein said modification is Topaquinone (TPQ) formation of one or more amino acid residues

423. The peptide according to item 382, wherein said modification is Porphyrin ring linkage of one or more amino acid residues

424. The peptide according to item 382, wherein said modification is glypiation (addition of glycosyl phosphatidyl inositol) of one or more amino acid residues

425. The peptide according to item 382, wherein said modification is addition of heme to one or more amino acid residues

426. The peptide according to item 382, wherein said modification is ubiquitination of one or more amino acid residues

427. The peptide according to item 382, wherein said modification is SUMOylation (Small Ubiquitin-like Modifier) of one or more amino acid residues

428. The peptide according to item 382, wherein said modification is ISGylation of one or more amino acid residues

429. The peptide according to item 382, wherein said modification is citrullination (or deimination) of one or more amino acid residues

430. The peptide according to item 382, wherein said modification is the formation of pyroglutamic acid (or pidolic acid) of one or more amino acid residues

431. The peptide according to item 382, wherein said modification is formation of disulfide bridges (or disulfide bond or SS-bond or persulfide connection) between two amino acid residues

432. The peptide according to item 382, wherein said modification is formation of a desmosine cross-link between two or more amino acid residues

433. The peptide according to item 382, wherein said modification is transglutamination between two or more amino acid residues

434. The peptide according to item 1, wherein any of X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, X_{10}, X_{11}, X_{12}, X_{13}, X_{14}, X_{15} and/or X_{16} is an uncommon or modified amino acid

435. The peptide according to item 434, wherein said uncommon amino acid is acetylalanine

436. The peptide according to item 434, wherein said uncommon amino acid is acetylaspartic acid

437. The peptide according to item 434, wherein said uncommon amino acid is acetylcysteine

438. The peptide according to item 434, wherein said uncommon amino acid is acetylglutamic acid

439. The peptide according to item 434, wherein said uncommon amino acid is acetylglutamine

440. The peptide according to item 434, wherein said uncommon amino acid is acetylglycine

441. The peptide according to item 434, wherein said uncommon amino acid is acetylisoleucine

442. The peptide according to item 434, wherein said uncommon amino acid is acetyllysine

443. The peptide according to item 434, wherein said uncommon amino acid is acetylmethionine

444. The peptide according to item 434, wherein said uncommon amino acid is acetylproline

445. The peptide according to item 434, wherein said uncommon amino acid is acetylserine

446. The peptide according to item 434, wherein said uncommon amino acid is acetylthreonine

447. The peptide according to item 434, wherein said uncommon amino acid is acetyltyrosine

448. The peptide according to item 434, wherein said uncommon amino acid is acetylvaline

449. The peptide according to item 434, wherein said uncommon amino acid is acetyllysine

450. The peptide according to item 434, wherein said uncommon amino acid is acetylcysteine

451. The peptide according to item 434, wherein said uncommon amino acid is alanine amide

452. The peptide according to item 434, wherein said uncommon amino acid is arginine amide

453. The peptide according to item 434, wherein said uncommon amino acid is asparagine amide

454. The peptide according to item 434, wherein said uncommon amino acid is aspartic acid amide

455. The peptide according to item 434, wherein said uncommon amino acid is cysteine amide

456. The peptide according to item 434, wherein said uncommon amino acid is glutamine amide

457. The peptide according to item 434, wherein said uncommon amino acid is glutamic acid amide

458. The peptide according to item 434, wherein said uncommon amino acid is glycine amide

459. The peptide according to item 434, wherein said uncommon amino acid is histidine amide

460. The peptide according to item 434, wherein said uncommon amino acid is isoleucine amide

461. The peptide according to item 434, wherein said uncommon amino acid is leucine amide

462. The peptide according to item 434, wherein said uncommon amino acid is lysine amide

463. The peptide according to item 434, wherein said uncommon amino acid is methionine amide

464. The peptide according to item 434, wherein said uncommon amino acid is phenylalanine amide

465. The peptide according to item 434, wherein said uncommon amino acid is proline amide

466. The peptide according to item 434, wherein said uncommon amino acid is serine amide

467. The peptide according to item 434, wherein said uncommon amino acid is threonine amide

468. The peptide according to item 434, wherein said uncommon amino acid is tryptophan amide

469. The peptide according to item 434, wherein said uncommon amino acid is tyrosine amide

470. The peptide according to item 434, wherein said uncommon amino acid is valine amide

471. The peptide according to item 434, wherein said uncommon amino acid is an amino acid alcohol

472. The peptide according to item 434, wherein said uncommon amino acid is Aminobenzoic Acid

473. The peptide according to item 434, wherein said uncommon amino acid is Aminobutyric Acid

474. The peptide according to item 434, wherein said uncommon amino acid is Aminocyanobutyric acid

475. The peptide according to item 434, wherein said uncommon amino acid is Aminocyanopropionic acid

476. The peptide according to item 434, wherein said uncommon amino acid is Aminocyclohexanoic acid

477. The peptide according to item 434, wherein said uncommon amino acid is Aminocyclopropanoic acid

478. The peptide according to item 434, wherein said uncommon amino acid is Aminocylopentanoic acid

479. The peptide according to item 434, wherein said uncommon amino acid is Aminodecanoic acid

480. The peptide according to item 434, wherein said uncommon amino acid is Aminododecanoic acid

481. The peptide according to item 434, wherein said uncommon amino acid is Aminohexanoic acid

482. The peptide according to item 434, wherein said uncommon amino acid is Aminoisobutyric acid

483. The peptide according to item 434, wherein said uncommon amino acid is Aminomethylbenzoic acid

484. The peptide according to item 434, wherein said uncommon amino acid is Aminomethylcyclohexanoic acid

485. The peptide according to item 434, wherein said uncommon amino acid is Aminononanoic acid

486. The peptide according to item 434, wherein said uncommon amino acid is Aminooctanoic acid

487. The peptide according to item 434, wherein said uncommon amino acid is Aminophenylalanine

488. The peptide according to item 434, wherein said uncommon amino acid is Amino Salicylic acid

489. The peptide according to item 434, wherein said uncommon amino acid is 2-Amino-2-Thiazoline-4-carboxylic acid

490. The peptide according to item 434, wherein said uncommon amino acid is Aminoundecanoic acid

491. The peptide according to item 434, wherein said uncommon amino acid is Aminovaleric acid

492. The peptide according to item 434, wherein said uncommon amino acid is 4-Benzoylphenylalanine

493. The peptide according to item 434, wherein said uncommon amino acid is Biphenylalanine

494. The peptide according to item 434, wherein said uncommon amino acid is Bromophenylalanine

495. The peptide according to item 434, wherein said uncommon amino acid is gamma-Carboxyglutamic acid

496. The peptide according to item 434, wherein said uncommon amino acid is canavanine

497. The peptide according to item 434, wherein said uncommon amino acid is Carnitine

498. The peptide according to item 434, wherein said uncommon amino acid is Chlorophenylalanine

499. The peptide according to item 434, wherein said uncommon amino acid is Chlorotyrosine

500. The peptide according to item 434, wherein said uncommon amino acid is Cine

501. The peptide according to item 434, wherein said uncommon amino acid is Citrulline

502. The peptide according to item 434, wherein said uncommon amino acid is 4-Cyano-2-Aminobutyric acid

503. The peptide according to item 434, wherein said uncommon amino acid is Cyclohexylalanine

504. The peptide according to item 434, wherein said uncommon amino acid is Cyclohexylglycine

505. The peptide according to item 434, wherein said uncommon amino acid is Diaminobenzoic acid

506. The peptide according to item 434, wherein said uncommon amino acid is 2,4-Diaminobutyric acid

507. The peptide according to item 434, wherein said uncommon amino acid is 2,3-Diaminopropionic acid

508. The peptide according to item 434, wherein said uncommon amino acid is Dibutylglycine

509. The peptide according to item 434, wherein said uncommon amino acid is Diethylglycine

510. The peptide according to item 434, wherein said uncommon amino acid is Dihydrotryptophan

511. The peptide according to item 434, wherein said uncommon amino acid is Dipropylglycine

512. The peptide according to item 434, wherein said uncommon amino acid is Fluorophenylalanine

513. The peptide according to item 434, wherein said uncommon amino acid is formylmethionine

514. The peptide according to item 434, wherein said uncommon amino acid is formylglycine

515. The peptide according to item 434, wherein said uncommon amino acid is formyllysine

516. The peptide according to item 434, wherein said uncommon amino acid is farnesylcysteine

517. The peptide according to item 434, wherein said uncommon amino acid is hydroxyfarnesylcysteine

518. The peptide according to item 434, wherein said uncommon amino acid is Homoalanine

519. The peptide according to item 434, wherein said uncommon amino acid is Homoarginine

520. The peptide according to item 434, wherein said uncommon amino acid is Homoasparagine

521. The peptide according to item 434, wherein said uncommon amino acid is Homoaspartic acid

522. The peptide according to item 434, wherein said uncommon amino acid is Homoglutamic acid

523. The peptide according to item 434, wherein said uncommon amino acid is Homoglutamine

524. The peptide according to item 434, wherein said uncommon amino acid is Homoisoleucine

525. The peptide according to item 434, wherein said uncommon amino acid is Homophenylalanine

526. The peptide according to item 434, wherein said uncommon amino acid is Homoserine

527. The peptide according to item 434, wherein said uncommon amino acid is Homotyrosine

528. The peptide according to item 434, wherein said uncommon amino acid is Hydroxyproline

529. The peptide according to item 434, wherein said uncommon amino acid is Hydroxylysine

530. The peptide according to item 434, wherein said uncommon amino acid is 2-Indanylglycine

531. The peptide according to item 434, wherein said uncommon amino acid is 2-Indolecarboxylic acid

532. The peptide according to item 434, wherein said uncommon amino acid is Indoleglycine

533. The peptide according to item 434, wherein said uncommon amino acid is Iodophenylalanine

534. The peptide according to item 434, wherein said uncommon amino acid is Isonipecotic Acid

535. The peptide according to item 434, wherein said uncommon amino acid is Kynurenine

536. The peptide according to item 434, wherein said uncommon amino acid is β-(S-Benzyl)Mercapto-β,β-cyclopentamethylene propionic acid

537. The peptide according to item 434, wherein said uncommon amino acid is Methyltyrosine

538. The peptide according to item 434, wherein said uncommon amino acid is Methylphenylalanine

539. The peptide according to item 434, wherein said uncommon amino acid is methylalanine

540. The peptide according to item 434, wherein said uncommon amino acid is trimethylalanine

541. The peptide according to item 434, wherein said uncommon amino acid is methylglycine

542. The peptide according to item 434, wherein said uncommon amino acid is methylmethionine

543. The peptide according to item 434, wherein said uncommon amino acid is methylphenylalanine

544. The peptide according to item 434, wherein said uncommon amino acid is dimethylproline

545. The peptide according to item 434, wherein said uncommon amino acid is dimethylarginine

546. The peptide according to item 434, wherein said uncommon amino acid is methylarginine

547. The peptide according to item 434, wherein said uncommon amino acid is methylasparagine

548. The peptide according to item 434, wherein said uncommon amino acid is methylglutamine

549. The peptide according to item 434, wherein said uncommon amino acid is methylhistidine

550. The peptide according to item 434, wherein said uncommon amino acid is trimethyllysine

551. The peptide according to item 434, wherein said uncommon amino acid is dimethyllysine

552. The peptide according to item 434, wherein said uncommon amino acid is methyllysine

553. The peptide according to item 434, wherein said uncommon amino acid is methylcysteine

554. The peptide according to item 434, wherein said uncommon amino acid is glutamic acid 5-methyl ester

555. The peptide according to item 434, wherein said uncommon amino acid is Naphthylalanine

556. The peptide according to item 434, wherein said uncommon amino acid is Nipecotic acid

557. The peptide according to item 434, wherein said uncommon amino acid is Nitrophenylalanine

558. The peptide according to item 434, wherein said uncommon amino acid is Norleucine

559. The peptide according to item 434, wherein said uncommon amino acid is Norvaline

560. The peptide according to item 434, wherein said uncommon amino acid is Octahydroindolecarboxylic acid

561. The peptide according to item 434, wherein said uncommon amino acid is ornithine

562. The peptide according to item 434, wherein said uncommon amino acid is Penicillamine

563. The peptide according to item 434, wherein said uncommon amino acid is Phenylglycine

564. The peptide according to item 434, wherein said uncommon amino acid is phosphocysteine

565. The peptide according to item 434, wherein said uncommon amino acid is phosphohistidine

566. The peptide according to item 434, wherein said uncommon amino acid is phosphoserine

567. The peptide according to item 434, wherein said uncommon amino acid is phosphothreonine

568. The peptide according to item 434, wherein said uncommon amino acid is phosphotyrosine

569. The peptide according to item 434, wherein said uncommon amino acid is phosphoarginine

570. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-adenosine)-tyrosine

571. The peptide according to item 434, wherein said uncommon amino acid is phosphopantetheine-serine

572. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-RNA)-serine

573. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-adenosine)-lysine

574. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-guanosine)-lysine

575. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-DNA)-serine

576. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-RNA)-tyrosine

577. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-adenosine)-threonine

578. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-DNA)-tyrosine

579. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-DNA)-threonine

580. The peptide according to item 434, wherein said uncommon amino acid is (phospho-5'-uridine)-tyrosine

581. The peptide according to item 434, wherein said uncommon amino acid is 4-Phosphonomethylphenylalanine

582. The peptide according to item 434, wherein said uncommon amino acid is palmitoylcysteine

583. The peptide according to item 434, wherein said uncommon amino acid is palmitoyllysine

584. The peptide according to item 434, wherein said uncommon amino acid is palmitoylthreonine

585. The peptide according to item 434, wherein said uncommon amino acid is palmitoylserine

586. The peptide according to item 434, wherein said uncommon amino acid is palmitoylcysteine

587. The peptide according to item 434, wherein said uncommon amino acid is phycoerythrobilin-bis-cysteine

588. The peptide according to item 434, wherein said uncommon amino acid is phycourobilin-bis-cysteine

589. The peptide according to item 434, wherein said uncommon amino acid is pyrrolidone-5-carboxylic acid

590. The peptide according to item 434, wherein said uncommon amino acid is Pipericolic Acid

591. The peptide according to item 434, wherein said uncommon amino acid is Propargylglycine

592. The peptide according to item 434, wherein said uncommon amino acid is Pyridinylalanine

593. The peptide according to item 434, wherein said uncommon amino acid is pyroglutamic acid

594. The peptide according to item 434, wherein said uncommon amino acid is Sarcosine

595. The peptide according to item 434, wherein said uncommon amino acid is Tert-Leucine

596. The peptide according to item 434, wherein said uncommon amino acid is Tetrahydoisoquinoline-3-carboxylic acid

597. The peptide according to item 434, wherein said uncommon amino acid is Thiazolidinecarboxylic acid

598. The peptide according to item 434, wherein said uncommon amino acid is Thyronine

599. The peptide according to item 434, wherein said uncommon amino acid is selenocysteine

600. The peptide according to item 434, wherein said uncommon amino acid is selenomethionine

601. The peptide according to item 434, wherein said uncommon amino acid is erythro-beta-hydroxyasparagine

602. The peptide according to item 434, wherein said uncommon amino acid is erythro-beta-hydroxyaspartic acid

603. The peptide according to item 434, wherein said uncommon amino acid is gamma-carboxyglutamic acid

604. The peptide according to item 434, wherein said uncommon amino acid is aspartic 4-phosphoric anhydride

605. The peptide according to item 434, wherein said uncommon amino acid is2'-[3-carboxamido-3-(trimethylammonio)propyl]-histidine

606. The peptide according to item 434, wherein said uncommon amino acid is glucuronoylglycine

607. The peptide according to item 434, wherein said uncommon amino acid is geranylgeranylcysteine

608. The peptide according to item 434, wherein said uncommon amino acid is myristoylglycine

609. The peptide according to item 434, wherein said uncommon amino acid is myristoyllysine

610. The peptide according to item 434, wherein said uncommon amino acid is cysteine methyl disulfide

611. The peptide according to item 434, wherein said uncommon amino acid is diacylglycerolcysteine

612. The peptide according to item 434, wherein said uncommon amino acid is isoglutamylcysteine

613. The peptide according to item 434, wherein said uncommon amino acid is cysteinylhistidine

614. The peptide according to item 434, wherein said uncommon amino acid is lanthionine

615. The peptide according to item 434, wherein said uncommon amino acid is mesolanthionine

616. The peptide according to item 434, wherein said uncommon amino acid is methyllanthionine

617. The peptide according to item 434, wherein said uncommon amino acid is cysteinyltyrosine

618. The peptide according to item 434, wherein said uncommon amino acid is carboxylysine

619. The peptide according to item 434, wherein said uncommon amino acid is carboxyethyllysine

620. The peptide according to item 434, wherein said uncommon amino acid is (4-amino-2-hydroxybutyl)-lysine

621. The peptide according to item 434, wherein said uncommon amino acid is biotinyllysine

622. The peptide according to item 434, wherein said uncommon amino acid is lipoyllysine

623. The peptide according to item 434, wherein said uncommon amino acid is pyridoxal phosphate-lysine

624. The peptide according to item 434, wherein said uncommon amino acid is retinal-lysine

625. The peptide according to item 434, wherein said uncommon amino acid is allysine

626. The peptide according to item 434, wherein said uncommon amino acid is lysinoalanine

627. The peptide according to item 434, wherein said uncommon amino acid is isoglutamyllysine

628. The peptide according to item 434, wherein said uncommon amino acid is glycyllysine

629. The peptide according to item 434, wherein said uncommon amino acid is isoaspartylglycine

630. The peptide according to item 434, wherein said uncommon amino acid is pyruvic acid

631. The peptide according to item 434, wherein said uncommon amino acid is phenyllactic acid

632. The peptide according to item 434, wherein said uncommon amino acid is oxobutanoic acid

633. The peptide according to item 434, wherein said uncommon amino acid is succinyltryptophan

634. The peptide according to item 434, wherein said uncommon amino acid is phycocyanobilincysteine

635. The peptide according to item 434, wherein said uncommon amino acid is phycoerythrobilincysteine

636. The peptide according to item 434, wherein said uncommon amino acid is phytochromobilincysteine

637. The peptide according to item 434, wherein said uncommon amino acid is heme-bis-cysteine

638. The peptide according to item 434, wherein said uncommon amino acid is heme-cysteine

639. The peptide according to item 434, wherein said uncommon amino acid is tetrakis-cysteinyl iron

640. The peptide according to item 434, wherein said uncommon amino acid is tetrakis-cysteinyl diiron disulfide

641. The peptide according to item 434, wherein said uncommon amino acid is tris-cysteinyl triiron trisulfide

642. The peptide according to item 434, wherein said uncommon amino acid is tris-cysteinyl triiron tetrasulfide

643. The peptide according to item 434, wherein said uncommon amino acid is tetrakis-cysteinyl tetrairon tetrasulfide

644. The peptide according to item 434, wherein said uncommon amino acid is cysteinyl homocitryl molybdenum-heptairon-nonasulfide

645. The peptide according to item 434, wherein said uncommon amino acid is cysteinyl molybdopterin

646. The peptide according to item 434, wherein said uncommon amino acid is (8alpha-FAD)-cysteine

647. The peptide according to item 434, wherein said uncommon amino acid is (8alpha-FAD)-histidine

648. The peptide according to item 434, wherein said uncommon amino acid is (8alpha-FAD)-tyrosine

649. The peptide according to item 434, wherein said uncommon amino acid is dihydroxyphenylalanine

650. The peptide according to item 434, wherein said uncommon amino acid is topaquinone

651. The peptide according to item 434, wherein said uncommon amino acid is tryptophyl quinine

652. The peptide according to item 434, wherein said uncommon amino acid is (tryptophan)-tryptophyl quinone

653. The peptide according to item 434, wherein said uncommon amino acid is glycosylasparagine

654. The peptide according to item 434, wherein said uncommon amino acid is glycosylcysteine

655. The peptide according to item 434, wherein said uncommon amino acid is glycosylhydroxylysine

656. The peptide according to item 434, wherein said uncommon amino acid is glycosylserine

657. The peptide according to item 434, wherein said uncommon amino acid is glycosylthreonine

658. The peptide according to item 434, wherein said uncommon amino acid is glycosyltryptophan

659. The peptide according to item 434, wherein said uncommon amino acid is glycosyltyrosine

660. The peptide according to item 434, wherein said uncommon amino acid is asparaginyl-glycosylphosphatidylinositolethanolamine

661. The peptide according to item 434, wherein said uncommon amino acid is aspartyl-glycosylphosphatidylinositolethanolamine

662. The peptide according to item 434, wherein said uncommon amino acid is cysteinyl-glycosylphosphatidylinositolethanolamine

663. The peptide according to item 434, wherein said uncommon amino acid is glycyl-glycosylphosphatidylinositolethanolamine

664. The peptide according to item 434, wherein said uncommon amino acid is seryl-glycosylphosphatidylinositolethanolamine

665. The peptide according to item 434, wherein said uncommon amino acid is seryl-glycosylsphingolipidinositolethanolamine

666. The peptide according to item 434, wherein said uncommon amino acid is (phosphoribosyl dephospho-coenzyme A)-serine

667. The peptide according to item 434, wherein said uncommon amino acid is (ADP-ribosyl)-arginine

668. The peptide according to item 434, wherein said uncommon amino acid is (ADP-ribosyl)-cysteine

669. The peptide according to item 434, wherein said uncommon amino acid is glutamyl-glycerylphosphorylethanolamine

670. The peptide according to item 434, wherein said uncommon amino acid is sulfocysteine

671. The peptide according to item 434, wherein said uncommon amino acid is sulfotyrosine

672. The peptide according to item 434, wherein said uncommon amino acid is bromohistidine

673. The peptide according to item 434, wherein said uncommon amino acid is bromophenylalanine

674. The peptide according to item 434, wherein said uncommon amino acid is triiodothyronine

675. The peptide according to item 434, wherein said uncommon amino acid is thyroxine

676. The peptide according to item 434, wherein said uncommon amino acid is bromotryptophan

677. The peptide according to item 434, wherein said uncommon amino acid is dehydroalanine

678. The peptide according to item 434, wherein said uncommon amino acid is dehydrobutyrine

679. The peptide according to item 434, wherein said uncommon amino acid is dehydrotyrosine

680. The peptide according to item 434, wherein said uncommon amino acid is seryl-imidazolinone glycine

681. The peptide according to item 434, wherein said uncommon amino acid is oxoalanine

682. The peptide according to item 434, wherein said uncommon amino acid is alanyl-imidazolinone glycine

683. The peptide according to item 434, wherein said uncommon amino acid is allo-isoleucine

684. The peptide according to item 434, wherein said uncommon amino acid is isoglutamyl-polyglycine

685. The peptide according to item 434, wherein said uncommon amino acid is isoglutamyl-polyglutamic acid

686. The peptide according to item 434, wherein said uncommon amino acid is aminovinyl-cysteine

687. The peptide according to item 434, wherein said uncommon amino acid is (aminovinyl)-methyl-cysteine

688. The peptide according to item 434, wherein said uncommon amino acid is cysteine sulfenic acid

689. The peptide according to item 434, wherein said uncommon amino acid is glycyl-cysteine

690. The peptide according to item 434, wherein said uncommon amino acid is hydroxycinnamyl-cysteine

691. The peptide according to item 434, wherein said uncommon amino acid is chondroitin sulfate glucuronyl-galactosyl-galactosyl-xylosyl-serine

692. The peptide according to item 434, wherein said uncommon amino acid is dermatan sulfate glucuronyl-galactosyl-galactosyl-xylosyl-serine

693. The peptide according to item 434, wherein said uncommon amino acid is heparan sulfate glucuronyl-galactosyl-galactosyl-xylosyl-serine

694. The peptide according to item 434, wherein said uncommon amino acid is glycosyl-hydroxyproline

695. The peptide according to item 434, wherein said uncommon amino acid is hydroxy-arginine

696. The peptide according to item 434, wherein said uncommon amino acid is isoaspartyl-cysteine

697. The peptide according to item 434, wherein said uncommon amino acid is alpha-mannosyl-tryptophan

698. The peptide according to item 434, wherein said uncommon amino acid is mureinyl-lysine

699. The peptide according to item 434, wherein said uncommon amino acid is chondroitin sulfate-aspartic acid ester

700. The peptide according to item 434, wherein said uncommon amino acid is (6-FMN)-cysteine

701. The peptide according to item 434, wherein said uncommon amino acid is diphytanylglycerol diether-cysteine

702. The peptide according to item 434, wherein said uncommon amino acid is bis-cysteinyl bis-histidino diiron disulfide

703. The peptide according to item 434, wherein said uncommon amino acid is hexakis-cysteinyl hexairon hexasulfide

704. The peptide according to item 434, wherein said uncommon amino acid is cysteine glutathione disulfide

705. The peptide according to item 434, wherein said uncommon amino acid is nitrosyl-cysteine

706. The peptide according to item 434, wherein said uncommon amino acid is (ADP-ribosyl)-asparagine

707. The peptide according to item 434, wherein said uncommon amino acid is beta-methylthioaspartic acid

708. The peptide according to item 434, wherein said uncommon amino acid is (lysine)-topaquinone

709. The peptide according to item 434, wherein said uncommon amino acid is hydroxymethyl-asparagine

710. The peptide according to item 434, wherein said uncommon amino acid is (ADP-ribosyl)-serine

711. The peptide according to item 434, wherein said uncommon amino acid is cysteine oxazolecarboxylic acid

712. The peptide according to item 434, wherein said uncommon amino acid is cysteine oxazolinecarboxylic acid

713. The peptide according to item 434, wherein said uncommon amino acid is glycine oxazolecarboxylic acid

714. The peptide according to item 434, wherein said uncommon amino acid is glycine thiazolecarboxylic acid

715. The peptide according to item 434, wherein said uncommon amino acid is serine thiazolecarboxylic acid

716. The peptide according to item 434, wherein said uncommon amino acid is phenyalanine thiazolecarboxylic acid

717. The peptide according to item 434, wherein said uncommon amino acid is cysteine thiazolecarboxylic acid

718. The peptide according to item 434, wherein said uncommon amino acid is lysine thiazolecarboxylic acid

719. The peptide according to item 434, wherein said uncommon amino acid is keratan sulfate glucuronyl-galactosyl-galactosyl-xylosyl-threonine

720. The peptide according to item 434, wherein said uncommon amino acid is selenocysteinyl molybdopterin guanine dinucleotide

721. The peptide according to item 434, wherein said uncommon amino acid is histidyl-tyrosine

722. The peptide according to item 434, wherein said uncommon amino acid is methionine sulfone

723. The peptide according to item 434, wherein said uncommon amino acid is dipyrrolylmethanemethyl-cysteine

724. The peptide according to item 434, wherein said uncommon amino acid is glutamyl-tyrosine

725. The peptide according to item 434, wherein said uncommon amino acid is glutamyl-poly-glutamic acid

726. The peptide according to item 434, wherein said uncommon amino acid is cysteine sulfinic acid

727. The peptide according to item 434, wherein said uncommon amino acid is trihydroxyphenylalanine

728. The peptide according to item 434, wherein said uncommon amino acid is (sn-1-glycerophosphoryl)-serine

729. The peptide according to item 434, wherein said uncommon amino acid is thioglycine

730. The peptide according to item 434, wherein said uncommon amino acid is heme P460-bis-cysteine-tyrosine

731. The peptide according to item 434, wherein said uncommon amino acid is tris-cysteinyl-cysteine persulfido-bis-glutamato-histidino tetrairon disulfide trioxide

732. The peptide according to item 434, wherein said uncommon amino acid is cysteine persulfide

733. The peptide according to item 434, wherein said uncommon amino acid is Lactic acid (2-hydroxypropanoic acid)

734. The peptide according to any of items 434 to 733, wherein said uncommon amino acid is the L-enantiomer

735. The peptide according to any of items 434 to 733, wherein said uncommon amino acid is the D-enantiomer

FIGURE LEGENDS

Figure 1. Schematic representation of MHC multimer. A MHC multimer consist of a multimerization domain whereto one or more MHC-peptide complexes are attached through one or more linkers. The multimerization domain comprice one or more carriers and/or one or more scaffolds. The MHC-peptide complexes comprice a peptide and a MHC molecule

Figure 2. Program for peptide sequence motifs prediction inhere called random prediction software.

Figure 3. Full List of HLA Class I alleles assigned as of January 2007 from http://www.anthonynolan.org.uk/HIG/lists/class1list.html

Figure 4. List of top 30 HLA class 1 alleles in different human ethnic groups

Figure 5. Reactive groups and the bonds formed upon their reaction

Figure 6. Cleavable linkers, conditions for cleaving them and the resulting products of the cleavage. Shown are cleavable linkers relevant for the present invention, as well as the conditions that lead to their cleavage, and the products of the cleavage reaction.

Figure 7. Size exclusion chromatography of folded HLA-A*0201-β2m –QLFEELQEL (SEQ ID NO 217775) peptide-complex. Purification of HLA-A*0201-β2m –QLFEELQEL (SEQ ID NO 217775) peptide-complex by size exclusion chromatography on a HiLoad 16/60 Superdex 75 column. Eluted protein was followed by measurement of the absorbance at 280 nm. The elution profile consisted of 4 peaks, corresponding to aggregated Heavy Chain, correctly folded MHC-complex, β2m and excess biotin and peptide.

Figure 8. MHC-SHIFT Assay. The SHIFT Assay shows that heavy chain is efficiently biotinylated, since the band corresponding to biotinylated heavy chain (lane 2) is shifted up-wards upon incubation with streptavidin.
Lane 1: Benchmark protein-ladder
Lane 2: Folded HLA-A*0201-β2m –QLFEELQEL (SEQ ID NO 217775) peptide-complex
Lane 3: Folded HLA-A*0201-β2m –QLFEELQEL (SEQ ID NO 217775) peptide-complex incubated with molar excess Streptavidin.

Figure 9. Composition of Fluorescein-linker molecule. (A) Schematic representation of an example of a Fluorescein-linker molecule. (B) Composition of a L15 linker.

Figure 10. List of the 24 MHC class 1 alleles used for peptide prediction by the database http://www.cbs.dtu.dk/services/NetMHC/ and the 14 MHC class 2 alleles used for peptide prediction by the database http://www.cbs.dtu.dk/services/NetMHCII/

Figure 11. Ex vivo ELISPOT analysis of BclX(L)-specific. CD8 positive T cells in PBL from a breast cancer patient either with or without the BclX(L) YLNDHLEPWI peptide (SEQ ID NO 217776). Analysis were performed in doublets and number of IFN-gamma producing T-cells are presented. (Reference: Sorensen RB, Hadrup SR, Kollgaard T, Svane IM, Thor Straten P, Andersen MH (2006) Efficient tumor cell lysis mediated by a Bcl-X(L) specific T cell clone isolated from a breast cancer patient.Cancer Immunol Immunother Apr;56(4)527-33)

Figure 12. PBL from a breast cancer patient analyzed by flow cytometry. PBL from a breast cancer patient was analyzed by flow cytometry to identify Bcl-X(L)173–182 (peptide YLNDHLEPWI (SEQ ID NO 217776)) specific CD8 T cells using the dextramer complex HLA-A2/Bcl-X(L)173–182-APC, 7-AAD-PerCP, CD3-FITC, and CD8-APC-Cy7. The dextramer complex HLA-A2/HIV-1 pol476–484-APC was used as negative control.
(Reference: Sorensen RB, Hadrup SR, Kollgaard T, Svane IM, Thor Straten P, Andersen MH (2006) Efficient tumor cell lysis mediated by a Bcl-X(L) specific T cell clone isolated from a breast cancer patient.Cancer Immunol Immunother Apr;56(4)527-33)

Figure 13. 51-Cr release assay of isolated T cell clones. Ten expanded T cell clones isolated by Flow sorting and then expanded were tested for their specificity by analysis in a standard 51-Cr release assay. For this purpose, T2 cells loaded with either Bcl-X(L)173–182, YLNDHLEPWI (SEQ ID NO 217776) peptide or an irrelevant peptide (BA4697–105, GLQHWVPEL (SEQ ID NO 217777)) were used as target cells.
(Reference: Sorensen RB, Hadrup SR, Kollgaard T, Svane IM, Thor Straten P, Andersen MH (2006) Efficient tumor cell lysis mediated by a Bcl-X(L) specific T cell clone isolated from a breast cancer patient.Cancer Immunol Immunother Apr;56(4)527-33)

Figure 14. Bcl-X(L)173–182 specific clone tested for its cytotoxic potential in 51Cr-release assays. A) Bcl-X(L)173–182 specific clone was tested for its cytotoxic potential

in 51Cr-release assays. Two assays were performed a Cell lysis of T2 cells pulsed with Bcl-X(L)173–182 peptide or an irrelevant peptide (BA4697–105, GLQHWVPEL (SEQ ID NO 217777)) in three E:T ratios. B) Cell lysis of T2 cells pulsed with different concentrations of Bcl-X(L)173–182 peptide at the E:T ratio 1:1. (Reference: Sorensen RB, Hadrup SR, Kollgaard T, Svane IM, Thor Straten P, Andersen MH (2006) Efficient tumor cell lysis mediated by a Bcl-X(L) specific T cell clone isolated from a breast cancer patient.Cancer Immunol Immunother Apr;56(4)527-33).

Figure 15. Detection of Borrelia specific T cells using MHC dextramers. Dot plots showing live gated $CD3^+/CD4^-$ lymphocytes from Borrelia patient stained with (A) Negative Control MHC Dextramer (HLA-A*0201(GLAGDVSAV) (SEQ ID NO 217778) or (B) pool of MHC Dextramers containing peptides from Borrelia antigen Osp A and Fla B. pool of MHC Dextramers containing peptides from Borrelia antigen. 0,05% of the live gated $CD3^+/CD4^-$ lymphocytes are positive for one or more of the MHC Dextramers in the pool.

Figure 16. Detection of CMV specific T cells using MHC dextramers Dot plots showing live gated $CD3^+/CD4^-$ lymphocytes from CMV infected patient stained with (A) Negative Control MHC Dextramers (HLA-A*0201(GLAGDVSAV)) (SEQ ID NO 217778) or (B) MHC Dextramers containing peptides from CMV pp65 antigen (HLA-A*0201(NLVPMVATV)) (SEQ ID NO 217779).

Figure 17. Conformational ELISA. The ELISA is carried out as a sandwich-ELISA. The ELISA-plate was coated with W6/32 mouse-anti-hHLA-ABC (DAKO M0736) antibody, which recognizes a conformational epitope on correctly folded MHC-complex. Then MHC complex in various concentrations was added. β2m in various concentrations was used as negative control. HRP-conjugated rabbit anti-β2m (DAKO PO174) was used for detection of bound MHC complex. TMB One-step substrate system (Dako) was used as a substrate for HRP, and color formation was followed by measurement of absorbance at 450 nm.

Figure 18. Carboxylate-modified beads coupled to TCR and stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779) or HLA-A*0201(ILKEPVHGV)/RPE (SEQ ID NO 217780) dextramers. TCR in various concentrations were coupled to carboxylate- modified beads and then stained with HLA-A*0201(NLVPMVATV)/RPE

(SEQ ID NO 217779) or HLA-A*0201(ILKEPVHGV)/RPE (SEQ ID NO 217780) dextramers in a flow cytometry experiment.
A) Histogram showing x-axis: Fluorescence intensity measured in the RPE channel (FL2), y-axis: events counted. Events measured in the Region R9 are regarded as negative, and events measured in Region R10 are regarded as positive.
B) Percentage of positively stained beads is shown for each preparation of beads.
Negative control samples:
1) Beads coupled with 10 µg TCR stained with HLA-A*0201(ILKEPVHGV)/RPE (SEQ ID NO 217780)
2) Beads coupled with 0 µg TCR stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779)
Positive control samples:
3) Beads coupled with 2 µg TCR stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779)
4) Beads coupled with 5 µg TCR stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779)
5) Beads coupled with 10 µg TCR stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779)
6) Beads coupled with 20 µg TCR stained with HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779)

Figure 19. Flow cytometry analysis of human cell samples added TCR-coated beads. TCR-beads were added into human peripheral whole blood (A) or HPBMC (B) and then the samples were analysed by flow cytometry. Region R1 represents TCR-beads; region R2 represents lymphocyte cell population of interest.

Figure 20. Flow cytometry analysis of MHC multimer constructs carrying nonsense peptides. Human Peripheral Blood Lymphocytes were ficoll purified from blood from a human donor and stained with mouse anti-human CD3/PE antibody and mouse anti-human CD8/PB antibody together with either of the MHC Dextramer molecule constructs A) HLA-A*0201(NLVPMVATV)/APC (SEQ ID NO 217779), B) HLA-A*0201(ILKEPVHGV)/APC (SEQ ID NO 217780), C) HLA-A*0201(nonsense peptide 1)/APC or D) HLA-A*0201(nonsense peptide 2)/APC. The staining was analysed on a CyAn ADP flow cytometer. Live-gated and CD3 positive lymphocytes are shown.

Figure 21. Summary of flow cytometry analysis of the binding of different MHC multimer constructs to specific T cells in purified Human Peripheral Blood. Mononuclear Cell samples. Purified HPBMC were stained with different MHC(peptide) molecules attached to APC labeled dextran270 multimerization domain and analyzed by flow cytometry . See example 58 for details on experimental procedures. 5 different MHC(peptide) molecules were investigated. Construct 1: HLA-A*0201(GLAGDVSAV) (SEQ ID NO 217778), construct 2: HLA-A*0201(ALIAPVHAV) (SEQ ID NO 217781), construct 3: HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), construct 4: HLA-A*0201(GLCTLVAML) (SEQ ID NO 217782) and construct 5: HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780). A positive staining is symbolized with a (+) and is here defined as the identification of a distinct CD8 positive and MHC (peptide) positive population when visualized in a dot plot (se Figure 20). Negative staining is symbolized wit a (-) and is defined as absence of a distinct CD8 positive and MHC (peptide) positive population when visualized in a dot plot. Nt means not determined. All samples have previously been analyzed for the presence of T-cells restricted by HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), HLA-A*0201(GLCTLVAML) (SEQ ID NO 217782) and HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) and these results are shown in italics in the figure (column 2 and 3).

Figure 22. Gating strategy for no-lyse no-wash procedure. Whole blood was stained with MHC multimer, anti-CD8/APC, anti-CD3/PB and CD45/CY antibody in a no-lyse no-wash procedure. For further details see text in example 65. During analysis of data the following gating strategy was used: CD45/PB antibody was used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells. This was done during data collection by gating on CD45/PB positive cells in a CD45/PB vs. side scatter dot plot as shown in A. After data collection and during data analysis CD3 positive cells were selected by gating CD3/FITC positive cells in a CD3/FITC vs side scatter plot as shown in B. The final data was illustrated in a MHC multimer/PE vs CD8/APC plot (see Figure 23).

Figure 23. Identification of CMV-specific T cells in a blood sample using no-lyse no-wash procedure. Whole blood from three different donors were analysed for the presence of CMV-specific T cells by flow cytometry using a no-lyse no-wash procedure. Donor 1 was stained with a MHC multimer consisting of PE-conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the

peptide NLVPMVATV (SEQ ID NO 217779) derived from Human Cytomegalo Virus (HCMV) (left panel) and with a negative control MHC multimer consisting of PE conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ILKEPVHGV (SEQ ID NO 217780) derived from Human Immunodeficiency Virus (HIV) (right panel). Donor 2 was stained with a MHC multimer consisting of PE-conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide VTEHDTLLY (SEQ ID NO 217783) derived from Human Cytomegalo Virus (HCMV) (left panel) and a negative control MHC multimer consisting of PE-conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide IVDCLTEMY (SEQ ID NO 217784) derived from ubiquitin specific peptidase 9 (USP9) (right panel). Donor 3 was stained with twoMHC multimers consisting of PE conjugated 270 kDa dextran coupled with HLA-B*0207 in complex with beta2microglobulin and either of the peptides TPRVTGGGAM (SEQ ID NO 217785) (left panel) or RPHERNGFTVL (SEQ ID NO 217786) (center panel) both derived from Human Cytomegalo Virus (HCMV) and with a negative control MHC multimer consisting of PE-conjugated 270 kDa dextran coupled with HLA- B*0207 in complex with beta2microglobulin and the peptide TPGPGVRYPL (SEQ ID NO 217787) derived from Human Immunodeficiency Virus (HIV) (right panel). All samples were also added Anti-CD45/PB, anti-CD3/FITC and anti-CD8/APC antibodies. The samples were gated as shown in Figure 22.

Figure 24. Enumeration of specific T cells using CytoCount™ beads. Whole blood from a human donor were analysed for the presence of CMV-specific T cells with MHC multimers by flow cytometry using a no-lyse no-wash procedure. 2 x 100 µl donor blood was analysed with two different MHC multimers: A) PE-conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide VTEHDTLLY (SEQ ID NO 217783) derived from Human Cytomegalo Virus (HCMV) and a negative control construct B) consisting of PE-conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide IVDCLTEMY (SEQ ID NO 217784) derived from ubiquitin specific peptidase 9 (USP9). To each sample Anti-CD45/CY, anti-CD3/APC and anti-CD8/PB antibody was added together with 50 µl CytoCount beads (1028 beads/µl). Following staining for 15 minutes PBS was added to 1 ml and the samples analysed on a CyAn flow cytometer. During analysis CD45/CY antibody was used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells and

CD3/APC antibody was used to gate for CD3 positive T lymphocytes. Amount of counted beads in sample A are shown in the histogram C and amount of beads counted in the negative control sample B are show in histogram D.
Concentration of HLA-A*0101(VTEHDTLLY) (SEQ ID NO 217783) specific T cells in the blood sample were determined as follows:
((count of MHC multimer+ CD8+ cells in A x concentration of beads x dilution factor of beads) /counted beads C))- ((counted MHC multimer+ CD8+ cells in B x concentration of beads x dilution factor of beads) /counted beads D) = ((1300 cells x 1028 beads/µl x 0,05) / 67225 beads) – ((2 cells x 1028 beads/µl x 0,05) / 72623 beads) = 0,9926 cells/ µl = 992,6 celler/ml

Figure 25. MHC dextramers can be embedded in a sugar matrix together with antibodies and used for detection of specific T cells in a blood sample. MHC dextramer constructs was embedded in a sugar matrix together with relevant gating reagents (anti-CD3/Pacific Blue, anti-CD8/Alexa700 and anti-CD45/Cascade Yellow antibodies) and the matrix dried. Then EDTA stabilized blood from a human donor were added and the samples analyzed by flow cytometry. Two different MHC construct were used HLA-A*0101(VTEHDTLLY)/PE dextramer (SEQ ID NO 217783) (A) and the negative control construct HLA-A*0101(IVDCLTEMY)/PE (SEQ ID NO 217784) (B). As a control antibodies and MHC dextramer constructs were used to stain blood from the same donor following a general staining procedure without embedding the antibodies and MHC dextramers in a sugar matrix as described elsewhere herein. (C) Staining with HLA-A*0101(VTEHDTLLY)/PE (SEQ ID NO 217783) dextramer following a normal staining procedure and (D) Staining with HLA-A*0101(IVDCLTEMY)/PE (SEQ ID NO 217784) dextramer following a normal staining procedure.

Figure 26. Borrelia genome survey for the three Borrelia species, B. burgdorferi, B. afzelii and B.garinii. Listed are the database accession numbers for the individual genomes and the known plasmids or variable plasmid segments of the three species. The specific strains of the individual species are denoted.

Figure 27. Complete list of all known and putative proteins encoded by the genome and plasmids of Borrelia burgdorferi (strain B31). The proteins are identified by their names or designations. Position of start and end of the gene, coding strand, amino acid length of the encoded protein, and the accession numbers and gene ID's are given.

Figure 28. Complete list of all known and putative proteins encoded by the genome and plasmids of Borrelia afzelii (strain PKo). The proteins are identified by their names or designations. Position of start and end of the gene, coding strand, amino acid length of the encoded protein, and the accession numbers and gene ID's are given.

Figure 29. Complete list of all known and putative proteins encoded by the genome, plasmids and known variable plasmid segments of Borrelia garinii (strain PBi). The proteins are identified by their names or designations. Position of start and end of the gene, coding strand, amino acid length of the encoded protein, and the accession numbers and gene ID's are given.

Figure 30. The amino acid sequences of Borrelia antigens of specific interest as sources for MHC binding peptides. Name and protein bank accession numbers are shown.

Figure 31. Borrelia MHC class 1 antigen peptides of 8-, 9-, 10- and 11 amino acids in length generated from the chosen protein sequences by random prediction software (see figure 2). Name and protein bank accession numbers are shown.

Figure 32. Borrelia MHC class 1 antigen peptides of 8-, 9-, 10- and 11 amino acids in length generated from the chosen protein sequences by use of software based on neural prediction of MHC binding peptides. Peptide sequences are grouped according to HLA binding alleles and sub-grouped according to peptide length.

Figure 33. Borrelia MHC class 2 antigen peptides of 13-, 14-, 15-, and 16 amino acids in length generated from the chosen protein sequences by random prediction software (see figure 2).

Figure 34. Borrelia MHC class 2 antigen peptides of 15 amino acids in length generated from the chosen protein sequences by use of software based on neural prediction of MHC binding peptides. Peptide sequences are grouped according to HLA binding alleles and sub-grouped according to peptide length. For each 15-mer binding peptide the essential 9-mer core sequence is given.

Figure 35. Summary flow chart ELISPOT. Summary flow chart showing measurement of antigen reactive T-Cells by IFN-γ capture in blood samples by ELISPOT. See example 31 for more detailed information.

Figure 36. Prediction of cancer antigen BclX(L) specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders. Prediction of cancer antigen BclX(L) specific MHC class 1, 8-, 9, 10-,11-mer peptide binders for 24 MHC class 1 alleles (see figure 10) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed. The peptides listed in figure 36 correspond to SEQ ID NO 216470-217262 in the sequence listing.

Figure 37. Prediction of cancer antigen BclX(L) specific MHC class 2, 15-mer peptide binders. Prediction of cancer antigen BclX(L) specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 10) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed. The peptides listed in Fig 37 correspond to SEQ ID NO 217263-217774 in the sequence listing.

Figure 38. The amino acid sequences of Borrelia antigens of specific interest as sources for MHC binding peptides. Name and protein bank accession numbers are shown.

Figure 39: Borrelia MHC class 1 and 2 antigen peptides of 8-, 9-, 10- and 11 amino acids and 13-, 14-, 15- and 16 amino acids in length generated from the chosen protein sequences by random prediction software. Name and protein bank accession numbers are shown.

Figure 40: NetMHC peptides. A) Borrelia burgdorferi MHC class1 & 2 epitopes, B) Borrelia afzelii MHC class1 & 2 epitopes, C) Borrelia garinii MHC class 1 & 2 epitopes. The NetMHC peptides are predicted by the http://www.cbs.dtu.dk/services/NetMHC/ database.

Figure 41: NetMHC peptide sequences from figure 40 are grouped according to HLA binding alleles and sub-grouped according to peptide length.

Figure 42: Selected peptides. The amino acid sequence from one or more Borrelia strains were aligned using the protein alignment programs Vector NTI from Invitrogen, and a homologous sequence for all analyzed strains were be identified. This homologous sequence were run through the "intelligent" peptide epitope prediction program NetMHC as described elsewhere herein to identify epitopes able to bind HLA-A*02 or HLA-A*03. The identified epitopes are shown in this figure. A) Special selected HLA-A*0201 binding peptides from Borrelia proteins; B) Special selected HLA-A*0301 binding peptides from Borrelia proteins.

Figure 43: Borrelia MHC class 1 and 2 antigen peptides of 8-, 9-, 10- and 11 amino acids and 13-, 14-, 15- and 16 amino acids in length generated from the chosen protein sequences by random prediction software (SEQ ID NO 180858 to SEQ ID NO 215925). NetMHC peptides predicted by the http://www.cbs.dtu.dk/services/NetMHC/ database (SEQ ID NO 215926 to SEQ ID NO216339). Name and protein bank accession numbers are shown.

Figure 44: Special selected HLA-A*0201 epitopes from Borrelia species. Some peptides may be identical to sequences in either Borrelia afzelii. B. garinii or B. burgdorferi but some will be optimized to show possible fit to more than one species ie. some amino acid position have been altered compared to the individual parent sequences.

Figure 45: Special selected HLA-A*03 epitopes from Borrelia species. Some peptides may be identical to sequences in either Borrelia afzelii. B. garinii or B. burgdorferi but some will be optimized to show possible fit to more than one species ie. some amino acid position have been altered compared to the individual parent sequences.

INDEX TO SEQUENCE LIST

The sequences in the figures and tables are included in the sequence list. The sequences have the SEQ ID NO's indicated below – the sequences in each figure or table are consecutively numbered.

Figure 30:
SEQ ID NO 1-44

Figure 31:

Antigen designation in Table 19	SEQ ID NO
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31]	45-1366
NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31	1367-2696
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31	2697-4074
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31	4075-5480
AAC70056.1 Decorin binding protein A; DbpA [Borrelia afzelii	5481-6126
AAC70057.1 Decorin binding protein A; DbpA [Borrelia garinii]	6127-6836
AAC70021.1 Decorin binding protein B; DbpB [Borrelia burgdorferi]	6837-7522
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31]	7523-10087
CAA44492.1| Outer surface protein A [Borrelia burgdorferi]	10088-11149
|BAA22351.1| Outer surface protein B [Borrelia garinii]	11150-12307
AAM22469.1| Outer surface protein C [Borrelia afzelii]	12308-13117
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]	13118-13799
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]	13800-14549
AAC44770.1| FlaA protein (Borrelia burgdorferi)	14550-15879
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]	15880-17189
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen Vlse Of Borrelia Burgdorferi	17190-18547
CAA57807.1 Associated protein A (BapA)[Borrelia burgdorferi]	18548-19189
Seq19	19190-20455
Seq 20	20456-22321

Seq 21	22322-23355
Seq 22	23356-24473
Seq 23	24474-25783
Seq 24	25784-27861
Seq 25	27862-28855
Seq 26	28856-31653
Seq 27	31564-33623
Seq 28	33624-35913
Seq 29	35914-36939
Seq 30	36940-38333
Seq 31	38334-38919
Seq 32	38920-39737
Seq 33	39738-40611
Seq 34	40612-42220
Seq 35	42221-43880
Seq 36	43881-44898
Seq 37	44899-45904
Seq 38	45905-46606
Seq 39	46607-47212
Seq 40	47213-48406
Seq 41	48407-49644
Seq 42	49645-51050
Seq 43	51051-52424
Seq 44	52425-54050

Figure 32

Antigen designation	SEQ ID NO
NP_212517.1; Basic membrane protein A (bmpA) [Borrelia burgdorferi B31; Seq1	54051-54446
NP_212516.1; Basic membrane protein B (bmpB) [Borrelia burgdorferi B31; Seq2	54447-54934
NP_212518.1; Basic membrane protein C (bmpC) [Borrelia burgdorferi B31; Seq3	54935-55486
NP_212519.1B; Basic membrane protein D (bmpD) [Borrelia burgdorferi B31; Seq4	55487-56052
AAC70056.1; Decorin binding protein A; DbpA [Borrelia afzelii; Seq5	56053-56237
AAC70057.1; Decorin binding protein A; DbpA [Borrelia garinii]; Seq6	56238-56436
AAC70021.1; Decorin binding protein B; DbpB [Borrelia burgdorferi]; Seq7	56437-56639
NP_212694.1; Heat shock protein 90 [Borrelia burgdorferi B31]; Seq8	56640-57579
CAA44492.1| Outer surface protein A [Borrelia burgdorferi]; Seq9	57580-57833
|BAA22351.1| Outer surface protein B [Borrelia garinii]; Seq10	57834-58137
AAM22469.1| Outer surface protein C [Borrelia afzelii]; Seq11	58138-58345
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]; Seq12	58346-58523
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]; Seq13	58524-58669
AAC44770.1| FlaA protein (Borrelia burgdorferi) ; Seq14	58670-59232
BAD18055.1 ; FlaB protein [Borrelia garinii]; Seq15	59233-59392
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]; Seq16	59393-59741
1L8W|A Chain A, Crystal Structure Of Lyme Disease	59742-60008

Variable Surface Antigen VlsE1 Of Borrelia Burgdorferi; Seq17	
CAA57807.1; Associated protein A (BapA)[Borrelia burgdorferi]; Seq18	60009-60203
AAL25643.1, P37-47 [Borrelia burgdorferi]; Seq19	60204-60500
NP_212481.1| fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31]; Seq20	60501-61184
AAC44656.1| P30 Borrelia burgdorferi; Seq21	61185-61566
NP_045619.1| immunogenic protein P37, putative [Borrelia burgdorferi B31]; Seq22	61567-61910
NP_212281.1| flagellin [Borrelia burgdorferi B31]; Seq23	61911-62261
NP_212463.1| oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) ; [Borrelia burgdorferi B31]; Seq24	62262-63060
AAC44381.1| outer membrane porin protein Oms28 precursor; Seq25	63061-63322
CAA49829.1| p93 [Borrelia burgdorferi]; Seq26	63323-64135
NP_212375.1| glycerol kinase (glpK) [Borrelia burgdorferi B31]; Seq27	64136-64773
NP_212342.1| hypothetical protein BB0208 [Borrelia burgdorferi B31]; Seq28	64774-65881
NP_045482.1| hypothetical protein BBG22 [Borrelia burgdorferi B31]; Seq29	65882-66290
NP_212885.1| hypothetical protein BB0751 [Borrelia burgdorferi B31]; Seq30	66291-66734
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31]; Seq31	66735-66934
NP_045709.1| lipoprotein BBA36[Borrelia burgdorferi B31]; Seq32	66935-67186
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi]; Seq33	67187-67422
NP_045739.1| BBA66 antigen, P35, putative [Borrelia burgdorferi B31]; Seq34	67423-67916

AAT93824.1|BBA66 antigen, P35, putative [Borrelia garinii PBi]; Seq35	67917-68425
NP_045742.1| hypothetical protein BBA69 [Borrelia burgdorferi B31]; Seq36	68426-68757
AAT93826.1| conserved hypothetical protein BBA69[Borrelia garinii PBi]; Seq37;	68758-69026
NP_045573.1| hypothetical protein BBI42 [Borrelia burgdorferi B31]; Seq38	69027-69299
NP_051318.1| revA protein[Borrelia burgdorferi B31]; Seq39	69300-69486
NP_045737.1| BBA64 antigen, P35 [Borrelia burgdorferi B31]; Seq40	69487-69835
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi]; Seq41	69836-70189
AAL84596.1| BBK32 [Borrelia burgdorferi]; Seq42	70190-70651
AAL84590.1| BBK32 [Borrelia afzelii]; Seq43	70652-71087
AAL84595.1| BBK32 [Borrelia garinii]; Seq44	71088-71575

Figure 33

Antigen designation	SEQ ID NO
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31	71576-72877
NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31	72848-74187
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31	74188-75545
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31	75546-76931
AAC70056.1 Decorin binding protein A; DbpA [Borrelia afzelii	76932-77557
AAC70057.1 Decorin binding protein A; DbpA [Borrelia garinii]	77558-78247
AAC70021.1 Decorin binding protein B; DbpB [Borrelia burgdorferi]	78248-78913

NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31]	78914-81459
CAA44492.1| Outer surface protein A [Borrelia burgdorferi]	81460-82502
|BAA22351.1| Outer surface protein B [Borrelia garinii]	82503-83640
AAM22469.1| Outer surface protein C [Borrelia afzelii]	83641-84430
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]	84431-85092
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]	85093-85822
AAC44770.1| FlaA protein (Borrelia burgdorferi)	85823-87132
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]	87133-88422
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen Vlse Of Borrelia Burgdorferi	88423-89760
CAA57807.1 Associated protein A (BapA)[Borrelia burgdorferi]	89761-90382
AAL25643.1, P37-47 [Borrelia burgdorferi]; Seq19	90383-91628
NP_212481.1| fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31]; Seq20	91629-93474
AAC44656.1| P30 Borrelia burgdorferi; Seq21	93475-94488
NP_045619.1| immunogenic protein P37, putative [Borrelia burgdorferi B31]; Seq22	94489-95586
NP_212281.1| flagellin [Borrelia burgdorferi B31]; Seq23	95587-96876
NP_212463.1| oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) ; [Borrelia burgdorferi B31]; Seq24	96877-98934
AAC44381.1| outer membrane porin protein Oms28 precursor; Seq25	98935-99908
CAA49829.1| p93 [Borrelia burgdorferi]; Seq26	99909-102686
NP_212375.1| glycerol kinase (glpK) [Borrelia burgdorferi B31]; Seq27	102687-104636
NP_212342.1| hypothetical protein BB0208 [Borrelia burgdorferi B31]; Seq28	104637-106906

NP_045482.1| hypothetical protein BBG22 [Borrelia burgdorferi B31]; Seq29	106907-107912
NP_212885.1| hypothetical protein BB0751 [Borrelia burgdorferi B31]; Seq30	107913-109286
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31]; Seq31	109287-109852
NP_045709.1| lipoprotein BBA36[Borrelia burgdorferi B31]; Seq32	109853-110650
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi]; Seq33	110651-111504
NP_045739.1| BBA66 antigen, P35, putative [Borrelia burgdorferi B31]; Seq34	111505-113094
AAT93824.1|BBA66 antigen, P35, putative [Borrelia garinii PBi]; Seq35	113095-114736
NP_045742.1| hypothetical protein BBA69 [Borrelia burgdorferi B31]; Seq36	114737-116378
AAT93826.1| conserved hypothetical protein BBA69[Borrelia garinii PBi]; Seq37;	116379-117364
NP_045573.1| hypothetical protein BBI42 [Borrelia burgdorferi B31]; Seq38	117365-118046
NP_051318.1| revA protein[Borrelia burgdorferi B31]; Seq39	118047-118632
NP_045737.1| BBA64 antigen, P35 [Borrelia burgdorferi B31]; Seq40	118633-119806
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi]; Seq41	119807-121024
AAL84596.1| BBK32 [Borrelia burgdorferi]; Seq42	121025-122410
AAL84590.1| BBK32 [Borrelia afzelii]; Seq43	122411-123764
AAL84595.1| BBK32 [Borrelia garinii]; Seq44	123765-125370

Figure 34

Antigen designation	SEQ ID NO
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31 Seq1	125371-126024

NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31 Seq2	126025-126584
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31 Seq3	126585-127288
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31 Seq4	127289-127904
AAC70056.1 Decorin binding protein A DbpA [Borrelia afzelii Seq5	127905-128186
AAC70057.1 Decorin binding protein A DbpA [Borrelia garinii] Seq6	128187-128428
AAC70021.1 Decorin binding protein B DbpB [Borrelia burgdorferi] Seq7	128429-128684
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31] Seq8	128685-129678
CAA44492.1| Outer surface protein A [Borrelia burgdorferi] Seq9	129679-129984
|BAA22351.1| Outer surface protein B [Borrelia garinii] Seq10	129985-130282
AAM22469.1| Outer surface protein C [Borrelia afzelii] Seq11	130283-130498
AAC62927.1| OspE-related lipoprotein [Borrelia garinii] Seq12	130499-130870
CAA57806.1| Outer surface protein G [Borrelia burgdorferi] Seq13	130871-131040
AAC44770.1| FlaA protein (Borrelia burgdorferi) Seq14	131041-131966
BAD18055.1 FlaB protein [Borrelia garinii] Seq15	131967-132356
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi] Seq16	132357-132940
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen VlsE1 Of Borrelia Burgdorferi Seq17	132941-133116
CAA57807.1 Associated protein A (BapA)[Borrelia burgdorferi] Seq18	133117-133398
AAL25643.1, P37-47 [Borrelia burgdorferi] Seq19	133399-133708

NP_212481.1| fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31] Seq20	133709-134764
AAC44656.1| P30 Borrelia burgdorferi Seq21	134765-135226
NP_045619.1| immunogenic protein P37, putative [Borrelia burgdorferi B31] Seq22	135227-135614
NP_212281.1| flagellin [Borrelia burgdorferi B31] Seq23	135615-136268
NP_212463.1| oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) [Borrelia burgdorferi B31] Seq24	136269-137092
AAC44381.1| outer membrane porin protein Oms28 precursor Seq25	137093-137570
CAA49829.1| p93 [Borrelia burgdorferi] Seq26	137571-138312
NP_212375.1| glycerol kinase (glpK) [Borrelia burgdorferi B31] Seq27	138313-139244
NP_212342.1| hypothetical protein BB0208 [Borrelia burgdorferi B31] Seq28	139245-139616
NP_045482.1| hypothetical protein BBG22 [Borrelia burgdorferi B31] Seq29	139617-140010
NP_212885.1| hypothetical protein BB0751 [Borrelia burgdorferi B31] Seq30	140011-140476
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31] Seq31	140477-140768
NP_045709.1| lipoprotein BBA36[Borrelia burgdorferi B31] Seq32	140769-141052
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi] Seq33	141053-141368
NP_045739.1| BBA66 antigen, P35, putative [Borrelia burgdorferi B31] Seq34	141369-142034
AAT93824.1|BBA66 antigen, P35, putative [Borrelia garinii PBi] Seq35	142035-142838
NP_045742.1| hypothetical protein BBA69 [Borrelia burgdorferi B31] Seq36	142839-143178
AAT93826.1| conserved hypothetical protein	143179-143468

BBA69[Borrelia garinii PBi] Seq37	
NP_045573.1| hypothetical protein BBI42 [Borrelia burgdorferi B31] Seq38	143469-143852
NP_051318.1| revA protein[Borrelia burgdorferi B31] Seq39	143853-144042
NP_045737.1| BBA64 antigen, P35 [Borrelia burgdorferi B31] Seq40	144043-144728
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi] Seq41	144729-145414
AAL84596.1| BBK32 [Borrelia burgdorferi] Seq42	145415-145890
AAL84590.1| BBK32 [Borrelia afzelii] Seq43	145891-146426
AAL84595.1| BBK32 [Borrelia garinii] Seq44	146427-146962

Figure 38

Antigen	SEQ ID NO
<ABX71745 CRASP-2,Borrelia Burgdorferi>	146963
<CAH10086 CRASP-1,Borrelia garinii>	146964
<AAU07022 4-alpha-glucanotransferase,Borrelia garinii PBi>	146965
<CAA59725 outer surface protein A,Borrelia afzelii>	146966
<CAA59727 outer surface protein A,Borrelia garinii>	146967
<YP_853838 outer surface protein B,Borrelia afzelii PKo>	146968
<NP_045689 outer surface protein B,Borrelia burgdorferi B31>	146969
AAN87995 OspC,Borrelia garinii>	146970
<NP_047005 outer surface protein C, Borrelia burgdorferi B31>	146971
<CAF34024 outer surface protein VlsE,Borrelia garinii>	146972
<CAF34027 outer surface protein VlsE,Borrelia afzelii PKo>	146973

Figure 39

Antigen	SEQ ID NO
<ABX71745 CRASP-2,Borrelia Burgdorferi>	146974-148805
<CAH10086 CRASP-1,Borrelia garinii>	148806-150757
<AAU07022 4-alpha-glucanotransferase,Borrelia garinii PBi>	150758-154717
<CAA59727 outer surface protein A,Borrelia garinii>	154718-156821
<CAA59725 outer surface protein A,Borrelia afzelii>	156822-158917
<YP_853838 outer surface protein B,Borrelia afzelii PKo>	158918-161221
<NP_045689 outer surface protein B,Borrelia burgdorferi B31>	161222-163501
AAN87995 OspC,Borrelia garinii>	163502-165005
<NP_047005 outer surface protein C, Borrelia burgdorferi B31>	165006-166597
<CAF34024 outer surface protein VlsE,Borrelia garinii>	166598-168853
<CAF34027 outer surface protein VlsE,Borrelia afzelii PKo>	168854-171149

Figure 40

Antigen	SEQ ID NO
<ABX71745 CRASP-2;Protein;Borrelia burgdorferi> Class 1 and 2	171150-171695
<NP_045689 outer surface protein B;Protein;Borrelia burgdorferi B31> Class 1 and 2	171696-172134
<NP_047005 outer surface protein C;Protein;Borrelia burgdorferi B31> Class 1 and 2	172135-172552
<CAA59725 outer surface protein	172553-172996

A;Protein;Borrelia afzelii> Class 1 and 2	
<YP_853838 outer surface protein B;Protein;Borrelia afzelii PKo> Class 1 and 2	172997-173522
<CAF34027 outer surface protein VlsE;Protein;Borrelia afzelii PKo> Class 1 and 2	173523-174053
<CAH10086 CRASP-1;Protein;Borrelia garinii> Class 1 and 2	174054-174491
<AAU07022 4-alpha-glucanotransferase;Protein;Borrelia garinii PBi> Class 1 and 2	174492-176082
<CAA59727 outer surface protein A;Protein;Borrelia garinii> Class 1 and 2	176083-176568
<AAN87995 Outer Surface Protein C;Protein;Borrelia garinii> Class 1 and 2	176569-176943
<CAF34024 outer surface protein VlsE;Protein;Borrelia garinii> Class 1 and 2	176944-177458

Figure 41

The peptides listed in Figure 41 are identical to the ones listed in Figure 40.

Figure 42

Peptide	SEQ ID NO
<OspA7;Protein;Borrelia species>FTLEGTLAA	177459
<OspA 8;Protein;Borrelia species>TLVSKKVTL	177460
<OspB 8;Protein;Borrelia species>IMLEGNLV	177461
<OspB 9;Protein;Borrelia species>TMSITDDL	177462
<OspC 7;Protein;Borrelia species>LMTLFLFI	177463
<OspC 8;Protein;Borrelia species>LLAGAYAI	177464

<FlaB 6;Protein;Borrelia species>QASWTLRV	177465
<FlaB 7;Protein;Borrelia species>IAVNIYAA	177466
<VlsE 8;Protein;Borrelia species>LSAIVTAA	177467
<VlsE 9;Protein;Borrelia species>ILSAIVTA	177468
<OspG 6;Protein;Borrelia species>IICAVFVL	177469
<FlaA 6;Protein;Borrelia species>IWSNPNYI	177470
<OspE 4;Protein;Borrelia species>IICAVFVL	177471
<OspE 5;Protein;Borrelia species>FSEFTVNI	177472
<BmpA 3;Protein;Borrelia species>MYSDGIDI	177473
<BmpA 4;Protein;Borrelia species>LAPNNVIT	177474
<BmpB 3;Protein;Borrelia species>LIGVVFRI	177475
<BmpB 4;Protein;Borrelia species>VGDALYLI	177476
<BmpC 3;Protein;Borrelia species>MTEDAYEV	177477
<BmpC 4;Protein;Borrelia species>LNQDQSYI	177478
<BmpD 2;Protein;Borrelia species>MYGYEAGA	177479
<BmpD 3;Protein;Borrelia species>LAPNNVLV	177480
<DbpA 3;Protein;Borrelia species>ILKAKIKA	177481
<DbpA 4;Protein;Borrelia species>TADGIIAI	177482
<DbpB 2;Protein;Borrelia species>LAACNFGL	177483
<DbpB 3;Protein;Borrelia species>LVACSIGL	177484
<BapA 4;Protein;Borrelia species>LFILSLSA	177485
<CRASP-1a;Protein;Borrelia species>KLNIIKLNI	177486
<CRASP-1b;Protein;Borrelia species>LNYEIEKI	177487
<CRASP-1c;Protein;Borrelia species>KLNILTTIL	177488
<CRASP-2a;Protein;Borrelia species>MLISISLL	177489
<CRASP-2b;Protein;Borrelia species>LIDDFAIEL	177490
<CRASP-2c;Protein;Borrelia species>LSCDVSRL	177491
<MalQ 4;Protein;Borrelia species>LLDFASFV	177492
<MalQ 5;Protein;Borrelia species>LNTNEDFV	177493
<MalQ 6;Protein;Borrelia species>IAYDSADV	177494
<BmpA 5;Protein;Borrelia species>IVFLSCSGK	177495
<BmpA 6;Protein;Borrelia species>FLTGYIAAK	177496
<BmpB 5;Protein;Borrelia species>EIFIKQILK	177497
<BmpB 6;Protein;Borrelia species>ALYLITGEY	177498

<BmpC 5;Protein;Borrelia species>KEMARFMYK	177499
<BmpC 6;Protein;Borrelia species>YIAAKMSRK	177500
<BmpD 5;Protein;Borrelia species>SLMYSLTKK	177501
<BmpD 6;Protein;Borrelia species>RSTASNMYR	177502
<DbpA 5;Protein;Borrelia species>IIAIVKVMK	177503
<DbpA 6;Protein;Borrelia species>FTNTQTGSK	177504
<DbpB 5;Protein;Borrelia species>FTGLKTGSK	177505
<DbpB 6;Protein;Borrelia species>LFEAFTGLK	177506
<HSP90 6;Protein;Borrelia species>LLTSGMPSK	177507
<OspA 7;Protein;Borrelia species>LILALIACK	177508
<OspA 8;Protein;Borrelia species>KTKNLVFTK	177509
<Osp A 9;Protein;Borrelia species>ISVNSQKTK	177510
<OspB 9;Protein;Borrelia species>VTLKKEIEK	177511
<OspB 10;Protein;Borrelia species>RTNGTTLEY	177512
<OspB 11;Protein;Borrelia species>MTDADNATK	177513
<OspC 9;Protein;Borrelia species>LANKAIGKK	177514
<OspC 10;Protein;Borrelia species>ILMTLFLFI	177515
<OspC 11;Protein;Borrelia species>AISTLITEK	177516
<OspE 6;Protein;Borrelia species>GSFKTSLYY	177517
<OspE 7;Protein;Borrelia species>NLGTLVIRK	177518
<OspG 7;Protein;Borrelia species>VFVLIISCK	177519
<FlaA 7;Protein;Borrelia species>RVSKSHSSK	177520
<FlaB 8;Protein;Borrelia species>SINAANLSK	177521
<FlaB 9;Protein;Borrelia species>KINTPASLS	177522
<FlaB 10;Protein;Borrelia species>SQASRNTSK	177523
<FlaB 11;Protein;Borrelia species>FQNRLESIK	177524
<VlsE 10;Protein;Borrelia species>AVSGEQILK	177525
<VlsE 11;Protein;Borrelia species>AIVLRGLAK	177526
<BapA 5;Protein;Borrelia species>KQILADLPK	177527
<BapA 6;Protein;Borrelia species>QLNSDKIDY	177528
<CRASP-1d;Protein;Borrelia species> RIIYSSLNY	177529
<CRASP-1e;Protein;Borrelia species>SSLNYEIEK	177530
<CRASP-2d;Protein;Borrelia species>RSRYNNFYK	177531
<CRASP-2e;Protein;Borrelia species> ESFDVISSK	177532

<CRASP-2f;Protein;Borrelia species>LIALKCIVK	177533
<MalQ 1;Protein;Borrelia species>RSFEKFKKK	177534
<MalQ 2;Protein;Borrelia species>FLFASSQSY	177535
<MalQ 3;Protein;Borrelia species>RINLNLKRK	177536
<Artificial;Protein>	177537
<Artificial;Protein>	177538

Table A: SEQ ID NO 177539-179138

Table B SEQ ID NO 179139-179392

Table C SEQ ID NO 179393-179552

Figure 36 SEQ ID NO 179553-180345

Figure 37 SEQ ID NO 180346-180857

Figure 43 SEQ ID NO 180858-216339

Figure 44 SEQ ID NO 216340-216404

Figure 45 SEQ ID NO 216405-216469

Fig 36 SEQ ID NO 216470-217262

Fig 37 SEQ ID NO 217263-217774

EXAMPLES

Example 1

This example describes how to make a MHC class I complex with a peptide in the peptide binding-groove using *in vitro refolding*. The MHC-complex in this example consisted of light chain β2m, the MHC class I Heavy Chain allele HLA-A*0201 (a truncated version in which the intracellular and transmembrane domains have been deleted) and the peptide QLFEELQEL (SEQ ID NO 217775).

MHC I-complexes consists of 3 components; Light Chain (β2m), Heavy Chain and a peptide of typically 8-10 amino acids. In this example MHC-complexes was generated by *in vitro* refolding of heavy chain, β2m and peptide in a buffer containing reduced and oxidized glutathione. By incubation in this buffer a non-covalent complex between Heavy Chain, β2m and peptide was formed. Heavy chain and β2m was expressed as inclusion bodies in *E.coli* prior to *in vitro* refolding following standard procedures as described in Garboczi et al., (1996), Nature 384, 134-141. Following refolding the MHC complexes was biotinylated using BirA enzyme able to biotinylate a specific amino acid residue in a recognition sequence fused to the C-terminal of the Heavy Chain by genetic fusion. Monomer MHC complexes was then purified by size exclusion chromatography.

1. 200 ml of refolding buffer (100 mM Tris, 400 mM L-arginin-HCL, 2 mM NaEDTA, 0.5 mM oxidized Gluthathione, 5 mM reduced Glutathione, pH 8.0) was supplied with protease inhibitors PMSF (phenylmethylsulphonyl fluoride), Pepstatin A and Leupeptin (to a final concentration of 1 mM, 1 mg/l and 1 mg/l, respectively). The refolding buffer was placed at 10 °C on a stirrer.
2. 12 mg of peptide QLFEELQEL (SEQ ID NO 217775) was dissolved in DMSO or another suitable solvent (300-500 µl), and added drop-wise to the refolding buffer at vigorous stirring.
3. 4.4 mg of human Light Chain β2m was added drop-wise to the refolding buffer at vigorous stirring.
4. 6.2 mg of Heavy Chain HLA-A*0201 (supplied with DTT to a concentration of 0.1 mM) was added drop-wise to the refolding buffer at vigorous stirring.
5. The folding reaction was placed at 10°C at slow stirring for 4-8 hours.
6. After 4-8 hours, step 3 and 4 was repeated and the folding reaction is placed at 10°C at slow stirring O/N.

7. Step 3 and 4 was repeated, and the folding reaction is placed at 10°C at slow stirring for 6-8 hours.

Optionally, steps 5-7 may be done in less time, e.g. a total of 0.5-5 hours.

8. After 6-8 hours the folding reaction was filtrated through a 0.2 μm filter to remove aggregates.
9. The folding reaction was concentrated O/N at 10°C shaking gently in a suitable concentrator with a 5000 mw cut-off filter. The folding reaction was concentrated to approximately 5-10 ml. (Optionally the filtrate can be stored at 4°C and reused for another folding with the same peptide and heavy chain.)
10. The concentrated folding reaction was buffer-exchanged at least 8 times, into a MHC-buffer (20 mM Tris-HCl, 50 mM NaCl, pH 8.0) and concentrated (at 10°C in a suitable concentrator with a 5000 mw cut-off filter) down to approximately 1 ml.
11. The heavy chain part of the MHC-complex was biotinylated by mixing the following components: approximately 1000 μl folded MHC-complex, 100 μl each of Biomix-A, Biomix-B and d-Biotin (all 3 from Biotin Protein Ligase Kit from Avidity, 10 μl birA enzyme (3 mg/ml, from Biotin Protein Ligase Kit from Avidity, 0.5 μl Pepstatin A (2 mg/ml) and 0.5 μl Leupeptin (2 mg/ml). The above was gently mixed and incubated O/N at room temperature.
12. The biotinylated and folded MHC-complex solution was centrifuged for 5 min. at 1700x g, room temperature.
13. Correctly folded MHC-complex was separated and purified from excess biotin, excess β2m, excesss heavy chain and aggregates thereoff, by size exclusion chromatography on a column that separates proteins in the 10-100 kDa range. Correctly folded monomer MHC-complex was eluted with a MHC-buffer (20 mM Tris-HCl, 50 mM NaCl, pH 8.0). The elution profile consisted of 4 peaks, corresponding to aggregated Heavy Chain, correctly folded monomer MHC-complex, β2m and excess biotin and peptide (See figure 7).
14. Fractions containing the folded MHC-complex were pooled and concentrated to approximately 1 ml in a suitable concentrator with a 5000 mw cut-off filter. The protein-concentration was estimated from its abosorption at 280 nm.
15. Folded MHC-complex can optionally be stored stored at –170°C before further use.
16. The grade of biotinylation was analyzed by a SDS PAGE SHIFT-assay with Streptavidin (figure 8) and correct folding was confirmed by ELISA, using the antibody W6/32 that recognizes correctly folded MHC-peptide complex.
17.

The above procedure may be used for folding any MHC I compexes consisting of any β2m, any heavy chain and any peptide approx. 8-11 amino acids long. Either of the components can be truncated or otherwise modified. The above procedure can also be used for generation of "empty" MHC I complexes consisting of β2m and heavy chain without peptide.

Example 2

This example describes how to generate soluble biotinylated MHC II complexes using a baculovirus expression system, where the MHC II complex was DR4 consisting of the α-chain DRA1*0101 and the β-chain DRB1*0401 as described by Svendsen et al., (2004), J. Immunol. 173(11):7037-45. Briefly, the hydrophobic transmembrane regions of the DRα and DRβ chains of DR4 were replaced by leucine zipper dimerization domains from the transcription factors Fos and Jun to promote DR α/β assembly. This was done by ligating cytoplasmic cDNA sequences of *DRA1*0101* and *DRB1*0401* to *fos*- and *jun*-encoding sequences. A *birA* site GLNDIFEAQKIEWH (SEQ ID NO 217788) was added to the 3' end of the *DRA1*0101-fos* template. Covalently bound peptide AGFKGEQGPKGEP (SEQ ID NO 217789) derived from collagen II amino acid 261–273 were genetically attached by a flexible linker peptide to the N terminus of the DRβ-chain. Finally, the modified DRA1*0101 and DRB1*0401 inserts were cloned into the expression vector pAcAb3. The pAcAB3-DRA1*0101/ DRB1*0401 plasmids were cotransfected with linearized baculovirus DNA (BD Pharmingen; BaculoGold kit) into Sf9 insect cells, according to the manufacturer's instructions. Following two rounds of plaque purification, clonal virus isolates were further amplified three times before preparation of high-titer virus (10^8–10^{10}/ml). These stocks were used to infect High Five or serum-free Sf21 insect cells (Invitrogen Life Technologies, Carlsbad, CA) for protein production. Spinner cultures (2–3 x 10^6 cells/ml) were infected at a multiplicity of infection of 1–3 in a volume of 150 ml per 2 L spinner flask. Supernatants were harvested and proteinase inhibitor tablets (Roche, Basel, Switzerland) were added before affinity purification on MiniLeak-Low columns (Kem-En-Tec) coupled with the anti-HLA-DR monoclonal antibody L243. HLA-DR4 complexes were eluted with diethylamine (pH 11) into neutralization buffer (2 M Tris, pH 6.5) and immediately buffer exchanged and concentrated in PBS, 0.01% NaN_3, using Millipore (Bedford, MA) concentrators. The purity of protein was confirmed by SDS-PAGE. The purified DR4 complexes were biotinylated *in vitro* as described for MHC I complexes elsewhere

herein. These complexes may now be used for coupling to any dimerization domain, e.g. divynylsulfone activated dextran 270coupled with SA and a fluorochrome.

Example 3

This example describes how to generate empty biotinylated MHC II complexes using a baculovirus expression system , where the MHC II complex consist of any α-chain and any β-chain, including truncated and otherwise modified versions of the two. Briefly, The hydrophobic transmembrane regions of the DRα and DRβ chains of MHC II are replaced by leucine zipper dimerization domains from the transcription factors Fos and Jun to promote DR α/β assembly. This is done by ligating cytoplasmic cDNA sequences of DRα and DRβ to *fos*- and *jun*-encoding sequences. A *birA* site GLNDIFEAQKIEWH (SEQ ID NO 217788) is added to the 3' end of either the DRα-*fos*/ DRα-*jun* or the DRβ-*jun*/ DRβ-*fos* template. The modified DRα and DRβ inserts is cloned into the expression vector pAcAb3 and cotransfected with linearized baculovirus DNA into Sf9 insect cells, according to the manufacturer's instructions. Following rounds of plaque purification, clonal virus isolates is further amplified before preparation of high-titer virus. These stocks are used to infect High Five or serum-free Sf21 insect cells (Invitrogen Life Technologies, Carlsbad, CA) for protein production, e.g. as Spinner cultures. Supernatants are harvested and proteinase inhibitors added before affinity purification, e.g. using a MiniLeak-Low columns (Kem-En-Tec) coupled with anti-MHC II antibody. The purified MHC II complexes is biotinylated *in vitro* as described for MHC I complexes elsewhere herein. These biotinylated MHC II complexes may now be used for coupling to any dimerization domain, e.g. divynylsulfone activated dextran 270coupled with SA and a fluorochrome.

Example 4

This example describes how to generate biotinylated MHC II complexes using a cell based protein expression system , where the MHC II complex consist of any α-chain and any β-chain, including truncated and otherwise modified versions of the two. The MHC II complex may also have a peptide bound in the peptide binding cleft.
The hydrophobic transmembrane regions of the MHC II α-chain and MHC II β-chain are replaced by leucine zipper dimerization domains from the transcription factors Fos and Jun to promote α/β chain assembly. This is done by ligating cytoplasmic cDNA sequences of α-chain and β-chain to *fos*- and *jun*-encoding sequences. A *birA* site GLNDIFEAQKIEWH (SEQ ID NO 217788) is added to the 3' end of the DRα-*fos*

template. Optionally covalently bound peptide is genetically attached by a flexible linker peptide to the N terminus of the DRβ-chain. The modified DRα and DRβ inserts is cloned into a suitable expression vector and transfected into a cell line capable of protein expression, e.g. insect cells, CHO cells or similar. Transfected cells are grown in culture, supernatants are harvested and proteinase inhibitors added before affinity purification, e.g. using a MiniLeak-Low columns (Kem-En-Tec) coupled with anti-MHC II antibody. Alternatively the expressed MHC II complexes may be purified by anion- or cation-exchange chromatography. The purified MHC II complexes is biotinylated *in vitro* as described for MHC I complexes elsewhere herein. These biotinylated MHC II complexes may now be used for coupling to any dimerization domain, e.g. divynylsulfone activated dextran 270coupled with SA and a fluorochrome.

Example 5

This is an example of how to make a MHC multimer that is a tetramer and where the MHC are attached to the multimerization domain through a non-covalent interaction The multimerization domain consist of Streptavidin. The MHC molecule was biotinylated DR4 consisting of the α-chain DRA1*0101 and the β-chain DRB1*0401 and the peptide AGFKGEQGPKGEP (SEQ ID NO 217789) derived from collagen II amino acid 261–273. The biotinylated MHC-peptide complexes was generated as described in a previous example herein.

Fluorescent DR4-peptide tetramer complexes were assembled by addition of ultra-avidin-R-PE (Leinco Technologies, St. Louis, MO) at a final molar ratio of biotinylated to DR4-peptide ultra-avidin-R-PE of 6:1. The resulting DR4-peptide multimer complexes were subjected to size exclusion on a Superdex-200 column to separate the tetramer complexes from protein aggregates and lower molecular weight complexes and excess fre DR4-peptide. The tetramer complexes were concentrated using Centicon-30 concentrators and stored at 0.1-0.3 mg/ml in a mixture of protease inhibitors.

These complexes could be used to detect specific T cells in a flow cytometry assay as described by Svendsen et al.(2004) Tracking of Proinflammatory Collagen-Specific T cells in Early and Late Collagen-Induced Arthritis in Humanized mice. J. Immunol. 173:7037-7045.

Example 6

This is and example of generation of a multimerization domain. The multimerization domain is an activated divinylsylfone-dextran(270kDa)(VS-dex270) was coupled with streptavidin (SA) and labelled with Allophycocyanin (APC).

1. Streptavidin (approx. 100 mg SA/ml in 10 mM HEPES, 0,1M NaCl, pH 7.85) was dialysed with gentle stirring for 2 days against 10 mM HEPES, 0.1M NaCl, pH 7.85 (20 fold excess volume) at 2-8°C with 1 buffer change/day.
2. 5 ml of APC from a homogen suspension (approx. 10 mg/ml) was centrifuged 40 min. at 3000 rpm. The supernatant was discharged and the precipitate dissolved in 5 ml of 10 mM HEPES, 0,1M NaCl, pH 7.85. This APC solution was dialysed with gentle stirring in the dark for 2 days against 10 mM HEPES, 0.1M NaCl, pH 7.85 (20 fold excess volume) at 2-8°C with 1 buffer change/day.
3. The APC-solution was concentrated to 1 ml and the concentration measured to 47 g/L at UV 650nm. The A650/A278-ratio was measured to 4.2.
4. The SA-solution was filtrated through a 0.45 μm filter and the protein concentration was measured to 61.8 g SA/L at UV 278nm .
5. Conjugation: The reagents was mixed to a total volume of 500 μl in the following order with 8.1 mol SA/mol Dex and 27 mol APC/mol Dex.:
    a) 90 μl water
    b) 160 μl activated VS-dex270
    c) 23 μl SA (61,8 g/L) ~ 8.1 equivalents,
    d) 177 μl APC (47 g/L) ~ 27 equivalents,
    e) 50 μl of 100 mM HEPES, 1M NaCl, pH 8

   The reaction was placed in a water bath with stirring at 30°C in the dark for 18 hours.
6. The coupling was stopped by adding 50 μl 0,1M ethanolamine, pH 8.0.
7. The conjugate was purified on a Sephacryl S-200 column with 10 mM HEPES, 0,1M NaCl buffer, pH 7.2.
8. 3 peaks were collected (peak 1: APC-SA-dex270; peak 2: Free APC; peak 3: Free SA). Volume, UV A650 and UV A278 were measured.
9. The concentration of dextran270, APC/Dex and SA/Dex were calculated to $22.4x10^{-8}$ M; 3.48 and 9.54 respectively.
10. The conjugate were added NaN_3 and BSA to a final concentration of 15 mM and 1% respectively. The volume was adjusted with 10 mM HEPES, 0.1M NaCl, pH 7.2 to a final concentration of $16x10^{-8}$ M Dex270.

11. The conjugate were kept at 2-8^{0}C in dark until further use.

Example 7

This is and example of generation of a multimerization domain. The multimerization domain is an activated divinylsylfone-dextran(270kDa)(VS-dex270) was coupled with streptavidin (SA) and the label is R-phycoerythrin (RPE).

The coupling procedure described for coupling of SA and APC to VS-dex270 (as described elsewhere herein) were followed with the exception that APC were replaced with RPE

Example 8

This is an example of how to couple MHC-peptide complexes to a multimerization domain, where the multimerization domain is dextran.

This example describes how to couple an empty MHC or a MHC-complex to a dextran multimerization domain through a non-covalent coupling, to generate a MHC-dextramer. The MHC-dextramer in this example consisted of APC-streptavidin (APC-SA)-conjugated 270kDA dextran and a biotinylated, folded MHC-complex composed of β2m, HLA-A*0201 heavy chain and the peptide NLVPMVATV (SEQ ID NO 217779).

The APC-SA conjugated 270kDA dextran contained 3,7 molecules of SA per dextran (each SA can bind 3 MHC-complexes) and the concentration was 16x10^{-8} M. The concentration of the HLA-A*0201/ NLVPMVATV-complex (SEQ ID NO 217779) was 4 mg/ml (1 μg = 20,663 pmol). The molecular concentration of the MHC-complex was 8,27x10^{-5}M .

The MHC-complex was attached to the dextran by a non-covalent Biotin-Streptavidin interaction between the biotinylated Heavy Chain part of the MHC-complex and the SA, conjugated to dextran.

Here follows a protocol for how to produce 1000 μl of a MHC-dextramer solution with a final concentration of approximately 32x10^{-9}M :

1. 200 μL 270 kDA vinylsulfone-activated dextran, corresponding to 3,2x10^{-11} mol, and 4 μl MHC-complex, corresponding to 3,55x10^{-10} mol was mixed and incubated at room temperature in the dark for 30 min.
2. A buffer of 0,05M Tris-HCl, 15 mM NaN_3, 1% BSA, pH 7,2 was added to a total volume of 1000 μl.

3. The resulting MHC-dextramer preparation may now be used in flow cytometry eksperiments.

Example 9

This is an example of how to make and use MHC multimers that are trimers consisting of a streptavidin multimerization domain with 3 biotinylated MHC complexs and 1 flourophore molecule attached to the biotin binding pockets of streptavidin.
MHC complexs consisting of HLA-A*0201 heavy chain, beta2microglobulin and NLVPMVATV (SEQ ID NO 217779) peptide or the negative control peptide GLAGDVSAV (SEQ ID NO 217778) were generated as described elsewhere herein.
The fluorophore in this example was Fluorescein-linker molecules as shown in figure 9. Each of these molecules consist of a linker-biotin molecule mounted with 4 trippel fluorescein-linker molecules. The linker-biotin molecule was here H-L30-Lys(NH_2)-L30-Lys(NH_2)-L30-Lys(NH_2)L300Lys(caproylamidobiotin)-NH_2 where L30 was a 30 atom large linker and L300 was a 300 atom large linker. Both L30 and L300 was composed of multiple L15 linkers with the structure shown in figure 9B. Linker-biotin molecules were generated as follows: Downloaded Boc-L300-Lys(Fmoc) resin (100 mg) was deprotected and subjected to coupling with Boc-Lys(2ClZ)-OH, Boc-L30-OH, Boc-Lys(2ClZ)-OH, Boc-L30-OH, Boc-Lys(2ClZ)-OH then Boc-L30-OH. The resin was Fmoc deprotected and reacted twice (2x 2 h) with caproylamido biotin NHS ester (25 mg in 0.5 mL NMP + 25 microL DIPEA). The resin was washed with TFA and the product cleaved off with TFA:TFMSA:mCresol:thioanisol (6:2:1:1), 1 mL, precipitated with diethyl ether and purified by RP-HPLC. MS calculated for $C_{300}H_{544}N_{64}O_{137}S$ is 7272.009 Da, found 7271.19 Da.
Alternatively linker-biotin molecule was H-L60- Lys(NH_2)-L60- Lys(NH_2)-L60-Lys(NH_2)L300Lys(caproylamidobiotin)-NH_2 and made from downloaded Boc-L300-Lys(Fmoc) resin (100 mg), and then prepared analogously to H-L30-Lys(NH_2)-L30-Lys(NH_2)-L30-Lys(NH_2)L300Lys(caproylamidobiotin)-NH_2. MS calculated for $C_{360}H_{652}N_{76}O_{167}S$ is 8749.5848 Da and was found to be 7271.19 Da. Yield 3 mg.
The trippel fluorescein-linker molecules was here betaalanin-L90-Lys(Flu)-L90-Lys(Flu)-L90-Lys(Flu)-NH_2 where Lys = Lysine, Flu = Fluorescein and L90 is a 90 atom linker (se figure 9 for further details). The trippel-fluorescein-linker molecule was generated as follows: Downloaded Boc-Lys(Fmoc) resin, 2 g,was Boc deprotected and subjected to 3 x coupling with Boc-L30-OH, Boc-Lys(Fmoc)-OH, 3 x Boc-L30-OH, Boc-

Lys(Fmoc)-OH, 3 x Boc-L30-OH. The three Fmoc groups were removed and carboxyfluorescein, 301 mg, activated with HATU, 274 mg, and DIPEA, 139 µL, in 8 mL NMP, was added to the resin twice for 30 min. The resin was Boc deprotected and subjected to 2 x 30 min coupling with beta-alanine-N,N-diacetic acid benzyl ester, followed by 5 min treatment with 20 % piperidine in NMP. The resin was washed with DCM, then TFA and the product was cleaved off the resin, precipitated with diethyl ether and purified by RP-HPLC. Yield was 621 mg. MS calculated for C268H402N44O116 is 6096.384 Da, while MS found was 6096 Da.

Biotin-linker molecule were coupled together with 4 trippel fluorescein-linker molecules as follows: (500 nmol) was dissolved in 88 microliter NMP + 2 µl pyridine and activated for 10 min at room temperature (conversion to cyclic anhydride) by addition of 10 µl N,N' diisopropylcarbodiimide. Following activation the trippel fluorescein-linker was precipitated with diethyl ether and redissolved in 100 microliter NMP containing 10 nmol biotin-linker. Once dissolved the coupling was initiated by addition of 5 µl diisopropyl ethyl amine, and was complete after 30 min.

Streptavidin and Fluorescein-linker molecules are then mixed in a molar ration of 1:1 and incubated for ½ hour. Then MHC complexes are added in 3-fold molar excess in respect to streptavidin and incubated for another ½ hour. Alternatively, MHC complexes are added first, then Fluorescein-linker molecules or MHC complexes are mixed with Fluorescein-linker molecules before addition to Streptavidin.

These MHC multimers are then used to stain CMV specific T cells in a flow Cytometry experiment. $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) are incubated with 10 µl of each of the two HLA-A*0201(peptide)/Fluorescein constructs described above for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. 10 µl of mouse-anti-human CD8/PB (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a flowcytometer.

In the above described example the Fluorescein-linker is as shown in figure 9 but the linker molecule can be any linker molecule as described in patent application WO 2007/015168 A2 (Lohse (2007)) or alternatively chemical biotinylated fluorochrom can be used instead of Fluorescein-linker molecules. The MHC complexes described in this

example is a MHC I molecule composed of HLA-A*0201 heavy chain, beta2microglobulin and NLVPMVATV (SEQ ID NO 217779) peptide but can in principle be any MHC complex or MHC like molecule as described elsewhere herein.

Example 10

This is an example of how to make and use MHC multimers that are trimers .
This is an example of how to make MHC multimers consisting of a streptavidin multimerization domain with 3 biotinylated MHC complexs attached to the biotin binding pockets of streptavidin and how to use such trimer MHC complexs to detect specific T cells by direct detection of individual cells in a flow cytometry experiment by addition of a biotinylated flourophore molecule. In this example the fluorophore is Fluorescein linker molecules constructed as described elsewhere herein.
MHC complexs consisting of HLA-A*0201 heavy chain, beta2microglobulin and peptide are generated as described elsewhere. MHC complexs are incubated with streptavidin in a molar ratio of 3:1 for ½ hour.
These trimer MHC multimers are then used to stain CMV specific T cells in a flow Cytometry experiment. $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) are incubated with 10 µl HLA-A*0201(peptide) multimer construct for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. Then Fluorescein linker molecules (as described in Example 9) are added and incubation continued for 5 minutes. 10 µl mouse-anti-human CD8/PB antibody (clone DK25 from Dako) is added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by addition of 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. Cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a flowcytometer.

In this example the Fluorescein-linker is as shown in figure 9 but the linker molecule can be any linker molecule as described in Lohse, Jesper, (2007), WO 2007/015168 A2 or alternative chemically biotinylated fluorochrome may be used. The MHC complexse described in this example is a MHC I molecule composed of HLA-A*0201 heavy chain, beta2microglobulin and NLVPMVATV (SEQ ID NO 217779) peptide but can in principle be any MHC complex or MHC like molecule as described elsewhere herein.

Example 11

This is an example of how to make MHC multimers where the multimerization domain is dextran and the MHC complexs are chemically conjugated to the dextran multimerization domain.

MHC complexs consisting of HLA-A*0201 heavy chain, beta2microglobulin and NLVPMVATV (SEQ ID NO 217779) peptide or the negative control peptide GLAGDVSAV (SEQ ID NO 217778) are generated as described elsewhere herein. Dextran with a molecular weight of 270 kDa is activated with divinylsulfone. Activated Dextran is then incubated with MHC and RPE in a 0.05 M $NaCHO_3$ buffer; pH = 9.5 with a molar ratio between MHC and Dextran of 30-60 and a molar ratio between RPE and dextran of 3-7 :1 The mixture is placed in a water bath at 30°C for 16 hours. Excess flourochrome, MHC and dextran are removed by FPLC using a sephacryl S-300 column.

These MHC/RPE dextramers are then used to stain CMV specific T cells in a flow Cytometry experiment. Briefly, $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) are incubated with 10 µl of each of the two HLA-A*0201(peptide)/RPE constructs described above for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. 10 µl mouse-anti-human CD8/PB antibody (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells are then resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a flow cytometer.

Example 12

This is an example of how to make MHC multimers where the multimerization domain is dextran and MHC complexs are MHC I molecules chemically conjugated to dextran multimerization domain and the dextran multimerization domain also have fluorochrome chemically coupled.

Human beta2microglobulin is coupled to dextran as follows. Dextran with a molecular weight of 270 kDa is activated with divinylsulfone. Activated dextran is incubated with human beta2microglobulin and RPE in a 0.05 M $NaCHO_3$ buffer; pH = 9.5 with a molar ratio between beta2microglobulin and Dextran of 30-60 and a molar ratio between RPE and dextran of 3-7:1. The molar ratio of the final product is preferable 4-6 RPE and 15-24 beta2microglobulin per dextran. The mixture is placed in a water bath at 30°C for 16

hours. Excess flourochrome, beta2microglobulin and dextran are removed by FPLC using a sephacryl S-300 column. The beta2microglobulin-RPE-dextran construct is then refolded in vitro together with heavy chain and peptide using the following procedure. 200 ml refolding buffer (100 mM Tris, 400 mM L-arginin-HCL, 2 mM NaEDTA, 0,5 mM oxidized Gluthathione, 5 mM reduced Glutathione, pH 8.0) supplied with protease inhibitors PMSF, Pepstatin A and Leupeptin (to a final concentration of 1 mM, 1 mg/l and 1 mg/l, respectively) is made and cooled to 10°C. 12 mg NLVPMVATV (SEQ ID NO 217779) peptide is dissolved in DMSO and added to the refolding buffer together with 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain. Incubation at 10°C for 4-8 hours, then 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain is added and incubation continued for 4-8 hours. Another 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain is added and incubation continued for 6-8 hours. The folding reaction is filtrated through a 0,2 μm filter to remove larger aggregates and then buffer exchanged into a buffer containing 20 mM Tris-HCl, 50 nM NaCl; pH = 8.0 followed by concentration to 1-2 ml sample. Dextran-RPE-MHC complexs are then separated from excess heavy chain and peptide by size exclusion chromatography using a sephacryl S-300, S-400 or sephacryl S-500 column.

These MHC/RPE dextramers may be used to stain CMV specific T cells in a flow Cytometry experiment. Briefly, $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) are incubated with 10 μl of each of the two HLA-A*0201(peptide)/RPE constructs described above for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. 10 μl of mouse-anti-human CD8/PB antibody (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells are then resuspended in 400-500 μl PBS; pH=7.2 and analyzed on a flowcytometer.

Example 13

The preparation of a Pentamer is described in e.g. (United States Patent application 20040209295). Briefly, the following steps lead to a fluorescent Pentamer reagent:

The following is a detailed example for cloning, expressing, and purifying a pentameric class I MHC complex, which comprises a chimeric fusion of .beta.2m with COMP. The

chimeric .beta.2m-COMP protein is expressed in insoluble inclusion bodies in E. coli and subsequently assembled as pentameric .beta.2m-COMP in vitro. The pentameric class I MHC peptide complex is then formed in a second refolding reaction by combining .beta.2m-COMP pentamers and the human MHC class I .alpha. molecule known as HLA-A*0201, in the presence of an appropriate synthetic binding peptide representing the T cell antigen. In this example, a well characterized antigen derived from Epstein-Barr virus BMLF1 protein, GLCTLVAML (SEQ ID NO 217782) (a.a. 289-297), is used. The resultant complex is labelled with a fluorescent entity and used as a staining reagent for detecting antigen-specific T cells from a mixed lymphocyte population, in a flow cytometry application.

The strategy involves the sequential cloning into pET-24c vector of .beta.2m, yielding a construct referred to as pETBMC01, followed by the insertion of the oligomerisation domain of cartilage oligomeric matrix protein (COMP) with a biotin acceptor sequence (BP) for site-specific biotinylation with the biotin-protein ligase BirA, yielding a construct referred to as pETBMC02. Thirdly a polyglycine linker is cloned in between .beta.2m and COMP, yielding a construct referred to as pETBMC03, and finally, a serine-residue is removed by site-directed mutagenesis, which serine residue precedes the poly-glycine linker, to give the final .beta.2m-COMP/pET-24c construct, referred to as pETBMC04 (see also FIG. 3). Removal of the serine residue is carried out to avoid steric hindrance when the .beta.2m molecule is associated with the MHC class I chain protein.

The extracellular portion of .beta.2m comprises of 99 amino acids (equivalent to Ile1-Met99 of the mature protein) encoded by 74 bp-370 bp of the DNA sequence. This region of the .beta.2m sequence is amplified from a normal human lymphocyte cDNA library, by polymerase chain reaction (PCR)

beta.2m PCR product is purified from the above reaction mix using a QIAquick.RTM. PCR purification kit according to the manufacturer's instructions (Qiagen). 200 ng of purified PCR product and 1 .mu.g pET-24c vector (Novagen) are each digested with BamH I (10 U) and Nde I (10 U) restriction enzymes (New England Biolabs, NEB) for 4 h at 37.degree. C., in accordance with the manufacturer's instructions, and purified.

The gel-purified insert and vector DNA are ligated at a 1:3 molar ratio (vector:insert, 50

ng: 7.5 ng) using T4 DNA ligase (5 U; Bioline), in T4 DNA ligase buffer (as supplied) for 16 hrs at 16.degree. C.

The ligation mixtures and appropriate controls are subsequently transformed into XL1-Blue strain competent E. coli cells, according to the manufacturer's instructions (Stratagene). Successful transformants are selected by plating the cells on Luria-Bertani (LB) agar plates containing 30 .mu.g/ml kanamycin, and incubating overnight at 37.degree. C.

A selection of single colonies from the bacterial transformation plates are screened by PCR with T7 promoter [SEQ ID NO: 4] (1 .mu.M) and T7 terminator [SEQ ID NO: 5] (1 .mu.M) primers (Sigma Genosys, see Appendix I for primer sequences), which are complementary to regions of the pET vector flanking the cloning site. Amplification is carried out using Taq DNA polymerase (1 U, Bioline) in Taq reaction buffer (as supplied), supplemented with 2 mM MgSO.sub.4 and 0.2 mM dNTPs, using 25 thermal-cycling reactions as detailed above. Successful transformants generated a DNA fragment of approximately 500 bp, ascertained by 1.5% agarose gel electrophoresis.

Bacterial transformants that generated the correct size of PCR products are inoculated into 6 ml of sterile LB-kanamycin medium and incubated overnight at 37.degree. C. with 200 rpm shaking. pETBMC01 plasmid DNA is recovered from the bacterial cultures using a QIAprep.RTM. Spin Mini-prep kit according to the manufacturer's instructions (Qiagen). The presence of the .beta.2m fragment in these plasmids is further verified by automated DNA sequencing.

The sequence of the oligomerisation domain of COMP is obtained from the Genbank database (accession #1705995) and a region encoding the coiled-coil domain (amino acids 21-85) is selected based on self-association experiments of COMP (Efinov et al., FEBS Letters 341:54-58 (1994)). A biotin acceptor sequence `BP`: SLNDIFEAQKIEWHE [SEQ ID NO: 6] is incorporated at the C terminus and an additional 14 amino acid linker, PQPQPKPQPKPEPET [SEQ ID NO:7] is included to provide a physical separation between the COMP oligomerising domain and BP.

The whole region is synthesized using the overlapping complementary

oligonucleotides, and purified COMP-BP and 1 .mu.g pETBMC01 vector are digested for 4 hrs at 37.degree. C. using Hind III (10 U) and Xho I (10 U) restriction enzymes (NEB), as described in Section 1.1. The digestion products are purified, ligated, transformed and PCR screened as in Section 1.1. Plasmids positive from the screen are purified and sequenced as described in Section 1.1.

The poly-glycine linker is synthesized by annealing overlapping oligonucleotides. Since the nucleotide sequence of the polyGlycine linker only incorporates the 5' overhang of the cut BamH I restriction site, and the 3' overhang of the cut Hind III nucleotide recognition motifs, there is no need to digest the annealed product to produce the complementary single-stranded overhangs suitable for subsequent ligation. The oligonucleotides are phosphorylated and annealed as described in Section 1.2.

pETBMC02 is digested with BamH I (10 U) and Hind III (10 U) . Ligation of the annealed poly-glycine linker into pETBMC02 was as described previously (Section 1.1), assuming 96 fmoles of annealed oligonucleotide/.mu.l. The transformation and PCR-screening reactions are as described in Section 1.1, but in addition, the presence of an inserted linker is verified by a restriction enzyme digestion of the PCR screen product to ascertain the presence or absence of a Sal I restriction site. Successful transformants are not susceptible to Sal I digestion, given the removal of the site from the plasmid vector backbone. Purification of pETBMC03 and automated sequencing is as described in Section 1.1.

Analysis of X-ray crystallography models of MHC class I molecules reveal that the C terminus of .beta.2m closely abuts the .alpha.3 domain of the .alpha. chain. It is therefore desirable to achieve maximum flexibility at the start of the poly-glycine linker.

The extracellular portion of HLA-A*0201 .alpha. chain (EMBL M84379) comprises of 276 amino acids (equivalent to Gly1-Pro276 of the mature protein) encoded by bases 73-900 of the messenger RNA sequence. This region of the A*0201 sequence is amplified from a normal human lymphocyte cDNA library by PCR, using the primers A2S#1 [SEQ ID NO: 20] and A2S#2 [SEQ ID NO: 21] which incorporated NcoI and BamHI restriction sites respectively. The procedure for cloning the A*0201 insert into Nco I/BamH I-digested pET-11d vector (Novagen) is essentially as described for .beta.2m in Section 1.1.

An identical procedure is carried out to produce either .beta.2m-COMP or A*0201 .alpha. chain proteins. Plasmid DNA is transformed into an E. coli expression host strain in preparation for a large scale bacterial prep. Protein is produced as insoluble inclusion bodies within the bacterial cells, and is recovered by sonication. Purified inclusion bodies are solubilised in denaturing buffer and stored at -80.degree. C. until required.

Purified plasmid DNA is transformed into the BL21(DE3)pLysS E. coli strain, which carries a chromosomal copy of the T7 RNA polymerase required to drive protein expression from pET-based constructs. Transformations into BL21(DE3)pLysS competent cells (Stratagene) are carried out with appropriate controls.

A single bacterial transformant colony is innoculated into 60 ml sterile LB medium, containing appropriate antibiotics for selection, and left to stand overnight in a warm room (.about.24.degree. C.) The resulting overnight culture is added to 6 litres of LB and grown at 37.degree. C. with shaking (.about.240 rpm), up to mid-log phase (OD.sub.600=0.3-0.4). Protein expression is induced at this stage by addition of 1.0 ml of 1M IPTG to each flask. The cultures are left for a further 4 h at 37.degree. C. with shaking, after which the cells are harvested by centrifugation and the supernatant discarded.

The bacterial cell pellet is resuspended in ice-cold balanced salt solution and sonicated (XL series sonicator; Misonix Inc., USA) in a small glass beaker on ice in order to lyse the cells and release the protein inclusion bodies. Once the cells are completely lysed the inclusion bodies are spun down in 50 ml polycarbonate Oak Ridge centrifuge tubes in a Beckman high-speed centrifuge (J2 series) at 15,000 rpm for 10 min. The inclusion bodies are then washed three times in chilled Triton.RTM. wash This is followed by a final wash in detergent-free wash buffer.

The resultant purified protein preparation is solubilised in 20-50 ml of 8 M urea buffer, containing 50 mM MES, pH 6.5, 0.1 mM EDTA and 1 mM DTT, and left on an end-over-end rotator overnight at 4.degree. C. Insoluble particles are removed by centrifugation and the protein yield is determined using Bradford's protein assay reagent (Bio-Rad Laboratories) and by comparison with known standards. Urea-

solubilised protein is dispensed in 10 mg aliquots and stored at -80.degree. C. for future use.

Assembly of .beta.2m-COMP from the urea-solubilised inclusion bodies is performed by diluting the protein into 20 mM CAPS buffer, pH 11.0, containing 0.2 M sodium chloride and 1 mM EDTA, to give a final protein concentration of 1.5 mg/ml. The protein is oxidised at room temperature by addition of oxidised and reduced glutathione to final concentrations of 20 mM and 2 mM, respectively. Following an overnight incubation, disulphide bond formation is analysed by non-reducing SDS-PAGE on 10% bis-tricine gels (Invitrogen).

The protein mixture is subsequently buffer exchanged into 20 mM Tris, pH 8.0, 50 mM sodium chloride (`S200 buffer`), and concentrated to a final volume of 4.5 ml, in preparation for enzymatic biotinylation with BirA (Affinity, Denver, Colo.). 0.5 ml of 10.times. BirA reaction buffer (as supplied) is added, and recombinant BirA enzyme at 10 .mu.M final concentration, supplemented with 10 mM ATP, pH 7.0. A selection of protease inhibitors is also used to preserve the proteins: 0.2 mM PMSF, 2 .mu.g/ml pepstatin and 2 .mu.g/ml leupeptin. The reaction is left for 4 hours at room temperature.

Biotinylated .beta.2m-COMP is purified by size exclusion chromatography (SEC) on a Superdex.RTM.200 HR 26/60 column (Amersham Biosciences), running S200 buffer.

500 ml of refolding buffer is prepared as follows: 100 mM Tris, pH 8.0, 400 mM Larginine hydrochloride, 2 mM EDTA, 5 mM reduced glutathione and 0.5 mM oxidised glutathione, dissolved in deionised water and left stirring at 4.degree. C. 15 mg of lyophilised synthetic peptide GLCTLVAML (SEQ ID NO 217782) is dissolved in 0.5 ml dimethylsulfoxide and added to the refolding buffer whilst stirring. 50 mg of biotinylated pentameric .beta.2m-COMP and 30 mg of A*0201 .alpha. chain is added sequentially, injected through a 23gauge hypodermic needle directly into the vigorously-stirred buffer, to ensure adequate dispersion. The refolding mixture is then left stirring gently for 16 hours at 4.degree. C.

The protein refolding mixture is subsequently concentrated from 500 ml to 20 ml using a MiniKros hollow fibre ultrafiltration cartridge (Spectrum Labs, Rancho Dominguez,

Calif.) with a 30 kD molecular weight cutoff. Further concentration of the complex from 20 ml to 5 ml is carried out in Centricon Plus-20 centrifugal concentrators (30 kD molecular weight cut-off) according to the manufacturers instructions, followed by buffer exchange into S200 buffer using disposable PD10 desalting columns (Amersham Biosciences), according to the manufacturer's instructions. Final volume is 7.5 ml. The concentrated protein refold mixture is first purified by SEC on a Superdex.RTM. 200 HR 26/60 gel filtration chromatography column, as in Section 4.2. Fractions containing protein complexes in the region of 310 kD is collected.

Fractions collected from SEC are pooled and subjected to further purification by anion exchange chromatography on a MonoQ.RTM. HR 5/5 column (Amersham Biosciences), running a salt gradient from 0-0.5 M sodium chloride in 20 mM Tris over 15 column volumes. The dominant peak is collected. Protein recovery is determined using the Bradford assay.

Since each streptavidin molecule is able to bind up to 4 biotin entities, final labelling with phycoerythrin (PE)-conjugated streptavidin is carried out in a molar ratio of 1:0.8, streptavidin to biotinylated pentamer complex respectively, taking into account the initial biotinylation efficiency measurement made for .beta.2m-COMP in Section 4.2. The total required amount of pentamer complex is subdivided (e.g. into 5 equal amounts) and titrated successively into streptavidin-PE. The concentration of A*0201 pentamer-streptavidin complex is adjusted to 1 mg/ml with phosphate buffered saline (PBS), supplemented with 0.01% azide and 1% BSA.

This resultant fluorescent Pentamer reagent is stored at 4.degree. C.

Example 14

Prediction of MHC class 1 peptide binders for human cancer protein BclX(L) using directed approach

This example describes the directed approach, applied to a known protein sequence, the cancer protein BclX(L) encoded by the human genome. The purpose is to predict BclX(L) peptide sequences that binds to MHC class 1 molecules for use in construction of MHC'mers designed to be used for analytical, diagnostic, prognostic, therapeutic and vaccine purposes, through the interaction of the MHC'mers with human BclX(L) specific T-cells. Prediction is carried out using the known preferences of the 42 HLA

class 1 alleles included in the http://www.cbs.dtu.dk/services/NetMHC/ database (figure 10).

The result of the prediction software is used to find all strong and weak 8-, 9-, 10- and 11-mer peptide binders of the 42 HLA class 1 alleles. The result can be seen in figure 36. The MHC class 1 alleles for whom no binders are predicted are omitted from the list. The
listed peptides are ranked according to decreased binding affinity for the individual MHC alleles. Strong binders are defined as binders with an affinity value of less than 50 nM and weak binders with a value of less than 500nM. Only peptides defined as weak or strong binders are shown.

Example 15

Prediction of MHC class 2 peptide binders for human cancer protein BclX(L) using directed approach

This example describes the directed approach, applied to a known protein sequence, the cancer protein BclX(L) encoded by the human genome. The purpose is to predict BclX(L) peptide sequences that binds to MHC class 2 molecules for use in construction of MHC'mers designed to be used for analytical, diagnostic, prognostic, therapeutic and vaccine purposes, through the interaction of the MHC'mers with human BclX(L) specific T-cells. Prediction is carried out using the known preferences of the 14 HLA class 2 alleles included in the http://www.cbs.dtu.dk/services/NetMHCII/ database (figure 10).

The result of the prediction software is used to find all strong and weak 15-mer peptide binders of the 14 HLA class 2 alleles. It also finds the important central nonamer core peptide sequence of each binding peptide. The result can be seen in figure 37. The MHC class 2 alleles for whom no binders are predicted are omitted from the list. The listed peptides are ranked according to decreased binding affinity for the individual MHC alleles. Strong binders are defined as binders with an affinity value of less than 50 nM and weak binders with a value of less than 500nM. Only peptides defined as weak or strong binders are shown.

Example 16

Prediction of MHC class 1 and 2 Borrelia afzelii OspC peptide binders

This example describes the prediction of MHC class 1 and 2 *Borrelia afzelii OspC* peptide sequences for use in construction of MHC'mers designed to be used for analytical, diagnostic, prognostic, therapeutic and vaccine purposes, through the interaction of the MHC'mers with *Borrelia afzelii OspC*-specific T-cells. The amino acid sequence of Borrelia afzelii OspC protein was found and retrieved from NCBI protein database (http://www.ncbi.nlm.nih.gov). Prediction of the 8-, 9-, 10-, 11-, 13-, 14-, 15- and 16-mer peptide sequences are carried out using the peptide generation software program described in figure 2. The outcome is shown in table A.

Example 17

Prediction of MHC class 1 Borrelia burgdorferi OspA peptide binders

This example describes the directed approach, applied to a known protein sequence, the Borrelia burgdorferi protein OspA encoded by the Borrelia genome. The purpose was to predict OspA peptide sequences that binds to MHC class 1 molecules for use in construction of MHC'mers designed to be used for analytical, diagnostic, prognostic, therapeutic and vaccine purposes, through the interaction of the MHC'mers with human OspA specific T-cells. The amino acid sequence of Borrelia burgdorferi OspA protein was found and retrieved from NCBI protein database (http://www.ncbi.nlm.nih.gov) Prediction was carried out using the known preferences of the 42 HLA class 1 alleles included in the http://www.cbs.dtu.dk/services/NetMHC/ database (figure 10).

The result of the prediction software was used to find all strong and weak 8-, 9-, 10- and 11-mer peptide binders of the 42 HLA class 1 alleles. The result can be seen in table B. The MHC class 1 alleles for whom no binders are predicted are omitted from the list. The listed peptides are ranked according to decreased binding affinity for the individual MHC alleles. Strong binders are defined as binders with an affinity value of less than 50 nM and weak binders with a value of less than 500nM. Only peptides defined as weak or strong binders are shown.

Example 18

Prediction of MHC class 1 Borrelia garinii FlaB peptide binders

This example describes the directed approach, applied to a known protein sequence, the Borrelia garinii protein FlaB encoded by the Borrelia genome. The purpose was to predict FlaB peptide sequences that binds to MHC class 1 molecules for use in construction of MHC'mers designed to be used for analytical, diagnostic, prognostic,

therapeutic and vaccine purposes, through the interaction of the MHC'mers with human FlaB specific T-cells. The amino acid sequence of Borrelia burgdorferi OspA protein was found and retrieved from NCBI protein database (http://www.ncbi.nlm.nih.gov). Prediction was carried out using the known preferences of the 42 HLA class 1 alleles included in the http://www.cbs.dtu.dk/services/NetMHC/ database (figure 10).

The result of the prediction software was used to find all strong and weak 8-, 9-, 10- and 11-mer peptide binders of the 42 HLA class 1 alleles. The result can be seen in table C. The MHC class 1 alleles for whom no binders are predicted are omitted from the list. The listed peptides are ranked according to decreased binding affinity for the individual MHC alleles. Strong binders are defined as binders with an affinity value of less than 50 nM and weak binders with a value of less than 500nM. Only peptides defined as weak or strong binders are shown.

Example 19

Test of predicted BclX(L) 10-mer binding peptide functionality in ELISPOT

In example 14 the best binding BclX(L) 10-mer peptide for HLA-A*0201 was identified to be YLNDHLEPWI. This peptide has then been tested in ELISPOT to see if it were able to detect the presence Bcl-X(L)-specific, CD8 positive T cells in PBL (Peripheral Blood Lymphocytes) from a breast cancer patient. PBL from a breast cancer patient was analyzed by ELISPOT ex vivo either with or without the Bcl-X(L)173–182 peptide (YLNDHLEPWII), 106 PBL/well in doublets. The number of spots was counted using the Immunospot Series 2.0 Analyzer (CTL Analysers). The result is given as number of spots above the pictures of the result as shown in Figure 11 and it clearly shows the presence of BclX(L) specific T-cells and thereby the functionality of the peptide as compared to the absence of added peptide.

This example is from Cancer Immunol Immunother Apr;56(4)527-33.

Example 20

Test of predicted BclX(L) 10-mer binding peptide functionality in Flow cytometry

In example 14 the best binding BclX(L) 10-mer peptide for HLA-A*0201 was identified to be YLNDHLEPWI. In the present example the functionality of the peptide is shown in a flow cytometric analysis of PBL from the patient was analyzed ex vivo by Flow cytometry to identify Bcl-X(L)173–182 specific CD8 T cells using the dextramer complex HLA-A2/Bcl-X(L)173–182-APC, 7-AAD-PerCP, CD3-FITC, and CD8-APC-

Cy7. The dextramer complex HLA-A2/HIV-1 pol476–484-APC was used as negative control. The result (figure 12) clearly demonstrate that a MHC Dextramer HLA-A*0201/YLNRHLHTWI complex detects BclX(L) antigen-specific CD-8 cells in the patient sample at a level of 0.03% as compared with the negative control using HIV specific MHC Dextramer.

This example is from Cancer Immunol Immunother Apr;56(4)527-33.

Example 21

Use of BclX(L) specific MHC Dextramer for sorting of antigen-specific CD8 T cells from patient sample

The antigen-specific CD8 positive T-cells of example 20 were sorted out during the flow cytometric analysis using the MHC Dextramer HLA-A*0201/YLNDHLEPWI. The detectable population of dextramer positive CD8 T cells was sorted as single cells into 96 well plates using the following protocol:

Small lymphocytes were gated by forward and side scatter profile, before cloning according to CD8/MHC-multimer double staining. CD8/MHC-multimer double-positive cells were sorted as single cells into 96 well plates (Nunc) already containing 10^5 cloning mix cells/well. The cloning mix was prepared containing 10^6 irradiated (20 Gy) lymphocytes from three healthy donors per ml in X-vivo with 5% heat-inactivated human serum, 25 mM HEPES buffer (GibcoBRL), 1 µg/ml phytohemagglutinin (PHA) (Peprotech) and 120 U/ml IL-2. The cloning mix was incubated for two hours at 37°C/5 $\%CO_2$, prior to cloning. After cloning, the plates were incubated at 37°C/5 $\%CO_2$. Every 3 - 4 days 50 µl fresh media were added containing IL-2 to a final concentration of 120U/ml. Following 10 - 14 days of incubation, growing clones were further expanded using cloning mix cells. Consequently, each of the growing clones were transferred (split) into two or three wells (depending on the number of growing cells) of a new 96 well plate containing 5 x 10^4 cloning mix cells/well. Clones that were not growing at this time were incubated for another week with IL-2, and then expanded. Subsequently, the specificity of the growing clones was tested in a ^{51}Cr-release assay or by FACS.

Out of twenty isolated dextramer positive CD8 T cells, ten were able to be expanded into T-cell clones.

This example is from Cancer Immunol Immunother Apr;56(4)527-33.

Example 22

Demonstration of specific cytolytic activity of isolated BclX(L) specific CD8 T-cells.

This is an example of a CTL killing assay.

The ten expanded T cell clones isolated by Flow sorting as shown in example 21 were tested for their specificity by analysis in a standard 51-Cr release assay. For this purpose, T2 cells loaded with either Bcl-X(L)173–182 peptide or an irrelevant peptide (BA4697–105, GLQHWVPEL (SEQ ID NO 217777)) were used as target cells. Five CD8 T-cell clones (Clone 8, 9, 10, 11, and 12) effectively lysed T2 cells pulsed with Bcl-X(L)173–182 without killing of T2 cells pulsed with an irrelevant peptide (Figure 13). One of these BclX(L)173–182 specific CD8 T-cell clones [Clone 9] were expanded for further analyses. The remaining five expanded clones (Clone 7, 13, 15, 17, and 18) did not show specific lysis against T2 cells pulsed with Bcl-X(L)173–182 peptide (figure 13).

This example is from Cancer Immunol Immunother Apr;56(4)527-33.

Example 23

Demonstration of the cytotoxic capacity of a BclX(L)173–182 specific CD8 T cell clone isolated by flow aided sorting of antigen (HLA-A*0201/YLNRHLHTWI) specific T cells.

The Bcl-X(L)173–182 specific clone 9 from example 22 was expanded for additional 2 weeks before the cytotoxic potential was examined further in 51Cr-release assays. Two assays were performed **a** Cell lysis of T2 cells pulsed with Bcl-X(L)173–182 peptide or an irrelevant peptide (BA4697–105, GLQHWVPEL (SEQ ID NO 217777)) in three E:T ratios. **b** Cell lysis of T2 cells pulsed with different concentrations of Bcl-X(L)173–182 peptide at the E:T ratio 1:1 The result is given in figure 14. As can be seen the presence of the specific peptide is necessary to get killing of the target cell and the effect of the peptide is significant even at low concentrations.

This example is from Cancer Immunol Immunother Apr;56(4)527-33.

Example 24

Synthesis of a comprehensive library of antigenic peptides of variable size derived from a full-length antigen sequence.

In this example it is described how virtually all of the possible 8'- to 20'-mer peptide epitopes of an antigen may be synthetically prepared by modification of the standard Fmoc peptide synthesis protocol.

N-(-amino acids are incorporated into a peptide of the desired sequence with one end of the sequence remaining attached to a solid support matrix. All soluble reagents can be removed from the peptide-solid support matrix by filtration and washed away at the end of each coupling step. After each of the coupling steps, and after the removal of reagents, a fraction of the generated peptides are removed and recovered from the polymeric support by cleavage of the cleavable linker that links the growing peptide to solid support.

The solid support can be a synthetic polymer that bears reactive groups such as -OH. These groups are made so that they can react easily with the carboxyl group of an N-(-protected amino acid, thereby covalently binding it to the polymer. The amino protecting group can then be removed and a second N-(-protected amino acid can be coupled to the attached amino acid. These steps are repeated until the desired sequence is obtained. At the end of the synthesis, a different reagent is applied to cleave the bond between the C-terminal amino acid and the polymer support; the peptide then goes into solution and can be obtained from the solution.

Initially, the first Fmoc amino acid (starting at the C-terminal end of the antigen sequence) is coupled to a precursor molecule on an insoluble support resin via an acid labile linker. Deprotection of Fmoc is accomplished by treatment of the amino acid with a base, usually piperidine. Before coupling the next amino acid, a fraction of the synthesized peptide (for example 0.1%) is detached from the solid support, and recovered. Then additional beads carrying only the precursor molecule including the linker (for example corresponding to 0.1% of the total amount of solid support in the reaction) is added. Then the next Fmoc amino acid is coupled utilizing a pre-activated species or in situ activation.

This cycle of amino acid coupling, removal of reagents, detachment of a small fraction of synthesized peptide and recovery of these, and activation of the immobilized peptide to prepare for the next round of coupling, goes on until the entire antigen sequence has been processed.

The recovered peptides thus represent different fragments of the antigen, with varying lengths. The peptide pool thus contains most or all of the possible peptide epitopes of the antigen, and may be used in the preparation of MHC multimers as a pool.

The entire process, including the detachment of a fraction of the peptides after each round of coupling, follows standard Fmoc peptide synthesis protocols, and involves weak acids such as TFA or TMSBr, typical scavengers such as thiol compounds, phenol and water, and involves standard protecting groups.

Example 25

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.

In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled dextran (Dextramers). The dextramers are used for direct detection of TCR in flow Cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein A (Table B) or Flagellin B (Table C) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide are generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes are then coupled to a 270 kDa dextran multimerization domain labelled with APC by interaction with streptavidin (SA) on the dextran multimerization domain. The dextran-APC-SA multimerization domain is generated as described elsewhere herein. MHC-peptide complexes are added in an amount corresponding to a ratio of three MHC- peptide molecules per SA molecule and each molecule dextran contains 3.7 SA molecule and 8.95 molecules APC. The final concentration of dextran is 3.8x10e-8 M. The following MHC(peptide)/APC dextran constructs are made:

1. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
2. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
3. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B
4. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B
5. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B
6. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC dextran is used to determine the presence of Osp A or Fla B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with 10 µl of each of the MHC(peptide)/APC dextran constructs described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako), mouse-anti-human CD4/FITC (clone MT310 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continues for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 300xg and the supernatant removed. The washing step is repeated twice. The washed cells are resuspended in 400-500 µl PBS + 1% BSA; pH=7.2 and analyzed on flowcytometer.
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and the MHC(peptide)/APC dextran constructs 1, 2, 3, 4 and 5 described above and thereby the presence of Borrelia specific T cells indicate that the patient are infected with Borrelia bacteria. Blood analysed with MHC(peptide)/APC dextran construct 6 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct. The result is shown in figure 15.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 26

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.

In this example the MHC multimer used are MHC complexes coupled to the fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow Cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein A (Table B) or Flagellin B (Table C) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes are then coupled SA labelled with APC. MHC-peptide complexes were added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes were purified from free SA, free monomeric MHC complex, SA carrying three, two and one MHC complexes.

The following SA- MHC(peptide)/APC tetramers are made:

7. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
8. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
9. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B.
10. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B.
11. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B.
12. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Osp A or Fla B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol. Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four SA- MHC(peptide)/APC tetramers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.

The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the SA-MHC(peptide)/APC tetramers 7, 8, 9, 10 or 11 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with SA- MHC(peptide)/APC tetramers 12 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC tetramer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 27

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.

In this example the MHC multimer used are MHC complexes coupled to any fluorophor-labelled multimerisation as described elsewhere herein. The MHC multimers are used for direct detection of TCR in flow cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein A (Table B) or Flagellin B (Table C) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding and purified or purified from antigen presenting cells. MHC-peptide complexes are then coupled to a multimerisation domain together with APC.

The following MHC(peptide)/APC multimers are made:

13. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
14. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
15. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B.
16. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B.

17. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B.
18. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Osp A or Fla B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol. Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four MHC(peptide)/APC multimers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti- human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the MHC(peptide)/APC multimers 13, 14, 15, 16 or 17 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with MHC(peptide)/APC multimer 18 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 28

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.

In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled dextran (Dextramers). The dextramers are used for direct detection of TCR in flow Cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0301 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein C (Table A) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes were then coupled to a 270 kDa dextran multimerization domain labelled with APC by interaction with streptavidin (SA) on the dextran multimerization domain. The dextran-APC-SA multimerization domain was generated as described elsewhere herein. MHC-peptide complexes were added in an amount corresponding to a ratio of three MHC- peptide molecules per SA molecule and each molecule dextran contained 3.7 SA molecule and 8.95 molecules APC. The final concentration of dextran was 3.8x10e-8 M. The following MHC(peptide)/APC dextran constructs were made:

19. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
20. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide ELANKAIGK derived from OspC.
21. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0301 in complex with beta2microglobulin and the HIV peptide QVPLRPMTYK.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Osp C specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.

Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with 10 µl of one of the MHC(peptide)/APC dextran constructs described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.

The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the MHC(peptide)/APC dextran constructs 19 or 20 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with MHC(peptide)/APC dextran construct 21 should show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the APC-SA conjugated 270 kDa dextran coupled MHC(peptide) constructs may be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 29

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.

In this example the MHC multimer used are MHC complexes coupled to the fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow Cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection

with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0301 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein C (Table A) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes are then coupled SA labelled with APC. MHC-peptide complexes were added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes were purified from free SA, free monomeric MHC complex, SA carrying three, two and one MHC complexes.
The following SA- MHC(peptide)/APC tetramers are made:

22. APC-SA coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
23. APC-SA coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide ELANKAIGK derived from OspC.
24. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the HIV peptide QVPLRPMTYK.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Osp C specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four SA- MHC(peptide)/APC tetramers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.

The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the SA-MHC(peptide)/APC tetramers 22 or 23 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with SA- MHC(peptide)/APC tetramers 24 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC tetramer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 30

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria.
In this example the MHC multimer used are MHC complexes coupled to any fluorophor-labelled multimerisation as described elsewhere herein. The MHC multimers are used for direct detection of TCR in flow cytometry. The antigen origin is Borrelia, thus, immune monitoring of a Borrelia infection.
Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein C (Table A) conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding and purified or purified from antigen presenting cells. MHC-peptide complexes are then coupled to a multimerisation domain together with APC.
The following MHC(peptide)/APC multimers are made:

25. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
26. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ELANKAIG derived from OspC.
27. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the HIV peptide QVPLRPMTYK.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Osp C specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four MHC(peptide)/APC multimers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti- human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the MHC(peptide)/APC multimers 25 or 26 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with MHC(peptide)/APC multimer 27 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Example 31

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples by ELISPOT.

This is an example of indirect detection of TCR, where individual cells are immobilized and measured by a chromogen assay.

The example provides a sensitive assay for the detection of T-cells reactive to an antigen by detecting a soluble factor whose secretion is induced by stimulation of the T-cell by the antigen.

A summary flow chart of the method is shown in FIG. 35. In brief, peripheral blood is diluted threefold in Dulbecco's phosphate buffered saline (DPBS), underlain with 15 ml of Ficoll (Pharmacia Ficoll-Paque #17-0840-02, Piscataway, N.J.) per 40 ml diluted blood in a 50 ml polypropylene centrifuge tube, and spun at 2000 RPM for 20 minutes in a Beckman CS-6R centrifuge (Beckman Inc., Palo Alto, Calif.). The buffy layer at the DPBS/Ficoll interface is removed, washed twice with DPBS and once with human tissue culture medium (hTCM: αMEM+5% heat inactivated human AB serum (Ultraserum, BioWhittaker, Walkersville, Md.), penicillin/streptomycin, 1-glutamine) at low RCF to remove platelets. Sixty percent of the PBMCs are resuspended in freezing medium (10% dimethyl sulfoxide(Sigma Chenical Co., St. Louis, Mo.), 90% fetal bovine serum to a concentration of $5x10^6$ cells/ml, frozen in a programmable Cryo-Med (New Baltimore, Mich.) cell freezer, and stored under liquid nitrogen until needed.

The purified PBMCs are plated at $2x10^5$ cells/well at a volume of 0.1 ml in 96 well Costar cell culture plates. An equal volume of antigen at 10 µg/ml is added to triplicate or sextuplet sets of wells and the plate is incubated in a 37°C., 5% CO_2 incubator. On day five, 10 µl/well of 100 U/ml stock recombinant IL-2 (Advanced Biotechnologies Inc., Columbia, Md.) is added to each well. On day 8, frozen PBMCs are thawed, washed in DPBS+0.5% bovine serum albumin (BSA) to remove DMSO, resuspended to a concentration of $4x10^6$ cells/ml in hTCM, and γ-irradiated (3,000 RADS). Fifty microliters/well are dispensed along with 50 µl of the appropriate antigen at a stock concentration of 40 µl/ml to give a final antigen concentration of 10 µg/ml.

To prepare a capture plate, IFN-γ capture antibody (monoclonal mouse anti-human IFN-g, Endogen #M700A, Cambridge, Mass.) is diluted to 10 µg/ml in sterile 0.1 M $Na(CO_3)_2$ pH 8.2 buffer, aliquotted at 50 µl/well in flat bottomed 96 well sterile microtiter

plates (Corning Costar Corp.), and incubated at 4°C for a minimum of 24 hours. Prior to use, excess antibody is removed and wells are washed twice with dPBS+1% Tween 20 (PBST). To block further nonspecific protein binding, plates are incubated with 250 µl/well of PBS+5% BSA at room temperature for 1 hour. After discarding the blocking solution, wells are washed once with PBST (0.1% Tween), followed by hTCM in preparation for the antigen stimulated cells.

On day 9 of the assay, twenty four hours after the second antigen stimulation, the stimulation plate is spun for 5 minutes at 1500 RPM in a Beckman CS-6R centrifuge and 90 µl of supernatant is carefully removed from each well with a micropipette. The pelleted cells are resuspended in 100 µl of hTCM, pooled in sterile tubes (Corning Costar corp sterile ClusterTAb #4411, Cambridge, Mass.), mixed and transferred into an equal number of wells of an anti IFN- γ capture plate. Capture plates are incubated undisturbed at 37°C for 16-20 hours. At the end of the IFN-γ secretion phase, the cells are discarded and the plates are washed three times with 0.1% PBST. A final aliquot of PBST is added to the wells for ten minutes, removed, and 100 µl of a 1:500 dilution of rabbit anti-human IFN-γ polyclonal antibody (Endogen #P700, Cambridge, Mass.) in PBST+1% BSA is added to each well for 3.5 hours at room temperature with gentle rocking. Unbound anti-IFN-γ polyclonal antibody is removed by three washes with PBST, followed by a wash with 250 µl of 1X Tris-buffered saline+0.05% Tween 20 (TBST). Next, a 100 µl aliquot of 1:5000 alkaline phosphatase-conjugated mouse anti-rabbit polyclonal antibody (Jackson Immunological #211-055-109, West Grove, Pa.) diluted in TBST is added to each well and incubated at room temperature for 1.5-2 hours with gentle rocking. Excess enzyme-conjugated antibody is removed by three washes with PBST and two washes with alkaline phosphatase buffer (APB=0.1 M NaCl, 0.05 M MgCl.sub.2, 0.1 M Tris HCl, pH 9.5) followed by addition of the substrate mix of p-Toluidine salt and nitroblue tetrazolium chloride (BCIP/NBT, GIBCO BRL #18280-016, Gaithersburg, Md.). To stop the calorimetric reaction, plates were washed three times in dH_2O, inverted to minimize deposition of dust in the wells, and dried overnight at 28°C in a dust free drying oven.

Images of the spots corresponding to the lymphokine secreted by individual antigen-stimulated T cells are captured with a CCD video camera and the image is analyzed by NIH image software. Captured images are enhanced using the Look Up Table which contrasts the images. Thresholding is then applied to every image and a wand tool is

used to highlight the border to effectively subtract the edge of the well so that background counts won't be high and artificial. Density slicing over a narrow range is then used to highlight the spots produced from secreting cells. Pixel limits are set to subtract out small debris and large particles, and the number of spots falling within the prescribed pixel range are counted by the software program. Totals from each well are then manually recorded for future analysis. Alternatively, spots can be counted by other commercially available or customized software applications, or may be quantitated manually by a technician using standard light microscopy. Spots can also be counted manually under a light microscope.

We conclude that the protocol detailed above can be used for the enumeration of single IFN-γ secreting T cells.

Example 32

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples by ELISPOT.

This is an example of indirect detection of TCR, where individual cells are immobilized and measured by a chromogen assay. The antigenic peptide origin is a library of antigens.

The example provides a sensitive assay for the detection of T-cells reactive to the antigen of a library generated as described in example 24, by detecting a soluble factor whose secretion is induced by stimulation of the T-cell by the antigen.

This example is similar to the experiment above. PMBC are isolated, prepared and stored as described in the example above.

The purified PBMCs are plated at $2x10^5$ cells/well at a volume of 0.1 ml in 96 well Costar cell culture plates. An equal volume of antigens from the library, at 10 µg/ml is added to triplicate or sextuplet sets of wells and the plate is incubated in a 37°C, 5% CO_2 incubator. On day five, 10 µl/well of 100 U/ml stock recombinant IL-2 is added to each well. On day 8, frozen PBMCs are thawed, washed in DPBS+0.5% BSA to remove DMSO, resuspended to a concentration of $4x10^6$ cells/ml in hTCM, and γ-irradiated (3,000 RADS). 50 µl/well are dispensed along with 50 µl of the appropriate antigen at a stock concentration of 40 µl/ml to give a final antigen concentration of 10 µg/ml.

A capture plate with IFN-γ antibody is prepared, washed and blocked as described in the example above.

On day 9 of the assay, twenty four hours after the second antigen stimulation, the stimulation plate is spun for 5 minutes at 1500 RPM and 90 µl of supernatant is carefully removed from each well with a micropipette. The pelleted cells are resuspended in 100 µl of hTCM, pooled in sterile tubes, mixed and transferred into an equal number of wells of an anti IFN- γ capture plate. Capture plates are incubated undisturbed at 37°C for 16-20 hours. At the end of the IFN-γ secretion phase, the cells are discarded and the plates are washed three times with 0.1% PBST. A final aliquot of PBST is added to the wells for ten minutes, removed, and 100 µl of a 1:500 dilution of rabbit anti-human IFN-γ polyclonal antibody in PBST+1% BSA is added to each well for 3.5 hours at room temperature with gentle rocking. Unbound anti-IFN-γ polyclonal antibody is removed by three washes with PBST, followed by a wash with 250 µl of 1X Tris-buffered saline+0.05% Tween 20 (TBST). Next, a 100 µl aliquot of 1:5000 alkaline phosphatase-conjugated mouse anti-rabbit polyclonal antibody diluted in TBST is added to each well and incubated at room temperature for 1.5-2 hours with gentle rocking. Excess enzyme-conjugated antibody is removed by three washes with PBST and two washes with alkaline phosphatase followed by addition of the substrate mix of p-Toluidine salt and nitroblue tetrazolium chloride. To stop the calorimetric reaction, plates were washed three times in dH_2O, inverted to minimize deposition of dust in the wells, and dried overnight at 28°C in a dust free drying oven.

Images of the spots corresponding to the lymphokine secreted by individual antigen-stimulated T cells are captured with a CCD video camera and the image is analyzed as described in the example above

We conclude that the experiment detailed above can be used for the enumeration of single IFN-γ secreting T cells in blood.

Example 33

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples from Borrelia patients by ELISPOT.

This is an example of indirect detection of TCR, where individual cells are immobilized and measured by a chromogen assay. The antigenic peptide origin is Borrelia, thus, immune monitoring of Borrelia.

The example provides a sensitive assay for the detection of T-cells reactive to the antigen OspC by detecting a soluble factor whose secretion is induced by stimulation of the T-cell by the antigen.

This example is similar to the experiment above. PBMCs from Borrelia patients are isolated, prepared and stored as described in the example above.

The purified PBMCs are plated at $2x10^5$ cells/well at a volume of 0.1 ml in 96 well Costar cell culture plates. An equal volume of a mix of antigenic peptides from OspC protein, at 10 µg/ml is added to triplicate or sextuplet sets of wells and the plate is incubated in a 37°C, 5% CO_2 incubator. On day five, 10 µl/well of 100 U/ml stock recombinant IL-2 is added to each well. On day 8, frozen PBMCs are thawed, washed in DPBS+0.5% BSA to remove DMSO, resuspended to a concentration of $4x10^6$ cells/ml in hTCM, and γ-irradiated (3,000 RADS). 50 µl/well are dispensed along with 50 µl of the appropriate antigen at a stock concentration of 40 µl/ml to give a final antigen concentration of 10 µg/ml.

A capture plate with IFN-γ antibody is prepared, washed and blocked as described in the example above.

On day 9 of the assay, twenty four hours after the second antigen stimulation, the stimulation plate is spun for 5 minutes at 1500 RPM and 90 µl of supernatant is carefully removed from each well with a micropipette. The pelleted cells are resuspended in 100 µl of hTCM, pooled in sterile tubes, mixed and transferred into an equal number of wells of an anti IFN- γ capture plate. Capture plates are incubated undisturbed at 37°C for 16-20 hours. At the end of the IFN-γ secretion phase, the cells are discarded and the plates are washed three times with 0.1% PBST. A final aliquot of PBST is added to the wells for ten minutes, removed, and 100 µl of a 1:500 dilution of rabbit anti-human IFN-γ polyclonal antibody in PBST+1% BSA is added to each well for 3.5 hours at room temperature with gentle rocking. Unbound anti-IFN-γ polyclonal antibody is removed by three washes with PBST, followed by a wash with 250 µl of 1X Tris-buffered saline+0.05% Tween 20 (TBST). Next, a 100 µl aliquot of 1:5000 alkaline

phosphatase-conjugated mouse anti-rabbit polyclonal antibody diluted in TBST is added to each well and incubated at room temperature for 1.5-2 hours with gentle rocking. Excess enzyme-conjugated antibody is removed by three washes with PBST and two washes with alkaline phosphatase followed by addition of the substrate mix of p-Toluidine salt and nitroblue tetrazolium chloride. To stop the calorimetric reaction, plates were washed three times in dH_2O, inverted to minimize deposition of dust in the wells, and dried overnight at 28°C in a dust free drying oven.

Images of the spots corresponding to the lymphokine secreted by individual antigen-stimulated T cells are captured with a CCD video camera and the image is analyzed as described in the example above

We conclude that the experiment detailed above can be used for the enumeration of single IFN-γ secreting T cells in blood from Borrelia patients.

Example 34

This is an example of how antigen-specific T-cells can be detected using a direct detection method detecting T cell immobilized in solid tissue. In this example MHC dextramers are used to detect antigen-specific T cells on frozen tissue sections using enzymatic chromogenic precipitation detection.

Equilibrate the cryosection tissue (e.g. section of spleen from transgenic mice) to –20°C in the cryostate. Cut 5 µm sections and then dry sections on slides at room temperature. Store slides frozen until use at –20°C.

Equilibrate frozen sections to room temperature. Fix with acetone for 5 min.

Immediately after fixation transfer slides to TBS buffer (50 mM Tris-HCL pH 7,6, 150 mM NaCl) for 10 min.

Incubate slides with FITC-conjugated MHC-dextramers at appropriate dilution (1:40-1:80) and incubate for 30 min at room temperature. Other dilution ranges, as well as incubation time and temperature, may be desirable.

Decant solution and gently tap slides against filter paper, submerge in TBS buffer.

Decant and wash for 10 min in TBS buffer.

Incubate with rabbit polyclonal anti-FITC antibody (Dako P5100) at 1:100 dilution in TBS at room temperature for 30 min.

Repeat step 5 and 6.

Incubate with Envision anti-Rabbit HRP (Dako K4003) at room temperature for 30 min. Other visualization systems may be used.
Repeat step 5 and 6.
Develop with DAB+ (Dako K3468) in fume hood for 10 min. Other substrates may be used
Rinse slides in tap-water for 5 min.
Counterstain with hematoxylin (Dako S3309) for 2 min.
Repeat step 12, mount slides.
The slides stained with MHC-Dextramers can now be evaluated by microscopy.

Example 35

This is an example of how antigen-specific T-cells can be detected using a direct detection method detecting T cell immobilized in solid tissue. In this example MHC dextramers are used to detect antigen-specific T cells on paraffin embedded tissue sections using enzymatic chromogenic precipitation detection.

Formaldehyde fixed paraffin-embedded tissue are cut in section and mounted on the glass slice, for subsequent IHC staining with MHC-dextramers. Tissue fixed and prepared according to other protocols may be used as well. E.g. fresh tissue, lightly fixed tissue section (e.g. tissue fixed in 2% formaldehyde) or formalin-fixed, paraffin-embedded tissue section.
Optimal staining may require target retrieval treatment with enzymes as well as heating in a suitable buffer before incubation with antibodies and MHC-dextramer.
The sample is stained for DNA using DAPI stain, followed by incubated with an antigen-specific MHCdex/FITC reagent, followed by addition of anti-FITC antibody labeled with HRP.
Then the substrate for HRP, “DAP” is added and the reaction allows to progress.
The sample is analyzed by light microscopy for the present of a colored precipitate on the cells (DAPI stained nucleus) positive for the specific MHC/dex reagent.
A digital image of the stained sample is obtained, and this can be analyzed manually in the same way as by microscopy. However, a digital image may be used for automatic determination of where and how many cells that are positive, related to the total amount of cells, determined by the DAPI staining, or other criteria or stainings.

Example 36

This example describes how the quality of a MHC multimer can be tested. The MHC multimer is in this example a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to TCRs immobilized on beads.

Recombinant TCRs (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific (SEQ ID NO 217779) TCR protein) specific for the MHC-peptide complex HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), where the letters in parenthesis denote the peptide complexed to the MHC-allel HLA-A*0201, were obtained from Altor Biosciences. The TCRs were dimers linked together via an IgG framework.
The purity of the TCRs was verified by SDS PAGE and was between 95-100% pure.
The quality of the TCRs was verified by their ability to recognize the relevant MHC-dextramer and not irrelevant MHC dextramers in ELISA experiments (data not shown).

Carboxylate-modified beads were coupled with dimeric TCR (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific TCR protein (SEQ ID NO 217779)), incubated with fluorescently labeled MHC-dextramers and the extend of cell staining analysed by flow cytometry, as follows:

Immobilization of TCR on carboxylate beads:
$3x10^9$ Carboxylate-modified beads, Duke Scientific Corporation, XPR-1536, 4µm, lot:4394 were washed in 2x 500µl Wash buffer 1 (0,05% Tetronic 1307, 0,1M MES-buffer (2-[N-morpholino]ethanesulfonic acid), pH 6,0), centrifuged 4 min at 15000 g, and the supernatant was discarded.
125 µl EDAC/Sulfo-NHS (50mM EDAC (1-ethyl-3-(3-dimethylaminopropyl)carbodiimide), 50mM Sulfo-NHS, in Wash buffer 1) was added to the beads, and the suspension incubated at room temperature for 20 min.
Beads were washed in 2x 250µl Wash buffer 1 and centrifuged 2 min at 15000 g, and the supernatant was discarded.
TCR was added in various concentrations from 0 µg to 20 µg, and incubated with slow shaking overnight at 4°C.
Beads were centrifuged 4 min at 15000 g, and the supernatant discarded.
Beads were washed in 2x 500µl Wash buffer 1 and centrifuged 4 min at 1500 g, and the supernatant was discarded.

125µl 20mM Glycin in Wash buffer 1 was added, and resuspended beads incubated for 1 hour at room temperature.
Beads were washed in 2x 500µl phosphate-buffered saline (PBS) pH 7.2, 0.5 % Tetronic 1307, and centrifuged 2 min at 15000 g, and the supernatant was discarded.
Beads were resuspended in 250µl PBS pH 7.2, 0,05% Tetronic 1307.

Bead concentration after resuspension was $1,2x10^7$ beads/µl. Beads coated with TCR were stored at 2-8°C until further use.

Flow cytometry analysis:
20µl beads ($1,2x10^7$ beads/µl) coated with 0-20µg TCRs, as described above were washed in 200µl Wash buffer 2 (5% FCS, PBS, pH 7.4).
Beads were centrifuged 3 min at 12000 g, and the supernatant was discarded, and beads resuspended in 50µl Wash buffer 2.
10µl MHC-dextramers were added, and samples were incubated 15 min. at room temperature in the dark.
Samples were washed in 1 ml Wash buffer 2, centrifuged at 300 g for 5 min. The supernatant was discarded, and pellet resuspended in 0.4 ml PBS pH 7.4, and kept at 4°C in the dark until analysis on flow cytometer.
Samples were analysed by flow cytometry on a CyAn instrument.

The results are shown in figure 18. Beads coated with 2-20µg TCR all showed positive staining with the specific HLA-A*0201(NLVPMVATV)/RPE (SEQ ID NO 217779) and not with an irrelevant HLA-A*0201(ILKEPVHGV)/RPE (SEQ ID NO 217780) dextramer.
It can be concluded that carboxylate beads coated with dimeric TCRs can be used to test the quality of the MHC-dextramers.

Example 37

This example describes how the quality of a MHC multimer can be tested. The MHC multimer was in this example a MHC-dextramer, and the test involved specific binding of the MHC-dextramer to monomeric and dimeric TCRs immobilized to different kind of beads.

Binding of MHC-dextramer to carboxylated beads coated with monomeric TCR:
Recombinant monomeric TCRs (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific TCR protein (SEQ ID NO 217779)) specific for the MHC-peptide complex HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), were obtained from Altor Biosciences.
The purity of the TCRs were verified by SDS PAGE. The quality of the TCRs were verified by their ability to recognize the relevant MHC-dextramer and not irrelevant MHC dextramers in ELISA experiments (data not shown).

Carboxylate modified beads were coupled with monomeric TCR (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific TCR protein (SEQ ID NO 217779)), incubated with fluorescently labeled MHC-dextramers and the extend of cell staining analysed by flow cytometry, as described in Example 8. 0-20 μg of monomeric TCRs were coupled to Carboxylate modified beads.
Flow cytometry analysis of beads coupled with 0-20 μg of monomeric TCRs showed a slightly stronger signal when stained with the relevant HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) dextramer than with an irrelevant MHC-dextramer (data not shown). It might be desirable to coat the beads with larger amounts of monomeric TCRs in order to increase the signal difference between relevant and irrelevant MHC-dextramer.
Beads couples with 0 μg of monomeric TCRs showed identical signal when stained with relevant and irrelevant MHC-dextramers.
We conclude that the monomeric TCRs coupled to Carboxylate modified beads can be used as positive control for the MHC-dextramer.

<u>Binding of MHC-dextramer to streptavidin beads coupled with biotinylated monomeric TCR:</u>
Recombinant monomeric, biotinylated TCRs (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific TCR protein (SEQ ID NO 217779)) specific for the MHC-peptide complex HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), were obtained from Altor Biosciences.
The purity of the TCRs were verified by SDS PAGE. The quality of the TCRs were verified by their ability to recognize the relevant MHC-dextramer and not irrelevant MHC dextramers in ELISA experiments (data not shown).

Streptavidin beads were coupled with monomeric biotinylated TCR (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV)-specific TCR protein (SEQ ID NO 217779)), incubated with fluorescently labeled MHC-dextramers and the extend of cell staining analysed by flow cytometry.

Immobilization of TCR on streptavidin beads:

$2x10^6$ Streptavidin Coated Compel Magnetic beads, Bangs laboratories, CM01N, lot: 6998, were washed in 2x 500µl phosphate-buffered saline (PBS) pH 7.2 centrifuged 5 min at 15000 g, and then the supernatant was discarded.
Beads were resuspended in 50µl PBS pH 7.2.
0-4µg TCRs was added. Incubated at room temperature for 30 min.
Beads were washed in 2x 500µl PBS, pH 7.2. Centrifuged 5 min at 15000 g, and the supernatant was discarded.
Beads were resuspended in 100µl PBS pH 7.2.

Bead concentration after resuspension was $2x10^4$ beads/µl. Beads coated with TCRs were stored at 2-8°C until further use.

Flow cytometry analysis:

50µl streptavidin beads (~$1x10^6$ beads) coated with 0-4µg TCRs were added 10µl MHC-dextramers, and samples were incubated at 4°C for 1 hour.
2x 500µl PBS pH 7.2 was added, and samples were centrifuged for 5 min at 15000 g, and supernatant discarded.
Beads were resuspended in 500µl PBS pH 7.2 and kept at 4°C in the dark until analysis on a flow cytometer.
Samples were analysed by flow cytometry on a CyAn instrument.

Beads were stained with HLA-A*0201(NLVPMVATV (SEQ ID NO 217779))-dextramers specific for the TCR and with irrelevant MHC-dextramers not able to bind the TCR.
Flow cytometry analysis of beads coupled with >0 µg TCRs showed a slightly stronger signal when stained with the relevant MHC-dextramer than with the irrelevant MHC-dextramer (data not shown). The staining intensity was identical when beads conjugated with 0 µg TCR were stained with either specific or non-specific MHC-dextramers. We conclude that the monomeric biotinylated TCRs bound to streptavidin coated beads can be used as positive control for the MHC-dextramer.

Binding of MHC-dextramers toamine-modified beads coupled with monomeric or dimeric TCRs:

Recombinant monomeric or dimeric TCRs (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV (SEQ ID NO 217779))-specific TCR protein) specific for the MHC-peptide complex HLA-A*0201(NLVPMVATV(SEQ ID NO 217779)), were obtained from Altor Biosciences.

The purity of the TCRs were verified by SDS PAGE. The quality of the TCRs were verified by their ability to recognize the relevant MHC-dextramer and not irrelevant MHC dextramers in ELISA experiments (data not shown).

Amine-modified beads were coupled with dimeric TCR (CMV3 TCRs; Soluble CMVpp65(NLVPMVATV (SEQ ID NO 217779))-specific TCR protein).

Immobilization of TCR on amine modified beads:

$3x10^9$ Amine modified beads, Duke Scentific XPR-1536, 4μm, lot:4393 were washed in 2x500μl phosphate-buffered saline (PBS) pH 7.5 centrifuged 4 min at 15000 g, and then the supernatant was discarded.

Resuspend beads in 0.3ml PBS pH 7.5

25μl 20mM solution of SPDP (N-Succinimidyl 3-(2-pyridyldithio) propionate) in DMSO was added to the beads, and the suspension incubated at room temperature for 30 min.

Beads were washed in 2x1ml PBS containing 1 mM EDTA, pH 7,5. Centrifuged 4 min at 15000 g, and the supernatant was discarded.

Resuspend beads in 0,3ml PBS containing 1 mM EDTA, pH 7.5.

10mg dithiothritol (DTT) was added, and suspension incubated at room temperature for 30 min.

Beads were washed in 2x 1ml PBS, pH 7.5. Centrifuged 4 min at 15000 g, and the supernatant was discarded.

Sedimented beads were added a freshly prepared SPDP-derivatized protein prepared according to the following outlines (step 14-15):

Treat protein (in this example dimeric TCR) 2–5mg/ml, in 0,1ml carbonate buffer, pH 8 with 10μl 20mM solution of SPDP in DMSO at room temperature for 30 min.

Remove excess reagent by passing through a small desalting column in PBS pH 7.5, or by rapid dialyse against PBS pH 7.5.

Add >1mg SPDS-protein per 10^9 beads, to the SPDP derivatized and reduced bead preparation from paragraph 13. 0-1mg of SPDS-protein per 10^9 beads might be desirable.
Resuspend beads in the SPDP-protein solution. Incubate with slow shaking overnight at 4°C.
Beads were washed in 2x 1ml PBS pH 7.5. Centrifuged 4 min at 15000 g, and the supernatant was discarded.
Resuspend beads in 250µl PBS pH 7.5.

Bead concentration after resuspension was $1.2x10^7$ beads/µl. Beads coated with TCRs were stored at 2-8°C. The quality of MHC-dextramer can now be analysed by examining the degree of binding of specific MHC-dextramer to the TCR-coated beads, versus the binding of irrelevant MHC-dextramer to the TCR coated beads.

Various reaction conditions (e.g various protein:bead ratios) and assay for optimal coupling yield can be explored. The latter can be done by using an ELISA technique (incubate protein/bead conjugated with an appropiate anti-protein enzyme conjugated (e.g. HRP Peroxidase) followed by washing and colour development with a suitable substrate (e.g. TMB/Peroxide)) or by flow cytometry (e.g. a fluorescence labelled anti-protein (in this example MHC multimer HLA-A*0201(NLVPMVATV (SEQ ID NO 217779))) to assess level of covalently bound protein to amine-modified beads.

We conclude that the TCRs coupled to amine-modified beads coupled can be used as positive controls for the MHC Dextramer as described in Example 38 and 39.

Example 38

This example describes how TCR-coated beads can be used as internal, positive controls when analysing suspensions of Human Peripheral Blood Mononuclear Cells (HPBMCs), whole blood samples or any other cell sample of interest. The MHC multimer employed in this example is a MHC-dextramer.

In this example TCR-coated carboxylated beads generated as described in Example 8 were added to a sample containing either HPBMCs or whole peripheral blood.

HPBMCs and TCR-beads were incubated with fluorescently labelled MHC-dextramers and the extent of cell staining analysed by flow cytometry according to this general staining procedure:

Transfer 1-3 x 10^6 lymphoid cells (PBMC or splenocytes) to a 12 x 75 mm polystyrene test tube. Other cells of interest can be used. Allocate only 2-5 x 10^5 cells per tube when staining T-cell clones or cell lines due to the high frequency of antigen-specific T cells

Add 2 ml 0,01 mol/L PBS containing 5% fetal calf serum and centrifuge at 300x g for 5 minutes. Remove supernatant and resuspend cells in remaining liquid.

Add 10 µl of MHC Dextramer and mix gently with a vortex mixer. Incubate in the dark at room temperature for 10 minutes.

Add an optimally titrated amount of anti-CD8 antibody conjugated with a relevant flourochrome (e.g. Dako clone DK25 for human lymphocytes or clone YTS169.4/KT15 for mouse lymphocytes). Incubate in the dark at 2-8°C for 20 min.

Add 2 ml of 0,01 mol/L PBS containing 5% fetal calf serum and centrifuge at 300x g for 5 minutes.

Resuspend pellet in an appropriate fluid for flow cytometry, e.g. 0.4 ml PBS. Analyse on a flow cytometer or store at 2-8°C in the dark until analysis. Do not store longer than 2 hours before analysis.

Human peripheral whole blood and TCR-beads were incubated with fluorescently labelled MHC-dextramers and the extent of cell staining analysed by flow cytometry as follows:

Transfer 100 µL whole blood to a 12 x 75 mm polystyrene test tube.

Add 10 µl of MHC Dextramer and mix with a vortex mixer. Incubate in the dark at room temperature for 10 minutes.

Add an optimally titrated amount of anti-CD8 antibody (e.g. Dako clone DK25) conjugated with a relevant fluorochromes and mix well. Continue incubation at 2-8 ºC in the dark for 20 minutes.

Add 2 mL EasyLyse™ working solution (Code No. S2364) and incubate for 10 minutes.

Centrifuge for 5 minutes at 300 x g and aspirate supernatant.

Add 2 mL 0.01 mol/L PBS and centrifuge for 5 minutes at 300 x g and aspirate supernatant.

Resuspend pellet in an appropriate fluid for flow cytometry, e.g. 0.4 mL PBS, and analyze on a flow cytometer or store at 2-8 ºC in the dark until analysis. Do not store longer than 2 hours before analysis.

Figure 19 shows examples of TCR-beads added into whole blood or HPBMC samples. In both experiments it is possible, by forward- vs. side-scatter measurements, to distinguish TCR-beads from cell populations in the sample. Region R1 is TCR-beads, and region R2 is lymphocyte cell population of interest in the analysis of MHC positive T cells.

The size and conditions of coating of beads might be optimized. The size of beads or labelling of beads (e.g. flourescent labelling) can be optimized to allow separation of cells of interest in the sample. In this example the forward- vs. side- scatter dot plot has been used for gating of cell populations of interest. Other parameters (e.g. fluorescence intensity) for cell populations of interest can be used.
Human peripheral whole blood and other cells (e.g. HPBMCs) can be stained with MHC Dextramers simultaneously with immuno-phenotyping of relevant antigens. The staining procedure describes the use of labelled CD8 antibody together with MHC dextramers; additional antibodies for detection of other extracellular antigens can be added. Likewise, detection of intracellular antigens can be performed simultaneously with MHC-detection (for protocol, see IntraStain procedure, cat no. K2311, Dako. Additional washing step prior to IntraStain Reagent A is essential for good results using MHC Dextramers together with this IntraStain procedure).

Example 39

This example describes how TCR-coated beads can be used as internal, positive controls when analysing suspensions of Human Peripheral Blood Mononuclear Cells (HPBMCs), whole blood samples or any cell sample of interest. The MHC multimer employed in this example is a MHC-tetramer.
In this example TCR-coated beads as described in Example 37 and 38 are added to a sample containing either HPBMCs or whole peripheral blood.

HPBMCs/whole peripheral blood and TCR-beads are incubated with fluorescently labelled MHC-tetramers and the extent of cell staining is analysed by flow cytometry

according to staining procedures as described for Tetramers in the product insert by Beckman Coulter.

Example 40

This example describes how TCR-coated beads can be used as internal, positive controls when analysing suspensions of Human Peripheral Blood Mononuclear Cells (HPBMCs), blood samples (red blood cell depleted) or any cell sample of interest. The MHC multimer employed in this example is a MHC-pentamer.

In this example TCR-coated beads as described in Example 37 and 38 are added to a sample containing either HPBMCs or blood.

HPBMCs/blood sample and TCR-beads are incubated with fluorescently labelled MHC-pentamers and the extent of cell staining is analysed by flow cytometry according to staining procedures as described for Petramers in the product insert by ProImmune.

Example 41

This example describes how it can be examined whether a MHC multimer is correctly folded. The MHC multimer is in this example a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to antibodies immobilized on beads.

Beads were coated with the antibody clone W6/32. W6/32 is an antibody recognizing all human MHC I HLA-A, B and, C alleles but only when they are in the correct conformation and properly loaded with antigenic peptide. The protocol for immobilization of proteins on carboxylate beads described elsewhere herein was followed. In the following these W6/32 antibody coated carboxylated beads are referred to as W/32-beads.

W6/32-beads were incubated with fluorescently labeled MHC-dextramers and the extent of cell staining analyzed by flow cytometry. The staining procedure described in example 37 was followed.

W6/32-beads incubated with correctly folded MHC-dextramers showed efficient staining. Experiments with W6/32-beads incubated with unfolded heavy chain attached to fluorescently labelled dextran, or a fluorescently labelled dextran without MHC complex attached, showed less fluorescence intensity compared to W6/32-beads incubated with correct folded MHC-dextramer.

We conclude that beads coupled with the antibody clone W6/32 can be used as positive control for all MHC alleles recognized by this antibody.

Other antibodies, or other types of molecules such as DNA aptamers recognizing correctly folded MHCs or parts of MHC could be used in similar experiments.

Example 42

This example describes how the quality of the MHC multimer can be tested. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The MHC multimer in this example is a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to TCRs or other MHC-recognizing molecules.

Experiments can be performed with any kind of TCRs or MHC-recognizing molecules immobilized on a bead or other solid support.

Procedures as described in examples elsewhere herein can be used, depending on the chemistry of the MHC recognizing molecules and type of solid support. Procedures for coupling of molecules and type of solid support can be chosen and optimized according to the chemistry of the molecules and solid support.

Alternatively, the experiments could be performed without including solid supports, e.g. by performing immunoprecipitation of formed MHC multimer-TCR complexes.

Example 43

This example describes how the quality of a MHC multimer can be tested. The example also describes how MHC multimers can be used for detection of a specific T-cell line.

The MHC multimer in this example is a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to a cell line that expresses specific TCRs and displays these on the cell surface.

A transfected Jurkat T cell line (JT3A) from Altor Biosciences specific for the MHC complex HLA-A*0201(NLVPMVATV (SEQ ID NO 217779)) was evaluated as positive control for the MHC-dextramer HLA-A*0201(NLVPMVATV (SEQ ID NO 217779)). The cells were cultured and treated to express TCR just before evaluation. Under the conditions used, 20-50% of the cells were expected to express and display TCR. After stimulation the cells were incubated with fluorescently labeled MHC-dextramers and the extent of cell staining analyzed by flow cytometry, as follows:

JT3A cells growing in log phase were incubated at room temperature for 2-3 hours to express TCRs (The TCRs are not stable expressed at 37°C).
After 3 hours cells were centrifuged for 5 min at 400 g, and the supernatant was discarded.
Cells were washed in PBS pH 7.4 + 5% FCS, and centrifuged for 5 min at 400 g. The supernatant was discarded, and cells resuspended in proper volume PBS pH 7.4 + 5% FCS for counting in a Bürker chamber.
$1x10^6$ cells per sample in 100µl PBS pH 7.4 + 5% FCS were added to each sample tube.
10µl MHC-dextramers were added. Incubation for 30 min at 4°C in the dark.
5µl anti-CD3 was added to each sample. Further incubation for 30 min at 4°C in the dark.
Samples were washed in 2 ml PBS, centrifuged for 5 min at 300 g. Supernatant discarded and sample resuspended in 0.4 ml PBS pH 7.4.
Samples were kept at 2-8°C in the dark until analysis on flow cytometer.
Samples were analyzed by flow cytometry on a CyAn instrument.

Data were analyzed by the Summit software. Stimulated JT3A cells were stained with the specific MHC-dextramer HLA-A*0201(NLVPMVATV (SEQ ID NO 217779)) and anti-CD3. Another sample of cells were stained with the irrelevant MHC-dextramer HLA-A*0201(GILGFVFTL) and anti-CD3. The cells stained with HLA-A*0201(GILGFVFTL) had weak signals (low fluorescent intensity), and therefore regarded as the negative population. A boundary was introduced in the dot plot, to mark the negative population. Cells with fluorescence higher than the negative boundary were hereafter regarded positive. 19% and 0.25% of the cells were regarded positive when stained with the relevant and irrelevant MHC-dextramer, respectively. See table below.

MHC-complex	Percentage of positive cells
HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779)	19%
HLA-A*0201(GILGFVFTL)	0,25%

The results thus correlate well with the expected 20-50% HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) positive JT3A cells after stimulation. We conclude that the

transfected Jurkat cell line (JT3A) can be used as positive control for the MHC-dextramer.

Example 44

This example describes how the quality of a MHC multimer can be tested. The example also describes how MHC multimers can be used for detection of specific T-cell lines.

The MHC multimer in this example is a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to cell preparations expressing TCRs.

Three different peptide specific T-cell preparations of Human cytotoxic T lymphocyte lines specific for viral peptides were incubated with fluorescently labeled MHC-dextramers and the extent of cell staining analyzed by flow cytometry. The following T-cell preparations were examined: (NLV) specific for MHC-dextramer HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779), (IPSI) specific for MHC-dextramer B*3501(IPSINVHHY) and (GLC) specific for MHC-dextramer A*0201(GLCLVALM).

Cells were added 1ml RPMI and then transfer to a tube with 9ml RPMI. Cells were centrifuged for 5 min at 300 g, and the supernatant was discarded.

Cells were washed in 10ml PBS pH 7.4 + 5% FCS, and centrifuged for 5 min at 300 g, and the supernatant was discarded.

$1x10^6$ cells per sample in 100µl PBS pH 7.4 + 5% FCS were added to sample tubes.

10µl MHC Dextramers were added, and incubated at room temperature in the dark for 10 min.

5µl anti-CD3 and anti-CD8 were added to each sample. Further incubation for 20 min at 4°C in the dark.

Samples were washed in 2ml PBS pH 7.4 + 5% FCS and centrifuged for 5 min at 300 g, and the supernatant was discarded.

Pellets were resuspended in 0.4 ml PBS pH 7.4.

Samples were kept in the dark at 2-8°C until analysis on a flow cytometer.

Samples were analyzed by flow cytometry on a CyAn instrument.

Data were analyzed by the Summit software. The cell preparations were stained with anti-CD3, anti-CD8, the respective specific MHC-dextramer, or an irrelevant MHC-dextramer. Anti-CD3 positive cells were positively gated and anti-CD8 vs. MHC-

dextramer were depicted in a dot plot. The main population of anti-CD8 positive cells stained with the irrelevant MHC-dextramer was regarded as negative, and a boundary was introduced in the dot plot to mark the negative population. Anti-CD8 positive cells with fluorescence higher than the negative boundary were regarded positive. In the NLV and IPSI cell preparations, approximately 95% of the $CD8^+$ cells were positive for the relevant MHC dextramer. 45% of the $CD8^+$ GLC cells were positive for relevant MHC Dextramers, see table below. Cell preparations were not stained by the irrelevant MHC-dextramer.

We conclude that the different peptide specific T-cell preparations can be used as positive controls for the relevant MHC-dextramer.

Cell preparation	MHC-complex	Percentage of positive cells
NLV	HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779)	97%
	HLA-B*3501(IPSINVHHY)	0,02%
IPSI	HLA-B*3501(IPSINVHHY)	95%
	HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779)	0,01%
GLC	HLA-A*0201(GLCLVALM)	45%
	HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780)	0,1%

Example 45

This example describes how the quality of the MHC multimer can be tested. The example also describes how MHC multimers can be used for detection of specific T-cell lines.

The MHC multimer in this example is a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to cell lines or other preparations expressing TCRs or MHC-recognizing molecules.

Experiments can be performed with any kind of TCRs or MHC-recognizing molecules displayed on cells (e.g. a cell line or a cell preparation).

Procedures as described in Example 43 and 44 can be used with any kind of TCRs or MHC-recognizing molecules displayed on cells. Stimulation of cells has to be optimized

for the specific experiments (e.g. stimulation with chemicals and/or temperature to express the TCR prior to analysis).
Results can be analyzed as in Example 43 and 44 and cell preparations stained with relevant MHC-dextramers will extent higher signal intensity than when stained with irrevant MHC-dextramers.

Example 46

This example describes how the quality of the MHC multimer can be tested. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support or attached to other molecule.
The MHC multimer in this example is a MHC-dextramer, and the test involves specific binding of the MHC-dextramer to TCRs or MHC recognizing motifs immobilized or expressed on molecules detectable in flow cytometry.
The experiments can be performed with any kind of molecule detectable in flow cytometry. MHC-recognizing molecules can be displayed on beads, cells, or other entities that are amenable to flow cytometry analysis.
MHC-recognizing molecules can be displayed on entities amenable in flow cytometry either naturally or artificially (e.g. chemical coupling). Procedures as described in the above examples can be applied, depending on the nature of the molecules.
Alternatively procedures optimized for the specific molecule can be applied.
Molecules can be stained with flourescently labeled MHC-dextramers and the extent of cell staining can be analyzed by flow cytometry. Molecules stained with relevant MHC-dextramers will extent higher signal intensity than when stained with irrelevant MHC-dextramers.

Example 47

This example describes how the quantity of correctly folded MHC can be determined by ELISA assay. The test involves specific binding of the MHC to anti-HLA-ABC antibody, clone W6/32. W6/32 is an antibody recognizing all human MHC I HLA-A, B and C alleles but only when they are in the correct conformation and properly loaded with antigenic peptide.
The ELISA can be carried out as follows. A preparation of MHC complexes is incubated in wells of a microtiter plate pre-coated with W6/32 antibody following standard ELISA procedure regarding washes, blocking etc. A secondary antibody recognizing MHC (e.g. anti-β_2m) is used for visualization. The secondary antibody can

be labbelled, e.g. with Horse raddish Peroxidase or it can be unlabelled, and a labeled compound specific for the secondary antibody is then employed (e.g. EnVision System) before visualization.. A compound for visualization is added, e.g. TMB One-Substrate System when Peroxidase enzyme is the label. The chromogenic intensity is measured and the result from the ELISA assay is evaluated. In parallel a standard curve of is generated, e.g. consisting of various concentrations of correctly folded MHC complexes. The chromogenic intensity of the tested MHC sample can now be converted to actual concentrations of correctly folded MHC using the standard curve. We conclude that the ELISA assay together with a standard curve can be used to quantify correctly folded MHC.

Example 48

This example describes how the quantity of correctly folded MHC can be determined by ELISA assay. The test involves specific binding of MHC complexes to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules).

As described elsewhere the quantity of correctly folded MHC can be measured in an ELISA assay using a molecule specific for correctly folded MHC complexes either for catching of the testet MHC complex preparation or for detection of it. The result obtained from bound MHC complex in the sample tested is correlated to a standard curve for determination of concentration. The ELISA assay can be conducted and optimized by various measures depending on the reagent and enzyme used.

Example 49

This example describes how the quantity of correctly folded MHC can be determined by competitive ELISA assay. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The test involves specific binding of MHC complexes to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules). The analysis is carried out as follows. A preparation of correctly folded MHC of known concentration is immobilized in wells of a microtiter plate. A mixture of a molecule recognizing correctly folded MHC (e.g. the antibody W6/32) and soluble MHC complex, containing a mixture of correctly and non-correctly folded MHC, is added to the microtiter plate. The molecules recognizing correctly folded MHC will now attach to either the immobilized MHC or the correctly folded MHC in the soluble

fraction. The amount of molecules recognizing correctly folded MHC bound to the immobilized MHC in the microtiter plate is measured, e.g. by addition of a secondary labeled or unlabeled antibody specific for the molecule recognizing correctly folded MHC. Depending on the characteristic of the secondary antibody visualization is performed. The result of the ELISA assay is evaluated. The amount of bound molecules specific for correctly folded MHC complexs is inversely proportional to the quantity of correctly folded MHC in the soluble fraction. The quantity of correctly folded MHC in the soluble fraction can be measured using a standard curve, obtained using known amounts of a pure preparation of MHC complexes and constant amount of molecules recognizing correctly folded MHC.

We conclude that an indirect competitive ELISA can be used to quantify correctly folded MHC.

Example 50

This example describes how the quantity of correctly folded MHC can be determined by competitive ELISA assay. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The test involves specific binding of MHC complexes to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules).

The analysis is carried out as follows. Molecules recognizing correctly folded MHC are immobilized in wells of a microtiter plate. A preparation of in vitro folded MHC complexes is mixed with a known amount of labeled correctly folded MHC and the mixure added to the microtiter plate. The correctly folded MHC in the mixture will now compete for binding to the molecules recognizing correctly folded MHC immobilized in the microtiter plate. The amount of bound labeled MHC can now be visualized and measured. The result is inversely proportional to the quantity of correctly folded MHC in the mixture. The quantity of correctly folded MHC in the mixture can be measured using a standard curve, obtained using known amounts of a pure preparation of MHC mixed with a constant amount of labeled MHC.

Example 51

This example describes how the quantity of correctly folded MHC can be determined by competitive ELISA assay. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The test involves specific binding of the MHC to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules) or to molecules recognizing MHC, correctly as well as non-correctly folded (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules).

A preparation of MHC complexes are immobilized in a microtiter plate and incubated with a labeled molecule recognizing MHC, correctly as well as non-correctly folded (in the following referred to as recognizing all MHC complexes).
Then an unlabeled molecule recognizing correctly folded MHC is added in major excess. These molecules will displace all the MHC recognizing molecules added in step 1 that binds correctly folded MHC complexes.
The amount of bound labeled molecule recognizing all MHC can now be visualized and measured.
The result is inversely proportional to the quantity of correctly folded MHC. The quantity of correctly folded MHC can be measured using a standard curve, obtained using known amounts of a MHC incubated with labeled molecule recognizing all MHC.

Example 52

This example describes how the quantity of correctly folded MHC can be determined.
The test involves specific binding of MHC complexes to anti-HLA-ABC antibody, clone W6/32. In this example W6/32 antibody is immobilized on magnetic beads.

The protein concentration in a purified preparation of MHC complexes is determined by spectofotometric measurement of OD_{280}. Other techniques can be used as well, e.g. BCA (bicinchoninic acid) assay or SDS-PAGE gel.
To measure the proportion of correctly folded MHC, a sample of the MHC complex preparation is incubated with W6/32 antibody coated magnetic beads.
After incubation the beads are sedimented or captured by a magnet and excess supernatant is withdrawn.
The concentration of protein in the supernatant is measured as in step 1.
The proportion of correctly folded MHC complex is calculated as follows:

X: Total protein concentration (step 1)

Y: Protein concentration after capture of correctly folded MHC (step 4)

% of correct folded MHC = (1- (Y/X))* 100 %

Ex. X = 10 mg/ml

Y = 2 mg/ml

% of correct folded MHC = (1- (2 mg/ml / 10 mg/ml))* 100 %

= 80%

The proportion of correctly folded MHC can be used as quality parameter, to measure the variation from production to production of a specific MHC-peptide complex.

Example 53

This example describes how the quantity of correctly folded MHC can be determined. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The test involves specific binding of MHC complexes to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules). The MHC recognizing molecules can be immobilized to a solid support (e.g. beads, microtiter plate or gel material).

The protein concentration in a purified preparation of MHC complexes is determined by spectofotometric measurement of OD_{280}. Other techniques can be used as well, e.g. BCA (bicinchoninic acid) assay or SDS-PAGE gel.

To measure the proportion of correctly folded MHC, a sample of the MHC complex preparation is incubated with a molecule recognizing correctly folded MHC complex immobilized to a solid support.

After incubation supernatant is withdrawn.

The concentration of protein in the supernatant is measured as in step 1.

The proportion of correctly folded MHC complex is calculated as follows:

X: Total protein concentration (step 1)

Y: Protein concentration after capture of correctly folded MHC (step 4)

% of correct folded MHC = (1- (Y/X))* 100 %

Ex. X = 10 mg/ml

Y = 2 mg/ml

% of correct folded MHC = (1- (2 mg/ml / 10 mg/ml))* 100 %
= 80%

The proportion of correctly folded MHC can be used as quality parameter, to measure the variation from production to production of a specific MHC-peptide complex.

Example 54

This example describes how the quantity of correctly folded MHC can be determined. The test involves specific binding of MHC complexes to anti-HLA-ABC antibody, clone W6/32. In this example W6/32 antibody is immobilized on magnetic beads.

A preparation of MHC complexes is incubated with W6/32 antibody coated magnetic beads and all correctly folded MHCs are thereby captured.
After incubation the beads are sedimented or captured by magnet, d the supernatant withdrawn and the amount of non-bound MHC complex (equal to not correctly folded MHC complex) is determined by ELISA.
To measure the quantity of MHC complexes in solution before and after incubation with W6/32 antibody coated magnetic beads an ELISA assay is applied. A microtiter plate is coated with an antibody recognizing all MHC complexes correct as well as non-correct folded.
Samples of MHC complex before and after incubation with W6/32 antibody coated magnetic beads are added to the coated microtiter plate.
A labeled secondary antibody recognizing MHC (e.g. anti-β_2m) is used for visualization. Alternatively the secondary antibody is unlabelled, and a labeled molcule specific for the secondary antibody is employed (e.g. EnVision System) before visualization.
The proportion between results from the sample after incubation with W6/32 antibody coated magnetic beads and the sample before incubation with W6/32 antibody coated magnetic beads is a measure of the amount of non correct folded MHC complex and thereby an indirect measure of the amount of correct folded MHC complex . To obtain exact values for the amount of MHC complex in each sample a standard curve can be generated.

Example 55

This example describes how the quantity of correctly folded MHC in a sample can be determined. The example also describes how MHC multimers can be used for detection of TCR immobilized to solid support.

The test involves specific binding of MHC complexes to a molecule recognizing correctly folded MHC complex (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules). The MHC recognizing molecules can be immobilized to any solid support (e.g. beads, microtiter plate or gel material). Correctly folded MHC complex in a sample is captured by addition of the sample to the immobilized MHC-binding molecule, then non-bound MHC-complex (equal to not corretly folded MHC complex) is removed. The proportion of MHC complex in the two fractions (before and after incubation with immobilized MHC-specific molecule) can be evaluated by any method capable of determination of the total amount of MHC complex (folded or undfodled).

Example 56

This example describes how the quantity of correctly folded MHC in a sample can be determined. The test involves specific binding of MHC complex to a molecule recognizing correctly folded MHC (e.g. antibody, TCR, aptamers, or other MHC-peptide complex binding molecules). The specific binding is evaluated by native protein gel electrophoresis.

A preparation of in vitro folded and purified MHC complex is incubated with a molecule recognizing correctly folded MHC, e.g. the antibody W6/32.

The product is analysed by native protein gel electrophoresis (lane 1) together with a sample of in vitro folded and purified MHC complex not incubated with MHC recognizing molecule (lane 2), and a sample of the molecule recognizing correctly folded MHC (lane 3). In the protein gel the different proteins are separated according to size. The various protein products are visualized in the gel e.g. by Comassie blue staining, isotope or chemiluminiscence. In the sample with MHC complex and MHC-binding molecule correctly folded MHC complex will bind the MHC-binding molecule and appear in the protein gel as one or more large bands in the top of the gel. In contrast non-correctly folded MHC complex will appear as monomer lower in the gel. The fraction of not correctly folded MHC (lane 1) can now be compared with the total amount of MHC in the sample (lane 2) and the difference between the two correlates with the amount of correctly folded MHC complex in the sample. The results can be

evaluated in different manners to determine the quantity of correctly folded MHC, e.g. comparison of intensity to the intensity of products of known concentration.

Example 57

This example describes how to verify that a MHC-complex is correctly folded by a sandwich-ELISA assay. W6/32 mouse-anti-HLA-ABC antibody (Dako M0736), that recognizes a conformational epitope on correctly folded MHC-complex, was used as coating-antibody. HRP-conjugated rabbit anti-β2m (Dako PO174) was used for visualization.

Wells of a microtiter plate was pre-coated with W6/32 antibody (Dako M0736, 5 μg/ml in 0.1M $NaHCO_3$, 1 mM $MgCl_2$, pH 9.8, 50 μl/well) following a standard ELISA procedure regarding washes and blocking ect.

After addition of 50 μl of 0.5M Tris-HCl, 0.1 M NaCl, 0.1% Tween 20, 0.01% Bronidox, pH 7.2 to each well, 50 μl of a sample of purified folded MHC-complex (in a concentration of approx. 0.4 mg/ml) was added to two wells in to columns in the microtiter plate, diluted 2-fold down the column and incubated 2 hours at 4°C. Light chain β2m (0.15 mg/ml in 0.5M Tris-HCl, 0.1 M NaCl, 0.1% Tween 20, 0.01% Bronidox, pH 7.2) was used as a negative control and the cell-line KG-1a, expressing HLA-A*30, HLA-A*31 and HLA-B*35 heavy chains, was used as positive control (10^6 cells/well).

After a standard ELISA wash, 50 μl of the detecting antibody; HRP-conjugated rabbit anti-β2m (Dako PO174), diluted 1:2500 in 1% Skimmed Milk in 0.5M Tris-HCl, 0.1 M NaCl, 0.1% Tween 20, 0.01% Bronidox, pH 7.2 was added to each well. The plate wass incubated 1 hour at 4°C.

After a standard ELISA wash, 50 μl of an amplifying antibody; HRP-Dextran500-conjugated goat anti-rabbit (Dako DM0106), diluted 1:2000 in 1% Skimmed Milk in 0.5M Tris-HCl, 0.1 M NaCl, 0.1% Tween 20, 0.01% Bronidox, 1% mouse serum (Dako X0190) pH 7.2 was added. The plate was incubated 30 min. at 20°C.

After a standard ELISA wash, 50 μl of Dako S1599 (TMB+Substrat Chromogen) was added to each well for visualization.

After 10 min. the visualization reaction was stopped with 50 μl 0,5M H_2SO_4/well.

The chromogenic intensity was measured at OD_{450} and the result from the ELISA assay evaluated.

As shown in figure 17 the OD_{450} values from wells with MHC complex was more than 6 times higher than OD_{450} values from wells with the negative control β2m. This ELISA procedure can be used to verify the presence of correctly folded MHC-peptide complexes in a preparation of MHC complexes.

Example 58

This example describes the generation and application of negative controls, where the MHC complex is HLA-A*0201 loaded with either of the nonsense peptides GLAGDVSAV (SEQ ID NO 217778) or ALIAPVHAV (SEQ ID NO 217781) and these MHC complexes are coupled to a 270 kDa dextran multimerization domain. The nonsense peptides have an amino acid sequence different from the linear sequence of any peptide derived from any known naturally occurring protein. This was analyzed by a blast search. The amino acids at position 2 and 9 can serve as anchor residues when binding to HLA-A*0201 molecules.

Purified MHC(peptide) molecules consisting of the allele HLA-A*0201, human beta2microglobulin and peptide was generated by in vitro refolding, purified and biotinylated as described elsewhere herin. Biotinylated HLA-A*0201(peptide) was mixed with APC-SA-conjugated 270 kDa dextran in an amount corresponding to a ratio of three biotinylated HLA-A*0201(peptide) molecules per SA molecule and incubated for 30 minutes in the dark at room temperature. The APC-SA-conjugated 270 kDa dextran contained 9 molecules APC and 3,7 molecules SA per dextran molecule. Following incubation the mixture was diluted into a buffer containing 0,05M Tris/HCl, 15 nM NaN_3 and 1% BSA to a final concentration of $3{,}8x10^{-8}$ M dextran.

By this procedure the following MHC multimer constructs were made:
A negative control construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated HLA-A*0201 in complex with beta2microglobulin and the nonsense peptide GLAGDVSAV ((SEQ ID NO 217778) nonsense peptide 1).
A negative control construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated HLA-A*0201 in complex with beta2microglobulin and the nonsense peptide ALIAPVHAV ((SEQ ID NO 217781) nonsense peptide 2).
A construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated HLA-A*0201 in complex with beta2microglobulin and the peptide NLVPMVATV (SEQ ID NO 217779) derived from pp65 protein from human cytomegalovirus (HCMV).

A construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated HLA-A*0201 in complex with beta2microglobulin and the peptide GLCTLVAML (SEQ ID NO 217782) derived from BMLF-1 protein from Epstein Barr virus (EBV).
A construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated HLA-A*0201 in complex with beta2microglobulin and the peptide ILKEPVHGV (SEQ ID NO 217780) Reverse Transcriptase from Human Immunodeficiency Virus (HIV).

The binding of the HLA-A*0201(peptide)/APC dextran constructs to Human Peripheral Blood Mononuclear Cells (HPBMC) from various donors was analyzed by flow cytometry following a standard flow cytometry protocol. Briefly, HPBMC from the blood of 9 individual donors were isolated, by a standard protocol using Ficoll-Hypaque. $1x10^6$ purified HPBMC at a concentration of $2x10^7$ cells/ml were incubated with 10 µl of one of the HLA-A*0201(peptide)/APC dextran constructs described above for 10 minutes in the dark at room temperature. 10 µl of each of the antibodies mouse-anti-human CD3/PE (clone UCHT1 from Dako) and mouse-anti-human CD8/PB (clone DK25 from Dako) were added and the incubation continued for another 20 minutes at 4°C in the dark. The samples were then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells were then resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a CYAN ADP flowcytometer.

Donor 1-5 were known to have detectable T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) and no detectable T cells specific for HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) while donor 6 were known not to have detectable specific T cells for either HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) nor HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780). Lymphocytes from these 6 donors were stained with MHC multimer construct 1, 2, 3, and 5. Donor 1-5 showed positive staining with MHC multimer construct 3 as expected while no staining was observed with the either of the negative control MHC complex constructs 1 and 2 or with MHC complex construct 5. An example showing the staining patterns for donor 2 is shown in figure 20. No specific staining was observed of lymphocytes from donor 6 with either of the MHC multimer constructs.
Donor 7-8 known to have detectable T cells specific for HLA-A*0201(GLCTLVAML) (SEQ ID NO 217782) and no detectable T cells recognizing HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) and donor 9 having no detectable T cells specific for either

HLA-A*0201(GLCTLVAML) (SEQ ID NO 217782) nor HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) were all stained with MHC multimer construct 1, 2, 4, and 5. Donor 7 and 8 demonstrated efficient staining with MHC multimer construct 4 as expected while no staining was observed with the other MHC multimer constructs tested. No staining was observed of lymphocytes from donor 9 with either of the MHC multimer constructs tested. A summary of the results is shown in figure 21.
In conclusion this experiment demonstrates that the negative MHC multimer constructs 1 and 2 did not stain any specific T cells in lymphocyte preparations from 10 different donors. Donors known to have specific T cells for either HLA-A*0201(GLCTLVAML) (SEQ ID NO 217782) or HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) also demonstrated positive staining with the corresponding MHC multimer constructs 3 and 4. None of the 10 donors were infected with HIV and as expected did not appear to have T cells specific for HLA-A*0201 in complex with the HIV derived peptide ILKEPVHGV (SEQ ID NO 217780), and as expected none of these donors showed staining with MHC multimere construct 5. MHC multimer construct 1 and 2 are therefore suitable negative controls when using HLA-A*0201(peptide) multimers for detection of specific T cells in Flow Cytometry.

Example 59

This is an example of how to generate and use negative controls, where the MHC complex is any MHC I or MHC II complex of human, mouse, rabbit, rat, swine or monkey origin loaded with a nonsense peptide. A nonsense peptide is here to be understood as a peptide having an amino acid sequence different from any peptide derived from any known naturally occurring protein, and preferably is not recognized by any T cell when presented by a MHC complex. The nonsense peptide has amino acid residues at relevant positions that anchor the peptide to the peptide-binding groove of the MHC complex. The MHC(nonsense peptide) complex is coupled to a 270 kDa dextran multimerization domain.

Purified MHC(peptide) molecules consisting of the alpha chain, human beta2microglobulin and peptide is generated by in vitro refolding, purified and biotinylated as described elsewhere. Biotinylated MHC(peptide) is mixed with APC-SA-conjugated 270 kDa dextran in amounts corresponding to a ratio of three biotinylated MHC(peptide) molecules per SA molecule and incubated for 30 minutes in the dark at room temperature. The APC-SA-conjugated 270 kDa dextran contains 9 molecules

APC and 3,7 molecules SA per dextran molecule. Following incubation the mixture is diluted into a buffer containing 0,05M Tris/HCl, 15 nM NaN_3 and 1% BSA to a final concentration of $3,8x10^{-8}$ M dextran.
By this procedure the following MHC complex constructs are made:

A negative control construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated alpha chain in complex with beta2microglobulin and a corresponding nonsense peptide. A nonsense peptide is here to be understood as a peptide with an amino acid sequence different from any peptide derived from any known naturally occurring protein and the nonsense peptide is not recognized by any T cell when presented by a MHC complex.
A construct comprising APC-SA-conjugated 270 kDa dextran and biotinylated alpha chain in complex with beta2microglobulin and a peptide derived from a known protein.

The binding of the MHC(peptide)/APC dextran constructs to Human Peripheral Blood Mononuclear Cells (HPBMC) from various donors is analyzed by flow cytometry following a standard flow cytometry protocol. Briefly, HPBMC from the blood of 9 individual donors are isolated by a standard protocol using Ficoll-Hypaque. $1x10^6$ purified HPBMC at a concentration of $2x10^7$ cells/ml is incubated with 10 µl of one of the MHC(peptide)/APC dextran constructs described above for 10 minutes in the dark at room temperature. 10 µl of each of each of the antibodies mouse-anti-human CD3/PE (clone UCHT1 from Dako) and mouse-anti-human CD8/PB (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a CYAN ADP flowcytometer.
The staining patterns of flow cytometry analysis with the two MHC(peptide)/APC constructs 1 and 2 are compared. There will be no staining observed with construct 1.

Example 60

This is an example of how to generate negative controls, where the MHC complexes is any MHC I or MHC II molecule of human, mouse, rabbit, rat, swine, monkey or any other origin loaded with a nonsense peptide and where the MHC(nonsense peptide) complexes are coupled to any multimerization domain. A nonsense peptide is here to

be understood as a peptide that have an amino acid sequence different from any peptide derived from any known naturally occurring protein and cannot be recognized by any T cell when presented by a MHC complex. The nonsense peptide carries amino acid residues at relevant positions that anchor the peptide to the peptide-binding groove of the MHC complex.

The MHC(nonsense peptide) complex can be made as described elsewhere herein, and can then be coupled to a relevant multimerization domain. The labelling of the multimerization domain can be optimized depending on later use of the negative control e.g. in flow cytometry analysis, IHC, ELISA or similar.

Example 61

This example describes the generation of a negative control, where the MHC complex is HLA-A*0201 coupled to a 270 kDa dextran, and where the MHC is loaded with the peptide ILAKFLHWL that have pivaloyl coupled to Lysine at position 4. ILAKFLHWL is a peptide derived from telomerase and is known to bind HLA-A*0201. Pivaloyl is a small molecule that confers high sterical hindrance. Because pivaloyl is placed at a central position in the peptide it is likely to inhibit or completely abrogate the interaction with a specific TCR, because TCR-recognition is normally directed to the middle of the peptide when bound in the peptide-binding cleft. In the following the pivaloyl-modified peptide will be designated ILAK^{p}FLHWL.

Purified HLA-A*0201(ILAK^{p}FLHWL) molecules consisting of the HLA-A*0201 heavy chain, human beta2microglobulin and ILAK^{p}FLHWL peptide is generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated HLA-A*0201(ILAK^{p}FLHWL) molecules are mixed with flourochrome-SA-conjugated 270 kDa dextran molecules. The resulting HLA-A*0201(ILAK^{p}FLHWL)/flourochrome-carrying dextran molecules can be used as negative controls in e.g. flow cytometric analysis.

Example 62

This example describes the generation of a negative control, where the MHC complex is any MHC I or MHC II molecule of human, mouse, rabbit, rat, swine, monkey or any other origin loaded with the peptide ILAK^{p}FLHWL and coupled to any multimerization domain labeled with fluorochrome, HRP or any other label. Purified MHC(ILAK^{p}FLHWL) complexes consisting of the heavy chain, human beta2microglobulin and ILAK^{p}FLHWL peptide is generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC(ILAK^{p}FLHWL)

complexes are mixed with labeled multimerization domain, thereby generating MHC(ILAK^{p}FLHWL) multimers. The MHC(ILAK^{p}FLHWL) multimers mayn be used as negative controls in e.g. flow cytometric analysis, IHC, ELISA or similar.

Example 63

This example describes the generation of a negative control where the MHC is HLA-A*0201 loaded with the peptide ILKEPVHGV (SEQ ID NO 217780) and coupled to a 270 kDa dextran multimerization domain. The peptide ILKEPVHGV (SEQ ID NO 217780) is derived from HIV. HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) complexes are generated, biotinylated and coupled with a labeled dextran multimerization domain as described elsewhere herein. Then these HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780)-dextran conjugates are used as negative controls in experiments with samples from humans that are HLA-A*0201 positive and not infected by HIV, because it is not likely that they have T cell's with a TCR specific for HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) in amounts that can be detected by MHC multimer reagents. The conjugates can also be used as negative control in samples from humans that are HLA-A*0201 negative or in samples from other species.

Example 64

This example describes the generation of a negative control. CD8 molecules on the surface of cytotoxic T-cells bind MHC I complexes by interaction with amino acids in the α3 domain of the heavy chain. When using MHC multimers this interaction can result in MHC multimer binding to CD8 positive T-cells that are not restricted by the MHC(peptide) complex in the MHC multimer. In this example a proper negative control showing these false positive cells is described. Such a negative control can consist of MHC I heavy chain or truncated versions of MHC I heavy chain bound to any multimerization domain. The heavy chain can be folded or unfolded, and can have a peptide bound in the peptide binding groove but does not have to comprise a peptide. A MHC I heavy chain-multimerization domain can be made in a way similar to what is described for the generation of MHC I-multimerization domains. Briefly, purified MHC I heavy chain is expressed as inclusion bodies in E.coli and purified by general procedures. The heavy chain is refolded in vitro, purified and biotinylated, or the heavy chain can be biotinylated directly without refolding. Biotinylated heavy chain is coupled to any multimerization domain. The multimerization domain can be labeled with any suitable label or can be unlabeled depending on later use. Such a negative control can

be used in experiments with MHC I multimers, e.g. in flow cytometry analysis, IHC, or ELISA.

Example 65

This example describes how to identify specific T cells in a blood sample with MHC multimers using flow cytometry analysis without lysis of red blood cells and without washing the cells after staining. MHC complexes in this example consisted of HLA-A*0201 heavy chain, human beta2microglobulin and different peptides, and the MHC complexes were coupled to a 270 kDa dextran multimerization domain.

Purified MHC-peptide complexes consisting of human heavy chain, human beta2microglobulin and peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes were then coupled to a 270 kDa dextran multimerization domain labelled with PE by interaction with streptavidin (SA) on the dextran multimerization domain. The SA-PE-dextran was made as described elsewhere herein. MHC-peptide complexes was added in an amount corresponding to a ratio of three MHC-peptide moleculess per SA molecule and each molecule dextran contained 6.1 SA molecule and 3.9 molecules PE. The final concentration of dextran was 3.8x10e-8 M. The following constructs were made:

PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide VTEHDTLLY (SEQ ID NO 217783) derived from Human Cytomegalo Virus (HCMV).

PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide IVDCLTEMY (SEQ ID NO 217784) derived from ubiquitin specific peptidase 9 (USP9).

PE conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLVPMVATV (SEQ ID NO 217779) derived from Human Cytomegalo Virus (HCMV).

PE conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ILKEPVHGV (SEQ ID NO 217780) derived from Human Immunodeficiency Virus (HIV).

PE/SA conjugated 270 kDa dextran coupled with HLA-B*0207 in complex with beta2microglobulin and the peptide TPRVTGGGAM (SEQ ID NO 217785) derived from Human Cytomegalo Virus (HCMV).

PE conjugated 270 kDa dextran coupled with HLA- B*0207 in complex with beta2microglobulin and the peptide RPHERNGFTVL (SEQ ID NO 217786) derived from Human Cytomegalo Virus (HCMV).
PE conjugated 270 kDa dextran coupled with HLA- B*0207 in complex with beta2microglobulin and the peptide TPGPGVRYPL (SEQ ID NO 217787) derived from Human Immunodeficiency Virus (HIV).

These seven MHC multimer constructs were used for detection of specific T cells in flow cytometry analysis using a no-lyse no-wash procedure. Blood samples from three individual donors were analyzed. The donors had previously been screened for the presence of specific T cells using a general staining procedure including lysis and wash of the cell sample, and donor one turned out to be positive for HLA*0201 in complex with the peptide NLVPMVATV (SEQ ID NO 217779), donor two were positive for HLA*0101 in complex with the peptide VTEHDTLLY (SEQ ID NO 217783) and donor three were positive for HLA-B*0207 in complex with the peptides TPRVTGGGAM (SEQ ID NO 217785) and RPHERNGFTVL (SEQ ID NO 217786). In this experiment blood from each donor were analyzed with the MHC multimer construct they were supposed to have specific T cells restricted for and with MHC multimers of same haplotype but carrying a negative control peptide. The negative control peptides were either derived from HIV or the self-protein USP 9. Self-protein here means a naturally occurring protein in normal cells of a human individual. Normal healthy donors not infected with HIV are not expected to have specific T cells recognizing HIV derived peptides or peptides derived from self-proteins in complex with any HLA molecule in an amount detectable with this analysis method.

The blood was stained as follows:
100 µl EDTA stabilized blood were incubated with 5 µl MHC(peptide)/PE dextran for 5 minutes at room temperature. Anti-CD45/PB, anti-CD3/FITC and anti-CD8/APC antibody in an amount of 0.4-1.2 µg/sample was added to each tube and the incubation continued for another 15 minutes. 850 µl PBS; pH = 7.2 was added and the sample analyzed on a CyAn ADP flowcytometry instrument with a speed of 150 µl/minute. A total of 20.000 CD8 positive cells were acquired. During analysis CD45/PB antibody was used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells (see figure 22A). Furthermore

CD3/FITC antibody was used to select CD3 positive cells in a second gating strategy (see figure 22B).

Blood from donor one showed specific staining with HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) multimer (construct 3) while no staining of specific T cells was observed with the negative control HLA-A*0201(ILKEPVHGV) (SEQ ID NO 217780) multimer (construct 4). Donor two showed specific staining with HLA-A*0101(VTEHDTLLY) (SEQ ID NO 217783) multimer (construct 1) and no staining was observed with the negative control HLA-A*0101(IVDCLTEMY) (SEQ ID NO 217784) multimer (construct 2). In blood from donor three a population of T cells were stained with HLA-B*0207(TPRVTGGGAM) (SEQ ID NO 217785) multimer (construct 5) and another population with HLA-B*0207(RPHERNGFTVL) (SEQ ID NO 217786) multimer (construct 6) while no specific staining was observed with the negative control HLA-B*0207(TPGPGVRYPL) (SEQ ID NO 217787) multimer (construct 7). The results are shown in figure 23.
We have shown that MHC multimers of three different haplotypes can be used to identify specific T cells in blood samples from three different donors using an approach without lysing red blood cells and without wash following staining with MHC multimer. This method is simple, fast and interfere as little as possible with cells in the blood sample.

Example 66

This example describes how to identify specific T cells in a blood sample with MHC multimers using flow cytometry analysis without lysis of red blood cells and without washing cells upon staining. The MHC complex is here any MHC I or MHC II molecule of human, rodent, bovine, monkey or any other origin loaded with any peptide able to bind the peptide-binding cleft of the MHC complex and where the MHC-peptide complexes are coupled to any multimerization domain.
Purified MHC-peptide complexes is generated as described elsewhere herein and coupled to any multimerization domain labelled with a fluorescent dye, preferable FITC, PE, APC, pacific blue, cascade yellow or any other flour chrome. These MHC multimers are used for detection of specific T cells by flow cytometry using the following procedure:

EDTA stabilized blood are incubated with MHC multimer at room temperature. The amount of blood analyzed is preferable 50-150 µl but could be any volume ranging from 1 -1000 µl. The amount of MHC multimer depends on the multimer construct and the volumen of blood and should be determined by titration prior to this type of experiment. The incubation time with MHC multimer is preferably 5-20 minutes but could be anything between 0 minutes and 1 hour. Then anti-CD45/CY, anti-CD3/APC and anti-CD8/PB antibody is added and the incubation continued. The incubation time is preferably 5-20 minutes but can be anything between 1 minute and 1 hour. The amount of antibody is preferable 0.4-1.2 µg /100 µl blood but these limits can be extended and should be determined by titration prior to this kind of experiments. The antibodies can be labelled with any fluorochrome as long as the fluorochrome is different from the fluorochrome on the MHC multimer. Next PBS; pH = 7.0-8.0 is added and the sample analyzed by a flowcytometer. The amount of PBS added is preferable 500-1000 µl but can also be more than 1000 µl and less than 500 µl. During analysis anti-CD45 antibody is used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells. Different gating strategies can then be applied to analyse data. Preferably cells are first gated on CD3 positive cells and then for CD8 positive cells, but can also be gated only for CD8 positive cells of only for CD3 positive cells. Alternatively “dump” gates can be applied excluding unwanted cells, e.g. B-cells, CD4-positive cells, NK-cells.

In the above example MHC multimers are added prior to antibodies but MHC multimers and antibodies can also be added simultaneously to the blood sample and incubated for preferably 5-30 minutes but the incubation time can be anything between 1 minute and 2 hours.

This method can be used to identify specific T cells in blood samples fromfdifferent donors using an approach without lysing red blood cells and without wash following staining with MHC multimer. This method is simple, fast and interfere as little as possible with cells in the blood sample

Example 67

This example illustrates how MHC multimers together with counting beads was used for exact numeration of MHC-peptide specific T cells in a flow cytometry analysis whit no lyses of red blood cells and no washing steps during or after staining. Counting beads in this example was CytoCount™, Count Control Beads from Dako that are polystyrene Fluorospheres with a diameter of 5.2 µm. The MHC multimer consisted of

HLA-A*0101 heavy chain complexed with human beta2microgloblin and a peptide and the MHC-peptide complexes were coupled to a 270 kDa dextran multimerization domain labelled with PE. MHC multimers were generated as described elsewhere herein and the following two constructs were made:

PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide VTEHDTLLY (SEQ ID NO 217783) derived from Human Cytomegalo Virus (HCMV).
PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide IVDCLTEMY (SEQ ID NO 217784) derived from ubiquitin specific peptidase 9 (USP9).

Construct 2 is a negative control for construct 1 in this example and both were used for detection of specific T cells by flow cytometry using a no-lyse no-wash procedure:
100 µl of EDTA stabilized blood from a donor positive for HLA*0101 in complex with the peptide VTEHDLLY were incubated with 5 µl MHC multimer for 5 minutes at room temperature. Anti-CD45/CY, anti-CD3/PB and anti-CD8/APC antibody in an amount of 0.4-1.2 µg/sample was added and the incubation continued for another 15 minutes. 850 µl PBS; pH = 7.2 was added together with precise 50 µl CytoCount beads 1028 bead/µl and the sample analyzed on a CyAn ADP flowcytometry instrument with a speed of 150 µl/minute. A total of 20.000 CD8 positive cells were acquired. During analysis CD45/CY antibody was used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells.
A dot plot was made for each sample showing MHC multimer vs CD8 positive events (se figure 24 A and B). Based on the negative control a gate containing events representing CD8 positive T cells specific for MHC multimer was defined. Similarly histogram plots for each sample were made showing FITC signal vs counts (figure 24 C and D). In these histograms the amount of beads in the analyzed sample were identified since the beads in contrast to the cells emit light in the FITC channel. In principle the beads could be visualized in any fluorochrome channel because they emit light in all channels but it was important to visualize the beads in a channel where there was no interfering signal from labelled cells.
The concentration of T cells specific for HLA-A*0101(VTEHDTLLY) (SEQ ID NO 217783) multimer (construct 1) in the blood sample were determined using the counting beads as an internal standard. Events obtained from staining with the

negative control MHC multimer, construct 2, were defined as background signals and subtracted from the result obtained from staining with construct 1.
Concentration of HLA-A*0101(VTEHDTLLY) (SEQ ID NO 217783) specific T cells in the blood sample =
((Count of MHC multimer+ CD8+ positive cells, construct 1 x concentration of beads x dilution factor of beads) /counted beads))- ((Counted MHC multimer+ CD8+ cells, construct 2 x concentration of beads x dilution factor of beads) /counted beads) = 992,6 cells/ml
For details see figure 24.
This experiment demonstrated how CytoCount™ counting beads together with MHC multimers could be used to determine the exact concentration of MHC-peptide specific T cells in a blood sample using a no-lyse no-wash method.

Example 68

This example describes an analysis of specific T cells in blood using MHC multimers where MHC multimers together with antibodies are pre-mixed and embedded in a matrix material to retain and immobilize the reagents prior to use. In this example the matrix was composed of Trehalose and Fructose and the MHC complex consisted of HLA-A*0101 heavy chain complexed with human beta2microglobulin and peptide. The MHC-peptide complexes were coupled to a 270 kDa dextran multimerization domain.

Purified MHC-peptide complexes consisting of heavy chain, human beta2microglobulin and peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC(peptide) complexes were coupled to a 270 kDa dextran multimerization domain labelled with PE, thereby generating PE labelled MHC multimers. The following MHC multimer constructs were made:

PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the peptide VTEHDTLLY (SEQ ID NO 217783) derived from Human Cytomegalo Virus (HCMV).
PE conjugated 270 kDa dextran coupled with HLA-A*0101 in complex with beta2microglobulin and the negative control peptide IVDCLTEMY (SEQ ID NO 217784) derived from ubiquitin specific peptidase 9 (USP9).

Tubes with a matrix material to retain and immobilize the above described MHC multimer constructs together with antibodies relevant for later flow cytometer analysis were made. The matrix material was made to retain MHC multimer and antibody in the container when dry but release them into the sample medium when a sample containing cells of interest was added to the tube.

Experimentally, solutions of 20% Fructose in water and 20% Trehalose in water were made and mixed in a 1:1 ratio. 15 µl of this mixture were transferred to two 5 ml Falcon tubes. A premix of antibodies were made consisting of 40 µl anti-CD8 Alexa700 labelled antibody in a concentration of 25 µg/ml + 40 µl anti-CD3 Pacific Blue labelled antibody in a concentration of 100 µg/ml + 160 µl anti-CD45 Cascade Yellow labelled antibody in a concentration of 200 µg/ml. 12 µl of this mixture were added to each Falcon tube together with 3 µl of either of the two MHC multimer constructs. 100 µl butylated hydroxytoluen (BHT) with a concentration of 99 mg/L were added. The mixtures were dried under vacuum a 2-8°C over night. 100 µl EDTA stabilized blood from a donor with T cells specific for HLA-A*0101 complexed with the peptide VTEHDTLLY (SEQ ID NO 217783) were added to each of the two tubes. As a control experiment 6 µl of the antibody premix described above were transferred to two empty 5 ml Falcon tubes together with 3 µl of either of the MHC multimer constructs and 100 µl blood from the same donor. All four tubes were incubated for 15 minutes at room temperature. Then 900 µl PBS; pH = 7.2 was added and the sample analyzed on a CyAn ADP flowcytometer instrument.

A total of 20.000 CD8 positive cells were acquired for each sample. During analysis CD45/CY antibody was used to set a trigger discriminator to allow the flow cytometer to distinguish between red blood cells and stained white blood cells.

As expected and shown in figure 25 a population of CD8 positive and HLA-A*0101(VTEHDTLLY) (SEQ ID NO 217783) multimer positive cells were observed in the two samples stained with construct 1. The amount of specific T cells detected in the matrix sample was comparable to the amount of specific T cells detected in the control sample without matrix material. No HLA-A*0101(IVDCLTEMY) (SEQ ID NO 217784) multimer specific CD8 positive cells were observed in the two samples stained with the negative control MHC multimer construct 2.

This experiment demonstrates that the MHC multimer constructs used in this experiment can be embedded in a sugar matrix and later used for analysis of specific T cells in a blood sample and that this method gives results comparable to results obtained from a no-lyse no-wash staining procedure.

Example 69

This example describes an analysis of specific T cells in blood or other samples with cells in solution using MHC multimers where MHC multimers together with antibodies are pre-mixed and embedded in a matrix material to retain and immobilize the reagents prior to use. In this example the matrix is composed of Trehalose and Fructose and the MHC multimer is any MHC I, MHC II or MHC like molecule.

Tubes with a matrix material to retain and immobilize MHC multimer constructs together with antibodies relevant for later flow cytometer analysis are made. The matrix material is made to retain MHC multimer and antibody in the container when dry but release them into the sample medium when a sample containing cells of interest is added to the tube. The matrix is preferable water-soluble sugar mixtures but can be any contiguous mass releasing its components upon addition of aqueous solution. The matrix embedding medium can comprise one or more compounds including carbohydrates, polymers, small proteins etc. Examples of carbohydrates for use in the matrix include saccharose, arabinose, ribulose, fructose, sorbose, glucose, mannose,gulose, galactose, sucrose, lactose, maltose, trehalose, raffinose and melizitose. Examples of suitable polymers for use in matrix include polyvinyl alcohols, polyethylene glycols, polyethylene imines, polyacryl amides, polyaziridines, glycols, polyacrylic acids, esters or derivatives thereof. Examples of small proteins include BSA, other albumins or protein fragments.

The matrix-embedding medium is transferred to tubes preferable 5 ml tubes or other tubes usable in flow cytometry. Fluorochrome antibodies are added and here means any antibody useable for gating when analysing samples with T lymphocytes. Preferable antibodies are directed against CD8, CD4, CD3, CD45, CD27, CD28, CD45RA, CD45RO and CD62L. Then MHC multimer constructs are added but can also be added simultaneously with the antibodies or before the antibodies. Addition of MHC multimer is not restricted to one type of MHC multimer but several different MHC multimers can be added to the same tube and thereby embedded in the same matrix sample. Optionally scavengers for oxygen-derived radicals can be added. Examples of such radical scavengers are ascorbic acid, beta-carotene, bilirubin, butylated hydroxytoluene, butylated hydroxyanisol, tert-butylhydroquinone, d-alpha-tocopherol, trolox and hydroxyanisol. The matrix mixtures are then dried under vacuum a 2-8°C over night.

Cell samples in solution are added to the dry or semidry matrix tubes. Cell samples here means any sample containing specific T cells. That is preferable whole blood, homogenized spleen, lymph nodes, tumors or similar or purified lymphocytes from any of the above. The samples are incubated at room temperature for 1minute to 2 hours, preferable 10-30 minutes. They can also be incubated at 4°C or 37°C or any temperature in between those two. The samples are analyzed on a flowcytometry instrument.

As an alternative to the above described method MHC multimers can be added to the sample after addition of cell sample thereby only embedding antibodies and not MHC multimer in the matrix. Similarly only MHC multimer are embedded in the matrix and antibodies added after addition of cell sample.

For enumeration of specific T cells in the samples counting beads can be embedded in the matrix medium. The beads are then added before, together with or after adding antibodies and MHC multimer. Alternatively counting beads are added following incubation with cell sample. The exact amount of specific T cells are determined as described elsewhere herein.

Example 70

This is an example of how to make and use MHC multimers where the multimerization domain is dextran and the MHC complexs are chemically conjugated to the dextran multimerization domain.

MHC complexs consisting of HLA-A*0201 heavy chain, beta2microglobulin and NLVPMVATV (SEQ ID NO 217779) peptide or the negative control peptide GLAGDVSAV (SEQ ID NO 217778) are generated as described elsewhere herein. Dextran with a molecular weight of 270 kDa is activated with divinylsulfone. Activated Dextran is then incubated with MHC and RPE in a 0.05 M $NaCHO_3$ buffer; pH = 9.5 with a molar ratio between MHC and Dextran of 30-60 and a molar ratio between RPE and dextran of 3-7 :1 The mixture is placed in a water bath at 30°C for 16 hours. Excess flourochrome, MHC and dextran are removed by FPLC using a sephacryl S-300 column.

These MHC/RPE dextramers are then used to stain CMV specific T cells in a flow Cytometry experiment. Briefly, $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV) (SEQ ID NO 217779) are incubated with 10 µl of each

of the two HLA-A*0201(peptide)/RPE constructs described above for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. 10 µl mouse-anti-human CD8/PB antibody (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells are then resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a flow cytometer.

Example 71

This is an example of how to make and use MHC multimers where the multimerization domain is dextran and MHC complexs are MHC I molecules chemically conjugated to dextran multimerization domain and the dextran multimerization domain also have fluorochrome chemically coupled.

Human beta2microglobulin is coupled to dextran as follows. Dextran with a molecular weight of 270 kDa is activated with divinylsulfone. Activated dextran is incubated with human beta2microglobulin and RPE in a 0.05 M $NaCHO_3$ buffer; pH = 9.5 with a molar ratio between beta2microglobulin and Dextran of 30-60 and a molar ratio between RPE and dextran of 3-7:1. The molar ratio of the final product is preferable 4-6 RPE and 15-24 beta2microglobulin per dextran. The mixture is placed in a water bath at 30°C for 16 hours. Excess flourochrome, beta2microglobulin and dextran are removed by FPLC using a sephacryl S-300 column. The beta2microglobulin-RPE-dextran construct is then refolded in vitro together with heavy chain and peptide using the following procedure. 200 ml refolding buffer (100 mM Tris, 400 mM L-arginin-HCL, 2 mM NaEDTA, 0,5 mM oxidized Gluthathione, 5 mM reduced Glutathione, pH 8.0) supplied with protease inhibitors PMSF, Pepstatin A and Leupeptin (to a final concentration of 1 mM, 1 mg/l and 1 mg/l, respectively) is made and cooled to 10°C. 12 mg NLVPMVATV (SEQ ID NO 217779) peptide is dissolved in DMSO and added to the refolding buffer together with 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain. Incubation at 10°C for 4-8 hours, then 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain is added and incubation continued for 4-8 hours. Another 20-30 mg beta2microglobulin-RPE-dex and 6 mg HLA-A*0201 heavy chain is added and incubation continued for 6-8 hours. The folding reaction is filtrated through a 0,2 µm filter to remove larger aggregates and then buffer exchanged into a buffer containing 20 mM Tris-HCl, 50 nM NaCl; pH = 8.0 followed by concentration to 1-2 ml sample. Dextran-RPE-MHC complexs are then separated from excess heavy chain

and peptide by size exclusion chromatography using a sephacryl S-300, S-400 or sephacryl S-500 column.

These MHC/RPE dextramers can be used to stain CMV specific T cells in a flow Cytometry experiment. Briefly, $1x10^6$ purified HPBMC from a donor with T cells specific for HLA-A*0201(NLVPMVATV (SEQ ID NO 217779)) are incubated with 10 µl of each of the two HLA-A*0201(peptide)/RPE constructs described above for 10 minutes in the dark at room temperature with a cell concentration of $2x10^7$ cells/ml. 10 µl of mouse-anti-human CD8/PB antibody (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The cells are then resuspended in 400-500 µl PBS; pH=7.2 and analyzed on a flowcytometer.

Example 72

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. The MHC multimer used are MHC complexes coupled to labeled dextran.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of a patient infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein B conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes were then coupled to a 270 kDa dextran multimerization domain labelled with APC by interaction with streptavidin (SA) on the dextran multimerization domain. The dextran-APC-SA multimerization domain was generated as described elsewhere herein. MHC-peptide complexes were added in an amount corresponding to a ratio of three MHC-peptide molecules per SA molecule and each molecule dextran contained 3.7 SA

molecule and 8.95 molecules APC. The final concentration of dextran was 3.8x10e-8 M. The following MHC(peptide)/APC dextran constructs were made:

APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTDGTITV derived from OspB.
APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SITDDLNTI derived from OspB.
APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KIKDFVFLT derived from OspB
APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Osp B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with 10 μl of one of the MHC(peptide)/APC dextran constructs described above for 10 minutes in the dark at room temperature. 5 μl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 μl PBS; pH=7.2 and analyzed on flowcytometer.
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the MHC(peptide)/APC dextran constructs 1, 2 or 3 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with MHC(peptide)/APC dextran construct 4 should show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

Example 73

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. The MHC multimer used are MHC complexes coupled to the multimerisation domain Streptavidin (SA).

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of patients infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein B conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding, purified and biotinylated as described elsewhere herein. Biotinylated MHC-peptide complexes are then coupled SA labelled with APC. MHC-peptide complexes were added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes were purified from free SA, free monomeric MHC complex, SA carrying three, two and one MHC complexes.
The following SA- MHC(peptide)/APC tetramers are made:

APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTDGTITV derived from OspB.
APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SITDDLNTI derived from OspB.
APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KIKDFVFLT derived from OspB
APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Osp B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.

Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four SA- MHC(peptide)/APC tetramers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.

The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the SA-MHC(peptide)/APC tetramers 1, 2 or 3 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria. Blood analysed with SA- MHC(peptide)/APC tetramers 4 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC tetramer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

Example 74

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. The MHC multimer used MHC complexes coupled to any multimerisation as described elsewhere herein.
Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of a patient infected with Borrelia.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Outer surface protein B conserved among the three species Borrelia Burgdorferi, Borrelia Garinii and Borrelia Afzelii or a negative control peptide were generated by in vitro refolding and purified or

purified from antigen presenting cells. MHC-peptide complexes are then coupled to a multimerisation domain together with APC.
The following MHC(peptide)/APC multimers are made:

APC-multimerisation domian coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTDGTITV derived from OspB.
APC-multimerisation domian coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SITDDLNTI derived from OspB.
APC-multimerisation domian coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KIKDFVFLT derived from OspB
APC-multimerisation domian coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV (SEQ ID NO 217778).

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Osp B specific T cells in the blood from Borrelia infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with Lyme disease is isolated and 100 ul of this blood is incubated with either of the four MHC(peptide)/APC multimers described above for 10 minutes in the dark at room temperature. 5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added and the incubation continued for another 20 minutes at 4°C in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed. The washing step is repeated. The washed cells are resuspended in 400-500 µl PBS; pH=7.2 and analyzed on flowcytometer.
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and either of the MHC(peptide)/APC multimers 1, 2 or 3 described above and thereby the presence of Borrelia specific T cells will indicate that the patient are infected with Borrelia bacteria.
Blood analysed with MHC(peptide)/APC multimer 4 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC tetramer.

The sensitivity of the above described diagnostic test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

Example 75

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. This is an example of indirect detection of individual specific T cells by measurement of produced soluble factor.

The MHC multimer used are antigen presenting cells expressing MHC molecules complexed with peptides derived from Borrelia antigen.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of a patient infected with Borrelia.

Activated effector T cells can be detected directly, via their secretion of cytokines, when presented with specific antigens. In this example the activation of individual effector T cells is detected by measurement of cytokines secreted from each individual T cell by capturing of the secreted cytokines in the proximity of each cell. The effector T cells secrete specific cytokine in response to stimulation by peptides from the Borrelia antigen OspB when these peptides are presented by antigen presenting cells, briefly:

A patient's blood sample is collected ficoll purified using aVacutainer® Cell Preparation Tubes™, which are spun to separate white blood cells, known as peripheral blood mononuclear cells (PBMCs)

PBMCs are washed in culture media to remove any background interference, counted to correct for a patient's immune status, and added in even amounts to the wells of a 96-well microtiter plate. These plate wells are pre-coated with a monoclonal antibody specific for the cytokine INFγ released by effector T cells in response to contact with specific antigens presented on antigen presenting cells (e.g. B cells that are a population in the PBMC pool)

The peptides FLTDGTITV, SITDDLNTI and KIKDFVFLT all derived from OspB from Borrelia bacteria are added to the appropriate wells to stimulate cytokine release (positive and nil controls are used as internal assay controls). A negative control is a non-sense peptide unable to stimulate antigen-specific T cells.

The assay plate is placed in a CO_2 incubator overnight to allow the effector T cells to encounter the antigen.
The plates are washed, removing both the T cells and the antigen from the wells and leaving any T cell secreted cytokine captured by the antibodies lining the wells.
An enzyme-conjugated secondary antibody that binds to another epitope on the captured cytokine is then added and incubated for 1 hour at room temperature.
The plates are washed to remove unbound secondary antibody.
Coloured spots are generated by the conjugated enzyme upon application of a colorimetric substrate. These spots reveal a footprint of the antigen-specific effector T cells in the sample.
The spots are counted to determine the number of T cells in the sample that reacted to the antigen relative to the negative control, thereby identifying infection.

Example 76

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. This is an example of indirect detection of a population of specific T cells by measurement of produced soluble factor.
The MHC multimer used are antigen presenting cells expressing MHC molecules complexed with peptides derived from Borrelia antigen.
Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of a patient infected with Borrelia.

Activated effector T cells can be detected directly, via their secretion of cytokines, when presented with specific antigens. In this example the activation of a pool of effector T cells is detected by measurement of cytokines secreted from the activated T cells in the analysed sample. In this example the effector T cells secrete the cytokine INFγ in response to stimulation by peptides derived from the Borrelia antigen OspB when these peptides are presented by antigen presenting cells.

Briefly, the procedure is as follows: Blood is collected in a heparin-coontaining tube, then the sample is aliquotated into the wells of a microtiterplate. Appropriate wells are incubated with the peptides FLTDGTITV, SITDDLNTI and KIKDFVFLT all derived from OspB from Borrelia bacteria within 12 hours of blood collection. Mix on a shaker, incubate for a day-ish. The supernatant plasma, is transferred to wells of another microtiterplate in various dilutions. The wells of the microtiterplate are previously coated with antibody specific for INFγ. An IFN-gamma standard dilution series is included as positive control. Mix, incubate, wash six times. An enzyme-conjugated secondary antibody that binds to another epitope on the captured INF is then added and incubated for 1 hour at room temperature Add enzyme substrate solution, incubate, add enzyme stopping solution. The OD of each well is determined. The OD value may be correlated to the amount of INF-gamma in the sample which is a surrogate marker for the presence of activated Borrelia specific T cells in the sample. The presence of activated Borrelia specific T cells in the sample is a surrogate marker for infection

Example 77

This is an example of how MHC multimers may be used for diagnosis of Lyme Disease in blood samples from humans infected with Borrelia bacteria. The MHC multimer used are MHC complexes coupled to labeled dextran, where theMHC molecules are complexed with peptides derived from Borrelia antigen.

Lyme disease is caused by infection by Borrelia bacteria. During acute infection Borrelia specific activated T cells will be present in increased amounts in an activated state compared to healthy individuals. The presences of an increased amount of activated Borrelia specific T cells may thereby act as a surrogate marker for infection with Borrelia bacterium. MHC multimers carrying borrelia specific antigenic peptides is in this example used to detect the presence of Borrelia specific T cells in the blood of a patient infected with Borrelia.

Activated effector T cells can be detected directly, via their production of cytokines, when presented with specific antigens. In this example the activation of individual effector T cells is detected by measurement of the intracellular production of cytokines in individual T cell in response to stimulation by peptides from the Borrelia antigen OspB when these peptides are presented by antigen presenting cells.

Briefly, a patient's blood sample is collected ficoll purified using aVacutainer® Cell Preparation Tubes™, which are spun to separate white blood cells, known as peripheral blood mononuclear cells (PBMCs)

PBMCs are washed in culture media to remove any background interference, counted to correct for a patient's immune status, and added in even amounts to the wells of cell culture plate.

The peptides FLTDGTITV, SITDDLNTI and KIKDFVFLT all derived from OspB from Borrelia bacteria are added to the appropriate wells to stimulate cytokine release (positive and nil controls are used as internal assay controls). A negative control is a non-sense peptide unable to stimulate antigen-specific T cells.

The assay plate is placed in a CO_2 incubator overnight to allow the effector T cells to encounter the antigen.

T cells from each well of the plate is transferred to 12 x 75 mm polystyrene test tubes and then analysed by flow cytometry using a procedure allowing for intracellular staining:

5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added to each sample and incubatied for 20 minutes at room temperature in the dark. The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed.

5 µl of each of each of the antibodies mouse-anti-human CD3/PB (clone UCHT1 from Dako) and mouse-anti-human CD8/PE (clone DK25 from Dako) are added to each sample and incubatied for 20 minutes at room temperature in the dark.

The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed.

Fixative is added. Mix gently with a vortex mixer to ensure that the cells are in suspension.

Incubate in the dark at room temperature for 15 minutes.

The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and then aspirate the supernatant, leaving approximately 50 µL of fluid. Mix thoroughly to ensure that the cells are in suspension.

Permeabilization reagent is added, to each test tube. Add an appropriate volume of fluorochrome-conjugated antibody specific for the intracellular antigen to be stained. Mix gently to ensure that the cells are in suspension.

Incubate in the dark at room temperature for 15 minutes.

The samples are then washed by adding 2 ml PBS; pH =7.2 followed by centrifugation for 5 minutes at 200xg and the supernatant removed.
Resuspend the pellet in an appropriate fluid for flow cytometric analysis.
Analyze on a flow cytometer
The presence of cells labeled with anti-CD3/PB, anti-CD8/PE and the antibody used for intracellular staining are cells that have been activated by Borrelia antigens and are thereby Borrelia specific T cells. The presence of activated Borrelia specific T cells in the sample is a surrogate marker for infection.

The sensitivity of the above described diagnostic test may be enhanced by addition of flourochrome labeled MHC multimers able to measure antigen-specific T cells and/or by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Borrelia specific T cells.

Example 78

This is an example of a CTL killing assay.
T cell clones can be tested for specificity for a given borrelia derived antigenic peptide able to bind a given HLA molecule using a CTL killing assay. In this example expanded T cell clones are tested for specificity for the borrelia derived Outer surface protein C (OspC) by analysis in a standard 51-Cr release assay. For this purpose, T2 cells expressing HLA-A*0201 molecules on their surface are loaded with either TLVSSIDEL peptide derived from OspC and able to bind HLA-A*0201 (se figure 32) or an irrelevant peptide GLAGDVSAV and used as target cells. CD8 T-cell clones that effectively lyse T2 cells pulsed with TLVSSIDEL without killing of T2 cells pulsed with the irrelevant peptide GLAGDVSAV are T cell clones specific for the OspC derived epitope TLVSSIDEL. Clones that do not show specific lysis against T2 cells pulsed with TLVSSIDEL peptide are not specific for OspC.

Example 79

This is an example of a CTL killing assay.
T cell clones can be tested for specificity for a given borrelia derived antigenic peptide able to bind a given HLA molecule using a CTL killing assay. In this example expanded T cell clones are tested for specificity for any borrelia derived protein by analysis in a standard 51-Cr release assay. For this purpose, T2 cells expressing HLA-A*0201 or any other cell type expressing specific HLA molecules are loaded with either antigenic

peptides derived from borrelia proteins and able to bind HLA molecules in question or an irrelevant peptide and used as target cells. CD8 T-cell clones that effectively lyse T2 cells pulsed with antigenic peptides derived from borrelia proteins without killing of T2 cells pulsed with the irrelevant peptide are T cell clones specific for the tested borrelia protein. Clones that do not show specific lysis against T2 cells pulsed with borrelia derived antigenic peptide are not specific for OspC.

Example 80

This is an example of indirect detection of a population of T cells, where cells in suspension are induced to produce soluble factor. The soluble factor produced is a cytokine (IFN-γ) and is detected by a chromogen assay using anti-cytokine antibodies. The antigenic peptides origin is Borrelia bacteria.

Blood from patients suspected to have Borrelia infection are withdrawn and the presence of IFN-γ releasing T cells are detected as described in the following.

The procedure used in this example is a whole blood IFN-γ assay (QuantiFERON [QFT]; Cellestis, Carnegie, Australia) and involves two stages: (*1*) overnight incubation of whole blood with antigens and (*2*) measurement of IFN-γ production in harvested plasma samples by ELISA.

Briefly, the procedure is as follows:

Within 12 hours of collection, 1-ml aliquots of blood samples are dispensed into 24-well tissue culture plates and antigens are added to appropriate wells. Three drops of saline (nil control) or phytohemagglutinin (5 µg/ml; mitogen-positive control), and 100 µl of a peptide cocktail, are added to separate wells to give a final peptide concentration of 1 µg/ml. The peptide cocktail contain 10 antigenic peptides selected from the Borrelia antigen OspB. The 10 peptides are able to bind different HLA clas 2 molecules and have the following sequences:
KKYLLGFALVLALIA; DTVKLFNDTKIFISK; SKVFKKQGSLTEETE; TAVWSDTSNTLTVSA; ETYDSSNTKVASKVF; MKKYLLGFALVLALI; TKAVETLKNGIMLEG; KAVETLKNGIMLEGN; TLEYSDMTNDENATK and ITVQNYDTAGTKLAG (see figure 34).

Blood samples were incubated with antigens for 16 to 24 hours at 37°C before harvesting about 300 µl of plasma from above the settled blood cells.

The concentration of IFN-γ produced in the four plasma samples from each subject, as a result of stimulation of specific T cells with antigen presenting cells displaying the above listed peptides, is determined by QuantiFERON-CMI ELISA or another IFN-γ measuring ELISA assay following the manufacturer's instructions.

Samples from up to 16 subjects are tested in each ELISA run, which also included a set of standards that are measured in duplicate. For an ELISA run to be valid, strict performance criteria (coefficient of variation less than 15% and correlation coefficient for the standard curve greater than 0.98) had to be met. ELISA data for the *Borrelia*–specific antigen OspB and the nil and mitogen controls are converted to international units per milliliter on the basis of the IFN-γ standard curve generated for each ELISA plate. For an individual's test to be deemed valid, their response to at least one antigen (OspB or mitogen) has to be at least 0.25 IU of IFN-γ per milliliter above that of their nil control (five times the limit of detection for the ELISA). Results for OspB are expressed as the concentration of IFN-γ detected minus the concentration of IFN-γ in the respective nil control plasma.

The presence of IFN-γ in blood of the tested individual indicates the presence of activated T cells specific for one or more of the investigated peptide epitopes from the Borrelia antigen OspB tested and can be regarded as a surrogate marker for infection with Borrelia bacteria.

Example 81

This is an example of indirect detection of a population of T cells, where cells in suspension are induced to produce soluble factor. The soluble factor produced is a cytokine (IFN-γ) and is detected by a chromogen assay using anti-cytokine antibodies. The antigenic peptides origin is Borrelia bacteria.

Blood from patients suspected to have Borrelia infection are withdrawn and the presence of IFN-γ releasing T cells are detected as described in the following.

The procedure used in this example is a whole blood IFN-γ assay (QuantiFERON [QFT]; Cellestis, Carnegie, Australia) and involves two stages: (*1*) overnight incubation of whole blood with antigens and (*2*) measurement of IFN-γ production in harvested plasma samples by ELISA.

Briefly, the procedure is as follows:

Within 12 hours of collection, 1-ml aliquots of blood samples are dispensed into 24-well tissue culture plates and antigens are added to appropriate wells. Three drops of saline (nil control) or phytohemagglutinin (5 µg/ml; mitogen-positive control), and 100 µl of a peptide cocktail, are added to separate wells to give a final peptide concentration of 1 µg/ml. The peptide cocktail contain 10-20 antigenic peptides selected from one or more Borrelia antigen(s). The 10-20 peptides are able to bind different HLA class 1 and/or 2 molecules and have sequences selected from the lists of borrelia derived antigenic peptide sequences enclosed in this application.

Blood samples were incubated with antigens for 16 to 24 hours at 37°C before harvesting about 300 µl of plasma from above the settled blood cells.

The concentration of IFN-γ produced in the four plasma samples from each subject, as a result of stimulation of specific T cells with antigen presenting cells displaying the above listed peptides, is determined by QuantiFERON-CMI ELISA or another IFN-γ measuring ELISA assay following the manufacturer's instructions.

Samples from up to 16 subjects are tested in each ELISA run, which also included a set of standards that are measured in duplicate. For an ELISA run to be valid, strict performance criteria (coefficient of variation less than 15% and correlation coefficient for the standard curve greater than 0.98) had to be met. ELISA data for the *Borrelia*–specific antigen(s) and the nil and mitogen controls are converted to international units per milliliter on the basis of the IFN-γ standard curve generated for each ELISA plate. For an individual's test to be deemed valid, their response to at least one antigen (Borrelia antigen or mitogen) has to be at least 0.25 IU of IFN-γ per milliliter above that of their nil control (five times the limit of detection for the ELISA). Results for Borrelia antigen(s) are expressed as the concentration of IFN-γ detected minus the concentration of IFN-γ in the respective nil control plasma.

The presence of IFN-γ in blood of the tested individual indicates the presence of activated T cells specific for one or more of the investigated antigenic peptide epitopes from the Borrelia antigen(s) tested and can be regarded as a surrogate marker for infection with Borrelia bacteria.

Example 82

This is an example of indirect detection of a population of T cells, where cells in suspension are induced to produce soluble factor. The soluble factor produced is a cytokine (IFN-γ) and is detected by a chromogen assay using anti-cytokine antibodies. The antigenic peptides origin is Borrelia bacteria.

Blood from patients suspected to have Borrelia infection are withdrawn and the presence of IFN-γ releasing T cells are detected as described in the following.

The procedure used in this example is a whole blood IFN-γ assay (QuantiFERON [QFT]; Cellestis, Carnegie, Australia) and involves two stages: (*1*) overnight incubation of whole blood with antigens and (*2*) measurement of IFN-γ production in harvested plasma samples by ELISA.
Briefly, the procedure is as follows:
Within 12 hours of collection, 1-ml aliquots of blood samples are dispensed into 24-well tissue culture plates and antigens are added to appropriate wells. Three drops of saline (nil control) or phytohemagglutinin (5 µg/ml; mitogen-positive control), and 100 µl of a peptide cocktail, are added to separate wells to give a final peptide concentration of 1 µg/ml. The peptide cocktail contain 10-20 antigenic polypeptides selected from one or more Borrelia antigen(s). The 10-20 peptides comprises antigenic peptides able to bind different HLA class 1 and/or 2 molecules and these antigenic peptides have sequences selected from the lists of borrelia derived antigenic peptide sequences enclosed in this application.

Blood samples were incubated with antigens for 16 to 24 hours at 37°C before harvesting about 300 µl of plasma from above the settled blood cells.

The concentration of IFN-γ produced in the four plasma samples from each subject, as a result of stimulation of specific T cells with antigen presenting cells displaying the above listed peptides, is determined by QuantiFERON-CMI ELISA or another IFN-γ measuring ELISA assay following the manufacturer's instructions.

Samples from up to 16 subjects are tested in each ELISA run, which also included a set of standards that are measured in duplicate. For an ELISA run to be valid, strict performance criteria (coefficient of variation less than 15% and correlation coefficient for the standard curve greater than 0.98) had to be met. ELISA data for the *Borrelia*–specific antigen(s) and the nil and mitogen controls are converted to international units

per milliliter on the basis of the IFN-ɣ standard curve generated for each ELISA plate. For an individual's test to be deemed valid, their response to at least one antigen (Borrelia antigen or mitogen) has to be at least 0.25 IU of IFN-ɣ per milliliter above that of their nil control (five times the limit of detection for the ELISA). Results for Borrelia antigen(s) are expressed as the concentration of IFN-ɣ detected minus the concentration of IFN-ɣ in the respective nil control plasma.

The presence of IFN-ɣ in blood of the tested individual indicates the presence of activated T cells specific for one or more of the investigated antigenic polypeptide epitopes from the Borrelia antigen(s) tested and can be regarded as a surrogate marker for infection with Borrelia bacteria.

Example 83

This is an example of how borrelia derived antigenic polypeptides can be used for vaccination of Gerbils.

To ascertain whether cross-protection between different OspC families was possible, OspC proteins were purified from B. burgdorferi strain ZS7 (OspC family 1), B. afzelii strain PKO (OspC family 7) and B. garinii strain W (OspC family 10) and used as immunogens in the gerbil model of Lyme borreliosis against a challenge with B. afzelii strain Orth (OspC family 5). To test protection within a family, the OspC from strain H7 (OspC family 5) was used as an immunoqen against strain Orth. The OspC from strain H7 belongs to the same serovar and RFLP-type as the OspC from strain Orth.

Gerbils were given either a single, subcutaneous immunization of purified OspC (20 .mu.g protein/200 .mu.l, adjuvanted with TiterMax #R-1 (CytRx), that is, were prepared as a water-in-oil (squalene) emulsion with a synthetic immunomodulator (copolymer CRL89-41) or two intraperitoneal injections of OspC (10 .mu.g protein/500 .mu.l) adjuvanted with aluminium hydroxide. The purified antigens were prepared from strains by methods described in U.S. patent application Ser. No. 07/903,580, the contents of which were previously incorporated above by reference. Three and a half weeks after the first immunization, blood samples were taken from the eye and plasma prepared so that the antibody response to the immunogen at the time of the challenge could be ascertained (unimmunized control animals were likewise treated). Four weeks after the first immunization, the animals were challenged intraperitoneally with 10.sup.4 cells

(25-100 ID.sub.50) of strain Orth, as were a group of unimmunized control animals. The challenge suspension was also titrated in unimmunized gerbils to determine the dose required to infect 50% of the animals. After a further two weeks, the animals challenged with the 10.sup.4 dose were killed and the bladder, heart, kidneys and spleens cultured in BSK medium. Cultures were inspected for spirochetes at weekly intervals, from the second to the sixth week post-inoculation, by dark-field microscopy. Blood also was taken and the resultant plasma analyzed by western blotting for sero-conversion, i.e. the development of antibodies post-challenge to antigens from strain Orth other than the immunogen. There was good agreement between the cultural and serological tests used to ascertain which animals were infected. Only serological testing was used for the ID(50) determinations but in this instance the animals were bled three weeks post-challenge, the extra time being given to ensure that the antibody response in infected gerbils was sufficiently strong to be easily detected.

There were no signs of cross-protection between species i.e. OspC proteins from OspC families 1 (B. burgdorferi) and (B. garinii) were ineffective as immunogens against the challenge strain Orth (B. afzelii). Likewise there was no sign of cross-protection between different OspC families of the same species i.e. the OspC protein from an OspC family 7 isolate (B. afzelii strain PKO) was ineffective as an immunogen against a challenge with strain Orth which expresses an OspC protein from OspC family 5. By contrast, immunization with the OspC protein from strain H7 (OspC family 5) was effective against a challenge strain Orth (OspC family 5). These data indicate that cross-protection between the OspC families is unlikely and that protection within a family is possible. A multivalent vaccine comprising one or more types of OspC proteins from each of the OspC families should be sufficient to protect against most Lyme disease Borrelia strains.

This example is modified from patent WO94/25596.

Example 84

This is an example of how a borrelia derived antigenic polypeptide can be used for vaccination of Gerbils.

In this example the antigenic polypeptide is the first 86 amino acids of the Borrelia Outer surface protein G (OspG). The amino acids sequences used is

MNKKMKNLIICAVFVLIISCKIDASSEDLKQNVKEKVEGFLDKELMQGDDPNNSLFNPP

PVLPASSHDNTPVLKAVQAKDGGQQEG and is derived from Borrelia burgdorferi strain ZS7. Genes encoding the antigenic polypeptide with this sequence are synthesized e.g. using Gene Assembler™ gene synthesis platform (made by GeneArt) and cloned into a suitable expression vector. Then this plasmid is transformed into E.coli, expressed and purified using standard procedures known by persons skilled in the art.

This OspG(1-86) antigenic polypeptide are used as immunogens in the gerbil model of Lyme borreliosis against a challenge with Borrelia burgdorferi.

Gerbils were given either a single, subcutaneous immunization of purified OspG(1-86) (20 .mu.g protein/200 .mu.l, adjuvanted with TiterMax #R-1 (CytRx), that is, were prepared as a water-in-oil (squalene) emulsion with a synthetic immunomodulator (copolymer CRL89-41) or two intraperitoneal injections of OspG(1-86) (10 .mu.g protein/500 .mu.l) adjuvanted with aluminium hydroxide.

Three and a half weeks after the first immunization, blood samples are taken from the eye and plasma prepared so that the antibody response to the immunogen at the time of the challenge can be ascertained (unimmunized control animals were likewise treated). Four weeks after the first immunization, the animals are challenged intraperitoneally with 10.sup.4 cells (25-100 ID.sub.50) of a Borreli burgdorferi strain (e.g. ZS7 or B31). The challenge suspension is also titrated in unimmunized gerbils to determine the dose required to infect 50% of the animals. After a further two weeks, the animals challenged with the 10.sup.4 dose are killed and the bladder, heart, kidneys and spleens cultured in BSK medium. Cultures are inspected for spirochetes at weekly intervals, from the second to the sixth week post-inoculation, by dark-field microscopy. Only serological testing was used for the ID(50) determinations but in this instance the animals are bled three weeks post-challenge, the extra time being given to ensure that the antibody response in infected gerbils is sufficiently strong to be easily detected.

It is expected that vaccination with the OspG(1-86) protein is effective against a challenge strain ZS7 and may also be effective against challenge with other strains since these strains have homologous sequences of the first 86 amino acids of the OspG proteins.

Example 85

This is an example of how several borrelia derived antigenic polypeptide can be used for vaccination of Gerbils.

In this example 10 different antigenic polypeptides with sequences derived from 1-10 different borrelia proteins are used to generate a vaccine against Lyme disease. Each sequence is selected to be homologous among many Borrelia species and strains. Genes encoding the antigenic polypeptides with these sequences are synthesized e.g. using Gene Assembler™ gene synthesis platform (made by GeneArt) and cloned into a suitable expression vectors. Then these plasmids are transformed into *E.coli*, expressed and purified using standard procedures known by persons skilled in the art. The antigenic polypeptides are used as immunogens in the gerbil model of Lyme borreliosis against a challenge with Borrelia burgdorferi, Borrelia Garinii and/or Borrelia afzelii.

Gerbils were given either a single, subcutaneous immunization of purified antigenic polypeptides (each 20 .mu.g protein/200 .mu.l, adjuvanted with TiterMax #R-1 (CytRx), that is, were prepared as a water-in-oil (squalene) emulsion with a synthetic immunomodulator (copolymer CRL89-41) or two intraperitoneal injections of antigenic polypeptide (each 10 .mu.g protein/500 .mu.l) adjuvanted with aluminium hydroxide. Three and a half weeks after the first immunization, blood samples are taken from the eye and plasma prepared so that the antibody response to the immunogen at the time of the challenge can be ascertained (unimmunized control animals were likewise treated). Four weeks after the first immunization, the animals are challenged intraperitoneally with 10.sup.4 cells (25-100 ID.sub.50) of a Borreli burgdorferi, Borrelia Garinii and/or Borrelia afzelii strain(s). The challenge suspension is also titrated in unimmunized gerbils to determine the dose required to infect 50% of the animals. After a further two weeks, the animals challenged with the 10.sup.4 dose are killed and the bladder, heart, kidneys and spleens cultured in BSK medium. Cultures are inspected for spirochetes at weekly intervals, from the second to the sixth week post-inoculation, by dark-field microscopy.

Only serological testing was used for the ID(50) determinations but in this instance the animals are bled three weeks post-challenge, the extra time being given to ensure that the antibody response in infected gerbils is sufficiently strong to be easily detected.

It is expected that vaccination with these antigenic polypeptides are effective against a challenge a wide range of Borrelia species and strain since these strains have homologous sequences of the amino acid sequence of the selected antigenic polypeptides.

A multivalent vaccine comprising one or more types of Borrelia derived proteins s should be sufficient to protect against most Lyme disease Borrelia strains. In general antigenic polypeptides comprising one/or more antigenic peptides sequence(s) as described herein can be used.

Example 86

This is an example of how several borrelia derived antigenic polypeptide can be used for vaccination of humans against Lyme disease.

In this example 10-20 different antigenic polypeptides with sequences derived from 1-20 different borrelia proteins are used to generate a vaccine against Lyme disease. Each sequence is selected to be homologous among many Borrelia species and strains.

Genes encoding the antigenic polypeptides with these sequences are synthesized , expressed and produced.

The antigenic polypeptides are used as vaccine components in humans

To protect against Borrelia burgdorferi, Borrelia Garinii and/or Borrelia afzelii strains.

The antigenic polypeptides are given in dosis suitable for humans and together with an adjuvant usefull in humans. The vaccine is given either as a single dose or as multiple dosis.

It is expected that vaccination with these antigenic polypeptides are effective against a challenge a wide range of Borrelia species and strain since these strains have homologous sequences of the amino acid sequence of the selected antigenic polypeptides.

A multivalent vaccine comprising one or more types of Borrelia derived proteins s should be sufficient to protect humans against most Lyme disease Borrelia strains. In general antigenic polypeptides comprising one/or more Borrelia derived antigenic peptide sequences as described in the present application can be used.

Example 87

This is an example of how several borrelia derived antigenic peptides can be used for vaccination of humans against Lyme disease.

In this example 10-20 different antigenic peptides with sequences derived from 1-20 different borrelia proteins are used to generate a vaccine against Lyme disease. Each sequence is selected to be homologous among many Borrelia species and strains.

Genes encoding the antigenic peptides with these sequences are synthesized , expressed and produced.
The antigenic peptides are used as vaccine components in humans
To protect against Borrelia burgdorferi, Borrelia Garinii and/or Borrelia afzelii strains.

The antigenic peptides are given in dosis suitable for humans and together with an adjuvant usefull in humans. The vaccine is given either as a single dose or as multiple dosis.
It is expected that vaccination with these antigenic peptides are effective against a challenge a wide range of Borrelia species and strain since these strains have homologous sequences of the amino acid sequence of the selected antigenic peptides. A multivalent vaccine comprising one or more types of Borrelia derived proteins s should be sufficient to protect humans against most Lyme disease Borrelia strains. In general any antigenic peptides comprising Borrelia derived amino acid sequences as described in the present application can be used.

Example 88

This is an example of how MHC multimers can be used as a borrelia vaccine for monkeys.
The vaccine is composed of a Dextran (270 kDa) carrier that has been derivatized by attaching Strepavidin (on average 8.6 Strepavidin molecules/Dextran molecule). Attached to the carrier are human HLA class 1 and 2 molecules containing antigenic peptides derived from the Borrelia antigen Basic membrane protein A (BmpA). The attached HLA-peptide complexes are:

HLA-A*0201(YLAPDNVIT), HLA-A*0101(YSDEIDIIH), HLA-B*0702(APDNVITST), HLA-DRB1*0401(IELVLKESSSNSYLS), HLA-BRB1*1501(MNKILLLILLESIVF) and HLA-DRB1*1101(SDLIWLIGYRFSDVA).

A single full dose of the final vaccine corresponds to, 100 µg of each MHC class 1; 113,5 □g of HLA class 2; 3x25.8 µg HSP70 and 3x162.2 µg dextran (corresponding to a total of approx 300 µg MHC multimer/kg body weight for a monkey of 3.5 kg) and consist of a 1:1:1 mixture of the following three MHC multimers:

MHC multimer 1:
HLA-A*0101(YSDEIDIIH) + HLA-DR*0401(IELVLKESSSNSYLS) +
HSP70 + Dextran carrier, in the molar ratio10/10/4/1

MHC multimer 2:
HLA-A*0201(YLAPDNVIT) + HLA-DR*1501(MNKILLLILLESIVF) +
HSP70 + Dextran carrier, in the molar ratio10/10/4/1

MHC multimer 2:
HLA-B*0702(APDNVITST) + HLA-DRB1*1101(SDLIWLIGYRFSDVA) +
HSP70 + Dextran carrier, in the molar ratio10/10/4/1

Administration:
The MHC multimer mix is emulsified with the adjuvant Titermax Gold as specified by the
manufacturer and administered as intramuscular injections at time points 0, 4, 8, and 16 weeks such that a full dose is given at 0 weeks and half-full dose at 4, 8, and 16 5 weeks. This vaccine may give protection against infection with Borrelia bacteria.

Example 89

This is an example of how MHC multimers can be used as a borrelia vaccine for monkeys.
The vaccine is composed of an antigen presenting cell (APC) e.g. a Dendritic cell expressing the HLA class 1 molecules HLA-A*0101 and HLA-B*0702. The APC is loaded with antigenic peptides derived from the Borrelia protein Basic membrane protein A (BmpA) by incubation with the peptides for 2-5 hours at 37ºC. The amino acid sequence of the peptides are YSDEIDIIH and APDNVITST (se figure 32).

Administration:
The peptide loaded APC are added the adjuvant Titermax Gold as specified by the manufacturer and administered as intramuscular injections at time points 0, 4, 8, and 16 weeks. This vaccine may give protection against infection with Borrelia bacteria.

Claims

1. An antigenic peptide, P, an antigenic polypeptide, a MHC monomer or a MHC multimer ,

wherein said MHC monomer comprise a-b-P, or wherein said MHC multimer comprises$(a\text{-}b\text{-}P)_n$, wherein $n > 1$,

wherein the polypeptides a and b together form a functional MHC protein capable of binding the peptide P,

wherein (a-b-P) is the MHC-peptide complex formed when the peptide P binds to the functional MHC protein,

wherein each MHC peptide complex of a MHC multimer is associated with one or more multimerization domains,

2. The MHC multimer according to claim 1, wherein the association is a covalent linkage so that one or more of the n MHC-peptide complexes is covalently linked to the one or more multimerization domains.

3. The MHC multimer according to claim 1, wherein the association is a non-covalent association so that one or more of the n MHC-peptide complexes is non-covalently associated with the one or more multimerization domains.

4. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more scaffolds.

5. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more carriers.

6. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises at least one scaffold and at least one carrier.

7. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprise one or more optionally substituted organic molecules.

8. The MHC multimer according to claim 7, wherein the optionally substituted organic molecule comprises one or more functionalized cyclic structures.

9. The MHC multimer according to claim 8, wherein the one or more functionalized cyclic structures comprises one or more benzene rings.

10. The MHC multimer according to claim 7, wherein the optionally substituted organic molecule comprises a scaffold molecule comprising at least three reactive groups, or at least three sites suitable for non-covalent attachment.

11. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more biological cells and/or cell-like structures, such as antigen presenting cells or dendritic cells.

12. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more membranes.

13. The MHC multimer according to claim 12, wherein the one or more membranes comprises liposomes or micelles.

14. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more polymers such as one or more synthetic polymers.

15. The MHC multimer according to claim 14, wherein the one or more polymers are selected from the group consisting of polysaccharides.

16. The MHC multimer according to claim 15, wherein the polysaccharide comprises one or more dextran moieties.

17. The MHC multimer according to claim 16, wherein the one or more dextran moieties are covalently attached to one or more MHC peptide complexes.

18. The MHC multimer according to claim 16, wherein the one or more dextran moieties are non-covalently attached to one or more MHC peptide complexes.

19. The MHC multimer according to claim 16, wherein the one or more dextran moieties are modified.

20. The MHC multimer according to claim 16, wherein the one or more dextran moieties comprises one or more Amino-dextrans.

21. The MHC multimer according to claim 16, wherein the one or more dextran moieties comprises one or more Amino-dextrans modified with divinyl sulfone.

22. The MHC multimer according to claim 16, wherein the one or more dextran moieties comprises one or more dextrans with a molecular weight of from 1,000 to 50,000, such as from 1,000 to 5,000, for example 5,000 to 10,000, such as from 10,000 to 15,000, for example 15,000 to 20,000, such as from 20,000 to 25,000, for example 25,000 to 30,000, such as from 30,000 to 35,000, for example 35,000 to 40,000, such as from 40,000 to 45,000, for example 45,000 to 50,000, including any consecutive combination of the afore-mentioned ranges.

23. The MHC multimer according to claim 16, wherein the one or more dextran moieties comprises one or more dextrans with a molecular weight of from 50,000 to 150,000, such as from 50,000 to 60,000, for example 60,000 to 70,000, such as from 70,000 to 80,000, for example 80,000 to 90,000, such as from 90,000 to 100,000, for example 100,000 to 110,000, such as from 110,000 to 120,000, for example 120,000 to 130,000, such as from 130,000 to 140,000, for example 140,000 to 150,000, including any consecutive combination of the afore-mentioned ranges.

24. The MHC multimer according to claim 16, wherein the one or more dextran moieties comprises one or more dextrans with a molecular weight of from 150,000-270,000 such as from 150,000 to 160,000, for example 160,000 to 170,000, such as from 170,000 to 180,000, for example 180,000 to 190,000, such as from 190,000 to 200,000, for example 200,000 to 210,000, such as from 210,000 to 220,000, for example 220,000 to 230,000, such as from 230,000 to 240,000, for example 240,000 to 250,000, such as from 250,000 to 260,000, for example 260,000 to 270,000, such as from 270,000 to 280,000, for example 280,000 to 290,000, such as from 290,000 to 300,000, for example 300,000 to 310,000 such as from 310,000 to 320,000, for

example 320,000 to 330,000 such as from 330,000 to 340,000, for example 340,000 to 350,000 such as from 350,000 to 360,000, for example 360,000 to 370,000 such as from 370,000 to 380,000, for example 380,000 to 390,000, such as from 390,000 to 400,000, including any consecutive combination of the afore-mentioned ranges.

25. The MHC multimer according to claim 16, wherein the one or more dextran moieties are linear.

26. The MHC multimer according to claim 16, wherein the one or more dextran moieties are branched.

27. The MHC multimer according to claim 14, wherein the one or more synthetic polymers are selected from the group consisting of PNA, polyamide and PEG.

28. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more entities selected from the group consisting of an IgG domain, a coiled-coil polypeptide structure, a DNA duplex, a nucleic acid duplex, PNA-PNA, PNA-DNA, DNA-RNA.

29. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises one or more avidins, such as one or more streptavidins.

30. The MHC multimer according to claim 29, wherein the one or more streptavidins comprises one or more tetrameric streptavidin variants.

31. The MHC multimer according to claim 29, wherein the one or more streptavidins comprises one or more monomeric streptavidin variants.

32. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises an antibody.

33. The MHC multimer according to claim 32, wherein the antibody is selected from the group consisting of polyclonal antibody, monoclonal antibody, IgA, IgG, IgM, IgD, IgE, IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM1, IgM2, humanized antibody, humanized monoclonal antibody, chimeric antibody, mouse antibody, rat antibody,

rabbit antibody, human antibody, camel antibody, sheep antibody, engineered human antibody, epitope-focused antibody, agonist antibody, antagonist antibody, neutralizing antibody, naturally-occurring antibody, isolated antibody, monovalent antibody, bispecific antibody, trispecific antibody, multispecific antibody, heteroconjugate antibody, immunoconjugates, immunoliposomes, labeled antibody, antibody fragment, domain antibody, nanobody, minibody, maxibody, diabody, fusion antibody.

34. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more small organic scaffold molecules.

35. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more small organic molecules.

36. The MHC multimer according to claim 35, wherein the one or more small organic molecules comprises one or more steroids.

37. The MHC multimer according to claim 35, wherein the one or more small organic molecules comprises one or more peptides.

38. The MHC multimer according to claim 35, wherein the one or more small organic molecules comprises one or more aromatic organic molecules.

39. The MHC multimer according to claim 38, wherein the one or more aromatic organic molecules comprises one or more monocyclic structures.

40. The MHC multimer according to claim 39, wherein the one or more monocyclic structures comprises one or more optionally functionalized or substituted benzene rings.

41. The MHC multimer according to claim 38, wherein the one or more aromatic organic molecules comprises one or more dicyclic structures.

42. The MHC multimer according to claim 38, wherein the one or more aromatic organic molecules comprises one or more polycyclic structures.

43. The MHC multimer according to claim 35, wherein the one or more small organic molecules comprises one or more aliphatic molecules.

44. The MHC multimer according to claim 43, wherein the one or more aliphatic molecules comprises one or more monocyclic molecules.

45. The MHC multimer according to claim 43, wherein the one or more aliphatic molecules comprises one or more dicyclic molecules.

46. The MHC multimer according to claim 43, wherein the one or more aliphatic molecules comprises one or more polycyclic molecules.

47. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more monomeric molecules able to polymerize.

48. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more biological polymers such as one or more proteins.

49. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more small molecule scaffolds.

50. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more supramolecular structure(s) such as one or more nanoclusters.

51. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more further polypeptides in addition to a and b.

52. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more protein complexes.

53. The MHC multimer according to claim 1, wherein the MHC multimer comprises one or more beads.

54. The MHC multimer according to claim 53, wherein the one or more beads can be selected from the groups consisting of beads that carry electrophilic groups e.g. divinyl sulfone activated polysaccharide, polystyrene beads that have been functionalized with tosyl-activated esters, magnetic polystyrene beads functionalized with tosyl-activated esters, and beads where MHC complexes have been covalently immobilized to these by reaction of nucleophiles comprised within the MHC complex with the electrophiles of the beads.

55. The MHC multimer according to claim 53, wherein the one or more beads can be selected from the groups consisting of sepharose beads, sephacryl beads, polystyrene beads, agarose beads, polysaccharide beads, polycarbamate beads and any other kind of beads that can be suspended in an aqueous buffer.

56. The MHC multimer according to claim 1, wherein the multimerization domain comprises one or more compounds selected from the group consisting of agarose, sepharose, resin beads, glass beads, pore-glass beads, glass particles coated with a hydrophobic polymer, chitosan-coated beads, SH beads, latex beads ,spherical latex beads, allele-type beads, SPA bead, PEG-based resins, PEG-coated bead, PEG-encapsulated bead, polystyrene beads, magnetic polystyrene beads, glutathione agarose beads, magnetic bead, paramagnetic beads, protein A and/or protein G sepharose beads, activated carboxylic acid bead, macroscopic beads, microscopic beads, insoluble resin beads, silica-based resins, cellulosic resins, cross-linked agarose beads, polystyrene beads, cross-linked polyacrylamide resins, beads with iron cores, metal beads, dynabeads, Polymethylmethacrylate beads activated with NHS, streptavidin-agarose beads, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, nitrocellulose, polyacrylamides, gabbros, magnetite, polymers, oligomers, non-repeating moieties, polyethylene glycol (PEG), monomethoxy-PEG, mono-(C_1-C_{10})alkoxy-PEG, aryloxy-PEG, poly-(N-vinyl pyrrolidone)PEG, tresyl monomethoxy PEG, PEG propionaldehyde, bis-succinimidyl carbonate PEG, polystyrene bead crosslinked with divinylbenzene, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, dextran, aminodextran, carbohydrate-based polymers, cross-linked dextran beads, polysaccharide beads, polycarbamate beads, divinyl sulfone activated polysaccharide, polystyrene beads that have been functionalized with tosyl-activated esters, magnetic polystyrene beads functionalized

with tosyl-activated esters, streptavidin beads, streptaivdin-monomer coated beads, streptaivdin-tetramer coated beads, Streptavidin Coated Compel Magnetic beads, avidin coated beads, dextramer coated beads, divinyl sulfone-activated dextran, Carboxylate-modified bead, amine-modified beads, antibody coated beads, cellulose beads, grafted co-poly beads, poly-acrylamide beads, dimethylacrylamide beads optionally crosslinked with N-N'-bis-acryloylethylenediamine, hollow fiber membranes, fluorescent beads, collagen-agarose beads, gelatin beads, collagen-gelatin beads, collagen-fibronectin-gelatin beads, collagen beads, chitosan beads, collagen-chitosan beads, protein-based beads, hydrogel beads, hemicellulose, alkyl cellulose, hydroxyalkyl cellulose, carboxymethylcellulose, sulfoethylcellulose, starch, xylan, amylopectine, chondroitin, hyarulonate, heparin, guar, xanthan, mannan, galactomannan, chitin and chitosan.

57. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a dimerization domain.

58. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a trimerization domain.

59. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a tetramerization domain.

60. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a pentamerization domain.

61. The MHC multimer according to claim 60, wherein the pentamerization domain comprises a coiled-coil polypeptide structure.

62. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a hexamerization domain.

63. The MHC multimer according to claim 62, wherein the hexamerization domain comprises three IgG domains.

64. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a polymer structure to which is attached one or more scaffolds.

65. The MHC multimer according to claim 64, wherein the polymer structure comprises a polysaccharide.

66. The MHC multimer according to claim 65, wherein the polysaccharide comprises one or more dextran moieties.

67. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a polyamide and/or a polyethylene glycol and/or a polysaccharide and/or a sepharose.

68. The MHC multimer according to claim 1, wherein the one or more multimerization domains comprises a carboxy methyl dextran and/or a dextran polyaldehyde and/or a carboxymethyl dextran lactone and/or a cyclodextrin.

69. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of less than 1,000 Da.

70. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of from 1,000 Da to preferably less than 10,000 Da.

71. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of from 10,000 Da to preferably less than 100,000 Da.

72. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of from 100,000 Da to preferably less than 1,000,000 Da.

73. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of more than 1,000,000 Da.

74. The MHC multimer according to claim 1, wherein the one or more multimerization domains have a molecular weight of from 50,000 Da to preferably less than 1,000,000 Da, such as from 50,000 Da to 980,000; for example from 50,000 Da to 960,000; such as from 50,000 Da to 940,000; for example from 50,000 Da to 920,000; such as from 50,000 Da to 900,000; for example from 50,000 Da to 880,000; such as from 50,000 Da to 860,000; for example from 50,000 Da to 840,000; such as from 50,000 Da to 820,000; for example from 50,000 Da to 800,000; such as from 50,000 Da to 780,000; for example from 50,000 Da to 760,000; such as from 50,000 Da to 740,000; for example from 50,000 Da to 720,000; such as from 50,000 Da to 700,000; for example from 50,000 Da to 680,000; such as from 50,000 Da to 660,000; for example from 50,000 Da to 640,000; such as from 50,000 Da to 620,000; for example from 50,000 Da to 600,000; such as from 50,000 Da to 580,000; for example from 50,000 Da to 560,000; such as from 50,000 Da to 540,000; for example from 50,000 Da to 520,000; such as from 50,000 Da to 500,000; for example from 50,000 Da to 480,000; such as from 50,000 Da to 460,000; for example from 50,000 Da to 440,000; such as from 50,000 Da to 420,000; for example from 50,000 Da to 400,000; such as from 50,000 Da to 380,000; for example from 50,000 Da to 360,000; such as from 50,000 Da to 340,000; for example from 50,000 Da to 320,000; such as from 50,000 Da to 300,000; for example from 50,000 Da to 280,000; such as from 50,000 Da to 260,000; for example from 50,000 Da to 240,000; such as from 50,000 Da to 220,000; for example from 50,000 Da to 200,000; such as from 50,000 Da to 180,000; for example from 50,000 Da to 160,000; such as from 50,000 Da to 140,000; for example from 50,000 Da to 120,000; such as from 50,000 Da to 100,000; for example from 50,000 Da to 80,000; such as from 50,000 Da to 60,000; for example from 100,000 Da to 1,000,000; such as from 100,000 Da to 980,000; for example from 100,000 Da to 960,000; such as from 100,000 Da to 940,000; for example from 100,000 Da to 920,000; such as from 100,000 Da to 900,000; for example from 100,000 Da to 880,000; such as from 100,000 Da to 860,000; for example from 100,000 Da to 840,000; such as from 100,000 Da to 820,000; for example from 100,000 Da to 800,000; such as from 100,000 Da to 780,000; for example from 100,000 Da to 760,000; such as from 100,000 Da to 740,000; for example from 100,000 Da to 720,000; such as from 100,000 Da to 700,000; for example from 100,000 Da to 680,000; such as from 100,000 Da to 660,000; for example from 100,000 Da to 640,000; such as from

100,000 Da to 620,000; for example from 100,000 Da to 600,000; such as from 100,000 Da to 580,000; for example from 100,000 Da to 560,000; such as from 100,000 Da to 540,000; for example from 100,000 Da to 520,000; such as from 100,000 Da to 500,000; for example from 100,000 Da to 480,000; such as from 100,000 Da to 460,000; for example from 100,000 Da to 440,000; such as from 100,000 Da to 420,000; for example from 100,000 Da to 400,000; such as from 100,000 Da to 380,000; for example from 100,000 Da to 360,000; such as from 100,000 Da to 340,000; for example from 100,000 Da to 320,000; such as from 100,000 Da to 300,000; for example from 100,000 Da to 280,000; such as from 100,000 Da to 260,000; for example from 100,000 Da to 240,000; such as from 100,000 Da to 220,000; for example from 100,000 Da to 200,000; such as from 100,000 Da to 180,000; for example from 100,000 Da to 160,000; such as from 100,000 Da to 140,000; for example from 100,000 Da to 120,000; such as from 150,000 Da to 1,000,000; for example from 150,000 Da to 960,000; such as from 150,000 Da to 940,000; for example from 150,000 Da to 920,000; such as from 150,000 Da to 900,000; for example from 150,000 Da to 880,000; such as from 150,000 Da to 860,000; for example from 150,000 Da to 840,000; such as from 150,000 Da to 820,000; for example from 150,000 Da to 800,000; such as from 150,000 Da to 780,000; for example from 150,000 Da to 760,000; such as from 150,000 Da to 740,000; for example from 150,000 Da to 720,000; such as from 150,000 Da to 700,000; for example from 150,000 Da to 680,000; such as from 150,000 Da to 660,000; for example from 150,000 Da to 640,000; such as from 150,000 Da to 620,000; for example from 150,000 Da to 600,000; such as from 150,000 Da to 580,000; for example from 150,000 Da to 560,000; such as from 150,000 Da to 540,000; for example from 150,000 Da to 520,000; such as from 150,000 Da to 500,000; for example from 150,000 Da to 480,000; such as from 150,000 Da to 460,000; for example from 150,000 Da to 440,000; such as from 150,000 Da to 420,000; for example from 150,000 Da to 400,000; such as from 150,000 Da to 380,000; for example from 150,000 Da to 360,000; such as from 150,000 Da to 340,000; for example from 150,000 Da to 320,000; such as from 150,000 Da to 300,000; for example from 150,000 Da to 280,000; such as from 150,000 Da to 260,000; for example from 150,000 Da to 240,000; such as from 150,000 Da to 220,000; for example from 150,000 Da to 200,000; such as from 150,000 Da to 180,000; for example from 150,000 Da to 160,000.

75. The MHC multimer according to claim 1 further comprising one or more scaffolds, carriers and/or linkers selected from the group consisting of streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-tranferase) glutathione affinity, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (Canavalia ensiformis) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity).

76. The MHC multimer according to claim 1, wherein n is 2.

77. The MHC multimer according to claim 1, wherein n is 3.

78. The MHC multimer according to claim 1, wherein n is 4.

79. The MHC multimer according to claim 1, wherein n is 5.

80. The MHC multimer according to claim 1, wherein n is 6.

81. The MHC multimer according to claim 1, wherein n is 7.

82. The MHC multimer according to claim 1, wherein n is 8.

83. The MHC multimer according to claim 1, wherein n is 9.

84. The MHC multimer according to claim 1, wherein n is 10.

85. The MHC multimer according to claim 1, wherein n is 11.

86. The MHC multimer according to claim 1, wherein n is 12.

87. The MHC multimer according to claim 1, wherein n ≥ 13.

88. The MHC multimer according to claim 1, wherein 1 < n ≥ 100.

89. The MHC multimer according to claim 1, wherein 1 < n ≥ 1000.

90. The MHC multimer according to claim 1, wherein n ≥ 1,000,000,000.

91. The MHC multimer according to claim 1, wherein n ≥ 1,000,000,000,000,000,000 (one trillion).

92. The MHC multimer according to any of claims 1 to 91, wherein n is selected from the group of integers consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900 and 1000.

93. The MHC multimer according to any of claims 1 to 91, wherein n has a value of from 1 to 1000, for example from 1 to 10, such as from 10 to 20, for example from 20 to 30, such as from 30 to 40, for example from 40 to 50, such as from 50 to 60, for example from 60 to 70, such as from 70 to 80, for example from 80 to 90, such as from 90 to 100, for example from 100 to 120, such as from 120 to 140, for example from 140 to 160, such as from 160 to 180, for example from 180 to 200, such as from 200 to 250, for example from 250 to 300, such as from 300 to 350, for example from 350 to 400, such as from 400 to 450, for example from 450 to 500, such as from 500 to 550, for example from 550 to 600, such as from 600 to 650, for example from 650 to 700, such as from 700 to 750, for example from 750 to 800, such as from 800 to 900, for example from 900 to 950, such as from 950 to 1000, including any consecutive combinations of the aforementioned ranges.

94. The MHC multimer according to claim 1, wherein a and/or b and/or P is of human origin.

95. The MHC multimer according to claim 1, wherein a and/or b and/or P is of mouse origin.

96. The MHC multimer according to claim 1, wherein a and/or b and/or P is of primate origin.

97. The MHC multimer according to claim 1, wherein a and/or b and/or P is of chimpansee origin.

98. The MHC multimer according to claim 1, wherein a and/or b and/or P is of gorilla origin.

99. The MHC multimer according to claim 1, wherein a and/or b and/or P is of orangutan origin.

100. The MHC multimer according to claim 1, wherein a and/or b and/or P is of monkey origin.

101. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Macaque origin.

102. The MHC multimer according to claim 1, wherein a and/or b and/or P is of porcine (swine/pig) origin.

103. The MHC multimer according to claim 1, wherein a and/or b and/or P is of bovine (cattle/antilopes) origin.

104. The MHC multimer according to claim 1, wherein a and/or b and/or P is of equine (horse) origin.

105. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Camelides (camels) origin.

106. The MHC multimer according to claim 1, wherein a and/or b and/or P is of ruminant origin.

107. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Canine (Dog) origin.

108. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Feline (Cat) origin.

109. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Bird origin.

110. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Chicken origin.

111. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Turkey origin.

112. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Fish origin.

113. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Reptile origin.

114. The MHC multimer according to claim 1, wherein a and/or b and/or P is of Amphibian origin.

115. The MHC multimer according to any of claims 1 to 114, wherein (a-b-P) is a class 1 MHC-peptide complex.

116. The MHC multimer according to any of claims 1 to 114, wherein (a-b-P) is a class 2 MHC-peptide complex.

117. The MHC multimer according to any of claims 1 to 116, wherein the MHC protein is the same or different MHC proteins selected from the group of HLA classes consisting of

A*01010101B*070201Cw*010201E*01010101F*01010101G*01010101,
A*01010102NB*070202Cw*010202E*01010102F*01010102G*01010102,
A*010102B*070203Cw*010203E*01010103F*01010103G*01010103,
A*010103B*070204Cw*010204E*01030101F*01010104G*01010104,
A*010104B*0703Cw*0103E*01030102F*01010105G*01010105,
A*0102B*0704Cw*0104E*010302F*01010106G*01010201,
A*0103B*070501Cw*0105E*010303F*01010107G*01010202,
A*0104NB*070502Cw*0106E*010304F*01010108G*010103,
A*0106B*070503Cw*0107E*0104F*01010201G*010104,
A*0107B*0706Cw*0108F*01010202G*010105,
A*0108B*0707Cw*0109F*01010203G*010106,
A*0109B*0708Cw*0110F*01010204G*010107,
A*0110B*0709Cw*0111F*01010205G*010108,
A*0111NB*0710Cw*0112F*01010301G*010109,
A*0112B*0711Cw*0113F*01010302G*010110,
A*0113B*0712Cw*020201F*01010303G*0102,
A*0114B*0713Cw*020202F*01010304G*0103,
A*0115NB*0714Cw*020203F*0102G*010401,
A*0116NB*0715Cw*020205F*01030101G*010402,
A*0117B*0716Cw*0203F*01030102G*010403,
A*0118NB*0717Cw*0204F*0104G*0105N, A*0119B*0718Cw*0205G*0106,
A*0120B*0719Cw*0206G*0107, A*02010101B*0720Cw*0207,
A*02010102LB*0721Cw*0208, A*020102B*0722Cw*0209,
A*020103B*0723Cw*0210, A*020104B*0724Cw*0211, A*020105B*0725Cw*0212,
A*020106B*0726Cw*0213, A*020107B*0727Cw*0214, A*020108B*0728Cw*0215,
A*020109B*0729Cw*0216, A*020110B*0730Cw*0217, A*020111B*0731Cw*030201,
A*020112B*0732Cw*030202, A*0202B*0733Cw*030301,
A*020301B*0734Cw*030302, A*020302B*0735Cw*030303,
A*0204B*0736Cw*030304, A*0205B*0737Cw*030305, A*020601B*0738Cw*030401,
A*020602B*0739Cw*030402, A*020603B*0740Cw*030403,
A*0207B*0741Cw*030404, A*0208B*0742Cw*030405, A*0209B*0743Cw*0305,
A*0210B*0744Cw*0306, A*0211B*0745Cw*0307, A*0212B*0746Cw*0308,
A*0213B*0747Cw*0309, A*0214B*0748Cw*0310, A*0215NB*0749NCw*031101,
A*0216B*0750Cw*031102, A*021701B*0751Cw*0312, A*021702B*080101Cw*0313,
A*0218B*080102Cw*0314, A*0219B*080103Cw*0315, A*022001B*0802Cw*0316,

A*022002B*0803Cw*0317, A*0221B*0804Cw*0318, A*0222B*0805Cw*0319, A*0224B*0806Cw*0320N, A*0225B*0807Cw*0321, A*0226B*0808NCw*0322Q, A*0227B*0809Cw*0323, A*0228B*0810Cw*0324, A*0229B*0811Cw*0325, A*0230B*0812Cw*0326, A*0231B*0813Cw*0327, A*0232NB*0814Cw*0328, A*0233B*0815Cw*0329, A*0234B*0816Cw*0330, A*023501B*0817Cw*0331, A*023502B*0818Cw*0332, A*0236B*0819NCw*0333, A*0237B*0820Cw*0334, A*0238B*0821Cw*0335, A*0239B*0822Cw*04010101, A*0240B*0823Cw*04010102, A*0241B*0824Cw*040102, A*0242B*0825Cw*040103, A*0243NB*0826Cw*040104, A*0244B*0827Cw*0403, A*0245B*0828Cw*040401, A*0246B*0829Cw*040402, A*0247B*0830NCw*0405, A*0248B*0831Cw*0406, A*0249B*1301Cw*0407, A*0250B*130201Cw*0408, A*0251B*130202Cw*0409N, A*0252B*130203Cw*0410, A*0253NB*1303Cw*0411, A*0254B*1304Cw*0412, A*0255B*1306Cw*0413, A*0256B*1307NCw*0414, A*0257B*1308Cw*0415, A*0258B*1309Cw*0416, A*0259B*1310Cw*0417, A*0260B*1311Cw*0418, A*0261B*1312Cw*0419, A*0262B*1313Cw*0420, A*0263B*1314Cw*0421, A*0264B*1315Cw*0423, A*0265B*1316Cw*0424, A*0266B*1317Cw*050101, A*0267B*1401Cw*050102, A*0268B*140201Cw*050103, A*0269B*140202Cw*0502, A*0270B*1403Cw*0503, A*0271B*1404Cw*0504, A*0272B*1405Cw*0505, A*0273B*140601Cw*0506, A*027401B*140602Cw*0507N, A*027402B*1407NCw*0508, A*0275B*15010101Cw*0509, A*0276B*15010102NCw*0510, A*0277B*150102Cw*0511, A*0278B*150103Cw*0512, A*0279B*150104Cw*0513, A*0280B*1502Cw*0514, A*0281B*1503Cw*0515, A*0282NB*1504Cw*06020101, A*0283NB*1505Cw*06020102, A*0284B*1506Cw*060202, A*0285B*1507Cw*0603, A*0286B*1508Cw*0604, A*0287B*1509Cw*0605, A*0288NB*1510Cw*0606, A*0289B*151101Cw*0607, A*0290B*151102Cw*0608, A*0291B*151103Cw*0609, A*0292B*1512Cw*0610, A*0293B*1513Cw*0611, A*0294NB*1514Cw*0612, A*0295B*1515Cw*0613, A*0296B*1516Cw*0614, A*0297B*15170101Cw*070101, A*0299B*15170102Cw*070102, A*03010101B*151702Cw*070103, A*03010102NB*1518Cw*070104, A*03010103B*1519Cw*070105, A*030102B*1520Cw*070106, A*030103B*1521Cw*070107, A*030104B*1523Cw*07020101, A*030105B*1524Cw*07020102, A*0302B*1525Cw*07020103, A*0303NB*1526NCw*0703, A*0304B*1527Cw*070401, A*0305B*1528Cw*070402, A*0306B*1529Cw*0705, A*0307B*1530Cw*0706, A*0308B*1531Cw*0707, A*0309B*1532Cw*0708, A*0310B*1533Cw*0709, A*0311NB*1534Cw*0710, A*0312B*1535Cw*0711,

A*0313B*1536Cw*0712, A*0314B*1537Cw*0713, A*0315B*1538Cw*0714, A*0316B*1539Cw*0715, A*0317B*1540Cw*0716, A*0318B*1542Cw*0717, A*0319B*1543Cw*0718, A*0320B*1544Cw*0719, A*0321NB*1545Cw*0720, A*0322B*1546Cw*0721, A*0323B*1547Cw*0722, A*0324B*1548Cw*0723, A*0325B*1549Cw*0724, A*0326B*1550Cw*0725, A*110101B*1551Cw*0726, A*110102B*1552Cw*0727, A*110103B*1553Cw*0728, A*110104B*1554Cw*0729, A*110105B*1555Cw*0730, A*110106B*1556Cw*0731, A*110201B*1557Cw*0732N, A*110202B*1558Cw*0733N, A*1103B*1560Cw*0734, A*1104B*1561Cw*0735, A*1105B*1562Cw*0736, A*1106B*1563Cw*0737, A*1107B*1564Cw*0738, A*1108B*1565Cw*0739, A*1109B*1566Cw*0740, A*1110B*1567Cw*0741, A*1111B*1568Cw*0742, A*1112B*1569Cw*0743, A*1113B*1570Cw*0744, A*1114B*1571Cw*0745, A*1115B*1572Cw*080101, A*1116B*1573Cw*080102, A*1117B*1574Cw*0802, A*1118B*1575Cw*0803, A*1301B*1576Cw*0804, A*1120B*1577Cw*0805, A*1121NB*1578Cw*0806, A*1122B*1579NCw*0807, A*1123B*1580Cw*0808, A*1124B*1581Cw*0809, A*1125B*1582Cw*0810, A*1126B*1583Cw*0811, A*1127B*1584Cw*0812, A*1128B*1585Cw*0813, A*1129B*1586Cw*0814, A*2301B*1587Cw*120201, A*2302B*1588Cw*120202, A*2303B*1589Cw*120203, A*2304B*1590Cw*12030101, A*2305B*1591Cw*12030102, A*2306B*1592Cw*120302, A*2307NB*1593Cw*120303, A*2308NB*1594NCw*120304, A*2309B*1595Cw*120401, A*2310B*1596Cw*120402, A*2311NB*1597Cw*1205, A*2312B*1598Cw*1206, A*2313B*1599Cw*1207, A*2314B*9501Cw*1208, A*24020101B*9502Cw*1209, A*24020102LB*9503Cw*1210, A*240202B*9504Cw*1211, A*240203B*9505Cw*1212, A*240204B*9506Cw*1213, A*240205B*9507Cw*1214, A*240206B*9508Cw*1215, A*240207B*9509Cw*1216, A*240208B*9510Cw*1217, A*240209B*9511NCw*1218, A*240210B*9512Cw*1219, A*240211B*9513Cw*140201, A*240212B*9514Cw*140202, A*240213B*9515Cw*140203, A*240301B*9516Cw*140204, A*240302B*9517Cw*1403, A*2404B*9518Cw*1404, A*2405B*9519Cw*1405, A*2406B*9520Cw*1406, A*2407B*9521Cw*1407N, A*2408B*9522Cw*1408, A*2409NB*180101Cw*150201, A*2410B*180102Cw*150202, A*2411NB*180103Cw*150203, A*2413B*1802Cw*1503, A*2414B*1803Cw*1504, A*2415B*1804Cw*150501, A*2417B*1805Cw*150502, A*2418B*1806Cw*150503, A*2419B*1807Cw*150504, A*2420B*1808Cw*1506, A*2421B*1809Cw*1507, A*2422B*1810Cw*1508, A*2423B*1811Cw*1509, A*2424B*1812Cw*1510,

A*2425B*1813Cw*1511, A*2426B*1814Cw*1512, A*2427B*1815Cw*1513, A*2428B*1817NCw*1514, A*2429B*1818Cw*1515, A*2430B*1819Cw*1516, A*2431B*1820Cw*1517, A*2432B*1821Cw*160101, A*2433B*1822Cw*160102, A*2434B*1823NCw*1602, A*2435B*1824Cw*160401, A*2436NB*2701Cw*1606, A*2437B*2702Cw*1607, A*2438B*2703Cw*1608, A*2439B*270401Cw*1609, A*2440NB*270402Cw*1701, A*2441B*270502Cw*1702, A*2442B*270503Cw*1703, A*2443B*270504Cw*1704, A*2444B*270505Cw*1801, A*2445NB*270506Cw*1802, A*2446B*270507, A*2447B*270508, A*2448NB*270509, A*2449B*2706, A*2450B*2707, A*2451B*2708, A*2452B*2709, A*2453B*2710, A*2454B*2711, A*2455B*2712, A*2456B*2713, A*2457B*2714, A*2458B*2715, A*2459B*2716, A*2460NB*2717, A*2461B*2718, A*2462B*2719, A*2463B*2720, A*2464B*2721, A*2465B*2723, A*2466B*2724, A*2467B*2725, A*2468B*2726, A*250101B*2727, A*250102B*2728, A*2502B*2729, A*2503B*2730, A*2504B*2731, A*2505B*2732, A*2506B*2733, A*260101B*2734, A*260102B*2735, A*260103B*2736, A*260104B*350101, A*2602B*350102, A*2603B*350103, A*2604B*350104, A*2605B*350105, A*2606B*350106, A*260701B*350201, A*260702B*350202, A*2608B*3503, A*2609B*350401, A*2610B*350402, A*2611NB*3505, A*2612B*3506, A*2613B*3507, A*2614B*350801, A*2615B*350802, A*2616B*350901, A*2617B*350902, A*2618B*3510, A*2619B*3511, A*2620B*3512, A*2621B*3513, A*2622B*351401, A*2623B*351402, A*2624B*3515, A*2625NB*3516, A*2626B*3517, A*2627B*3518, A*2628B*3519, A*2629B*3520, A*2630B*3521, A*2631B*3522, A*2632B*3523, A*2633B*3524, A*2634B*3525, A*29010101B*3526, A*29010102NB*3527, A*290201B*3528, A*290202B*3529, A*290203B*3530, A*2903B*3531, A*2904B*3532, A*2905B*3533, A*2906B*3534, A*2907B*3535, A*2908NB*3536, A*2909B*3537, A*2910B*3538, A*2911B*3539, A*2912B*3540N, A*2913B*3541, A*2914B*3542, A*2915B*3543, A*2916B*3544, A*300101B*3545, A*300102B*3546, A*300201B*3547, A*300202B*3548, A*300203B*3549, A*3003B*3550, A*3004B*3551, A*3006B*3552, A*3007B*3553N, A*3008B*3554, A*3009B*3555, A*3010B*3556, A*3011B*3557, A*3012B*3558, A*3013B*3559, A*3014LB*3560, A*3015B*3561, A*3016B*3562, A*3017B*3563, A*3018B*3564, A*3019B*3565Q, A*310102B*3566, A*3102B*3567, A*3103B*3568, A*3104B*3569, A*3105B*3570, A*3106B*3571, A*3107B*3572, A*3108B*370101, A*3109B*370102, A*3110B*370103, A*3111B*370104, A*3112B*3702, A*3113B*3703N, A*3114NB*3704, A*3115B*3705, A*3201B*3706, A*3202B*3707, A*3203B*3708, A*3204B*3709, A*3205B*3710, A*3206B*3711, A*3207B*3712,

A*3208B*380101, A*3209B*380102, A*3210B*380201, A*3211QB*380202, A*3212B*3803, A*3213B*3804, A*3214B*3805, A*3301B*3806, A*330301B*3807, A*330302B*3808, A*3304B*3809, A*3305B*3810, A*3306B*3811, A*3307B*3812, A*3308B*3813, A*3309B*3814, A*3401B*3815, A*3402B*39010101, A*3403B*39010102L, A*3404B*390103, A*3405B*390104, A*3406B*390201, A*3407B*390202, A*3408B*3903, A*3601B*3904, A*3602B*3905, A*3603B*390601, A*3604B*390602, A*4301B*3907, A*6601B*3908, A*6602B*3909, A*6603B*3910, A*6604B*3911, A*6605B*3912, A*6606B*391301, A*680101B*391302, A*680102B*3914, A*680103B*3915, A*680104B*3916, A*680105B*3917, A*68020101B*3918, A*68020102B*3919, A*680301B*3920, A*680302B*3922, A*6804B*3923, A*6805B*3924, A*6806B*3925N, A*6807B*3926, A*6808B*3927, A*6809B*3928, A*6810B*3929, A*6811NB*3930, A*6812B*3931, A*6813B*3932, A*6814B*3933, A*6815B*3934, A*6816B*3935, A*6817B*3936, A*6818NB*3937, A*6819B*3938Q, A*6820B*3939, A*6821B*3940N, A*6822B*3941, A*6823B*400101, A*6824B*400102, A*6825B*400103, A*6826B*400104, A*6827B*400105, A*6828B*400201, A*6829B*400202, A*6830B*400203, A*6831B*4003, A*6832B*4004, A*6833B*4005, A*6834B*40060101, A*6835B*40060102, A*6836B*400602, A*6901B*4007, A*7401B*4008, A*7402B*4009, A*7403B*4010, A*7404B*4011, A*7405B*4012, A*7406B*4013, A*7407B*401401, A*7408B*401402, A*7409B*401403, A*7410B*4015, A*7411B*4016, A*7412NB*4018, A*8001B*4019, A*9201B*4020, A*9202B*4021, A*9203B*4022N, A*9204B*4023, A*9205B*4024, A*9206B*4025, A*9207B*4026, A*9208B*4027, A*9209B*4028, B*4029, B*4030, B*4031, B*4032, B*4033, B*4034, B*4035, B*4036, B*4037, B*4038, B*4039, B*4040, B*4042, B*4043, B*4044, B*4045, B*4046, B*4047, B*4048, B*4049, B*4050, B*4051, B*4052, B*4053, B*4054, B*4055, B*4056, B*4057, B*4058, B*4059, B*4060, B*4061, B*4062, B*4063, B*4064, B*4065, B*4066, B*4067, B*4068, B*4069, B*4070, B*4101, B*4102, B*4103, B*4104, B*4105, B*4106, B*4107, B*4108, B*4201, B*4202, B*4204, B*420501, B*420502, B*4206, B*4207, B*4208, B*4209, B*44020101, B*44020102S, B*440202, B*440203, B*440204, B*440301, B*440302, B*4404, B*4405, B*4406, B*4407, B*4408, B*4409, B*4410, B*4411, B*4412, B*4413, B*4414, B*4415, B*4416, B*4417, B*4418, B*4419N, B*4420, B*4421, B*4422, B*4423N, B*4424, B*4425, B*4426, B*4427, B*4428, B*4429, B*4430, B*4431, B*4432, B*4433, B*4434, B*4435, B*4436, B*4437, B*4438, B*4439, B*4440, B*4441, B*4442, B*4443, B*4444, B*4445, B*4446, B*4447, B*4448, B*4449,

B*4450, B*4451, B*4501, B*4502, B*4503, B*4504, B*4505, B*4506, B*4507, B*460101, B*460102, B*4602, B*4603, B*4604, B*4605, B*4606, B*4607N, B*4608, B*4609, B*47010101, B*47010102, B*4702, B*4703, B*4704, B*4705, B*4801, B*4802, B*480301, B*480302, B*4804, B*4805, B*4806, B*4807, B*4808, B*4809, B*4810, B*4811, B*4812, B*4813, B*4814, B*4815, B*4816, B*4901, B*4902, B*4903, B*4904, B*4905, B*5001, B*5002, B*5004, B*510101, B*510102, B*510103, B*510104, B*510105, B*510106, B*510107, B*510201, B*510202, B*5103, B*5104, B*5105, B*5106, B*5107, B*5108, B*5109, B*5110, B*5111N, B*5112, B*511301, B*511302, B*5114, B*5115, B*5116, B*5117, B*5118, B*5119, B*5120, B*5121, B*5122, B*5123, B*5124, B*5126, B*5127N, B*5128, B*5129, B*5130, B*5131, B*5132, B*5133, B*5134, B*5135, B*5136, B*5137, B*5138, B*5139, B*5140, B*5141N, B*5142, B*5143, B*5144N, B*5145, B*5146, B*520101, B*520102, B*520103, B*520104, B*5202, B*5203, B*5204, B*5205, B*5206, B*5207, B*5208, B*5209, B*5210, B*530101, B*530102, B*530103, B*530104, B*5302, B*5303, B*5304, B*5305, B*5306, B*5307, B*5308, B*5309, B*5310, B*5311, B*5312, B*5401, B*5402, B*5403, B*5404, B*5405N, B*5406, B*5407, B*5408N, B*5409, B*5410, B*5411, B*5412, B*550101, B*550102, B*550103, B*550104, B*550201, B*550202, B*5503, B*5504, B*5505, B*5507, B*5508, B*5509, B*5510, B*5511, B*5512, B*5513, B*5514, B*5515, B*5516, B*5517, B*5518, B*5519, B*5520, B*5521, B*5522, B*5523, B*5524, B*5601, B*5602, B*5603, B*5604, B*560501, B*560502, B*5606, B*5607, B*5608, B*5609, B*5610, B*5611, B*5612, B*5613, B*5614, B*5615, B*5616, B*5617, B*5618, B*5619N, B*570101, B*570102, B*570103, B*5702, B*570301, B*570302, B*5704, B*5705, B*5706, B*5707, B*5708, B*5709, B*5710, B*5711, B*5801, B*5802, B*5804, B*5805, B*5806, B*5807, B*5808, B*5809, B*5810N, B*5811, B*5812, B*5813, B*5814, B*5901, B*5902, B*670101, B*670102, B*6702, B*7301, B*7801, B*780201, B*780202, B*7803, B*7804, B*7805, B*8101, B*8102, B*8201, B*8202, B*8301, H*01010101J*01010101K*01010101L*01010101P*01010101, H*01010102J*01010102K*01010102L*01010102P*01010102, H*01010103J*01010103K*01010103L*01010103P*02010101, H*0102J*01010104K*01010104L*010102P*02010102, H*02010101J*01010105K*0102L*0102, H*02010102J*01010106K*0103, H*0202J*01010107, H*0203J*01010108, H*0204J*0201, H*0205, H*0206 and, H*0301.

118. The MHC multimer according to any of claims 1 to 116, wherein the MHC protein is the same or different MHC proteins selected from the group of HLA classes consisting of A*0201, C*0701, A*0101, A*0301, C*0702, C*0401, B*4402, B*0702, B*0801, C*0501, C*0304, C*0602, A*1101, B*4001, A*2402, B*3501, C*0303, B*5101, C*1203, B*1501, A*2902, A*2601, A*3201, C*0802, A*2501, B*5701, B*1402, C*0202, B*1801, B*4403, C*0401, C*0701, C*0602, A*0201, A*2301, C*0202, A*0301, C*0702, B*5301, B*0702, C*1601, B*1503, B*5801, A*6802, C*1701, B*4501, B*4201, A*3001, B*3501, A*0101, C*0304, A*3002, B*0801, A*3402, A*7401, A*3303, C*1801, A*2902, B*4403, B*4901, A*0201, C*0401, A*2402, C*0702, C*0701, C*0304, A*0301, B*0702, B*3501, C*0602, C*0501, A*0101, A*1101, B*5101, C*1601, B*4403, C*0102, A*2902, C*0802, B*1801, A*3101, B*5201, B*1402, C*0202, C*1203, A*2601, A*6801, B*0801, A*3002, B*4402, A*1101, A*2402, C*0702, C*0102, A*3303, C*0801, C*0304, A*0201, B*4001, C*0401, B*5801, B*4601, B*5101, C*0302, B*3802, A*0207, B*1501, A*0206, C*0303, B*1502, A*0203, B*4403, C*1402, B*3501, C*0602, B*5401, B*1301, B*4002, B*5502, A*2601.

119. The MHC multimer according to any claims 1 to 116 comprising one or more covalently attached labels.

120. The MHC multimer according to any of claims 1 to 116 comprising one or more non-covalently attached labels.

121. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to the polypeptide a.

122. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to the polypeptide b.

123. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to the peptide P.

124. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to the one or more multimerization domains.

125. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to $(a\text{-}b\text{-}P)_n$.

126. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to the polypeptide a.

127. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to the polypeptide b.

128. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to P.

129. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to the one or more multimerization domains.

130. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to $(a\text{-}b\text{-}P)_n$.

131. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to the antibody in the mutimerization domain.

132. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to an antibody in the mutimerization domain.

133. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to an aptamer in the mutimerization domain.

134. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to an aptamer in the mutimerization domain.

135. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to a molecule in the mutimerization domain.

136. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to a molecule in the mutimerization domain.

137. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to a protein in the mutimerization domain.

138. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to a protein in the mutimerization domain.

139. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to a sugar residue in the mutimerization domain.

140. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to a sugar residue in the mutimerization domain.

141. The MHC multimer according to claim 120, wherein the one or more labels is non-covalently attached to a DNA in the mutimerization domain.

142. The MHC multimer according to claim 119, wherein the one or more labels is covalently attached to a DNA in the mutimerization domain.

143. The MHC multimer according to any of the claims 119 to 142, wherein the attachment is directly between reactive groups in the labelling molecule and reactive groups in the marker molecule.

144. The MHC multimer according to any of the claims 119 to 142, wherein the attachment is through a linker connecting labelling molecule and marker.

145. The MHC multimer according to any of the claims 119 to 144, wherein one label is used.

146. The MHC multimer according to any of the claims 119 to 144, wherein more than one label is used.

147. The MHC multimer according to claim 146, wherein the more than one label are all identical.

148. The MHC multimer according to claim 146, wherein at least two labels are different.

149. The MHC multimer according to any of claims 119 to 148, wherein the one or more labels is attached to $(a\text{-}b\text{-}P)_n$ via a streptavidin-biotin linkage.

150. The MHC multimer according to any of claims 119 to 148, wherein the one or more labels is a fluorophore label.

151. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group of fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

152. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 2-(4'-maleimidylanilino)naphthalene-6- sulfonic acid, sodium salt

153. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 5-((((2-iodoacetyl)amino)ethyl)amino) naphthalene-1-sulfonic acid

154. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Pyrene-1-butanoic acid

155. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of AlexaFluor 350 (7-amino-6-sulfonic acid-4-methyl coumarin-3-acetic acid

156. The MHC multimer according to claim 150 wherein the one or more fluorophore label are selected from the group consisting of AMCA (7-amino-4-methyl coumarin-3-acetic acid

157. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-4-methyl coumarin-3-acetic acid

158. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Marina Blue (6,8-difluoro-7-hydroxy-4-methyl coumarin-3-acetic acid

159. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 7-dimethylamino-coumarin-4-acetic acid

160. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Fluorescamin-N-butyl amine adduct

161. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-coumarine-3-carboxylic acid

162. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of CascadeBlue (pyrene-trisulphonic acid acetyl azide

163. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Cascade Yellow

164. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Pacific Blue (6,8 difluoro-7-hydroxy coumarin-3-carboxylic acid

165. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 7-diethylamino-coumarin-3-carboxylic acid

166. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of N-(((4-azidobenzoyl)amino)ethyl)- 4-amino-3,6-disulfo-1,8-naphthalimide, dipotassium salt

167. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Alexa Fluor 430

168. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 3-perylenedodecanoic acid

169. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 8-hydroxypyrene-1,3,6-trisulfonic acid, trisodium salt

170. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 12-(N-(7-nitrobenz-2-oxa-1,3- diazol-4-yl)amino)dodecanoic acid

171. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of N,N'-dimethyl-N-(iodoacetyl)-N'-(7-nitrobenz-2- oxa-1,3-diazol-4-yl)ethylenediamine

172. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Oregon Green 488 (difluoro carboxy fluorescein)

173. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of 5-iodoacetamidofluorescein

174. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of propidium iodide-DNA adduct

175. The MHC multimer according to claim 150, wherein the one or more fluorophore label are selected from the group consisting of Carboxy fluorescein

176. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a fluorescent label.

177. The MHC multimer according to claim 176, wherein the one or more fluorescent label is a simple fluorescent label

178. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Fluor dyes, Pacific Blue™, Pacific Orange™, Cascade Yellow™

179. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group AlexaFluor®(AF), AF405, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750, AF800.

180. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Quantum Dot based dyes, QDot® Nanocrystals (Invitrogen, MolecularProbs), Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800.

181. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group DyLight™ Dyes (Pierce) (DL); DL549, DL649, DL680, DL800.

182. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Fluorescein (Flu) or any derivate of that, such as FITC

183. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Cy-Dyes, Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7.

184. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Fluorescent Proteins, RPE, PerCp, APC, Green fluorescent proteins; GFP and GFP derivated mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine, mStrawberry, mCherry.

185. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group Tandem dyes, RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed, APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

186. The MHC multimer according to claim 177, wherein the one or more simple fluorescent label is selected from the group multi fluorochrome assemblies, Multiple fluorochromes attached to a polymer molecule, such as a peptide/protein, Dextrane, polysaccharide, any combination of the fluorescent dyes involving in generation of FRET (Fluorescence resonance energy transfer) based techniques.

187. The MHC multimer according to claim 177 wherein the one or more simple fluorescent label is selected from the group ionophors; ion chelating fluorescent props, props that change wavelength when binding a specific ion, such as Calcium, props that change intensity when binding to a specific ion, such as Calcium.

188. The MHC multimer according to any of claims 119-148, wherein the one or more labels is capable of absorption of light

189. The MHC multimer according to claim 188, wherein the one or more labels capable of absorption of light is a chromophore.

190. The MHC multimer according to claim 188, wherein the one or more labels capable of absorption of light is a dye.

191. The MHC multimer according to any of claims 119-148, wherein the one or more labels is capable of emission of light after excitation

192. The MHC multimer according to claim 191, wherein the one or more labels capable of emission of light is one or more fluorochromes.

193. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the AlexaFluor®(AF) family, which include AF®350, AF405, AF430, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750 and AF800

194. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the Quantum Dot (Qdot®) based dye family, which include Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800

195. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the DyLight™ Dyes (DL) family, which include DL549, DL649, DL680, DL800

196. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Small fluorescing dyes, which include FITC, Pacific Blue™, Pacific Orange™, Cascade Yellow™, Marina blue™, DSred, DSred-2, 7-AAD, TO-Pro-3.

197. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Cy-Dyes, which include Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7

198. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Phycobili Proteins, which include R-Phycoerythrin (RPE), PerCP, Allophycocyanin (APC), B-Phycoerythrin, C-Phycocyanin.

199. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Fluorescent Proteins, which include (E)GFP and GFP ((enhanced) green fluorescent protein) derived mutant proteins;

BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine.

200. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Tandem dyes with RPE, which include RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed.

201. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Tandem dyes with APC, which include APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

202. The MHC multimer according to claim 192, wherein the one or more fluorochrome is selected from the family of Calcium dyes, which include Indo-1-Ca^{2+} Indo-2-Ca^{2+}.

203. The MHC multimer according to any of claims 119-148, wherein the one or more labels is capable of reflection of light.

204. The MHC multimer according to claim 203, wherein the one or more labels capable of reflection of light comprises gold.

205. The MHC multimer according to claim 203, wherein the one or more labels capable of reflection of light comprises plastic.

206. The MHC multimer according to claim 203, wherein the one or more labels capable of reflection of light comprises glass.

207. The MHC multimer according to claim 203, wherein the one or more labels capable of reflection of light comprises polystyrene.

208. The MHC multimer according to claim 203, wherein the one or more labels capable of reflection of light comprises pollen.

209. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a chemiluminescent label.

210. The MHC multimer according to claim 209, wherein the chemiluminescent labels is selected from the group luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

211. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a bioluminescent label.

212. The MHC multimer according to claim 211, wherein the bioluminescent labels is selected from the group luciferin, luciferase and aequorin.

213. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a radioactive label.

214. The MHC multimer according to claim 213, wherein the one or more radioactive labels is a radionuclide.

215. The MHC multimer according to claim 213 wherein the one or more radioactive labels is an isotope.

216. The MHC multimer according to claim 213, wherein the one or more radioactive labels comprises α rays.

217. The MHC multimer according to claim 213, wherein the one or more radioactive labels comprises β rays.

218. The MHC multimer according to claim 213, wherein the one or more radioactive labels comprises γ rays.

219. The MHC multimer according to any of claims 119-148, wherein the one or more labels is detectable by NMR (nuclear magnetic resonance form paramagnetic molecules).

220. The MHC multimer according to any of claims 119-148, wherein the one or more labels is an enzyme label.

221. The MHC multimer according to claim 220, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, producing a light signal (chemi-luminescence).

222. The MHC multimer according to claim 220, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitation of chromophor dyes.

223. The MHC multimer according to claim 220, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitates that can be detected by an additional layer of detection molecules.

224. The MHC multimer according to claim 220, wherein the enzyme label is selected from the group peroxidases, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate, dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase.

225. The MHC multimer according to claim 220, wherein the enzyme label is horseradish peroxidase.

226. The MHC multimer according to claim 220, wherein the enzyme label is horseradish peroxidase and the substrate is diaminobenzidine (DAB).

227. The MHC multimer according to claim 220, wherein the enzyme label is horseradish peroxidase and the substrate is 3-amino-9-ethyl-carbazole (AEC+).

228. The MHC multimer according to claim 220, wherein the enzyme label is horseradish peroxidase and the substrate is biotinyl tyramide.

229. The MHC multimer according to claim 220, wherein the enzyme label is horseradish peroxidase and the substrate is fluorescein tyramide.

230. The MHC multimer according to claim 220, wherein the enzyme label is alkaline phosphatase.

231. The MHC multimer according to claim 220, wherein the enzyme label is alkaline phosphatase and the substrate is Fast red dye.

232. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a ionophore or chelating chemical compound binding to specific ions such as Ca^{2+}.

233. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a lanthanide.

234. The MHC multimer according to claim 233, wherein the lanthanide comprises fluorescence.

235. The MHC multimer according to claim 233, wherein the lanthanide comprises Phosphorescence.

236. The MHC multimer according to claim 233, wherein the lanthanide is paramagnetic.

237. The MHC multimer according to any of claims 119-148, wherein the one or more labels is a DNA fluorescing stain.

238. The MHC multimer according to claim 237, wherein the DNA fluorescing stain is Propidium iodide.

239. The MHC multimer according to claim 237, wherein the DNA fluorescing stain is Hoechst stain.

240. The MHC multimer according to claim 237, wherein the DNA fluorescing stain is DAPI.

241. The MHC multimer according to claim 237, wherein the DNA fluorescing stain is AMC.

242. The MHC multimer according to claim 237, wherein the DNA fluorescing stain is DraQ5™

243. The MHC multimer according to claim 237 wherein the DNA fluorescing stain is Acridine orange.

244. The MHC multimer according to claim 1, wherein the MHC-peptide complex (a-b-P) is attached to a multimerization domain comprising an avidin or streptavidin via a linkage comprising a biotin moiety.

245. The MHC multimer according to any of claims 1 to 244, wherein P is chemically modified.

246. The MHC multimer according to any of claims 1 to 244, wherein P is pegylated.

247. The MHC multimer according to any of claims 1 to 244, wherein P is phosphorylated.

248. The MHC multimer according to any of claims 1 to 244, wherein P is glycosylated.

249. The MHC multimer according to any of claims 1 to 244, wherein one of the amino acid residues of the peptide P is substituted with another amino acid.

250. The MHC multimer according to any of claims 1 to 244, wherein a and b are both full-length peptides.

251. The MHC multimer according to any of claims 1 to 244, wherein a is a full-length peptide.

252. The MHC multimer according to any of claims 1 to 244, wherein b is a full-length peptide.

253. The MHC multimer according to any of claims 1 to 244, wherein a is truncated.

254. The MHC multimer according to any of claims 1 to 244, wherein b is truncated.

255. The MHC multimer according to any of claims 1 to 244, wherein a and b are both truncated.

256. The MHC multimer according to any of claims 1 to 244, wherein a is covalently linked to b.

257. The MHC multimer according to any of claims 1 to 244, wherein a is covalently linked to P.

258. The MHC multimer according to any of claims 1 to 244, wherein b is covalently linked to P.

259. The MHC multimer according to any of claims 1 to 244, wherein a, b and P are all covalently linked.

260. The MHC multimer according to any of claims 1 to 244, wherein a is non-covalently linked to b.

261. The MHC multimer according to any of claims 1 to 244, wherein a is non-covalently linked to P.

262. The MHC multimer according to any of claims 1 to 244, wherein b is non-covalently linked to P.

263. The MHC multimer according to any of claims 1 to 244, wherein a, b and P are all non-covalently linked.

264. The MHC multimer according to any of claims 1 to 244, wherein a is not included in the (a-b-P) complex.

265. The MHC multimer according to any of claims 1 to 244, wherein b is not included in the (a-b-P) complex.

266. The MHC multimer according to any of claims 1 to 244, wherein P is not included in the (a-b-P) complex.

267. The MHC multimer according to any of claims 1 to 244, wherein P consists of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acids.

268. The MHC multimer according to any of claims 1 to 244, wherein P consist of more than 30 amino acids such as/or more than 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 amino acids.

269. The MHC multimer according to any of claims 1 to 244, wherein the MHC-peptide complex is linked to at least one of the one or more multimerization domains by a linker moiety.

270. The MHC multimer according to claim 269, wherein the MHC-peptide complex is linked to at least one of the one or more multimerization domains by a covalent linker moiety.

271. The MHC multimer according to claims 269 and 270, wherein the linkage of at least one of the one or more multimerization domains and at least one MHC-peptide complexes is formed by a binding entity X attached to, or being part of, at least one of the one or more multimerization domains, and a binding entity Y attached to, or being part of at least one of the MHC-peptide complexes.

272. The MHC multimer according to claim 269 and 270, wherein the linker moiety linking at least one of the one or more multimerization domains and the MHC-peptide complex comprises the linker moiety XY, wherein the linker moiety XY results from a reaction of the moiety X comprising one or more reactive groups and the moiety Y

comprising one or more reactive groups, wherein at least some of said reactive groups are capable of reacting with each other.

273. The MHC multimer according to any of claims 271 and 272, wherein the moiety X comprises a nucleophilic group.

274. The MHC multimer according to claim 273, wherein the nucleophilic group is selected from the group consisting of $-NH_2$, -OH, -SH, $-NH-NH_2$.

275. The MHC multimer according to claim 272, wherein the moiety Y comprises an electrophilic group.

276. The MHC multimer according to claim 275, wherein the electrophilic group is selected from the group consisting of CHO, COOH and CO.

277. The MHC multimer according to claims 269 and 270, wherein at least one of the reactive groups on one of the moieties X and Y comprises a radical capable of reacting with a reactive group forming part of the other moiety.

278. The MHC multimer according to claims 269 and 270, wherein X and Y comprises reactive groups natively associated with the one or more multimerization domains and/or the MHC-peptide complexes.

279. The MHC multimer according to claims 269 and 270, wherein X and Y comprises reactive groups not natively associated with the one or more multimerization domains and/or the MHC-peptide complex.

280. The MHC multimer according to claims 269 and 270, wherein the linker moiety forms a covalent link between at least one of the one or more multimerization domains and at least one of the MHC-peptide complexes.

281. The MHC multimer according to claims 269 and 270, wherein the reactive groups of MHC-peptide complexes include amino acid side chains selected from the group $-NH_2$, -OH, -SH, and -NH-

282. The MHC multimer according to claims 277 and 279, wherein the reactive groups of multimerization domains include hydroxyls of polysaccharides such as dextrans.

283. The MHC multimer according to claims 277 and 279, wherein the reactive groups of multimerization domains are selected from the group amino acid side chains comprising -NH_2, -OH, -SH, and -NH- of polypeptides.

284. The MHC multimer according to claims 269 and 270, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the multimerization domain.

285. The MHC multimer according to claims 269 and 270, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the multimerization domain, wherein an acyl group and an amino group react to form an amide bond.

286. The MHC multimer according to claim 1, wherein one of the polypeptides of the MHC-peptide complex is a β2M polypeptide.

287. The MHC multimer according to claim 1, wherein one of the polypeptides of the MHC-peptide complex is a heavy chain polypeptide.

288. The MHC multimer according to claim 1, wherein the peptides P of the MHC-peptide complex is an antigenic peptide.

289. The MHC multimer according to claim 1, wherein one of the polypeptides of the MHC-peptide complex is linked by non-native reactive groups to the multimerization domain.

290. The MHC multimer according to claim 289, wherein the non-native reactive groups include reactive groups that are attached to the multimerization domain through association of a linker molecule comprising the reactive group.

291. The MHC multimer according to claim 289, wherein the non-native reactive groups include reactive groups that are attached to the MHC-peptide complex through association of a linker molecule comprising the reactive group.

292. The MHC multimer according to claim 291, wherein a dextran is activated by reaction of the dextran hydroxyls with divinyl sulfon.

293. The MHC multimer according to claim 291, wherein dextran is activated by a multistep reaction that results in the decoration of the dextran with maleimide groups.

294. The MHC multimer according to claim 1, wherein the multimerization domain comprises one or more nucleophilic groups.

295. The MHC multimer according to claim 294, wherein the nucleophilic group is selected from the group consisting of $–NH_2$, -OH, -SH, -CN, $-NH-NH_2$.

296. The MHC multimer according to claim 1, wherein the multimerization domain is selected from the group polysaccharides, polypeptides comprising e.g. lysine, serine, and cysteine.

297. The MHC multimer according to claim 1, wherein the multimerization domain comprises one or more electrophilic groups.

298. The MHC multimer according to claim 297, wherein the electrophilic group is selected from the group –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides.

299. The MHC multimer according to claim 1, wherein reactive groups involved in forming an association between the multimerization domain and the MHC peptide complex are located on glutamate or aspartate residues, or on a vinyl sulfone activated dextran.

300. The MHC multimer according to claim 1, wherein the multimerization domain is associated with the MHC peptide complex by a radical reaction.

301. The MHC multimer according to claim 1, wherein the multimerization domain comprises one or more conjugated double bonds.

302. The MHC multimer according to claim 1, wherein the MHC-peptide complex comprises one or more nucleophilic groups.

303. The MHC multimer according to claim 302, wherein the nucleophilic group is selected from the group consisting of $–NH_2$, -OH, -SH, -CN, -NH-NH_2.

304. The MHC multimer according to claim 1, wherein the MHC-peptide complex comprises one or more electrophilic groups.

305. The MHC multimer according to claim 304, wherein the electrophilic group is selected from the group consisting of –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides.

306. The MHC multimer according to claim 1, wherein the MHC-peptide complex comprises one or more radicals.

307. The MHC multimer according to claim 1, wherein the MHC-peptide complex comprises one or more conjugated double bonds.

308. The MHC multimer according to claim 53, wherein the multimerization domain comprising one or more beads further comprises a linker moiety

309. The MHC multimer according to claim 308, wherein the linker is a flexible linker.

310. The MHC multimer according to claim 308, wherein the linker is a rigid linker.

311. The MHC multimer according to claim 308, wherein the linker is a water-soluble linker.

312. The MHC multimer according to claim 308, wherein the linker is a cleavable linker.

313. The MHC multimer according to claim 312, wherein the cleavable linker is selected from linkers depicted in Figure 6 herein.

314. The MHC multimer according to claim 312, wherein the cleavable linker is cleavable at physiological conditions

315. The MHC multimer according to claim 1, wherein the MHC-peptide complex is linked to at least one of the one or more multimerization domains by a non-covalent linker moiety.

316. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises natural dimerization.

317. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises protein-protein interactions.

318. The MHC multimer according to claim 317, wherein the protein-protein interactions comprises one or more Fos/Jun interactions.

319. The MHC multimer according to claim 317, wherein the protein-protein interactions comprises one or more Acid/Base coiled coil structure based interactions.

320. The MHC multimer according to claim 317, wherein the protein-protein interactions comprises one or more antibody/antigen interactions.

321. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises polynucleotide-polynucleotide interactions.

322. The MHC multimer according to claim 315 wherein the non-covalent linkage comprises protein-small molecule interactions.

323. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises combinations of non-covalent linker molecules.

324. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises synthetic molecule-synthetic molecule interactions.

325. The MHC multimer according to claim 316, wherein the natural dimerization comprises antigen-antibody pairs

326. The MHC multimer according to claim 316, wherein the natural dimerization comprises DNA-DNA interactions

327. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises natural interactions.

328. The MHC multimer according to claim 327, wherein the natural interaction comprises biotin and streptavidin.

329. The MHC multimer according to claim 53, wherein the bead is coated with streptavidin monomers, which in turn are associated with biotinylated MHC peptide complexes.

330. The MHC multimer according to claim 53, wherein the bead is coated with streptavidin tetramers each of which being independently associated with 0, 1, 2, 3, or 4 biotinylated MHC complexes.

331. The MHC multimer according to claim 53, wherein the bead is coated with polysaccharide, such as a polysaccharide comprising dextran moieties.

332. The MHC multimer according to claim 327, wherein the natural interaction comprises the interaction of MHC complexes (comprising full-length polypeptide chains, including the transmembrane portion) with the cell membrane of for example dendritic cells.

333. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises artificial interactions.

334. The MHC multimer according to claim 333, wherein the artificial interaction comprises His_6 tag interacting with Ni-NTA.

335. The MHC multimer according to claim 333, wherein the artificial interaction comprises PNA-PNA.

336. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises non-specific adsorption.

337. The MHC multimer according to claim 334, wherein the non-specific adsorption comprises adsorption of proteins onto surfaces.

338. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises the pentamer structure.

339. The MHC multimer according to claim 315, wherein the non-covalent linkage comprises interactions selected from the group streptavidin/biotin, avidin/biotin, antibody/antigen, DNA/DNA, DNA/PNA, DNA/RNA, PNA/PNA, LNA/DNA, leucine zipper e.g. Fos/Jun, IgG dimeric protein, IgM multivalent protein, acid/base coiled-coil helices, chelate/metal ion-bound chelate, streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-transferase) glutathione affinity, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (Canavalia ensiformis) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity).

340. The MHC multimer according to any of claims 1 to 339 further comprising one or more molecules with adjuvant effect.

341. The MHC multimer according to any of claims 1 to 339 further comprising one or more immune targets.

342. The MHC multimer according to any of claim 341, wherein the one or more immune targets is an antigen.

343. The MHC multimer according to any of claims 1 to 342 further comprising one or more molecules with biological activity.

344. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises proteins such as MHC Class I-like proteins like MIC A, MIC B, CD1d, HLA E, HLA F, HLA G, HLA H, ULBP-1, ULBP-2, and ULBP-3.

345. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises co-stimulatory molecules such as CD2, CD3, CD4, CD5, CD8, CD9, CD27, CD28, CD30, CD69, CD134 (OX40), CD137 (4-1BB), CD147, CDw150 (SLAM), CD152 (CTLA-4), CD153 (CD30L), CD40L (CD154), NKG2D, ICOS, HVEM, HLA Class II, PD-1, Fas (CD95), FasL expressed on T and/or NK cells, CD40, CD48, CD58, CD70, CD72, B7.1 (CD80), B7.2 (CD86), B7RP-1, B7-H3, PD-L1, PD-L2, CD134L, CD137L, ICOSL, LIGHT expressed on APC and/or tumour cells.

346. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises cell modulating molecules such as CD16, NKp30, NKp44, NKp46, NKp80, 2B4, KIR, LIR, CD94/NKG2A, CD94/NKG2C expressed on NK cells, IFN-alpha, IFN-beta, IFN-gamma, IL-1, IL-2, IL-3, IL-4, IL-6, IL-7, IL-8, IL-10, IL-11, IL-12, IL-15, CSFs (colony-stimulating factors), vitamin D3, IL-2 toxins, cyclosporin, FK-506, rapamycin, TGF-beta, clotrimazole, nitrendipine, and charybdotoxin.

347. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises accessory molecules such as LFA-1, CD11a/18, CD54 (ICAM-1), CD106 (VCAM), and CD49a,b,c,d,e,f/CD29 (VLA-4).

348. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more non-classical MHC complexes and other MHC-like molecules such as protein products of MHC Ib and MHC IIb genes, β2m-associated cell-surface molecules, HLA-E, HLA-G, HLA-F, HLA-H, MIC A, MIC B, ULBP-1, ULBP-2, ULBP-3, H2-M, H2-Q, H2-T, Rae, Non-classical MHC II molecules, protein products of MHC IIb genes, HLA–DM, HLA-DO, H2-DM, H2-DO, and/or CD1.

349. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more artificial molecules capable of binding specific TCRs such as antibodies that bind TCRs including full length antibodies of isotype IgG, IgM, IgE, IgA and truncated versions of these, antibody fragments like Fab fragments and scFv as well as antibodies of antibody fragments displayed on various supramolecular structures or solid supports, including filamentous phages, yeast, mammalian cells, fungi, artificial cells or micelles, and beads with various surface chemistries.

350. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more peptides that bind TCRs including one or more peptides composed of natural, non-natural and/or chemically modified amino acids with a length of 8-20 amino acid.

351. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more aptamers such as natural nucleic acids (e.g. RNA and DNA) or unnatural nucleic acids (e.g. PNA, LNA, morpholinos) capable of binding TCR, said aptamer molecules consist of natural or modified nucleotides in various lengths.

352. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more ankyrin repeat proteins or other repeat proteins.

353. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more Avimers.

354. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises one or more small chemical molecules capable of binding TCR with a dissociation constant smaller than 10^{-3} M.

355. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises adhesion molecules such as ICAM-1, ICAM-2, GlyCAM-1, CD34, anti-LFA-1, anti-CD44, anti-beta7, chemokines, CXCR4, CCR5, anti-selectin L, anti-selectin E, and anti-selectin P.

356. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises toxic molecules selected from toxins, enzymes, antibodies, radioisotopes, chemiluminescent substances, bioluminescent substances, polymers, metal particles, and haptens, such as cyclophosphamide, methrotrexate, Azathioprine, mizoribine, 15-deoxuspergualin, neomycin, staurosporine, genestein, herbimycin A, Pseudomonas exotoxin A, saporin, Rituxan, Ricin, gemtuzumab ozogamicin, Shiga toxin, heavy metals like inorganic and organic mercurials, and FN18-CRM9, radioisotopes such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor, and haptens such as DNP, and digoxiginin.

357. The MHC multimer according to claim 343, wherein the one or more molecules with biological activity comprises antibodies such as monoclonal antibodies, polyclonal antibodies, recombinant antibodies, antibody derivatives or fragments thereof.

358. The MHC multimer according to any of claims 1 to 357 further comprising one or more molecules with a cytotoxic effect.

359. The MHC multimer according to any of claims 1 to 357 further comprising one or more molecules selected from the group consisting of enzymes, regulators of receptor activity, receptor ligands, immune potentiators, drugs, toxins, co-receptors, proteins, peptides, sugar moieties, lipid groups, nucleic acids including siRNA, nano particles, and small molecules.

360. The MHC multimer according to any of claims 1 to 357 further comprising one or more molecules selected from the group consisting of HIV gp120, HIV-GAG gp 27, HSP70, and MHC class II proteins or peptides or combinations thereof.

361. The MHC multimer according to any of claims 1 to 360 comprising a plurality of identical or different multimerization domains linked by a multimerization domain linking moiety,

wherein at least one of said multimerization domains is associated with $(a\text{-}b\text{-}P)_n$, wherein $n > 1$,

wherein a and b together form a functional MHC protein capable of binding the peptide P,

wherein (a-b-P) is the MHC-peptide complex formed when the peptide P binds to the functional MHC protein.

362. The MHC multimer according to claim 361, wherein the plurality of identical or different multimerization domains is in the range of from 2 to 100, suach as 2 to 5, 5 to 10, 10 to 20, 20 to 30, 30 to 40, 40 to 50, 50 to 60, 60 to 70, 70 to 80, 80 to 90, 90 to 100.

363. The MHC multimer according to claim 361, wherein the MHC multimer comprises a first multimerization domain linked to a second multimerization domain.

364. The MHC multimer according to claim 363, wherein the first multimerization domain and the second multimerization domain is independently selected from the group consisting of multimerization domains cited in any of claims 4 to 75.

365. The MHC multimer according to claim 363, wherein the association is a covalent linkage so that one or more of the n MHC-peptide complexes is covalently linked to the first multimerization domains.

366. The MHC multimer according to claim 363, wherein the association is a non-covalent association so that one or more of the n MHC-peptide complexes is non-covalently associated with the first multimerization domain.

367. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more scaffolds.

368. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more carriers.

369. The MHC multimer according to claim 363, wherein the first multimerization domain comprises at least one scaffold and at least one carrier.

370. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more optionally substituted organic molecules.

371. The MHC multimer according to claim 370, wherein the optionally substituted organic molecule comprises one or more functionalized cyclic structures.

372. The MHC multimer according to claim 371, wherein the one or more functionalized cyclic structures comprises one or more optionally substituted benzene rings.

373. The MHC multimer according to claim 370, wherein the optionally substituted organic molecule comprises a scaffold molecule comprising at least three reactive groups, or at least three sites suitable for non-covalent attachment.

374. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more biological cells, such as antigen presenting cells or dendritic cells.

375. The MHC multimer according to claim 374, wherein the one or more biological cells are alive and mitotic active.

376. The MHC multimer according to claim 374, wherein the one or more biological cells are alive and mitotic inactive e.g. as a result of irradiation and/or chemically treatment.

377. The MHC multimer according to claim 374, wherein the one or more biological cells are dead.

378. The MHC multimer according to claim 374, wherein the one or more biological cells have a natural expression of MHC (i.e. not stimulated).

379. The MHC multimer according to claim 374, wherein the one or more biological cells have to be induced/stimulated by e.g. Inf-γ to express MHC.

380. The MHC multimer according to claim 374, wherein the one or more biological cells are macrophages.

381. The MHC multimer according to claim 374, wherein the one or more biological cells are Kupfer cells.

382. The MHC multimer according to claim 374, wherein the one or more biological cells are Langerhans cells.

383. The MHC multimer according to claim 374, wherein the one or more biological cells are B-cells.

384. The MHC multimer according to claim 374, wherein the one or more biological cells are MHC expressing cells.

385. The MHC multimer according to claim 374, wherein the one or more biological cells are one or more transfected cells expressing MHC.

386. The MHC multimer according to claim 374, wherein the one or more biological cells are one or more hybridoma cells expressing MHC.

387. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more cell-like structures.

388. The MHC multimer according to claim 387, wherein the one or more cell-like structures comprises one or more membrane-based structures carrying MHC-peptide complexes in their membranes such as micelles, liposomes, and other structures of membranes, and phages such as filamentous phages.

389. The MHC multimer according to claim 363 wherein the first multimerization domain comprises one or more membranes.

390. The MHC multimer according to claim 389, wherein the one or more membranes comprises liposomes or micelles.

391. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more polymers.

392. The MHC multimer according to claim 391, wherein the one or more polymers are selected from the group consisting of the group consisting of polysaccharides.

393. The MHC multimer according to claim 392, wherein the polysaccharide comprises one or more dextran moieties.

394. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more entities selected from the group consisting of an IgG domain, a coiled-coil polypeptide structure, a DNA duplex, a nucleic acid duplex, PNA-PNA, PNA-DNA, DNA-RNA.

395. The MHC multimer according to claim 363, wherein the first multimerization domain comprises an avidin, such as streptavidin.

396. The MHC multimer according to claim 363, wherein the first multimerization domain comprises an antibody.

397. The MHC multimer according to claim 396, wherein the antibody is selected from the group consisting of polyclonal antibody, monoclonal antibody, IgA, IgG, IgM, IgD, IgE, IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM1, IgM2, humanized antibody, humanized monoclonal antibody, chimeric antibody, mouse antibody, rat antibody, rabbit antibody, human antibody, camel antibody, sheep antibody, engineered human antibody, epitope-focused antibody, agonist antibody, antagonist antibody, neutralizing antibody, naturally-occurring antibody, isolated antibody, monovalent antibody, bispecific antibody, trispecific antibody, multispecific antibody, heteroconjugate antibody, immunoconjugates, immunoliposomes, labeled antibody, antibody fragment, domain antibody, nanobody, minibody, maxibody, diabody, fusion antibody.

398. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more small organic scaffold molecules.

399. The MHC multimer according to claim 363, wherein the first multimerization comprises one or more further polypeptides in addition to a and b.

400. The MHC multimer according to claim 363, wherein the first multimerization comprises one or more protein complexes.

401. The MHC multimer according to claim 363, wherein the first multimerization comprises one or more beads.

402. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more compounds selected from the group consisting of agarose, sepharose, resin beads, glass beads, pore-glass beads, glass particles coated with a hydrophobic polymer, chitosan-coated beads, SH beads, latex beads, spherical latex beads, allele-type beads, SPA bead, PEG-based resins, PEG-coated bead, PEG-encapsulated bead, polystyrene beads, magnetic polystyrene beads, glutathione agarose beads, magnetic bead, paramagnetic beads, protein A and/or protein G sepharose beads, activated carboxylic acid bead, macroscopic beads, microscopic beads, insoluble resin beads, silica-based resins, cellulosic resins, cross-linked agarose beads, polystyrene beads, cross-linked polyacrylamide resins, beads with iron cores, metal beads, dynabeads, Polymethylmethacrylate beads

activated with NHS, streptavidin-agarose beads, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, nitrocellulose, polyacrylamides, gabbros, magnetite, polymers, oligomers, non-repeating moieties, polyethylene glycol (PEG), monomethoxy-PEG, mono-(C_1-C_{10})alkoxy-PEG, aryloxy-PEG, poly-(N-vinyl pyrrolidone)PEG, tresyl monomethoxy PEG, PEG propionaldehyde, bis-succinimidyl carbonate PEG, polystyrene bead crosslinked with divinylbenzene, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, dextran, aminodextran, carbohydrate-based polymers, cross-linked dextran beads, polysaccharide beads, polycarbamate beads, divinyl sulfone activated polysaccharide, polystyrene beads that have been functionalized with tosyl-activated esters, magnetic polystyrene beads functionalized with tosyl-activated esters, streptavidin beads, streptaivdin-monomer coated beads, streptaivdin-tetramer coated beads, Streptavidin Coated Compel Magnetic beads, avidin coated beads, dextramer coated beads, divinyl sulfone-activated dextran, Carboxylate-modified bead, amine-modified beads, antibody coated beads, cellulose beads, grafted co-poly beads, poly-acrylamide beads, dimethylacrylamide beads optionally crosslinked with N-N'-bis-acryloylethylenediamine, hollow fiber membranes, fluorescent beads, collagen-agarose beads, gelatin beads, collagen-gelatin beads, collagen-fibronectin-gelatin beads, collagen beads, chitosan beads, collagen-chitosan beads, protein-based beads, hydrogel beads, hemicellulose, alkyl cellulose, hydroxyalkyl cellulose, carboxymethylcellulose, sulfoethylcellulose, starch, xylan, amylopectine, chondroitin, hyarulonate, heparin, guar, xanthan, mannan, galactomannan, chitin and chitosan.

403. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a dimerization domain.

404. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a trimerization domain.

405. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a tetramerization domain.

406. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a pentamerization domain.

407. The MHC multimer according to claim 406, wherein the pentamerization domain comprises a coiled-coil polypeptide structure.

408. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a hexamerization domain.

409. The MHC multimer according to claim 408, wherein the hexamerization domain comprises three IgG domains.

410. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a polymer structure to which is attached one or more scaffolds.

411. The MHC multimer according to claim 410, wherein the polymer structure comprises a polysaccharide.

412. The MHC multimer according to claim 411, wherein the polysaccharide comprises one or more dextran moieties.

413. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a polyamide and/or a polyethylene glycol and/or a polysaccharide and/or a sepharose.

414. The MHC multimer according to claim 363, wherein the first multimerization domain comprises a carboxy methyl dextran and/or a dextran polyaldehyde and/or a carboxymethyl dextran lactone and/or or a cyclodextrin.

415. The MHC multimer according to claim 363, wherein one or more labels is covalently attached to the first multimerization domain.

416. The MHC multimer according to claim 363, wherein one or more labels is non-covalently attached to the first multimerization domain.

417. The MHC multimer according to claim 416, wherein the one or more labels is non-covalently attached to an antibody in the first mutimerization domain.

418. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to an antibody in the first multimerization domain.

419. The MHC multimer according claim 416, wherein the one or more labels is non-covalently attached to an aptamer in the first mutimerization domain.

420. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to an aptamer in the first mutimerization domain.

421. The MHC multimer according claim 416, wherein the one or more labels is non-covalently attached to a molecule in the first mutimerization domain.

422. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to a molecule in the first mutimerization domain.

423. The MHC multimer according claim 416, wherein the one or more labels is non-covalently attached to a protein in the first mutimerization domain.

424. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to a protein in the first mutimerization domain.

425. The MHC multimer according claim 416, wherein the one or more labels is non-covalently attached to a sugar residue in the first mutimerization domain.

426. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to a sugar residue in the first mutimerization domain.

427. The MHC multimer according claim 416, wherein the one or more labels is non-covalently attached to a DNA in the first mutimerization domain.

428. The MHC multimer according claim 415, wherein the one or more labels is covalently attached to a DNA in the first mutimerization domain.

429. The MHC multimer according to any of the claims 415 to 428, wherein the attachment is directly between reactive groups in the labelling molecule and reactive groups in the marker molecule.

430. The MHC multimer according to any of the claims 415 to 428, wherein the attachment is through a linker connecting labelling molecule and marker.

431. The MHC multimer according to any of the claims 415 to 430, wherein one label is used.

432. The MHC multimer according to any of the claims 415 to 430, wherein more than one label is used.

433. The MHC multimer according to claim 432, wherein the more than one labels are all identical.

434. The MHC multimer according to claim 432, wherein at least two labels are different.

435. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a fluorophore.

436. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of selected from the group fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

437. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 2-(4'-maleimidylanilino)naphthalene-6- sulfonic acid, sodium salt

438. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 5-((((2-iodoacetyl)amino)ethyl)amino) naphthalene-1-sulfonic acid

439. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Pyrene-1-butanoic acid

440. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of AlexaFluor 350 (7-amino-6-sulfonic acid-4-methyl coumarin-3-acetic acid

441. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of AMCA (7-amino-4-methyl coumarin-3-acetic acid

442. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-4-methyl coumarin-3-acetic acid.

443. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Marina Blue (6,8-difluoro-7-hydroxy-4-methyl coumarin-3-acetic acid.

444. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 7-dimethylamino-coumarin-4-acetic acid.

445. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Fluorescamin-N-butyl amine adduct.

446. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-coumarine-3-carboxylic acid.

447. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of CascadeBlue (pyrene-trisulphonic acid acetyl azide.

448. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Cascade Yellow.

449. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Pacific Blue (6,8 difluoro-7-hydroxy coumarin-3-carboxylic acid.

450. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 7-diethylamino-coumarin-3-carboxylic acid.

451. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of N-(((4-azidobenzoyl)amino)ethyl)- 4-amino-3,6-disulfo-1,8-naphthalimide, dipotassium salt.

452. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Alexa Fluor 430.

453. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 3-perylenedodecanoic acid.

454. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 8-hydroxypyrene-1,3,6-trisulfonic acid, trisodium salt.

455. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 12-(N-(7-nitrobenz-2-oxa-1,3- diazol-4-yl)amino)dodecanoic acid.

456. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of N,N'-dimethyl-N-(iodoacetyl)-N'-(7-nitrobenz-2- oxa-1,3-diazol-4-yl)ethylenediamine.

457. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Oregon Green 488 (difluoro carboxy fluorescein).

458. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of 5-iodoacetamidofluorescein.

459. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of propidium iodide-DNA adduct.

460. The MHC multimer according to claim 435, wherein the one or more fluorophore label are selected from the group consisting of Carboxy fluorescein.

461. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a fluorescent label.

462. The MHC multimer according to claim 461, wherein the one or more fluorescent label is a simple fluorescent label.

463. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Fluor dyes, Pacific Blue™, Pacific Orange™, Cascade Yellow™.

464. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group AlexaFluor®(AF), AF405, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750, AF800.

465. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Quantum Dot based dyes, QDot® Nanocrystals (Invitrogen, MolecularProbs), Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800.

466. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group DyLight™ Dyes (Pierce) (DL); DL549, DL649, DL680, DL800.

467. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Fluorescein (Flu) or any derivate of that, such as FITC.

468. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Cy-Dyes, Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7.

469. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Fluorescent Proteins, RPE, PerCp, APC, Green fluorescent proteins; GFP and GFP derivated mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine, mStrawberry, mCherry.

470. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group Tandem dyes, RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed, APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

471. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group multi fluorochrome assemblies, Multiple fluorochromes attached to a polymer molecule, such as a peptide/protein, Dextrane, polysaccharide, any combination of the fluorescent dyes involving in generation of FRET (Fluorescence resonance energy transfer) based techniques.

472. The MHC multimer according to claim 462, wherein the one or more simple fluorescent label is selected from the group ionophors; ion chelating fluorescent props, props that change wavelength when binding a specific ion, such as Calcium, props that change intensity when binding to a specific ion, such as Calcium.

473. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is capable of absorption of light

474. The MHC multimer according to claim 473, wherein the one or more labels capable of absorption of light is a chromophore.

475. The MHC multimer according to claim 473, wherein the one or more labels capable of absorption of light is a dye.

476. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is capable of emission of light after excitation

477. The MHC multimer according to claim 476, wherein the one or more labels capable of emission of light is one or more fluorochromes.

478. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the AlexaFluor®(AF) family, which include AF®350, AF405, AF430, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750 and AF800

479. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the Quantum Dot (Qdot®) based dye family, which include Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800

480. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the DyLight™ Dyes (DL) family, which include DL549, DL649, DL680, DL800

481. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Small fluorescing dyes, which include FITC, Pacific Blue™, Pacific Orange™, Cascade Yellow™, Marina blue™, DSred, DSred-2, 7-AAD, TO-Pro-3.

482. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Cy-Dyes, which include Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7

483. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Phycobili Proteins, which include R-Phycoerythrin (RPE), PerCP, Allophycocyanin (APC), B-Phycoerythrin, C-Phycocyanin.

484. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Fluorescent Proteins, which include (E)GFP and GFP ((enhanced) green fluorescent protein) derived mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine.

485. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Tandem dyes with RPE, which include RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed.

486. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Tandem dyes with APC, which include APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

487. The MHC multimer according to claim 477, wherein the one or more fluorochrome is selected from the family of Calcium dyes, which include Indo-1-Ca^{2+} Indo-2-Ca^{2+}.

488. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is capable of reflection of light

489. The MHC multimer according to claim 488, wherein the one or more labels capable of reflection of light comprises gold

490. The MHC multimer according to claim 488, wherein the one or more labels capable of reflection of light comprises plastic

491. The MHC multimer according to claim 488, wherein the one or more labels capable of reflection of light comprises glass

492. The MHC multimer according to claim 488, wherein the one or more labels capable of reflection of light comprises polystyrene

493. The MHC multimer according to claim 488, wherein the one or more labels capable of reflection of light comprises pollen

494. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a chemiluminescent label.

495. The MHC multimer according to claim 494, wherein the chemiluminescent labels is selected from the group luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

496. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a bioluminescent label.

497. The MHC multimer according to claim 496, wherein the bioluminescent labels is selected from the group luciferin, luciferase and aequorin.

498. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a radioactive label.

499. The MHC multimer according to claim 498, wherein the one or more radioactive labels is a radionuclide.

500. The MHC multimer according to claim 498, wherein the one or more radioactive labels is an isotope.

501. The MHC multimer according to claim 498, wherein the one or more radioactive labels comprises α rays.

502. The MHC multimer according to claim 498, wherein the one or more radioactive labels comprises β rays.

503. The MHC multimer according to claim 498, wherein the one or more radioactive labels comprises γ rays.

504. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is detectable by NMR (nuclear magnetic resonance form paramagnetic molecules)

505. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is an enzyme label.

506. The MHC multimer according to claim 505, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, producing a light signal (chemi-luminescence).

507. The MHC multimer according to claim 505, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitation of chromophor dyes.

508. The MHC multimer according to claim 505, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitates that can be detected by an additional layer of detection molecules.

509. The MHC multimer according to claim 505, wherein the enzyme label is selected from the group peroxidases, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate, dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-

galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase.

510. The MHC multimer according to claim 505, wherein the enzyme label is horseradish peroxidase.

511. The MHC multimer according to claim 505, wherein the enzyme label is horseradish peroxidase and the substrate is diaminobenzidine (DAB).

512. The MHC multimer according to claim 505, wherein the enzyme label is horseradish peroxidase and the substrate is 3-amino-9-ethyl-carbazole (AEC+).

513. The MHC multimer according to claim 505, wherein the enzyme label is horseradish peroxidase and the substrate is biotinyl tyramide.

514. The MHC multimer according to claim 505, wherein the enzyme label is horseradish peroxidase and the substrate is fluorescein tyramide.

515. The MHC multimer according to claim 505, wherein the enzyme label is alkaline phosphatase.

516. The MHC multimer according to claim 505, wherein the enzyme label is alkaline phosphatase and the substrate is Fast red dye.

517. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a ionophore or chelating chemical compound binding to specific ions such as Ca^{2+}

518. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a lanthanide.

519. The MHC multimer according to claim 518, wherein the lanthanide comprises fluorescence.

520. The MHC multimer according to claim 518, wherein the lanthanide comprises Phosphorescence.

521. The MHC multimer according to claim 518, wherein the lanthanide is paramagnetic.

522. The MHC multimer according to any of claims 415 to 434, wherein the one or more labels is a DNA fluorescing stain.

523. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is Propidium iodide.

524. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is Hoechst stain.

525. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is DAPI.

526. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is AMC.

527. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is DraQ5™

528. The MHC multimer according to claim 522, wherein the DNA fluorescing stain is Acridine orange.

529. The MHC multimer according to claim 361, wherein the MHC-peptide complex (a-b-P) is attached to the first multimerization domain comprising an avidin or streptavidin via a linkage comprising a biotin moiety.

530. The MHC multimer according to any of claims 361 to 529, wherein the MHC-peptide complex is linked to the first multimerization domain by a first linker moiety.

531. The MHC multimer according to claim 530, wherein the MHC-peptide complex is linked to the first multimerization domain by a covalent linker moiety.

532. The MHC multimer according to claims 530 and 531, wherein the association of the first multimerization domain and at least one MHC-peptide complexes is formed by a binding entity X attached to, or being part of, the first multimerization domain, and a binding entity Y attached to, or being part of at least one of the MHC-peptide complexes.

533. The MHC multimer according to claims 530 and 531, wherein the linker moiety linking the first multimerization domain and the MHC-peptide complex comprises the linker moiety XY, wherein the linker moiety XY results from a reaction of the moiety X comprising one or more reactive groups and the moiety Y comprising one or more reactive groups, wherein at least some of said reactive groups are capable of reacting with each other.

534. The MHC multimer according to any of claims 532 and 533, wherein the moiety X comprises a nucleophilic group.

535. The MHC multimer according to claim 534, wherein the nucleophilic group is selected from the group consisting of $-NH_2$, -OH, -SH, $-NH-NH_2$.

536. The MHC multimer according to any of claims 532 and 533, wherein the moiety Y comprises an electrophilic group.

537. The MHC multimer according to claim 536, wherein the electrophilic group is selected from the group consisting of CHO, COOH and CO.

538. The MHC multimer according to claims 532 and 533, wherein at least one reactive group on one of the moieties X and Y comprises a radical capable of reacting with a reactive group forming part of the other moiety.

539. The MHC multimer according to claims 532 and 533, wherein X and Y comprises reactive groups natively associated with the first multimerization domain and/or the MHC-peptide complexes.

540. The MHC multimer according to claims 532 and 533, wherein X and Y comprises reactive groups not natively associated with the first multimerization domain and/or the MHC-peptide complex.

541. The MHC multimer according to claims 530 and 531, wherein the linker moiety forms a covalent link between the first multimerization domain and at least one of the MHC-peptide complexes.

542. The MHC multimer according to claims 532 and 533, wherein the reactive groups of MHC-peptide complexes include amino acid side chains selected from the group consisting of $-NH_2$, -OH, -SH, and -NH-

543. The MHC multimer according to claims 532 and 533, wherein the reactive groups of the first multimerization domain include hydroxyls of polysaccharides such as dextrans

544. The MHC multimer according to claims 532 and 533, wherein the reactive groups of the first multimerization domain selected from the group consisting of amino acid side chains comprising $-NH_2$, -OH, -SH, and -NH- of polypeptides

545. The MHC multimer according to claims 530 and 531, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the first multimerization domain

546. The MHC multimer according to claims 530 and 531, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the first multimerization domain, wherein an acyl group and an amino group react to form an amide bond

547. The MHC multimer according to claim 361, wherein one of the polypeptides of the MHC-peptide complex is linked by non-native reactive groups to the first multimerization domain.

548. The MHC multimer according to claim 361, wherein the reactive groups include reactive groups that are attached to the first multimerization domain through association of a linker molecule comprising the reactive group.

549. The MHC multimer according to claim 361, wherein the reactive groups include reactive groups that are attached to the MHC-peptide complex through association of a linker molecule comprising the reactive group.

550. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more nucleophilic groups

551. The MHC multimer according to claim 550, wherein the nucleophilic group is selected from the group consisting of $–NH_2$, -OH, -SH, -CN, $-NH-NH_2$

552. The MHC multimer according to claim 363, wherein the first multimerization domain is selected from the group consisting of polysaccharides, polypeptides comprising e.g. lysine, serine, and cysteine.

553. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more electrophilic groups.

554. The MHC multimer according to claim 553, wherein the electrophilic group is selected from the group consisting of –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides.

555. The MHC multimer according to claim 363, wherein the first multimerization domain is selected from the group consisting of polypeptides comprising e.g. glutamate and aspartate, or vinyl sulfone activated dextran.

556. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more radicals.

557. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more conjugated double bonds.

558. The MHC multimer according to claim 363, wherein the first multimerization domain comprises one or more beads, further comprising a linker moiety

559. The MHC multimer according to any of the claims 530 to 558, wherein the linker is a flexible linker.

560. The MHC multimer according to any of the claims 530 to 558, wherein the linker is a rigid linker.

561. The MHC multimer according to any of the claims 530 to 558, wherein the linker is a water-soluble linker.

562. The MHC multimer according to any of the claims 530 to 558, wherein the linker is a cleavable linker.

563. The MHC multimer according to claim 562, wherein the cleavable linker is selected from linkers depicted in Figure 6 herein.

564. The MHC multimer according to claim 562, wherein the cleavable linker is cleavable at physiological conditions.

565. The MHC multimer according to claims 530 or 531, wherein the MHC-peptide complex is linked to the first multimerization domain by a non-covalent linker moiety.

566. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises natural dimerization

567. The MHC multimer according to claim 566, wherein the natural dimerization comprises antigen-antibody pairs

568. The MHC multimer according to claim 566, wherein the natural dimerization comprises DNA-DNA interactions

569. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises natural interactions

570. The MHC multimer according to claim 569, wherein the natural interaction comprises biotin and streptavidin

571. The MHC multimer according to claim 401, wherein the bead is coated with streptavidin monomers, which in turn are associated with biotinylated MHC complexes

572. The MHC multimer according to claim 401, wherein the bead is coated with streptavidin tetramers, each of which being independently associated with 0, 1, 2, 3, or 4 biotinylated MHC complexes

573. The MHC multimer according to claim 401, wherein the bead is coated with a polysaccharide, such as a polysaccharide comprising dextran moieties.

574. The MHC multimer according to claim 569, wherein the natural interaction comprises the interaction of MHC complexes (comprising full-length polypeptide chains, including the transmembrane portion) with the cell membrane of for example dendritic cells

575. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises artificial interactions

576. The MHC multimer according to claim 575, wherein the artificial interaction comprises His_6 tag interacting with Ni-NTA

577. The MHC multimer according to claim 575, wherein the artificial interaction comprises PNA-PNA

578. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises non-specific adsorption

579. The MHC multimer according to claim 578, wherein the non-specific adsorption comprises adsorption of proteins onto surfaces

580. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises the pentamer structure

581. The MHC multimer according to claim 565, wherein the non-covalent linkage comprises interactions selected from the group streptavidin/biotin, avidin/biotin, antibody/antigen, DNA/DNA, DNA/PNA, DNA/RNA, PNA/PNA, LNA/DNA, leucine zipper e.g. Fos/Jun, IgG dimeric protein, IgM multivalent protein, acid/base coiled-coil helices, chelate/metal ion-bound chelate, streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-transferase) glutathione affinity, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (Canavalia ensiformis) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity).

582. The MHC multimer according to claim 365, wherein the association is a covalent linkage so that one or more of the n MHC-peptide complexes is covalently linked to the second multimerization domains.

583. The MHC multimer according to claim 365 wherein the association is a non-covalent association so that one or more of the n MHC-peptide complexes is non-covalently associated with the second multimerization domain.

584. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more scaffolds.

585. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more carriers.

586. The MHC multimer according to claim 363, wherein the second multimerization domain comprises at least one scaffold and at least one carrier.

587. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more optionally substituted organic molecules.

588. The MHC multimer according to claim 587, wherein the optionally substituted organic molecule comprises one or more functionalized cyclic structures.

589. The MHC multimer according to claim 588 wherein the one or more functionalized cyclic structures comprises one or more benzene rings.

590. The MHC multimer according to claim 587, wherein the optionally substituted organic molecule comprises a scaffold molecule comprising at least three reactive groups, or at least three sites suitable for non-covalent attachment.

591. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more biological cells, such as antigen presenting cells or dendritic cells.

592. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more membranes.

593. The MHC multimer according to claim 592, wherein the one or more membranes comprises liposomes or micelles.

594. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more polymers.

595. The MHC multimer according to claim 594 wherein the one or more polymers are selected from the group consisting of the group consisting of polysaccharides.

596. The MHC multimer according to claim 595, wherein the polysaccharide comprises one or more dextran moieties.

597. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more entities selected from the group consisting of an IgG domain, a coiled-coil polypeptide structure, a DNA duplex, a nucleic acid duplex, PNA-PNA, PNA-DNA, DNA-RNA.

598. The MHC multimer according to claim 363, wherein the second multimerization domain comprises an avidin, such as streptavidin.

599. The MHC multimer according to claim 363, wherein the second multimerization domain comprises an antibody.

600. The MHC multimer according to claim 599, wherein the antibody is selected from the group consisting of polyclonal antibody, monoclonal antibody, IgA, IgG, IgM, IgD, IgE, IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM1, IgM2, humanized antibody, humanized monoclonal antibody, chimeric antibody, mouse antibody, rat antibody, rabbit antibody, human antibody, camel antibody, sheep antibody, engineered human antibody, epitope-focused antibody, agonist antibody, antagonist antibody, neutralizing antibody, naturally-occurring antibody, isolated antibody, monovalent antibody, bispecific antibody, trispecific antibody, multispecific antibody, heteroconjugate antibody, immunoconjugates, immunoliposomes, labeled antibody, antibody fragment, domain antibody, nanobody, minibody, maxibody, diabody, fusion antibody.

601. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more small organic scaffold molecules.

602. The MHC multimer according to claim 363, wherein the second multimerization comprises one or more further polypeptides in addition to a and b.

603. The MHC multimer according to claim 363, wherein the second multimerization comprises one or more protein complexes.

604. The MHC multimer according to claim 363, wherein the second multimerization comprises one or more beads

605. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more compounds selected from the group consisting of agarose, sepharose, resin beads, glass beads, pore-glass beads, glass particles coated with a hydrophobic polymer, chitosan-coated beads, SH beads, latex beads ,spherical latex beads, allele-type beads, SPA bead, PEG-based resins, PEG-coated bead, PEG-encapsulated bead, polystyrene beads, magnetic polystyrene beads, glutathione agarose beads, magnetic bead, paramagnetic beads, protein A and/or protein G sepharose beads, activated carboxylic acid bead, macroscopic beads, microscopic beads, insoluble resin beads, silica-based resins, cellulosic resins, cross-linked agarose beads, polystyrene beads, cross-linked polyacrylamide resins, beads with iron cores, metal beads, dynabeads, Polymethylmethacrylate beads activated with NHS, streptavidin-agarose beads, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, nitrocellulose, polyacrylamides, gabbros, magnetite, polymers, oligomers, non-repeating moieties, polyethylene glycol (PEG), monomethoxy-PEG, mono-(C_1-C_{10})alkoxy-PEG, aryloxy-PEG, poly-(N-vinyl pyrrolidone)PEG, tresyl monomethoxy PEG, PEG propionaldehyde, bis-succinimidyl carbonate PEG, polystyrene bead crosslinked with divinylbenzene, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, dextran, aminodextran, carbohydrate-based polymers, cross-linked dextran beads, polysaccharide beads, polycarbamate beads, divinyl sulfone activated polysaccharide, polystyrene beads that have been functionalized with tosyl-activated esters, magnetic polystyrene beads functionalized with tosyl-activated esters, streptavidin beads, streptaivdin-monomer coated beads, streptaivdin-tetramer coated beads, Streptavidin Coated Compel Magnetic beads, avidin coated beads, dextramer coated beads, divinyl sulfone-activated dextran, Carboxylate-modified bead, amine-modified beads, antibody coated beads, cellulose beads, grafted co-poly beads, poly-acrylamide beads, dimethylacrylamide beads optionally crosslinked with N-N'-bis-acryloylethylenediamine, hollow fiber membranes, fluorescent beads, collagen-agarose beads, gelatin beads, collagen-gelatin beads, collagen-fibronectin-gelatin beads, collagen beads, chitosan beads, collagen-chitosan beads, protein-based beads, hydrogel beads, hemicellulose, alkyl cellulose, hydroxyalkyl cellulose, carboxymethylcellulose, sulfoethylcellulose, starch, xylan, amylopectine, chondroitin, hyarulonate, heparin, guar, xanthan, mannan, galactomannan, chitin and chitosan.

606. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a dimerization domain.

607. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a trimerization domain.

608. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a tetramerization domain.

609. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a pentamerization domain.

610. The MHC multimer according to claim 609, wherein the pentamerization domain comprises a coiled-coil polypeptide structure.

611. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a hexamerization domain.

612. The MHC multimer according to claim 611, wherein the hexamerization domain comprises three IgG domains.

613. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a polymer structure to which is attached one or more scaffolds.

614. The MHC multimer according to claim 613, wherein the polymer structure comprises a polysaccharide.

615. The MHC multimer according to claim 614, wherein the polysaccharide comprises one or more dextran moieties.

616. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a polyamide and/or a polyethylene glycol and/or a polysaccharide and/or a sepharose.

617. The MHC multimer according to claim 363, wherein the second multimerization domain comprises a carboxy methyl dextran and/or a dextran polyaldehyde and/or a carboxymethyl dextran lactone and/or a cyclodextrin.

618. The MHC multimer according to claim 363, wherein one or more labels is covalently attached to the second multimerization domain.

619. The MHC multimer according to claim 363, wherein one or more labels is non-covalently attached to the second multimerization domain.

620. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to an antibody in the second mutimerization domain.

621. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to an antibody in the second mutimerization domain.

622. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to an aptamer in the second mutimerization domain.

623. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to an aptamer in the second mutimerization domain.

624. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to a molecule in the second mutimerization domain.

625. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to a molecule in the second mutimerization domain.

626. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to a protein in the second mutimerization domain.

627. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to a protein in the second mutimerization domain.

628. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to a sugar residue in the second mutimerization domain.

629. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to a sugar residue in the second mutimerization domain.

630. The MHC multimer according to claim 619, wherein the one or more labels is non-covalently attached to a DNA in the second mutimerization domain.

631. The MHC multimer according to claim 618, wherein the one or more labels is covalently attached to a DNA in the second mutimerization domain.

632. The MHC multimer according to any of the claims 618 to 631, wherein the attachment is directly between reactive groups in the labelling molecule and reactive groups in the marker molecule.

633. The MHC multimer according to any of the claims 618 to 631, wherein the attachment is through a linker connecting labelling molecule and marker.

634. The MHC multimer according to any of the claims 618 to 631, wherein one label is used.

635. The MHC multimer according to any of the claims 618 to 631, wherein more than one label is used.

636. The MHC multimer according to claim 635, wherein the more than one label are all identical.

637. The MHC multimer according to claim 635, wherein at least two labels are different.

638. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a fluorophore.

639. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of selected from the group fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

640. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 2-(4'-maleimidylanilino)naphthalene-6- sulfonic acid, sodium salt

641. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 5-((((2-iodoacetyl)amino)ethyl)amino) naphthalene-1-sulfonic acid

642. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Pyrene-1-butanoic acid

643. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of AlexaFluor 350 (7-amino-6-sulfonic acid-4-methyl coumarin-3-acetic acid

644. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of AMCA (7-amino-4-methyl coumarin-3-acetic acid

645. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-4-methyl coumarin-3-acetic acid

646. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Marina Blue (6,8-difluoro-7-hydroxy-4-methyl coumarin-3-acetic acid

647. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 7-dimethylamino-coumarin-4-acetic acid

648. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Fluorescamin-N-butyl amine adduct

649. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 7-hydroxy-coumarine-3-carboxylic acid

650. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of CascadeBlue (pyrene-trisulphonic acid acetyl azide

651. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Cascade Yellow

652. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Pacific Blue (6,8 difluoro-7-hydroxy coumarin-3-carboxylic acid

653. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 7-diethylamino-coumarin-3-carboxylic acid

654. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of N-(((4-azidobenzoyl)amino)ethyl)- 4-amino-3,6-disulfo-1,8-naphthalimide, dipotassium salt

655. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Alexa Fluor 430

656. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 3-perylenedodecanoic acid

657. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 8-hydroxypyrene-1,3,6-trisulfonic acid, trisodium salt

658. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 12-(N-(7-nitrobenz-2-oxa-1,3- diazol-4-yl)amino)dodecanoic acid

659. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of N,N'-dimethyl-N-(iodoacetyl)-N'-(7-nitrobenz-2- oxa-1,3-diazol-4-yl)ethylenediamine

660. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Oregon Green 488 (difluoro carboxy fluorescein)

661. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of 5-iodoacetamidofluorescein

662. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of propidium iodide-DNA adduct

663. The MHC multimer according to claim 638, wherein the one or more fluorophore label are selected from the group consisting of Carboxy fluorescein

664. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a fluorescent label.

665. The MHC multimer according to claim 664, wherein the one or more fluorescent label is a simple fluorescent label

666. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Fluor dyes, Pacific Blue™, Pacific Orange™, Cascade Yellow™

667. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group AlexaFluor®(AF), AF405, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750, AF800.

668. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Quantum Dot based dyes, QDot® Nanocrystals (Invitrogen, MolecularProbs), Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800.

669. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group DyLight™ Dyes (Pierce) (DL); DL549, DL649, DL680, DL800.

670. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Fluorescein (Flu) or any derivate of that, such as FITC

671. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Cy-Dyes, Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7.

672. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Fluorescent Proteins, RPE, PerCp, APC, Green fluorescent proteins; GFP and GFP derivated mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine, mStrawberry, mCherry.

673. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group Tandem dyes, RPE-Cy5, RPE-Cy5.5,

RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed, APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

674. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group multi fluorochrome assemblies, Multiple fluorochromes attached to a polymer molecule, such as a peptide/protein, Dextrane, polysaccharide, any combination of the fluorescent dyes involving in generation of FRET (Fluorescence resonance energy transfer) based techniques.

675. The MHC multimer according to claim 664, wherein the one or more simple fluorescent label is selected from the group ionophors; ion chelating fluorescent props, props that change wavelength when binding a specific ion, such as Calcium, props that change intensity when binding to a specific ion, such as Calcium.

676. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is capable of absorption of light

677. The MHC multimer according to claim 676, wherein the one or more labels capable of absorption of light is a chromophore.

678. The MHC multimer according to claim 676, wherein the one or more labels capable of absorption of light is a dye.

679. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is capable of emission of light after excitation

680. The MHC multimer according to claim 679, wherein the one or more labels capable of emission of light is one or more fluorochromes.

681. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the AlexaFluor®(AF) family, which include AF®350, AF405, AF430, AF488,AF500, AF514, AF532, AF546, AF555, AF568, AF594, AF610, AF633, AF635, AF647, AF680, AF700, AF710, AF750 and AF800

682. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the Quantum Dot (Qdot®) based dye family, which include Qdot®525, Qdot®565, Qdot®585, Qdot®605, Qdot®655, Qdot®705, Qdot®800

683. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the DyLight™ Dyes (DL) family, which include DL549, DL649, DL680, DL800

684. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Small fluorescing dyes, which include FITC, Pacific Blue™, Pacific Orange™, Cascade Yellow™, Marina blue™, DSred, DSred-2, 7-AAD, TO-Pro-3.

685. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Cy-Dyes, which include Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7

686. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Phycobili Proteins, which include R-Phycoerythrin (RPE), PerCP, Allophycocyanin (APC), B-Phycoerythrin, C-Phycocyanin.

687. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Fluorescent Proteins, which include (E)GFP and GFP ((enhanced) green fluorescent protein) derived mutant proteins; BFP,CFP, YFP, DsRed, T1, Dimer2, mRFP1,MBanana, mOrange, dTomato, tdTomato, mTangerine.

688. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Tandem dyes with RPE, which include RPE-Cy5, RPE-Cy5.5, RPE-Cy7, RPE-AlexaFluor® tandem conjugates; RPE-Alexa610, RPE-TxRed.

689. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Tandem dyes with APC, which include APC-Aleca600, APC-Alexa610, APC-Alexa750, APC-Cy5, APC-Cy5.5.

690. The MHC multimer according to claim 680, wherein the one or more fluorochrome is selected from the family of Calcium dyes, which include Indo-1-Ca^{2+} Indo-2-Ca^{2+}.

691. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is capable of reflection of light

692. The MHC multimer according to claim 691, wherein the one or more labels capable of reflection of light comprises gold

693. The MHC multimer according to claim 691, wherein the one or more labels capable of reflection of light comprises plastic

694. The MHC multimer according to claim 691, wherein the one or more labels capable of reflection of light comprises glass

695. The MHC multimer according to claim 691, wherein the one or more labels capable of reflection of light comprises polystyrene

696. The MHC multimer according to claim 691, wherein the one or more labels capable of reflection of light comprises pollen

697. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a chemiluminescent label.

698. The MHC multimer according to claim 697, wherein the chemiluminescent labels is selected from the group luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

699. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a bioluminescent label.

700. The MHC multimer according to claim 699, wherein the bioluminescent labels is selected from the group consisting of luciferin, luciferase and aequorin.

701. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a radioactive label.

702. The MHC multimer according to claim 701, wherein the one or more radioactive labels is a radionuclide.

703. The MHC multimer according to claim 701, wherein the one or more radioactive labels is an isotope.

704. The MHC multimer according to claim 701, wherein the one or more radioactive labels comprises α rays.

705. The MHC multimer according to claim 701, wherein the one or more radioactive labels comprises β rays.

706. The MHC multimer according to claim 701, wherein the one or more radioactive labels comprises γ rays.

707. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is detectable by NMR (nuclear magnetic resonance form paramagnetic molecules)

708. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is an enzyme label.

709. The MHC multimer according to claim 708, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, producing a light signal (chemi-luminescence)

710. The MHC multimer according to claim 708, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitation of chromophor dyes

711. The MHC multimer according to claim 708, wherein the enzyme catalyze a reaction between chemicals in the near environment of the labeling molecules, resulting in precipitates that can be detected by an additional layer of detection molecules

712. The MHC multimer according to claim 708, wherein the enzyme label is selected from the group peroxidases, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate, dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase.

713. The MHC multimer according to claim 708, wherein the enzyme label is horseradish peroxidase.

714. The MHC multimer according to claim 708, wherein the enzyme label is horseradish peroxidase and the substrate is diaminobenzidine (DAB).

715. The MHC multimer according to claim 708, wherein the enzyme label is horseradish peroxidase and the substrate is 3-amino-9-ethyl-carbazole (AEC+).

716. The MHC multimer according to claim 708, wherein the enzyme label is horseradish peroxidase and the substrate is biotinyl tyramide.

717. The MHC multimer according to claim 708, wherein the enzyme label is horseradish peroxidase and the substrate is fluorescein tyramide.

718. The MHC multimer according to claim 708, wherein the enzyme label is alkaline phosphatase.

719. The MHC multimer according to claim 708, wherein the enzyme label is alkaline phosphatase and the substrate is Fast red dye

720. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a ionophore or chelating chemical compound binding to specific ions such as Ca^{2+}

721. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a lanthanide.

722. The MHC multimer according to claim 721, wherein the lanthanide comprises fluorescence.

723. The MHC multimer according to claim 721, wherein the lanthanide comprises Phosphorescence.

724. The MHC multimer according to claim 721, wherein the lanthanide is paramagnetic

725. The MHC multimer according to any of claims 618 to 637, wherein the one or more labels is a DNA fluorescing stain

726. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is Propidium iodide

727. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is Hoechst stain

728. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is DAPI

729. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is AMC

730. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is DraQ5™

731. The MHC multimer according to claim 725, wherein the DNA fluorescing stain is Acridine orange

732. The MHC multimer according to claim 361, wherein the MHC-peptide complex (a-b-P) is attached to the second multimerization domain comprising an avidin or streptavidin via a linkage comprising a biotin moiety.

733. The MHC multimer according to any of claims 582 to 732, wherein the MHC-peptide complex is linked to the second multimerization domain by a second linker moiety.

734. The MHC multimer according to claim 733, wherein the MHC-peptide complex is linked to the second multimerization domain by a covalent linker moiety.

735. The MHC multimer according to claims 733 and 734, wherein the linkage of the second multimerization domain and at least one MHC-peptide complexes is formed by a binding entity X attached to, or being part of, the second multimerization domain, and a binding entity Y attached to, or being part of at least one of the MHC-peptide complexes.

736. The MHC multimer according to claims 733 and 734, wherein the linker moiety linking the second multimerization domain and the MHC-peptide complex comprises the linker moiety XY, wherein the linker moiety XY results from a reaction of the moiety X comprising one or more reactive groups and the moiety Y comprising one or more reactive groups, wherein at least some of said reactive groups are capable of reacting with each other.

737. The MHC multimer according to claim 736, wherein the moiety X comprises a nucleophilic group.

738. The MHC multimer according to claim 737, wherein the nucleophilic group is selected from the group consisting of $-NH_2$, -OH, -SH, $-NH-NH_2$.

739. The MHC multimer according to claim 736, wherein the moiety Y comprises an electrophilic group.

740. The MHC multimer according to claim 739, wherein the electrophilic group is selected from the group consisting of CHO, COOH and CO.

741. The MHC multimer according to claims 733 and 734, wherein at least one of the reactive groups on one of the moieties X and Y comprises a radical capable of reacting with a reactive group forming part of the other moiety.

742. The MHC multimer according to claims 733 and 734, wherein X and Y comprises reactive groups natively associated with the second multimerization domain and/or the MHC-peptide complexes.

743. The MHC multimer according to claims 733 and 734, wherein X and Y comprises reactive groups not natively associated with the second multimerization domain and/or the MHC-peptide complex.

744. The MHC multimer according to claims 733 and 734, wherein the linker moiety forms a covalent link between the second multimerization domain and at least one of the MHC-peptide complexes.

745. The MHC multimer according to claims 733 and 734, wherein the reactive groups of MHC-peptide complexes include amino acid side chains selected from the group consisting of $-NH_2$, -OH, -SH, and -NH-

746. The MHC multimer according to claims 733 and 734, wherein the reactive groups of the second multimerization domain include hydroxyls of polysaccharides such as dextrans

747. The MHC multimer according to claims 733 and 734, wherein the reactive groups of the second multimerization domain selected from the group consisting of amino acid side chains comprising $-NH_2$, -OH, -SH, and -NH- of polypeptides

748. The MHC multimer according to claims 733 and 734, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the second multimerization domain

749. The MHC multimer according to claims 733 and 734, wherein one of the polypeptides of the MHC-peptide complex is linked by a protein fusion to the second multimerization domain, wherein an acyl group and an amino group react to form an amide bond

750. The MHC multimer according to claim 363, wherein one of the polypeptides of the MHC-peptide complex is linked by non-native reactive groups to the second multimerization domain.

751. The MHC multimer according to claim 363, wherein the reactive groups include reactive groups that are attached to the second multimerization domain through association of a linker molecule comprising the reactive group.

752. The MHC multimer according to claim 363, wherein the reactive groups include reactive groups that are attached to the MHC-peptide complex through association of a linker molecule comprising the reactive group.

753. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more nucleophilic groups

754. The MHC multimer according to claim 753, wherein the nucleophilic group is selected from the group consisting of $–NH_2$, -OH, -SH, -CN, $-NH-NH_2$

755. The MHC multimer according to claim 363, wherein the second multimerization domain is selected from the group consisting of polysaccharides, polypeptides comprising e.g. lysine, serine, and cysteine.

756. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more electrophilic groups.

757. The MHC multimer according to claim 756, wherein the electrophilic group is selected from the group consisting of –COOH, -CHO, -CO, NHS-ester, tosyl-activated ester, and other activated esters, acid-anhydrides.

758. The MHC multimer according to claim 363, wherein the second multimerization domain is selected from the group consisting of polypeptides comprising e.g. glutamate and aspartate, or vinyl sulfone activated dextran.

759. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more radicals.

760. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more conjugated double bonds.

761. The MHC multimer according to claim 363, wherein the second multimerization domain comprises one or more beads, further comprising a linker moiety

762. The MHC multimer according to any of the claims 733 to 761, wherein the linker is a flexible linker.

763. The MHC multimer according to any of the claims 733 to 761, wherein the linker is a rigid linker.

764. The MHC multimer according to any of the claims 733 to 761, wherein the linker is a water-soluble linker.

765. The MHC multimer according to any of the claims 733 to 761, wherein the linker is a cleavable linker.

766. The MHC multimer according to claim 765, wherein the cleavable linker is selected from linkers depicted in (fig 6).

767. The MHC multimer according to claim 765, wherein the cleavable linker is cleavable at physiological conditions

768. The MHC multimer according to claims 733 and 733, wherein the MHC-peptide complex is linked to the second multimerization domain by a non-covalent linker moiety.

769. The MHC multimer according to claim 768, wherein the non-covalent linkage comprises natural dimerization

770. The MHC multimer according to claim 769, wherein the natural dimerization comprises antigen-antibody pairs.

771. The MHC multimer according to claim 769, wherein the natural dimerization comprises DNA-DNA interactions

772. The MHC multimer according to claim 768, wherein the non-covalent linkage comprises natural interactions

773. The MHC multimer according to claim 772, wherein the natural interaction comprises biotin and streptavidin.

774. The MHC multimer according to claim 604, wherein the bead is coated with streptavidin monomers, which in turn are associated with biotinylated MHC complexes.

775. The MHC multimer according to claim 604, wherein the bead is coated with streptavidin tetramers, which in turn are associated with 0, 1, 2, 3, or 4 biotinylated MHC complexes.

776. The MHC multimer according to claim 604, wherein the bead is coated with a polysaccharide, such as a polysaccharide comprising a dextran moiety.

777. The MHC multimer according to claim 772, wherein the natural interaction comprises the interaction of MHC complexes (comprising full-length polypeptide chains, including the transmembrane portion) with the cell membrane of for example dendritic cells.

778. The MHC multimer according to claim 768, wherein the non-covalent linkage comprises artificial interactions.

779. The MHC multimer according to claim 778, wherein the artificial interaction comprises His_6 tag interacting with Ni-NTA.

780. The MHC multimer according to claim 778, wherein the artificial interaction comprises PNA-PNA

781. The MHC multimer according to claim 768, wherein the non-covalent linkage comprises non-specific adsorption.

782. The MHC multimer according to claim 781, wherein the non-specific adsorption comprises adsorption of proteins onto surfaces.

783. The MHC multimer according to claim 768 wherein the non-covalent linkage comprises the pentamer structure.

784. The MHC multimer according to claim 768, wherein the non-covalent linkage comprises interactions selected from the group streptavidin/biotin, avidin/biotin, antibody/antigen, DNA/DNA, DNA/PNA, DNA/RNA, PNA/PNA, LNA/DNA, leucine zipper e.g. Fos/Jun, IgG dimeric protein, IgM multivalent protein, acid/base coiled-coil helices, chelate/metal ion-bound chelate, streptavidin (SA) and avidin and derivatives thereof, biotin, immunoglobulins, antibodies (monoclonal, polyclonal, and recombinant), antibody fragments and derivatives thereof, leucine zipper domain of AP-1 (jun and fos), hexa-his (metal chelate moiety), hexa-hat GST (glutathione S-transferase) glutathione affinity, Calmodulin-binding peptide (CBP), Strep-tag, Cellulose Binding Domain, Maltose Binding Protein, S-Peptide Tag, Chitin Binding Tag, Immuno-reactive Epitopes, Epitope Tags, E2Tag, HA Epitope Tag, Myc Epitope, FLAG Epitope, AU1 and AU5 Epitopes, Glu-Glu Epitope, KT3 Epitope, IRS Epitope, Btag Epitope, Protein Kinase-C Epitope, VSV Epitope, lectins that mediate binding to a diversity of compounds, including carbohydrates, lipids and proteins, e.g. Con A (Canavalia ensiformis) or WGA (wheat germ agglutinin) and tetranectin or Protein A or G (antibody affinity).

785. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from a virus polypeptide.

786. The monomer or MHC multimer according to claim 785, wherein the virus is selected from the group consisting of Adenovirus (subgropus A-F), BK-virus, CMV (Cytomegalo virus, HHV-5), EBV (Epstein Barr Virus, HHV-4), HBV (Hepatitis B Virus), HCV (Hepatitis C virus), HHV-6a and b (Human Herpes Virus-6a and b), HHV-7, HHV-8, HSV-1 (Herpes simplex virus-1, HHV-1), HSV-2 (HHV-2), JC-virus, SV-40 (Simian virus 40), VZV (Varizella-Zoster-Virus, HHV-3), Parvovirus B19, Haemophilus influenza, HIV-1 (Human immunodeficiency Virus-1), HTLV-1 (Human T-lymphotrophic virus-1), HPV (Human Papillomavirus giving rise to clinical manifestions such as Hepatitis, AIDS, Measles, Pox, Chicken pox, Rubella, and Herpes.

787. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from a bacterial polypeptide.

788. The monomer or MHC multimer according to claim 787, wherein the bacterium is selected from the group consisting of Gram positive bacteria, Gram negative bacteria, intracellular bacterium, extracellular bacterium, Mycobacterium tuberculosis, Mycobacterium bovis, Mycobacterium avium subsp. paratuberculosis Borrelia burgdorferi, other spirochetes, Helicobacter pylori, Streptococcus pneumoniae, Listeria monocytogenes, Histoplasma capsulatum, Bartonella henselae, Bartonella quintana giving rise to clinical manifestations, such as Tuberculosis, Pneumonia, Stomach ulcers, and Paratuberculosis.

789. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from a fungal polypeptide.

790. The monomer or MHC multimer according to claim 789, wherein the virus is selected from the group consisting of Aspergillus fumigatus, Candida albicans, Cryptococcus neoformans, and Pneumocystis carinii giving rise to clinical manifestations, such as skin-, nail-, and mucosal infections, Meningitis, and Sepsis.

791. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from a polypeptide produced by a parasitic organism.

792. The monomer or MHC multimer according to claim 791, wherein the parasitic organism is selected from the group consisting of Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae, Schistosoma mansoni, Schistosoma japonicum, Schistosoma haematobium, Trypanosoma cruzi, Trypanosoma rhodesiense, Trypanosoma gambiense, Leishmania donovani, and Leishmania tropica.

793. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from a polypeptide produced by Birch, Hazel, Elm, Ragweed, Wormwood, Grass, Mould, and Dust Mite giving rise to clinical manifestations such as Asthma.

794. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from minor histocompatibility antigens, such as HA-1, HA-8, USP9Y, SMCY, TPR-protein, HB-1Y.

795. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from proteins from Borrelia.

796. The monomer or MHC multimer according to any of claims 1 to 784, wherein the peptide P originates from and/or is isolated from antigens, such as GAD64, Collagen, human cartilage glycoprotein 39, β-amyloid, Aβ42, APP, and Presenilin 1.

797. The monomer or MHC multimer according to any of claims 1 to 797, wherein the peptide P is selected from the group of antigenic peptides according to any one of the claims 1 and 1509-1537.

798. A method for generating the MHC multimer according to any of claims 1 to 797, said method comprising the steps of

i) providing one or more peptides P;
ii) providing one or more functional MHC proteins,
iii) optionally providing one or more multimerization domains, and
iv) contacting or reacting the one or more peptides P and the one or more functional MHC proteins and the one or more multimerization domains simultaneously or sequentialy in any order, thereby obtaining MHC multimers according to the present invention.

799. The method of claim 798, wherein said reaction(s) involves a covalent coupling of the MHC-peptide complex and the multimerization domain(s) comprising nucleophilic substitution by activation of electrophiles, preferably acylation, such as amide formation, pyrazolone formation, isoxazolone formation; alkylation; vinylation; and disulfide formation.

800. The method of claim 798, wherein said reaction(s) involves a covalent coupling of the MHC-peptide complex and the multimerization domain comprising addition to carbon-hetero multiple bonds, preferably by alkene formation by reaction of phosphonates with aldehydes or ketones; or arylation; alkylation of arenes/hetarenes by reaction with alkyl boronates or enolethers.

801. The method of claim 798, wherein said reaction(s) involves a covalent coupling of the MHC-peptide complex and the multimerization domain comprising nucleophilic substitution using activation of nucleophiles, preferably by condensations; alkylation of aliphatic halides or tosylates with enolethers or enamines.

802. The method of claim 798, wherein said reaction involves a covalent coupling of the MHC-peptide complex and the multimerization domain comprises cycloadditions.

803. The method of claim 798, wherein the one or more MHC peptide complexes comprises MHC class I heavy chain and/or beta2-Microglobulin.

804. The method of claim 803, wherein the MHC class I heavy chain and/or beta2-Microglobulin is derived from natural sources.

805. The method of claim 803, wherein the MHC class I heavy chain and/or beta2-Microglobulin is generated by recombinant means.

806. The method of claim 805, wherein the recombinant means comprises in vitro translation of mRNA obtained from expressing cells.

807. The method of claim 805, wherein the recombinant means comprises use of beta2-microglubulin and/or MHC class I Heavy chain transfected cells.

808. The method of claim 807, wherein the use of beta-2-microglubulin and/or MHC class I Heavy chain transfected cells comprises use of genetic material isolated from natural origin such as cells, one or more tissues and/or one or more organisms.

809. The method of claim 807, wherein the use of beta-2-microglubulin and/or MHC class I Heavy chain transfected cells comprises use of one or more synthetic genes identical to natural DNA sequence and/or modified.

810. The method of claim 807, wherein the beta-2-microglubulin is full length.

811. The method of claim 807, wherein the beta-2-microglubulin is a fragment.

812. The method of claim 803, wherein the MHC class I Heavy chain is full length.

813. The method of claim 803, wherein the MHC class I Heavy chain is a fragment.

814. The method of claim 813, wherein the MHC class I Heavy chain fragment comprises and/or consists of the complete chain minus the intramembrane domain.

815. The method of claim 813, wherein the MHC class I Heavy chain fragment comprises and/or consists of the alpha1 and alpha 2 class 1 heavy chain domains.

816. The method of claims 803 and 815, wherein the beta2-microglubulin and/or MHC class I Heavy chain fragment comprises one or more added designer domain(s) and/or sequences(s).

817. The method of claim 803, wherein the MHC class I heavy chain and/or beta2-Microglobulin is generated by chemical synthesis.

818. The method of claim 817, wherein the chemical synthesis comprises solid phase synthesis.

819. The method of claim 798, wherein the one or more MHC peptide complexes comprises MHC class II alpha and/or beta chain.

820. The method of claim 819, wherein the MHC class II alpha and/or beta chain is derived from natural sources.

821. The method of claim 819, wherein the MHC class II alpha and/or beta chain is generated by recombinant means.

822. The method of claim 821, wherein the recombinant means comprises in vitro translation of mRNA obtained from expressing cells.

823. The method of claim 821, wherein the recombinant means comprises use of MHC class II alpha and/or beta chain transfected cells.

824. The method of claim 823, wherein the use of MHC class II alpha and/or beta chain transfected cells comprises use of genetic material isolated from natural origin such as cells, one or more tissues and/or one or more organisms.

825. The method of claim 823, wherein the use of MHC class II alpha and/or beta chain transfected cells comprises use of one or more synthetic genes identical to natural DNA sequence and/or modified.

826. The method of claim 823, wherein the MHC class II alpha and/or beta chain is full length.

827. The method of claim 823, wherein the MHC class II alpha and/or beta chain is a fragment.

828. The method of claim 827, wherein the MHC class II alpha and/or beta chain fragment comprises and/or consists of the MHC class 2 α- and β-chain fragments consisting of, the complete α- and β-chains minus the intramembrane domains of either or both chains.

829. The method of claim 827, wherein the MHC class II alpha and/or beta chain fragment comprises and/or consists of α- and β-chains consisting of only the extracellular domains of either or both, i.e α1 plus α2 and β1 plus β2 domains, respectively.

830. The method of claim 827, wherein the MHC class II alpha and/or beta chain fragment comprises and/or consists of the MHC class II molecule fragments consisting of domains starting from the amino terminal in consecutive order, MHC class 2 β1 plus MHC class 2 α1 plus MHC class 1 α3 domains or in alternative order, MHC class 2 α1 plus MHC class 2 β1 plus MHC class 1 α3 domains.

831. The method of claim 819 to 830, wherein the MHC class II alpha and/or beta chain fragment comprises one or more modified or added designer domain(s) and/or sequence(s).

832. The method of claim 798, wherein the one or more MHC peptide complexes are modified.

833. The method of claim 832, wherein the one or more MHC peptide complexes that are modified are one or more MHC class I complexes and/or one or more MHC class II complexes.

834. The method of claim 833, wherein the one or more MHC class I complexes and/or one or more MHC class II complexes are modified by mutagenesis.

835. The method of claim 834, wherein the mutagenesis comprises one or more substitutions of one or more natural and/or non-natural amino acids.

836. The method of claim 834, wherein the mutagenesis comprises one or more deletions of one or more natural and/or non-natural amino acids.

837. The method of claim 834, wherein the mutagenesis comprises one or more insertions of one or more natural and/or non-natural amino acids.

838. The method of claim 834, wherein the mutagenesis comprises one or more mutations in the α3 subunit of MHC I heavy chain.

839. The method of claim 834, wherein the mutagenesis comprises one or more mutations in areas of the β2-domain of MHC II molecules responsible for binding CD4 molecules.

840. The method of claim 833, wherein the one or more MHC class I complexes and/or one or more MHC class II complexes are modified by one or more chemical modification(s).

841. The method of claim 840, wherein the one or more chemical modification(s) comprises one or more chemical modification(s) of the peptide in the peptide-binding cleft such as attachment of a dinitrophenyl group.

842. The method of claim 840, wherein the one or more chemical modification(s) comprises one or more chemical modification(s) of MHC I or MHC II fusion proteins.

843. The method of claim 840, wherein the one or more chemical modification(s) comprises one or more chemical modification(s) of MHC complexes fused with genes encoding an amino acid sequence (biotinylation sequence) capable of being biotinylated with a Bir A enzyme.

844. The method of claim 843, wherein the biotinylation sequence is fused with the COOH-terminal of β2m or the heavy chain of MHC I molecules or the COOH-terminal of either the α-chain or β-chain of MHC II.

845. The method of claim 843, wherein the biotinylation sequence is fused with the NH_2-terminal of β2m or the heavy chain of MHC I molecules or the NH_2-terminal of either the α-chain or β-chain of MHC II.

846. The method of claim 840, wherein the one or more chemical modification(s) comprises one or more chemical modification(s) of MHC complexes fused with genes encoding an amino acid sequence capable of being chemically modified.

847. The method of claim 846, wherein the one or more genes encoding an amino acid sequence capable of being chemically modified are fused with the COOH-terminal of β2m or the heavy chain of MHC I molecules or the COOH-terminal of either the α-chain or β-chain of MHC II.

848. The method of claim 846, wherein the one or more genes encoding an amino acid sequence capable of being chemically modified are fused with the NH_2-terminal of β2m or the heavy chain of MHC I molecules or the NH_2-terminal of either the α-chain or β-chain of MHC II.

849. The method of claim 798, wherein the one or more MHC peptide complexes and/or empty MHC complexes are stabilized.

850. The method of claim 849, wherein the one or more MHC peptide complexes and/or empty MHC complexes that are stabilized are one or more MHC class I complexes.

851. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises generation of covalent protein-fusions.

852. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers between the individual components of the MHC I complex.

853. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers resulting in generation of a complex comprising a heavy chain fused with β2m through a linker and a soluble peptide.

854. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers resulting in generation of a complex comprising a heavy chain fused to β2m through a linker.

855. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers resulting in generation of a complex comprising a heavy chain /β2m dimer covalently linked to a peptide through a linker to either heavy chain or β2m, and where there can or can not be a linker between the heavy chain and β2m.

856. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers resulting in generation of a complex comprising a heavy chain fused to a peptide through a linker.

857. The method of claim 851, wherein the generation of covalent protein-fusions comprises introduction of one or more linkers resulting in generation of a complex comprising the α1 and α2 subunits of the heavy chain fused to a peptide through a linker.

858. The method of claim 852-857, wherein the heavy chain, beta2-microglubulin and/or the peptide is truncated.

859. The method of claim 852-857, wherein the linker is a flexible linker.

860. The method of claim 859 wherein the flexible linker is made of glycine and/or serine.

861. The method of claim 859, wherein the flexible linker is between 5-20 residues long such as 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 residues long.

862. The method of claim 852-857, wherein the linker is rigid with a defined structure.

863. The method of claim 962, wherein the rigid linker is made of amino acids like glutamate, alanine, lysine, and leucine creating e.g. a more rigid structure.

864. The method of claim 863, wherein the rigid linker is between 5-20 residues long such as 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 residues long.

865. The method of claim 863, wherein the one or more stabilized MHC peptide complexes and/or empty MHC complexes comprises heavy chain-β2m fusion proteins.

866. The method of claim 865, wherein the heavy chain-β2m fusion proteins is constructed so that the COOH terminus of β2m is covalently linked to the NH_2 terminus of the heavy chain.

867. The method of claim 865, wherein the heavy chain-β2m fusion proteins is constructed so that the NH_2 terminus of β2m is linked to the COOH terminus of the heavy chain.

868. The method of claim 849, wherein the one or more stabilized MHC peptide complexes and/or empty MHC complexes comprises one or more peptide-β2m fusion proteins.

869. The method of claim 868, wherein one or more peptide-β2m fusion proteins are constructed so that the COOH terminus of the peptide is linked to the NH_2 terminus of β2m.

870. The method of claim 868, wherein one or more peptide-β2m fusion proteins are constructed so that the peptide is linked to the COOH terminal of β2m via its NH_2 terminus.

871. The method of claim 849, wherein the one or more stabilized MHC peptide complexes and/or empty MHC complexes comprises one or more heavy chain-peptide fusion proteins.

872. The method of claim 871, wherein the one or more heavy chain-peptide fusion proteins are constructed so that the NH_2 terminus of the heavy chain is fused to the COOH terminus of the peptide.

873. The method of claim 871, wherein the one or more heavy chain-peptide fusion proteins are constructed so that the COOH terminus of the heavy chain is fused to the NH_2 terminus of the peptide.

874. The method of claim 849, wherein the one or more stabilized MHC peptide complexes and/or empty MHC complexes comprises one or more heavy chain-β2m-peptide fusion proteins.

875. The method of claim 874, wherein the one or more heavy chain-β2m-peptide fusion proteins is constructed so that the NH_2 terminus of the heavy chain is fused to the COOH terminus of β2m and the NH_2 terminus of β2m is fused to the COOH terminus of the peptide.

876. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises non-covalent stabilization by binding to one or more unnatural component.

877. The method of claim 876, wherein the one or more unnatural component bind to both the heavy chain and the β2m and thereby promote the assemble of the complex, and/or stabilize the formed complex.

878. The method of claim 876, wherein the one or more unnatural component bind to either β2m or heavy chain, and in this way stabilize the polypeptide in its correct conformation, and in this way increase the affinity of the heavy chain for β2m and/or peptide, or increase the affinity of β2m for peptide.

879. The method of claim 876, wherein the one or more unnatural component comprises one or more antibodies.

880. The method of claim 879, wherein the one or more antibodies can be selected from the group consisting of truncated or full-length antibodies of isotype IgG, IgM, IgA, IgE, Fab, scFv or bi-Fab fragments or diabodies.

881. The method of claim 879, wherein the one or more antibodies comprises one or more antibodies binding the MHC I molecule by interaction with the heavy chain as well as β2m.

882. The method of claim 879, wherein the one or more antibodies comprises one or more bispecific antibodies that binds with one arm to the heavy chain and the other arm to the β2m of the MHC complex.

883. The method of claim 879, wherein the one or more antibodies comprises one or more monospecific antibodies which bind at the interface between heavy chain and β2m.

884. The method of claim 879, wherein the one or more antibodies comprises one or more antibodies that bind the correctly folded heavy chain with higher affinity than non-correctly folded heavy chain.

885. The method of claim 879, wherein the one or more antibodies comprises an antibody like the one produced by the clone W6/32 (M0736 from Dako, Denmark) that recognizes a conformational epitope on intact human and some monkey MHC complexes containing β2m, heavy chain and peptide.

886. The method of claim 876, wherein the one or more unnatural component comprises one or more peptides.

887. The method of claim 876, wherein the one or more unnatural component comprises one or more aptamers.

888. The method of claim 876, wherein the one or more unnatural component comprises one or more molecule with the ability to bind to the surface of the MHC complex.

889. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises generation of modified proteins or protein components.

890. The method of claim 889, wherein the generation of modified proteins or protein components results in an increase of the affinity of the peptide P for the MHC complex.

891. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by mutation/substitution of amino acids at relevant positions in the peptide.

892. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by chemical modifications of amino acids at relevant positions in the peptide.

893. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by introduction of non-natural amino acids at relevant positions in the peptide.

894. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions in the peptide binding cleft, i.e. in the binding pockets that accommodate peptide side chains responsible for anchoring the peptide to the peptide binding cleft.

895. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by introduction of reactive groups into the antigenic peptide; before, during or upon binding of the peptide.

896. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by mutations/substitutions, chemical modifications, insertion of natural or non-natural amino acids or deletions in the heavy chain and/or β2m at positions outside the peptide-binding cleft.

897. The method of claim 890, wherein the increase of the affinity of the peptide P for the MHC complex is caused by removal of cysteine residues in the heavy chain by mutation, chemical modification, amino acid exchange or deletion.

898. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises stabilization with soluble additives.

899. The method of claim 898, wherein the stabilization with soluble additives comprises addition of one or more additives selected from the group consisting of salts, detergents organic solvent and polymers.

900. The method of claim 898, wherein the stabilization with soluble additives comprises addition one or more additives that increase surface tension of the MHC molecule without binding the molecule.

901. The method of claim 900, wherein the one or more additives that increase surface tension of the MHC molecule without binding the molecule can be selected from the group consisting of sucrose, mannose, glycine, betaine, alanine, glutamine, glutamic acid and ammoniumsulfate.

902. The method of claim 898, wherein the stabilization with soluble additives comprises addition one or more additives that increase surface tension of the MHC molecule.

903. The method of claim 902, wherein the one or more additives that increase surface tension of the MHC molecule can be selected from the group consisting of glycerol, mannitol and sorbitol.

904. The method of claim 898, wherein the stabilization with soluble additives comprises addition one or more additives that increase surface tension of the MHC molecule and simultaneously interact with charged groups in the protein.

905. The method of claim 904, wherein the one or more additives that increase surface tension of the MHC molecule and simultaneously interact with charged groups in the protein can be selected from the group consisting of $MgSO_4$, NaCl, polyethylenglycol, 2-methyl-2,4-pentandiol and guanidiniumsulfate.

906. The method of claim 898, wherein the stabilization with soluble additives comprises addition of molar excess of peptide.

907. The method of claim 898, wherein the stabilization with soluble additives comprises addition of excess of β2m.

908. The method of claim 898, wherein the stabilization with soluble additives comprises addition BSA, fetal and bovine calf serum and/or individual protein components in serum with a protein stabilizing effect.

909. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises stabilization with soluble additives, said additives are added during the refolding process.

910. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises stabilization with soluble additives, said additives are added to the soluble monomer.

911. The method of claim 850, wherein the stabilization of one or more MHC class I complexes comprises stabilization with soluble additives, said additives are added to a solutions containing MHC I bound to a carrier.

912. The method of claim 849, wherein the one or more MHC peptide complexes and/or empty MHC complexes that are stabilized are one or more MHC class II complexes.

913. The method of claim 912, wherein the stabilization of one or more MHC class I complexes and/or one or more MHC class II complexes comprises generation of covalent protein-fusions.

914. The method of claim 913, wherein the generation of covalent protein-fusions comprises stabilization of MHC II complexes by introduction of one or more linkers between the individual components of the MHC II complex.

915. The method of claim 913, wherein the generation of covalent protein-fusions comprises stabilization of MHC II complexes by construction of a α/β dimer with a linker between α-chain and β-chain.

916. The method of claim 913, wherein the generation of covalent protein-fusions comprises stabilization of MHC II complexes by construction of a α/β dimer covalently linked to the peptide via a linker to either the α-chain or β-chain.

917. The method of claim 913, wherein the generation of covalent protein-fusions comprises stabilization of MHC II complexes by construction of a α/β dimer, covalently linked by a linker between the α-chain and β-chain, and where the dimer is covalently linked to the peptide.

918. The method of claim 913, wherein the generation of covalent protein-fusions comprises stabilization of MHC II complexes by construction of a α/β dimer with a linker between α-chain and β-chain, where the dimer is combined with a peptide covalently linked to either α-chain or β-chain.

919. The method of claim 913, wherein the generation of covalent protein-fusions comprises one or more linkers.

920. The method of claim 919, wherein the one or more linkers comprises one or more flexible linker(s).

921. The method of claim 920, wherein the one or more flexible linker(s) comprises glycine and/or serine.

922. The method of claim 920, wherein the one or more flexible linker(s) are between 5-20 residues long such as 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 residues long.

923. The method of claim 919, wherein the one or more linker(s) comprises one or more rigid linker with a more defined structure.

924. The method of claim 923, wherein the one or more rigid linker(s) comprises glutamate, alanine, lysine, and/or leucine.

925. The method of claim 919, wherein the one or more linker(s) result in that the one or more peptide is linked to the NH_2- or COOH-terminus of either α-chain or β-chain.

926. The method of claim 919, wherein the one or more linker(s) result in that the one or more peptides are linked to the NH_2-terminus of the β-chain via their COOH-terminus.

927. The method of claim 919, wherein the one or more linker(s) result in that the α-chain is linked to the β-chain via the COOH-terminus of the β-chain to the NH_2-terminus of the α-chain or from the COOH-terminus of the α-chain to the NH_2-terminus of the β-chain.

928. The method of claim 919, wherein the one or more linker result in that formation of a three-molecule fusion protein consisting of α-chain, β-chain and peptide, wherein some linker(s) connect the COOH-terminus of the β-chain with the NH_2-terminus of the α-chain and other linker(s) connect the COOH-terminal of the peptide with the NH_2-terminal of the β-chain.

929. The method of claim 919, wherein the one or more linker result in that formation of a three-molecule fusion protein consisting of α-chain, β-chain and peptide, wherein one linker joins the COOH-terminus of the α-chain with the NH_2-terminus of the β-chain and a second linker joins the NH_2-terminus of the peptide with the COOH-terminus of the β-chain.

930. The method of claim 927, wherein the stabilization of one or more MHC class I complexes and/or one or more MHC class II complexes comprises non-covalent stabilization by binding ligand.

931. The method of claim 930, wherein the non-covalent stabilization by binding ligand results in bridging of α- and β-chain.

932. The method of claim 930, wherein the non-covalent stabilization by binding ligand results in binding to either of the α- or β-chains, and in this way stabilize the conformation of α or β, that binds β or α, respectively, and/or that binds the peptide.

933. The method of claim 930, wherein the non-covalent stabilization by binding ligand comprises one or more compounds selected from the group consisting of antibodies, peptides, aptamers or any other molecules with the ability to bind proteins.

934. The method of claim 933, wherein the one or more antibodies comprises one or more antibodies which bind the MHC complex distal to the interaction site with TCR, i.e. distal to the peptide-binding cleft.

935. The method of claim 933, wherein the one or more antibodies comprises one or more antibodies selected from the group consisting of truncated or full length antibody of any isotype IgG, IgM, IgA or IgE, a bi-Fab fragment or a diabody.

936. The method of claim 933, wherein the one or more antibodies comprises one or more bispecific antibodies e.g. with one arm binding to the α-chain and the other arm binding to the β-chain.

937. The method of claim 933, wherein the one or more antibodies comprises one or more monospecific antibodies e.g. directed to a sequence fused to the α-chain as well as to the β-chain.

938. The method of claim 933, wherein the one or more antibodies comprises one or more monospecific antibodies which are capable of binding to a surface of the complex that involves both the α- and β-chain, e.g. both the α2- and β2- domain or both the α1- and β1- domain.

939. The method of claim 933, wherein the one or more antibodies comprises one or more antibodies capable of binding more central in the MHC II molecule, but still interacting with both α- and β-chain.

940. The method of claim 933, wherein the one or more antibodies comprises one or more antibodies which are capable of binding a conformational epitope.

941. The method of claim 912, wherein the stabilization of one or more MHC class I complexes and/or one or more MHC class II complexes comprises non-covalent stabilization by induced multimerization.

942. The method of claim 941, wherein the non-covalent stabilization by induced multimerization comprises anchoring of the α- and/or β-chains in the cell membrane.

943. The method of claim 941, wherein the non-covalent stabilization by induced multimerization comprises anchoring the α/β-dimer by attachment of the MHC II chains to the Fc regions of an antibody.

944. The method of claim 941, wherein the non-covalent stabilization by induced multimerization comprises anchoring of one or more MHC II monomers and/or dimers into one or more artificial membrane spheres like liposomes or lipospheres.

945. The method of claim 941, wherein the non-covalent stabilization by induced multimerization comprises the steps of biotinylation of α- as well as β-chain, followed by the binding of biotinylated α-chain and β-chain to streptavidin, to form an association between α-chain and β-chain.

946. The method of claim 912, wherein the stabilization of one or more MHC class I complexes and/or one or more MHC class II complexes comprises generation of modified proteins or protein components.

947. The method of claim 946, wherein the generation of modified proteins or protein components comprises one or more covalent modifications of the protein.

948. The method of claim 946, wherein the generation of modified proteins or protein components comprises exchange of the natural amino acids with other natural or non-natural amino acids at relevant positions in the peptide or by chemical modifications of amino acids at relevant positions in the peptide.

949. The method of claim 9346, wherein the generation of modified proteins or protein components comprises mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions in the peptide-binding cleft.

950. The method of claim 946, wherein the generation of modified proteins or protein components comprises mutations, chemical modifications, insertion of natural or non-natural amino acids or deletions in α- and/or β- chain at positions outside the peptide-binding cleft.

951. The method of claim 946, wherein the generation of modified proteins or protein components comprises replacement of the hydrophobic transmembrane regions of α-chain and β-chain with leucine zipper dimerisation domains (e.g. Fos-Jun leucine zipper; acid-base coiled-coil structure) to promote assembly of α-chain and β-chain.

952. The method of claim 946, wherein the generation of modified proteins or protein components comprises introduction of one or more cysteine residues by amino acid exchange at the COOH-terminal of both α-chain and β-chain, to create disulfide bridges between the two chains upon assembly of the MHC complex.

953. The method of claim 946, wherein the generation of modified proteins or protein components comprises removal of cysteine residues in either of the chains by mutation, chemical modification, amino acid exchange or deletion.

954. The method of claim 946, wherein the generation of modified proteins or protein components comprises stabilization of MHC II complexes by stabilized by chemically linking together the subunits and the peptide.

955. The method of claim 912, wherein the one or more MHC class I complexes and/or one or more MHC class II complexes comprises stabilization with one or more soluble additives.

956. The method of claim 955, wherein the one or more soluble additives can be selected from the group consisting of salts, detergents, organic solvent, polymers and any other soluble additives can be added to increase the stability of MHC complexes.

957. The method of claim 955, wherein the one or more soluble additives that can increase the surface tension of the MHC complex.

958. The method of claim 957, wherein the one or more soluble additives that can increase the surface tension of the MHC complex can be selected from the group consisting of sucrose, mannose, glycine, betaine, alanine, glutamine, glutamic acid and ammonium sulphate, glycerol, mannitol, sorbitol, $MgSO_4$, NaCl, polyethylenglycol, 2-methyl-2,4-pentanediol and guanidiniumsulphate.

959. The method of claim 957, wherein the one or more soluble additives comprises excess of peptide.

960. The method of claim 957, wherein the one or more soluble additives comprises excess of β2m.

961. The method of claim 957, wherein the one or more soluble additives comprises BSA, fetal and bovine calf serum, and other protein components in serum with a protein stabilizing effect.

962. The method of claim 849, wherein the one or more MHC peptide complexes and/or empty MHC complexes are stabilized by chemical modification.

963. The method of claim 962, wherein the chemical modification results in cross-linking of MHC I and/or MHC II complexes.

964. The method of claim 962, wherein the chemical modification comprises nucleophilic substitution by activation of electrophiles.

965. The method of claim 962, wherein the chemical modification comprises acylation.

966. The method of claim 962, wherein the chemical modification comprises amide formation.

967. The method of claim 962, wherein the chemical modification comprises pyrazolone formation.

968. The method of claim 962, wherein the chemical modification comprises isoxazolone formation.

969. The method of claim 962, wherein the chemical modification comprises alkylation.

970. The method of claim 962, wherein the chemical modification comprises vinylation.

971. The method of claim 962, wherein the chemical modification comprises disulfide formation.

972. The method of claim 962, wherein the chemical modification comprises addition to carbon-hetero multiple bonds.

973. The method of claim 962, wherein the chemical modification comprises alkene formation by reaction of phosphonates with aldehydes or ketones.

974. The method of claim 962, wherein the chemical modification comprises arylation.

975. The method of claim 962, wherein the chemical modification comprises alkylation of arenes/hetarenes by reaction with alkyl boronates or enolethers.

976. The method of claim 962, wherein the chemical modification comprises nucleophilic substitution using activation of nucleophiles.

977. The method of claim 962, wherein the chemical modification comprises condensations.

978. The method of claim 962, wherein the chemical modification comprises alkylation of aliphatic halides or tosylates with enolethers or enamines.

979. The method of claim 962, wherein the chemical modification comprises cycloadditions.

980. The method of claim 962, wherein the chemical modification comprises use of one or more reagents selected from the group consisting of activated carboxylic acids, NHS-ester, tetra and pentafluoro phenolic esters, anhydrides, acid chlorides and fluorides, sulphonyl chlorides, iso-Cyanates, isothiocyanates, aldehydes, formaldehyde, and glutardialdehyde.

981. The method of claim 962, wherein the chemical modification comprises modification of one or more cysteine(s).

982. The method of claim 962, wherein the chemical modification comprises modification of one or more cysteine(s) by maleimides, vinyl sulphones and/or halides.

983. The method of claim 962, wherein the chemical modification comprises modification of one or more carboxylic acids at the C-terminal of both chains and/or peptide, as well as on the side chains of glutamic and aspartic acid, by introduction of one or more cross-links e.g. by carbodiimides treatment.

984. The method of claim 962, wherein the chemical modification comprises use of two or more reagents i.e. GMBS can be used to introduce maleimides on the α-chain, and iminothiolane can be used to introduce thiols on the β-chain; the malemide and thiol can then form a thioether link between the two chains.

985. The method of claim 962, wherein the chemical modification comprises that the folded MHC-complex is reacted with dextrans possessing a large number (up to many hundreds) of vinyl sulphones; said vinyl sulphones react with lysine residues on both the α and β chains as well as with lysine residues on the peptide protruding from the binding site, effectively cross linking the entire MHC-complex.

986. The method of claim 962, wherein the chemical modification comprises that one or more lysine residues are inserted into the α-chain, juxtaposed with glutamic

acids in the β-chain, where after the introduced amino groups and carboxylic acids are reacted by addition of carbodiimide.

987. The method of claim 962, wherein the chemical modification comprises that a dextran multimerization domain is cross-linked with appropriately modified MHC-complexes; i.e. one or both chains of the MHC complex can be enriched with lysine residues, increasing reactivity towards the vinylsulphone dextran.

988. The method of claim 962, wherein the chemical modification comprises use of extended and flexible cross-linkers.

989. The method of claim 798, wherein the one or more peptides P are selected either from the group consisting of 8-, 9-, 10,- and 11-mer peptides, or from the group consisting of 13-, 14-, 15-, 16-, 17- and 18-mer peptides; corresponding to peptides of MHC classes I and II, such as any of the antigenic peptides as defined in any of the claims 1 and 1509-1537.

990. The method of claim 989 comprising the further step of confirming the antigenicity of a peptide P and/or determining the sequence of a peptide P, said method comprising the steps of

selecting one or more MHC alleles; and

obtaining and optionally identifying one or more peptides P of a predetermined length derived from a specific protein, and

assaying the association formed between a) said one or more peptides P, when forming part of a functional MHC protein in a MHC monomer or MHC multimer, and b) a T-cell receptor representative of the selected MHC allelle, and

optionally modifying said one or more peptides P,

thereby confirming or generating one or more optionally modified peptides P of general utility in diagnosing or treating a disease in an individual.

991. The method of claim 990, wherein identification of the one or more peptides P derived from a specific protein for a given MHC allele comprises computational analysis.

992. The method of claim 991, wherein the computational analysis comprises a prediction of theoretical binding affinity of the peptide to the MHC molecules using www.syfpeithi.de.

993. The method of claim 991, wherein the computational analysis comprises prediction of theoretical binding affinity of the peptide to the MHC molecules using http://www-bimas.cit.nih.gov/molbio/hla_bind/.

994. The method of claim 991, wherein the computational analysis comprises prediction of theoretical binding affinity of the peptide to the MHC molecules using www.cbs.dtu.dk/services/NetMHC/.

995. The method of claim 991, wherein the computational analysis comprises prediction of theoretical binding affinity of the peptide to the MHC molecules using www.cbs.dtu.dk/services/NetMHCII/.

996. The method of claim 991, wherein the computational analysis comprises translation of the DNA sequence (genomic DNA) in all three reading frames in both directions leading to a total of six amino acid sequences for a given genome; said amino acid sequences are used to predict the MHC molecule peptides P.

997. The method of claim 991, wherein the computational analysis comprises translation of one or more cDNA sequences into the amino acid sequences; said amino acid sequences are used to predict the MHC molecule peptides P.

998. The method of claim 991, wherein the computational analysis comprises prediction of MHC molecule peptides P from one or more known amino acid sequences.

999. The method of claim 990, wherein the modification of the one or more antigenic peptides comprises the use of one or more peptides homologous to the predicted

peptide sequences; said peptides homologous having an amino acid sequence identity greater than e.g. more than 90%, more than 80% or more than 70%.

1000. The method of claim 999, wherein the one or more homologues MHC peptide sequences arise from the existence of multiple strongly homologous alleles.

1001. The method of claim 999, wherein the one or more homologues MHC peptide sequences arise from one or more insertions.

1002. The method of claim 999, wherein the one or more homologues MHC peptide sequences arise from one or more deletions.

1003. The method of claim 999, wherein the one or more homologues MHC peptide sequences arise from one or more inversions.

1004. The method of claim 999, wherein the one or more homologues MHC peptide sequences arise from one or more substitutions.

1005. The method of claim 990, wherein the modification of the one or more peptides P comprises the use of one or more peptides with one or more un-common amino acids such as selenocysteine and/or pyrrolysine.

1006. The method of claim 990, wherein the modification of the one or more peptides P comprises the use of one or more peptides with one or more artificial amino acids such as the isomeric D-form.

1007. The method of claim 990, wherein the modification of the one or more peptides P comprises the use of one or more peptides with one or more chemically modified amino acids.

1008. The method of claim 990, wherein the modification of the one or more peptides P comprises the use of one or more split- or combinatorial epitope origin i.e. formed by linkage of peptide fragments derived from two different peptide fragments and/or proteins.

1009. The method of claim 990, wherein the modification of the one or more peptides P comprises one or more modifications at any position of the one or more peptides e.g. at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and/or 18.

1010. The method of claim 990, wherein the modification of the one or more peptides P comprises one or more post translational modifications.

1011. The method of claim 1010, wherein the one or more post translational modifications comprises acylation.

1012. The method of claim 1010, wherein the one or more post translational modifications comprises alkylation.

1013. The method of claim 1010, wherein the one or more post translational modifications comprises methylation.

1014. The method of claim 1010, wherein the one or more post translational modifications comprises demethylation.

1015. The method of claim 1010, wherein the one or more post translational modifications comprises amidation at C-terminus.

1016. The method of claim 1010, wherein the one or more post translational modifications comprises biotinylation.

1017. The method of claim 1010, wherein the one or more post translational modifications comprises formylation.

1018. The method of claim 1010, wherein the one or more post translational modifications comprises gamma-carboxylation.

1019. The method of claim 1010, wherein the one or more post translational modifications comprises glutamylation.

1020. The method of claim 1010, wherein the one or more post translational modifications comprises glycosylation.

1021. The method of claim 1010, wherein the one or more post translational modifications comprises glycation.

1022. The method of claim 1010, wherein the one or more post translational modifications comprises glycylation.

1023. The method of claim 1010, wherein the one or more post translational modifications comprises covalently attachment of one or more heme moieties.

1024. The method of claim 1010, wherein the one or more post translational modifications comprises hydroxylation.

1025. The method of claim 1010, wherein the one or more post translational modifications comprises iodination.

1026. The method of claim 1010, wherein the one or more post translational modifications comprises isoprenylation.

1027. The method of claim 1010, wherein the one or more post translational modifications comprises lipoylation.

1028. The method of claim 1010, wherein the one or more post translational modifications comprises prenylation.

1029. The method of claim 1010, wherein the one or more post translational modifications comprises GPI anchor formation.

1030. The method of claim 1010, wherein the one or more post translational modifications comprises myristoylation.

1031. The method of claim 1010, wherein the one or more post translational modifications comprises farnesylation.

1032. The method of claim 1010, wherein the one or more post translational modifications comprises geranylation.

1033. The method of claim 1010, wherein the one or more post translational modifications comprises covalently attachment of nucleotides or derivatives thereof.

1034. The method of claim 1010, wherein the one or more post translational modifications comprises ADP-ribosylation.

1035. The method of claim 1010, wherein the one or more post translational modifications comprises flavin attachment.

1036. The method of claim 1010, wherein the one or more post translational modifications comprises oxidation.

1037. The method of claim 1010, wherein the one or more post translational modifications comprises pegylation.

1038. The method of claim 1010, wherein the one or more post translational modifications comprises addition of poly-ethylen-glycol groups to a protein.

1039. The method of claim 1010, wherein the one or more post translational modifications comprises modification of one or more reactive amino acids include lysine, cysteine, histidine, arginine, aspartic acid, glutamic acid, serine, threonine, tyrosine.

1040. The method of claim 1010, wherein the one or more post translational modifications comprises covalently attachment of phosphatidylinositol.

1041. The method of claim 1010, wherein the one or more post translational modifications comprises phosphopantetheinylation.

1042. The method of claim 1010, wherein the one or more post translational modifications comprises phosphorylation.

1043. The method of claim 1010, wherein the one or more post translational modifications comprises pyroglutamate formation.

1044. The method of claim 1010, wherein the one or more post translational modifications comprises racemization of proline by prolyl isomerase.

1045. The method of claim 1010, wherein the one or more post translational modifications comprises tRNA-mediated addition of amino acids such as arginylation.

1046. The method of claim 1010, wherein the one or more post translational modifications comprises sulfation.

1047. The method of claim 1010, wherein the one or more post translational modifications comprises Selenoylation (co-translational incorporation of selenium in selenoproteins).

1048. The method of claim 1010, wherein the one or more post translational modifications comprises ISGylation.

1049. The method of claim 1010, wherein the one or more post translational modifications comprises SUMOylation.

1050. The method of claim 1010, wherein the one or more post translational modifications comprises ubiquitination.

1051. The method of claim 1010, wherein the one or more post translational modifications comprises citrullination, or deimination the conversion of arginine to citrulline.

1052. The method of claim 1010, wherein the one or more post translational modifications comprises deamidation, the conversion of glutamine to glutamic acid or asparagine to aspartic acid.

1053. The method of claim 1010, wherein the one or more post translational modifications comprises modifications of a single amino acid or more than one i.e. in combinations.

1054. The method of claim 990, wherein the one or more antigenic peptides are obtained by digestion and/or proteolysis of natural proteins or proteins derived by in vitro translation of mRNA.

1055. The method of claim 990, wherein the sequence of the one or more antigenic peptides is determined by elution of peptides from the MHC binding groove of a naturally existing MHC complex.

1056. The method of claim 990, wherein the one or more antigenic peptides are derived from one or more recombinant sources.

1057. The method of claim 1056, wherein the one or more recombinant sources comprises one or more monomeric or multimeric peptides.

1058. The method of claim 1056, wherein the one or more recombinant sources comprises one or more parts of a bigger recombinant protein.

1059. The method of claim 1056, wherein the one or more recombinant sources comprises one or more MHC class 1 peptides P.

1060. The method of claim 1059, wherein the one or more MHC class 1 peptides P comprises Peptide-linker-β2m, β2m being full length or truncated.

1061. The method of claim 1059, wherein the one or more MHC class 1 peptides P comprises Peptide-linker-MHC class 1 heavy chain, the heavy chain being full length or truncated.

1062. The method of claim 1059, wherein the one or more MHC class 1 peptides P comprises truncated class I heavy chain consisting of the extracellular part i.e the α1, α2, and α domains.

1063. The method of claim 1059, wherein the one or more MHC class 1 binding peptides comprises heavy chain fragment containing the α1 and α2 domains, or α1 domain alone, or any fragment or full length β2m or heavy chain attached to a designer domain(s) or protein fragment(s).

1064. The method of claim 1054, wherein the one or more recombinant sources comprises one or more MHC class 2 binding peptides.

1065. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises Peptide-linker-MHC class 2 alpha-chain, full length or truncated.

1066. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises Peptide-linker-MHC class 2 beta-chain, full length or truncated.

1067. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises Peptide-linker-MHC class 2 α-chain-linker-MHC class 2 β-chain, both chains are full length or truncated, truncation involve, omission of α- and/or β-chain intermembrane domain, or omission of α- and/or β-chain intermembrane plus cytoplasmic domains.

1068. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises MHC class 2 part of the construction consisting of fused domains from NH2-terminal, MHC class 2 β1domain-MHC class 2 α1domain-constant α3 of MHC class 1, or alternatively of fused domains from NH2-terminal, MHC class 2 α1domain-MHC class 2 β1domain-constant α3 of MHC class 1.

1069. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises β2m associated non-covalently in the folded MHC complex.

1070. The method of claim 1054, wherein the one or more MHC class 2 binding peptides comprises β2m covalently associated in the folded MHC class 2 complex.

1071. The method of claim 989, wherein the one or more peptides P are obtained from chemical synthesis.

1072. The method of claim 1071, wherein the chemical synthesis comprises solid phase synthesis.

1073. The method of claim 1071, wherein the chemical synthesis comprises fluid phase synthesis.

1074. The method of claim 1071, wherein the chemical synthesis method comprises the further step of loading of the peptide into the functional MHC protein.

1075. The method of claim 1074, wherein the loading of the peptide into the functional MHC protein comprises the step of loading of free peptide P during the folding of the functional MHC protein and the formation of the MHC peptide complex.

1076. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises that the peptide to be folded into the binding groove is encoded together with e.g. the α heavy chain or fragment hereof by a gene construct having the structure, heavy chain-flexible linker- peptide followed by folding in vitro.

1077. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises that the peptide is part of a recombinant protein construct.

1078. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions.

1079. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions in solution.

1080. The method of claim 10674, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions “in situ”.

1081. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions by aided exchange.

1082. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions by in vivo loading.

1083. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more in vitro exchange reactions where a peptide already in place in the binding groove are being exchanged by another peptide species.

1084. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions where the parent molecule is attached to other molecules, structures, surfaces, artificial or natural membranes and nano-particles.

1085. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions where the parent construct is made with a peptide containing a meta-stable amino acid analog that is split by either light or chemically induction thereby leaving the parent structure free for access of the desired peptide in the binding groove.

1086. The method of claim 1074 wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions comprising in vivo loading of MHC class I and II molecules expressed on the cell surface with the desired peptides.

1087. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions comprising that cells are transfected by the peptides themselves or by the mother proteins that are then being processed leading to an in vivo analogous situation where the peptides are bound in the groove during the natural cause of MHC expression by the transfected cells.

1088. The method of claim 1074, wherein the loading of the peptide into the MHCmer comprises one or more exchange reactions comprising one or more professional antigen presenting cells e.g. dendritic cells, macrophages, or Langerhans cells.

1089. The method of claim 1074 further comprising a step to verify correct folding of the one or more MHC-peptide complexes.

1090. A composition comprising a plurality of MHC monomers and/or MHC multimers according to any of claims 1 to 797, wherein the MHC multimers are identical, and a carrier.

1091. A composition comprising a plurality of MHC multimers according to any of claims 1 to 779, wherein the MHC multimers are different, and a carrier.

1092. A kit comprising a MHC monomer or a MHC multimer according to any of claims 1 to 797, or the composition according to any of claims 1090 and 1091, and at least one additional component, such as a positive control and/or instructions for use.

1093. A method for immune monitoring one or more diseases comprising the following steps
i) providing the MHC monomer or MHC multimer according to any of the claims 1 to 797, or the individual components thereof, or the antigenic peptide according to any of the claims 1 and 1509-1537, or the antigenic polypeptide according to claim 1585,
ii) providing a population of T cells, and
iii) measuring the number, activity or state of T cells specific for said peptide, polypeptide, MHC monomer or MHC multimer, thereby immune monitoring said one or more diseases.

1094. A method for diagnosing one or more diseases comprising the following steps:
i) providing the MHC monomer or MHC multimer according to any of the claims 1 to 797, or the individual components thereof or the antigenic peptide according to any of the claims 1 and 1509-1537, or the antigenic polypeptide according to claim 1580 or 1581,
ii) providing a population T cells, and
iii) measuring the number, activity or state T cells specific for said antigenic peptide, antigenic polypeptide, MHC monomer or MHC multimer, thereby diagnosing said one or more diseases.

1095. A method for isolation of one or more antigen-specific T cells, said method comprising the steps of

i) providing the MHC monomer or MHC multimer according to any of the claims 1 to 797, or individual components
ii) providing a population of T cells, and
iii) isolating T cells specific for said MHC monomer or MHC multimer.

1096. The method of any of claims 1093 to 1095, wherein the measurement of T cells comprises the step of counting of T cells specific for the said antigenic peptide, antigenic polypeptide, MHC monomer or MHC multimer.

1097. The method of any of claims 1093 to 1095, wherein the measurement of T cells comprises the step of sorting of T cells specific for said antigenic peptide, antigenic polypeptide, MHC monomer or MHC multimer.

1098. The method of any of claims 1093 to 1095, wherein the measurement of T cells comprises the step of isolation of T cells specific for the peptide, polypeptide, MHC monomer or MHC multimer.

1099. The method of any of claims 1093 to 1095, wherein the number of T cells specific for said MHC monomer or MHC multimer is determined from the number of T cells that are bound by more than a given threshold number of MHC multimers.

1100. The method of claim 1099, wherein the amount of MHC multimers bound to an individual T cell is measured by flow cytometry.

1101. The method of claim 1099, where the amount of MHC multimers bound to an individual T cell is measured by microscopy.

1102. The method of claim 1099 where the amount of MHC multimers bound to an individual T cell is measured by capture on solid support, optionally followed by elution of T cells.

1103. The method of claim 1099 where the amount of MHC multimers bound to a population of T cells is determined by the total number of MHC multimers bound to the population of T cells.

1104. The method of any of claims 1093 to 1095, where the T cells of step (ii) are immobilized.

1105. The method of claim 1104 where the MHC multimers are labelled, and the number of individual T cells specific for said MHC multimer is determined using microscopy.

1106. The method of claim 1104 where the MHC multimers are labelled, and the number of T cells specific for said MHC multimer is determined from the total signal of the population of T cells

1107. The method of claims 1104-1106 where the immobilized T cells are part of a solid tissue

1108. The method of claim 1107 where the solid tissue is part of a living animal and the detection of T cells specific for the MHC multimer is performed in vivo.

1109. The method of claim 1108 where the detection of T cells involves magnetic resonance imaging or electron spin resonance scanning.

1110. The method any of claims 1093 to 1095, where the number, activity or state of the T cells specific for said MHC multimer or MHC monomer, are determined from the result of the interaction of said MHC with said T cells.

1111. The method of claim 1110 where the result of the interaction of said MHC multimer or MHC monomer with said T cells is an up- or down-regulation, such as an increased or decreased production, of the amount of a specific factor.

1112. The method of claim 1111 where the specific factor is a secreted soluble factor.

1113. The method of claim 1111 where the specific factor is an intracellular factor.

1114. The method of claim 1111 where the specific factor is a mRNA

1115. The method of claim 1111 where the specific factor is a cytokine

1116. The method of claim 1111 where the specific factor is a surface receptor of T cells

1117. The method of claim 1111 where the specific factor is a secreted soluble factor that is captured on solid support.

1118. The method of claim 1111 where the specific factor is interferon-gamma (INF-gamma).

1119. The method of claims 1110-1118 where individual T cells are measured.

1120. The method of claims 1110-1118 where populations of T cells are measured.

1121. The method of claims 1110-1118 where the specific factor is immobilized on solid support before measurement of its amount.

1122. The method of claims 1110-1118 where the specific factor is in solution when its amount is measured.

1123. The method of claim 1110 where the result of the interaction of said MHC multimer with the T cell is T cell apoptosis.

1124. The method of claim 1110 where the result of the interaction of said MHC multimer with the T cell is T cell apoptosis.

1125. The method of claim 1110 where the result of the interaction of said MHC multimer with the T cell is T cell differentiation.

1126. The method of claim 1110 where the result of the interaction of said MHC multimer with the T cell is T cell inactivation.

1127. The method of claim 1110 where the measurement of T cells specific for said MHC multimer with the T cell involves flow cytometry.

1128. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells comprises flow cytometry.

1129. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells comprises indirect measurement of individual T cells.

1130. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells comprises indirect measurement of populations of T cells.

1131. The method of claims 1110-1130 where in step (i) an antigenic peptide or antigenic polypeptide is added instead of a MHC monomer or MHC multimer.

1132. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells involves immunohistochemistry (IHC).

1133. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells involves limited dilution assay (LDA).

1134. The method of any of claims 1093 to 1095, wherein the measurement of antigen-specific T cells involves microscopy.

1135. The method of any of claims 1093 to 1095, wherein the method comprises the step of detecting one or more marker molecules associated with the MHC monomer or MHC multimer.

1136. The method of claim 1135, wherein the one or more marker molecules comprises one or more antibodies and/or antibody fragments.

1137. The method of claim 1135, wherein the one or more marker molecules comprises one or more aptamers.

1138. The method of claim 1135, wherein the one or more marker molecules comprises one or more proteins.

1139. The method of claim 1135, wherein the one or more marker molecules comprises one or more peptides.

1140. The method of claim 1135, wherein the one or more marker molecules comprises one or more small organic molecules.

1141. The method of claim 1135, wherein the one or more marker molecules comprises one or more natural compounds such as one or more steroids.

1142. The method of claim 1135, wherein the one or more marker molecules comprises one or more non-peptide polymers.

1143. The method of any of the claims 1093 to 1095, wherein the method comprises the further step of providing one or more labelling molecules.

1144. The method of claim 1143, wherein the one or more labelling molecules comprises one or more labelling molecules that results in directly detectable T cells.

1145. The method of claim 1143, wherein the one or more labelling molecules comprises one or more labelling molecules that results in indirectly detectable T cells.

1146. The method of claim 1143, wherein the one or more labelling molecules are attached via one or more linkers.

1147. The method of claim 1143, wherein the one or more labelling molecules comprises one or more fluorescent labels.

1148. The method of claim 1147, wherein the one or more fluorescent labels can be selected from the group consisting of 5-(and 6)-carboxyfluorescein, 5- or 6-carboxyfluorescein, 6-(fluorescein)-5-(and 6)-carboxamido hexanoic acid, fluorescein isothiocyanate (FITC), rhodamine, tetramethylrhodamine, and dyes such as Cy2, Cy3, and Cy5, optionally substituted coumarin including AMCA, PerCP,

phycobiliproteins including R-phycoerythrin (RPE) and allophycoerythrin (APC), Texas Red, Princeston Red, Green fluorescent protein (GFP) and analogues thereof, and conjugates of R-phycoerythrin or allophycoerythrin and e.g. Cy5 or Texas Red, and inorganic fluorescent labels based on semiconductor nanocrystals (like quantum dot and Qdot™ nanocrystals), and time-resolved fluorescent labels based on lanthanides like Eu3+ and Sm3+.

1149. The method of claim 1143, wherein the one or more labelling molecules comprises one or more enzyme labels.

1150. The method of claim 1149, wherein the one or more enzyme labels can be selected from the group consisting of horse radish peroxidase (HRP), alkaline phosphatase (AP), beta-galactosidase (GAL), glucose-6-phosphate dehydrogenase, beta-N-acetylglucosaminidase, ß-glucuronidase, invertase, Xanthine Oxidase, firefly luciferase and glucose oxidase (GO),

1151. The method of claim 1143, wherein the one or more labelling molecules comprises one or more radioisotopes.

1152. The method of claim 1151, wherein the one or more radioisotopes can be selected from the group consisting of isotopes of iodide, cobalt, selenium, tritium, and/or phosphor.

1153. The method of claim 1143, wherein the one or more labelling molecules comprises one or more chemiluminescent labels.

1154. The method of claim 1143, wherein the one or more labelling molecules comprises one or more luminescent labels.

1155. The method of claim 1154, wherein the one or more luminescent labels can be selected from the group consisting of luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines.

1156. The method of claim 1143, wherein the one or more labelling molecules comprises one or more polymers.

1157. The method of claim 1143, wherein the one or more labelling molecules comprises one or more metal particles.

1158. The method of claim 1143, wherein the one or more labelling molecules comprises one or more haptens.

1159. The method of claim 1158, wherein the one or more haptens can be selected from the group consisting of DNP, biotin, and digoxiginin.

1160. The method of claim 1143, wherein the one or more labelling molecules comprises one or more antibodies.

1161. The method of claim 1143, wherein the one or more labelling molecules comprises one or more dyes.

1162. The method of any of the claims 1093 to 1095, wherein the method comprises a detection step based on flow cytometry or flow cytometry-like analysis.

1163. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of TCRs attached to a lipid bilayer.

1164. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more individual T cells in a fluid sample.

1165. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more populations of T cells in a fluid sample.

1166. The method of claim 1164, where in the direct detection of one or more individual T cells in a fluid sample comprises flow cytometry.

1167. The method of claim 1164, where in the direct detection of one or more populations of T cells in a fluid sample comprises flow cytometry.

1168. The method of claim 1164, where in the direct detection of one or more individual T cells in a fluid sample comprises microscopy.

1169. The method of claim 1164, where in the direct detection of one or more populations of T cells in a fluid sample comprises microscopy.

1170. The method of claim 1164, where in the direct detection of one or more individual T cells in a fluid sample comprises capture of T cells on a solid support followed by elution of said T cells.

1171. The method of claim 1164, where in the direct detection of one or more populations of T cells in a fluid sample comprises capture of T cells on a solid support followed by elution of said T cells.

1172. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more individual immobilized T cells.

1173. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more populations of immobilized T cells.

1174. The method of claim 1172, wherein one or more individual T cells are immobilized on a solid support such as particles, beads, biodegradable particles, sheets, gels, filters, membranes, nylon membranes, fibres, capillaries, needles, microtitre strips, tubes, plates, wells, combs, pipette tips, micro arrays, chips and slides.

1175. The method of claim 1173, wherein one or more populations of T cells are immobilized on a solid support such as particles, beads, biodegradable particles, sheets, gels, filters, membranes, nylon membranes, fibres, capillaries, needles, microtitre strips, tubes, plates, wells, combs, pipette tips, micro arrays, chips and slides.

1176. The method of claim 1172, wherein the immobilization of one or more individual T cells are directly immobilized on the solid support.

1177. The method of claim 1173, wherein the immobilization of one or more populations of T cells are directly immobilized on the solid support.

1178. The method of claim 1172, wherein the immobilization of one or more individual T cells are directly immobilized through a linker on the solid support.

1179. The method of claim 1173, wherein the immobilization of one or more individual T cells are directly immobilized through a linker on the solid support.

1180. The method of any of the claims 1093 to 1095, wherein the direct detection of one or more individual immobilized T cells comprises phenotyping a T cell sample using MHC multimer beads.

1181. The method of any of the claims 1093 to 1095, wherein the direct detection of one or more populations of immobilized T cells comprises phenotyping a T cell sample using MHC multimer beads.

1182. The method of any of the claims 1093 to 1095, wherein the direct detection of one or more individual immobilized T cells comprises detection of T cells immobilized to solid support in a defined pattern.

1183. The method of any of the claims 1093 to 1095, wherein the direct detection of one or more populations of immobilized T cells comprises detection of T cells immobilized to solid support in a defined pattern.

1184. The method of any of claims 1180 to 1183, wherein the direct detection of one or more individual immobilized T cells is followed by sorting of said T cells.

1185. The method of any of claims 1180 to 1183, wherein the direct detection one or more populations of immobilized T cells is followed by sorting of said T cells.

1186. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more individual T cells in a solid tissue either in vitro or in vivo.

1187. The method of any of the claims 1093 to 1095, wherein the method comprises direct detection of one or more populations of T cells in a solid tissue either in vitro or in vivo.

1188. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of one or more populations of T cells in a sample.

1189. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of one or more individual T cells in a sample.

1190. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of one or more individual T cells in a sample by measurement of activation.

1191. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of one or more populations of T cells in a sample by measurement of activation.

1192. The method of 1191, wherein the indirect detection of one or more individual T cells in a sample comprises measurement of secretion of soluble factors.

1193. The method of 1191, wherein the indirect detection of one or more populations of T cells in a sample comprises measurement of secretion of soluble factors.

1194. The method of claim 1192, wherein the measurement of secretion of soluble factors comprises measurement of extracellular secreted soluble factors.

1195. The method of claim 1194, wherein the measurement of extracellular secreted soluble factors comprises analysis of a fluid sample.

1196. The method of claim 1194, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells by capture of extracellular secreted soluble factor on a solid support.

1197. The method of claim 1194, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells immobilized to solid support in a defined pattern.

1198. The method of claim 1194, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells by measurement of effect of extracellular secreted soluble factor.

1199. The method of claim 1193, wherein the measurement of secretion of soluble factors comprises measurement of intracellular secreted soluble factors.

1200. The method of 1192, wherein the indirect detection of individual or populations of T cells in a sample comprises measurement of expression of one or more receptors.

1201. The method of 1192, wherein the indirect detection of individual or populations of T cells in a sample comprises measurement of T cell effector function.

1202. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of individual or populations of T cells in a sample by measurement of T cell proliferation.

1203. The method of any of the claims 1093 to 1095, wherein the method comprises indirect detection of individual or populations of T cells in a sample by measurement of T cell inactivation such as measuremet of blockage of TCR and/or measurement of induction of apoptosis.

1204. The method of any of the claims 1093 to 1095, wherein the method comprises immunohistochemistry or immunohistochemistry-like analysis.

1205. The method of any of claims 1093 to 1095, wherein the method comprises a measuring step involving an ELISA or ELISA-like analysis.

1206. The method of any of the claims 1093 to 1095, wherein the antigen-specific T cells are isolated using MHC multimers immobilized on a solid phase.

1207. The method of claim 1206, wherein the solid phase is a bead.

1208. The method of claim 1206, wherein the solid phase is immunotubes.

1209. The method of claim 1206, wherein the solid phase is microtiter plates.

1210. The method of claim 1206, wherein the solid phase is microchips.

1211. The method of claim 1206, wherein the solid phase is microarrays.

1212. The method of claim 1206, wherein the solid phase is test strips.

1213. The method of any of the claims 1093 to 1095, wherein the method comprises blocking of the sample with a protein solution such as BSA or skim milk.

1214. The method of any of the claims 1093 to 1095, wherein the method comprises blocking of the MHC multimer with a protein solution such as BSA or skim milk.

1215. The method of any of the claims 1093 to 1095, wherein the method comprises mixing of MHC multimer coated beads with the cell sample.

1216. The method of any of the claims 1093 to 1095, wherein the method comprises incubation of MHC multimer coated beads with the cell sample.

1217. The method of any of the claims 1093 to 1095, wherein the method comprises a washing step after incubation of MHC multimer coated beads with the cell sample.

1218. The method of any of the claims 1093 to 1095, wherein the method comprises release of the immobilized T cells from the beads.

1219. The method of claim 1218, wherein the T cells are released by cleavage of the linker.

1220. The method of claim 1218, wherein the T cells are released by changing the pH.

1221. The method of claim 1218, wherein the T cells are released by changing the salt concentration.

1222. The method of claim 1218, wherein the T cells are released by addition of one or more competitive binders.

1223. The method of claim 1218, wherein the T cells are released by a method that does not disrupts the integrity of the cells.

1224. The method of any of the claims 1093 to 1095, wherein the method comprises manipulation of the T cells after release from the beads.

1225. The method of claim 1224, wherein the manipulation is induction of apoptosis.

1226. The method of claim 1224, wherein the manipulation is induction of proliferation.

1227. The method of claim 1224, wherein the manipulation is induction of differentiation.

1228. The method of any of the claims 1093 to 1095, wherein the sample to be analysed is acquired from the bone marrow, the blood, the lymph, a solid tissue sample or a suspension of a tissue sample.

1229. The method of any of the claims 1093 to 1095, wherein the sample to be analysed is acquired from solid tissue, solid tissue section or a fluid such as whole blood, serum, plasma, nasal secretions, sputum, urine, sweat, saliva, transdermal exudates, pharyngeal exudates, bronchoalveolar lavage, tracheal aspirations, cerebrospinal fluid, synovial fluid, fluid from joints, vitreous fluid, vaginal or urethral

secretions, or disaggregated cellular tissues such as hair, skin, synovial tissue, tissue biopsies and nail scrapings.

1230. The method of any of the claims 1093 to 1095, wherein the sample to be analysed is acquired from cell suspensions derived from tissue samples or cell lines.

1231. The method of claims 1093 to 1095 for use in a method of diagnosing an infection in an individual, such as an animal, for example a human being.

1232. The method of claims 1231, wherein the infection is caused by a bacteria.

1233. The method of claims 1231, wherein the infection is caused by a Borrelia species or subspecies selected from the group consisting of: Borrelia anserina, Borrelia barbouri, Borrelia afzelii, Borrelia afzelii ACA-1, Borrelia afzelii K78, Borrelia afzelii PKo, Borrelia andersonii, Borrelia bissettii, Borrelia burgdorferi, Borrelia burgdorferi 118a, Borrelia burgdorferi 156a, Borrelia burgdorferi 29805, Borrelia burgdorferi 64b, Borrelia burgdorferi 72a, Borrelia burgdorferi 80a, Borrelia burgdorferi 94a, Borrelia burgdorferi B31, Borrelia burgdorferi Bol26, Borrelia burgdorferi CA-11.2a, Borrelia burgdorferi WI91-23, Borrelia burgdorferi ZS7, Borrelia californiensis, Borrelia garini, Borrelia garini PBi, Borrelia garini PBr, Borrelia genomosp. 1, Borrelia genomosp. 2, Borrelia japonica, Borrelia lusitaniae, Borrelia spielmanii, Borrelia spielmanii A14S, Borrelia tanukii, Borrelia turdi, Borrelia valaisiana, Borrelia valaisiana VS116, Candidatus Borrelia texasensis, Borrelia sp. AA4Pool, Borrelia sp. Al-1, Borrelia sp. B31, Borrelia sp. BC-1, Borrelia sp. CA1133, Borrelia sp. CA1176, Borrelia sp. CA128, Borrelia sp. CA13, Borrelia sp. CA134, Borrelia sp. CA142, Borrelia sp. CA20, Borrelia sp. CA22, Borrelia sp. CA27, Borrelia sp. CA28, Borrelia sp. CA29, Borrelia sp. CA31, Borrelia sp. CA33, Borrelia sp. CA370, Borrelia sp. CA372, Borrelia sp. CA378, Borrelia sp. CA388, Borrelia sp. CA393, Borrelia sp. CA394, Borrelia sp. CA395, Borrelia sp. CA399, Borrelia sp. CA400, Borrelia sp. CA401, Borrelia sp. CA402, Borrelia sp. CA404, Borrelia sp. CA411, Borrelia sp. CA426, Borrelia sp. CA443, Borrelia sp. CA446, Borrelia sp. CA448, Borrelia sp. CA462, Borrelia sp. CA468, Borrelia sp. CA502, Borrelia sp. CA504, Borrelia sp. CA507, Borrelia sp. CA547, Borrelia sp. CA552, Borrelia sp. CA8, Borrelia sp. D22, Borrelia sp. D35, Borrelia sp. FD-1, Borrelia sp. FL18, Borrelia sp. FL27, Borrelia sp. FL35, Borrelia sp. FL42, Borrelia sp. HN6, Borrelia sp. HN7,

Borrelia sp. HN8, Borrelia sp. HNM13, Borrelia sp. HNM14, Borrelia sp. HNM19, Borrelia sp. IA1, Borrelia sp. Ir-3519, Borrelia sp. Ir-4721, Borrelia sp. Ir-4812, Borrelia sp. Ir-5215, Borrelia sp. LV5, Borrelia sp. MI-2, Borrelia sp. MI-5, Borrelia sp. MI-6, Borrelia sp. MI-8, Borrelia sp. MI-9, Borrelia sp. MOD-1, Borrelia sp. MOD-5, Borrelia sp. MOK-3a, Borrelia sp. MOS-1b, Borrelia sp. NE49, Borrelia sp. NE581, Borrelia sp. PHaP, Borrelia sp. PSigII, Borrelia sp. SCGT-10, Borrelia sp. SCGT-8a, Borrelia sp. SCI-2, Borrelia sp. SCW-30h, Borrelia sp. SI-1, Borrelia sp. SI-10, Borrelia sp. SM-1, Borrelia sp. SV1, Borrelia sp. W97F51, Borrelia sp. Z41293, Borrelia sp. Z41493, Borrelia coriaceae, Borrelia crocidurae, Borrelia duttonii, Borrelia duttonii Ly, Borrelia hermsii, Borrelia hermsii DAH, Borrelia hispanica, Borrelia lonestari, Borrelia miyamotoi, Borrelia parkeri, Borrelia persica, Borrelia recurrentis, Borrelia recurrentis A1, Borrelia sinica, Borrelia theileri, Borrelia turcica, Borrelia turicatae, Borrelia turicatae 91E135, Borrelia sp., Borrelia sp. 'Lake Gaillard', Borrelia sp. 000133, Borrelia sp. 010298, Borrelia sp. 10MT, Borrelia sp. 5145, Borrelia sp. 57Nsk, Borrelia sp. 5MT, Borrelia sp. 6T04-2, Borrelia sp. BR, Borrelia sp. BR 2007, Borrelia sp. C5-N52, Borrelia sp. CB-A1, Borrelia sp. CB-A11, Borrelia sp. CB-A3, Borrelia sp. EFL-S0100110, Borrelia sp. IK/23, Borrelia sp. IM/16, Borrelia sp. IM/19, Borrelia sp. KR1, Borrelia sp. KR3, Borrelia sp. LB-2001, Borrelia sp. LB-M56, Borrelia sp. LB-W100, Borrelia sp. MK-N61, Borrelia sp. NR-N8, Borrelia sp. OkME1, Borrelia sp. PAnz, Borrelia sp. PJes, Borrelia sp. PMai, Borrelia sp. PMew, Borrelia sp. R57, Borrelia sp. strain Spain, Borrelia sp. TA1, Borrelia sp. TM, Borrelia sp. TM1 and Borrelia sp. TM2.

1234. The method of claims 1231, wherein the infection is caused by *Borrelia burgdorferi*.

1235. The method of claims 1231, wherein the infection is caused by *Borrelia afzelii*.

1236. The method of claims 1231, wherein the infection is caused by *Borrelia garinii*.

1237. The method of claims 1231, wherein the infection is caused by *Borrelia burgdorferi* such as burgdorferi 118a, 156a, 29895, 64b,72a, 80a, 94a, B31, zBol26, CA-11.2a, ZS7 or WI91-23.

1238. The method of claims 1231, wherein the infection is caused by a *Borrelia californiensis*.

1239. The method of claims 1231, wherein the infection is caused by *Borrelia garinii* PBi or PBr.

1240. The method of claims 1231, wherein the infection is caused by *Borrelia genomosp. 1* or *genomosp. 2*.

1241. The method of claims 1231, wherein the infection is caused by *Borrelia anserine*.

1242. The method of claims 1231, wherein the infection is caused by *Borrelia barbouri.*

1243. The method of claims 1231, wherein the infection is caused *Borrelia japonica*.

1244. The method of claims 1231, wherein the infection is caused by *Borrelia lustaniae*.

1245. The method of claims 1231, wherein the infection is caused by *Borrelia spielmanii*.

1246. The method of claims 1231, wherein the infection is caused by *Borrelia tanukii*.

1247. The method of claims 1231, wherein the infection is caused by *Borrelia valaisiana*.

1248. The method of claims 1093 to 1095 for use in diagnosis of allergic disease in an individual, such as an animal, for example a human being.

1249. The method of claims 1093 to 1095 for use in diagnosis a borrelia infection.

1250. The method of claims 1093 to 1095 for use in diagnosis of autoimmune disease in an individual, such as an animal, for example a human being.

1251. The method of claims 1093 to 1095 for use in diagnosis of inflammation in an individual, such as an animal, for example a human being.

1252. The method of any of the claims 1093 to 1095 for use in monitoring of an adaptive immune response in an individual, such as an animal, for example a human being.

1253. The method of any of the claims 1093 to 1095 for use in monitoring of autoimmune diseases in an individual, such as an animal, for example a human being.

1254. The method of any of the claims 1093 to 1095 for use in diagnosis of autoimmune diseases in an individual, such as an animal, for example a human being.

1255. The method of any of the claims 1093 to 1095 for use in determining the prognosis of autoimmune diseases in an individual, such as an animal, for example a human being.

1256. The method of any of the claims 1093 to 1095 for use in development of vaccines for autoimmune diseases in an individual, such as an animal, for example a human being.

1257. The method of any of the claims 1093 to 1095 for use in development of therapy for autoimmune diseases in an individual, such as an animal, for example a human being.

1258. The method of any of the claims 1093 to 1095 for use in determination of the prognosis for diseases associated with the immune system in an individual, such as an animal, for example a human being.

1259. The method of any of the claims 1093 to 1095 for use in diagnostics for diseases associated with the immune system in an individual, such as an animal, for example a human being.

1260. The method of any of the claims 1093 to 1095 for use in monitoring a vaccine response in an individual, such as an animal, for example a human being.

1261. The method of any of the claims 1093 to 1095 for use in development of a vaccine in an individual, such as an animal, for example a human being.

1262. The method of any of the claims 1093 to 1095 for use of determination of the overall wellness of the immune system in an individual, such as an animal, for example a human being.

1263. The method of any of the claims 1093 to 1095 for use of determination of the efficacy of an anti HIV treatment in an individual, such as an animal, for example a human being.

1264. The method of any of the claims 1093 to 1095 for use of development of an anti HIV treatment in an individual, such as an animal, for example a human being.

1265. The method of any of the claims 1093 to 1095, wherein T cells specific for Cytomegalovirus (CMV) are detected.

1266. The method of any of the claims 1093 to 1095, wherein T cells specific for allergens are detected.

1267. The method of any of the claims 1093 to 1095, wherein T cells specific for auto antigens are detected.

1268. The method of any of the claims 1093 to 1095, wherein T cells specific for disease associated proteins are detected.

1269. The method of any of the claims 1093 to 1095, wherein the measuring of said T cells is predictive for treatment efficiency.

1270. The method of any of the claims 1093 to 1095, wherein the outcome of an vaccination is monitored in an individual, such as an animal, for example a human being.

1271. The method of any of the claims 1093 to 1095, wherein the method is used for adjustment of an immune suppressive treatment in an individual, such as an animal, for example a human being.

1272. The method of any of the claims 1093 to 1095, wherein the method is used for monitoring an immune suppressive treatment in an individual, such as an animal, for example a human being.

1273. The method of any of the claims 1093 to 1095, wherein the method is used for monitoring an immune suppressive treatment in an individual, such as an animal, for example a human being.

1274. The method of any of the claims 1093 to 1095, wherein the method comprises the provision of one or more derivatives of MHC multimers.

1275. The method of any of the claims 1093 to 1095, wherein the said method comprises detection of and/or analysis of and/or manipulation of one or more specific T cells with MHC multimers comprising antigenic peptides from antigens selected from the group consisting of Adenovirus (subgropus A-F), BK-virus, CMV (Cytomegalo virus, HHV-5), EBV (Epstein Barr Virus, HHV-4), HBV (Hepatitis B Virus), HCV (Hepatitis C virus), HHV-6a and b (Human Herpes Virus-6a and b), HHV-7, HHV-8, HSV-1 (Herpes simplex virus-1, HHV-1), HSV-2 (HHV-2), JC-virus, SV-40 (Simian virus 40), VZV (Varizella-Zoster-Virus, HHV-3), Parvovirus B19, Haemophilus influenza, HIV-1 (Human immunodeficiency Virus-1), HTLV-1 (Human T-lymphotrophic virus-1), HPV (Human Papillomavirus), Mycobacterium tuberculosis,

Mycobacterium bovis, Borrelia burgdorferi, Helicobacter pylori, Streptococcus pneumoniae, Listeria monocytogenes, Histoplasma capsulatum, Aspergillus fumigatus, Candida albicans, Cryptococcus neoformans, Pneumocystis carinii, Plasmodium falciparum, Plasmodium vivax, Plasmodium malariae, Schistosoma mansoni, Schistosoma japonicum, Schistosoma haematobium, Trypanosoma cruzi, Trypanosoma rhodesiense, Trypanosoma gambiense, Leishmania donovani, Leishmania tropica, Birch, Hazel, Elm, Ragweed, Wormwood, Grass, Mould and Dust Mite.

1276. The method of any of the claims 1093 to 1095, wherein the said method comprises detection of and/or analysis of and/or manipulation of one or more specific T cells with antigenic peptides or MHC multimers comprising antigenic peptides from antigens selected from the group consisting of: any of the proteins shown in figures 27, 28, 29 and 30 .

1277. A method for performing a vaccination of an individual in need thereof, said method comprising the steps of

providing a MHC monomer or a MHC multimer according to any of the claims 1 to 797, or the individual components thereof , or the antigenic peptide (P), according to any of the claims 1 and 1509-1537, or the antigenic polypeptide (poly-P) according to claim 1580 or 1581, and

administering said MHC monomer or MHC multimer or antigenic peptide or antigenic polypeptide to said individual and obtaining a protective immune response, thereby performing a vaccination of the said individual.

1278. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered alone to said individual.

1279. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered together with one or more adjuvant(s) to said individual.

1280. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual more than once such as twice or three times.

1281. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual cutaneously.

1282. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual subcutaneously (SC).

1283. The method according to claim 1277, wherein P , poly-P or the MHC multimer is administered to said individual by intramuscular (IM) administration.

1284. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual by intravenous (IV) administration.

1285. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual by Per-oral (PO) administration.

1286. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual inter peritoneally.

1287. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual pulmonally.

1288. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual vaginally.

1289. The method according to claim 1277, wherein P, poly-P or the MHC multimer is administered to said individual rectally.

1290. The method according to claim 1277, wherein the vaccination is a therapeutic vaccination i.e. vaccination “teaching” the immune system to fight an existing infection or disease.

1291. A method for performing therapeutic treatment of an individual comprising the steps of

Providing the MHC multimer according to claim 1 to 797, or individual components thereof, and

Isolating or obtaining T-cells from a source, such as an individual or an ex-vivo library or cell bank, wherein said isolated or obtained T-cells are specific for said provided MHC multimer,

Optionally manipulating said T-cells, and

Introducing said isolated or obtianed T-cells into an individual to be subjected to a therapeutic treatment, wherein the individual can be the same individual or a different individual from the source individual.

1292. A method for minimization of undesired binding of the MHC multimer according to any of the claims 1 to 784.

1293. The method of claim 1292, wherein the method comprises mutagenesis of the MHC multimer.

1294. The method of claim 1293, wherein the method comprises mutagenesis in areas of the MHC multimer responsible for binding to unwanted cells.

1295. The method of claim 1293, wherein the method comprises mutagenesis in the α3-domain of the α-chain of MHC I molecules.

1296. The method of claim 1296, wherein the method comprises mutagenesis in a sub domain in the β2 domain of the β-chain of MHC II molecules.

1297. The method of claim 1293, wherein the method comprises mutagenesis in areas of MHC multimers that are involved in interactions with T cell surface receptors different from TCR, CD8 and CD4, or that bind surface receptors on B cells, NK cells, Eosiniophils, Neutrophils, Basophiles, Dendritic cells or monocytes.

1298. The method of any of the claims 1293 to 1297, wherein the mutation is a substitution.

1299. The method of any of the claims 1293 to 1297, wherein the mutation is an insertion.

1300. The method of any of the claims 1293 to 1297, wherein the mutation is a deletion.

1301. The method of any of the claims 1293 to 1300, wherein the one or more target residues are natural amino acids.

1302. The method of any of the claims 1293 to 1300, wherein the one or more target residues are non-natural amino acids.

1303. The method of any of the claims 1293 to 1300, wherein the target residues are a combination of natural and non-natural amino acids.

1304. The method of any of the claims 1293 to 1303, wherein a single amino acid is mutated.

1305. The method of any of the claims 1293 to 1303, wherein more than one amino acid is mutated.

1306. The method for minimization of undesired binding of the MHC multimer according to claim 1292, wherein the method comprises chemical alterations in the MHC multimer.

1307. The method of claim 1306, wherein the method comprises one or more chemical alterations of surface areas of the MHC multimer responsible for binding to unwanted cells.

1308. The method of claim 1306, wherein the method comprises one or more chemical alterations in the α3-domain of the α-chain of MHC I molecules.

1309. The method of claim 1306, wherein the method comprises one or more chemical alterations in a sub domain in the β2 domain of the β-chain of MHC II molecules.

1310. The method of claim 1306, wherein the method comprises one or more chemical alterations of surface areas of MHC multimers that are involved in interactions with T cell surface receptors different from TCR, CD8 and CD4, or that bind surface receptors on B cells, NK cells, Eosiniophils, Neutrophils, Basophiles, Dendritic cells or monocytes.

1311. The method of any of the claims 1306 to 1310, wherein a single amino acid is altered.

1312. The method of any of the claims 1306 to 1310, wherein more than one amino acid is altered.

1313. The method of claim 1392, wherein the method comprises the addition of one or more components of a MHC multimer, predicted to be responsible for the undesired binding.

1314. The method of claim 1313, wherein the added component is one or more MHC multimers that contain nonsense peptides.

1315. The method of claim 1313, wherein the added component is one or more soluble MHC multimers not coupled to a multimerization domain, and with or without peptide bound in the peptide binding cleft.

1316. The method of claim 1313, wherein the added component is individual components of the MHC multimer.

1317. The method of claim 1316, wherein one or more individual components of the MHC multimer is selected from the group consisting of I α-chain, subunits of MHC I α-chain, beta2microglobulin, subunits of beta2microglobulin , α/β-chain of MHC II, subunits of α/β-chain of MHC II.

1318. The method of claim 1316, wherein the one or more individual subunits are folded.

1319. The method of claim 1316, wherein the one or more individual subunits are un-folded.

1320. The method of claim 1316, wherein the individual subunits are folded and un-folded.

1321. The method of claim 1316, wherein the one or more individual subunits are attached to one or more multimerization domains identical or different from the one used in the MHC multimer employed in the analysis.

1322. The method of claim 1316, wherein the one or more individual subunits are one or more multimerization domain similar or identical to the multimerization domain used in the MHC multimer or individual components of the multimerization domain.

1323. The method of any of the claims 1316 to 1322, wherein the added component is not labelled.

1324. The method of any of the claims 1316 to 1322, wherein the added component is labelled with a label different from the label of the MHC multimer used for analysis.

1325. The method of claim 1292, wherein one or more reagents able to identify specific cell types are included.

1326. The method of claim 1325, wherein the one or more reagents comprises gating reagents for use in flow cytometry experiments.

1327. The method of claim 1326, wherein the flow cytometry experiment comprises removal of signals from MHC multimer stained cells not expressing the specific TCR by introducing an exclusion gate.

1328. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD3.

1329. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD8.

1330. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD3 and CD8.

1331. The method of claim 1330, wherein the CD3 and CD8 are labelled with distinct labels such as fluorochromes.

1332. The method of claim 1330, wherein the CD3 and CD8 are labelled with the same labels such as fluorochromes.

1333. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD4.

1334. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD3 and CD4.

1335. The method of claim 1334, wherein the CD3 and CD4 are labelled with distinct labels such as fluorochromes.

1336. The method of claim 1334, wherein the CD3 and CD4 are labelled with the same labels such as fluorochromes.

1337. The method of claim 1326, wherein the one or more reagents comprises fluorescent antibodies directed against specific surface markers.

1338. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD2.

1339. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD27 and/or CD28.

1340. The method of claim 1326, wherein the one or more gating reagents comprises anti-Foxp3.

1341. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD45RA.

1342. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD45RO.

1343. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CD62L.

1344. The method of claim 1326, wherein the one or more gating reagents comprises reagents binding to CCR7.

1345. The method of any of the claims 1325 to 1344, wherein the reagent identifies specific cell types by selection.

1346. The method of any of the claims 1325 to 1344, wherein the reagent identifies specific cell types by exclusion.

1347. The method of claim 1346, wherein the reagent identifies CD45 expressed on red blood cells.

1348. The method of claim 1346, wherein the reagent identifies CD19 expressed on B cells.

1349. The method of claim 1346, wherein the reagent identifies CD56 expressed on NK cells.

1350. The method of claim 1346, wherein the reagent identifies CD4 expressed on T helper cells.

1351. The method of claim 1346, wherein the reagent identifies CD8 expressed on cytotoxic T cells.

1352. The method of claim 1346, wherein the reagent identifies CD14 expressed on monocytes.

1353. The method of claim 1346, wherein the reagent identifies CD15 expressed on granulocytes.

1354. The method of claim 1346, wherein the reagent identifies CD15 expressed on monocytes.

1355. The method of claim 1292 further comprising co-staining with reagents according to any of the claims 1 to 784.

1356. A method for performing a control experiment comprising the step of counting of particles comprising the MHC multimer according to any of the claims 1 to 797.

1357. A method for performing a control experiment comprising the step of sorting of particles comprising the MHC multimer according to any of the claims 1 to 797.

1358. A method for performing a control experiment comprising the step of performing flow cytometry analysis of particles comprising the MHC multimer according to any of the claims 1 to 797.

1359. A method for performing a control experiment comprising the step of performing a immunohistochemistry analysis comprising the MHC multimer according to any of the claims 1 to 797.

1360. A method for performing a control experiment comprising the step of performing a immunocytochemistry analysis comprising the MHC multimer according to any of the claims 1 to 797.

1361. A method for performing a control experiment comprising the step of performing an ELISA analysis comprising the MHC multimer according to any of the claims 1 to 797.

1362. The method of any of the claims 1356 to 1361, further comprising a positive control (recognizing the MHC multimers comprising correctly folded MHC).

1363. The method of claim 1362, wherein the positive control comprises one or more beads with immobilized TCR's.

1364. The method of claim 1362, wherein the positive control comprises one or more "solid support" scaffolds with immobilized TCR's.

1365. The method of claim 1362, wherein the positive control comprises a solid surface with immobilized TCR's.

1366. The method of claim 1365, wherein the solid surface is a microtiter plate.

1367. The method of claim 1362, wherein the positive control comprises one or more micelles with immobilized TCR's.

1368. The method of claim 1362, wherein the positive control comprises one or more liposomes with immobilized TCR's.

1369. The method of claim 1362, wherein the positive control comprises soluble TCR's.

1370. The method of any of the claims 1363 to 1369, wherein the TCR's are full-length.

1371. The method of any of the claims 1363 to 1369, wherein the TCR's are truncated.

1372. The method of any of the claims 1363 to 1369, wherein the TCR's are full-length or truncated.

1373. The method of any of the claims 1363 to 1369, wherein the TCR's only comprises the extracellular domains.

1374. The method of any of the claims 1363 to 1369, wherein the TCR's are recombinant.

1375. The method of any of the claims 1363 to 1369, wherein the TCR's are chemically modified.

1376. The method of any of the claims 1363 to 1369, wherein the TCR's are enzymatically modified.

1377. The method of claim 1362, wherein the positive control comprises one or more beads with immobilized aptamers.

1378. The method of claim 1362, wherein the positive control comprises one or more "solid support" scaffolds with immobilized aptamers.

1379. The method of claim 1362, wherein the positive control comprises a solid surface with immobilized aptamers.

1380. The method of claim 1379, wherein the solid surface is a microtiter plate.

1381. The method of claim 1362, wherein the positive control comprises one or more micelles with immobilized aptamers.

1382. The method of claim 1362, wherein the positive control comprises one or more liposomes with immobilized aptamers.

1383. The method of claim 1362, wherein the positive control comprises one or more soluble aptamers.

1384. The method of claim 1362, wherein the positive control comprises one or more beads with immobilized antibody specific for the MCH mutimer.

1385. The method of claim 1362, wherein the positive control comprises one or more “solid support” scaffolds with immobilized antibody specific for the MCH mutimer.

1386. The method of claim 1362, wherein the positive control comprises a solid surface with immobilized antibody specific for the MCH mutimer.

1387. The method of claim 1386, wherein the solid surface is a microtiter plate.

1388. The method of claim 1362, wherein the positive control comprises one or more micelles with immobilized antibody specific for the MCH mutimer.

1389. The method of claim 1362, wherein the positive control comprises one or more liposomes with immobilized antibody specific for the MCH mutimer.

1390. The method of claim 1362, wherein the positive control comprises one or more soluble antibody specific for the MCH mutimer.

1391. The method of claim 1362, wherein the positive control comprises one or more beads with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1392. The method of claim 1362, wherein the positive control comprises one or more “solid support” scaffolds with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1393. The method of claim 1362, wherein the positive control comprises a solid surface with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1394. The method of claim 1393, wherein the solid surface is a microtiter plate.

1395. The method of claim 1362, wherein the positive control comprises one or more micelles with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1396. The method of claim 1362, wherein the positive control comprises one or more liposomes with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1397. The method of claim 1362, wherein the positive control comprises one or more soluble molecule that recognize correctly folded MHC-peptide complexes.

1398. The method of claim 1362, wherein the positive control comprises one or more cell lines that display MHC multimer-binding molecules that recognize the MHC-peptide complexes.

1399. The method of claim 1398, wherein the cell line is a T-cell line.

1400. The method of claim 1398, wherein the MHC multimer-binding molecules are TCR's.

1401. The method of claim 1362, wherein the positive control comprises cells from blood samples that carry receptor molecules specific for the MHC multimer.

1402. The method of claim 1362, wherein the positive control comprises cells from preparations of purified lymphocytes (HPBMCs) that carry receptor molecules specific for the MHC multimer.

1403. The method of claim 1362, wherein the positive control comprises cells from bodily fluids that carry receptor molecules specific for the MHC multimer.

1404. The method of claim 1362, wherein the positive control comprises cells from bodily fluids that carry receptor molecules specific for the MHC multimer.

1405. The method of claim 1362, wherein the said method comprises density-gradient centrifugation (e.g. in CsCl).

1406. The method of claim 1362, wherein the said method comprises size exclusion chromatography.

1407. The method of claim 1362, wherein the said method comprises PAGE.

1408. The method of claim 1362, wherein the said method comprises chromatography.

1409. The method of any of the claims 1356 to 1361, wherein the MHC multimer binding is visualized with a labelled secondary component that binds the MHC multimer

1410. The method of claim 1409, wherein the label of the secondary component is selected from the group consisting of fluorophores, chromophores, chemiluminescent labels, bioluminescent labels, radioactive labels, enzyme labels.

1411. The method of any of the claims 1409 and 1410, wherein the MHC multimer binding is visualized by binding of a labelled compound specific for the secondary component that binds the MHC multimer selected from the group of TCR's, aptamers, antibodies, streptavidin or other MHC-peptide complex binding molecules.

1412. The method of claim 1410, wherein the label of the compound specific for the secondary component is selected from the group consisting of fluorophores, chromophores, chemiluminescent labels, bioluminescent labels, radioactive labels, enzyme labels.

1413. The method of any of the claims 1356 to 1412, wherein a negative control is included.

1414. The method of claim 1413, wherein the method comprises MHC multimers carrying nonsense peptides.

1415. The method of claim 1413, wherein the method comprises MHC multimers carrying nonsense chemically modified peptides.

1416. The method of claim 1413, wherein the method comprises MHC multimers carrying naturally occurring peptides different from the peptide used for analysis of specific T cells in the sample.

1417. The method of claim 1413, wherein the method comprises empty MHC multimers.

1418. The method of claim 1413, wherein the method comprises MHC heavy chain or MHC multimers comprising MHC heavy chain and not the MHC light chain

1419. The method of claim 1418, wherein the MHC heavy chain is MHC I

1420. The method of claim 1418, wherein the MHC heavy chain is MHC II

1421. The method of claims 1419 and 1420, wherein the MHC heavy chain is truncated

1422. The method of claims 1419 and 1420, wherein the MHC heavy chain is full-length.

1423. The method of claims 1419 and 1420, wherein the MHC heavy chain is folded.

1424. The method of claims 1419 and 1420, wherein the MHC heavy chain is un-folded.

1425. The method of claim 1419, wherein the MHC I heavy chain is the MHC I alpha chain comprising the $\alpha 3$ domain that binds CD8 molecules on cytotoxic T cells.

1426. The method of claim 1420, wherein the MHC II heavy chain is the MHC II β chain comprising the $\beta 2$ domain that binds CD4 on the surface of helper T cells.

1427. The method of claim 1426, wherein the method comprises Beta2microglobulin.

1428. The method of claim 1413, wherein the method comprises subunits of beta2microglobulin.

1429. The method of claim 1413, wherein the method comprises MHC multimers comprising Beta2microglobulin.

1430. The method of claim 1413, wherein the method comprises MHC multimers comprising subunits of beta2microglobulin.

1431. The method of claims 1427 to 1430, wherein the Beta2microglobulin is un-folded.

1432. The method of claims 1427 to 1430, wherein the Beta2microglobulin is folded.

1433. The method of claims 1427 to 1430, wherein the subunit of Beta2microglobulin is un-folded.

1434. The method of claims 1427 to 1430, wherein the subunit of Beta2microglobulin is folded.

1435. The method of claim 1413, wherein the method comprises MHC-like complexes.

1436. The method of claim 1435, wherein the MHC-like complexes are folded.

1437. The method of claim 1435, wherein the MHC-like complexes are un-folded.

1438. The method of claim 1435, wherein the MHC-like complexes are CD1 molecules.

1439. The method of claim 1436, wherein the method comprises multimerization domains without MHC or MHC-like molecules.

1440. The method of claim 1413, wherein the method comprises one or more multimerization domains selected from the group consisting of dextran, streptavidin, IgG, coiled-coil-domain, liposomes.

1441. The method of claim 1413, wherein the method comprises one or more labels selected from the group FITC, PE, APC, pacific blue, cascade yellow.

1442. The method of any of the claims 1356 to 1361, wherein a negative and a positive control is included.

1443. The method according to any of the claims 1093 to 1442, wherein the method comprises use of one or more MHC monomer and/or one or more MHC multimer according to any of the claims 1 to 797, wherein said one or more MHC monomers and/or MHC multimers are part of an array or other kind of library of MHC monomers or MHC multimers.

1444. The method according to claim 1443, wherein said array or library of MHC monomers or MHC multimers comprises at least 10, such as at least 100, such as at least 1000, such as at least 10.000, such as at least 100.000, such as at least 1.000.0000, such as at least 10.000.000 different antigenic peptides.

1445. The method according to claim 1444, wherein the antigenic peptides are made by organic synthesis.

1446. The method according to claim 1444, wherein the antigenic peptides comprise all possible 8'-, 9'-, 10'-, and 11'-mers of one antigen.

1447. The method according to claim 1444, wherein the antigenic peptides comprise all possible 13'-, 14'-, 15'-, and 16'-mers of one antigen.

1448. The method of any of the claims 1444-1447, where the antigenic peptides are derived from a Borrelia antigen such as an antigen selected from the Borrelia

antigens listed in this application including the Borrelia antigens listed in Figure 27, Figure 28, Figure 29, Figure 30, Figure 38 and Figure 39 or where the antigenic peptides is selected from any on of the sequnces identified by SEQ ID NO 1-221774.

1449. The MHC monomer or MHC multimer according to any of the claims 1 to 797, wherein said MHC monomer or MHC multimer comprises one of the possible 8'-, 9'-, 10'-, 11'-,13'-, 14'-, 15'-, or 16'-mers of an antigen.

1450. The MHC monomer or MHC multimer according to claim 1449, wherein the antigen is a Borrelia antigen such as an antigen selected from the Borrelia antigens listed in this application including the Borrelia antigens listed in Figure 27, Figure 28, Figure 29, Figure 30, Figure 38 and Figure 39.

1451. The composition according to claim 1090 and 1091, wherein the composition comprises at least 10 different antigenic peptides, such as at least 100, such as at least 1000, such as at least 10.000, such as at least 100.000, such as at least 1.000.0000, such as at least 10.000.000 different antigenic peptides.

1452. The composition according to claim 1090 and 1091, wherein the composition comprises least 10 different antigenic peptides derived from one antigen, such as at least 100, such as at least 1000, such as at least 10.000, such as at least 100.000, such as at least 1.000.0000, such as at least 10.000.000 different antigenic peptides derived from one antigen.

1453. The composition according to claim 1452, wherein the antigenic peptides are made by organic synthesis on solid support, and wherein a partial cleavage of the linker that connects the growing antigenic peptide to the solid support is performed before, during or after each additional amino acid that is coupled to the growing antigenic peptide.

1454. A MHC monomer or MHC multimer, wherein the MHC monomer or MHC multimer is comprised within the composition of claim 1453.

1455. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain.

1456. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain combined with a MHC I beta2microglobulin chain.

1457. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain in complex with a MHC I beta2microglobulin chain.

1458. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain combined with MHC I beta2microglobulin chain through a linker.

1459. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain covalently linked to a MHC I beta2microglobulin chain through a linker.

1460. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain combined with an antigenic peptide.

1461. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain in complex with an antigenic peptide.

1462. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain combined with an antigenic peptide through a linker.

1463. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain covalently linked with an antigenic peptide through a linker.

1464. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain/MHC I beta2microglobulin dimer combined with an antigenic peptide.

1465. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain/MHC I beta2microglobulin dimer in complex with an antigenic peptide.

1466. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain/MHC I beta2microglobulin dimer combined with an antigenic peptide through a linker to the heavy chain or beta2microglobulin.

1467. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain/MHC I beta2microglobulin dimer covalently linked to an antigenic peptide through a linker to the heavy chain or beta2microglobulin.

1468. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC I heavy chain and/or beta2microglobulin-chain where the heavy chain or beta2microglobulin-chain is at least 99%, such as at least 98%, such as at least 95%, such as at least 90%, such as at least 80%, such as at least 70%, such as at least 60%, such as at least 50%, such as at least 40%, such as at least 30% identical to wild type MHC I heavy chain or beta2microglobulin.

1469. The MHC monomer or MHC multimer of any of the preceding claims where the MHC I molecule chains differ from wild type MHC I molecule chains by substitution of single or cohorts of native amino acids.

1470. The MHC monomer or MHC multimer of any of the preceding claims where the MHC I molecule chains differ from wild type MHC I molecule chains by inserts or deletions.

1471. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha-chain and a MHC II beta-chain, i.e. is a MHC II alpha/beta-dimer.

1472. The MHC monomer or MHC multimer of any of the preceding claims comprising an MHC II alpha/beta dimer with an antigenic peptide.

1473. The MHC monomer or MHC multimer of any of the preceding claims comprising an MHC II alpha/beta dimer in complex with an antigenic peptide.

1474. The MHC monomer or MHC multimer of any of the preceding claims comprising an MHC II alpha/beta dimer combined with an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1475. The MHC monomer or MHC multimer of any of the preceding claims comprising an MHC II alpha/beta dimer covalently linked to an antigenic peptide through a flexible linker to the MHC II alpha or MHC II beta chain.

1476. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha/beta dimer combined through an interaction by affinity tags.

1477. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha/beta dimer held together through an interaction by affinity tags.

1478. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha/beta dimer combined through an interaction by affinity tags and further combined with an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1479. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha/beta dimer held together through an interaction by affinity tags and further covalently linked to an antigenic peptide through a flexible linker to the MHC II alpha or MHC II beta chain.

1480. The MHC monomer or MHC multimer of any of the preceding claims comprising a MHC II alpha- or beta-chain where the alpha- and/or beta-chain are at least 99%, such as at least 98%, such as at least 95%, such as at least 90%, such as at least 80%, such as at least 70%, such as at least 60%, such as at least 50% identical to wild type MHC II alpha- or beta-chains.

1481. The MHC monomer or MHC multimer of any of the preceding claims where the MHC II molecule chains differ from wild type MHC II by substitution of single or cohorts of native amino acids.

1482. The MHC monomer or MHC multimer of any of the preceding claims where the MHC II molecule chains differ from wild type MHC II molecule chains by inserts or deletions.

1483. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain.

1484. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain combined with a MHC I beta2microglobulin chain.

1485. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain in complex with a MHC I beta2microglobulin chain.

1486. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain combined with MHC I beta2microglobulin chain through a linker.

1487. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain covalently linked to a MHC I beta2microglobulin chain through a linker.

1488. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain combined with an antigenic peptide.

1489. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain in complex with an antigenic peptide.

1490. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain combined with an antigenic peptide through a linker.

1491. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain covalently linked with an antigenic peptide through a linker.

1492. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain/MHC I beta2microglobulin dimer combined with an antigenic peptide.

1493. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain/MHC I beta2microglobulin dimer in complex with an antigenic peptide.

1494. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain/MHC I beta2microglobulin dimer combined with an antigenic peptide through a linker to the heavy chain or beta2microglobulin.

1495. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC I heavy chain/MHC I beta2microglobulin dimer covalently linked to an antigenic peptide through a linker to the heavy chain or beta2microglobulin.

1496. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises MHC II molecule chains that differ from wild type MHC I molecule chains by substitution of single or cohorts of native amino acids.

1497. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises MHC II molecule chains that differ from wild type MHC I molecule chains by inserts or deletions.

1498. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises MHC II alpha-chain and a MHC II beta-chain, i.e. is a MHC II alpha/beta-dimer.

1499. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises an MHC II alpha/beta dimer with an antigenic peptide.

1500. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises an MHC II alpha/beta dimer in complex with an antigenic peptide.

1501. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises an MHC II alpha/beta dimer combined with an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1502. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises an MHC II alpha/beta dimer covalently linked to an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1503. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC II alpha/beta dimer combined through an interaction by affinity tags.

1504. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC II alpha/beta dimer held together through an interaction by affinity tags.

1505. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC II alpha/beta dimer combined through an interaction by affinity tags and further combined with an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1506. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises a MHC II alpha/beta dimer held together through an interaction by affinity tags and further covalently linked to an antigenic peptide through a linker to the MHC II alpha or MHC II beta chain.

1507. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises MHC II molecule chains that differ from wild type MHC II by substitution of single or cohorts of native amino acids.

1508. The method of any of the preceding claims wherein the MHC monomer or MHC multimer comprises MHC II molecule chains that differ from wild type MHC II molecule chains by inserts or deletions.

1509. The antigenic peptide, P, according to claim 1, wherein said antigenic peptide comprises or consists of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774 and modified sequences obtained by modification of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774.

1510. The antigenic peptide according to claim 1509, wherein the peptide comprises or consists of a modified sequence obtained by modification of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774.

1511. The antigenic peptide according to claim 1510, wherein the modified sequence has at least 50 %, such as at least 60 %, such as at least 70 %, such as at least 85 %, such as at least 95 % or such as at least 99 % identity with a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774.

1512. The antigenic peptide according to claim 1510 or 1511, wherein said modified sequence has one or more amino acid substitutions.

1513. The antigenic peptide according to claim 1512, wherein said modified sequence has at most 10 amino acid substitutions, such as at most 9, such as at most 8, such as at most 7, such as at most 6, such as at most 5, such as at most 4, such as at most 3, such as at most 2 or such as at most 1 amino acid substitution.

1514. The antigenic peptide according to any of the claims 1512-1513, wherein the amino acid substitutions are amino acid substitutions with equivalent amino acid residues.

1515. The antigenic peptide according to any of the claims 1512-1513, wherein the amino acid substitutions are amino acid substitutions with non-equivalent amino acid residues.

1516. The antigenic peptide according to any of the claims 1509-1515, wherein the peptide consists of at most 30 amino acids, such as at the most 25 amino acids, such as at most 20 amino acids or such as at most 18 amino acids.

1517. The antigenic peptide according to any of the claims 1509-1516, wherein the peptide consists of at least 8, such as at least 9, such as at least 10, such as at least 11, such as at least 12, such as at least 13, such as at least 14, such as at least 15, such as at least 16, such as at least 17 or such as at least 18 amino acid residues.

1518. The antigenic peptide according to any of the claims 1509-1517, wherein the peptide consists of 8, 9, 10 or 11 amino acid residues.

1519. The antigenic peptide according to any of the claims 1509-1518, wherein the sequence or the modified sequence comprises an anchor motif selected form the group of HLA motifs presented in table 6.

1520. The antigenic peptide according to any of the claims 1509-1519, wherein the sequence or the modified sequence comprises a primary anchoring amino acid residue in position 2 and/or 9 in accordance with table 6.

1521. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 2 in the sequence with an amino acid residue selected from the group consisting of: alanine, threonine, serine, valine, leucine, isoleucine, methionine, glutamine, phenylalanine, tryptophan and tyrosine.

1522. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 2 in the sequence with an amino acid residue selected from the group consisting of: alanine, threonine, serine, valine, leucine, isoleucine, methionine and glutamine.

1523. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 2 in the sequence with an amino acid residue selected from the group consisting of: argennine, histidine and lysine.

1524. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 2 in the sequence with an amino acid residue selected from the group consisting of: aspartic acid and glutamic acid.

1525. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 2 in the sequence with an amino acid residue selected from the group consisting of: alanine, threonine and serine.

1526. The antigenic peptide according to any of the claims 1512-1518, wherein the amino substitution substitutes the amino acid residue in position 9 or 10 in the sequence with an amino acid residue selected from the group consisting of: phenylalanine, tryptophan, tyrosine, leucine, isoleucine, valine, glutamine, alanine, argentine, histidine, lysine and methionine.

1527. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 9 or 10 in the sequence with an amino acid residue selected from the group consisting of: phenylalanine, tryptophan, tyrosine, leucine, isoleucine, valine, glutamine, alanine and methionine.

1528. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 9 or 10 in the sequence with an amino acid residue selected from the group consisting of: leucine, isoleucine, valine, glutamine, alanine and methionine.

1529. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substitution substitutes the amino acid residue in position 9 or 10 in the sequence with an amino acid residue seleceted from the group consisting of: phenylalanine, tryptophan, tyrosine, leucine, isoleucine and methionine.

1530. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substituion substitutes the amino acid residue in position 9 or 10 in the sequence with an amino acid residue seleceted from glutamine and alanine.

1531. The antigenic peptide according to any of the claims 1512-1518, wherein the amino acid substituion substitutes the amino acid residues in position 9 or 10 in the sequence with an amino acid residue seleceted from tyrosine, arginine and lysine.

1532. The antigenic peptide according to any of the claims 1509-1516, wherein the peptide consists of 13, 14, 15, 16, 17 or 18 amino acid residues.

1533. The antigenic peptide according to claim 1532, wherein the sequence or the modified sequence comprises a MHC class II 9'mer core sequence.

1534. The antigenic peptide according to claim 1533, wherein the MHC class II 9'mer core sequence is in accordance with table 7.

1535. The antigenic peptide according to any of claims 1534-1535, wherein the 9'mer core sequence starts at any one of the positions 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 from the N-terminus of the antigenic peptide.

1536. The antigenic peptide according to any of the claims 1533-1535, wherein the peptide comprises or consiststs of a modified sequence comprising an amino acid substituion in position 1, 4, 6 and/or 9 of an MHC class II 9'mer core sequence.

1537. The antigenic peptide according to claim 1536, wherein the amino acid substitution is in accordance with table 7.

1538. A composition comprising a plurality of antigenic peptides according to any of claims 1, 1509-1537, wherein the antigenic peptides are identical.

1539. A composition comprising a plurality of antigenic peptides according to any of claims 1, 1509-1537, wherein the antigenic peptides are different.

1540. A kit comprising an antigenic peptide according to any of claims 1, 1509-1537 or the composition according to any of claims 1537 and 1538, and at least one additional component, such as a positive control and/or instructions for use.

1541. A vaccine comprising one or more antigenic peptides and/or one or more antigenic polypeptides and/or one or more MHC monomers and/or one or more MHC Multimers or a nucleic acid encoding said peptides and/or MHC monomers and/or multimers.

1542. The vaccine according to claim 1541, wherein vaccine comprise one or more antigenic peptides according to any of the claims 1 and 1509-1537 or one or more antigenic polypeptides according to claim 1580 or 1581.

1543. The vaccine according to claim 1541, wherein the one or more MHC monomers and/or one or more MHC Multimers are according to any of the claim 1-797.

1544. The vaccine according to any of the claims 1541-1543, wherein the peptides and/or MHC monomers and/or MHC multimers are encoded by one or more vira or one or more DNA vectors.

1545. The vaccine according to any of the previous claims 1541-1544, wherein the vaccine further comprises one or more cells.

1546. The vaccine according to claim 1545, wherein the one or more cells comprises cells expressing MHC molecules.

1547. The vaccine according to claim 1545, wherein the one or more cells comprises cells expressing MHC molecules that have been loaded with said one or more antigenic peptides.

1548. The vaccine according to claim 1545, wherein the one or more cells comprises cells expressing MHC molecules that have been loaded with said one or more antigenic peptides in vitro.

1549. The vaccine according to claim 1645, wherein the one or more cells comprises cells expressing MHC molecules that have been loaded with said one or more antigenic peptides in vivo.

1550. The vaccine according to any of the claims 1541-1543, wherein the one or more antigenic polypeptides or the one or more antigenic peptides or the antigenic peptides comprised by the one or more MHC monomers or the one or more multimers are made by organic synthesis.

1551. The vaccine according to any of the claims 1541-1550, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise one or more 8'-, 9'-, 10'-, and 11'-mers of one or more antigens.

1552. The vaccine according to any of the claims 1541-1551, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise one or more 13'-, 14'-, 15'-, and 16'-mers of one or more antigen.

1553. The vaccine according to any of the claims 1541-1550, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise all possible 8'-, 9'-, 10'-, and 11'-mers of one or more antigens.

1554. The vaccine according to any of the claims 1541-1550, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise all possible 13'-, 14'-, 15'-, and 16'-mers of one or more antigens.

1555. The vaccine according any of the claims 1541-1554, where the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers are derived from an Borrelia antigen selected from the group consisting of: the Borrelia antigens listed in the figures 27, 28, 29, 30, 38 and 39.

1556. The vaccine according to any of claims 1541-1555, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise or consist of one or more sequences selected from the group of sequences consisting of: SEQ ID N0 1 to 217774 and modified sequences obtained by modification of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774.

1557. The vaccine according to any of the previous claims 1541-1556, wherein the one or more antigenic peptides or the antigenic peptides comprised by the one or more antigenic polypeptides or the one or more MHC monomers or the one or more multimers comprise or consist of one or more sequences selected from the group of sequences consisting of: SEQ ID N0 1 to 217774 and modified sequences obtained by modification of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774, wherein the sequence is characterized by items 1 to 735.

1558. The vaccine according to any of the claims 1541-1557, wherein the vaccine further comprise one or more biologically active molecules.

1559. The vaccine according to claim 1558, wherein the one or more biologically active molecules comprise one or more molecules selected from the group consisting of one or more molecules with adjuvant effects, one or more

immune targets such as one or more antigens, one or more enzymes, one or more regulators of receptor activity, one or more receptor ligands, one or more immune potentiators, one or more drugs, one or more toxins, one or more co-receptors, one or more proteins, one or more peptides, one or more sugar moieties, one or more lipid groups, one or more nucleic acids, one or more siRNAs, one or more microRNAs, one or more nano particles, small molecules, one or more membranes, and one or more liposomes.

1560. The vaccine according to any of the claims 1541-1559, wherein the vaccine further comprises one or more immunological active molecules.

1561. The vaccine according to claim 1560, wherein the one or more immunological active molecules comprises one or more molecules selected from the group consisting of proteins, co-stimulatory molecules, cell modulating molecules, receptors, accessory molecules, adhesion molecules, natural ligands, toxic molecules, antibodies and recombinant binding molecules to any of the foregoing, and combinations thereof.

1562. The vaccine according to claim 1561, wherein the one or more immunological active molecules comprises one or more molecules selected from the group consisting of MHC Class 1 proteins like HLA-A, HLA-B, HLA-C alone or in complex with HLA-b2Microglobulin with or without peptide in the binding groove, MICA, MICB, CD1d, HLA-E, HLA-F, HLA-G, HLA-H, ULBP-1, ULBP-2, ULBP-3, HLA-DR (HLA-DRA, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5), HLA-DQ (HLA-DQA1, HLADQA2, HLA-DQB1, HLA-DQB2), HLA-DP (HLA-DPA1, HLA-DPB1), HLA-DO (HLA-DOA, HLA-DOB), HLA-DM (HLA-DMA, HLA-DMB) alone or in complexes consisting of class 2 A- and B-chains with or without peptide in the binding groove, Cytokines; IFN-alpha, IFN-beta, IFN-gamma, IL-1, IL-2, IL-3, IL-4, IL-6, IL-7, IL-8, IL-10, IL-11, IL-12, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, IL-21, IL-22, IL-23, IL-24, IL-25, IL-26, IL-27, IL-28,-IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, CSFs (colony-stimulating factors), c-Kit, EPO, TNF-alfa, TNF-beta, Lymphotoxin; Cytokine receptors like IL-1R, IL-2R, IL-3R, IL-4R, IL-5R, IL-6R, IL-7R, IL-8R, IL-9-R, IL-10R, IL-11R, IL-12R, IL-13R, IL-15R, IL-18R, IL-20R, IL-21R, IL-22R, IL-23R, IL-27R, IL-28R; Chemokines such as CXCL1, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10,

CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CCL1, CCL2, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL8, CCL9, CCL10, CCL11, CCL12, CCL13, CCL14, CCL15, CCL16, CCL17, CCL18, CCL19, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CXCR4, CCRL2; Chemokine receptors like CCR1, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CCR10, CCR11, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, CXCR7, CX3CR1, Toll-like receptors, TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, Toll like receptor ligands, multiple triacyl lipopeptides, multiple diacyl lipopeptides, multiple glycolipids, multiple lipopeptides, multiple lipoproteins, lipoteichoic acid, peptidoglycans, heat shock proteins (HSP70, HSP90 and others), zymosan, single- and double-stranded RNA, Poly I:C, lipo-polysaccharides, fibrinogen, heparin sulphate fragments, hyaluronic acid fragments, flagellin, imidazoquinoline, loxoribine (guanosine analogue), bropirimine, Imiquimod, unmethylated CpG DNA, Viral entry receptors/molecules, Ku70, Pvr, Prr1, HVEM, EphrinB2, cellular integrins (in particular alpha2beta1, alpha6beta1 alphaVbeta3), CD81, CD155, SR-B1, claudin-1, xCT, human nectin-2, LIGHT, TLR3, LIR, Heparan sulphate proteoglycans, GPI anchored proteins, hemeagglutinin receptor, Bacterial entry receptors/molecules, CD48, CEACAM-1, -2, -3, -4, -5, -6, invasion, internalin (InlA), InlB; Fc receptors like ε (FcεRI, FcεRII) - γ (FcγRI, FcγRII, FcγRIII) - α/μ (FcαRI, Fcα/μR) - Neonatal FcR, Lymphocyte homing receptors, CD44, L-selectin, VLA-4 (CD49a, b, c, d, e, f), LFA-1, Co-stimulatory molecules, CD2, CD3, CD4, CD5, CD8, CD9, CD27, CD28, CD30, CD69, CD134 (OX40), CD120, CD137 (4-1BB), CD147, CDw150 (SLAM), CD152 (CTLA-4), CD153 (CD30L), CD40L (CD154), NKG2D, ICOS, PD-1, Fas (CD95), FasL, CD40, CD58, CD70, CD72, B7.1 (CD80), B7.2 (CD86), B7RP-1, B7- H3, PD-L1, PD-L2, CD134L, CD137L, ICOSL, NK cell receptors/molecules, CD16, NKp30, NKp44, NKp46, NKp80,2B4, KIR3DL1, KIR3DL", KIR3DS1, KIR2DL1,KIRDL2, KIR2DL3, KIR2DL4, KIR2DL5, CD94/NKG2A, CD94/NKG2C, CD94/NKG2E, CD94/NKG2H, NKG2ADNKG2D, Adhesion molecules, ICAM-1, ICAM-2, GlyCAM-1, VCAM, CD34, Anti microbial peptides, Defensins, cathelicidin derived peptide LL-37, anti-LFA-1, anti-CD44, anti-beta7, anti-selectin L, anti-selectin E, anti- selectin P, toxic molecules selected from toxins, enzymes, antibodies, radioisotopes, chemiluminescent substances, bioluminescent substances, polymers, metal particles, and haptens, such as cyclophosphamide, methrotrexate, Azathioprine, mizoribine, 15-deoxuspergualin, neomycin,

staurosporine, genestein, herbimycin A, Pseudomonas exotoxin A, saporin, Rituxan, Ricin, gemtuzumab ozogamicin, Shiga toxin, vitamin D3, IL-2 toxins, cyclosporin, FK-506, rapamycin, TGF- beta, clotrimazole, nitrendipine, and charybdotoxin, heavy'metals, inorganic and organic mercurials, and FN18-CRM9, radioisotopes, incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor, and haptens such as DNP, and digoxiginin, and combinations of any of the foregoing, as well as antibodies (monoclonal, polyclonal, and recombinant) to the foregoing.

1563. The vaccine according to any of the claims 1541-1562, wherein the vaccine further comprises one or more vaccine adjuvant(s).

1564. The vaccine according to claim 1563, wherein the one or more vaccine adjuvant(s) can be selected from the group consisting of one or more antigenic determinant(s), one or more haptenic determinant(s), one or more mineral adjuvant(s), one or more aluminium compounds, one or more aluminium salt(s), aluminium hydroxide, one or more bacterial adjuvant(s), lipid A, Interleukin 1, Interleukin 2, one or more cloned host mediator(s), Bordetella pertussis, one or more lipopolysaccharide(s), Freund's Complete Adjuvant (FCA), Titermax, ISCOMS, Quil A, ALUN, one or more Lipid A derivatives, one or more choleratoxin derivatives, one or more HSP derivatives, one or more LPS derivatives, one or more synthetic peptide matrixes, GMDP, one or more lipopolysaccharide(s) and/or derivatis thereof, one or more liposome(s), one or more lipid emulsion(s), one or more plant adjuvant(s), saponin, one or more animal products adjuvant(s), chitin, one or more synthetic adjuvant(s), one or more host adjuvant(s), one or more antigens precipitated with aluminum salt(s), one or more antigens mixed with or adsorbed to performed aluminum compounds, one or more oil emulsion(s), one or more synthetic polymer(s), Alhydrogel, MF59, the proprietary Montanide ISA720, $AlK(SO_4)_2$, $AlNa(SO_4)_2$, $AlNH_4(SO_4)$, silica, alum, $Al(OH)_3$, $Ca_3(PO_4)_2$, kaolin, carbon, aluminum hydroxide, muramyl dipeptides, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-DMP), N-acetyl-nornuramyl-L-alanyl-D-isoglutamine (CGP 11687, also referred to as nor-MDP), N-acetylmuramyul-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'2'-dipalmitoyl-sn -glycero-3-hydroxphosphoryloxy)-ethylamine (CGP 19835A, also referred to as MTP-PE), RIBI (MPL+TDM+CWS) in a 2% squalene/Tween-

80.RTM. emulsion, lipopolysaccharides and its various derivatives, including lipid A, Freund's Complete Adjuvant (FCA), Freund´s Incomplete Adjuvants, Merck Adjuvant 65, polynucleotides (for example, poly IC and poly AU acids), wax D from Mycobacterium, tuberculosis, substances found in Corynebacterium parvum, Bordetella pertussis, and members of the genus Brucella, liposomes or other lipid emulsions, Titermax, ISCOMS, Quil A, ALUN (see US 58767 and 5,554,372), Lipid A derivatives, choleratoxin derivatives, HSP derivatives, LPS derivatives, synthetic peptide matrixes or GMDP, Interleukin 1, Interleukin 2, Montanide ISA-51 and QS-21, Freund's complete or incomplete adjuvant, and killed *B. pertussis* organisms, used e.g. in combination with alum precipitated antigen.

1565. A method for performing a vaccination of an individual in need thereof, said method comprising the steps of:

providing a vaccine according to any of the claims 1541-1564

administering said vaccine to said individual and obtaining a protective immune response and thereby performing a vaccination of the said individual.

1566. The method for vaccination according to claim 1565, wherein the vaccination is for treatment of one or more diseases.

1567. The method for vaccination according to claim 1566, wherein the one or more diseases can be selected from the group consisting of: Lyme disease, birrekuisus and recurring fever

1568. The method for vaccination according to any of the claims 1565-1567, wherein the vaccination comprises combination therapy such as co-administration of the vaccine and one or more medicaments.

1569. The method for vaccination according to claim 1568, wherein the co-administration comprises that the vaccine and the one or more medicaments can be administered simulatenously.

1570. The method for vaccination according to claim 1568, wherein the co-administration comprises that the vaccine and the one or more medicaments can be administered sequentially in any order.

1571. The method for vaccination according to claim 1568, wherein the one or more medicaments can be an anti-infection medicaments.

1572. The method for vaccination according to claim 1568, wherein the one or more medicaments can be an immunotherapeutic agent.

1573. The method for vaccination according to claim 1568, wherein the combination therapy comprises gene therapy.

1574. A kit-of-parts comprising the vaccine according to any of claims 1541 to 1564 and at least one addition component.

1575. Use of the kit-of-parts according to claim 1574 for vaccination of an individual in need thereof.

1576. The antigenic peptide according to any of the previous claims 1, 1509-1537 where in the peptide comprises or consists of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774 and modified sequences obtained by modification of a sequence selected from the group of sequences consisting of: SEQ ID N0 1 to 217774, wherein the sequence is characterized by items 1 to 735.

1577. The MHC monomer or multimer according to any of the claims 1-797 and 1449, 1450, 1455-1482, wherein the antigenic peptide comprised by said MHC is as defined in claim 1576.

1578. The compositions or kits according to any of the claims 1090, 1091, 1092, 1451-1453 and 1538-1540 wherein the antigenic peptide alone or comprised by a MHC is as defined in claim 1576.

1579. The methods according to any of the claims 798-1089 and 1093-1448, 1483-1508, wherein the antigenic peptide alone or comprised by a MHC is as defined in claim 1576.

1580. A polypeptide comprising one or more antigenic peptides according to any the claims 1, 1509-1537 and 1576.

1581. The polypeptide according to claim 1580, wherein said polypeptide has a total length of between 20 to 30, such as 30-40, for example 40-50, such as 50-60, for example 60-70, such as 70-80, for example 80-90, such as 90-100, for example 100-150, such as 150-200, for example 200-250, such as 250-300, for example 300-500 amino acid residues.

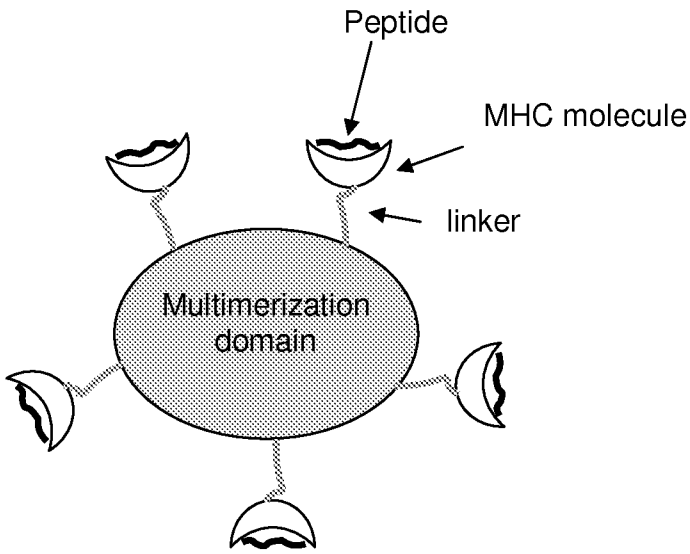

Fig 1. Schematic representation of MHC multimer

Fig. 2.
Program for peptide sequence motifs prediction

```
Imports System.IO

Public Class Form1

   Dim TRACE_LOG = ""
   Dim CR = "-"
   Dim BACKSLASH = "\"
   Dim COLON = ":"
   Dim SPACE = " "

   Private Sub Button_valgmappe_Click(ByVal sender As System.Object, ByVal e As
System.EventArgs) Handles Button_valgmappe.Click
      Dim fdlg As FolderBrowserDialog = New FolderBrowserDialog()

      If fdlg.ShowDialog() = Windows.Forms.DialogResult.OK Then
         Txt_mappe.Text = fdlg.SelectedPath
      End If
   End Sub

   Private Sub Button_gem_Click(ByVal sender As System.Object, ByVal e As
System.EventArgs) Handles Button_gem.Click
      If Txt_sekvens.Text = Nothing Then
         MessageBox.Show("Indtast sekvens")
         Exit Sub
      End If
      If Txt_fil.Text = Nothing Then
         MessageBox.Show("Indtast filnavn")
         Exit Sub
      End If
      If Txt_mappe.Text = Nothing Then
         MessageBox.Show("Vælg mappe")
         Exit Sub
      End If

      TRACE_LOG = Txt_mappe.Text + "/" + Txt_fil.Text + ".txt"
      If File.Exists(TRACE_LOG) Then
         MessageBox.Show("Filen findes allerede og kan ikke overskrives")
         Exit Sub
      End If

      Dim n = Txt_sekvens.Text.Length
      Trace_skriv("Sequence length: " & n)
      Trace_skriv("CR")
```

```
        Trace_skriv("CR")

        Dim min = CInt(Txt_min.Text)
        Dim max = CInt(Txt_max.Text)
        Dim j As Integer
        Dim i As Integer
        Dim tmptxt As String
        Dim peptid As String

        For j = min To max
            Trace_skriv(j & " mers:")
            Trace_skriv("CR")
            tmptxt = ""
            For i = 0 To n - j
                peptid = Txt_sekvens.Text.Substring(i, j)
                If CheckBox_validering.Checked Then
                    If valideret(peptid) Then
                        tmptxt = tmptxt + peptid & CR
                    End If
                Else
                    tmptxt = tmptxt + peptid & CR
                End If
            Next
            Trace_skriv(tmptxt)
            Trace_skriv("CR")
            Trace_skriv("CR")
        Next

    End Sub

    Private Function valideret(ByVal peptid As String)
        If CheckBox_validering_stopkodon.Checked Then
            If InStr(peptid, "*") Then
                Return False
            Else
                Return True
            End If
        Else
            Return True
        End If
    End Function

    Private Sub Form1_Load(ByVal sender As System.Object, ByVal e As
System.EventArgs) Handles MyBase.Load
        Txt_min.Text = 8
        Txt_max.Text = 11
```

```
    End Sub

    Friend Sub Trace_skriv(ByVal texttoadd As String)
        Dim logtext() As String
        Dim fileline() As String
        Dim fs As StreamWriter
        Dim strace As New StackTrace(True)
        Try
            If Not File.Exists(TRACE_LOG) Then
                fs = File.CreateText(TRACE_LOG)
                'fs.Write("Trace Log " & Format(Now) & CR & CR)
                fs.Flush()
                fs.Close()
            End If
            logtext = strace.GetFrame(1).ToString.Split(Space)
            fileline = logtext(6).Split(BACKSLASH)
            Dim i As Integer = fileline.GetUpperBound(0)
            fs = File.AppendText(TRACE_LOG)
            If texttoadd = "CR" Then
                fs.WriteLine()
            Else
                Dim tmp = Split(texttoadd, CR)
                If UBound(tmp) = 0 Then
                    fs.Write(tmp(0))
                Else
                    For i = LBound(tmp) To UBound(tmp) - 1
                        fs.Write(tmp(i))
                        If Me.CheckBox_semikolon.Checked Then
                            fs.Write("; ")
                        End If
                        If Me.CheckBox_linie.Checked And i < UBound(tmp) - 1 Then
                            fs.WriteLine()
                        End If
                    Next
                End If
            End If
            fs.Flush()
            fs.Close()
        Catch ex As Exception
            MsgBox(ex.ToString)
        End Try
    End Sub
End Class
```

Fig. 3.

Full List of HLA Class I alleles assigned as of January 2007 from http://www.anthonynolan.org.uk/HIG/lists/class1list.html

HLA-AHLA-BHLA-CHLA-EHLA-FHLA-G
A*01010101B*070201Cw*010201E*01010101F*01010101G*01010101
A*01010102NB*070202Cw*010202E*01010102F*01010102G*01010102
A*010102B*070203Cw*010203E*01010103F*01010103G*01010103
A*010103B*070204Cw*010204E*01030101F*01010104G*01010104
A*010104B*0703Cw*0103E*01030102F*01010105G*01010105
A*0102B*0704Cw*0104E*010302F*01010106G*01010201
A*0103B*070501Cw*0105E*010303F*01010107G*01010202
A*0104NB*070502Cw*0106E*010304F*01010108G*010103
A*0106B*070503Cw*0107E*0104F*01010201G*010104
A*0107B*0706Cw*0108F*01010202G*010105
A*0108B*0707Cw*0109F*01010203G*010106
A*0109B*0708Cw*0110F*01010204G*010107
A*0110B*0709Cw*0111F*01010205G*010108
A*0111NB*0710Cw*0112F*01010301G*010109
A*0112B*0711Cw*0113F*01010302G*010110
A*0113B*0712Cw*020201F*01010303G*0102
A*0114B*0713Cw*020202F*01010304G*0103
A*0115NB*0714Cw*020203F*0102G*010401
A*0116NB*0715Cw*020205F*01030101G*010402
A*0117B*0716Cw*0203F*01030102G*010403
A*0118NB*0717Cw*0204F*0104G*0105N
A*0119B*0718Cw*0205G*0106
A*0120B*0719Cw*0206G*0107
A*02010101B*0720Cw*0207
A*02010102LB*0721Cw*0208
A*020102B*0722Cw*0209
A*020103B*0723Cw*0210
A*020104B*0724Cw*0211
A*020105B*0725Cw*0212
A*020106B*0726Cw*0213
A*020107B*0727Cw*0214
A*020108B*0728Cw*0215
A*020109B*0729Cw*0216
A*020110B*0730Cw*0217
A*020111B*0731Cw*030201
A*020112B*0732Cw*030202
A*0202B*0733Cw*030301
A*020301B*0734Cw*030302
A*020302B*0735Cw*030303
A*0204B*0736Cw*030304
A*0205B*0737Cw*030305

A*020601B*0738Cw*030401
A*020602B*0739Cw*030402
A*020603B*0740Cw*030403
A*0207B*0741Cw*030404
A*0208B*0742Cw*030405
A*0209B*0743Cw*0305
A*0210B*0744Cw*0306
A*0211B*0745Cw*0307
A*0212B*0746Cw*0308
A*0213B*0747Cw*0309
A*0214B*0748Cw*0310
A*0215NB*0749NCw*031101
A*0216B*0750Cw*031102
A*021701B*0751Cw*0312
A*021702B*080101Cw*0313
A*0218B*080102Cw*0314
A*0219B*080103Cw*0315
A*022001B*0802Cw*0316
A*022002B*0803Cw*0317
A*0221B*0804Cw*0318
A*0222B*0805Cw*0319
A*0224B*0806Cw*0320N
A*0225B*0807Cw*0321
A*0226B*0808NCw*0322Q
A*0227B*0809Cw*0323
A*0228B*0810Cw*0324
A*0229B*0811Cw*0325
A*0230B*0812Cw*0326
A*0231B*0813Cw*0327
A*0232NB*0814Cw*0328
A*0233B*0815Cw*0329
A*0234B*0816Cw*0330
A*023501B*0817Cw*0331
A*023502B*0818Cw*0332
A*0236B*0819NCw*0333
A*0237B*0820Cw*0334
A*0238B*0821Cw*0335
A*0239B*0822Cw*04010101
A*0240B*0823Cw*04010102
A*0241B*0824Cw*040102
A*0242B*0825Cw*040103
A*0243NB*0826Cw*040104
A*0244B*0827Cw*0403
A*0245B*0828Cw*040401
A*0246B*0829Cw*040402
A*0247B*0830NCw*0405

A*0248B*0831Cw*0406
A*0249B*1301Cw*0407
A*0250B*130201Cw*0408
A*0251B*130202Cw*0409N
A*0252B*130203Cw*0410
A*0253NB*1303Cw*0411
A*0254B*1304Cw*0412
A*0255B*1306Cw*0413
A*0256B*1307NCw*0414
A*0257B*1308Cw*0415
A*0258B*1309Cw*0416
A*0259B*1310Cw*0417
A*0260B*1311Cw*0418
A*0261B*1312Cw*0419
A*0262B*1313Cw*0420
A*0263B*1314Cw*0421
A*0264B*1315Cw*0423
A*0265B*1316Cw*0424
A*0266B*1317Cw*050101
A*0267B*1401Cw*050102
A*0268B*140201Cw*050103
A*0269B*140202Cw*0502
A*0270B*1403Cw*0503
A*0271B*1404Cw*0504
A*0272B*1405Cw*0505
A*0273B*140601Cw*0506
A*027401B*140602Cw*0507N
A*027402B*1407NCw*0508
A*0275B*15010101Cw*0509
A*0276B*15010102NCw*0510
A*0277B*150102Cw*0511
A*0278B*150103Cw*0512
A*0279B*150104Cw*0513
A*0280B*1502Cw*0514
A*0281B*1503Cw*0515
A*0282NB*1504Cw*06020101
A*0283NB*1505Cw*06020102
A*0284B*1506Cw*060202
A*0285B*1507Cw*0603
A*0286B*1508Cw*0604
A*0287B*1509Cw*0605
A*0288NB*1510Cw*0606
A*0289B*151101Cw*0607
A*0290B*151102Cw*0608
A*0291B*151103Cw*0609
A*0292B*1512Cw*0610

A*0293B*1513Cw*0611
A*0294NB*1514Cw*0612
A*0295B*1515Cw*0613
A*0296B*1516Cw*0614
A*0297B*15170101Cw*070101
A*0299B*15170102Cw*070102
A*03010101B*151702Cw*070103
A*03010102NB*1518Cw*070104
A*03010103B*1519Cw*070105
A*030102B*1520Cw*070106
A*030103B*1521Cw*070107
A*030104B*1523Cw*07020101
A*030105B*1524Cw*07020102
A*0302B*1525Cw*07020103
A*0303NB*1526NCw*0703
A*0304B*1527Cw*070401
A*0305B*1528Cw*070402
A*0306B*1529Cw*0705
A*0307B*1530Cw*0706
A*0308B*1531Cw*0707
A*0309B*1532Cw*0708
A*0310B*1533Cw*0709
A*0311NB*1534Cw*0710
A*0312B*1535Cw*0711
A*0313B*1536Cw*0712
A*0314B*1537Cw*0713
A*0315B*1538Cw*0714
A*0316B*1539Cw*0715
A*0317B*1540Cw*0716
A*0318B*1542Cw*0717
A*0319B*1543Cw*0718
A*0320B*1544Cw*0719
A*0321NB*1545Cw*0720
A*0322B*1546Cw*0721
A*0323B*1547Cw*0722
A*0324B*1548Cw*0723
A*0325B*1549Cw*0724
A*0326B*1550Cw*0725
A*110101B*1551Cw*0726
A*110102B*1552Cw*0727
A*110103B*1553Cw*0728
A*110104B*1554Cw*0729
A*110105B*1555Cw*0730
A*110106B*1556Cw*0731
A*110201B*1557Cw*0732N
A*110202B*1558Cw*0733N

A*1103B*1560Cw*0734
A*1104B*1561Cw*0735
A*1105B*1562Cw*0736
A*1106B*1563Cw*0737
A*1107B*1564Cw*0738
A*1108B*1565Cw*0739
A*1109B*1566Cw*0740
A*1110B*1567Cw*0741
A*1111B*1568Cw*0742
A*1112B*1569Cw*0743
A*1113B*1570Cw*0744
A*1114B*1571Cw*0745
A*1115B*1572Cw*080101
A*1116B*1573Cw*080102
A*1117B*1574Cw*0802
A*1118B*1575Cw*0803
A*1119B*1576Cw*0804
A*1120B*1577Cw*0805
A*1121NB*1578Cw*0806
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H*0203J*01010108
H*0204J*0201
H*0205
H*0206
H*0301

Fig. 4.
Top 30 HLA class 1 allele frequency in human ethnic groups

% chance of allele expressed in an individual

Top 30 expressed alleles

Allele	Caucasian	Allele	African-American	Allele	Hispanic	Allele	Oriental
A*0201	45.6%	C*0401	29.0%	A*0201	37.1%	A*1101	38.4%
C*0701	27.7%	C*0701	25.4%	C*0401	25.4%	A*2402	33.7%
A*0101	27.4%	C*0602	23.0%	A*2402	24.9%	C*0702	33.3%
A*0301	23.8%	A*0201	22.3%	C*0702	24.2%	C*0102	27.7%
C*0702	21.5%	A*2301	20.7%	C*0701	20.8%	A*3303	23.3%
C*0401	21.2%	C*0202	19.0%	C*0304	14.4%	C*0801	21.6%
B*4402	20.2%	A*0301	18.7%	A*0301	14.3%	C*0304	19.9%
B*0702	18.1%	C*0702	18.1%	B*0702	13.2%	A*0201	18.1%
B*0801	18.1%	B*5301	18.1%	B*3501	12.8%	B*4001	15.2%
C*0501	17.2%	B*0702	15.8%	C*0602	12.3%	C*0401	14.0%
C*0304	16.8%	C*1601	15.7%	C*0501	11.9%	B*5801	13.3%
C*0602	15.7%	B*1503	13.9%	A*0101	11.4%	B*4601	12.7%
A*1101	15.3%	B*5801	13.5%	A*1101	11.0%	B*5101	12.4%
B*4001	13.6%	A*6802	12.7%	B*5101	10.8%	C*0302	12.0%
A*2402	12.1%	C*1701	11.7%	C*1601	10.6%	B*3802	11.4%
B*3501	10.7%	B*4501	10.8%	B*4403	9.9%	A*0207	11.0%
C*0303	10.6%	B*4201	10.5%	C*0102	9.7%	B*1501	9.4%
B*5101	10.4%	A*3001	10.4%	A*2902	9.7%	A*0206	9.3%
C*1203	9.9%	B*3501	10.1%	C*0802	9.3%	C*0303	9.2%
B*1501	9.6%	A*0101	10.0%	B*1801	9.1%	B*1502	9.1%
A*2902	8.9%	C*0304	9.3%	A*3101	8.9%	A*0203	8.8%
A*2601	8.2%	A*3002	9.2%	B*5201	8.6%	B*4403	8.6%
A*3201	8.2%	B*0801	8.5%	B*1402	8.6%	C*1402	8.4%
C*0802	7.7%	A*3402	8.4%	C*0202	7.6%	B*3501	7.2%
A*2501	7.5%	A*7401	8.4%	C*1203	7.6%	C*0602	7.0%
B*5701	7.1%	A*3303	8.0%	A*2601	7.6%	B*5401	6.9%
B*1402	6.7%	C*1801	7.3%	A*6801	7.1%	B*1301	6.6%
C*0202	6.6%	A*2902	7.2%	B*0801	7.0%	B*4002	6.3%
B*1801	6.4%	B*4403	6.9%	A*3002	6.8%	B*5502	6.3%
B*4403	6.4%	B*4901	6.9%	B*4402	6.5%	A*2601	6.0%

Data from HLA Matchmaker, http://tpis.upmc.edu/tpis/HLAMatchmaker/

A

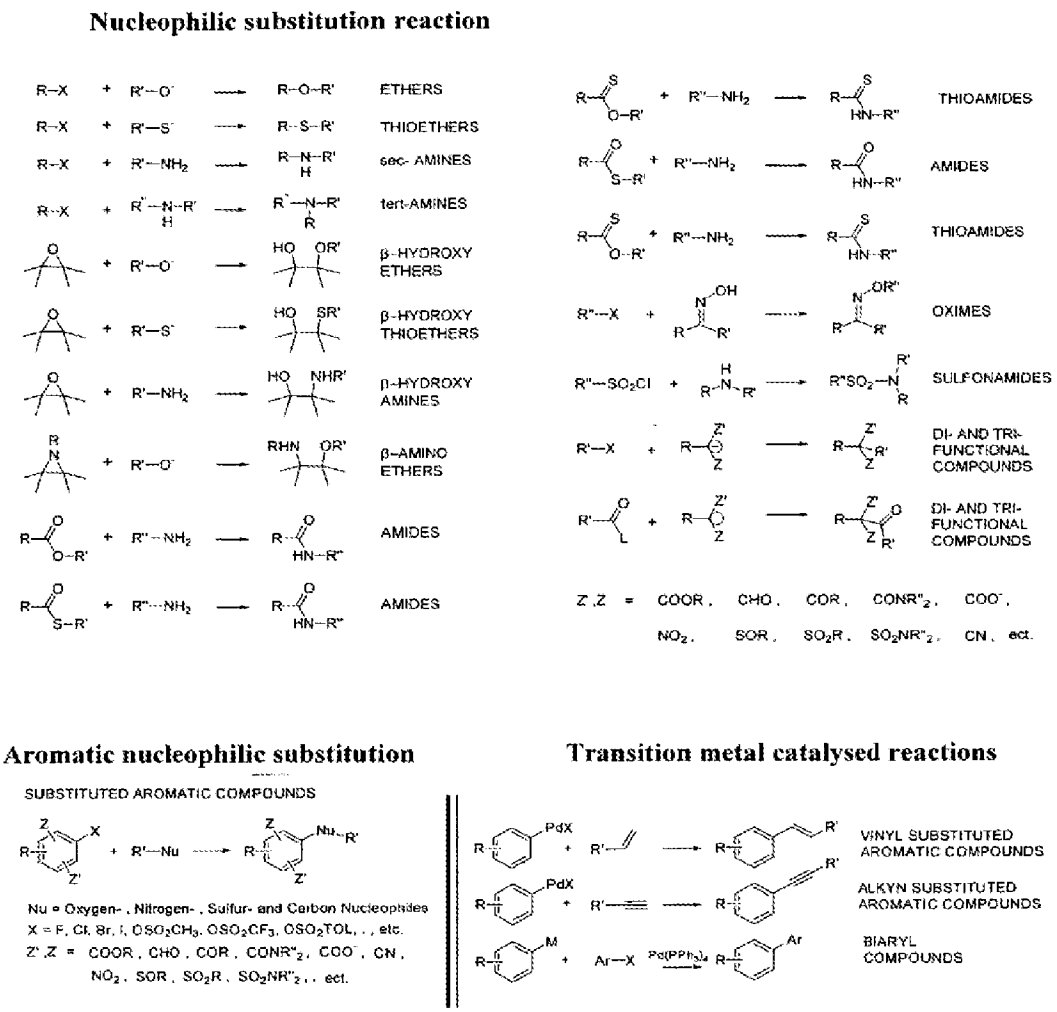


Fig. 5. Reactive groups and the bonds formed upon their reaction.

B

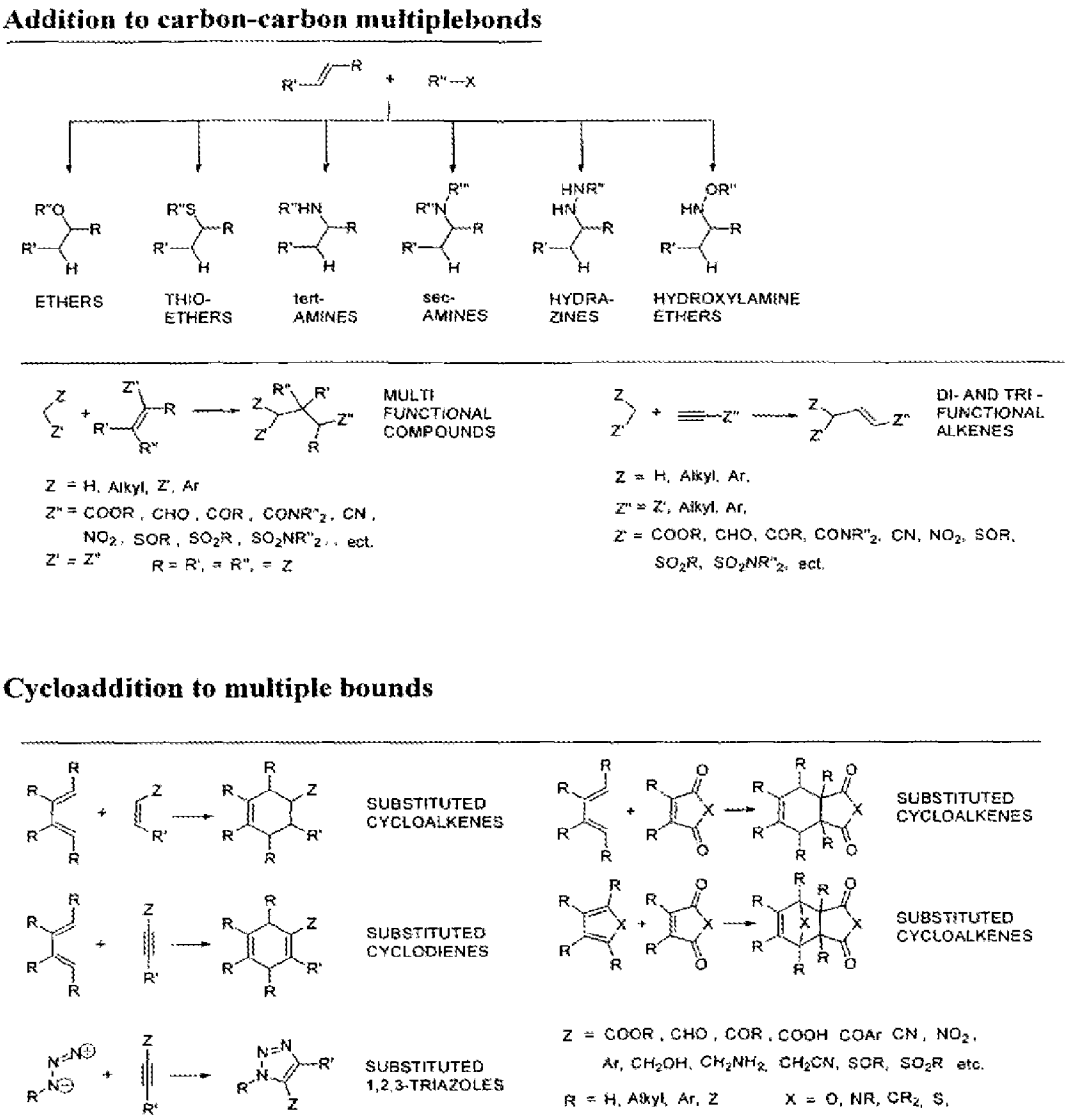


Fig. 5., continued. Reactive groups and the bonds formed upon their reaction.

C

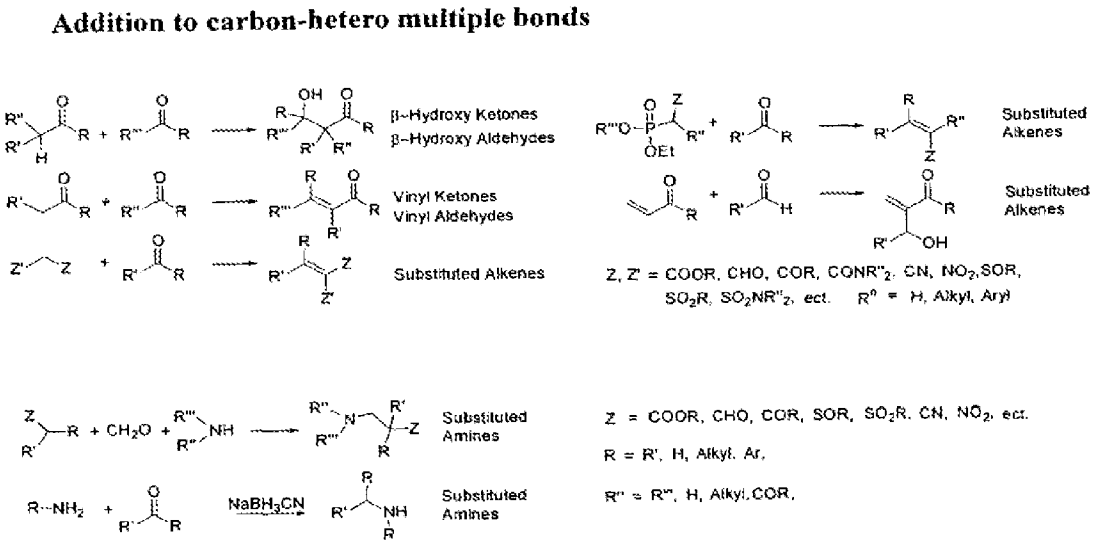
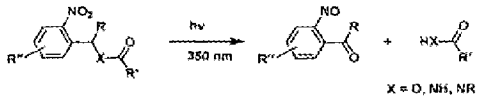
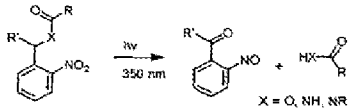


Fig. 5., continued. Reactive groups and the bonds formed upon their reaction.

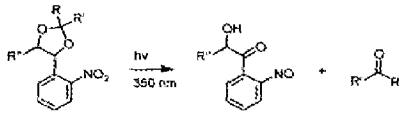
A. Linker for the formation of Ketones, Aldehydes, Amides and Acids



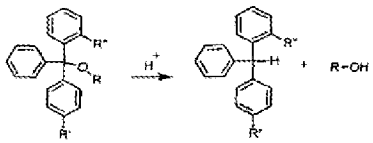
B. Linker for the formation of Ketones, Amides and Acids



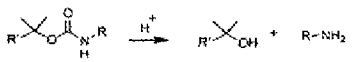
C. Linker for the formation of Aldehydes and Ketones



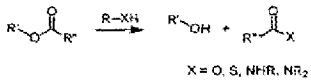
D. Linker for the formation of Alcohols and Acids



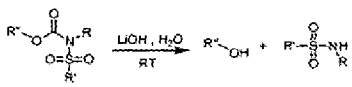
E. Linker for the formation of Amines and Alcohols



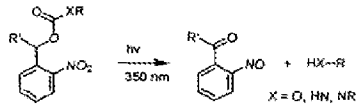
F. Linker for the formation of Esters, Thioesters , Amides and Alcohols



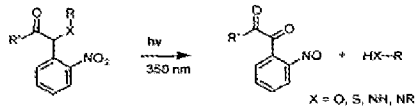
G. Linker for the formation of Sulfonamides and Alcohols



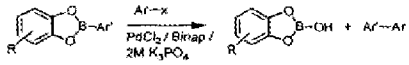
H. Linker for the formation of Ketones, Amines and Alcohols



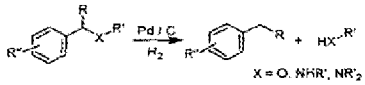
I. Linker for the formation of Ketones, Amines, Alcohols and Mercaptanes



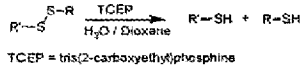
J. Linker for the formation of Biaryl and Bihetaryl



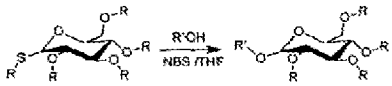
K. Linker for the formation of Benzyles, Amines, Anilins Alcohols and Phenoles



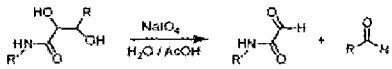
L. Linker for the formation of Mercaptanes



M. Linker for the formation of Glycosides



N. Linker for the formation of Aldehydes and Glyoxylamides



O. Linker for the formation of Aldehydes, Ketones and Aminoalcohols

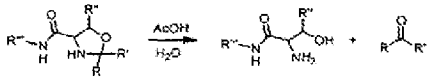


Fig. 6. Cleavable linkers, conditions for cleaving them and the resulting products of the cleavage.

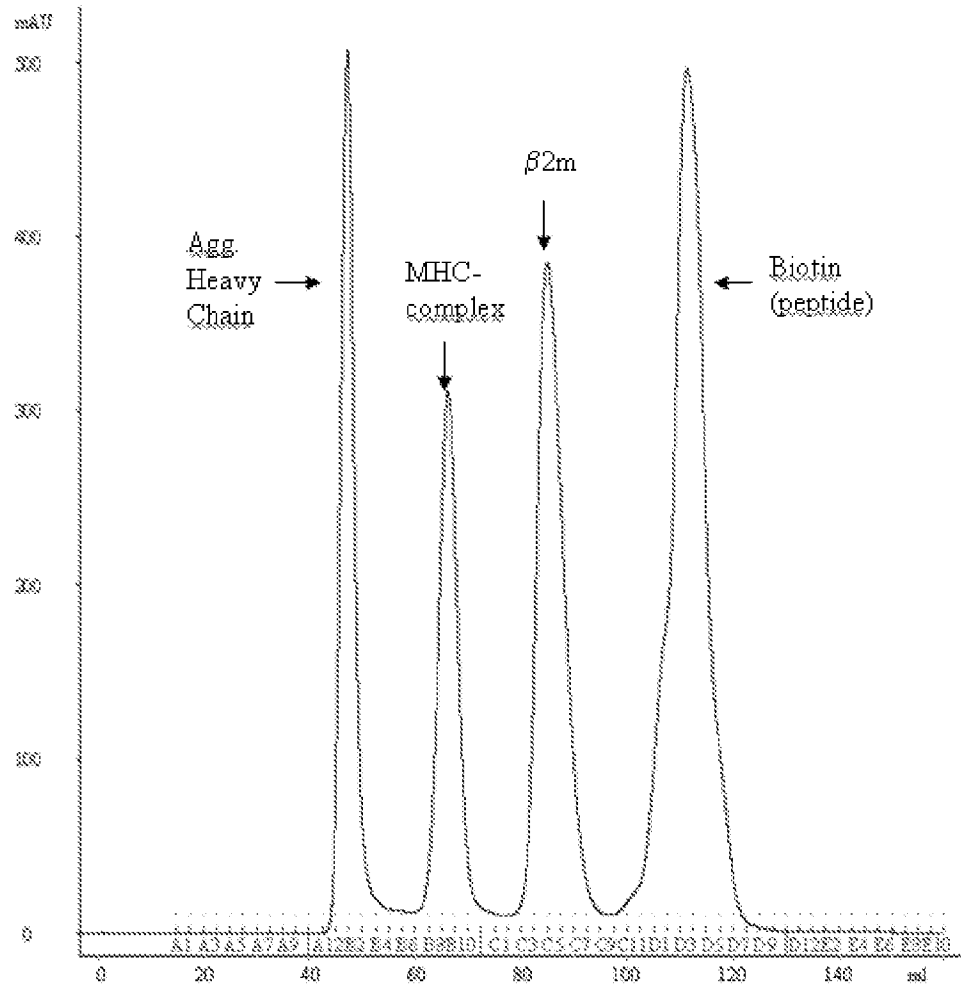


Fig 7. Size exclusion chromatography of folded HLA-A*0201-β2m-QLFEELQEL-complex.

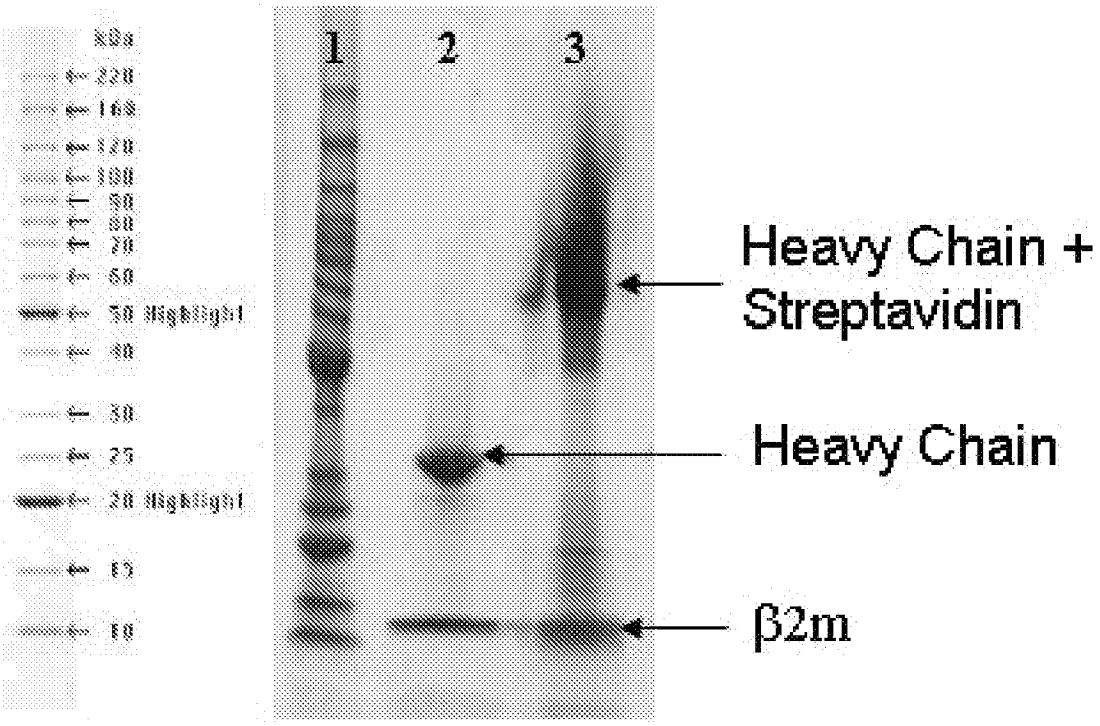
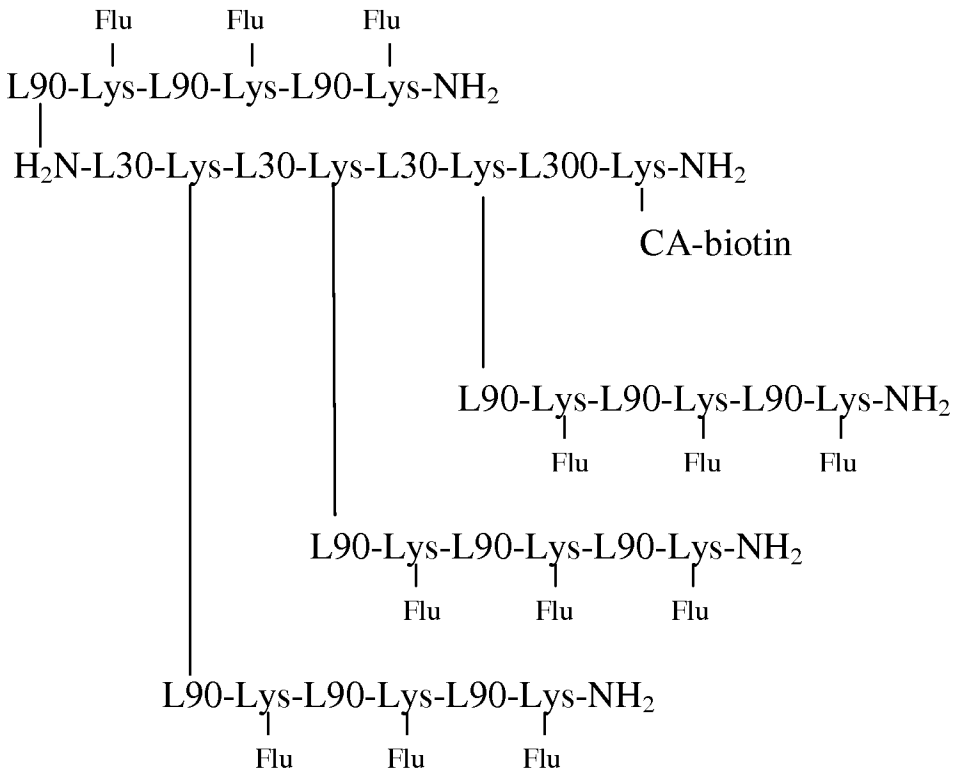


Fig. 8. MHC-SHIFT Assay

A



B

L15 linker composition:

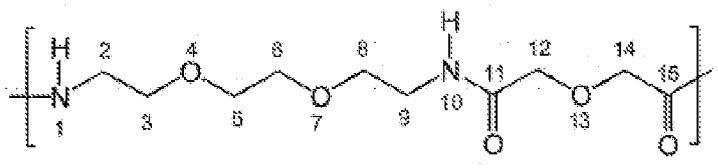


Fig. 9. Composition of a Fluorescein-linker molecule

Database	Alleles
http://www.cbs.dtu.dk/services/NetMHC/	HLA-A0101, HLA-A0201, HLA-A0202, HLA-A0203, HLA-A0204, HLA-A0206, HLA-A0211, HLA-A0212, HLA-A0216, HLA-A0219, HLA-A0301, HLA-A1101, HLA-A2301, HLA-A2402, HLA-A2403, HLA-A2601, HLA-A2602, HLA-A2902, HLA-A3002, HLA-A3101, HLA-A3301, HLA-A6801, HLA-A6802, HLA-A6901
http://www.cbs.dtu.dk/services/NetMHCII/	HLA-DRB1*0101, HLA-DRB1*0301, HLA-DRB1*0401, HLA-DRB1*0404, HLA-DRB1*0405, HLA-DRB1*0701, HLA-DRB1*0802, HLA-DRB1*0901, HLA-DRB1*1101, HLA-DRB1*1302, HLA-DRB1*1501, HLA-DRB3*0101, HLA-DRB4*0101, HLA-DRB1*0501

Fig. 10. HLA alleles of the NetMHC databases

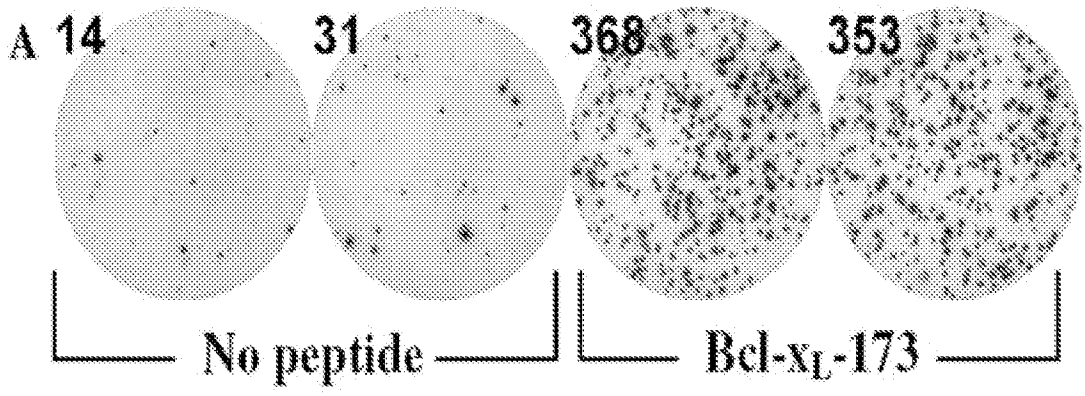


Fig. 11. Ex vivo ELISPOT analysis of BclX(L)-specific

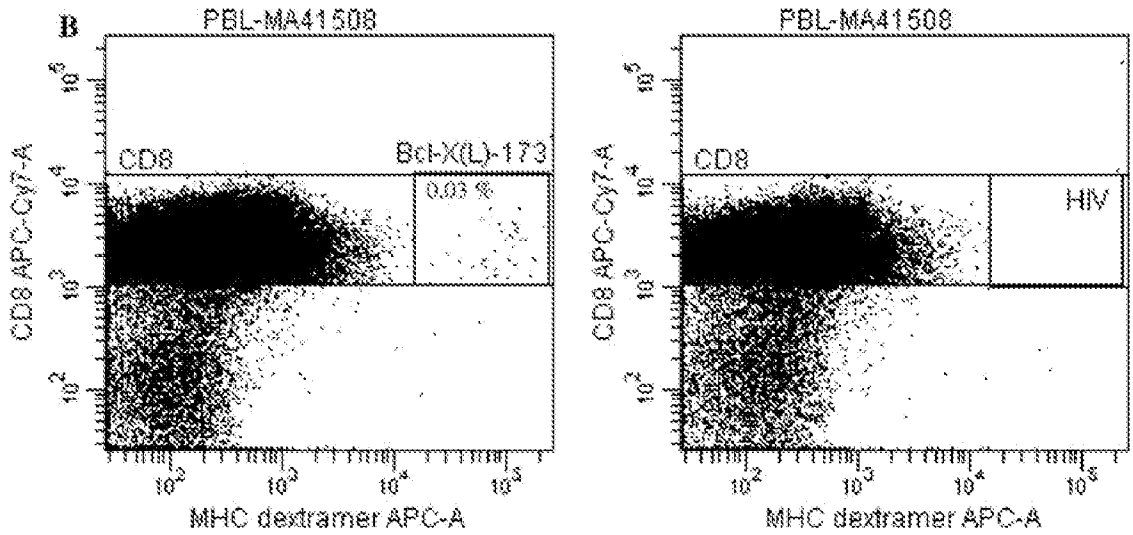


Fig 12. PBL from a breast cancer patient analyzed by flow cytometry.

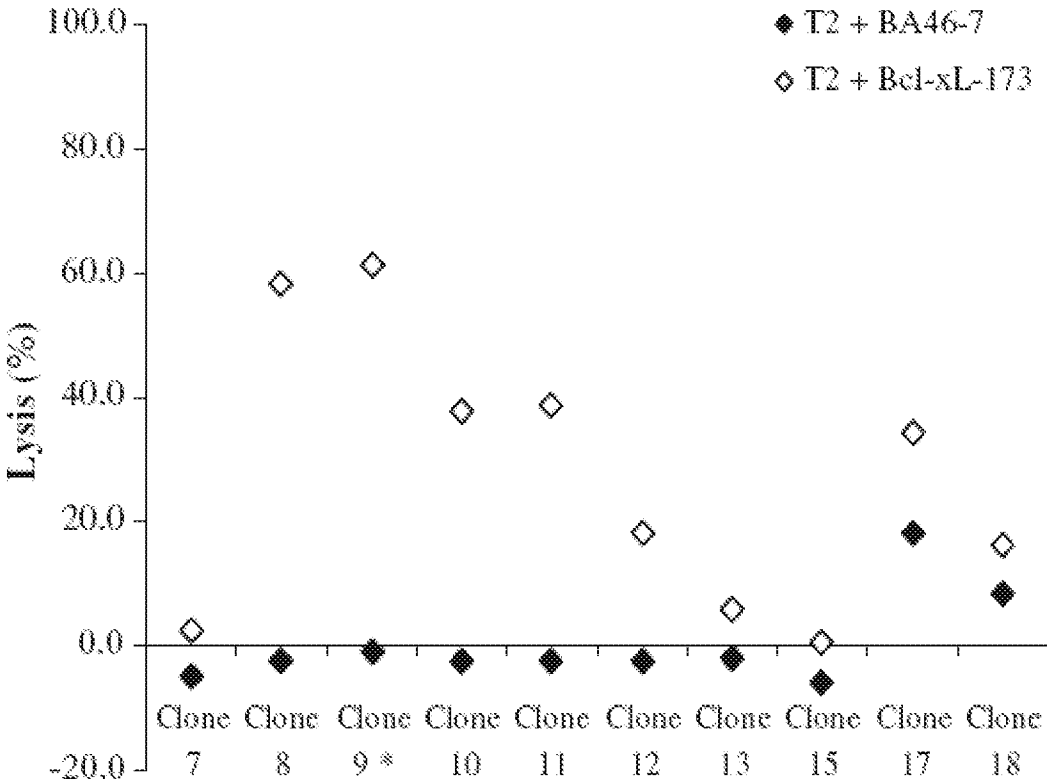


Fig. 13. 51-Cr release assay of isolated T cell clones.

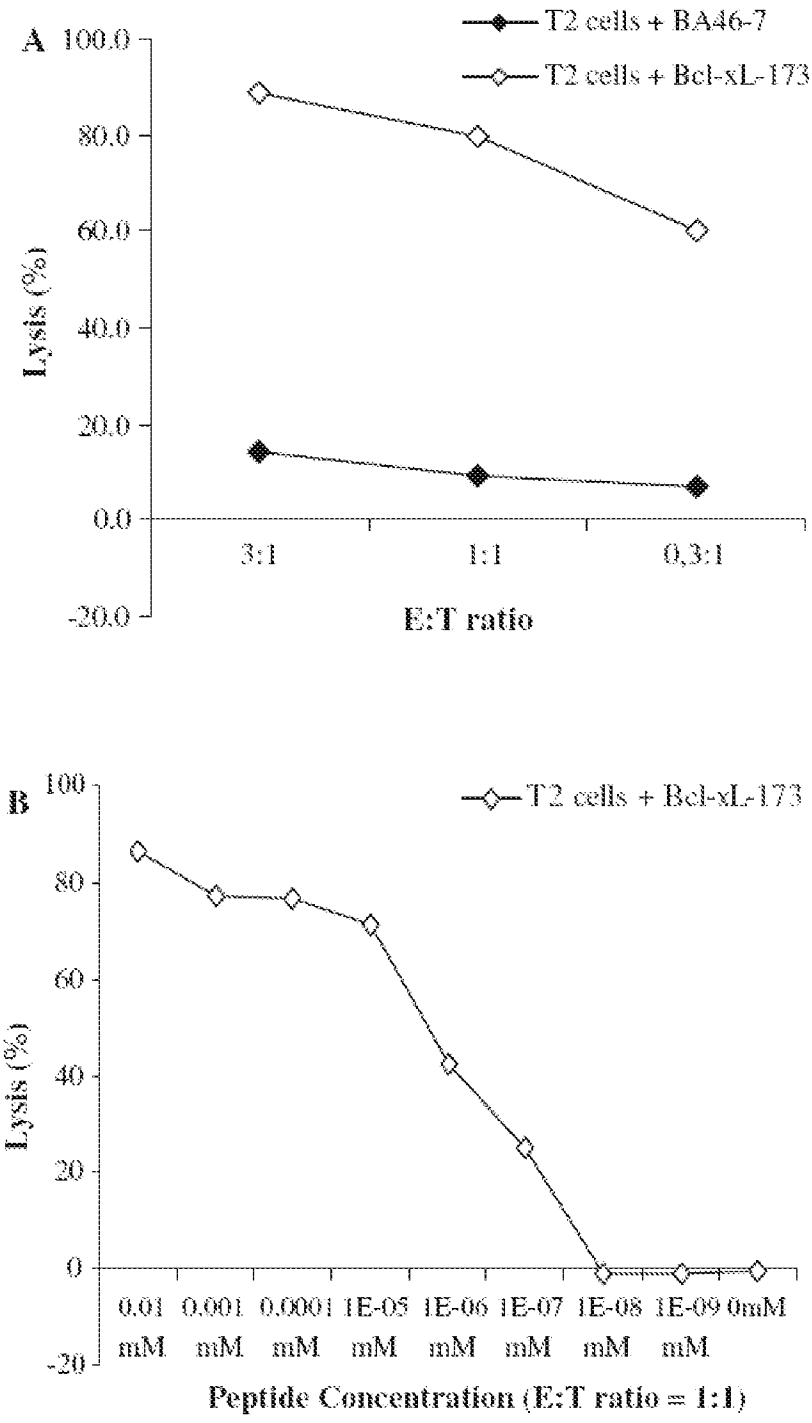
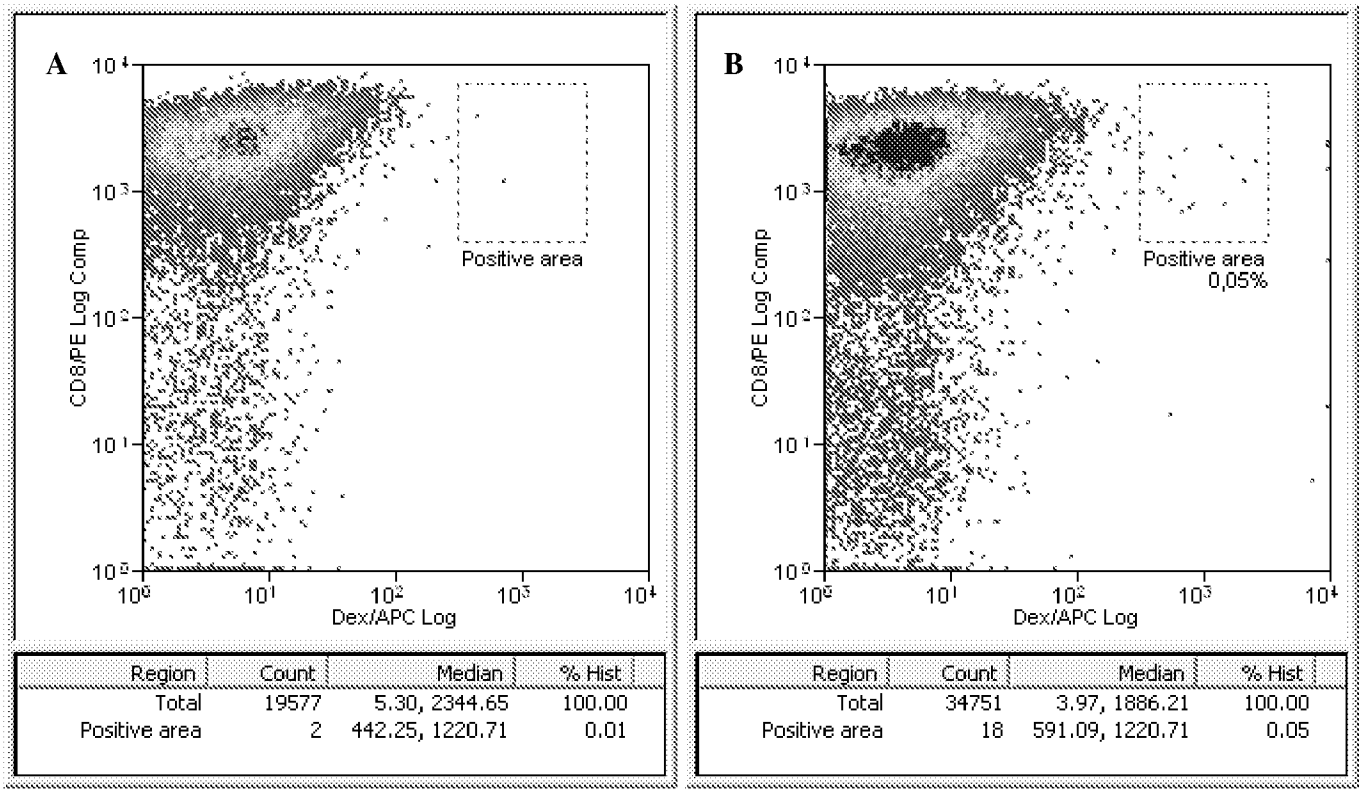


Fig. 14. Bcl-X(L)173–182 specific clone tested for its cytotoxic potential in 51Cr-release assays.



Region	Count	Median	% Hist
Total	19577	5.30, 2344.65	100.00
Positive area	2	442.25, 1220.71	0.01

Region	Count	Median	% Hist
Total	34751	3.97, 1886.21	100.00
Positive area	18	591.09, 1220.71	0.05

Fig. 15. Detection of Borrelia specific T cells using MHC dextramers

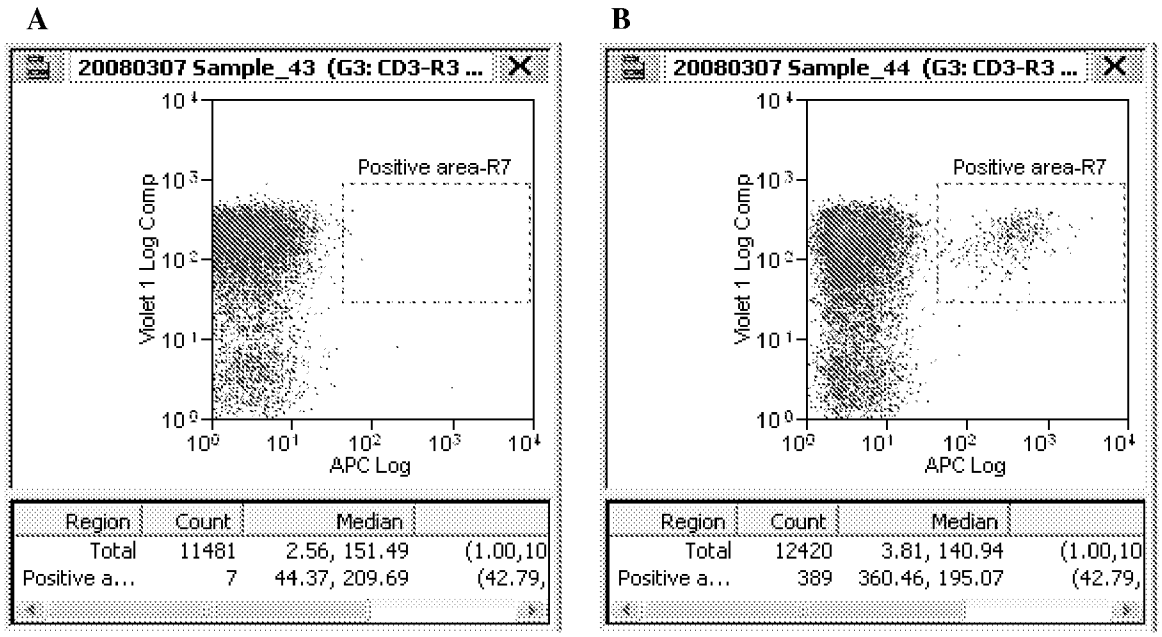


Fig. 16. Detection of CMV specific T cells using MHC dextramers

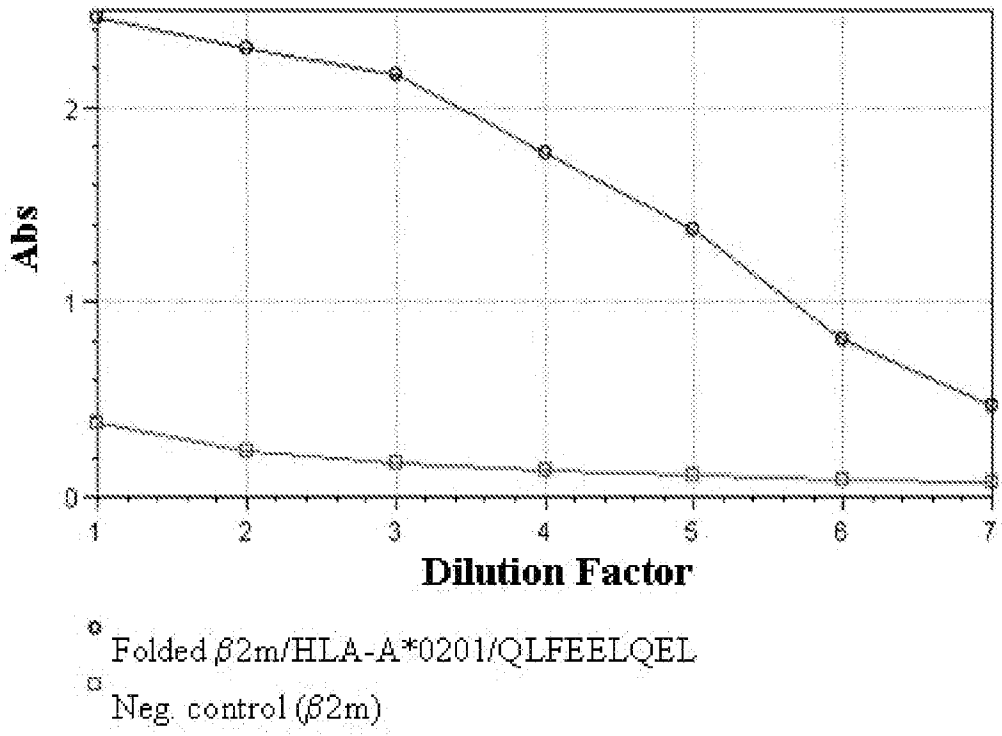
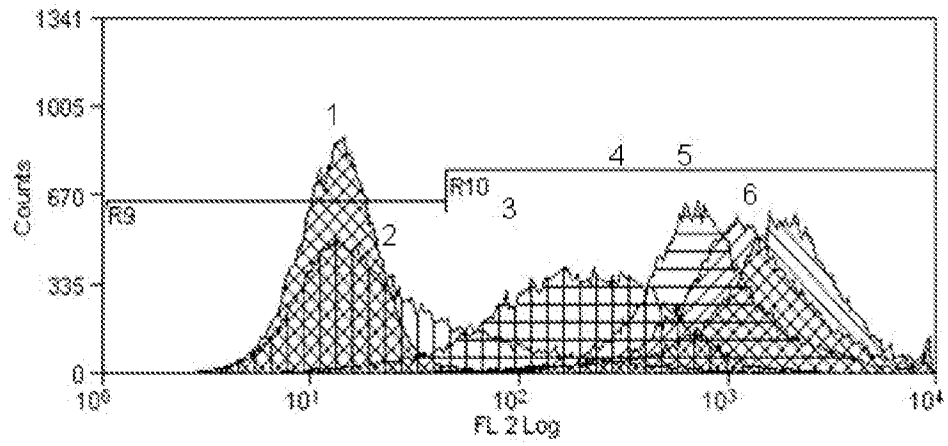


Fig. 17. Conformational ELISA

A



B

MHC-complex	TCR	Percentage of cells in R10 (Positive events)
HLA-A*0201(NLVPMVATV)	20 µg dimeric TCR	99,8%
HLA-A*0201(NLVPMVATV)	10 µg dimeric TCR	99,8%
HLA-A*0201(NLVPMVATV)	5 µg dimeric TCR	99,7%
HLA-A*0201(NLVPMVATV)	2 µg dimeric TCR	93,1%
HLA-A*0201(NLVPMVATV)	0 µg dimeric TCR	25,1%
HLA-A*0201(ILKEPVHGV)	10 ug dimeric TCR	1,5%

Fig. 18. Carboxylate-modified beads coupled to different amounts of TCR and stained with HLA-A*0201(NLVPMVATV)/RPE or HLA-A*0201(ILKEPVHGV)/RPE.

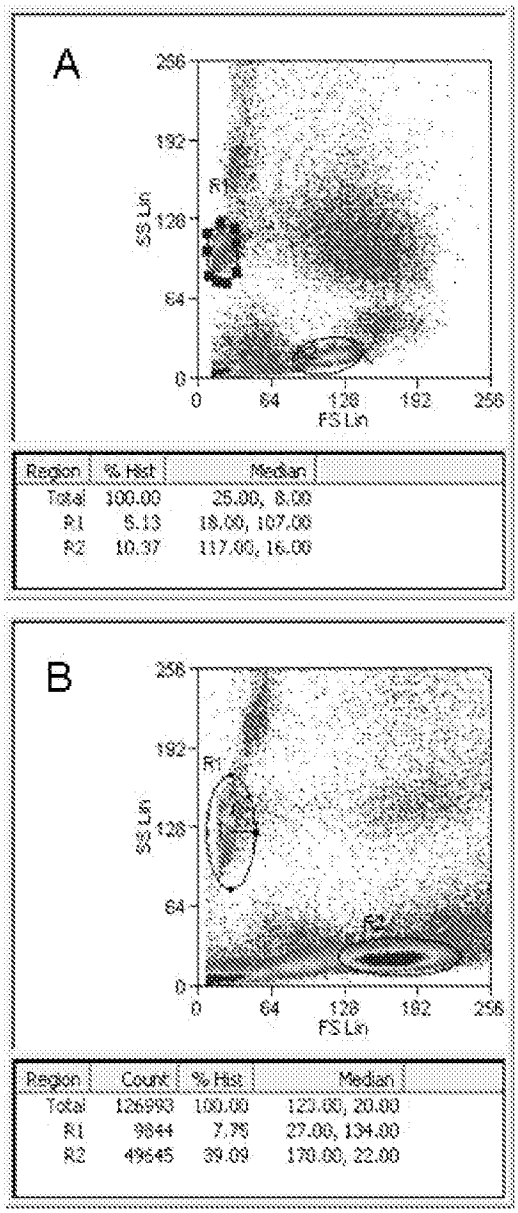


Fig. 19. TCR added into human peripheral whole blood (A), or into HPBMCs (B).

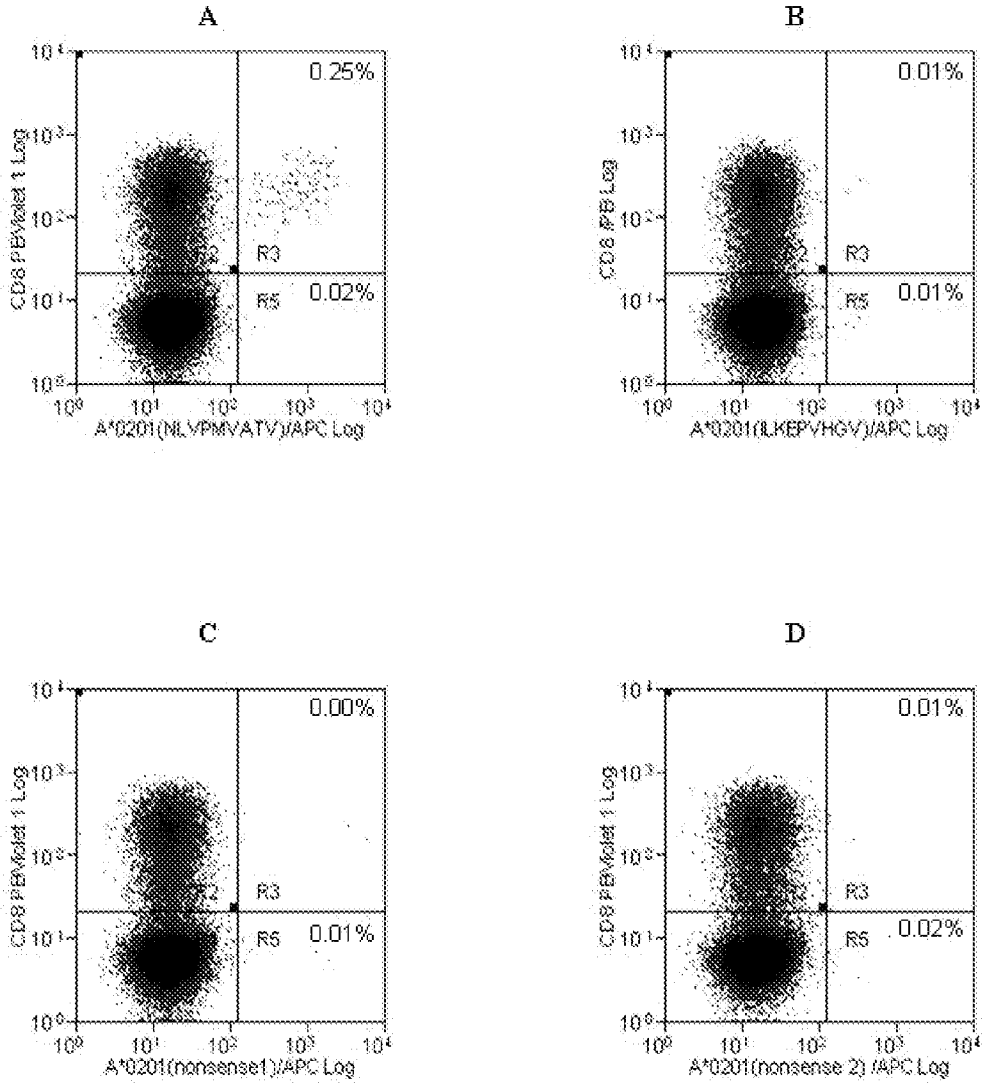


Fig. 20. Flow cytometry analysis of MHC multimer constructs carrying nonsense peptides

	Positive	*Negative*	Construct 1	Construct 2	Construct 3	Construct 4	Construct 5
Donor							
1	–	*A2(NLVPMVATV) A2(ILKEPVHGV)*	-	-	-	nt	-
2	*A2(NLVPMVATV)*	*A2(ILKEPVHGV)*	-	-	+	nt	-
3	*A2(NLVPMVATV)*	*A2(ILKEPVHGV)*	-	-	+	nt	-
4	*A2(NLVPMVATV)*	*A2(ILKEPVHGV)*	-	-	+	nt	-
5	*A2(NLVPMVATV)*	*A2(ILKEPVHGV)*	-	-	+	nt	-
6	*A2(NLVPMVATV)*	*A2(ILKEPVHGV)*	-	-	+	nt	-
7	-	*A2(ILKEPVHGV) A2(GLCTLVAML)*	-	-	nt	-	-
8	*A2(GLCTLVAML)*	*A2(ILKEPVHGV)*	-	-	nt	+	-
9	*A2(GLCTLVAML)*	*A2(ILKEPVHGV)*	-	-	nt	+	-

Fig. 21. Summary of flow cytometry analysis of the binding of different MHC multimer constructs to specific T cells in purified Human Peripheral Blood

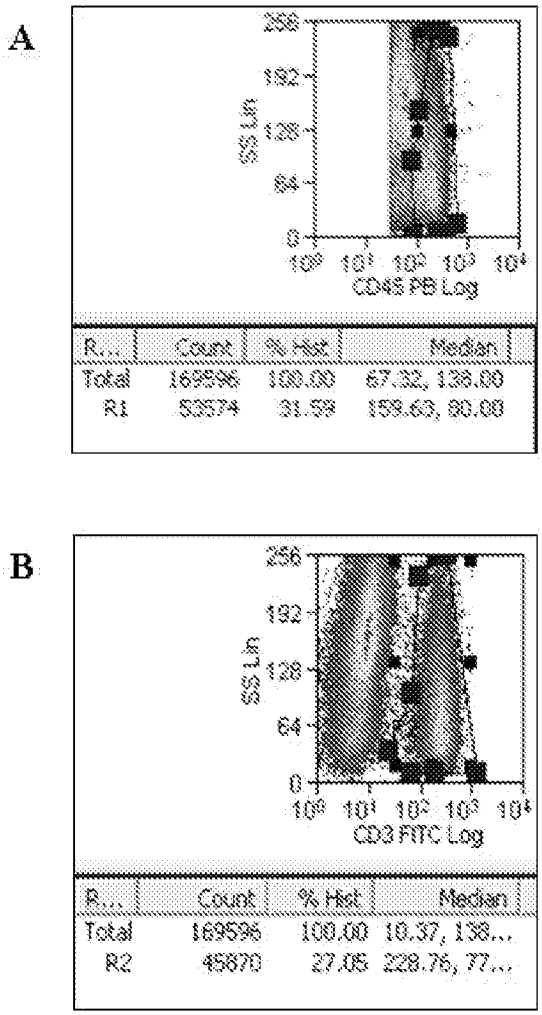
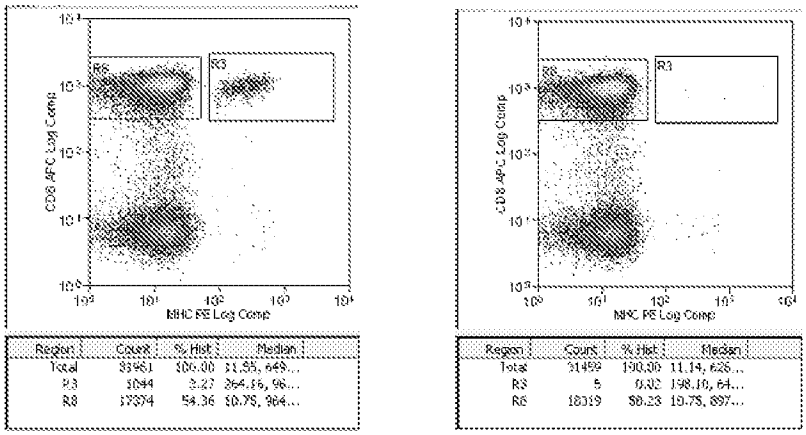
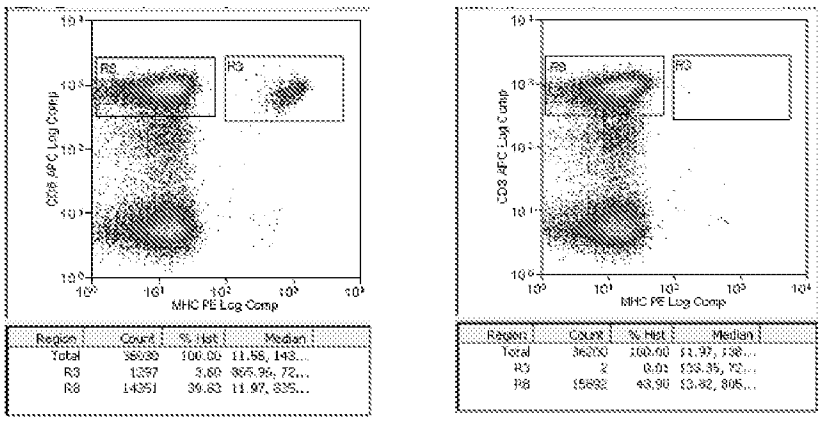


Fig. 22. Gating strategy for no-lyse no-wash procedure

Donor 1



Donor 2



Donor 3

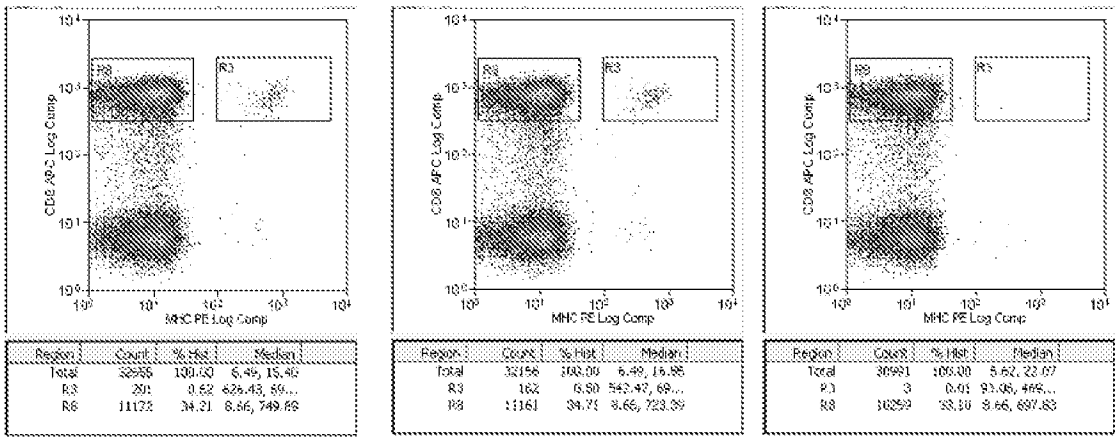


Fig. 23. Identification of CMV-specific T cells in a blood sample using no-lyse no-wash procedure

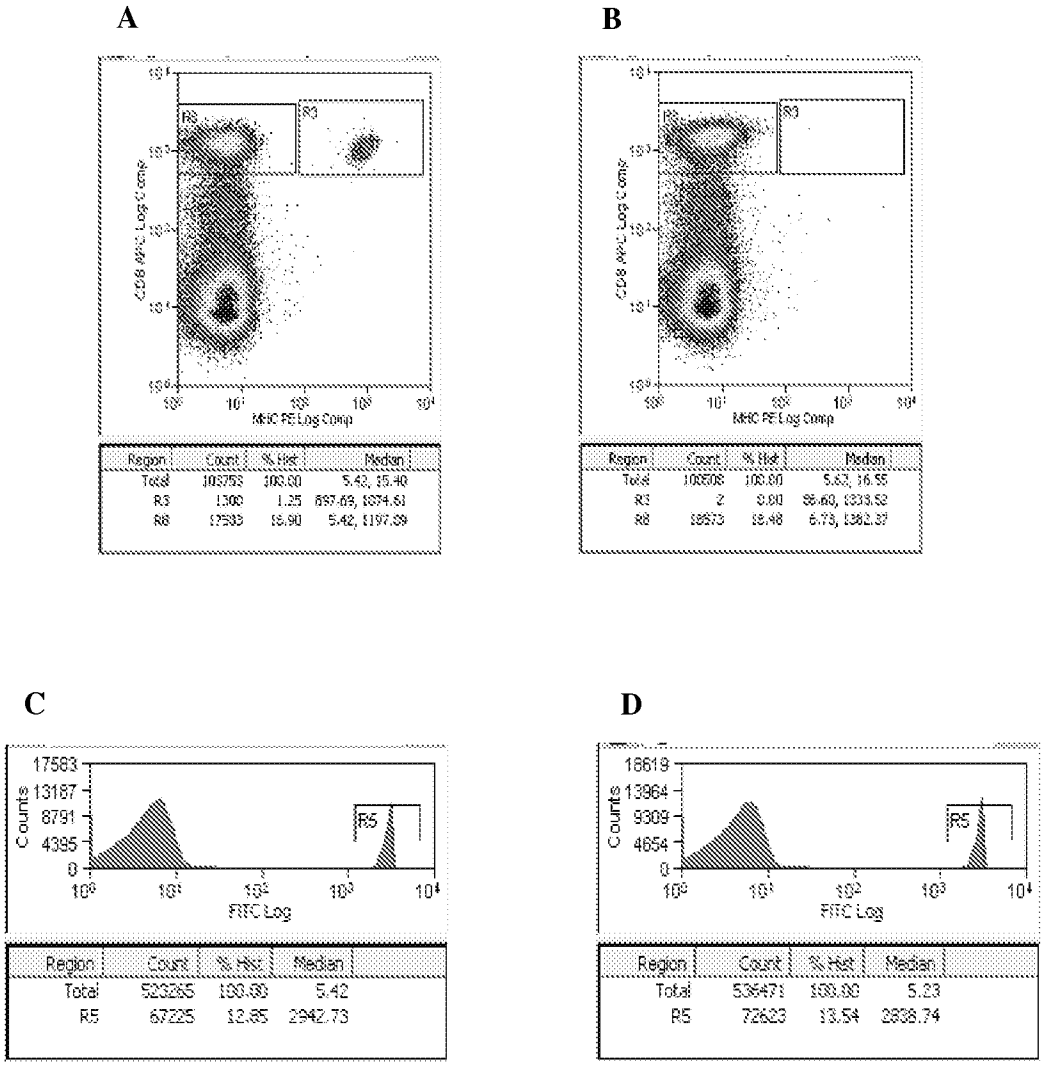


Fig. 24. Enumeration of specific T cells using CytoCount™ beads.

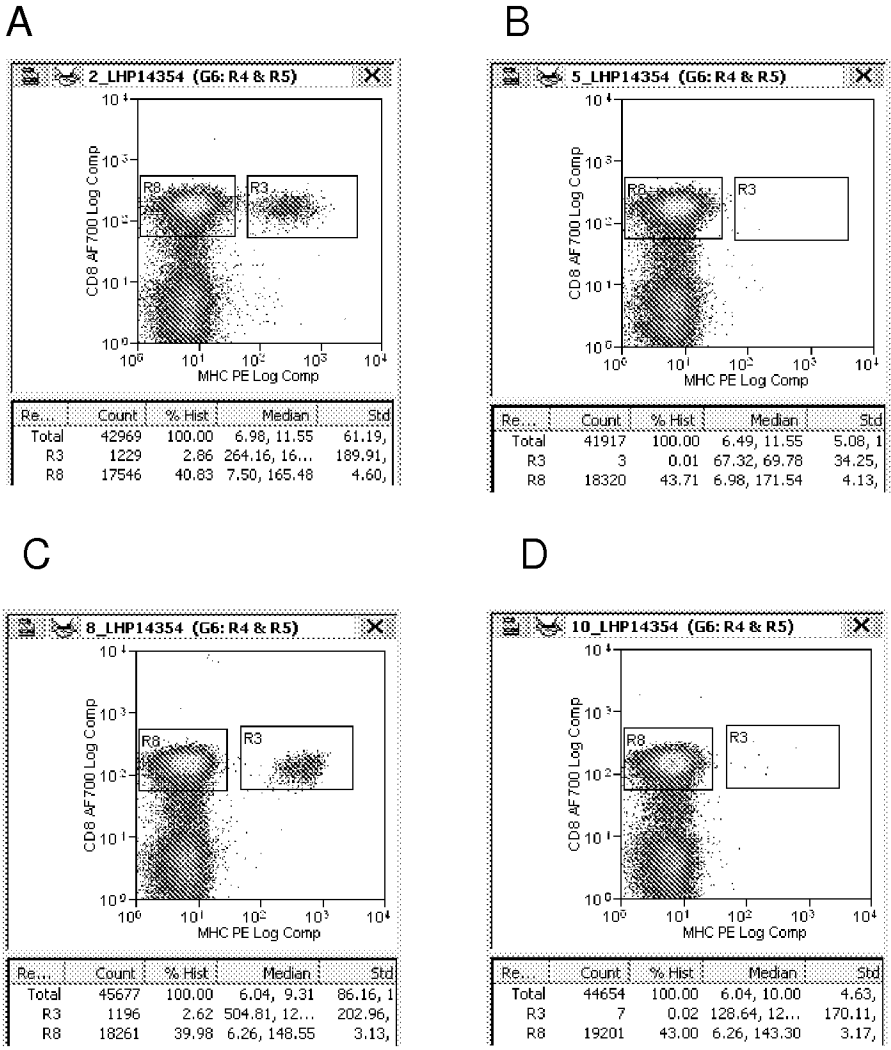


Fig. 25. MHC-peptide complexes can be embedded in a sugar matrix together with antibodies and used for detection of specific T cells in a blood sample

Borrelia	**burgdorferi B31**	**afzelii PKo**	**garini PBi**
Genome	NC_001318 851 proteins	NC_008277 855 proteins	NC_006156 832 proteins
Plasmids	lp5 NC_000957	lp25 NC_008569	lp54 NC_006129
	lp 17 NC_001849	lp28 NC_0085698	cp26 NC_006128
	lp21 NC_000955	lp32 NC_008567	Variable plasmid segments not finally assembled to whole plasmids NT_108239; NT_108263; NT_108262; NT_108261 NT_108260; NT_108259 NT_108258; NT_108257 NT_108256; NT_108255 NT_108254; NT_108253 NT_108252; NT_108251 NT_108250; NT_108249 NT_108248; NT_108247 NT_108246, NT_108245 NT_108244, NT_108243 NT_108242, NT_108241 NT_108238, NT_108237 NT_108236, NT_108235 NT_108234, NT_108233 NT_108232, NT_108231 NT_108230, NT_108229 NT_108228, NT_108227
	lp25 NC_001850	lp34 NC_008566	
	lp28-1 NC_001851	lp60 NC_008564	
	lp28-2 NC_001852	lp60-2 NC_008565	
	lp28-3 NC_001853	cp27 NC_008274	
	lp28-4 NC_001854	cp30 NC_008273	
	lp36 NC_001855		
	lp38 NC_001856		
	lp56 NC_000956		
	cp9 NC_001904		
	cp26 NC_001903		
	cp32-1 NC_000948		
	cp32-3 NC_000949		
	cp32-4 NC_000950		
	cp32-6 NC_000951		
	cp32-7 NC_000952		
	cp32-8 NC_000953		
	cp32-9 NC_000954		

Fig. 26.

Fig. 27. Borrelia bulgdorferi

Plasmid or genome	Product Name	Start	End	Strand	Length	Gi	GeneID
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P01	66	1289	+	407	11497090	1194468
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P02	1306	1998	+	230	11497091	1194469
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P03	2011	2568	+	185	11497092	1194470
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P04	2575	3339	+	254	11497093	1194471
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P05	3369	3941	+	190	11497094	1194472
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P06	3948	4922	+	324	11497064	1194442
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P07	4936	5397	+	153	11497065	1194443
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P08	5379	5780	+	133	11497066	1194444
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P09	5768	6157	+	129	11497067	1194445
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P10	6154	6720	+	188	11497068	1194446
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P11	6701	7813	+	370	11497095	1194473
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P12	7828	8256	+	142	11497096	1194474
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P13	8272	8727	+	151	11497097	1194475
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P14	8724	8960	+	78	11497098	1194476
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P15	8968	10242	+	424	11497099	1194477
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P16	10265	10948	+	227	11497100	1194478

Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P17	10952	11902	+	316	11497101	1194479
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P18	11920	12465	+	181	11497102	1194480
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P19	12495	12827	+	110	11497069	1194447
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P20	12824	13699	+	291	11497070	1194448
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P21	13709	14314	+	201	11497071	1194449
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P22	14324	15139	+	271	11497072	1194450
Plasmid cp32-1(Accession number NC_000948)	pore-forming hemolysin	15215	15418	+	67	11497073	1194451
Plasmid cp32-1(Accession number NC_000948)	hemolysin accessory protein	15422	15769	+	115	11497074	1194452
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P25	15759	16094	+	111	11497075	1194453
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P26	16081	16440	+	119	11497076	1194454
Plasmid cp32-1(Accession number NC_000948)	rev protein	16578	17060	-	160	11497077	1194455
Plasmid cp32-1(Accession number NC_000948)	lipoprotein	17232	17678	+	148	11497078	1194456
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P29	17715	18728	-	337	11497079	1194457
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P30	19114	20214	+	366	11497080	1194458
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P31	20224	20790	+	188	11497081	1194459
Plasmid cp32-1(Accession number NC_000948)	plasmid partition protein, putative	20766	21506	+	246	11497082	1194460
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P33	21510	22118	+	202	11497083	1194461
Plasmid cp32-1(Accession number	BdrA	22131	22763	+	210	11497084	1194462

NC_000948)							
Plasmid cp32-1(Accession number NC_000948)	BppA	23231	24556	+	441	11497085	1194463
Plasmid cp32-1(Accession number NC_000948)	BppB	24609	25034	+	141	11497086	1194464
Plasmid cp32-1(Accession number NC_000948)	BppC	25040	25816	-	258	11497087	1194465
Plasmid cp32-1(Accession number NC_000948)	ErpA	26247	26768	+	173	11497061	1194439
Plasmid cp32-1(Accession number NC_000948)	ErpB	26796	27932	+	378	11497062	1194440
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P40	28074	28655	+	193	11497088	1194466
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P41	28835	29401	+	188	11497089	1194467
Plasmid cp32-1(Accession number NC_000948)	hypothetical protein BB_P42	29398	30750	+	450	11497063	1194441
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S01	66	1289	+	407	11497136	1194513
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S02	1306	1998	+	230	11497137	1194514
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S03	2011	2568	+	185	11497138	1194515
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S04	2575	3339	+	254	11497139	1194516
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S05	3369	3941	+	190	11497140	1194517
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S06	3963	4922	+	319	11497125	1194502
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S07	4936	5397	+	153	11497126	1194503
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S08	5379	5780	+	133	11497127	1194504
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S09	5768	6157	+	129	11497128	1194505

Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S10	6154	6720	+	188	11497129	1194506
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S11	6701	7813	+	370	11497141	1194518
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S12	7828	8256	+	142	11497142	1194519
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S13	8272	8727	+	151	11497143	1194520
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S14	8724	8960	+	78	11497144	1194521
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S15	8968	10242	+	424	11497145	1194522
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S16	10265	10948	+	227	11497146	1194523
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S17	10952	11902	+	316	11497147	1194524
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S18	11920	12465	+	181	11497148	1194525
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S19	12495	12827	+	110	11497130	1194507
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S20	12824	13699	+	291	11497131	1194508
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S21	13784	14314	+	176	11497104	1194481
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S22	14324	15136	+	270	11497105	1194482
Plasmid cp32-3 (Accession number NC_000949)	pore-forming hemolysin	15212	15415	+	67	11497106	1194483
Plasmid cp32-3 (Accession number NC_000949)	hemolysin accessory protein	15419	15766	+	115	11497107	1194484
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S25	15756	16091	+	111	11497108	1194485
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S26	16078	16437	+	119	11497109	1194486
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S27	16586	16903	+	105	11497132	1194509

Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S28	16915	17049	+	44	11497133	1194510
Plasmid cp32-3 (Accession number NC_000949)	BdrF	17068	17697	+	209	11497110	1194487
Plasmid cp32-3 (Accession number NC_000949)	lipoprotein	17803	18249	+	148	11497111	1194488
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S31	18287	19159	-	290	11497112	1194489
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S32	19198	19395	+	65	11497113	1194490
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S33	19605	20705	+	366	11497114	1194491
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S34	20715	21281	+	188	11497115	1194492
Plasmid cp32-3 (Accession number NC_000949)	plasmid partition protein, putative	21257	21997	+	246	11497116	1194493
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S36	22038	22580	+	180	11497117	1194494
Plasmid cp32-3 (Accession number NC_000949)	BdrE	22593	23183	+	196	11497118	1194495
Plasmid cp32-3 (Accession number NC_000949)	BppA	23649	25016	+	455	11497119	1194496
Plasmid cp32-3 (Accession number NC_000949)	BppB	25069	25494	+	141	11497120	1194497
Plasmid cp32-3 (Accession number NC_000949)	BppC	25500	26276	-	258	11497121	1194498
Plasmid cp32-3 (Accession number NC_000949)	ErpG	26708	27298	+	196	11497122	1194499
Plasmid cp32-3 (Accession number NC_000949)	BapA	27410	27919	+	169	11497123	1194500
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S43	28067	28249	+	60	11497134	1194511
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S44	28236	28874	+	212	11497135	1194512
Plasmid cp32-3 (Accession number NC_000949)	hypothetical protein BB_S45	28871	30223	+	450	11497124	1194501

Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R01	66	1289	+	407	11497179	1194556
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R03	2013	2576	+	187	11497180	1194557
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R04	2580	3347	+	255	11497181	1194558
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R05	3340	3951	+	203	11497182	1194559
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R06	3958	4932	+	324	11497153	1194529
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R07	4952	5407	+	151	11497154	1194530
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R08	5389	5790	+	133	11497155	1194531
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R09	5778	6167	+	129	11497156	1194532
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R10	6164	6730	+	188	11497157	1194533
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R11	6711	7823	+	370	11497183	1194560
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R12	7838	8266	+	142	11497184	1194561
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R13	8282	8737	+	151	11497185	1194562
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R14	8734	8970	+	78	11497186	1194563
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R15	8978	10273	+	431	11497187	1194564
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R16	10296	10892	+	198	11497188	1194565
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R17	10896	11846	+	316	11497189	1194566
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R18	11864	12418	+	184	11497190	1194567
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R19	12448	12780	+	110	11497158	1194534

Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R20	12777	13652	+	291	11497159	1194535
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R21	13662	14267	+	201	11497160	1194536
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R22	14277	15092	+	271	11497161	1194537
Plasmid cp32-4 (Accession number NC_000950)	pore-forming hemolysin	15167	15370	+	67	11497162	1194538
Plasmid cp32-4 (Accession number NC_000950)	hemolysin accessory protein	15374	15721	+	115	11497163	1194539
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R25	15711	16046	+	111	11497164	1194540
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R26	16033	16392	+	119	11497165	1194541
Plasmid cp32-4 (Accession number NC_000950)	BdrH	16467	16997	+	176	11497166	1194542
Plasmid cp32-4 (Accession number NC_000950)	lipoprotein	17103	17525	+	140	11497167	1194543
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R29	17573	18664	-	363	11497168	1194544
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R30	18734	18829	-	31	11497191	1194568
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R31	18960	20057	+	365	11497169	1194545
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R32	20067	20633	+	188	11497170	1194546
Plasmid cp32-4 (Accession number NC_000950)	plasmid partition protein, putative	20609	21364	+	251	11497171	1194547
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R34	21415	21960	+	181	11497172	1194548
Plasmid cp32-4 (Accession number NC_000950)	BdrG	21974	22252	+	92	21538986	1194549
Plasmid cp32-4 (Accession number NC_000950)	BppA	22831	24156	+	441	11497173	1194550
Plasmid cp32-4 (Accession number	BppB	24210	24635	+	141	11497174	1194551

NC_000950)							
Plasmid cp32-4 (Accession number NC_000950)	BppC	24641	25435	-	264	11497175	1194552
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R39	25535	25636	-	33	11497192	1194569
Plasmid cp32-4 (Accession number NC_000950)	ErpH	25865	25969	+	34	11497176	1194553
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R41	26077	26820	+	247	11497150	1194526
Plasmid cp32-4 (Accession number NC_000950)	ErpY	26853	27527	+	224	11497151	1194527
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R43	27634	28203	+	189	11497177	1194554
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R44	28384	28950	+	188	11497178	1194555
Plasmid cp32-4 (Accession number NC_000950)	hypothetical protein BB_R45	28947	30299	+	450	11497152	1194528
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M01	66	1289	+	407	11497225	1194601
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M02	1306	1998	+	230	11497226	1194602
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M03	2010	2573	+	187	11497227	1194603
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M04	2577	3344	+	255	11497228	1194604
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M05	3337	3948	+	203	11497229	1194605
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M06	3955	4929	+	324	11497215	1194591
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M07	4949	5404	+	151	11497216	1194592
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M08	5386	5787	+	133	11497217	1194593
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M09	5775	6164	+	129	11497218	1194594

Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M10	6161	6730	+	189	11497219	1194595
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M11	6711	7823	+	370	11497230	1194606
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M12	7838	8266	+	142	11497231	1194607
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M13	8282	8737	+	151	11497232	1194608
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M14	8734	8970	+	78	11497233	1194609
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M15	8978	10252	+	424	11497234	1194610
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M16	10275	10958	+	227	11497235	1194611
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M17	10962	11912	+	316	11497220	1194596
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M18	11930	12484	+	184	11497221	1194597
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M19	12514	12846	+	110	11497194	1194570
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M20	12843	13718	+	291	11497195	1194571
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M21	13728	14333	+	201	11497196	1194572
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M22	14343	15155	+	270	11497197	1194573
Plasmid cp32-6 (Accession number NC_000951)	pore-forming hemolysin	15231	15434	+	67	11497198	1194574
Plasmid cp32-6 (Accession number NC_000951)	hemolysin accessory protein	15438	15785	+	115	11497199	1194575
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M25	15775	16110	+	111	11497200	1194576
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M26	16097	16456	+	119	11497201	1194577
Plasmid cp32-6 (Accession number NC_000951)	rev protein	16593	17075	-	160	11497202	1194578

Plasmid cp32-6 (Accession number NC_000951)	lipoprotein	17247	17696	+	149	11497203	1194579
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M29	17733	18680	-	315	11497204	1194580
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M30	19069	20169	+	366	11497205	1194581
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M31	20179	20745	+	188	11497206	1194582
Plasmid cp32-6 (Accession number NC_000951)	plasmid partition protein, putative	20721	21470	+	249	11497207	1194583
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M33	21520	22098	+	192	11497208	1194584
Plasmid cp32-6 (Accession number NC_000951)	BdrK	22102	22770	+	222	11497209	1194585
Plasmid cp32-6 (Accession number NC_000951)	BppA	23241	24566	+	441	11497210	1194586
Plasmid cp32-6 (Accession number NC_000951)	BppB	24619	25044	+	141	11497211	1194587
Plasmid cp32-6 (Accession number NC_000951)	BppC	25050	25820	-	256	11497212	1194588
Plasmid cp32-6 (Accession number NC_000951)	ErpK	26245	27015	+	256	11497213	1194589
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M39	27077	27745	-	222	11497223	1194599
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M40	27731	27853	+	40	11497222	1194598
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M41	27923	28489	+	188	11497224	1194600
Plasmid cp32-6 (Accession number NC_000951)	hypothetical protein BB_M42	28486	29838	+	450	11497214	1194590
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O01	65	1288	+	407	11497267	1194642
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O02	1305	1997	+	230	11497268	1194643

Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O03	2010	2567	+	185	11497269	1194644
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O04	2574	3338	+	254	11497270	1194645
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O05	3368	3940	+	190	11497271	1194646
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O06	3962	4921	+	319	11497248	1194623
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O07	4935	5396	+	153	11497249	1194624
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O08	5378	5779	+	133	11497250	1194625
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O09	5767	6156	+	129	11497251	1194626
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O10	6153	6722	+	189	11497252	1194627
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O11	6703	7815	+	370	11497272	1194647
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O12	7830	8258	+	142	11497273	1194648
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O13	8274	8729	+	151	11497274	1194649
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O14	8726	8962	+	78	11497275	1194650
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O15	8970	10304	+	444	11497276	1194651
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O16	10317	10958	+	213	11497277	1194652
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O17	10962	11903	+	313	11497278	1194653
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O18	11904	12473	+	189	11497279	1194654
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O19	12503	12835	+	110	11497253	1194628

Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O20	12832	13710	+	292	11497254	1194629
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O21	13716	14321	+	201	11497255	1194630
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O22	14331	15146	+	271	11497256	1194631
Plasmid cp32-7 (Accession number NC_000952)	pore-forming hemolysin	15222	15425	+	67	11497257	1194632
Plasmid cp32-7 (Accession number NC_000952)	hemolysin accessory protein	15429	15785	+	118	11497258	1194633
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O25	15766	16101	+	111	11497259	1194634
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O26	16088	16447	+	119	11497260	1194635
Plasmid cp32-7 (Accession number NC_000952)	BdrN	16522	17139	+	205	11497261	1194636
Plasmid cp32-7 (Accession number NC_000952)	lipoprotein	17245	17667	+	140	11497262	1194637
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O29	17712	18770	-	352	11497280	1194655
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O30	19117	20214	+	365	11497237	1194612
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O31	20224	20790	+	188	11497238	1194613
Plasmid cp32-7 (Accession number NC_000952)	plasmid partition protein, putative	20766	21515	+	249	11497239	1194614
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O33	21522	22076	+	184	11497240	1194615
Plasmid cp32-7 (Accession number NC_000952)	BdrM	22088	22660	+	190	11497241	1194616
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O35	22627	22755	-	42	11497263	1194638
Plasmid cp32-7 (Accession number NC_000952)	BppA	23093	24460	+	455	11497242	1194617
Plasmid cp32-7 (Accession number	BppB	24513	24938	+	141	11497243	1194618

NC_000952)							
Plasmid cp32-7 (Accession number NC_000952)	BppC	24944	25720	-	258	11497244	1194619
Plasmid cp32-7 (Accession number NC_000952)	ErpL	26152	26841	+	229	11497245	1194620
Plasmid cp32-7 (Accession number NC_000952)	ErpM	26893	27984	+	363	11497246	1194621
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O41	28004	28117	-	37	11497264	1194639
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O42	28134	28703	+	189	11497265	1194640
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O43	28885	29451	+	188	11497266	1194641
Plasmid cp32-7 (Accession number NC_000952)	hypothetical protein BB_O44	29448	30800	+	450	11497247	1194622
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L01	66	1289	+	407	11497312	1194686
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L02	1306	1998	+	230	11497313	1194687
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L03	2011	2568	+	185	11497314	1194688
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L04	2575	3339	+	254	11497315	1194689
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L05	3369	3941	+	190	11497316	1194690
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L06	3948	4922	+	324	11497293	1194667
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L07	4936	5397	+	153	11497294	1194668

Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L08	5379	5780	+	133	11497295	1194669
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L09	5768	6157	+	129	11497296	1194670
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L10	6154	6720	+	188	11497297	1194671
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L11	6701	7813	+	370	11497317	1194691
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L12	7828	8256	+	142	11497318	1194692
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L13	8272	8727	+	151	11497319	1194693
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L14	8724	8960	+	78	11497320	1194694
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L15	8968	10242	+	424	11497321	1194695
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L16	10265	10948	+	227	11497322	1194696
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L17	10952	11902	+	316	11497323	1194697
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L18	11920	12465	+	181	11497324	1194698
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L19	12495	12827	+	110	11497298	1194672

Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L20	12824	13699	+	291	11497299	1194673
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L21	13709	14314	+	201	11497300	1194674
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L22	14324	15139	+	271	11497301	1194675
Plasmid cp32-8 (Accession number NC_000953)	pore forming hemolysin	15215	15418	+	67	11497302	1194676
Plasmid cp32-8 (Accession number NC_000953)	hemolysin accessory protein	15422	15769	+	115	11497303	1194677
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L25	15759	16094	+	111	11497304	1194678
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L26	16081	16440	+	119	11497305	1194679
Plasmid cp32-8 (Accession number NC_000953)	BdrP	16515	17099	+	194	11497306	1194680
Plasmid cp32-8 (Accession number NC_000953)	lipoprotein	17205	17651	+	148	11497307	1194681
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L29	17688	18761	-	357	11497308	1194682
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L30	19091	20188	+	365	11497282	1194656
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L31	20198	20764	+	188	11497283	1194657
Plasmid cp32-8 (Accession number NC_000953)	plasmid partition protein, putative	20740	21480	+	246	11497284	1194658

Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L33	21467	21559	+	30	11497309	1194683
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L34	21540	22100	+	186	11497285	1194659
Plasmid cp32-8 (Accession number NC_000953)	BdrO	22113	22691	+	192	11497286	1194660
Plasmid cp32-8 (Accession number NC_000953)	BppA	23306	24691	+	461	11497287	1194661
Plasmid cp32-8 (Accession number NC_000953)	BppB	24744	25169	+	141	11497288	1194662
Plasmid cp32-8 (Accession number NC_000953)	BppC	25175	25951	-	258	11497289	1194663
Plasmid cp32-8 (Accession number NC_000953)	ErpN	26370	26903	+	177	11497290	1194664
Plasmid cp32-8 (Accession number NC_000953)	ErpO	26931	28067	+	378	11497291	1194665
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L41	28209	28790	+	193	11497310	1194684
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L42	28970	29536	+	188	11497311	1194685
Plasmid cp32-8 (Accession number NC_000953)	hypothetical protein BB_L43	29533	30885	+	450	11497292	1194666
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN01	66	1292	+	408	11497348	1194725
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN02	1309	2001	+	230	11497349	1194726
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN03	2013	2579	+	188	11497350	1194727

Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN04	2583	3350	+	255	11497351	1194728
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN07	4958	5413	+	151	11497326	1194699
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN08	5395	5796	+	133	11497327	1194700
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN09	5784	6173	+	129	11497328	1194701
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN10	6170	6736	+	188	11497329	1194702
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN11	6717	7805	+	362	11497352	1194729
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN12	7845	8273	+	142	11497353	1194730
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN14	8742	8978	+	78	11497354	1194731
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN15	8986	10260	+	424	11497355	1194732
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN17	11041	11991	+	316	11497356	1194733
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN19	12593	12925	+	110	11497330	1194703
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN20	12922	13797	+	291	11497331	1194704

Plasmid cp32-9 (Accession number NC_000954)	pore-forming hemolysin	15312	15515	+	67	11497332	1194707
Plasmid cp32-9 (Accession number NC_000954)	hemolysin accessory protein	15519	15866	+	115	11497333	1194708
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN25	15856	16191	+	111	11497334	1194709
Plasmid cp32-9 (Accession number NC_000954)	outer surface protein, putative	16178	16537	+	119	11497335	1194710
Plasmid cp32-9 (Accession number NC_000954)	BdrR	16612	17196	+	194	11497336	1194711
Plasmid cp32-9 (Accession number NC_000954)	lipoprotein	17302	17730	+	142	11497337	1194712
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN30	19164	20264	+	366	11497338	1194714
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN31	20275	20841	+	188	11497339	1194715
Plasmid cp32-9 (Accession number NC_000954)	plasmid partition protein, putative	20817	21572	+	251	11497340	1194716
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN33	21614	22174	+	186	11497341	1194717
Plasmid cp32-9 (Accession number NC_000954)	BdrQ	22184	22723	+	179	11497342	1194718
Plasmid cp32-9 (Accession number NC_000954)	BppA	23194	24519	+	441	11497343	1194719
Plasmid cp32-9 (Accession number NC_000954)	BppB	24572	24997	+	141	11497344	1194720
Plasmid cp32-9 (Accession number NC_000954)	BppC	25558	25779	-	73	21538987	1194721
Plasmid cp32-9 (Accession number	ErpP	26210	26770	+	186	11497345	1194722

NC_000954)							
Plasmid cp32-9 (Accession number NC_000954)	ErpQ	26798	27829	+	343	11497346	1194723
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN40	27881	27991	-	36	11497358	1194735
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN41	27984	28544	+	186	11497357	1194734
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN42	28736	29302	+	188	11497359	1194736
Plasmid cp32-9 (Accession number NC_000954)	hypothetical protein BBN43	29299	30651	+	450	11497347	1194724
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU01	184	618	+	144	11497367	1194744
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU02	746	1114	+	122	11497368	1194745
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU03	1238	1357	-	39	11497369	1194746
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU04	1486	2628	+	380	11497361	1194737
Plasmid lp21 (Accession number NC_000955)	plasmid partition protein, putative	2868	3656	+	262	11497362	1194738
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU06	14633	15235	+	200	11497363	1194739
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU07	15349	15813	+	154	11497364	1194740

Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU08	15791	16084	+	97	11497370	1194747
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU09	16228	16548	-	106	11497365	1194741
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU10	16603	16800	+	65	11497371	1194748
Plasmid lp21 (Accession number NC_000955)	hypothetical protein BBU11	16886	17878	+	330	11497366	1194742
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q01	279	548	+	89	11497373	1194749
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q02	710	802	+	30	11497407	1194793
Plasmid lp56 (Accession number NC_000956)	outer membrane protein, putative	856	1407	+	183	11497374	1194750
Plasmid lp56 (Accession number NC_000956)	antigen, P35, putative	2744	3496	+	250	11497375	1194752
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q06	3623	4108	+	161	11497376	1194753
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q07	4249	4986	-	245	11497377	1194754
Plasmid lp56 (Accession number NC_000956)	plasmid partition protein, putative	5069	5830	-	253	11497378	1194755
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q09	5803	6339	-	178	11497379	1194756

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q10	6336	6674	-	112	11497408	1194794
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q12	6800	7411	+	203	11497409	1194795
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q13	7418	8392	+	324	11497380	1194757
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q14	8406	8867	+	153	11497381	1194758
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q15	8849	9250	+	133	11497382	1194759
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q17	9624	10190	+	188	11497383	1194761
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q18	10171	11283	+	370	11497410	1194796
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q19	11276	11725	+	149	11497411	1194797
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q20	11741	12196	+	151	11497412	1194798
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q21	12193	12429	+	78	11497413	1194799
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q22	12437	13732	+	431	11497414	1194800
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q23	13755	14438	+	227	11497415	1194801

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q24	14442	15392	+	316	11497416	1194802
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q25	15410	15964	+	184	11497417	1194803
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q26	15994	16326	+	110	11497384	1194762
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q27	16323	17198	+	291	11497385	1194763
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q28	17208	17813	+	201	11497386	1194764
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q29	17823	18638	+	271	11497387	1194765
Plasmid lp56 (Accession number NC_000956)	pore-forming hemolysin	18713	18916	+	67	11497388	1194766
Plasmid lp56 (Accession number NC_000956)	hemolysin accessory protein	18920	19267	+	115	11497389	1194767
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q32	19257	19592	+	111	11497390	1194768
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q33	19579	19938	+	119	11497391	1194769
Plasmid lp56 (Accession number NC_000956)	BdrW	20022	20738	+	238	11497392	1194770
Plasmid lp56 (Accession number NC_000956)	MlpJ	20844	21455	+	203	11497393	1194771
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q36	21424	21516	+	30	11497418	1194804

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q37	21532	22479	-	315	11497394	1194772
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q38	22869	23966	+	365	11497395	1194773
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q39	23976	24542	+	188	11497396	1194774
Plasmid lp56 (Accession number NC_000956)	plasmid partition protein, putative	24518	25273	+	251	11497397	1194775
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q41	25317	25877	+	186	11497398	1194776
Plasmid lp56 (Accession number NC_000956)	BdrV	25890	26426	+	178	11497399	1194777
Plasmid lp56 (Accession number NC_000956)	BppA	26879	28246	+	455	11497400	1194778
Plasmid lp56 (Accession number NC_000956)	BppB	28299	28724	+	141	11497401	1194779
Plasmid lp56 (Accession number NC_000956)	BppC	28730	29506	-	258	11497402	1194780
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q46	29559	29654	+	31	11497419	1194805
Plasmid lp56 (Accession number NC_000956)	ErpX	29937	30974	+	345	11497403	1194781
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q48	31117	31710	+	197	11497420	1194806
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q49	31892	32458	+	188	11497421	1194807
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q50	32455	33807	+	450	11497404	1194782

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q52	35115	35807	+	230	11497422	1194808
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q53	35819	36385	+	188	11497423	1194809
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q54	36389	37135	+	248	11497424	1194810
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q56	37669	37809	-	46	11497425	1194811
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q57	37816	38223	-	135	11497426	1194812
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q58	38416	38514	-	32	11497427	1194813
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q59	38565	39077	-	170	11497428	1194814
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q61	39357	39482	-	41	11497429	1194815
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q62	39531	39905	+	124	11497430	1194816
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q64	39959	40186	-	75	11497431	1194817
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q66	40317	40412	+	31	11497432	1194818
Plasmid lp56 (Accession number NC_000956)	adenine specific DNA methyltransferase	40436	43732	-	1098	11497405	1194785

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q68	43915	44232	-	105	11497433	1194819
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q70	44508	44612	-	34	11497434	1194820
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q72	45314	45430	+	38	11497435	1194821
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q76	46982	47080	+	32	11497436	1194822
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q78	47295	47396	+	33	11497437	1194823
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q82	49344	49538	-	64	11497438	1194824
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q83	49752	49868	-	38	11497439	1194825
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q84	50395	50550	-	51	11497440	1194826
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q85	51172	51528	-	118	11497406	1194792
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q86	51719	51823	-	34	11497441	1194827
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q87	51918	52067	-	49	11497442	1194828
Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q88	52135	52608	-	157	11497443	1194829

Plasmid lp56 (Accession number NC_000956)	hypothetical protein BB_Q89	52532	52726	-	64	11497444	1194830
Plasmid lp5 (Accession number NC_000957)	hypothetical protein BB_T01	195	638	+	147	11497450	1194835
Plasmid lp5 (Accession number NC_000957)	hypothetical protein BB_T02	744	1097	+	117	11497446	1194831
Plasmid lp5 (Accession number NC_000957)	hypothetical protein BB_T03	1208	1576	+	122	11497451	1194836
Plasmid lp5 (Accession number NC_000957)	hypothetical protein BB_T04	2148	3254	+	368	11497447	1194832
Plasmid lp5 (Accession number NC_000957)	hypothetical protein BB_T06	3340	4332	+	330	11497448	1194833
Plasmid lp5 (Accession number NC_000957)	outer membrane protein	4388	4819	+	143	11497449	1194834
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD01	332	805	+	157	11496586	1194013
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD02	873	1022	+	49	11496599	1194028
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD03	1117	1221	+	34	11496598	1194027
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD04	1412	1768	+	118	11496585	1194012
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD05	2389	2544	+	51	11496584	1194011

Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD06	3143	3607	+	154	11496596	1194024
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD07	4257	4373	-	38	11496606	1194035
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD08	4707	4805	+	32	11496605	1194034
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD09	5058	5741	+	227	11496595	1194023
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD10	5876	6454	-	192	11496594	1194022
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD11	6681	7634	+	317	11496593	1194021
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD12	7621	7752	-	43	11496604	1194033
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD13	7787	8113	+	108	11496592	1194020
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD14	8269	9381	+	370	11496591	1194019
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD15	9593	10015	-	140	11496590	1194018
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD16	10425	10520	-	31	11496603	1194032
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD17	10591	10686	+	31	11496601	1194030

Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD18	10986	11648	-	220	11496588	1194015
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD19	12057	12170	+	37	11496600	1194029
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD21	13341	14081	+	246	11496587	1194014
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD22	14072	14341	+	89	11496589	1194017
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD24	15891	16121	-	76	11496597	1194026
Plasmid lp17 (Accession number NC_001849)	hypothetical protein BBD25	16212	16370	+	52	11496602	1194031
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE01	154	255	-	33	11496632	1194063
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE02	323	4156	-	1277	11496616	1194047
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE03	4419	4613	-	64	11496617	1194048
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE04	4719	4859	+	46	11496618	1194049
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE05	5377	5529	+	50	11496615	1194046
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE06	5757	5906	+	49	11496625	1194056

Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE07	6182	6355	-	57	11496626	1194057
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE08	6555	6701	-	48	11496627	1194058
Plasmid lp25 (Accession number NC_001850)	protein p23	6898	7761	+	287	11496612	1194043
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE10	7874	7972	-	32	11496628	1194059
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE11	8312	8446	-	44	11496629	1194060
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE12	8521	8646	-	41	11496630	1194061
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE13	8863	8958	+	31	11496631	1194062
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE14	9163	9378	+	71	11496633	1194064
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE15	9353	9490	-	45	11496634	1194065
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE16	9567	10187	-	206	11496635	1194066
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE17	10200	10709	-	169	11496636	1194067
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE18	11498	12079	-	193	11496613	1194044
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE19	12096	12854	-	252	11496614	1194045

Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE20	12830	13393	-	187	11496608	1194036
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE21	13403	14530	-	375	11496609	1194037
Plasmid lp25 (Accession number NC_001850)	pyrazinamidase/nicotinamidase (pncA)	15042	15578	-	178	11496610	1194038
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE23	15973	16158	+	61	11496620	1194051
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE25	18502	18606	-	34	11496621	1194052
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE26	18586	18714	+	42	11496619	1194050
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE27	19055	19198	+	47	11496622	1194053
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE28	19337	19489	-	50	11496623	1194054
Plasmid lp25 (Accession number NC_001850)	hypothetical protein BBE30	21558	21704	+	48	11496624	1194055
Plasmid lp25 (Accession number NC_001850)	antigen, P35, putative	21946	22677	-	243	11496611	1194040
Plasmid lp28-1 (Accession number NC_001851)	erpD protein, putative	467	1465	+	332	11496643	1194073
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF02	1720	2076	+	118	11496642	1194072

Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF03	2098	2619	-	173	11496641	1194071
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF04	2658	2807	+	49	11496658	1194094
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF05	2777	3076	+	99	11496657	1194093
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF06	3201	3380	+	59	11496640	1194070
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF07	3410	3529	-	39	11496656	1194092
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF08	3682	3849	-	55	11496655	1194091
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF09	4027	4182	+	51	11496654	1194090
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF10	4488	4985	+	165	11496653	1194089
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF11	5435	5542	+	35	11496652	1194088
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF13	6632	7381	-	249	11496639	1194069
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF14	7354	7911	-	185	11496638	1194068
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF15	8239	8370	+	43	11496651	1194087

Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF16	8389	8574	+	61	11496650	1194086
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF17	8772	9029	+	85	11496660	1194096
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF20	10698	10991	-	97	11496649	1194079
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF21	11446	11550	-	34	11496659	1194095
Plasmid lp28-1 (Accession number NC_001851)	protein p23, putative	11791	12018	-	75	11496648	1194078
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF23	12441	12992	-	183	11496647	1194077
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF24	13029	13793	-	254	11496646	1194076
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF25	13769	14329	-	186	11496645	1194075
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF26	14351	15451	-	366	11496644	1194074
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF27	15755	15925	-	56	11496663	1194099
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF28	15998	16129	-	43	11496662	1194098
Plasmid lp28-1 (Accession number NC_001851)	hypothetical protein BBF30	17167	17415	-	82	11496661	1194097

Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG01	116	1009	+	297	11496686	1194123
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG02	1047	1928	+	293	11496666	1194101
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG04	2750	2857	-	35	11496687	1194124
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG06	4208	5368	+	386	11496667	1194102
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG07	5378	5950	+	190	11496668	1194103
Plasmid lp28-2 (Accession number NC_001852)	stage 0 sporulation protein J (spoOJ)	5911	6678	+	255	11496669	1194104
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG09	6737	7288	+	183	11496670	1194105
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG10	7483	10779	-	1098	11496688	1194125
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG11	10776	11015	-	79	11496689	1194126
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG12	11063	11491	-	142	11496690	1194127
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG13	11501	12355	-	284	11496691	1194128
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG14	12309	12752	-	147	11496676	1194113

Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG15	12681	13169	+	162	11496692	1194129
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG16	13157	13495	-	112	11496677	1194114
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG17	13508	14341	-	277	11496678	1194115
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG18	14376	14885	-	169	11496679	1194116
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG19	14886	15431	-	181	11496680	1194117
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG20	15457	16482	-	341	11496681	1194118
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG21	16494	17684	-	396	11496682	1194119
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG22	18030	18827	-	265	11496683	1194120
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG23	18837	19619	-	260	11496684	1194121
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG24	19620	22310	-	896	11496685	1194122
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG25	22273	22659	-	128	11496665	1194100
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG26	22659	23033	-	124	11496693	1194130

Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG27	23033	23725	-	230	11496671	1194106
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG28	23722	24108	-	128	11496694	1194131
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG29	24489	25955	+	488	11496672	1194107
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG30	25962	26390	+	142	11496695	1194132
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG31	26567	27085	+	172	11496673	1194108
Plasmid lp28-2 (Accession number NC_001852)	replicative DNA helicase, putative	27113	27940	+	275	11496674	1194109
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG33	28031	28831	+	266	11496675	1194110
Plasmid lp28-2 (Accession number NC_001852)	hypothetical protein BBG34	28854	29618	-	254	11496696	1194133
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH01	273	467	+	64	11496702	1194139
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH02	391	858	+	155	11496704	1194141
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH03	926	1075	+	49	11496709	1194148
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH04	1045	1368	+	107	11496698	1194134

Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH05	1498	1680	+	60	11496703	1194140
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH06	2260	2970	-	236	11496710	1194149
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH08	3590	3730	-	46	11496711	1194150
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH09	3892	7728	-	1278	11496712	1194151
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH10	8000	8203	-	67	11496713	1194152
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH11	8701	8796	-	31	11496714	1194153
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH12	9455	9592	+	45	11496715	1194154
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH13	9848	10516	-	222	11496699	1194136
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH14	10818	10934	-	38	11496716	1194155
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH15	10910	11005	-	31	11496717	1194156
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH16	11068	11190	+	40	11496732	1194171
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH17	11837	12028	+	63	11496733	1194172

Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH18	12105	13220	+	371	11496734	1194173
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH19	13590	13712	+	40	11496718	1194157
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH22	14763	14870	-	35	11496719	1194158
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH23	15051	15161	+	36	11496720	1194159
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH24	15136	15345	+	69	11496721	1194160
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH25	15565	15810	-	81	11496722	1194161
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH26	16519	17415	+	298	11496723	1194162
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH27	17408	17974	+	188	11496705	1194142
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH28	17947	18702	+	251	11496706	1194143
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH29	18798	19427	+	209	11496707	1194144
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH31	20997	21107	+	36	11496725	1194164
Plasmid lp28-3 (Accession number NC_001853)	antigen, P35, putative	21470	22219	+	249	11496708	1194146

Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH33	22678	22953	+	91	11496726	1194165
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH34	23189	23383	-	64	11496727	1194166
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH35	23447	23563	+	38	11496728	1194167
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH36	24028	24180	-	50	11496729	1194168
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH37	25433	26371	-	312	11496730	1194169
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH38	26495	26614	-	39	11496731	1194170
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH39	26754	26858	+	34	11496724	1194163
Plasmid lp28-3 (Accession number NC_001853)	transposase-like protein, putative	26978	27445	-	155	11496700	1194137
Plasmid lp28-3 (Accession number NC_001853)	hypothetical protein BBH41	27625	28197	-	190	11496701	1194138
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI01	174	608	+	144	11496764	1194202
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI02	736	1104	+	122	11496742	1194180
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI03	1847	1972	-	41	11496765	1194203

Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI04	2124	2219	-	31	11496766	1194204
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI05	2188	2310	-	40	11496767	1194205
Plasmid lp28-4 (Accession number NC_001854)	pfs protein (pfs)	2536	3351	+	271	11496743	1194181
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI07	3343	3441	-	32	11496768	1194206
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI08	3576	3755	+	59	11496749	1194187
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI09	3745	3882	+	45	11496750	1194188
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI10	3911	4315	+	134	11496751	1194189
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI11	4623	4721	-	32	11496752	1194190
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI12	5128	5346	+	72	11496753	1194191
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI13	5609	5707	+	32	11496736	1194174
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI14	6159	6272	+	37	11496754	1194192
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI15	6603	6833	+	76	11496755	1194193

Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI16	7183	8538	+	451	11496756	1194194
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI17	8821	8967	-	48	11496757	1194195
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI18	10495	10647	-	50	11496758	1194196
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI19	10749	11927	+	392	11496737	1194175
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI20	11924	12478	+	184	11496738	1194176
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI21	12454	13206	+	250	11496739	1194177
Plasmid lp28-4 (Accession number NC_001854)	conserved hypothetical protein,	13265	13837	+	190	11496740	1194178
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI23	13989	14093	+	34	11496759	1194197
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI24	14334	14441	+	35	11496760	1194198
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI25	15211	15342	+	43	11496769	1194207
Plasmid lp28-4 (Accession number NC_001854)	multidrug-efflux transporter	15352	16530	+	392	11496744	1194182
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI27	17093	17272	-	59	11496770	1194208

Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI28	17302	17874	-	190	11496771	1194209
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI29	18518	19183	-	221	11496772	1194210
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI30	19403	19510	+	35	11496773	1194211
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI31	19615	20127	-	170	11496747	1194185
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI32	20270	20479	-	69	11496774	1194212
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI33	20482	20592	+	36	11496775	1194213
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI34	20771	21562	-	263	11496776	1194214
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI35	21992	22093	+	33	11496777	1194215
Plasmid lp28-4 (Accession number NC_001854)	antigen, P35, putative	22095	22931	-	278	11496748	1194186
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI37	23056	23157	+	33	11496778	1194216
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI38	23159	23995	-	278	11496761	1194199
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI39	24223	25089	-	288	11496762	1194200

Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI40	25518	25805	+	95	11496741	1194179
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI41	25794	26036	-	80	11496763	1194201
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI42	26360	26914	+	184	11496745	1194183
Plasmid lp28-4 (Accession number NC_001854)	hypothetical protein BBI43	26881	27069	-	62	11496746	1194184
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK01	188	1081	+	297	11496795	1194235
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK02	1210	2478	-	422	11496796	1194236
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK03	2818	3222	-	134	11496797	1194237
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK04	3416	3595	-	59	11496798	1194238
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK05	4902	5096	-	64	11496799	1194239
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK06	5126	5236	+	36	11496800	1194240
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK07	5288	6040	-	250	11496801	1194241
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK08	6177	6281	-	34	11496802	1194242

Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK09	6366	6650	+	94	11496803	1194243
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK10	6804	6983	-	59	11496805	1194245
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK11	6956	7063	+	35	11496804	1194244
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK12	7335	8033	+	232	11496806	1194246
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK13	8164	8880	-	238	11496780	1194217
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK14	8921	9016	+	31	11496807	1194247
Plasmid lp36 (Accession number NC_001855)	antigen, P35, putative	9373	9999	+	208	11496781	1194218
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK16	10098	10223	-	41	11496819	1194259
Plasmid lp36 (Accession number NC_001855)	adenine deaminase (adeC)	10301	11947	+	548	11496787	1194225
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK18	12051	12143	-	30	11496788	1194226
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK19	12602	13237	+	211	11496820	1194260
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK20	13212	13304	+	30	11496821	1194261
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK21	13577	14326	-	249	11496789	1194227

Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK22	14302	14841	-	179	11496790	1194228
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK23	14834	15760	-	308	11496822	1194262
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK24	16275	16886	+	203	11496791	1194229
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK26	18346	18465	+	39	11496823	1194263
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK27	18804	19094	-	96	11496809	1194249
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK28	19232	19351	+	39	11496810	1194250
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK29	19715	19807	-	30	11496811	1194251
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK30	19935	20036	+	33	11496812	1194252
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK31	20026	20169	+	47	11496813	1194253
Plasmid lp36 (Accession number NC_001855)	immunogenic protein P35	20389	21453	+	354	11496782	1194219
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK33	21720	21893	+	57	11496808	1194248
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK34	21912	22133	+	73	11496814	1194254

Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK35	22294	22467	+	57	11496815	1194255
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK36	22545	22649	+	34	11496816	1194256
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK38	23919	24146	-	75	11496824	1194264
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK39	24293	24670	+	125	11496825	1194265
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK40	25103	25657	+	184	11496792	1194231
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK41	25813	26379	-	188	11496826	1194266
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK42	26585	26803	-	72	11496827	1194267
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK43	26937	27044	+	35	11496828	1194268
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK44	27234	27353	+	39	11496829	1194269
Plasmid lp36 (Accession number NC_001855)	immunogenic protein P37, putative	27383	28315	-	310	11496793	1194232
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK47	29477	30463	-	328	11496830	1194270
Plasmid lp36 (Accession number NC_001855)	immunogenic protein P37, putative	30719	31585	-	288	11496794	1194233

Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK49	31827	32822	-	331	11496817	1194257
Plasmid lp36 (Accession number NC_001855)	immunogenic protein P37	33081	34079	-	332	11496783	1194221
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK51	34232	34330	+	32	11496818	1194258
Plasmid lp36 (Accession number NC_001855)	protein p23	34595	35443	-	282	11496784	1194222
Plasmid lp36 (Accession number NC_001855)	outer membrane protein	35868	36422	+	184	11496785	1194223
Plasmid lp36 (Accession number NC_001855)	hypothetical protein BBK54	36389	36577	-	62	11496786	1194224
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ01	482	667	+	61	11496862	1194305
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ02	927	1211	+	94	11496863	1194306
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ03	1593	1745	+	50	11496840	1194283
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ04	2268	2381	-	37	11496841	1194284
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ06	3486	3632	+	48	11496842	1194285
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ07	4164	4307	-	47	11496843	1194286
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ08	4576	5496	+	306	11496844	1194287

Plasmid lp38 (Accession number NC_001856)	outer surface protein D (ospD)	6089	6862	+	257	11496832	1194272
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ10	7270	7476	+	68	11496845	1194288
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ11	7780	7965	-	61	11496846	1194289
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ12	8633	8725	-	30	11496847	1194290
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ13	8877	9155	-	92	11496848	1194291
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ14	9125	9286	+	53	11496833	1194273
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ15	10040	10168	-	42	11496849	1194292
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ16	10518	11105	-	195	11496834	1194274
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ17	11152	11889	-	245	11496835	1194275
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ18	11862	12452	-	196	11496836	1194276
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ19	12445	13440	-	331	11496837	1194277
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ20	13772	13936	-	54	11496864	1194307

Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ21	15514	15660	+	48	11496865	1194308
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ22	15902	16003	-	33	11496866	1194309
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ23	16505	17329	+	274	11496867	1194310
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ24	17388	18170	+	260	11496868	1194311
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ25	18202	19254	+	350	11496869	1194312
Plasmid lp38 (Accession number NC_001856)	ABC transporter, ATP-binding protein	19313	20008	+	231	11496838	1194278
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ27	19995	21230	+	411	11496870	1194313
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ28	21220	21948	+	242	11496850	1194293
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ29	21971	23008	+	345	11496851	1194294
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ30	23018	23122	+	34	11496852	1194295
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ31	23366	24088	+	240	11496853	1194296
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ32	24386	24517	-	43	11496854	1194297

Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ33	24681	24794	+	37	11496855	1194298
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ34	25337	26407	-	356	11496856	1194299
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ35	26858	26962	+	34	11496857	1194300
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ36	26995	28053	-	352	11496858	1194301
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ37	28278	28442	-	54	11496859	1194302
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ38	28605	28703	-	32	11496860	1194303
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ39	29264	29401	-	45	11496861	1194304
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ40	29827	29922	+	31	11496871	1194314
Plasmid lp38 (Accession number NC_001856)	antigen, P35, putative	29905	30771	-	288	11496839	1194279
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ42	30942	31133	-	63	11496872	1194315
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ43	31220	32140	+	306	11496873	1194316
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ44	32150	32254	+	34	11496874	1194317

Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ45	32498	33220	+	240	11496875	1194318
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ46	34372	34668	-	98	11496876	1194319
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ47	34905	35591	-	228	11496877	1194320
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ48	35634	36272	-	212	11496878	1194321
Plasmid lp38 (Accession number NC_001856)	hypothetical protein BBJ49	36312	36455	-	47	11496879	1194322
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB01	16	324	+	102	11497020	1194411
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB02	308	751	-	147	11497029	1194420
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB03	837	2186	-	449	11497028	1194419
Plasmid cp26 (Accession number NC_001903)	PTS system, cellobiose-specific IIC component (celB)	2476	3807	-	443	11497019	1194410
Plasmid cp26 (Accession number NC_001903)	PTS system, cellobiose-specific IIA component (celC)	4084	4431	+	115	11497018	1194409

Plasmid cp26 (Accession number NC_001903)	PTS system, cellobiose-specific IIB component (celA)	4440	4757	+	105	11497017	1194408
Plasmid cp26 (Accession number NC_001903)	outer surface protein, putative	4769	5866	+	365	11497016	1194407
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB08	5888	6517	-	209	11497027	1194418
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB09	6677	7714	+	345	11497026	1194417
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB10	7836	8765	+	309	11497015	1194406
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB11	8781	9299	+	172	11497014	1194405
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB12	9275	10036	+	253	11497013	1194404
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB13	10104	10652	+	182	11497012	1194403
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB14	10920	11417	-	165	11497011	1194402
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB15	11636	11740	+	34	11497025	1194416

Plasmid cp26 (Accession number NC_001903)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppAIV)	12014	13606	+	530	11497010	1194401
Plasmid cp26 (Accession number NC_001903)	inositol-5-monophosphate dehydrogenase	13893	15107	-	404	11497009	1194400
Plasmid cp26 (Accession number NC_001903)	bifunctional GMP synthase/glutamine amidotransferase protein	15132	16718	-	528	11497008	1194399
Plasmid cp26 (Accession number NC_001903)	outer surface protein C (ospC)	16903	17535	+	210	11497024	1194415
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB20	17623	17733	-	36	11497036	1194427
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB21	17750	17845	+	31	11497035	1194426
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB22	17966	19321	-	451	11497023	1194414
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB23	19431	20822	-	463	11497022	1194413
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB24	20858	21364	-	168	11497034	1194425
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB25	21339	21851	-	170	11497033	1194424

Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB26	21898	22593	+	231	11497032	1194423
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB27	22603	23154	-	183	11497031	1194422
Plasmid cp26 (Accession number NC_001903)	hypothetical protein BBB28	23255	24499	+	414	11497030	1194421
Plasmid cp26 (Accession number NC_001903)	PTS system, maltose and glucose-specific IIABC component (malX)	24825	26453	+	542	11497021	1194412
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC01	163	1272	+	369	11497057	1194436
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC02	1282	1839	+	185	11497049	1194428
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC03	1892	2452	+	186	11497050	1194429
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC04	2590	2700	-	36	11497058	1194437
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC05	2804	3712	+	302	11497051	1194430
Plasmid cp9 (Accession number NC_001904)	exported protein A (eppA)	3853	4377	-	174	11497052	1194431
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC07	4504	4788	-	94	11497059	1194438

Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC08	5534	5980	+	148	11497053	1194432
Plasmid cp9 (Accession number NC_001904)	rev protein (rev)	6281	6808	-	175	11497054	1194433
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC11	6974	7771	+	265	11497055	1194434
Plasmid cp9 (Accession number NC_001904)	hypothetical protein BBC12	7911	9203	-	430	11497056	1194435
Complete genome (Accession number NC_001318)	hypothetical protein BB0001	105	677	+		15594347	1194837
Complete genome (Accession number NC_001318)	beta-N-acetylhexosaminidase, putative	768	1796	-		15594348	1194838
Complete genome (Accession number NC_001318)	hypothetical protein BB0003	1784	3148	-		15594349	1194839
Complete genome (Accession number NC_001318)	phosphoglucomutase (femD)	3395	5188	+		15594350	1194840
Complete genome (Accession number NC_001318)	tryptophanyl-tRNA synthetase	5251	6312	-		15594351	1194841
Complete genome (Accession number NC_001318)	hypothetical protein BB0006	6309	7433	-		15594352	1194842
Complete genome (Accession number NC_001318)	hypothetical protein BB0007	7458	8315	-		15594353	1194843
Complete genome (Accession number NC_001318)	hypothetical protein BB0008	8412	9197	+		15594354	1194844

Complete genome (Accession number NC_001318)	hypothetical protein BB0009	9202	10206	+		15594355	1194845
Complete genome (Accession number NC_001318)	holo-acyl-carrier protein synthase, putative	10203	10577	+		15594356	1194846
Complete genome (Accession number NC_001318)	hypothetical protein BB0011	10581	11420	+		15594357	1194847
Complete genome (Accession number NC_001318)	tRNA pseudouridine synthase A	11421	12161	+		15594358	1194848
Complete genome (Accession number NC_001318)	hypothetical protein BB0013	12154	12753	+		15594359	1194849
Complete genome (Accession number NC_001318)	primosomal protein N (priA)	12746	14728	+		15594360	1194850
Complete genome (Accession number NC_001318)	uridine kinase	14725	15348	-		15594361	1194851
Complete genome (Accession number NC_001318)	glpE protein (glpE)	15345	15722	-		15594362	1194852
Complete genome (Accession number NC_001318)	hypothetical protein BB0017	15845	16804	+		15594363	1194853
Complete genome (Accession number NC_001318)	hypothetical protein BB0018	16807	17817	-		15594364	1194854
Complete genome (Accession number NC_001318)	hypothetical protein BB0019	17792	18304	-		15594365	1194855
Complete genome (Accession number NC_001318)	diphosphate--fructose-6-phosphate 1-phosphotransferase	18312	19979	-		15594366	1194856

Complete genome (Accession number NC_001318)	S-adenosylmethionine: tRNA ribosyltransferase-isomerase	20445	21092	-		15594367	1194857
Complete genome (Accession number NC_001318)	Holliday junction DNA helicase B	21058	22101	-		15594368	1194858
Complete genome (Accession number NC_001318)	Holliday junction DNA helicase (ruvA)	22146	22739	-		15594369	1194859
Complete genome (Accession number NC_001318)	hypothetical protein BB0024	22819	23958	+		15594370	1194860
Complete genome (Accession number NC_001318)	hypothetical protein BB0025	23965	24696	-		15594371	1194861
Complete genome (Accession number NC_001318)	methylenetetrahydrofolate dehydrogenase (folD)	24697	25623	-		15594372	1194862
Complete genome (Accession number NC_001318)	hypothetical protein BB0027	25753	26391	+		15594373	1194863
Complete genome (Accession number NC_001318)	hypothetical protein BB0028	26399	27448	+		15594374	1194864
Complete genome (Accession number NC_001318)	hypothetical protein BB0029	27434	27865	-		15594375	1194865
Complete genome (Accession number NC_001318)	signal peptidase I (lepB-1)	27855	28490	-		15594376	1194866
Complete genome (Accession number NC_001318)	signal peptidase I (lepB-2)	28492	29472	-		15594377	1194867

Complete genome (Accession number NC_001318)	hypothetical protein BB0032	29543	31015	+		15594378	1194868
Complete genome (Accession number NC_001318)	SsrA-binding protein	31027	31479	+		15594379	1194869
Complete genome (Accession number NC_001318)	hypothetical protein BB0034	31550	32089	-		15594380	1194870
Complete genome (Accession number NC_001318)	DNA topoisomerase IV subunit A	32157	34037	-		15594381	1194871
Complete genome (Accession number NC_001318)	DNA topoisomerase IV subunit B	34037	35836	-		15594382	1194872
Complete genome (Accession number NC_001318)	1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC)	35857	36609	-		15594383	1194873
Complete genome (Accession number NC_001318)	hypothetical protein BB0038	36606	38123	-		15594384	1194874
Complete genome (Accession number NC_001318)	hypothetical protein BB0039	38136	39638	-		15594385	1194875
Complete genome (Accession number NC_001318)	chemotaxis protein methyltransferase (cheR-1)	39826	40677	+		15594386	1194876
Complete genome (Accession number NC_001318)	hypothetical protein BB0041	40677	40769	+		15594387	1194877
Complete genome (Accession number NC_001318)	phosphate transport system regulatory protein (phoU)	40761	41432	-		15594388	1194878

Complete genome (Accession number NC_001318)	hypothetical protein BB0043	41443	42483	-		15594389	1194879
Complete genome (Accession number NC_001318)	hypothetical protein BB0044	42480	42881	-		15594390	1194880
Complete genome (Accession number NC_001318)	P115 protein	42907	45366	-		15594391	1194881
Complete genome (Accession number NC_001318)	ribonuclease H (rnhB)	45446	45991	+		15594392	1194882
Complete genome (Accession number NC_001318)	hypothetical protein BB0047	46011	46394	-		15594393	1194883
Complete genome (Accession number NC_001318)	hypothetical protein BB0048	46601	46771	-		15594394	1194884
Complete genome (Accession number NC_001318)	hypothetical protein BB0049	46921	47040	-		15594395	1194885
Complete genome (Accession number NC_001318)	hypothetical protein BB0050	47167	47841	+		15594396	1194886
Complete genome (Accession number NC_001318)	hypothetical protein BB0051	47905	48606	+		15594397	1194887
Complete genome (Accession number NC_001318)	spoU protein (spoU)	48603	49259	-		15594398	1194888
Complete genome (Accession number NC_001318)	uracil-DNA glycosylase	49341	50012	+		15594399	1194889
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecG	50112	50489	-		15594400	1194890
Complete genome (Accession number NC_001318)	triosephosphate isomerase	50490	51251	-		15594401	1194891

Complete genome (Accession number NC_001318)	phosphoglycerate kinase	51253	52434	-		15594402	1194892
Complete genome (Accession number NC_001318)	glyceraldehyde 3-phosphate dehydrogenase (gap)	52454	53461	-		15594403	1194893
Complete genome (Accession number NC_001318)	hypothetical protein BB0058	53534	55504	-		15594404	1194894
Complete genome (Accession number NC_001318)	hemolysin (tlyC)	55501	56280	-		15594405	1194895
Complete genome (Accession number NC_001318)	hypothetical protein BB0060	56281	56748	-		15594406	1194896
Complete genome (Accession number NC_001318)	thioredoxin (trxA)	56832	57185	-		15594407	1194897
Complete genome (Accession number NC_001318)	hypothetical protein BB0062	57259	57975	+		15594408	1194898
Complete genome (Accession number NC_001318)	hypothetical protein BB0063	58029	59036	-		15594409	1194899
Complete genome (Accession number NC_001318)	methionyl-tRNA formyltransferase (fmt)	59101	60039	-		15594410	1194900
Complete genome (Accession number NC_001318)	polypeptide deformylase (def)	60036	60554	-		15594411	1194901
Complete genome (Accession number NC_001318)	hypothetical protein BB0066	60568	61257	-		15594412	1194902
Complete genome (Accession number NC_001318)	peptidase, putative	61254	63032	-		15594413	1194903

Complete genome (Accession number NC_001318)	hypothetical protein BB0068	63147	64028	+		15594414	1194904
Complete genome (Accession number NC_001318)	aminopeptidase II	64038	65276	+		15594415	1194905
Complete genome (Accession number NC_001318)	hypothetical protein BB0070	65291	65752	+		15594416	1194906
Complete genome (Accession number NC_001318)	hypothetical protein BB0071	65768	67240	+		15594417	1194907
Complete genome (Accession number NC_001318)	hypothetical protein BB0072	67248	69569	+		15594418	1194908
Complete genome (Accession number NC_001318)	hypothetical protein BB0073	69566	70126	+		15594419	1194909
Complete genome (Accession number NC_001318)	peptide chain release factor 2	70173	71219	+		15594420	1194910
Complete genome (Accession number NC_001318)	hypothetical protein BB0075	71201	72610	+		15594421	1194911
Complete genome (Accession number NC_001318)	cell division protein, putative	72647	73492	+		15594422	1194912
Complete genome (Accession number NC_001318)	hypothetical protein BB0077	73489	74517	+		15594423	1194913
Complete genome (Accession number NC_001318)	hypothetical protein BB0078	74518	75039	+		15594424	1194914
Complete genome (Accession number NC_001318)	hypothetical protein BB0079	75110	75772	+		15594425	1194915

Complete genome (Accession number NC_001318)	ABC transporter, ATP-binding protein	75732	76454	+		15594426	1194916
Complete genome (Accession number NC_001318)	hypothetical protein BB0081	76451	77701	+		15594427	1194917
Complete genome (Accession number NC_001318)	hypothetical protein BB0082	77711	79009	-		15594428	1194918
Complete genome (Accession number NC_001318)	hypothetical protein BB0083	79002	79376	-		15594429	1194919
Complete genome (Accession number NC_001318)	aminotransferase (nifS)	79505	80773	+		15594430	1194920
Complete genome (Accession number NC_001318)	hypothetical protein BB0085	80983	81408	+		15594431	1194921
Complete genome (Accession number NC_001318)	hypothetical protein BB0086	81405	82940	+		15594432	1194922
Complete genome (Accession number NC_001318)	L-lactate dehydrogenase (ldh)	82970	83920	-		15594433	1194923
Complete genome (Accession number NC_001318)	GTP-binding protein LepA	84041	85720	-		15594434	1194924
Complete genome (Accession number NC_001318)	hypothetical protein BB0089	85880	86854	-		15594435	1194925
Complete genome (Accession number NC_001318)	V-type ATP synthase subunit K	86926	87360	-		15594436	1194926
Complete genome (Accession number NC_001318)	V-type ATP synthase subunit I	87377	89203	-		15594437	1194927

Complete genome (Accession number NC_001318)	V-type ATP synthase subunit D	89200	89814	-		15594438	1194928
Complete genome (Accession number NC_001318)	V-type ATP synthase subunit B	89811	91115	-		15594439	1194929
Complete genome (Accession number NC_001318)	V-type ATP synthase subunit A	91137	92864	-		1,62E+08	1194930
Complete genome (Accession number NC_001318)	hypothetical protein BB0095	92878	93423	-		15594441	1194931
Complete genome (Accession number NC_001318)	V-type ATP synthase subunit E	93433	94035	-		15594442	1194932
Complete genome (Accession number NC_001318)	hypothetical protein BB0097	94219	94605	-		15594443	1194933
Complete genome (Accession number NC_001318)	recombination and DNA strand exchange inhibitor protein	94611	96953	-		15594444	1194934
Complete genome (Accession number NC_001318)	hypothetical protein BB0099	96943	97866	-		15594445	1194935
Complete genome (Accession number NC_001318)	glutamate racemase (murI)	97863	98648	-		15594446	1194936
Complete genome (Accession number NC_001318)	asparaginyl-tRNA synthetase	98805	100205	+		15594447	1194937
Complete genome (Accession number NC_001318)	hypothetical protein BB0102	100228	100749	+		15594448	1194938
Complete genome (Accession number NC_001318)	hypothetical protein BB0103	100746	101339	-		15594449	1194939

Complete genome (Accession number NC_001318)	periplasmic serine protease DO (htrA)	101525	102976	-		15594450	1194940
Complete genome (Accession number NC_001318)	methionine aminopeptidase (map)	103016	103771	-		15594451	1194941
Complete genome (Accession number NC_001318)	hypothetical protein BB0106	103764	105473	-		15594452	1194942
Complete genome (Accession number NC_001318)	transcription antitermination protein NusB	105418	105855	-		15594453	1194943
Complete genome (Accession number NC_001318)	basic membrane protein	105884	106894	-		15594454	1194944
Complete genome (Accession number NC_001318)	acetyl-CoA C-acetyltransferase (fadA)	106974	108170	-		15594455	1194945
Complete genome (Accession number NC_001318)	hypothetical protein BB0110	108307	109671	+		15594456	1194946
Complete genome (Accession number NC_001318)	replicative DNA helicase (dnaB)	109675	111042	-		15594457	1194947
Complete genome (Accession number NC_001318)	50S ribosomal protein L9	111046	111567	-		15594458	1194948
Complete genome (Accession number NC_001318)	30S ribosomal protein S18	111585	111875	-		15594459	1194949
Complete genome (Accession number NC_001318)	single-stranded DNA-binding protein (ssb)	111889	112338	-		15594460	1194950

Complete genome (Accession number NC_001318)	30S ribosomal protein S6	112350	112769	-		15594461	1194951
Complete genome (Accession number NC_001318)	PTS system, maltose and glucose-specific IIABC component (malX)	112909	114633	-		15594462	1194952
Complete genome (Accession number NC_001318)	hemolysin III (yplQ)	114807	115508	+		15594463	1194953
Complete genome (Accession number NC_001318)	zinc protease, putative	115505	116818	-		15594464	1194954
Complete genome (Accession number NC_001318)	phosphatidate cytidylyltransferase	116825	117763	-		15595197	1195711
Complete genome (Accession number NC_001318)	hypothetical protein BB0120	117678	118370	-		15594465	1194955
Complete genome (Accession number NC_001318)	ribosome releasing factor (frr)	118375	118929	-		15594466	1194956
Complete genome (Accession number NC_001318)	elongation factor Ts	118964	119803	-		15594467	1194957
Complete genome (Accession number NC_001318)	30S ribosomal protein S2	119807	120589	-		15594468	1194958
Complete genome (Accession number NC_001318)	hypothetical protein BB0124	120804	121082	-		15594469	1194959
Complete genome (Accession number NC_001318)	hypothetical protein BB0125	121101	121823	-		15594470	1194960
Complete genome (Accession number NC_001318)	hypothetical protein BB0126	121880	122491	-		15594471	1194961

Complete genome (Accession number NC_001318)	30S ribosomal protein S1	122491	124152	-		15594472	1194962
Complete genome (Accession number NC_001318)	cytidylate kinase (cmk-1)	124149	124814	-		15594473	1194963
Complete genome (Accession number NC_001318)	hypothetical protein BB0129	124798	125547	-		15594474	1194964
Complete genome (Accession number NC_001318)	hypothetical protein BB0130	125534	126301	-		15594475	1194965
Complete genome (Accession number NC_001318)	recombinase A	126316	127413	-		15594476	1194966
Complete genome (Accession number NC_001318)	transcript cleavage factor/unknown domain fusion protein	127427	130132	-		15594477	1194967
Complete genome (Accession number NC_001318)	hypothetical protein BB0133	130170	131114	-		15594478	1194968
Complete genome (Accession number NC_001318)	hypothetical protein BB0134	131277	132425	+		15594479	1194969
Complete genome (Accession number NC_001318)	histidyl-tRNA synthetase	132472	133845	-		15594480	1194970
Complete genome (Accession number NC_001318)	penicillin-binding protein (pbp-1)	133975	135864	+		15594481	1194971
Complete genome (Accession number NC_001318)	long-chain-fatty-acid CoA ligase	135874	137766	-		15594482	1194972
Complete genome (Accession number NC_001318)	hypothetical protein BB0138	137880	138089	-		15594483	1194973

Complete genome (Accession number NC_001318)	hypothetical protein BB0139	138434	138823	-		15594484	1194974
Complete genome (Accession number NC_001318)	acriflavine resistance protein (acrB)	138850	141960	-		15594485	1194975
Complete genome (Accession number NC_001318)	membrane fusion protein (mtrC)	141979	142935	-		15594486	1194976
Complete genome (Accession number NC_001318)	hypothetical protein BB0142	142944	144266	-		15594487	1194977
Complete genome (Accession number NC_001318)	alpha-hemolysin (hlyA)	144307	144597	+		15594488	1194978
Complete genome (Accession number NC_001318)	glycine betaine, L-proline ABC transporter, glycine/betaine/L-proline-binding protein (proX)	144586	145458	-		15594489	1194979
Complete genome (Accession number NC_001318)	glycine betaine, L-proline ABC transporter, permease protein (proW)	145471	146370	-		15594490	1194980
Complete genome (Accession number NC_001318)	glycine betaine, L-proline ABC transporter, ATP-binding protein (proV)	146377	147495	-		15594491	1194981
Complete genome (Accession number	flagellin	147649	148659	-		15594492	1194982

NC_001318)							
Complete genome (Accession number NC_001318)	hypothetical protein BB0148	148710	148805	+		15594493	1194983
Complete genome (Accession number NC_001318)	flagellar hook-associated protein FliD	148786	150783	-		15594494	1194984
Complete genome (Accession number NC_001318)	hypothetical protein BB0150	150805	150897	-		15594495	1194985
Complete genome (Accession number NC_001318)	N-acetylglucosamine-6-phosphate deacetylase (nagA)	150974	152179	+		15594496	1194986
Complete genome (Accession number NC_001318)	glucosamine-6-phosphate deaminase	152206	153012	+		15594497	1194987
Complete genome (Accession number NC_001318)	superoxide dismutase (sodA)	153075	153719	-		15594498	1194988
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecA	153701	156400	-		15594499	1194989
Complete genome (Accession number NC_001318)	hypothetical protein BB0155	156462	157598	+		15594500	1194990
Complete genome (Accession number NC_001318)	hypothetical protein BB0156	157627	158061	+		15594501	1194991
Complete genome (Accession number NC_001318)	hypothetical protein BB0157	158058	158474	+		15594502	1194992

Complete genome (Accession number NC_001318)	antigen, S2, putative	158628	159344	+		15594503	1194993
Complete genome (Accession number NC_001318)	hypothetical protein BB0159	159368	160042	+		15594504	1194994
Complete genome (Accession number NC_001318)	alanine racemase (alr)	160090	161208	+		15594505	1194995
Complete genome (Accession number NC_001318)	hypothetical protein BB0161	161200	162864	-		15594506	1194996
Complete genome (Accession number NC_001318)	hypothetical protein BB0162	162878	163045	+		15594507	1194997
Complete genome (Accession number NC_001318)	hypothetical protein BB0163	163072	164820	-		15594508	1194998
Complete genome (Accession number NC_001318)	Na+/Ca+ exchange protein, putative	164901	165914	-		15594509	1194999
Complete genome (Accession number NC_001318)	hypothetical protein BB0165	165915	167759	-		15594510	1195000
Complete genome (Accession number NC_001318)	4-alpha-glucanotransferase (malQ)	167879	169399	-		15594511	1195001
Complete genome (Accession number NC_001318)	outer membrane protein (tpn50)	169539	170708	+		15594512	1195002
Complete genome (Accession number NC_001318)	dnaK suppressor, putative	170720	171097	-		15594513	1195003
Complete genome (Accession number NC_001318)	translation initiation factor IF-1	171212	171484	+		15594514	1195004

Complete genome (Accession number NC_001318)	hypothetical protein BB0170	171532	173580	-		15594515	1195005
Complete genome (Accession number NC_001318)	hypothetical protein BB0171	173529	174116	-		15594516	1195006
Complete genome (Accession number NC_001318)	hypothetical protein BB0172	174098	175138	-		15594517	1195007
Complete genome (Accession number NC_001318)	hypothetical protein BB0173	175081	176106	-		15594518	1195008
Complete genome (Accession number NC_001318)	hypothetical protein BB0174	176069	176974	-		15594519	1195009
Complete genome (Accession number NC_001318)	hypothetical protein BB0175	176978	177853	-		15594520	1195010
Complete genome (Accession number NC_001318)	methanol dehydrogenase regulator (moxR)	177868	178881	-		15594521	1195011
Complete genome (Accession number NC_001318)	glucose inhibited division protein B (gidB)	178917	179543	-		15594522	1195012
Complete genome (Accession number NC_001318)	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	179540	181423	-		15594523	1195013
Complete genome (Accession number NC_001318)	tRNA modification GTPase TrmE	181408	182802	-		15594524	1195014

Complete genome (Accession number NC_001318)	flagellar protein, putative	182886	183380	+		15594525	1195015
Complete genome (Accession number NC_001318)	flagellar hook-associated protein FlgK	183392	185275	+		15594526	1195016
Complete genome (Accession number NC_001318)	flagellar hook-associated protein FlgL	185278	186552	+		15594527	1195017
Complete genome (Accession number NC_001318)	flagellar assembly protein FliW	186554	186946	+		15594528	1195018
Complete genome (Accession number NC_001318)	carbon storage regulator (csrA)	186949	187194	+		15594529	1195019
Complete genome (Accession number NC_001318)	hypothetical protein BB0185	187178	187831	-		15594530	1195020
Complete genome (Accession number NC_001318)	hypothetical protein BB0186	187824	188237	-		15594531	1195021
Complete genome (Accession number NC_001318)	hypothetical protein BB0187	188234	188494	-		15594532	1195022
Complete genome (Accession number NC_001318)	50S ribosomal protein L20	188708	189055	-		15594533	1195023
Complete genome (Accession number NC_001318)	50S ribosomal protein L35	189076	189276	-		15594534	1195024
Complete genome (Accession number NC_001318)	translation initiation factor IF-3	189299	189859	-		15594535	1195025
Complete genome (Accession number NC_001318)	hypothetical protein BB0191	189949	190044	+		15594536	1195026

Complete genome (Accession number NC_001318)	hypothetical protein BB0192	190064	190717	+		15594537	1195027
Complete genome (Accession number NC_001318)	hypothetical protein BB0193	190719	191459	+		15594538	1195028
Complete genome (Accession number NC_001318)	hypothetical protein BB0194	191518	192327	-		15594539	1195029
Complete genome (Accession number NC_001318)	cell division control protein 27, putative	192324	193463	-		15594540	1195030
Complete genome (Accession number NC_001318)	peptide chain release factor 1	193800	194873	+		15594541	1195031
Complete genome (Accession number NC_001318)	protoporphyrinogen oxidase, putative	194876	195736	+		15594542	1195032
Complete genome (Accession number NC_001318)	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (spoT)	195693	197696	+		15594543	1195033
Complete genome (Accession number NC_001318)	hypothetical protein BB0199	197686	199950	+		15594544	1195034
Complete genome (Accession number NC_001318)	D-alanine--D-alanine ligase (ddlA)	199965	201035	-		15594545	1195035

Complete genome (Accession number NC_001318)	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (murE)	201052	202578	-		15594546	1195036
Complete genome (Accession number NC_001318)	hemolysin, putative	202850	204088	+		15594547	1195038
Complete genome (Accession number NC_001318)	Lambda CII stability-governing protein (hflK)	204137	205072	+		15594548	1195039
Complete genome (Accession number NC_001318)	Lambda CII stability-governing protein (hflC)	205073	206044	+		15594549	1195040
Complete genome (Accession number NC_001318)	hypothetical protein BB0205	206529	208106	+		15594550	1195042
Complete genome (Accession number NC_001318)	hypothetical protein BB0206	208084	208653	-		15594551	1195043
Complete genome (Accession number NC_001318)	UTP--glucose-1-phosphate uridylyltransferase (gtaB)	208706	209542	+		15594552	1195044
Complete genome (Accession number NC_001318)	hypothetical protein BB0208	209529	211274	+		15594553	1195045
Complete genome (Accession number NC_001318)	hypothetical protein BB0209	211301	212068	+		15594554	1195046

Complete genome (Accession number NC_001318)	surface-located membrane protein 1 (lmp1)	212061	215420	+		15594555	1195047
Complete genome (Accession number NC_001318)	DNA mismatch repair protein (mutL)	215427	217259	+		15594556	1195048
Complete genome (Accession number NC_001318)	hypothetical protein BB0212	217278	218312	+		15594557	1195049
Complete genome (Accession number NC_001318)	hypothetical protein BB0213	218425	219078	-		15594558	1195050
Complete genome (Accession number NC_001318)	translation elongation factor P (efp)	219056	219634	-		15594559	1195051
Complete genome (Accession number NC_001318)	phosphate ABC transporter, periplasmic phosphate-binding protein (pstS)	219797	220639	+		15594560	1195052
Complete genome (Accession number NC_001318)	phosphate ABC transporter, permease protein (pstC)	220729	221637	+		15594561	1195053
Complete genome (Accession number NC_001318)	phosphate ABC transporter, permease protein (pstA)	222192	223178	+		15594562	1195054

Complete genome (Accession number NC_001318)	phosphate ABC transporter, ATP-binding protein (pstB)	223179	223961	+		15594563	1195055
Complete genome (Accession number NC_001318)	gufA protein	223964	224785	-		15594564	1195056
Complete genome (Accession number NC_001318)	alanyl-tRNA synthetase	224826	226610	-		15594565	1195057
Complete genome (Accession number NC_001318)	flagellar motor switch protein (fliG-1)	226610	227836	-		15594566	1195058
Complete genome (Accession number NC_001318)	glucose-6-phosphate 1-dehydrogenase, putative	227814	228521	-		15594567	1195059
Complete genome (Accession number NC_001318)	hypothetical protein BB0223	228542	228895	-		15594568	1195060
Complete genome (Accession number NC_001318)	hypothetical protein BB0224	228864	229148	-		15594569	1195061
Complete genome (Accession number NC_001318)	tRNA-dihydrouridine synthase A	229217	230224	+		15594570	1195062
Complete genome (Accession number NC_001318)	seryl-tRNA synthetase	230214	231491	-		15594571	1195063
Complete genome (Accession number NC_001318)	hypothetical protein BB0227	231621	232322	+		15594572	1195064
Complete genome (Accession number NC_001318)	hypothetical protein BB0228	232338	235253	+		15594573	1195065

Complete genome (Accession number NC_001318)	50S ribosomal protein L31 type B	235289	235534	-		15594574	1195066
Complete genome (Accession number NC_001318)	transcription termination factor Rho	235595	237142	-		15594575	1195067
Complete genome (Accession number NC_001318)	hypothetical protein BB0231	237222	237629	-		15594576	1195068
Complete genome (Accession number NC_001318)	hbbU protein	237630	237956	-		15594577	1195069
Complete genome (Accession number NC_001318)	30S ribosomal protein S20	237969	238226	-		1,62E+08	1195070
Complete genome (Accession number NC_001318)	hypothetical protein BB0234	238301	239128	-		15594579	1195071
Complete genome (Accession number NC_001318)	translation-associated GTPase	239144	240250	-		15594580	1195072
Complete genome (Accession number NC_001318)	hypothetical protein BB0236	240283	242289	-		15594581	1195073
Complete genome (Accession number NC_001318)	apolipoprotein N-acyltransferase	242438	244003	+		15594582	1195074
Complete genome (Accession number NC_001318)	hypothetical protein BB0238	243943	244731	-		15594583	1195075
Complete genome (Accession number NC_001318)	deoxyguanosine/deoxyadenosine kinase(I) subunit 2 (dck)	244777	245394	-		15594584	1195076

Complete genome (Accession number NC_001318)	glycerol uptake facilitator (glpF)	245790	246554	+		15594585	1195077
Complete genome (Accession number NC_001318)	glycerol kinase (glpK)	246597	248102	+		15594586	1195078
Complete genome (Accession number NC_001318)	hypothetical protein BB0242	248156	248434	+		15594587	1195079
Complete genome (Accession number NC_001318)	glycerol-3-phosphate dehydrogenase, anaerobic (glpA)	248506	250089	+		15594588	1195080
Complete genome (Accession number NC_001318)	hypothetical protein BB0244	250176	250670	-		15594589	1195081
Complete genome (Accession number NC_001318)	hypothetical protein BB0245	250657	251211	-		15594590	1195082
Complete genome (Accession number NC_001318)	hypothetical protein BB0246	251212	252237	-		15594591	1195083
Complete genome (Accession number NC_001318)	hypothetical protein BB0247	252434	253039	+		15594592	1195084
Complete genome (Accession number NC_001318)	oligoendopeptidase F (pepF)	253159	254931	+		15594593	1195085
Complete genome (Accession number NC_001318)	phosphatidyltransferase	254945	255649	+		15594594	1195086
Complete genome (Accession number NC_001318)	dedA protein (dedA)	255646	256260	+		15594595	1195087
Complete genome (Accession number NC_001318)	leucyl-tRNA synthetase	256463	258985	+		15594596	1195088

Complete genome (Accession number NC_001318)	hypothetical protein BB0252	259000	261303	+		15594597	1195089
Complete genome (Accession number NC_001318)	ATP-dependent protease LA (lon-1)	261292	263712	-		15594598	1195090
Complete genome (Accession number NC_001318)	single-stranded-DNA-specific exonuclease (recJ)	263988	266114	+		15594599	1195091
Complete genome (Accession number NC_001318)	hypothetical protein BB0255	266095	267051	+		15594600	1195092
Complete genome (Accession number NC_001318)	30S ribosomal protein S21	267066	267275	+		15594601	1195093
Complete genome (Accession number NC_001318)	cell division protein, putative	267313	269676	-		15594602	1195094
Complete genome (Accession number NC_001318)	undecaprenyl pyrophosphate phosphatase	269673	270473	-		15594603	1195095
Complete genome (Accession number NC_001318)	hypothetical protein BB0259	270488	272701	-		15594604	1195096
Complete genome (Accession number NC_001318)	hypothetical protein BB0260	272634	273647	-		15594605	1195097
Complete genome (Accession number NC_001318)	hypothetical protein BB0261	273854	275236	+		15594606	1195098
Complete genome (Accession number NC_001318)	hypothetical protein BB0262	275243	276496	-		15594607	1195099

Complete genome (Accession number NC_001318)	signal peptidase I (lepB-3)	276558	277064	+		15594608	1195100
Complete genome (Accession number NC_001318)	heat shock protein 70 (dnaK-1)	277090	278565	-		15594609	1195101
Complete genome (Accession number NC_001318)	hypothetical protein BB0265	278537	279058	-		15594610	1195102
Complete genome (Accession number NC_001318)	hypothetical protein BB0266	279078	279386	-		15594611	1195103
Complete genome (Accession number NC_001318)	hypothetical protein BB0267	279407	281311	-		15594612	1195104
Complete genome (Accession number NC_001318)	hypothetical protein BB0268	281314	281793	-		15594613	1195105
Complete genome (Accession number NC_001318)	ATP-binding protein (ylxH-1)	281800	282687	-		15594614	1195106
Complete genome (Accession number NC_001318)	flagellar biosynthesis regulator FlhF	282699	283865	-		15594615	1195107
Complete genome (Accession number NC_001318)	flagellar biosynthesis protein A	283869	285962	-		15594616	1195108
Complete genome (Accession number NC_001318)	flagellar biosynthesis protein FlhB	285971	287089	-		15594617	1195109
Complete genome (Accession number NC_001318)	flagellar biosynthesis protein (fliR)	287089	287898	-		15594618	1195110

Complete genome (Accession number NC_001318)	flagellar biosynthesis protein (fliQ)	287910	288173	-		15594619	1195111
Complete genome (Accession number NC_001318)	flagellar biosynthesis protein FliP	288182	288946	-		15594620	1195112
Complete genome (Accession number NC_001318)	flagellar biosynthesis protein (fliZ)	288957	289583	-		15594621	1195113
Complete genome (Accession number NC_001318)	flagellar motor switch protein (fliN)	289576	289917	-		15594622	1195114
Complete genome (Accession number NC_001318)	flagellar motor switch protein FliM	289963	291021	-		15594623	1195115
Complete genome (Accession number NC_001318)	flagellar basal body-associated protein FliL	291059	291595	-		15594624	1195116
Complete genome (Accession number NC_001318)	flagellar motor protein MotB	291644	292426	-		15594625	1195117
Complete genome (Accession number NC_001318)	flagellar motor rotation protein A (motA)	292426	293208	-		15594626	1195118
Complete genome (Accession number NC_001318)	flagellar protein (flbD)	293205	293429	-		15594627	1195119
Complete genome (Accession number NC_001318)	flagellar hook protein FlgE	293452	294780	-		15594628	1195120

Complete genome (Accession number NC_001318)	flagellar basal body rod modification protein	294785	295228	-		15594629	1195121
Complete genome (Accession number NC_001318)	flagellar protein (flbC)	295242	296426	-		15594630	1195122
Complete genome (Accession number NC_001318)	flagellar protein (flbB)	296428	297051	-		15594631	1195123
Complete genome (Accession number NC_001318)	flagellar protein (flbA)	297038	297469	-		15594632	1195124
Complete genome (Accession number NC_001318)	flagellum-specific ATP synthase (fliI)	297466	298776	-		15594633	1195125
Complete genome (Accession number NC_001318)	flagellar assembly protein H	298795	299715	-		15594634	1195126
Complete genome (Accession number NC_001318)	flagellar motor switch protein G	299730	300764	-		15594635	1195127
Complete genome (Accession number NC_001318)	flagellar MS-ring protein	300780	302489	-		15594636	1195128
Complete genome (Accession number NC_001318)	flagellar hook-basal body protein FliE	302504	302839	-		15594637	1195129
Complete genome (Accession number NC_001318)	flagellar basal body rod protein FlgC	302851	303309	-		15594638	1195130
Complete genome (Accession number NC_001318)	flagellar basal body rod protein FlgB	303333	303740	-		15594639	1195131

Complete genome (Accession number NC_001318)	ATP-dependent protease ATP-binding subunit	303774	305141	-		15594640	1195132
Complete genome (Accession number NC_001318)	ATP-dependent protease peptidase subunit	305113	305661	-		15594641	1195133
Complete genome (Accession number NC_001318)	smg protein	305671	306618	-		15594642	1195134
Complete genome (Accession number NC_001318)	hypothetical protein BB0298	306625	307317	-		15594643	1195135
Complete genome (Accession number NC_001318)	cell division protein FtsZ	307318	308532	-		15594644	1195136
Complete genome (Accession number NC_001318)	cell division protein (ftsA)	308539	309780	-		15594645	1195137
Complete genome (Accession number NC_001318)	cell division protein (divIB)	309780	310523	-		15594646	1195138
Complete genome (Accession number NC_001318)	cell division protein (ftsW)	310559	311653	-		15594647	1195139
Complete genome (Accession number NC_001318)	phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)	311660	312715	-		15594648	1195140

Complete genome (Accession number NC_001318)	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase (murF)	312729	314123	-		15594649	1195141
Complete genome (Accession number NC_001318)	hypothetical protein BB0305	314146	314427	-		15594650	1195142
Complete genome (Accession number NC_001318)	hypothetical protein BB0306	314424	315314	-		15594651	1195143
Complete genome (Accession number NC_001318)	hypothetical protein BB0307	315307	316143	-		15594652	1195144
Complete genome (Accession number NC_001318)	hypothetical protein BB0308	316140	317216	-		15594653	1195145
Complete genome (Accession number NC_001318)	hypothetical protein BB0309	317247	318026	-		15594654	1195146
Complete genome (Accession number NC_001318)	hypothetical protein BB0310	318119	318256	-		15594655	1195147
Complete genome (Accession number NC_001318)	hypothetical protein BB0311	318277	319158	-		15594656	1195148
Complete genome (Accession number NC_001318)	purine-binding chemotaxis protein (cheW-1)	319106	319636	-		15594657	1195149
Complete genome (Accession number NC_001318)	cell division protein (ftsJ)	319680	320258	-		15594658	1195150

Complete genome (Accession number NC_001318)	octaprenyl-diphosphate synthase (ispB)	320309	321352	+		15594659	1195151
Complete genome (Accession number NC_001318)	hypothetical protein BB0315	321352	322038	+		15594660	1195152
Complete genome (Accession number NC_001318)	hypothetical protein BB0316	322040	322846	-		15594661	1195153
Complete genome (Accession number NC_001318)	hypothetical protein BB0317	322847	323779	-		15594662	1195154
Complete genome (Accession number NC_001318)	methylgalactoside ABC transporter, ATP-binding protein (mglA)	323776	325236	-		15594663	1195155
Complete genome (Accession number NC_001318)	exported protein (tpn38b)	325236	326288	-		15594664	1195156
Complete genome (Accession number NC_001318)	hypothetical protein BB0320	326325	326432	-		15594665	1195157
Complete genome (Accession number NC_001318)	hypothetical protein BB0321	326469	326666	-		15594666	1195158
Complete genome (Accession number NC_001318)	hypothetical protein BB0322	326699	327757	-		15594667	1195159
Complete genome (Accession number NC_001318)	hypothetical protein BB0323	328032	329165	+		15594668	1195160
Complete genome (Accession number NC_001318)	hypothetical protein BB0324	329262	329621	+		15594669	1195161

Complete genome (Accession number NC_001318)	hypothetical protein BB0325	329643	330752	-		15594670	1195162
Complete genome (Accession number NC_001318)	hypothetical protein BB0326	330803	333598	-		15594671	1195163
Complete genome (Accession number NC_001318)	glycerol-3-phosphate O-acyltransferase, putative	333619	334515	-		15594672	1195164
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-1)	334919	336508	+		15594673	1195165
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2)	336629	338215	+		15594674	1195166
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-3)	338358	339983	+		15594675	1195167
Complete genome (Accession number NC_001318)	hypothetical protein BB0331	340062	340217	-		15594676	1195168

Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, permease protein (oppB-1)	340341	341261	+		15594677	1195169
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, permease protein (oppC-1)	341274	342323	+		15594678	1195170
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, ATP-binding protein (oppD)	342335	343207	+		15594679	1195171
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, ATP-binding protein (oppF)	343208	344179	+		15594680	1195172
Complete genome (Accession number NC_001318)	P26	344192	344947	-		15594681	1195173
Complete genome (Accession number NC_001318)	enolase (eno)	345063	346364	+		15594682	1195174
Complete genome (Accession number NC_001318)	30S ribosomal protein S9	346431	346841	-		15594683	1195175
Complete genome (Accession number NC_001318)	50S ribosomal protein L13	346861	347301	-		15594684	1195176
Complete genome (Accession number NC_001318)	hypothetical protein BB0340	347351	348160	-		15594685	1195177

Complete genome (Accession number NC_001318)	aspartyl/glutamyl-tRNA amidotransferase subunit B	348153	349610	-		15594686	1195178
Complete genome (Accession number NC_001318)	glu-tRNA amidotransferase, subunit A (gluA)	349600	351090	-		15594687	1195179
Complete genome (Accession number NC_001318)	aspartyl/glutamyl-tRNA amidotransferase subunit C	351056	351331	-		15594688	1195180
Complete genome (Accession number NC_001318)	DNA helicase (uvrD)	351341	353440	-		15594689	1195181
Complete genome (Accession number NC_001318)	hypothetical protein BB0345	353440	354636	-		15594690	1195182
Complete genome (Accession number NC_001318)	hypothetical protein BB0346	354648	355298	-		15594691	1195183
Complete genome (Accession number NC_001318)	fibronectin/fibrinogen-binding protein, putative	355482	356909	+		15594692	1195184
Complete genome (Accession number NC_001318)	pyruvate kinase	357007	358440	+		15594693	1195185
Complete genome (Accession number NC_001318)	hypothetical protein BB0349	358458	359198	+		15594694	1195186
Complete genome (Accession number NC_001318)	50S ribosomal protein L28	359217	359495	-		15594695	1195187
Complete genome (Accession number NC_001318)	hypothetical protein BB0351	359513	361081	-		15594696	1195188

Complete genome (Accession number NC_001318)	hypothetical protein BB0352	361188	362321	+		15594697	1195189
Complete genome (Accession number NC_001318)	hypothetical protein BB0353	362318	364117	-		15594698	1195190
Complete genome (Accession number NC_001318)	hypothetical protein BB0354	364130	365170	-		15594699	1195191
Complete genome (Accession number NC_001318)	transcription factor, putative	365115	365603	-		15594700	1195192
Complete genome (Accession number NC_001318)	hypothetical protein BB0356	365643	366137	-		15594701	1195193
Complete genome (Accession number NC_001318)	hypothetical protein BB0357	366144	366236	-		15594702	1195194
Complete genome (Accession number NC_001318)	hypothetical protein BB0358	366229	366960	-		15594703	1195195
Complete genome (Accession number NC_001318)	carboxyl-terminal protease (ctp)	366964	368391	-		15594704	1195196
Complete genome (Accession number NC_001318)	hypothetical protein BB0360	368456	368881	+		15594705	1195197
Complete genome (Accession number NC_001318)	ATP-binding protein (ylxH-2)	368885	370027	+		15594706	1195198
Complete genome (Accession number NC_001318)	prolipoprotein diacylglyceryl transferase	370027	371013	+		15594707	1195199
Complete genome (Accession number NC_001318)	periplasmic protein	371034	373046	+		15594708	1195200
Complete genome (Accession number NC_001318)	methylglyoxal synthase	373140	373520	+		15594709	1195201

Complete genome (Accession number NC_001318)	lipoprotein LA7	373567	374151	-		15594710	1195202
Complete genome (Accession number NC_001318)	putative aminopeptidase 1	374277	375653	+		15594711	1195203
Complete genome (Accession number NC_001318)	hypothetical protein BB0367	375661	375939	+		15594712	1195204
Complete genome (Accession number NC_001318)	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	375961	377052	-		15594713	1195205
Complete genome (Accession number NC_001318)	ATP-dependent Clp protease, subunit A (clpA)	377039	379330	-		15594714	1195206
Complete genome (Accession number NC_001318)	tyrosyl-tRNA synthetase (tyrS)	379341	380558	-		15594715	1195207
Complete genome (Accession number NC_001318)	glycyl-tRNA synthetase	380555	381892	-		15594716	1195208
Complete genome (Accession number NC_001318)	glutamyl-tRNA synthetase	381910	383382	-		15594717	1195209
Complete genome (Accession number NC_001318)	hypothetical protein BB0373	383395	384162	-		15594718	1195210
Complete genome (Accession number NC_001318)	hypothetical protein BB0374	384287	385426	+		15594719	1195211
Complete genome (Accession number NC_001318)	pfs protein (pfs-1)	385449	386162	+		15594720	1195212

Complete genome (Accession number NC_001318)	S-adenosylmethionine synthetase	386159	387337	+		15594721	1195213
Complete genome (Accession number NC_001318)	S-ribosylhomocysteinase	387334	387807	+		1,62E+08	1195214
Complete genome (Accession number NC_001318)	hypothetical protein BB0378	387818	388480	-		15594723	1195215
Complete genome (Accession number NC_001318)	protein kinase C1 inhibitor (pkcI)	388507	388956	-		15594724	1195216
Complete genome (Accession number NC_001318)	Mg2+ transport protein (mgtE)	388977	390341	-		15594725	1195217
Complete genome (Accession number NC_001318)	hypothetical protein BB0381	390392	391819	-		15594726	1195218
Complete genome (Accession number NC_001318)	basic membrane protein B (bmpB)	391932	392957	-		15594727	1195219
Complete genome (Accession number NC_001318)	basic membrane protein A (bmpA)	393044	394063	-		15594728	1195220
Complete genome (Accession number NC_001318)	basic membrane protein C (bmpC)	394105	395166	-		15594729	1195221
Complete genome (Accession number NC_001318)	basic membrane protein D (bmpD)	395481	396563	-		15594730	1195222
Complete genome (Accession number NC_001318)	30S ribosomal protein S7	396604	397077	-		15594731	1195223

Complete genome (Accession number NC_001318)	30S ribosomal protein S12	397102	397476	-		15594732	1195224
Complete genome (Accession number NC_001318)	DNA-directed RNA polymerase subunit beta'	397544	401677	-		15594733	1195225
Complete genome (Accession number NC_001318)	DNA-directed RNA polymerase subunit beta	401693	405160	-		15594734	1195226
Complete genome (Accession number NC_001318)	50S ribosomal protein L7/L12	405243	405617	-		15594735	1195227
Complete genome (Accession number NC_001318)	50S ribosomal protein L10	405688	406194	-		15594736	1195228
Complete genome (Accession number NC_001318)	50S ribosomal protein L1	406181	406861	-		15594737	1195229
Complete genome (Accession number NC_001318)	50S ribosomal protein L11	406861	407292	-		15594738	1195230
Complete genome (Accession number NC_001318)	transcription antitermination factor (nusG)	407344	407898	-		15594739	1195231
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecE	407922	408092	-		15594740	1195232
Complete genome (Accession number NC_001318)	50S ribosomal protein L33	408201	408380	-		15594741	1195234

Complete genome (Accession number NC_001318)	hypothetical protein BB0397	408554	409402	-		15594742	1195235
Complete genome (Accession number NC_001318)	hypothetical protein BB0398	409416	410447	-		15594743	1195236
Complete genome (Accession number NC_001318)	hypothetical protein BB0399	410787	411446	+		15594744	1195237
Complete genome (Accession number NC_001318)	hypothetical protein BB0400	411456	413006	-		15594745	1195238
Complete genome (Accession number NC_001318)	glutamate transporter, putative	413113	414315	+		15594746	1195239
Complete genome (Accession number NC_001318)	prolyl-tRNA synthetase	414327	415793	-		15594747	1195240
Complete genome (Accession number NC_001318)	hypothetical protein BB0403	415846	416523	-		15594748	1195241
Complete genome (Accession number NC_001318)	hypothetical protein BB0404	416689	417105	+		15594749	1195242
Complete genome (Accession number NC_001318)	hypothetical protein BB0405	417102	417713	+		15594750	1195243
Complete genome (Accession number NC_001318)	hypothetical protein BB0406	417724	418335	+		15594751	1195244
Complete genome (Accession number NC_001318)	mannose-6-phosphate isomerase (manA)	418388	419506	-		15594752	1195245

Complete genome (Accession number NC_001318)	PTS system, fructose-specific IIABC component (fruA-1)	419503	421380	-		15594753	1195246
Complete genome (Accession number NC_001318)	hypothetical protein BB0409	421554	422183	+		15594754	1195247
Complete genome (Accession number NC_001318)	hypothetical protein BB0410	422180	422299	+		15594755	1195248
Complete genome (Accession number NC_001318)	endonuclease precursor (nucA)	422471	423058	+		15594756	1195249
Complete genome (Accession number NC_001318)	hypothetical protein BB0412	423055	423834	+		15594757	1195250
Complete genome (Accession number NC_001318)	hypothetical protein BB0413	423822	424445	-		15594758	1195251
Complete genome (Accession number NC_001318)	chemotaxis protein methyltransferase (cheR-2)	424694	425551	+		15594759	1195252
Complete genome (Accession number NC_001318)	protein-glutamate methylesterase (cheB-1)	425584	426711	+		15594760	1195253
Complete genome (Accession number NC_001318)	pheromone shutdown protein (traB)	426736	427950	+		15594761	1195254
Complete genome (Accession number NC_001318)	adenylate kinase (adk)	427987	428622	+		15594762	1195255
Complete genome (Accession number NC_001318)	hypothetical protein BB0418	428646	429674	+		15594763	1195256

Complete genome (Accession number NC_001318)	response regulatory protein (rrp-1)	429693	430616	-		15594764	1195257
Complete genome (Accession number NC_001318)	sensory transduction histidine kinase, putative	430619	435103	-		15594765	1195258
Complete genome (Accession number NC_001318)	hydrolase	441713	442552	-		15594766	1195263
Complete genome (Accession number NC_001318)	3-methyladenine DNA glycosylase (mag)	442688	443248	-		15594767	1195264
Complete genome (Accession number NC_001318)	hypothetical protein BB0423	443763	444053	-		15594768	1195266
Complete genome (Accession number NC_001318)	hypothetical protein BB0424	444150	444299	+		15594769	1195267
Complete genome (Accession number NC_001318)	hypothetical protein BB0425	446113	446205	-		15594770	1195270
Complete genome (Accession number NC_001318)	hypothetical protein BB0426	446327	446890	-		15594771	1195271
Complete genome (Accession number NC_001318)	hypothetical protein BB0427	446969	447760	-		15594772	1195272
Complete genome (Accession number NC_001318)	hypothetical protein BB0428	447855	448172	+		15594773	1195273
Complete genome (Accession number NC_001318)	hypothetical protein BB0429	448202	448591	-		15594774	1195274
Complete genome (Accession number NC_001318)	proline dipeptidase (pepQ)	448705	449310	+		15594775	1195275

Complete genome (Accession number NC_001318)	hypothetical protein BB0431	449419	450171	+		15594776	1195276
Complete genome (Accession number NC_001318)	hypothetical protein BB0432	450174	450887	+		15594777	1195277
Complete genome (Accession number NC_001318)	hypothetical protein BB0433	450972	451070	-		15594778	1195278
Complete genome (Accession number NC_001318)	stage 0 sporulation protein J (spo0J)	451139	451921	-		15594779	1195279
Complete genome (Accession number NC_001318)	DNA gyrase, subunit A (gyrA)	452040	454472	-		15594780	1195280
Complete genome (Accession number NC_001318)	DNA gyrase, subunit B (gyrB)	454484	456403	-		15594781	1195281
Complete genome (Accession number NC_001318)	chromosomal replication initiator protein (dnaA)	456576	458036	+		15594782	1195282
Complete genome (Accession number NC_001318)	DNA polymerase III, subunit beta (dnaN)	458277	459434	+		15594783	1195283
Complete genome (Accession number NC_001318)	hypothetical protein BB0439	459525	459824	+		15594784	1195284
Complete genome (Accession number NC_001318)	50S ribosomal protein L34	459916	460071	+		15594785	1195285
Complete genome (Accession number NC_001318)	ribonuclease P protein component (rnpA)	460052	460411	+		15594786	1195286

Complete genome (Accession number NC_001318)	putative inner membrane protein translocase component YidC	460398	462032	+		15594787	1195287
Complete genome (Accession number NC_001318)	spoIIIJ-associated protein (jag)	462045	462773	+		15594788	1195288
Complete genome (Accession number NC_001318)	nucleotide sugar epimerase	462819	463886	+		15594789	1195289
Complete genome (Accession number NC_001318)	fructose-bisphosphate aldolase	464053	465132	+		15594790	1195290
Complete genome (Accession number NC_001318)	aspartyl-tRNA synthetase	465518	467278	-		1,62E+08	1195291
Complete genome (Accession number NC_001318)	Na+/H+ antiporter (napA)	467282	469387	-		15594792	1195292
Complete genome (Accession number NC_001318)	phosphocarrier protein HPr (ptsH-1)	469390	469665	-		15594793	1195293
Complete genome (Accession number NC_001318)	hypothetical protein BB0449	469678	469971	-		15594794	1195294
Complete genome (Accession number NC_001318)	RNA polymerase sigma-54 factor (ntrA)	469961	471220	-		15594795	1195295
Complete genome (Accession number NC_001318)	chromate transport protein, putative	471223	471756	-		15594796	1195296
Complete genome (Accession number NC_001318)	hypothetical protein BB0452	471771	472475	-		15594797	1195297

Complete genome (Accession number NC_001318)	hypothetical protein BB0453	472566	473408	+		15594798	1195298
Complete genome (Accession number NC_001318)	lipopolysaccharide biosynthesis-related protein	473405	474556	-		15594799	1195299
Complete genome (Accession number NC_001318)	hypothetical protein BB0455	474613	475602	+		15594800	1195300
Complete genome (Accession number NC_001318)	hypothetical protein BB0456	475606	476211	+		15594801	1195301
Complete genome (Accession number NC_001318)	excinuclease ABC, subunit C (uvrC)	476263	478074	-		15594802	1195302
Complete genome (Accession number NC_001318)	hypothetical protein BB0458	478139	479716	+		15594803	1195303
Complete genome (Accession number NC_001318)	hypothetical protein BB0459	479709	481019	+		15594804	1195304
Complete genome (Accession number NC_001318)	hypothetical protein BB0460	481344	482057	-		15594805	1195305
Complete genome (Accession number NC_001318)	DNA polymerase III subunits gamma and tau	482600	484282	+		15594806	1195307
Complete genome (Accession number NC_001318)	hypothetical protein BB0462	484254	484586	+		15594807	1195308
Complete genome (Accession number NC_001318)	nucleoside-diphosphate kinase (ndk)	484757	485266	+		15594808	1195309

Complete genome (Accession number NC_001318)	hypothetical protein BB0464	485550	486077	+		15594809	1195310
Complete genome (Accession number NC_001318)	hypothetical protein BB0465	486074	486769	+		15594810	1195311
Complete genome (Accession number NC_001318)	ABC transporter, ATP-binding protein	486705	487538	+		15594811	1195312
Complete genome (Accession number NC_001318)	hypothetical protein BB0467	487535	488224	+		15594812	1195313
Complete genome (Accession number NC_001318)	hypothetical protein BB0468	488226	488972	+		15594813	1195314
Complete genome (Accession number NC_001318)	signal peptidase II	488983	489495	+		15594814	1195315
Complete genome (Accession number NC_001318)	hypothetical protein BB0470	489492	489719	+		15594815	1195316
Complete genome (Accession number NC_001318)	hypothetical protein BB0471	489733	490554	+		15594816	1195317
Complete genome (Accession number NC_001318)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	490599	491927	+		15594817	1195318
Complete genome (Accession number NC_001318)	hypothetical protein BB0473	492588	493952	+		15594818	1195319
Complete genome (Accession number NC_001318)	hypothetical protein BB0474	493991	494092	+		15594819	1195320

Complete genome (Accession number NC_001318)	hypothetical protein BB0475	494150	494542	-		15594820	1195321
Complete genome (Accession number NC_001318)	elongation factor Tu	495033	496217	+		1,62E+08	1195322
Complete genome (Accession number NC_001318)	30S ribosomal protein S10	496268	496579	+		15594822	1195323
Complete genome (Accession number NC_001318)	50S ribosomal protein L3	496615	497235	+		15594823	1195324
Complete genome (Accession number NC_001318)	50S ribosomal protein L4	497245	497874	+		15594824	1195325
Complete genome (Accession number NC_001318)	50S ribosomal protein L23	497880	498191	+		15594825	1195326
Complete genome (Accession number NC_001318)	50S ribosomal protein L2	498213	499046	+		15594826	1195327
Complete genome (Accession number NC_001318)	30S ribosomal protein S19	499056	499334	+		15594827	1195328
Complete genome (Accession number NC_001318)	50S ribosomal protein L22	499341	499703	+		15594828	1195329
Complete genome (Accession number NC_001318)	30S ribosomal protein S3	499707	500588	+		15594829	1195330
Complete genome (Accession number NC_001318)	50S ribosomal protein L16	500593	501009	+		15594830	1195331
Complete genome (Accession number NC_001318)	50S ribosomal protein L29	501012	501212	+		15594831	1195332
Complete genome (Accession number NC_001318)	30S ribosomal protein S17	501215	501469	+		15594832	1195333

Complete genome (Accession number NC_001318)	50S ribosomal protein L14	501497	501865	+		1,62E+08	1195334
Complete genome (Accession number NC_001318)	50S ribosomal protein L24	501880	502185	+		15594834	1195335
Complete genome (Accession number NC_001318)	50S ribosomal protein L5	502191	502739	+		15594835	1195336
Complete genome (Accession number NC_001318)	30S ribosomal protein S14	502756	502941	+		1,62E+08	1195337
Complete genome (Accession number NC_001318)	30S ribosomal protein S8	502951	503349	+		15594837	1195338
Complete genome (Accession number NC_001318)	50S ribosomal protein L6	503366	503908	+		15594838	1195339
Complete genome (Accession number NC_001318)	50S ribosomal protein L18	503926	504285	+		15594839	1195340
Complete genome (Accession number NC_001318)	30S ribosomal protein S5	504298	504795	+		15594840	1195341
Complete genome (Accession number NC_001318)	ribosomal protein L30 (rpmD)	504799	505104	+		15594841	1195342
Complete genome (Accession number NC_001318)	50S ribosomal protein L15	505104	505541	+		15594842	1195343
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecY	505554	506858	+		15594843	1195344
Complete genome (Accession number NC_001318)	50S ribosomal protein L36	506865	506984	+		15594844	1195345

Complete genome (Accession number NC_001318)	30S ribosomal protein S13	507002	507379	+		15594845	1195346
Complete genome (Accession number NC_001318)	30S ribosomal protein S11	507394	507798	+		15594846	1195347
Complete genome (Accession number NC_001318)	DNA-directed RNA polymerase subunit alpha	507811	508848	+		15594847	1195348
Complete genome (Accession number NC_001318)	50S ribosomal protein L17	508870	509241	+		15594848	1195349
Complete genome (Accession number NC_001318)	hypothetical protein BB0504	509314	510846	+		15594849	1195350
Complete genome (Accession number NC_001318)	hypothetical protein BB0505	510836	511624	+		15594850	1195351
Complete genome (Accession number NC_001318)	hemolysin (tlyA)	511605	512396	+		15594851	1195352
Complete genome (Accession number NC_001318)	hypothetical protein BB0507	512393	513148	-		15594852	1195353
Complete genome (Accession number NC_001318)	GTP-binding protein EngA	513226	514527	+		15594853	1195354
Complete genome (Accession number NC_001318)	hypothetical protein BB0509	514524	515783	+		15594854	1195355
Complete genome (Accession number NC_001318)	hypothetical protein BB0510	515780	515998	+		15594855	1195356
Complete genome (Accession number NC_001318)	hypothetical protein BB0511	516090	516473	+		15594856	1195357

Complete genome (Accession number NC_001318)	hypothetical protein BB0512	516493	522993	+		15594857	1195358
Complete genome (Accession number NC_001318)	phenylalanyl-tRNA synthetase subunit alpha	522990	524576	+		15594858	1195359
Complete genome (Accession number NC_001318)	phenylalanyl-tRNA synthetase subunit beta	524554	526254	+		15594859	1195360
Complete genome (Accession number NC_001318)	thioredoxin reductase (trxB)	526325	527305	+		15594860	1195361
Complete genome (Accession number NC_001318)	rRNA methylase (yacO)	527361	528047	-		15594861	1195362
Complete genome (Accession number NC_001318)	heat shock protein (dnaJ-1)	528104	529198	-		15594862	1195363
Complete genome (Accession number NC_001318)	molecular chaperone DnaK	529198	531105	-		15594863	1195364
Complete genome (Accession number NC_001318)	grpE protein (grpE)	531129	531692	-		15594864	1195365
Complete genome (Accession number NC_001318)	hypothetical protein BB0520	531851	531967	-		15594865	1195366
Complete genome (Accession number NC_001318)	hypothetical protein BB0521	532069	532521	+		15594866	1195367
Complete genome (Accession number NC_001318)	NH(3)-dependent NAD+ synthetase	532938	533606	+		15594867	1195368
Complete genome (Accession number NC_001318)	hypothetical protein BB0523	533980	534072	+		15594868	1195369

Complete genome (Accession number NC_001318)	inositol monophosphatase	534301	535155	+		15594869	1195370
Complete genome (Accession number NC_001318)	hypothetical protein BB0525	535178	535600	-		15594870	1195371
Complete genome (Accession number NC_001318)	hypothetical protein BB0526	535704	537527	+		15594871	1195372
Complete genome (Accession number NC_001318)	pantothenate kinase	537520	538308	+		15594872	1195373
Complete genome (Accession number NC_001318)	aldose reductase, putative	538328	539275	-		15594873	1195374
Complete genome (Accession number NC_001318)	hypothetical protein BB0529	539256	539372	+		15594874	1195375
Complete genome (Accession number NC_001318)	hypothetical protein BB0530	539367	540020	-		15594875	1195376
Complete genome (Accession number NC_001318)	hypothetical protein BB0531	540159	540773	-		15594876	1195377
Complete genome (Accession number NC_001318)	hypothetical protein BB0532	541182	542069	-		15594877	1195378
Complete genome (Accession number NC_001318)	phnP protein (phnP)	542263	543024	+		15594878	1195379
Complete genome (Accession number NC_001318)	exodeoxyribonuclease III (exoA)	543049	543816	+		15594879	1195380
Complete genome (Accession number NC_001318)	hypothetical protein BB0535	543832	544605	+		15594880	1195381
Complete genome (Accession number NC_001318)	zinc protease, putative	544586	547387	+		15594881	1195382

Complete genome (Accession number NC_001318)	hypothetical protein BB0537	547846	548490	-		15594882	1195384
Complete genome (Accession number NC_001318)	hypothetical protein BB0538	548487	548885	-		15594883	1195385
Complete genome (Accession number NC_001318)	hypothetical protein BB0539	548920	549618	-		15594884	1195386
Complete genome (Accession number NC_001318)	elongation factor G	549642	551723	-		15594885	1195387
Complete genome (Accession number NC_001318)	hypothetical protein BB0541	552007	552225	+		15594886	1195388
Complete genome (Accession number NC_001318)	hypothetical protein BB0542	552440	553018	+		15594887	1195389
Complete genome (Accession number NC_001318)	hypothetical protein BB0543	553133	553789	+		15594888	1195390
Complete genome (Accession number NC_001318)	phosphoribosylpyrophosphate synthetase	553992	555212	+		15594889	1195391
Complete genome (Accession number NC_001318)	xylulokinase (xylB)	555216	556580	+		15594890	1195392
Complete genome (Accession number NC_001318)	hypothetical protein BB0546	556563	557423	-		15594891	1195393
Complete genome (Accession number NC_001318)	dephospho-CoA kinase	557407	558024	-		15594892	1195394
Complete genome (Accession number NC_001318)	DNA polymerase I (polA)	558006	560732	-		15594893	1195395
Complete genome (Accession number NC_001318)	hypothetical protein BB0549	560729	561127	-		15594894	1195396

Complete genome (Accession number NC_001318)	flagellar protein (flaJ)	561117	561554	-		15594895	1195397
Complete genome (Accession number NC_001318)	chemotaxis response regulator (cheY-1)	561563	561964	-		15594896	1195398
Complete genome (Accession number NC_001318)	DNA ligase (lig)	562185	564167	+		15594897	1195399
Complete genome (Accession number NC_001318)	hypothetical protein BB0553	564188	565681	-		15594898	1195400
Complete genome (Accession number NC_001318)	hypothetical protein BB0554	565943	567823	+		15594899	1195401
Complete genome (Accession number NC_001318)	hypothetical protein BB0555	567810	568277	+		15594900	1195402
Complete genome (Accession number NC_001318)	hypothetical protein BB0556	568270	569139	+		15594901	1195403
Complete genome (Accession number NC_001318)	phosphocarrier protein HPr (ptsH-2)	569278	569538	+		15594902	1195404
Complete genome (Accession number NC_001318)	phosphoenolpyruvate-protein phosphatase (ptsI)	569559	571280	+		15594903	1195405
Complete genome (Accession number NC_001318)	glucose-specific PTS system component	571283	571852	+		15594904	1195406
Complete genome (Accession number NC_001318)	heat shock protein 90	571890	573842	-		15594905	1195407

Complete genome (Accession number NC_001318)	6-phosphogluconate dehydrogenase	573853	575247	+		15594906	1195408
Complete genome (Accession number NC_001318)	hypothetical protein BB0562	575274	575816	-		15594907	1195409
Complete genome (Accession number NC_001318)	hypothetical protein BB0563	575981	576526	-		15594908	1195410
Complete genome (Accession number NC_001318)	hypothetical protein BB0564	576582	577187	-		15594909	1195411
Complete genome (Accession number NC_001318)	purine-binding chemotaxis protein (cheW-2)	577395	577937	+		15594910	1195412
Complete genome (Accession number NC_001318)	hypothetical protein BB0566	577950	578261	+		15594911	1195413
Complete genome (Accession number NC_001318)	chemotaxis histidine kinase (cheA-1)	578277	580421	+		15594912	1195414
Complete genome (Accession number NC_001318)	protein-glutamate methylesterase (cheB-2)	580486	581643	+		15594913	1195415
Complete genome (Accession number NC_001318)	hypothetical protein BB0569	581645	583417	+		15594914	1195416
Complete genome (Accession number NC_001318)	chemotaxis response regulator (cheY-2)	583458	583832	+		15594915	1195417
Complete genome (Accession number NC_001318)	uridylate kinase	584191	584880	-		15594916	1195418
Complete genome (Accession number NC_001318)	glycosyl transferase (lgtD)	585080	586156	+		15594917	1195419

Complete genome (Accession number NC_001318)	ABC transporter, ATP-binding protein	586212	587024	+		15594918	1195420
Complete genome (Accession number NC_001318)	hypothetical protein BB0574	587031	587882	+		15594919	1195421
Complete genome (Accession number NC_001318)	CTP synthetase	588066	589667	+		15594920	1195422
Complete genome (Accession number NC_001318)	hypothetical protein BB0576	589684	590232	-		15594921	1195423
Complete genome (Accession number NC_001318)	hypothetical protein BB0577	590348	590935	+		15594922	1195424
Complete genome (Accession number NC_001318)	methyl-accepting chemotaxis protein (mcp-1)	591188	592357	+		15594923	1195425
Complete genome (Accession number NC_001318)	DNA polymerase III subunit alpha	592446	595931	+		15594924	1195426
Complete genome (Accession number NC_001318)	hypothetical protein BB0580	595943	596521	+		15594925	1195427
Complete genome (Accession number NC_001318)	DNA recombinase (recG)	596531	598591	+		15594926	1195428
Complete genome (Accession number NC_001318)	carboxypeptidase, putative	598588	599376	-		15594927	1195429
Complete genome (Accession number NC_001318)	hypothetical protein BB0583	599495	600844	+		15594928	1195430
Complete genome (Accession number NC_001318)	hypothetical protein BB0584	600998	602344	+		15594929	1195431

Complete genome (Accession number NC_001318)	UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD)	602374	603729	+		15594930	1195432
Complete genome (Accession number NC_001318)	femA protein (femA)	603726	604769	-		15594931	1195433
Complete genome (Accession number NC_001318)	methionyl-tRNA synthetase	604779	606983	-		15594932	1195434
Complete genome (Accession number NC_001318)	pfs protein (pfs-2)	607138	607935	+		15594933	1195435
Complete genome (Accession number NC_001318)	phosphate acetyltransferase (pta)	608020	609078	+		15594934	1195436
Complete genome (Accession number NC_001318)	dimethyladenosine transferase	609061	609906	-		15594935	1195437
Complete genome (Accession number NC_001318)	competence locus E, putative	609943	611193	-		15594936	1195438
Complete genome (Accession number NC_001318)	hypothetical protein BB0592	611309	612022	+		15594937	1195439
Complete genome (Accession number NC_001318)	long-chain-fatty-acid CoA ligase	612048	613985	+		15594938	1195440
Complete genome (Accession number NC_001318)	arginyl-tRNA synthetase	614014	615789	-		15594939	1195441
Complete genome (Accession number NC_001318)	hypothetical protein BB0595	615764	616390	-		15594940	1195442

Complete genome (Accession number NC_001318)	methyl-accepting chemotaxis protein (mcp-2)	616412	618559	-		15594941	1195443
Complete genome (Accession number NC_001318)	methyl-accepting chemotaxis protein (mcp-3)	618828	621035	+		15594942	1195444
Complete genome (Accession number NC_001318)	UDP-N-acetylmuramate dehydrogenase (murB)	621045	621953	-		15594943	1195445
Complete genome (Accession number NC_001318)	cysteinyl-tRNA synthetase (cysS)	622005	623447	+		15594944	1195446
Complete genome (Accession number NC_001318)	hypothetical protein BB0600	623451	625007	+		15594945	1195447
Complete genome (Accession number NC_001318)	serine hydroxymethyltransferase (glyA)	625007	626260	+		15594946	1195448
Complete genome (Accession number NC_001318)	chaperonin, putative	626286	627038	+		15594947	1195449
Complete genome (Accession number NC_001318)	membrane-associated protein p66	627092	628948	-		15594948	1195450
Complete genome (Accession number NC_001318)	L-lactate permease (lctP)	629196	630698	-		15594949	1195451
Complete genome (Accession number NC_001318)	serine-type D-Ala-D-Ala carboxypeptidase (dacA)	630769	631986	+		15594950	1195452
Complete genome (Accession number NC_001318)	hypothetical protein BB0606	631991	632482	+		15594951	1195453

Complete genome (Accession number NC_001318)	rep helicase, single-stranded DNA-dependent ATPase (rep)	632485	634464	+		15594952	1195454
Complete genome (Accession number NC_001318)	aminoacyl-histidine dipeptidase (pepD)	634581	636011	+		15594953	1195455
Complete genome (Accession number NC_001318)	hypothetical protein BB0609	636024	636134	-		15594954	1195456
Complete genome (Accession number NC_001318)	trigger factor	636593	637957	+		15594955	1195459
Complete genome (Accession number NC_001318)	ATP-dependent Clp protease proteolytic component (clpP-1)	637963	638556	+		15594956	1195460
Complete genome (Accession number NC_001318)	ATP-dependent protease ATP-binding subunit	638580	639872	+		15594957	1195461
Complete genome (Accession number NC_001318)	ATP-dependent protease LA (lon-2)	639808	642249	+		15594958	1195462
Complete genome (Accession number NC_001318)	hypothetical protein BB0614	642289	642441	+		15594959	1195463
Complete genome (Accession number NC_001318)	30S ribosomal protein S4	642500	643129	-		15594960	1195464

Complete genome (Accession number NC_001318)	hypothetical protein BB0616	643295	644650	-		15594961	1195465
Complete genome (Accession number NC_001318)	hypothetical protein BB0617	644772	645140	+		15594962	1195466
Complete genome (Accession number NC_001318)	cytidine deaminase (cdd)	645137	645601	-		15594963	1195467
Complete genome (Accession number NC_001318)	hypothetical protein BB0619	645689	646681	+		15594964	1195468
Complete genome (Accession number NC_001318)	beta-glucosidase, putative	646659	648326	-		15594965	1195469
Complete genome (Accession number NC_001318)	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ)	648553	649107	+		15594966	1195471
Complete genome (Accession number NC_001318)	acetate kinase (ackA)	649170	650411	-		15594967	1195472
Complete genome (Accession number NC_001318)	transcription-repair coupling factor (mfd)	650413	653790	-		15594968	1195473
Complete genome (Accession number NC_001318)	hypothetical protein BB0624	653887	654849	+		15594969	1195474
Complete genome (Accession number NC_001318)	N-acetylmuramoyl-L-alanine amidase, putative	654809	656902	+		15594970	1195475

Complete genome (Accession number NC_001318)	hypothetical protein BB0626	656998	657543	-		15594971	1195477
Complete genome (Accession number NC_001318)	putative aminopeptidase 2	657546	658817	-		15594972	1195478
Complete genome (Accession number NC_001318)	hypothetical protein BB0628	658898	659623	+		15594973	1195479
Complete genome (Accession number NC_001318)	PTS system, fructose-specific IIABC component (fruA-2)	659644	661524	-		15594974	1195480
Complete genome (Accession number NC_001318)	1-phosphofructokinase (fruK)	661606	662529	+		15594975	1195481
Complete genome (Accession number NC_001318)	hypothetical protein BB0631	662603	662917	-		15594976	1195482
Complete genome (Accession number NC_001318)	exodeoxyribonuclease V, alpha chain (recD)	663179	665011	-		15594977	1195484
Complete genome (Accession number NC_001318)	exodeoxyribonuclease V, beta chain (recB)	665008	668517	-		15594978	1195485
Complete genome (Accession number NC_001318)	exodeoxyribonuclease V, gamma chain (recC)	668848	671763	-		15594979	1195486
Complete genome (Accession number NC_001318)	nicotinate phosphoribosyltransferase	671767	673212	-		15594980	1195487

Complete genome (Accession number NC_001318)	glucose-6-phosphate 1-dehydrogenase	673342	674778	+		15594981	1195488
Complete genome (Accession number NC_001318)	Na+/H+ antiporter (nhaC-1)	675029	676378	+		15594982	1195489
Complete genome (Accession number NC_001318)	Na+/H+ antiporter (nhaC-2)	676472	677860	+		15594983	1195490
Complete genome (Accession number NC_001318)	spermidine/putrescine ABC transporter, spermidine/putrescine-binding periplasmic protein (potD)	677892	678938	-		15594984	1195491
Complete genome (Accession number NC_001318)	spermidine/putrescine ABC transporter, permease protein (potC)	678959	679750	-		15594985	1195492
Complete genome (Accession number NC_001318)	spermidine/putrescine ABC transporter, permease protein (potB)	679754	680563	-		15594986	1195493
Complete genome (Accession number NC_001318)	spermidine/putrescine ABC transporter, ATP-binding protein (potA)	680563	681606	-		15594987	1195494
Complete genome (Accession number NC_001318)	ribosomal biogenesis GTPase	681685	682524	-		15594988	1195495

Complete genome (Accession number NC_001318)	N-acetylmannosamine-6-phosphate 2-epimerase	682679	683377	+		15594989	1195496
Complete genome (Accession number NC_001318)	PTS system, glucose-specific IIBC component (ptsG)	683423	684967	+		15594990	1195497
Complete genome (Accession number NC_001318)	hypothetical protein BB0646	684997	685980	-		15594991	1195498
Complete genome (Accession number NC_001318)	ferric uptake regulation protein (fur)	685977	686507	-		15594992	1195499
Complete genome (Accession number NC_001318)	serine/threonine kinase, putative	686607	688295	-		15594993	1195500
Complete genome (Accession number NC_001318)	chaperonin GroEL	688490	690127	+		15594994	1195501
Complete genome (Accession number NC_001318)	hypothetical protein BB0650	690151	690489	+		15594995	1195502
Complete genome (Accession number NC_001318)	hypothetical protein BB0651	690482	690799	+		15594996	1195503
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecD	690885	692645	+		15594997	1195504
Complete genome (Accession number NC_001318)	preprotein translocase subunit SecF	692629	693528	+		15594998	1195505

Complete genome (Accession number NC_001318)	hypothetical protein BB0654	693554	694696	+		15594999	1195506
Complete genome (Accession number NC_001318)	heat shock protein (dnaJ-2)	694693	695523	-		15595000	1195507
Complete genome (Accession number NC_001318)	oxygen-independent coproporphyrinogen III oxidase, putative	695631	696764	+		15595001	1195508
Complete genome (Accession number NC_001318)	ribose 5-phosphate isomerase (rpi)	696751	697437	-		15595002	1195509
Complete genome (Accession number NC_001318)	phosphoglycerate mutase (gpmA)	697571	698332	+		15595003	1195510
Complete genome (Accession number NC_001318)	lysyl-tRNA synthetase	698400	699965	-		15595004	1195511
Complete genome (Accession number NC_001318)	GTP-binding protein Era	700052	700924	-		15595005	1195512
Complete genome (Accession number NC_001318)	hypothetical protein BB0661	701014	701385	+		15595006	1195513
Complete genome (Accession number NC_001318)	hypothetical protein BB0662	701395	701805	+		15595007	1195514
Complete genome (Accession number NC_001318)	hypothetical protein BB0663	701825	702274	+		15595008	1195515
Complete genome (Accession number NC_001318)	hypothetical protein BB0664	702283	702966	-		15595009	1195516

Complete genome (Accession number NC_001318)	hypothetical protein BB0665	703009	703968	+		15595010	1195517
Complete genome (Accession number NC_001318)	hypothetical protein BB0666	703931	704959	+		15595011	1195518
Complete genome (Accession number NC_001318)	hypothetical protein BB0667	704949	705500	+		15595012	1195519
Complete genome (Accession number NC_001318)	flagellar filament outer layer protein (flaA)	705571	706605	+		15595013	1195520
Complete genome (Accession number NC_001318)	chemotaxis histidine kinase (cheA-2)	706673	709267	+		15595014	1195521
Complete genome (Accession number NC_001318)	purine-binding chemotaxis protein (cheW-3)	709274	710674	+		15595015	1195522
Complete genome (Accession number NC_001318)	chemotaxis operon protein (cheX)	710686	711171	+		15595016	1195523
Complete genome (Accession number NC_001318)	chemotaxis response regulator (cheY-3)	711211	711651	+		15595017	1195524
Complete genome (Accession number NC_001318)	hypothetical protein BB0673	711692	712207	-		15595018	1195525
Complete genome (Accession number NC_001318)	hypothetical protein BB0674	712204	713250	-		15595019	1195526
Complete genome (Accession number NC_001318)	hypothetical protein BB0675	713244	714107	-		15595020	1195527

Complete genome (Accession number NC_001318)	phosphoglycolate phosphatase (gph)	714104	714766	-		15595021	1195528
Complete genome (Accession number NC_001318)	ribose/galactose ABC transporter, ATP-binding protein (mglA)	715009	716619	+		15595022	1195529
Complete genome (Accession number NC_001318)	ribose/galactose ABC transporter, permease protein (rbsC-1)	716620	717771	+		15595023	1195530
Complete genome (Accession number NC_001318)	ribose/galactose ABC transporter, permease protein (rbsC-2)	717734	718669	+		15595024	1195531
Complete genome (Accession number NC_001318)	methyl-accepting chemotaxis protein (mcp-4)	718827	721088	+		15595025	1195532
Complete genome (Accession number NC_001318)	methyl-accepting chemotaxis protein (mcp-5)	721110	723020	+		15595026	1195533
Complete genome (Accession number NC_001318)	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	723063	724130	-		15595027	1195534
Complete genome (Accession number NC_001318)	3-hydroxy-3-methylglutaryl-CoA synthase	724224	725447	+		15595028	1195535

Complete genome (Accession number NC_001318)	isopentenyl pyrophosphate isomerase	725413	726495	+		15595029	1195536
Complete genome (Accession number NC_001318)	3-hydroxy-3-methylglutaryl-CoA reductase (mvaA)	726458	727753	+		15595030	1195537
Complete genome (Accession number NC_001318)	mevalonate pyrophosphate decarboxylase	727737	728675	+		15595031	1195538
Complete genome (Accession number NC_001318)	phosphomevalonate kinase, putative	728666	729619	+		15595032	1195539
Complete genome (Accession number NC_001318)	mevalonate kinase	729613	730506	+		15595033	1195540
Complete genome (Accession number NC_001318)	hypothetical protein BB0689	730632	731099	-		15595034	1195542
Complete genome (Accession number NC_001318)	neutrophil activating protein (napA)	731151	731720	+		15595035	1195543
Complete genome (Accession number NC_001318)	elongation factor G	731794	733803	+		15595036	1195544
Complete genome (Accession number NC_001318)	hypothetical protein BB0692	733809	733922	+		15595037	1195545
Complete genome (Accession number NC_001318)	xylose operon regulatory protein (xylR-1)	734081	735289	+		15595038	1195546
Complete genome (Accession number NC_001318)	signal recognition particle protein (ffh)	735343	736686	+		15595039	1195547

Complete genome (Accession number NC_001318)	30S ribosomal protein S16	736699	736959	+		15595040	1195548
Complete genome (Accession number NC_001318)	hypothetical protein BB0696	736960	737208	+		15595041	1195549
Complete genome (Accession number NC_001318)	hypothetical protein BB0697	737212	737712	+		15595042	1195550
Complete genome (Accession number NC_001318)	tRNA (guanine-N(1)-)-methyltransferase	737709	738428	+		15595043	1195551
Complete genome (Accession number NC_001318)	50S ribosomal protein L19	738406	738771	+		15595044	1195552
Complete genome (Accession number NC_001318)	hypothetical protein BB0700	738851	738964	+		15595045	1195553
Complete genome (Accession number NC_001318)	hypothetical protein BB0701	739144	739683	+		15595046	1195554
Complete genome (Accession number NC_001318)	lipopolysaccharide biosynthesis-related protein (kdtB)	739685	740176	+		15595047	1195555
Complete genome (Accession number NC_001318)	50S ribosomal protein L32	740240	740422	+		15595048	1195556
Complete genome (Accession number NC_001318)	acyl carrier protein	740446	740688	+		15595049	1195557
Complete genome (Accession number NC_001318)	ribonuclease III (rnc)	740685	741425	+		15595050	1195558

Complete genome (Accession number NC_001318)	polynucleotide adenylyltransferase (papS)	741396	742628	-		15595051	1195559
Complete genome (Accession number NC_001318)	hypothetical protein BB0707	742690	744516	+		15595052	1195560
Complete genome (Accession number NC_001318)	hypothetical protein BB0708	744522	744845	+		15595053	1195561
Complete genome (Accession number NC_001318)	hypothetical protein BB0709	745302	746333	+		15595054	1195563
Complete genome (Accession number NC_001318)	DNA primase (dnaG)	746339	747910	+		15595055	1195564
Complete genome (Accession number NC_001318)	hypothetical protein BB0711	747925	748119	+		15595056	1195565
Complete genome (Accession number NC_001318)	RNA polymerase sigma factor RpoD	748123	750018	+		15595057	1195566
Complete genome (Accession number NC_001318)	hypothetical protein BB0713	750028	750789	+		15595058	1195567
Complete genome (Accession number NC_001318)	hypothetical protein BB0714	751191	752159	+		15595059	1195568
Complete genome (Accession number NC_001318)	rod shape-determining protein (mreB-1)	752134	753219	+		15595060	1195569
Complete genome (Accession number NC_001318)	rod shape-determining protein (mreC)	753223	754068	+		15595061	1195570
Complete genome (Accession number NC_001318)	hypothetical protein BB0717	754068	754550	+		15595062	1195571

Complete genome (Accession number NC_001318)	penicillin-binding protein (pbp-2)	754550	756349	+		15595063	1195572
Complete genome (Accession number NC_001318)	rod shape-determining protein (mreB-2)	756291	757670	+		15595064	1195573
Complete genome (Accession number NC_001318)	threonyl-tRNA synthetase (thrZ)	757836	759581	+		15595065	1195574
Complete genome (Accession number NC_001318)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	759586	760215	+		15595066	1195575
Complete genome (Accession number NC_001318)	hypothetical protein BB0722	760202	761647	+		15595067	1195576
Complete genome (Accession number NC_001318)	hypothetical protein BB0723	761621	762154	-		15595068	1195577
Complete genome (Accession number NC_001318)	K+ transport protein (ntpJ)	762242	763573	+		15595069	1195578
Complete genome (Accession number NC_001318)	hypothetical protein BB0725	763570	764361	+		15595070	1195579
Complete genome (Accession number NC_001318)	ATP-binding protein (ylxH-3)	764371	765342	+		15595071	1195580
Complete genome (Accession number NC_001318)	diphosphate--fructose-6-phosphate 1-phosphotransferase	765370	766716	+		15595072	1195581

Complete genome (Accession number NC_001318)	coenzyme A disulfide reductase	766733	768067	-		15595073	1195582
Complete genome (Accession number NC_001318)	glutamate transporter (gltP)	768079	769470	-		15595074	1195583
Complete genome (Accession number NC_001318)	glucose-6-phosphate isomerase	769547	771145	-		15595075	1195584
Complete genome (Accession number NC_001318)	hypothetical protein BB0731	771162	771563	-		15595076	1195585
Complete genome (Accession number NC_001318)	penicillin-binding protein (pbp-3)	771570	774368	-		15595077	1195586
Complete genome (Accession number NC_001318)	hypothetical protein BB0733	774632	775462	+		15595078	1195587
Complete genome (Accession number NC_001318)	hypothetical protein BB0734	775666	776679	-		15595079	1195588
Complete genome (Accession number NC_001318)	rare lipoprotein A (rlpA)	776746	777573	+		15595080	1195589
Complete genome (Accession number NC_001318)	hypothetical protein BB0736	777625	777768	+		15595081	1195590
Complete genome (Accession number NC_001318)	histidine phosphokinase/phophatase, putative	777747	778754	+		15595082	1195591
Complete genome (Accession number NC_001318)	valyl-tRNA synthetase	778758	781385	+		15595083	1195592
Complete genome (Accession number NC_001318)	hypothetical protein BB0739	781486	782073	-		15595084	1195593

Complete genome (Accession number NC_001318)	hypothetical protein BB0740	782152	782829	-		15595085	1195594
Complete genome (Accession number NC_001318)	co-chaperonin GroES	782976	783257	-		15595086	1195595
Complete genome (Accession number NC_001318)	ABC transporter, ATP-binding protein	783324	785021	+		15595087	1195596
Complete genome (Accession number NC_001318)	hypothetical protein BB0743	785057	786754	+		15595088	1195597
Complete genome (Accession number NC_001318)	antigen, p83/100	786860	788962	+		15595089	1195598
Complete genome (Accession number NC_001318)	endonuclease III (nth)	789270	789938	+		15595090	1195601
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, permease protein (oppC-2)	789947	790807	-		15595091	1195602
Complete genome (Accession number NC_001318)	oligopeptide ABC transporter, permease protein (oppB-2)	790807	791787	-		15595092	1195603
Complete genome (Accession number NC_001318)	hypothetical protein BB0748	791794	792252	-		15595093	1195604
Complete genome (Accession number NC_001318)	hypothetical protein BB0749	792333	793625	+		15595094	1195605
Complete genome (Accession number NC_001318)	hypothetical protein BB0750	793693	793836	+		15595095	1195606

Complete genome (Accession number NC_001318)	hypothetical protein BB0751	793842	794915	-		15595096	1195607
Complete genome (Accession number NC_001318)	hypothetical protein BB0752	794875	796383	-		15595097	1195608
Complete genome (Accession number NC_001318)	membrane spanning protein, putative	796388	797122	-		15595098	1195609
Complete genome (Accession number NC_001318)	ABC transporter, ATP-binding protein	797119	798048	-		15595099	1195610
Complete genome (Accession number NC_001318)	ribonuclease Z	798057	799016	-		15595100	1195611
Complete genome (Accession number NC_001318)	hypothetical protein BB0756	799208	800275	-		15595101	1195612
Complete genome (Accession number NC_001318)	ATP-dependent Clp protease proteolytic subunit	800452	801072	+		15595102	1195613
Complete genome (Accession number NC_001318)	hypothetical protein BB0758	800996	801778	+		15595103	1195614
Complete genome (Accession number NC_001318)	hypothetical protein BB0759	801941	802798	-		15595104	1195616
Complete genome (Accession number NC_001318)	hypothetical protein BB0760	802838	803212	-		15595105	1195617
Complete genome (Accession number NC_001318)	hypothetical protein BB0761	803278	804165	+		15595106	1195618
Complete genome (Accession number NC_001318)	hypothetical protein BB0762	804240	804353	-		15595107	1195619

Complete genome (Accession number NC_001318)	response regulatory protein (rrp-2)	804417	805778	-		15595108	1195620
Complete genome (Accession number NC_001318)	sensory transduction histidine kinase, putative	805775	806923	-		15595109	1195621
Complete genome (Accession number NC_001318)	hypothetical protein BB0765	806920	807966	-		15595110	1195622
Complete genome (Accession number NC_001318)	colicin V production protein, putative	807976	808464	-		15595111	1195623
Complete genome (Accession number NC_001318)	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (murG)	808461	809552	-		15595112	1195624
Complete genome (Accession number NC_001318)	pyridoxal kinase (pdxK)	809701	810495	-		15595113	1195625
Complete genome (Accession number NC_001318)	O-sialoglycoprotein endopeptidase	810470	811510	-		15595114	1195626
Complete genome (Accession number NC_001318)	hypothetical protein BB0770	811507	812388	-		15595115	1195627
Complete genome (Accession number NC_001318)	RNA polymerase sigma factor (rpoS)	812439	813239	-		15595116	1195628

Complete genome (Accession number NC_001318)	flagellar basal body P-ring protein	813690	814697	-		15595117	1195629
Complete genome (Accession number NC_001318)	hypothetical protein BB0773	814868	815302	-		15595118	1195630
Complete genome (Accession number NC_001318)	flagellar basal body rod protein FlgG	815502	816299	-		15595119	1195631
Complete genome (Accession number NC_001318)	flagellar hook-basal body complex protein (flhO)	816312	817214	-		15595120	1195632
Complete genome (Accession number NC_001318)	hypothetical protein BB0776	817393	817956	+		15595121	1195633
Complete genome (Accession number NC_001318)	adenine phosphoribosyltransferase	818018	818548	+		15595122	1195634
Complete genome (Accession number NC_001318)	50S ribosomal protein L21	818605	818916	+		15595123	1195635
Complete genome (Accession number NC_001318)	hypothetical protein BB0779	818922	819242	+		15595124	1195636
Complete genome (Accession number NC_001318)	50S ribosomal protein L27	819242	819487	+		15595125	1195637
Complete genome (Accession number NC_001318)	GTPase ObgE	819542	820528	+		15595126	1195638
Complete genome (Accession number NC_001318)	hypothetical protein BB0782	820568	821188	+		15595127	1195639

Complete genome (Accession number NC_001318)	hypothetical protein BB0783	821185	822369	+		15595128	1195640
Complete genome (Accession number NC_001318)	hypothetical protein BB0784	822335	822694	+		15595129	1195641
Complete genome (Accession number NC_001318)	regulatory protein SpoVG	822810	823103	+		15595130	1195642
Complete genome (Accession number NC_001318)	50S ribosomal protein L25/general stress protein Ctc	823263	823811	+		1,62E+08	1195643
Complete genome (Accession number NC_001318)	peptidyl-tRNA hydrolase	823816	824382	+		15595132	1195645
Complete genome (Accession number NC_001318)	hypothetical protein BB0788	824382	825704	+		15595133	1195646
Complete genome (Accession number NC_001318)	cell division protein (ftsH)	825701	827620	+		15595134	1195647
Complete genome (Accession number NC_001318)	hypothetical protein BB0790	827625	829112	+		15595135	1195648
Complete genome (Accession number NC_001318)	thymidine kinase (tdk)	829218	830321	+		15595136	1195649
Complete genome (Accession number NC_001318)	hypothetical protein BB0792	830318	830941	-		15595137	1195650
Complete genome (Accession number NC_001318)	thymidylate kinase (tmk)	830955	831728	-		15595138	1195651
Complete genome (Accession number NC_001318)	hypothetical protein BB0794	831646	836043	+		15595139	1195652
Complete genome (Accession number NC_001318)	outer membrane protein	836061	838526	+		15595140	1195653

Complete genome (Accession number NC_001318)	hypothetical protein BB0796	838523	839080	+		15595141	1195654
Complete genome (Accession number NC_001318)	DNA mismatch repair protein	839244	841832	+		15595142	1195655
Complete genome (Accession number NC_001318)	competence protein F, putative	841834	842451	+		15595143	1195656
Complete genome (Accession number NC_001318)	hypothetical protein BB0799	842501	842989	+		15595144	1195657
Complete genome (Accession number NC_001318)	transcription elongation factor NusA	843003	844451	+		15595145	1195658
Complete genome (Accession number NC_001318)	translation initiation factor IF-2	844454	847102	+		15595146	1195659
Complete genome (Accession number NC_001318)	ribosome-binding factor A (rbfA)	847105	847488	+		15595147	1195660
Complete genome (Accession number NC_001318)	tRNA pseudouridine 55 synthase (truB)	847491	848339	+		15595148	1195661
Complete genome (Accession number NC_001318)	30S ribosomal protein S15	848538	848804	+		15595149	1195662
Complete genome (Accession number NC_001318)	polynucleotide phosphorylase/polyadenylase	848819	850987	+		15595150	1195663
Complete genome (Accession number NC_001318)	hypothetical protein BB0806	850994	852514	+		15595151	1195664

Complete genome (Accession number NC_001318)	hypothetical protein BB0807	852489	853778	+		15595152	1195665
Complete genome (Accession number NC_001318)	hypothetical protein BB0808	853775	854842	+		15595153	1195666
Complete genome (Accession number NC_001318)	tRNA-guanine transglycosylase (tgt)	854869	855996	+		15595154	1195667
Complete genome (Accession number NC_001318)	virulence factor mviN protein (mviN) (SP:P37169)	855971	857509	+		15595155	1195668
Complete genome (Accession number NC_001318)	hypothetical protein BB0811	857506	858915	+		15595156	1195669
Complete genome (Accession number NC_001318)	pantothenate metabolism flavoprotein (dfp)	858939	860111	-		15595157	1195670
Complete genome (Accession number NC_001318)	hypothetical protein BB0813	860186	860362	+		15595158	1195671
Complete genome (Accession number NC_001318)	sodium/panthothenate symporter	860440	861774	+		15595159	1195672
Complete genome (Accession number NC_001318)	hypothetical protein BB0815	861784	862677	+		15595160	1195673
Complete genome (Accession number NC_001318)	hypothetical protein BB0816	862696	863646	+		15595161	1195674

Complete genome (Accession number NC_001318)	UDP-N-acetylmuramate--L-alanine ligase	863636	865042	+		15595162	1195675
Complete genome (Accession number NC_001318)	hypothetical protein BB0818	865053	865919	+		15595163	1195676
Complete genome (Accession number NC_001318)	cytidylate kinase	865916	866458	+		15595164	1195677
Complete genome (Accession number NC_001318)	hypothetical protein BB0820	866494	866694	+		15595165	1195678
Complete genome (Accession number NC_001318)	2-methylthio-N6-isopentyladenosine tRNA modification enzyme (miaA)	866681	867601	+		15595166	1195679
Complete genome (Accession number NC_001318)	hypothetical protein BB0822	867605	867700	+		15595167	1195680
Complete genome (Accession number NC_001318)	hypothetical protein BB0823	867743	868114	-		15595168	1195681
Complete genome (Accession number NC_001318)	hypothetical protein BB0824	868189	868740	+		15595169	1195682
Complete genome (Accession number NC_001318)	hypothetical protein BB0825	868733	869515	-		15595170	1195683
Complete genome (Accession number NC_001318)	hypothetical protein BB0826	869508	870023	-		15595171	1195684
Complete genome (Accession number NC_001318)	ATP-dependent helicase (hrpA)	870112	872583	-		15595172	1195685

Complete genome (Accession number NC_001318)	DNA topoisomerase I (topA)	872586	875132	-		15595173	1195686
Complete genome (Accession number NC_001318)	exonuclease SbcD (sbcD)	875207	876448	+		15595174	1195687
Complete genome (Accession number NC_001318)	exonuclease SbcC (sbcC)	876429	879281	+		15595175	1195688
Complete genome (Accession number NC_001318)	xylose operon regulatory protein (xylR-2)	879303	880250	+		15595176	1195689
Complete genome (Accession number NC_001318)	hypothetical protein BB0832	880267	881091	-		15595177	1195690
Complete genome (Accession number NC_001318)	isoleucyl-tRNA synthetase	881085	884213	-		15595178	1195691
Complete genome (Accession number NC_001318)	ATP-dependent Clp protease, subunit C (clpC)	884228	886447	-		15595179	1195692
Complete genome (Accession number NC_001318)	phosphomannomutase (cpsG)	886470	888182	-		15595180	1195693
Complete genome (Accession number NC_001318)	excinuclease ABC subunit B	888297	890318	+		15595181	1195694
Complete genome (Accession number NC_001318)	excinuclease ABC, subunit A (uvrA)	890322	893174	+		15595182	1195695
Complete genome (Accession number NC_001318)	hypothetical protein BB0838	893129	896569	+		15595183	1195696
Complete genome (Accession number NC_001318)	hypothetical protein BB0839	897096	897740	-		15595184	1195697

Complete genome (Accession number NC_001318)	hypothetical protein BB0840	897704	899320	-		15595185	1195698
Complete genome (Accession number NC_001318)	arginine deiminase (arcA)	899499	900731	+		15595186	1195699
Complete genome (Accession number NC_001318)	ornithine carbamoyltransferase, catabolic (arcB)	900796	901782	+		15595187	1195700
Complete genome (Accession number NC_001318)	hypothetical protein BB0843	901810	903258	+		15595188	1195701
Complete genome (Accession number NC_001318)	hypothetical protein BB0844	903929	904900	-		15595189	1195702
Complete genome (Accession number NC_001318)	hypothetical protein BB0845	905120	905227	+		15595190	1195703
Complete genome (Accession number NC_001318)	hypothetical protein BB0846	905752	905865	-		15595191	1195704
Complete genome (Accession number NC_001318)	hypothetical protein BB0847	905839	905946	+		15595192	1195705
Complete genome (Accession number NC_001318)	hypothetical protein BB0848	905928	906032	+		15595193	1195706
Complete genome (Accession number NC_001318)	hypothetical protein BB0849	906162	906263	+		15595194	1195707
Complete genome (Accession number NC_001318)	hypothetical protein BB0851	907935	908081	+		15595195	1195708
Complete genome (Accession number NC_001318)	hypothetical protein BB0852	908407	909591	+		15595196	1195709

Fig. 28. Borrelia afzelli

Plasmid or genome	Product Name	Start	End	Strand	Length	Gi	GeneID
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4000	63	632	+	189	111074075	4227522
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4001	671	916	-	81	111074076	4227523
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4002	1038	1367	-	109	111074077	4227524
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4003	1371	1568	-	65	111074078	4227525
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4004	1642	2457	-	271	111074079	4227485
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4005	2569	3081	-	170	111074080	4227486
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4006	3078	3956	-	292	111074081	4227487
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4007	3953	4285	-	110	111074082	4227488
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4008	4403	4564	+	53	111074083	4227489

Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4009	4795	4875	-	26	111074084	4227490
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4010	4877	4996	-	39	111074085	4227491
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4011	5038	5883	-	281	111074086	4227492
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4012	5887	6519	-	210	111074087	4227493
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4013	6513	7817	-	434	111074088	4227494
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4014	7825	8061	-	78	111074089	4227495
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4015	8058	8180	-	40	111074090	4227496
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4016	8186	8503	-	105	111074091	4227497
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4017	8519	8947	-	142	111074092	4227498
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4018	8961	10073	-	370	111074093	4227499

Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4019	10054	10623	-	189	111074094	4227500
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4020	10620	11006	-	128	111074095	4227501
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4021	10994	11377	-	127	111074096	4227502
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4022	11377	11832	-	151	111074097	4227503
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4023	11851	12810	-	319	111074098	4227504
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4024	12832	13404	-	190	111074099	4227505
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4025	13429	14187	-	252	111074100	4227506
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4026	14195	14758	-	187	111074101	4227507
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4027	14770	15465	-	231	111074102	4227508
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4028	15482	16705	-	407	111074103	4227266

Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4029	16771	18123	-	450	111074104	4227267
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4030	18154	18639	-	161	111074105	4227509
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4031	18809	19525	+	238	111074106	4227510
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4032	19660	20169	-	169	111074107	4227511
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4033	20281	20901	-	206	111074108	4227512
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4034	20929	21477	-	182	111074109	4227513
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4035	21910	22686	+	258	111074110	4227514
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4036	22691	23038	-	115	111074111	4227515
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4037	23168	24496	-	442	111074112	4227516
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4038	25236	25760	-	174	111074113	4227517

Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4039	25773	26330	-	185	111074114	4227518
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4040	26372	27127	-	251	111074115	4227519
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4041	27103	27681	-	192	111074116	4227520
Plasmid cp30 (Accession number NC_008273)	hypothetical protein BAPKO_4042	27691	28785	-	364	111074117	4227521
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5000	46	327	+	93	111074119	4227268
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5001	311	757	-	148	111074120	4227269
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5002	843	2192	-	449	111074121	4227270
Plasmid cp27 (Accession number NC_008274)	PTS system, cellobiose-specific IIC component	2436	3758	-	440	111074122	4227271
Plasmid cp27 (Accession number NC_008274)	PTS system, cellobiose-specific IIA component	3961	4308	+	115	111074123	4227272

Plasmid cp27 (Accession number NC_008274)	PTS system, cellobiose-specific IIB component	4317	4643	+	108	111074124	4227273
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5006	4645	5742	+	365	111074125	4227274
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5007	5764	6393	-	209	111074126	4227275
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5008	6535	7563	+	342	111074127	4227276
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5009	7695	8633	+	312	111074128	4227277
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5010	8633	9151	+	172	111074129	4227278
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5011	9127	9888	+	253	111074130	4227279
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5012	9954	10523	+	189	111074131	4227280
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5013	10773	11270	-	165	111074132	4227281

Plasmid cp27 (Accession number NC_008274)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	12028	13620	+	530	111074133	4227282
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5015	13672	13800	-	42	111074134	4227283
Plasmid cp27 (Accession number NC_008274)	inositol-5-monophosphate dehydrogenase	13901	15112	-	403	111074135	4227284
Plasmid cp27 (Accession number NC_008274)	bifunctional GMP synthase/glutamine amidotransferase protein	15137	16672	-	511	111074136	4227285
Plasmid cp27 (Accession number NC_008274)	outer surface protein C	16925	17563	+	212	111074137	4227286
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5019	17997	19352	-	451	111074138	4227287
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5020	19461	20816	-	451	111074139	4227288
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5021	20891	21394	-	167	111074140	4227289
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5022	21369	21881	-	170	111074141	4227290

Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5023	21928	22623	+	231	111074142	4227291
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5024	22633	23184	-	183	111074143	4227292
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5025	23286	24530	+	414	111074144	4227293
Plasmid cp27 (Accession number NC_008274)	hypothetical protein BAPKO_5026	24831	24926	-	31	111074145	4227294
Plasmid cp27 (Accession number NC_008274)	PTS system, maltose and glucose-specific IIABC component	24925	26487	+	520	111074146	4227295
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2000	782	1336	-	184	117621571	4491022
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2001	1691	2500	+	269	117621572	4491023
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2002	2785	2973	+	62	117621573	4491024
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2003	3222	3707	+	161	117621574	4491025
Plasmid lp60 (Accession number NC_008564)	outer membrane protein	3949	4467	+	172	117621575	4491026
Plasmid lp60 (Accession number NC_008564)	antigen, S2	4545	5387	-	280	117621576	4491027
Plasmid lp60 (Accession number NC_008564)	antigen, S1	5488	6735	-	415	117621577	4491028

Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2007	6967	7086	-	39	117621578	4491029
Plasmid lp60 (Accession number NC_008564)	chpAI protein, putative	7147	7617	-	156	117621579	4491050
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2009	7788	8123	+	111	117621580	4491051
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2010	8120	8992	+	290	117621581	4491052
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2011	8995	9621	+	208	117621582	4491053
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2012	9677	10711	+	344	117621583	4491054
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2013	10735	10914	+	59	117621584	4491055
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2014	10911	11330	+	139	117621585	4491056
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2015	11320	11685	+	121	117621586	4491057
Plasmid lp60 (Accession number NC_008564)	outer surface protein A	11891	12712	+	273	117621587	4491058
Plasmid lp60 (Accession number NC_008564)	outer surface protein B	12726	13625	+	299	117621588	4491059
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2018	14200	15399	+	399	117621589	4491060
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2019	15447	16031	+	194	117621590	4491061
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2020	16007	16759	+	250	117621591	4491062

Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2021	16789	17334	+	181	117621592	4491063
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2022	17599	17718	+	39	117621593	4491064
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2023	18044	18475	+	143	117621594	4491065
Plasmid lp60 (Accession number NC_008564)	decorin binding protein A	18591	19103	-	170	117621595	4491066
Plasmid lp60 (Accession number NC_008564)	decorin binding protein B	19219	19770	-	183	117621596	4491067
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2026	20199	20516	-	105	117621597	4491068
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2027	20638	21231	+	197	117621598	4491069
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2028	21235	22587	+	450	117621599	4491070
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2029	22676	22804	+	42	117621600	4491071
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2030	22886	23311	+	141	117621601	4491072
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2031	23444	23638	+	64	117621602	4491073
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2032	23801	24340	+	179	117621603	4491074
Plasmid lp60 (Accession number NC_008564)	oligopeptide ABC transporter, periplasmic	24430	26016	-	528	117621604	4491075
Plasmid lp60 (Accession number NC_008564)	lipoprotein	26531	27181	+	216	117621605	4491076

Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2035	27289	27897	+	202	117621606	4491077
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2036	28263	29492	+	409	117621607	4491078
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2037	29504	30103	+	199	117621608	4491079
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2038	30158	30769	+	203	117621609	4491080
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2039	30786	31703	+	305	117621610	4491081
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2040	31706	32161	+	151	117621611	4491082
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2041	32158	32547	+	129	117621612	4491083
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2042	32544	32897	+	117	117621613	4491084
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2043	32894	33433	+	179	117621614	4491085
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2044	33492	34562	+	356	117621615	4491086
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2045	34562	34984	+	140	117621616	4491087
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2046	35026	35517	+	163	117621617	4491088
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2047	35510	35728	+	72	117621618	4491030
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2048	35737	37116	+	459	117621619	4491031

Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2049	37147	37710	+	187	117621620	4491032
Plasmid lp60 (Accession number NC_008564)	outer membrane protein	37750	38667	+	305	117621621	4491033
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2051	38748	39026	+	92	117621622	4491034
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2052	39056	39328	+	90	117621623	4491035
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2053	39391	40329	+	312	117621624	4491036
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2054	40319	40882	+	187	117621625	4491037
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2055	40946	42145	-	399	117621626	4491038
Plasmid lp60 (Accession number NC_008564)	lipoprotein	42628	42861	-	77	117621627	4491039
Plasmid lp60 (Accession number NC_008564)	surface lipoprotein P27	42958	43734	-	258	117621628	4491040
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2058	44112	44738	-	208	117621629	4491041
Plasmid lp60 (Accession number NC_008564)	lipoprotein	44987	45166	+	59	117621630	4491042
Plasmid lp60 (Accession number NC_008564)	antigen, P35	45371	46345	-	324	117621631	4491043
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2061	46511	47362	-	283	117621632	4491044
Plasmid lp60 (Accession number NC_008564)	antigen, P35, putative	47529	48776	-	415	117621633	4491045

Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2063	48934	49629	-	231	117621634	4491046
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2064	49707	50426	-	239	117621635	4491047
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2065	50661	51437	-	258	117621636	4491048
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2066	51638	52450	-	270	117621637	4491049
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2067	52651	53397	-	248	117621638	4491014
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2068	53673	54398	-	241	117621639	4491015
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2069	54670	55425	-	251	117621640	4491016
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2070	55736	56434	-	232	117621641	4491017
Plasmid lp60 (Accession number NC_008564)	antigen, P35, putative	56660	57541	-	293	117621642	4491018
Plasmid lp60 (Accession number NC_008564)	hypothetical protein BAPKO_2072	57699	57836	-	45	117621643	4491019
Plasmid lp60 (Accession number NC_008564)	outer membrane porin	58076	58897	+	273	117621644	4491020
Plasmid lp60 (Accession number NC_008564)	FAD-dependent thymidylate synthase	59105	59908	+	267	117621645	4491021
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2500	120	683	+	187	117621647	4491089
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2501	866	1363	+	165	117621648	4491090

Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2502	1360	1545	-	61	117621649	4491091
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2503	1777	1989	+	70	117621650	4491092
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2504	2513	3337	+	274	117621651	4491093
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2505	3901	4251	+	116	117621652	4491094
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2506	4400	5080	+	226	117621653	4491095
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2507	5952	6845	+	297	117621654	4491096
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2508	7447	11277	-	1276	117621655	4491097
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2509	11397	11627	-	76	117621656	4491098
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2510	11700	11903	-	67	117621657	4491099
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2511	11818	11961	-	47	117621658	4491100
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2512	12703	13620	+	305	117621659	4491101
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2513	13613	14179	+	188	117621660	4491102
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2514	14152	14907	+	251	117621661	4491103
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2515	15003	15632	+	209	117621662	4491104

Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2516	15791	16135	+	114	117621663	4491105
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2517	16427	16534	+	35	117621664	4491106
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2518	16914	17174	-	86	117621665	4491107
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2519	17628	18611	-	327	117621666	4491108
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2520	19291	20145	+	284	117621667	4491109
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2521	20892	21902	-	336	117621668	4491110
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2522	22598	23146	+	182	117621669	4491111
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2523	23546	24028	-	160	117621670	4491112
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2524	24605	24928	-	107	117621671	4491113
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2525	25621	26796	-	391	117621672	4491114
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2526	26919	27104	-	61	117621673	4491115
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2527	27194	31027	-	1277	117621674	4491116
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2528	32613	32786	+	57	117621675	4491117
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2529	32875	33033	-	52	117621676	4491118

Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2530	34078	34218	+	46	117621677	4491119
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2531	34708	34941	+	77	117621678	4491120
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2532	36466	36561	-	31	117621679	4491121
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2533	36485	36577	-	30	117621680	4491122
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2534	36811	36957	-	48	117621681	4491123
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2535	37016	37069	-	17	117621682	4491124
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2536	37128	37880	-	250	117621683	4491125
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2537	37856	38410	-	184	117621684	4491126
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2538	38452	39522	-	356	117621685	4491127
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2539	39691	39885	+	64	117621686	4491128
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2540	40723	40896	+	57	117621687	4491129
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2541	41188	41796	-	202	117621688	4491130
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2542	43297	44079	-	260	117621689	4491131
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2543	44529	44606	-	25	117621690	4491132

Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2544	45087	45770	-	227	117621691	4491133
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2545	46660	46971	+	103	117621692	4491134
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2546	47035	47256	-	73	117621693	4491135
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2547	47854	48042	+	62	117621694	4491136
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2548	48072	48290	+	72	117621695	4491137
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2549	48442	49368	-	308	117621696	4491138
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2550	49361	49819	-	152	117621697	4491139
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2551	50125	50427	-	100	117621698	4491140
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2552	51127	51678	+	183	117621699	4491141
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2553	51837	52424	-	195	117621700	4491142
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2554	55948	57054	+	368	117621701	4491143
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2555	57064	57300	+	78	117621702	4491144
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2556	57293	58045	+	250	117621703	4491145
Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2557	58340	58684	+	114	117621704	4491146

Plasmid lp60-2 (Accession number NC_008565)	hypothetical protein BAPKO_2558	58870	59328	+	152	117621705	4491147
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3000	921	1748	+	275	117621707	4491157
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3001	2473	2664	-	63	117621708	4491158
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3002	3113	3391	-	92	117621709	4491159
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3003	3345	3806	-	153	117621710	4491160
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3004	3796	3912	-	38	117621711	4491161
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3005	4259	4783	-	174	117621712	4491162
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3006	5150	5473	-	107	117621713	4491163
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3007	5657	5908	-	83	117621714	4491164
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3008	6922	7803	-	293	117621715	4491165
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3009	8618	8731	+	37	117621716	4491166
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3010	8863	9375	+	170	117621717	4491167
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3011	9826	10143	-	105	117621718	4491168
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3012	11425	12402	+	325	117621719	4491169

Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3013	12395	12874	+	159	117621720	4491170
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3014	12956	13693	+	245	117621721	4491171
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3015	13740	14360	+	206	117621722	4491172
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3016	15785	16540	-	251	117621723	4491173
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3017	17870	18028	+	52	117621724	4491174
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3018	18237	18410	+	57	117621725	4491175
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3019	18705	18905	+	66	117621726	4491176
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3020	19482	19679	-	65	117621727	4491177
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3021	19801	20007	-	68	117621728	4491178
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3022	20673	20780	-	35	117621729	4491179
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3023	20844	21080	-	78	117621730	4491180
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3024	22176	22337	-	53	117621731	4491181
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3025	24087	25163	-	358	117621732	4491182
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3026	25511	26326	+	271	117621733	4491183

Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3027	26254	26343	-	29	117621734	4491148
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3028	26358	26489	+	43	117621735	4491149
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3029	26500	26748	+	82	117621736	4491150
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3030	27001	27123	+	40	117621737	4491151
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3031	28470	28571	+	33	117621738	4491152
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3032	28516	29262	+	248	117621739	4491153
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3033	29847	31493	+	548	117621740	4491154
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3034	32390	33085	-	231	117621741	4491155
Plasmid lp34 (Accession number NC_008566)	hypothetical protein BAPKO_3035	33488	34153	+	221	117621742	4491156
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3500	598	1212	-	204	117621744	4491204
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3501	1714	1890	+	58	117621745	4491205
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3502	1863	2105	+	80	117621746	4491206
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3503	2247	2402	-	51	117621747	4491207
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3504	2426	2809	+	127	117621748	4491208

Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3505	2877	3035	+	52	117621749	4491209
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3506	3342	3674	+	110	117621750	4491210
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3507	3722	4102	+	126	117621751	4491211
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3508	4166	4321	+	51	117621752	4491212
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3509	4522	4776	+	84	117621753	4491213
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3510	5340	5537	+	65	117621754	4491214
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3511	5719	6273	+	184	117621755	4491215
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3512	6397	6852	+	151	117621756	4491216
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3513	7298	7624	+	108	117621757	4491217
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3514	7706	8302	+	198	117621758	4491218
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3515	8264	8374	-	36	117621759	4491219
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3516	8394	8510	+	38	117621760	4491220
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3517	9142	9468	-	108	117621761	4491221
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3518	9888	13100	+	1070	117621762	4491222

Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3519	13803	14180	+	125	117621763	4491223
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3520	14183	14701	+	172	117621764	4491224
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3521	14691	14912	+	73	117621765	4491225
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3522	14928	15380	+	150	117621766	4491226
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3523	15496	15654	+	52	117621767	4491227
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3524	15983	16051	+	22	117621768	4491228
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3525	16044	16397	+	117	117621769	4491229
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3526	16571	17122	+	183	117621770	4491230
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3527	16984	17187	-	67	117621771	4491184
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3528	17240	17329	+	29	117621772	4491185
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3529	17274	17435	+	53	117621773	4491186
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3530	17756	17926	-	56	117621774	4491187
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3531	17878	18561	-	227	117621775	4491188
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3532	18637	18795	-	52	117621776	4491189

Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3533	19187	20278	+	363	117621777	4491190
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3534	20288	20845	+	185	117621778	4491191
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3535	20821	21576	+	251	117621779	4491192
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3536	21620	22180	+	186	117621780	4491193
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3537	22193	22444	+	83	117621781	4491194
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3538	22965	23087	+	40	117621782	4491195
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3539	23555	23836	-	93	117621783	4491196
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3540	23848	24291	-	147	117621784	4491197
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3541	24303	24521	-	72	117621785	4491198
Plasmid lp32 (Accession number NC_008567)	outer surface protein D	25555	26034	+	159	117621786	4491199
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3543	26148	26282	+	44	117621787	4491200
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3544	26530	26595	-	21	117621788	4491201
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3545	26598	26840	-	80	117621789	4491202
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3546	27551	27685	-	44	117621790	4491203

Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3547	28099	28935	+	278	117621791	4491231
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3548	29331	29852	-	173	117621792	4491232
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3549	29895	30086	-	63	117621793	4491233
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3550	30228	30452	+	74	117621794	4491234
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3551	30445	30498	+	17	117621795	4491235
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3552	30521	30640	+	39	117621796	4491236
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3553	30809	31156	+	115	117621797	4491237
Plasmid lp32 (Accession number NC_008567)	hypothetical protein BAPKO_3554	31215	31841	+	208	117621798	4491238
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4500	351	542	-	63	117621800	4491239
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4501	699	926	-	75	117621801	4491240
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4502	1398	1670	-	90	117621802	4491241
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4503	1661	2401	-	246	117621803	4491242
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4504	4910	5569	+	219	117621804	4491243
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4505	6396	7079	+	227	117621805	4491244

Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4506	7231	7809	-	192	117621806	4491245
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4507	7986	8990	+	334	117621807	4491246
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4508	9140	9466	+	108	117621808	4491254
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4509	9622	10728	+	368	117621809	4491255
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4510	10600	10833	-	77	117621810	4491256
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4511	11681	11857	+	58	117621811	4491257
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4512	11916	12974	+	352	117621812	4491258
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4513	13919	14218	+	99	117621813	4491259
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4514	14600	15385	-	261	117621814	4491260
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4515	16400	17338	-	312	117621815	4491261
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4516	17467	17592	+	41	117621816	4491262
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4517	18068	18586	-	172	117621817	4491263
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4518	18866	18955	+	29	117621818	4491264
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4519	19045	19212	+	55	117621819	4491265

Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4520	19406	20053	+	215	117621820	4491266
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4521	20238	20570	-	110	117621821	4491267
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4522	20905	22041	+	378	117621822	4491268
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4523	22127	22345	-	72	117621823	4491269
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4524	22338	22457	-	39	117621824	4491270
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4525	22828	22908	+	26	117621825	4491271
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4526	22903	23469	-	188	117621826	4491272
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4527	23475	23708	-	77	117621827	4491247
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4528	23953	24729	+	258	117621828	4491248
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4529	24757	25074	+	105	117621829	4491249
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4530	25091	26446	-	451	117621830	4491250
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4531	26427	27755	-	442	117621831	4491251
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4532	27974	28156	-	60	117621832	4491252
Plasmid lp28 (Accession number NC_008568)	hypothetical protein BAPKO_4533	28389	28526	-	45	117621833	4491253

Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5500	685	1254	-	189	117621835	4491275
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5501	1351	2727	-	458	117621836	4491276
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5502	2747	3385	-	212	117621837	4491277
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5503	3469	3903	-	144	117621838	4491278
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5504	3928	5292	-	454	117621839	4491279
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5505	5658	6032	+	124	117621840	4491280
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5506	6025	6471	+	148	117621841	4491281
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5507	6497	6829	+	110	117621842	4491282
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5508	6842	9544	+	900	117621843	4491283
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5509	9544	10374	+	276	117621844	4491284
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5510	10383	10721	+	112	117621845	4491285
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5511	10738	11130	+	130	117621846	4491286
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5512	11127	11570	+	147	117621847	4491287
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5513	11560	12378	+	272	117621848	4491288

Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5514	12399	12827	+	142	117621849	4491289
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5515	12917	13114	+	65	117621850	4491290
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5516	13111	14988	+	625	117621851	4491291
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5517	15006	15458	+	150	117621852	4491292
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5518	15487	15564	+	25	117621853	4491293
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5519	15565	16116	+	183	117621854	4491294
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5520	16514	17086	+	190	117621855	4491295
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5521	17236	17775	+	179	117621856	4491296
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5522	17751	18512	+	253	117621857	4491297
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5523	18584	19141	+	185	117621858	4491298
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5524	19296	19838	-	180	117621859	4491299
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5525	19869	20411	-	180	117621860	4491300
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5526	20545	22722	+	725	117621861	4491301
Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5527	22650	23780	+	376	117621862	4491273

Plasmid lp25 (Accession number NC_008569)	hypothetical protein BAPKO_5528	23844	24347	-	167	117621863	4491274
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0001	531	1550	-	339	111114824	4227028
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0002	1538	3013	-	491	111114825	4227029
Complete genome (Accession number NC_008277)	phosphoglucomutase	3156	4946	+	596	111114826	4227030
Complete genome (Accession number NC_008277)	tryptophanyl-tRNA synthetase	5023	6069	-	348	111114827	4227031
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0005	6072	7160	-	362	111114828	4227032
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0006	7218	8075	-	285	111114829	4227033
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0007	8184	8954	+	256	111114830	4227034
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0008	8959	9963	+	334	111114831	4227174
Complete genome (Accession number NC_008277)	holo-acyl-carrier protein synthase, putative	9960	10334	+	124	111114832	4227175
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0010	10338	11177	+	279	111114833	4227176
Complete genome (Accession	tRNA pseudouridine synthase A	11178	11918	+	246	111114834	4227177

number NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0012	11911	12510	+	199	111114835	4227178
Complete genome (Accession number NC_008277)	primosomal protein N	12503	14494	+	663	111114836	4227179
Complete genome (Accession number NC_008277)	uridine kinase	14491	15114	-	207	111114837	4227180
Complete genome (Accession number NC_008277)	glpE protein	15114	15488	-	124	111114838	4227181
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0016	15616	16590	+	324	111114839	4227182
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0017	16587	17567	-	326	111114840	4227183
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0018	17574	18086	-	170	111114841	4227184
Complete genome (Accession number NC_008277)	diphosphate--fructose-6-phosphate 1-phosphotransferase	18094	19761	-	555	111114842	4227185
Complete genome (Accession number NC_008277)	S-adenosylmethionine: tRNA ribosyltransferase- isomerase	19841	20881	-	346	111114843	4227186
Complete genome (Accession number NC_008277)	Holliday junction DNA helicase B	20856	21899	-	347	111114844	4227187
Complete genome (Accession number	Holliday junction DNA helicase	21959	22549	-	196	111114845	4227188

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0023	22619	23758	+	379	111114846	4227189
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0024	23773	24504	-	243	111114847	4227190
Complete genome (Accession number NC_008277)	methylenetetrahydrofolate dehydrogenase	24505	25410	-	301	111114848	4227191
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0026	25557	26192	+	211	111114849	4227192
Complete genome (Accession number NC_008277)	lipoprotein, putative	26200	27249	+	349	111114850	4227035
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0028	27235	27666	-	143	111114851	4227036
Complete genome (Accession number NC_008277)	signal peptidase I	27656	28291	-	211	111114852	4227037
Complete genome (Accession number NC_008277)	signal peptidase I	28293	29273	-	326	111114853	4227038
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0031	29344	30807	+	487	111114854	4227039
Complete genome (Accession number NC_008277)	SsrA-binding protein	30810	31262	+	150	111114855	4227040
Complete genome (Accession number	hypothetical protein BAPKO_0033	31133	31285	-	50	111114856	4227041

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0034	31344	31880	-	178	111114857	4227042
Complete genome (Accession number NC_008277)	DNA topoisomerase IV subunit A	31948	33828	-	626	111114858	4227043
Complete genome (Accession number NC_008277)	DNA topoisomerase IV subunit B	33828	35627	-	599	111114859	4227044
Complete genome (Accession number NC_008277)	1-acyl-sn-glycerol-3-phosphate acyltransferase	35648	36385	-	245	111114860	4227045
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0038	36394	37917	-	507	111114861	4227046
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0039	37930	39432	-	500	111114862	4227047
Complete genome (Accession number NC_008277)	chemotaxis protein methyltransferase	39622	40479	+	285	111114863	4227048
Complete genome (Accession number NC_008277)	phosphate transport system regulatory protein	40544	41215	-	223	111114864	4227049
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0042	41226	42260	-	344	111114865	4227050
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0043	42257	42658	-	133	111114866	4227051
Complete genome (Accession number	P115 protein	42684	45134	-	816	111114867	4227052

NC_008277)							
Complete genome (Accession number NC_008277)	ribonuclease H	45227	45772	+	181	111114868	4227053
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0047	45790	46161	-	123	111114869	4227054
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0049	46695	46814	-	39	111114870	4227592
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0050	46933	47607	+	224	111114871	4227593
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0051	47654	48373	+	239	111114872	4227594
Complete genome (Accession number NC_008277)	spoU protein	48370	49038	-	222	111114873	4227595
Complete genome (Accession number NC_008277)	uracil-DNA glycosylase	49108	49779	+	223	111114874	4227596
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecG	49853	50215	-	120	111114875	4227597
Complete genome (Accession number NC_008277)	triosephosphate isomerase	50231	50992	-	253	111114876	4227598
Complete genome (Accession number NC_008277)	phosphoglycerate kinase	50994	52175	-	393	111114877	4227599
Complete genome (Accession number NC_008277)	glyceraldehyde 3-phosphate dehydrogenase	52200	53207	-	335	111114878	4227600

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0058	53282	55252	-	656	111114879	4227601
Complete genome (Accession number NC_008277)	hemolysin	55249	56028	-	259	111114880	4227602
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0060	56029	56487	-	152	111114881	4227603
Complete genome (Accession number NC_008277)	thioredoxin	56570	56923	-	117	111114882	4227604
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0062	56997	57713	+	238	111114883	4227605
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0063	57764	58771	-	335	111114884	4227606
Complete genome (Accession number NC_008277)	methionyl-tRNA formyltransferase	58821	59768	-	315	111114885	4227607
Complete genome (Accession number NC_008277)	polypeptide deformylase	59765	60262	-	165	111114886	4227608
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0066	60269	60322	-	17	111114887	4227722
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0067	60295	60981	-	228	111114888	4227723
Complete genome (Accession number NC_008277)	peptidase, putative	60978	62756	-	592	111114889	4227724

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0069	62871	63779	+	302	111114890	4227725
Complete genome (Accession number NC_008277)	aminopeptidase II	63764	65002	+	412	111114891	4227726
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0071	65017	65478	+	153	111114892	4227727
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0072	65495	66967	+	490	111114893	4227728
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0073	66975	69293	+	772	111114894	4227729
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0074	69290	69850	+	186	111114895	4227730
Complete genome (Accession number NC_008277)	peptide chain release factor 2	70134	70943	+	269	111114896	4227731
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0076	70925	72334	+	469	111114897	4227732
Complete genome (Accession number NC_008277)	signal recognition particle-docking protein FtsY	72371	73216	+	281	111114898	4227733
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0078	73213	74241	+	342	111114899	4227734
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0079	74242	75495	+	417	111114900	4227735

Complete genome (Accession number NC_008277)	ABC transporter, ATP-binding protein	75485	76177	+	230	111114901	4227736
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0081	76174	77427	+	417	111114902	4227737
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0082	77438	78733	-	431	111114903	4227738
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0083	78726	79046	-	106	111114904	4227829
Complete genome (Accession number NC_008277)	nifS protein	79231	80499	+	422	111114905	4227424
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0085	80709	81137	+	142	111114906	4227425
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0086	81134	82669	+	511	111114907	4227333
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0087	82507	82698	-	63	111114908	4227334
Complete genome (Accession number NC_008277)	L-lactate dehydrogenase	82699	83649	-	316	111114909	4227335
Complete genome (Accession number NC_008277)	GTP-binding protein LepA	83770	85575	-	601	111114910	4227336
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0090	85609	86571	-	320	111114911	4227337

Complete genome (Accession number NC_008277)	V-type ATP synthase subunit K	86658	87092	-	144	111114912	4227338
Complete genome (Accession number NC_008277)	V-type ATP synthase subunit I	87109	88962	-	617	111114913	4227339
Complete genome (Accession number NC_008277)	V-type ATP synthase subunit D	88946	89545	-	199	111114914	4227340
Complete genome (Accession number NC_008277)	V-type ATP synthase subunit B	89548	90852	-	434	111114915	4227341
Complete genome (Accession number NC_008277)	V-type ATP synthase subunit A	90874	92628	-	584	111114916	4227342
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0096	92615	93157	-	180	111114917	4227343
Complete genome (Accession number NC_008277)	V-type ATP synthase subunit E	93170	93769	-	199	111114918	4227344
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0098	93955	94341	-	128	111114919	4227345
Complete genome (Accession number NC_008277)	DNA mismatch repair protein, putative	94347	96683	-	778	111114920	4227346
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0100	96673	97596	-	307	111114921	4227347
Complete genome (Accession number NC_008277)	glutamate racemase	97593	98378	-	261	111114922	4227348

Complete genome (Accession number NC_008277)	asparaginyl-tRNA synthetase	98540	99928	+	462	111114923	4227349
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0103	99951	100472	+	173	111114924	4227350
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0104	100469	101062	-	197	111114925	4227351
Complete genome (Accession number NC_008277)	periplasmic serine protease DO	101193	102617	-	474	111114926	4227385
Complete genome (Accession number NC_008277)	methionine aminopeptidase	102684	103439	-	251	111114927	4227386
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0107	103432	105099	-	555	111114928	4227387
Complete genome (Accession number NC_008277)	transcription antitermination protein NusB	105101	105514	-	137	111114929	4227388
Complete genome (Accession number NC_008277)	basic membrane protein	105551	106561	-	336	111114930	4227389
Complete genome (Accession number NC_008277)	acetyl-CoA C-acetyltransferase	106639	107832	-	397	111114931	4227390
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0111	107947	109311	+	454	111114932	4227391
Complete genome (Accession number NC_008277)	replicative DNA helicase	109328	110695	-	455	111114933	4227392

Complete genome (Accession number NC_008277)	50S ribosomal protein L9	110699	111220	-	173	111114934	4227393
Complete genome (Accession number NC_008277)	30S ribosomal protein S18	111237	111527	-	96	111114935	4227394
Complete genome (Accession number NC_008277)	single-stranded DNA-binding protein	111542	111991	-	149	111114936	4227395
Complete genome (Accession number NC_008277)	30S ribosomal protein S6	112003	112422	-	139	111114937	4227396
Complete genome (Accession number NC_008277)	PTS system, maltose and glucose-specific IIABC component	112561	114255	-	564	111114938	4227397
Complete genome (Accession number NC_008277)	hemolysin III	114457	115158	+	233	111114939	4227398
Complete genome (Accession number NC_008277)	zinc protease, putative	115155	116456	-	433	111114940	4227399
Complete genome (Accession number NC_008277)	phosphatidate cytidylyltransferase	116478	117320	-	280	111114941	4227400
Complete genome (Accession number NC_008277)	undecaprenyl diphosphate synthase	117325	118017	-	230	111114942	4227401
Complete genome (Accession number NC_008277)	ribosome releasing factor	118023	118577	-	184	111114943	4227402
Complete genome (Accession number NC_008277)	elongation factor Ts	118615	119454	-	279	111114944	4227403

Complete genome (Accession number NC_008277)	30S ribosomal protein S2	119451	120224	-	257	111114945	4227404
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0125	120452	120730	-	92	111114946	4227366
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0126	120561	120740	-	59	111114947	4227367
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0127	120749	121390	-	213	111114948	4227368
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0128	121531	122142	-	203	111114949	4227369
Complete genome (Accession number NC_008277)	30S ribosomal protein S1	122142	123797	-	551	111114950	4227370
Complete genome (Accession number NC_008277)	cytidylate kinase	123800	124465	-	221	111114951	4227371
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0131	124449	125198	-	249	111114952	4227372
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0132	125185	125949	-	254	111114953	4227373
Complete genome (Accession number NC_008277)	recombinase A	125964	127061	-	365	111114954	4227374
Complete genome (Accession number NC_008277)	transcript cleavage factor/unknown domain fusion protein	127075	129777	-	900	111114955	4227375

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0135	129814	130758	-	314	111114956	4227376
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0136	130943	132070	+	375	111114957	4227377
Complete genome (Accession number NC_008277)	histidyl-tRNA synthetase	132115	133485	-	456	111114958	4227378
Complete genome (Accession number NC_008277)	penicillin-binding protein	133618	135504	+	628	111114959	4227379
Complete genome (Accession number NC_008277)	long-chain-fatty-acid CoA ligase	135505	137397	-	630	111114960	4227380
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0140	137747	137875	-	42	111114961	4227381
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0141	137875	138261	-	128	111114962	4227382
Complete genome (Accession number NC_008277)	acriflavine resistance protein	138185	141397	-	1070	111114963	4227383
Complete genome (Accession number NC_008277)	membrane fusion protein	141416	142369	-	317	111114964	4227384
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0144	142381	143616	-	411	111114965	4227426
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0145	143745	144035	+	96	111114966	4227427

Complete genome (Accession number NC_008277)	glycine betaine, L-proline ABC transporter, binding protein	144024	144908	-	294	111114967	4227428
Complete genome (Accession number NC_008277)	glycine betaine, L-proline ABC transporter, permease protein	144923	145822	-	299	111114968	4227429
Complete genome (Accession number NC_008277)	glycine betaine, L-proline ABC transporter, ATP- binding protein	145829	146947	-	372	111114969	4227430
Complete genome (Accession number NC_008277)	flagellin	147100	148110	-	336	111114970	4227431
Complete genome (Accession number NC_008277)	flagellar hook-associated protein FliD	148233	150230	-	665	111114971	4227432
Complete genome (Accession number NC_008277)	N-acetylglucosamine-6-phosphate deacetylase	150413	151618	+	401	111114972	4227433
Complete genome (Accession number NC_008277)	glucosamine-6-phosphate deaminase	151645	152451	+	268	111114973	4227434
Complete genome (Accession number NC_008277)	superoxide dismutase	152514	153125	-	203	111114974	4227435
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecA	153140	155839	-	899	111114975	4227436
Complete genome (Accession number NC_008277)	lipoprotein, putative	155909	157045	+	378	111114976	4227437
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0157	157074	157502	+	142	111114977	4227438

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0158	157506	157922	+	138	111114978	4227439
Complete genome (Accession number NC_008277)	antigen, S2, putative	158071	158805	+	244	111114979	4227440
Complete genome (Accession number NC_008277)	antigen S2-related protein	158832	159506	+	224	111114980	4227441
Complete genome (Accession number NC_008277)	alanine racemase	159571	160671	+	366	111114981	4227442
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0162	160663	162264	-	533	111114982	4227443
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0163	162340	162507	+	55	111114983	4227444
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0164	162535	164283	-	582	111114984	4227445
Complete genome (Accession number NC_008277)	Na+/Ca+ exchange protein, putative	164363	165349	-	328	111114985	4227092
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0166	165377	167215	-	612	111114986	4227093
Complete genome (Accession number NC_008277)	4-alpha-glucanotransferase	167341	168861	-	506	111114987	4227094
Complete genome (Accession number NC_008277)	outer membrane protein	169002	170171	+	389	111114988	4227095

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0169	170160	170237	-	25	111114989	4227096
Complete genome (Accession number NC_008277)	dnaK suppressor, putative	170182	170559	-	125	111114990	4227097
Complete genome (Accession number NC_008277)	translation initiation factor IF-1	170725	170946	+	73	111114991	4227098
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0172	170994	173000	-	668	111114992	4227099
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0173	172994	173581	-	195	111114993	4227100
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0174	173563	174603	-	346	111114994	4227101
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0175	174546	175547	-	333	111114995	4227102
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0176	175534	176433	-	299	111114996	4227103
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0177	176437	177312	-	291	111114997	4227104
Complete genome (Accession number NC_008277)	MoxR-related protein	177326	178318	-	330	111114998	4227105
Complete genome (Accession number NC_008277)	glucose inhibited division protein B	178375	179001	-	208	111114999	4227106

Complete genome (Accession number NC_008277)	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	178998	180863	-	621	111115000	4227617
Complete genome (Accession number NC_008277)	tRNA modification GTPase TrmE	180866	182260	-	464	111115001	4227959
Complete genome (Accession number NC_008277)	flagellar protein, putative	182343	182837	+	164	111115002	4227960
Complete genome (Accession number NC_008277)	flagellar hook-associated protein FlgK	182849	184732	+	627	111115003	4227961
Complete genome (Accession number NC_008277)	flagellar hook-associated protein FlgL	184735	186009	+	424	111115004	4227783
Complete genome (Accession number NC_008277)	flagellar assembly protein FliW	186011	186409	+	132	111115005	4227784
Complete genome (Accession number NC_008277)	carbon storage regulator	186412	186657	+	81	111115006	4227785
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0187	186641	187294	-	217	111115007	4227786
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0188	187287	187700	-	137	111115008	4227787
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0189	187697	187957	-	86	111115009	4227788
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0190	188164	188295	+	43	111115010	4227789

Complete genome (Accession number NC_008277)	50S ribosomal protein L20	188172	188519	-	115	111115011	4227790
Complete genome (Accession number NC_008277)	50S ribosomal protein L35	188540	188740	-	66	111115012	4227791
Complete genome (Accession number NC_008277)	translation initiation factor IF-3	188763	189323	-	186	111115013	4227792
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0194	189517	190170	+	217	111115014	4227793
Complete genome (Accession number NC_008277)	lipoprotein, putative	190157	190912	+	251	111115015	4227794
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0196	190968	191774	-	268	111115016	4227795
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0197	191774	192913	-	379	111115017	4227796
Complete genome (Accession number NC_008277)	peptide chain release factor 1	193251	194324	+	357	111115018	4227797
Complete genome (Accession number NC_008277)	HemK family methylase, putative	194327	195148	+	273	111115019	4227798
Complete genome (Accession number NC_008277)	guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	195145	197148	+	667	111115020	4227799
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0201	197138	199399	+	753	111115021	4227800

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0202	199344	199454	-	36	111115022	4227801
Complete genome (Accession number NC_008277)	D-alanine--D-alanine ligase	199396	200481	-	361	111115023	4227802
Complete genome (Accession number NC_008277)	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	200483	202000	-	505	111115024	4227686
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0206	202273	202647	+	124	111115025	4227688
Complete genome (Accession number NC_008277)	hemolysin, putative	202743	203510	+	255	111115026	4227689
Complete genome (Accession number NC_008277)	Lambda CII stability-governing protein	203563	204498	+	311	111115027	4227690
Complete genome (Accession number NC_008277)	Lambda CII stability-governing protein	204499	205470	+	323	111115028	4227691
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0212	205930	207480	+	516	111115029	4227694
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0213	207485	208054	-	189	111115030	4227695
Complete genome (Accession number NC_008277)	UTP--glucose-1-phosphate uridylyltransferase	208107	208943	+	278	111115031	4227696
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0215	208930	210669	+	579	111115032	4227697

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0216	210706	211473	+	255	111115033	4227698
Complete genome (Accession number NC_008277)	surface-located membrane protein 1	211466	214507	+	1013	111115034	4227699
Complete genome (Accession number NC_008277)	DNA mismatch repair protein	214514	216349	+	611	111115035	4227700
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0219	216368	217402	+	344	111115036	4227701
Complete genome (Accession number NC_008277)	lipoprotein, putative	217515	218168	-	217	111115037	4227831
Complete genome (Accession number NC_008277)	translation elongation factor P	218146	218724	-	192	111115038	4227832
Complete genome (Accession number NC_008277)	phosphate ABC transporter, periplasmic phosphate-binding protein	218890	219729	+	279	111115039	4227833
Complete genome (Accession number NC_008277)	phosphate ABC transporter, permease protein	219819	220727	+	302	111115040	4227834
Complete genome (Accession number NC_008277)	phosphate ABC transporter, permease protein	220724	222268	+	514	111115041	4227835
Complete genome (Accession number NC_008277)	phosphate ABC transporter, ATP-binding protein	222269	223051	+	260	111115042	4227836
Complete genome (Accession number NC_008277)	gufA protein	223054	223875	-	273	111115043	4227837
Complete genome	alanyl-tRNA synthetase	223916	225700	-	594	111115044	4227838

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	flagellar motor switch protein	225700	226917	-	405	111115045	4227839
Complete genome (Accession number NC_008277)	6-phosphoglucon olactonase	226904	227611	-	235	111115046	4227840
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0231	227716	227853	-	45	111115047	4227841
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0232	227874	228041	-	55	111115048	4227842
Complete genome (Accession number NC_008277)	tRNA-dihydrouridine synthase A	228118	229119	+	333	111115049	4227843
Complete genome (Accession number NC_008277)	seryl-tRNA synthetase	229109	230386	-	425	111115050	4227844
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0235	230526	231242	+	238	111115051	4227845
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0236	231243	234161	+	972	111115052	4227846
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0237	234158	234232	-	24	111115053	4227847
Complete genome (Accession number NC_008277)	50S ribosomal protein L31 type B	234198	234443	-	81	111115054	4227702
Complete genome (Accession number	transcription termination factor Rho	234504	236051	-	515	111115055	4227703

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0240	236131	236538	-	135	111115056	4227704
Complete genome (Accession number NC_008277)	hbbU protein	236539	236865	-	108	111115057	4227705
Complete genome (Accession number NC_008277)	30S ribosomal protein S20	236878	237135	-	85	111115058	4227706
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0243	237206	238033	-	275	111115059	4227707
Complete genome (Accession number NC_008277)	translation-associated GTPase	238043	239149	-	368	111115060	4227708
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0245	239185	241191	-	668	111115061	4227709
Complete genome (Accession number NC_008277)	apolipoprotein N-acyltransferase	241352	242920	+	522	111115062	4227710
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0247	242857	243630	-	257	111115063	4227711
Complete genome (Accession number NC_008277)	deoxyguanosine/deoxyadenosine kinase(I) subunit 2	243695	244297	-	200	111115064	4227712
Complete genome (Accession number NC_008277)	glycerol uptake facilitator	244705	245469	+	254	111115065	4227713
Complete genome (Accession number	glycerol kinase	245507	247012	+	501	111115066	4227714

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0251	247067	247306	+	79	111115067	4227715
Complete genome (Accession number NC_008277)	glycerol-3-phosphate dehydrogenase, anaerobic	247440	249008	+	522	111115068	4227716
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0253	249095	249589	-	164	111115069	4227717
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0254	249576	250130	-	184	111115070	4227718
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0255	250131	251156	-	341	111115071	4227719
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0256	251354	251959	+	201	111115072	4227720
Complete genome (Accession number NC_008277)	oligoendopeptidase F	252079	253851	+	590	111115073	4227721
Complete genome (Accession number NC_008277)	phosphatidyltransferase	253865	254569	+	234	111115074	4227466
Complete genome (Accession number NC_008277)	dedA protein	254566	255180	+	204	111115075	4227467
Complete genome (Accession number NC_008277)	leucyl-tRNA synthetase	255376	257898	+	840	111115076	4227469
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0262	257913	260216	+	767	111115077	4227470

Complete genome (Accession number NC_008277)	ATP-dependent protease LA	260205	262625	-	806	111115078	4227471
Complete genome (Accession number NC_008277)	single-stranded-DNA-specific exonuclease	262898	265018	+	706	111115079	4227472
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0265	265011	265955	+	314	111115080	4227473
Complete genome (Accession number NC_008277)	30S ribosomal protein S21	265970	266179	+	69	111115081	4227474
Complete genome (Accession number NC_008277)	cell division protein, putative	266218	268569	-	783	111115082	4227475
Complete genome (Accession number NC_008277)	undecaprenyl pyrophosphate phosphatase	268573	269367	-	264	111115083	4227476
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0269	269382	271550	-	722	111115084	4227477
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0270	271528	272538	-	336	111115085	4227478
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0271	272741	274123	+	460	111115086	4227479
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0272	274130	275383	-	417	111115087	4227480
Complete genome (Accession number NC_008277)	signal peptidase I	275559	275951	+	130	111115088	4227481
Complete genome	heat shock protein 70	275975	277444	-	489	111115089	4227482

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0275	277422	277943	-	173	111115090	4227483
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0276	277963	278265	-	100	111115091	4227260
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0277	278292	280196	-	634	111115092	4227261
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0278	280199	280678	-	159	111115093	4227262
Complete genome (Accession number NC_008277)	minD-related ATP-binding protein	280688	281575	-	295	111115094	4227263
Complete genome (Accession number NC_008277)	flagellar biosynthesis regulator FlhF	281587	282753	-	388	111115095	4227264
Complete genome (Accession number NC_008277)	flagellar biosynthesis protein A	282758	284848	-	696	111115096	4227265
Complete genome (Accession number NC_008277)	flagellar biosynthesis protein FlhB	284860	285978	-	372	111115097	4227618
Complete genome (Accession number NC_008277)	flagellar biosynthesis protein	285978	286766	-	262	111115098	4227619
Complete genome (Accession number NC_008277)	flagellar biosynthesis protein	286802	287065	-	87	111115099	4227620
Complete genome (Accession number	flagellar biosynthesis protein FliP	287073	287837	-	254	111115100	4227621

NC_008277)							
Complete genome (Accession number NC_008277)	flagellar biosynthesis protein	287848	288474	-	208	111115101	4227622
Complete genome (Accession number NC_008277)	flagellar motor switch protein	288467	288808	-	113	111115102	4227623
Complete genome (Accession number NC_008277)	flagellar motor switch protein FliM	288851	289909	-	352	111115103	4227624
Complete genome (Accession number NC_008277)	flagellar basal body-associated protein FliL	289930	290466	-	178	111115104	4227625
Complete genome (Accession number NC_008277)	flagellar motor protein MotB	290514	291296	-	260	111115105	4227626
Complete genome (Accession number NC_008277)	flagellar motor rotation protein A	291296	292078	-	260	111115106	4227627
Complete genome (Accession number NC_008277)	flagellar protein	292075	292299	-	74	111115107	4227628
Complete genome (Accession number NC_008277)	flagellar hook protein FlgE	292320	293648	-	442	111115108	4227629
Complete genome (Accession number NC_008277)	flagellar basal body rod modification protein	293653	294096	-	147	111115109	4227630
Complete genome (Accession number NC_008277)	flagellar protein	294110	295294	-	394	111115110	4227631
Complete genome (Accession number	flagellar protein	295302	295919	-	205	111115111	4227213

NC_008277)							
Complete genome (Accession number NC_008277)	flagellar protein	295912	296343	-	143	111115112	4227214
Complete genome (Accession number NC_008277)	flagellum-specific ATP synthase	296340	297650	-	436	111115113	4227215
Complete genome (Accession number NC_008277)	flagellar assembly protein H	297669	298589	-	306	111115114	4227216
Complete genome (Accession number NC_008277)	flagellar motor switch protein G	298604	299638	-	344	111115115	4227217
Complete genome (Accession number NC_008277)	flagellar MS-ring protein	299654	301363	-	569	111115116	4227218
Complete genome (Accession number NC_008277)	flagellar hook-basal body protein FliE	301378	301713	-	111	111115117	4227219
Complete genome (Accession number NC_008277)	flagellar basal body rod protein FlgC	301725	302183	-	152	111115118	4227220
Complete genome (Accession number NC_008277)	flagellar basal body rod protein FlgB	302207	302614	-	135	111115119	4227221
Complete genome (Accession number NC_008277)	ATP-dependent protease ATP-binding subunit	302648	303994	-	448	111115120	4227222
Complete genome (Accession number NC_008277)	ATP-dependent protease peptidase subunit	303987	304535	-	182	111115121	4227223
Complete genome (Accession number NC_008277)	smf protein	304544	305491	-	315	111115122	4227224

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0308	305498	306190	-	230	111115123	4227225
Complete genome (Accession number NC_008277)	cell division protein FtsZ	306191	307390	-	399	111115124	4227226
Complete genome (Accession number NC_008277)	cell division protein	307412	308653	-	413	111115125	4227227
Complete genome (Accession number NC_008277)	cell division protein	308653	309396	-	247	111115126	4227228
Complete genome (Accession number NC_008277)	cell division protein	309432	309989	-	185	111115127	4227229
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0313	310062	310490	-	142	111115128	4227230
Complete genome (Accession number NC_008277)	phospho-N-acetylmuramoyl-pentapeptide-transferase	310533	311588	-	351	111115129	4227231
Complete genome (Accession number NC_008277)	UDP-N-acetylmuramoyl alanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanine	311606	312997	-	463	111115130	4227405
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0316	313020	313301	-	93	111115131	4227406
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0317	313298	314188	-	296	111115132	4227407
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0318	314181	315017	-	278	111115133	4227408

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0319	315014	316090	-	358	111115134	4227409
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0320	316120	316878	-	252	111115135	4227410
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0321	317194	318033	-	279	111115136	4227411
Complete genome (Accession number NC_008277)	purine-binding chemotaxis protein	318023	318553	-	176	111115137	4227412
Complete genome (Accession number NC_008277)	cell division protein	318599	319168	-	189	111115138	4227413
Complete genome (Accession number NC_008277)	octaprenyl-diphosphate synthase	319228	320271	+	347	111115139	4227414
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0325	320271	320954	+	227	111115140	4227415
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0326	320956	321762	-	268	111115141	4227416
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0327	321763	322695	-	310	111115142	4227417
Complete genome (Accession number NC_008277)	methylgalactoside ABC transporter, ATP-binding protein	322692	324152	-	486	111115143	4227418
Complete genome (Accession number NC_008277)	exported protein	324152	325189	-	345	111115144	4227419

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0330	325323	325574	-	83	111115145	4227420
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0331	325609	326667	-	352	111115146	4227421
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0332	326941	328080	+	379	111115147	4227422
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0333	328176	328541	+	121	111115148	4227423
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0334	328548	329657	-	369	111115149	4227647
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0335	329708	332512	-	934	111115150	4227667
Complete genome (Accession number NC_008277)	glycerol-3-phosphate O-acyltransferase, putative	332536	333429	-	297	111115151	4227668
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	333829	335400	+	523	111115152	4227669
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	335499	337082	+	527	111115153	4227670
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	337227	338852	+	541	111115154	4227671
Complete genome (Accession number	oligopeptide ABC transporter, permease	339148	340068	+	306	111115155	4227672

NC_008277)	protein						
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, permease protein	340081	341130	+	349	111115156	4227673
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0342	341102	341185	+	27	111115157	4227674
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, ATP-binding protein	341142	342017	+	291	111115158	4227675
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, ATP-binding protein	342018	342989	+	323	111115159	4227676
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0345	343003	343734	-	243	111115160	4227677
Complete genome (Accession number NC_008277)	enolase	343868	345169	+	433	111115161	4227678
Complete genome (Accession number NC_008277)	30S ribosomal protein S9	345234	345644	-	136	111115162	4227679
Complete genome (Accession number NC_008277)	50S ribosomal protein L13	345646	346104	-	152	111115163	4227680
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0349	346157	346966	-	269	111115164	4227681
Complete genome (Accession number NC_008277)	aspartyl/glutamyl-tRNA amidotransferase subunit B	346959	348416	-	485	111115165	4227682
Complete genome (Accession	Glu-tRNA(Gln) amidotransferase, subunit A	348406	349851	-	481	111115166	4227683

number NC_008277)							
Complete genome (Accession number NC_008277)	aspartyl/glutamyl-tRNA amidotransferase subunit C	349862	350137	-	91	111115167	4227684
Complete genome (Accession number NC_008277)	DNA helicase	350147	352243	-	698	111115168	4227685
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0354	352246	353445	-	399	111115169	4227446
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0355	353456	354106	-	216	111115170	4227447
Complete genome (Accession number NC_008277)	fibronectin/fibrinogen-binding protein, putative	354298	355716	+	472	111115171	4227448
Complete genome (Accession number NC_008277)	pyruvate kinase	355812	357245	+	477	111115172	4227449
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0358	357314	358003	+	229	111115173	4227450
Complete genome (Accession number NC_008277)	50S ribosomal protein L28	358022	358300	-	92	111115174	4227451
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0360	358322	359884	-	520	111115175	4227452
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0361	359994	361127	+	377	111115176	4227453
Complete genome (Accession	hypothetical protein BAPKO_0362	361124	362923	-	599	111115177	4227454

number NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0363	362936	363886	-	316	111115178	4227455
Complete genome (Accession number NC_008277)	transcription factor, putative	363920	364408	-	162	111115179	4227456
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0365	364448	365041	-	197	111115180	4227457
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0366	365034	365765	-	243	111115181	4227458
Complete genome (Accession number NC_008277)	carboxyl-terminal protease	365769	367202	-	477	111115182	4227459
Complete genome (Accession number NC_008277)	minD-related ATP-binding protein	367702	368844	+	380	111115183	4227460
Complete genome (Accession number NC_008277)	prolipoprotein diacylglyceryl transferase	368844	369815	+	323	111115184	4227461
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0370	369850	371862	+	670	111115185	4227462
Complete genome (Accession number NC_008277)	methylglyoxal synthase	371958	372341	+	127	111115186	4227463
Complete genome (Accession number NC_008277)	lipoprotein LA7	372384	372971	-	195	111115187	4227464
Complete genome (Accession number	putative aminopeptidase 1	373108	374484	+	458	111115188	4227465

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0375	374435	374770	+	111	111115189	4227554
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0376	374754	375215	+	153	111115190	4227555
Complete genome (Accession number NC_008277)	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	374792	375850	-	352	111115191	4227556
Complete genome (Accession number NC_008277)	ATP-dependent Clp protease, subunit A	375868	378165	-	765	111115192	4227557
Complete genome (Accession number NC_008277)	tyrosyl-tRNA synthetase	378176	379393	-	405	111115193	4227558
Complete genome (Accession number NC_008277)	glycyl-tRNA synthetase	379390	380727	-	445	111115194	4227559
Complete genome (Accession number NC_008277)	glutamyl-tRNA synthetase	380745	382217	-	490	111115195	4227560
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0382	382230	382997	-	255	111115196	4227561
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0383	383127	384263	+	378	111115197	4227562
Complete genome (Accession number NC_008277)	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative	384285	384998	+	237	111115198	4227563
Complete genome	S-adenosylmethio	384995	386173	+	392	111115199	4227564

(Accession number NC_008277)	nine synthetase						
Complete genome (Accession number NC_008277)	S-ribosylhomocysteinase	386170	386643	+	157	111115200	4227565
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0387	386654	387316	-	220	111115201	4227566
Complete genome (Accession number NC_008277)	protein kinase C1 inhibitor	387343	387762	-	139	111115202	4227567
Complete genome (Accession number NC_008277)	Mg2+ transport protein	387811	389175	-	454	111115203	4227568
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0390	389229	390653	-	474	111115204	4227569
Complete genome (Accession number NC_008277)	basic membrane protein B	390767	391792	-	341	111115205	4227570
Complete genome (Accession number NC_008277)	basic membrane protein A	391879	392898	-	339	111115206	4227571
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0393	392942	393100	-	52	111115207	4227572
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0394	393299	393385	-	28	111115208	4227803
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0395	393563	394582	-	339	111115209	4227804
Complete genome (Accession number	hypothetical protein BAPKO_0396	394626	394904	-	92	111115210	4227805

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0397	394980	395066	-	28	111115211	4227806
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0398	395244	396263	-	339	111115212	4227807
Complete genome (Accession number NC_008277)	basic membrane protein C	396307	397368	-	353	111115213	4227808
Complete genome (Accession number NC_008277)	basic membrane protein D	397682	398707	-	341	111115214	4227809
Complete genome (Accession number NC_008277)	30S ribosomal protein S7	398808	399281	-	157	111115215	4227810
Complete genome (Accession number NC_008277)	30S ribosomal protein S12	399306	399680	-	124	111115216	4227811
Complete genome (Accession number NC_008277)	DNA-directed RNA polymerase subunit beta'	399748	403881	-	1377	111115217	4227812
Complete genome (Accession number NC_008277)	DNA-directed RNA polymerase subunit beta	403897	407364	-	1155	111115218	4227813
Complete genome (Accession number NC_008277)	50S ribosomal protein L7/L12	407447	407821	-	124	111115219	4227814
Complete genome (Accession number NC_008277)	50S ribosomal protein L10	407892	408380	-	162	111115220	4227815
Complete genome (Accession number	50S ribosomal protein L1	408385	409065	-	226	111115221	4227816

NC_008277)							
Complete genome (Accession number NC_008277)	50S ribosomal protein L11	409065	409496	-	143	111115222	4227817
Complete genome (Accession number NC_008277)	transcription antitermination factor	409550	410104	-	184	111115223	4227818
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecE	410128	410298	-	56	111115224	4227819
Complete genome (Accession number NC_008277)	50S ribosomal protein L33	410406	410585	-	59	111115225	4227821
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0414	410750	411607	-	285	111115226	4227610
Complete genome (Accession number NC_008277)	lipoprotein, putative	411621	412643	-	340	111115227	4227611
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0416	412990	413601	+	203	111115228	4227612
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0417	413658	415313	-	551	111115229	4227613
Complete genome (Accession number NC_008277)	glutamate transporter, putative	415314	416516	+	400	111115230	4227614
Complete genome (Accession number NC_008277)	prolyl-tRNA synthetase	416528	417994	-	488	111115231	4227615
Complete genome (Accession number	hypothetical protein BAPKO_0420	418047	418724	-	225	111115232	4227616

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0421	418888	419304	+	138	111115233	4227739
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0422	419301	419906	+	201	111115234	4227740
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0423	419917	420528	+	203	111115235	4227741
Complete genome (Accession number NC_008277)	mannose-6-phosphate isomerase	420581	421696	-	371	111115236	4227742
Complete genome (Accession number NC_008277)	PTS system, fructose-specific IIABC component	421697	423574	-	625	111115237	4227743
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0426	423746	424375	+	209	111115238	4227744
Complete genome (Accession number NC_008277)	endonuclease precursor	424372	425253	+	293	111115239	4227745
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0428	425250	426029	+	259	111115240	4227746
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0429	426017	426637	-	206	111115241	4227747
Complete genome (Accession number NC_008277)	chemotaxis protein methyltransferase	426883	427740	+	285	111115242	4227748
Complete genome (Accession number	protein-glutamate methylesterase	427773	428900	+	375	111115243	4227749

NC_008277)							
Complete genome (Accession number NC_008277)	pheromone shutdown protein	428926	430140	+	404	111115244	4227750
Complete genome (Accession number NC_008277)	adenylate kinase	430179	430814	+	211	111115245	4227751
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0434	430815	431864	+	349	111115246	4227752
Complete genome (Accession number NC_008277)	response regulatory protein	431896	432819	-	307	111115247	4227753
Complete genome (Accession number NC_008277)	sensory transduction histidine kinase/response regulator	432822	437303	-	1493	111115248	4227754
Complete genome (Accession number NC_008277)	hydrolase	443902	444744	-	280	111115249	4227759
Complete genome (Accession number NC_008277)	3-methyladenine DNA glycosylase	444880	445440	-	186	111115250	4227760
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0443	445966	446049	+	27	111115251	4227761
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0448	450181	450729	-	182	111115253	4227575
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0449	450819	451496	-	225	111115254	4227576
Complete genome (Accession number	hypothetical protein BAPKO_0450	451709	452026	+	105	111115255	4227577

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0451	452057	452446	-	129	111115256	4227578
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0452	452573	453169	+	198	111115257	4227579
Complete genome (Accession number NC_008277)	chromosome segregation protein, putative	453278	454030	+	250	111115258	4227580
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0454	454033	454746	+	237	111115259	4227581
Complete genome (Accession number NC_008277)	stage 0 sporulation protein J	455034	455816	-	260	111115260	4227582
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0456	455862	455951	+	29	111115261	4227583
Complete genome (Accession number NC_008277)	DNA gyrase, subunit A	455934	458366	-	810	111115262	4227584
Complete genome (Accession number NC_008277)	DNA gyrase, subunit B	458378	460282	-	634	111115263	4227585
Complete genome (Accession number NC_008277)	chromosomal replication initiator protein	460469	461926	+	485	111115264	4227586
Complete genome (Accession number NC_008277)	DNA polymerase III, subunit beta	462159	463319	+	386	111115265	4227587
Complete genome (Accession number	hypothetical protein BAPKO_0461	463411	463710	+	99	111115266	4227588

NC_008277)							
Complete genome (Accession number NC_008277)	50S ribosomal protein L34	463802	463957	+	51	111115267	4227589
Complete genome (Accession number NC_008277)	ribonuclease P protein component	463938	464273	+	111	111115268	4227590
Complete genome (Accession number NC_008277)	putative inner membrane protein translocase component YidC	464284	465918	+	544	111115269	4227764
Complete genome (Accession number NC_008277)	spoIIIJ-associtated protein	465932	466660	+	242	111115270	4227765
Complete genome (Accession number NC_008277)	nucleotide sugar epimerase	466704	467771	+	355	111115271	4227766
Complete genome (Accession number NC_008277)	fructose-bisphosphate aldolase	467933	469012	+	359	111115272	4227767
Complete genome (Accession number NC_008277)	aspartyl-tRNA synthetase	469419	471179	-	586	111115273	4227768
Complete genome (Accession number NC_008277)	Na+/H+ antiporter	471183	473288	-	701	111115274	4227769
Complete genome (Accession number NC_008277)	phosphocarrier protein HPr	473291	473566	-	91	111115275	4227770
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0471	473579	473872	-	97	111115276	4227771
Complete genome (Accession	RNA polymerase sigma-54 factor	473862	475121	-	419	111115277	4227772

number NC_008277)							
Complete genome (Accession number NC_008277)	chromate transport protein, putative	475124	475657	-	177	111115278	4227773
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0474	475654	476259	-	201	111115279	4227774
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0475	476471	477313	+	280	111115280	4227775
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0476	477288	477404	-	38	111115281	4227776
Complete genome (Accession number NC_008277)	lipopolysaccharide biosynthesis-related protein	477310	478458	-	382	111115282	4227777
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0478	478533	479504	+	323	111115283	4227778
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0479	479508	480146	+	212	111115284	4227779
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0480	480209	480352	+	47	111115285	4227780
Complete genome (Accession number NC_008277)	excinuclease ABC, subunit C	480235	481962	-	575	111115286	4227781
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0482	482153	483670	+	505	111115287	4227782
Complete genome (Accession number	hypothetical protein BAPKO_0483	483663	484973	+	436	111115288	4227352

NC_008277)							
Complete genome (Accession number NC_008277)	lipoprotein, putative	485299	486024	-	241	111115289	4227641
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0489	486225	486536	+	103	111115290	4227644
Complete genome (Accession number NC_008277)	DNA polymerase III subunits gamma and tau	486587	488287	+	566	111115291	4227645
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0491	488292	488591	+	99	111115292	4227646
Complete genome (Accession number NC_008277)	nucleoside-diphosphate kinase	488761	489270	+	169	111115293	4227254
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0493	489566	490093	+	175	111115294	4227255
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0494	490090	490785	+	231	111115295	4227256
Complete genome (Accession number NC_008277)	ABC transporter, ATP-binding protein	490754	491554	+	266	111115296	4227257
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0496	491551	492240	+	229	111115297	4227258
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0497	492242	492988	+	248	111115298	4227259
Complete genome (Accession number	signal peptidase II	492999	493511	+	170	111115299	4227949

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0499	493508	493735	+	75	111115300	4227950
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0500	493749	494570	+	273	111115301	4227951
Complete genome (Accession number NC_008277)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	494676	495959	+	427	111115302	4227952
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0502	496449	497813	+	454	111115303	4227953
Complete genome (Accession number NC_008277)	lipoprotein, putative	497902	498291	-	129	111115304	4227954
Complete genome (Accession number NC_008277)	elongation factor Tu	498782	499966	+	394	111115305	4227955
Complete genome (Accession number NC_008277)	30S ribosomal protein S10	500018	500329	+	103	111115306	4227956
Complete genome (Accession number NC_008277)	50S ribosomal protein L3	500365	500985	+	206	111115307	4227957
Complete genome (Accession number NC_008277)	50S ribosomal protein L4	500995	501624	+	209	111115308	4227958
Complete genome (Accession number NC_008277)	50S ribosomal protein L23	501645	501941	+	98	111115309	4227164
Complete genome (Accession number NC_008277)	50S ribosomal protein L2	501963	502796	+	277	111115310	4227165

Complete genome (Accession number NC_008277)	30S ribosomal protein S19	502806	503084	+	92	111115311	4227166
Complete genome (Accession number NC_008277)	50S ribosomal protein L22	503092	503454	+	120	111115312	4227167
Complete genome (Accession number NC_008277)	30S ribosomal protein S3	503458	504333	+	291	111115313	4227168
Complete genome (Accession number NC_008277)	50S ribosomal protein L16	504338	504754	+	138	111115314	4227169
Complete genome (Accession number NC_008277)	50S ribosomal protein L29	504757	504957	+	66	111115315	4227170
Complete genome (Accession number NC_008277)	30S ribosomal protein S17	504960	505214	+	84	111115316	4227171
Complete genome (Accession number NC_008277)	50S ribosomal protein L14	505242	505610	+	122	111115317	4227172
Complete genome (Accession number NC_008277)	50S ribosomal protein L24	505625	505930	+	101	111115318	4227173
Complete genome (Accession number NC_008277)	50S ribosomal protein L5	505936	506484	+	182	111115319	4227895
Complete genome (Accession number NC_008277)	30S ribosomal protein S14	506502	506687	+	61	111115320	4227896
Complete genome (Accession number NC_008277)	30S ribosomal protein S8	506697	507095	+	132	111115321	4227897

Complete genome (Accession number NC_008277)	50S ribosomal protein L6	507112	507654	+	180	111115322	4227898
Complete genome (Accession number NC_008277)	50S ribosomal protein L18	507672	508031	+	119	111115323	4227899
Complete genome (Accession number NC_008277)	30S ribosomal protein S5	508044	508541	+	165	111115324	4227900
Complete genome (Accession number NC_008277)	ribosomal protein L30	508545	508856	+	103	111115325	4227901
Complete genome (Accession number NC_008277)	50S ribosomal protein L15	508849	509286	+	145	111115326	4227902
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecY	509299	510603	+	434	111115327	4227903
Complete genome (Accession number NC_008277)	50S ribosomal protein L36	510616	510729	+	37	111115328	4227904
Complete genome (Accession number NC_008277)	30S ribosomal protein S13	510747	511124	+	125	111115329	4227905
Complete genome (Accession number NC_008277)	30S ribosomal protein S11	511152	511544	+	130	111115330	4227906
Complete genome (Accession number NC_008277)	DNA-directed RNA polymerase subunit alpha	511560	512594	+	344	111115331	4227907
Complete genome (Accession number NC_008277)	50S ribosomal protein L17	512616	512987	+	123	111115332	4227908

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0532	513064	514593	+	509	111115333	4227909
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0533	514583	515371	+	262	111115334	4227910
Complete genome (Accession number NC_008277)	hemolysin	515352	516143	+	263	111115335	4227911
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0535	516140	516886	-	248	111115336	4227912
Complete genome (Accession number NC_008277)	GTP-binding protein EngA	516973	518274	+	433	111115337	4227913
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0537	518271	519530	+	419	111115338	4227193
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0538	519527	520213	+	228	111115339	4227194
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0539	520233	526721	+	2162	111115340	4227195
Complete genome (Accession number NC_008277)	phenylalanyl-tRNA synthetase subunit alpha	526733	528295	+	520	111115341	4227196
Complete genome (Accession number NC_008277)	phenylalanyl-tRNA synthetase subunit beta	528283	529986	+	567	111115342	4227197
Complete genome (Accession number NC_008277)	thioredoxin reductase	530055	531035	+	326	111115343	4227198
Complete genome	rRNA methylase	531056	531796	-	246	111115344	4227199

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	heat shock protein	531798	532892	-	364	111115345	4227200
Complete genome (Accession number NC_008277)	heat shock protein 70	532892	534799	-	635	111115346	4227201
Complete genome (Accession number NC_008277)	grpE protein	534823	535386	-	187	111115347	4227202
Complete genome (Accession number NC_008277)	NH(3)-dependent NAD+ synthetase	535764	537302	+	512	111115348	4227203
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0548	537545	537724	+	59	111115349	4227204
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0549	538068	538154	+	28	111115350	4227205
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0550	538208	539062	+	284	111115351	4227206
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0551	539089	539511	-	140	111115352	4227207
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0552	539616	541427	+	603	111115353	4227208
Complete genome (Accession number NC_008277)	pantothenate kinase	541420	542196	+	258	111115354	4227209
Complete genome (Accession number	aldose reductase, putative	542231	543178	-	315	111115355	4227210

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0555	543264	544073	-	269	111115356	4227211
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0556	544057	544671	-	204	111115357	4227212
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0557	544674	545981	-	435	111115358	4227128
Complete genome (Accession number NC_008277)	phnP protein	546177	546938	+	253	111115359	4227129
Complete genome (Accession number NC_008277)	exodeoxyribonuclease III	546959	547726	+	255	111115360	4227130
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0560	547742	548512	+	256	111115361	4227131
Complete genome (Accession number NC_008277)	zinc protease, putative	548493	551294	+	933	111115362	4227132
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0565	551746	552390	-	214	111115363	4227136
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0566	552387	552743	-	118	111115364	4227137
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0567	552828	553526	-	232	111115365	4227138
Complete genome (Accession number	elongation factor G	553561	555642	-	693	111115366	4227139

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0569	555941	556168	+	75	111115367	4227140
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0570	556400	556927	+	175	111115368	4227141
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0571	557048	557698	+	216	111115369	4227142
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0572	557771	557905	+	44	111115370	4227143
Complete genome (Accession number NC_008277)	phosphoribosyl pyrophosphate synthetase	557892	559112	+	406	111115371	4227108
Complete genome (Accession number NC_008277)	xylulokinase	559116	560480	+	454	111115372	4227109
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0575	560463	561209	-	248	111115373	4227110
Complete genome (Accession number NC_008277)	dephospho-CoA kinase	561193	561810	-	205	111115374	4227111
Complete genome (Accession number NC_008277)	DNA polymerase I	561792	564461	-	889	111115375	4227112
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0578	564515	564925	-	136	111115376	4227113
Complete genome (Accession number NC_008277)	flagellar protein	564915	565334	-	139	111115377	4227114

Complete genome (Accession number NC_008277)	chemotaxis response regulator	565343	565723	-	126	111115378	4227115
Complete genome (Accession number NC_008277)	DNA ligase	565973	567955	+	660	111115379	4227116
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0582	567979	569484	-	501	111115380	4227117
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0583	569764	571626	+	620	111115381	4227118
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0584	571613	571984	+	123	111115382	4227119
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0585	572073	572942	+	289	111115383	4227120
Complete genome (Accession number NC_008277)	phosphocarrier protein HPr	573080	573340	+	86	111115384	4227121
Complete genome (Accession number NC_008277)	phosphoenolpyruvate-protein phosphatase	573361	575082	+	573	111115385	4227122
Complete genome (Accession number NC_008277)	glucose-specific PTS system component	575085	575654	+	189	111115386	4227123
Complete genome (Accession number NC_008277)	heat shock protein 90	575691	577541	-	616	111115387	4227124
Complete genome (Accession number NC_008277)	6-phosphogluconate dehydrogenase	577654	579048	+	464	111115388	4227125

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0591	579079	579624	-	181	111115389	4227126
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0592	579727	579816	+	29	111115390	4227127
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0593	579809	580327	-	172	111115391	4227296
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0594	580410	580997	-	195	111115392	4227297
Complete genome (Accession number NC_008277)	purine-binding chemotaxis protein	581210	581746	+	178	111115393	4227298
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0596	581759	582070	+	103	111115394	4227299
Complete genome (Accession number NC_008277)	chemotaxis histidine kinase	582086	584227	+	713	111115395	4227300
Complete genome (Accession number NC_008277)	protein-glutamate methylesterase	584285	585442	+	385	111115396	4227301
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0599	585445	587217	+	590	111115397	4227302
Complete genome (Accession number NC_008277)	chemotaxis response regulator	587258	587632	+	124	111115398	4227303
Complete genome (Accession number NC_008277)	uridylate kinase	587959	588648	-	229	111115399	4227305
Complete genome	glycosyl transferase	588861	589925	+	354	111115400	4227306

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	ABC transporter, ATP-binding protein	589988	590794	+	268	111115401	4227307
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0605	590801	591652	+	283	111115402	4227308
Complete genome (Accession number NC_008277)	CTP synthetase	591839	593440	+	533	111115403	4227309
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0607	593457	593981	-	174	111115404	4227310
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0608	594119	594709	+	196	111115405	4227311
Complete genome (Accession number NC_008277)	methyl-accepting chemotaxis protein	594956	596128	+	390	111115406	4227312
Complete genome (Accession number NC_008277)	DNA polymerase III subunit alpha	596216	599701	+	1161	111115407	4227313
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0611	599710	600291	+	193	111115408	4227914
Complete genome (Accession number NC_008277)	DNA recombinase	600301	602361	+	686	111115409	4227915
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0613	602358	603146	-	262	111115410	4227916
Complete genome (Accession number	hypothetical protein BAPKO_0614	603275	604624	+	449	111115411	4227917

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0615	604779	606125	+	448	111115412	4227918
Complete genome (Accession number NC_008277)	UDP-N-acetylmuramoylalanine--D-glutamateligase	606144	607499	+	451	111115413	4227919
Complete genome (Accession number NC_008277)	femA protein	607496	608539	-	347	111115414	4227920
Complete genome (Accession number NC_008277)	methionyl-tRNA synthetase	608549	610723	-	724	111115415	4227921
Complete genome (Accession number NC_008277)	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative	610882	611676	+	264	111115416	4227922
Complete genome (Accession number NC_008277)	phosphate acetyltransferase	611768	612805	+	345	111115417	4227923
Complete genome (Accession number NC_008277)	dimethyladenosine transferase	612788	613633	-	281	111115418	4227924
Complete genome (Accession number NC_008277)	competence locus E, putative	613666	614922	-	418	111115419	4227925
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0623	615078	615752	+	224	111115420	4227926
Complete genome (Accession number NC_008277)	long-chain-fatty-acid CoA ligase	615778	617715	+	645	111115421	4227927
Complete genome	arginyl-tRNA synthetase	617744	619501	-	585	111115422	4227928

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0626	619494	619544	-	16	111115423	4227929
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0627	619547	620146	-	199	111115424	4227930
Complete genome (Accession number NC_008277)	methyl-accepting chemotaxis protein	620168	622315	-	715	111115425	4227931
Complete genome (Accession number NC_008277)	methyl-accepting chemotaxis protein	622583	624790	+	735	111115426	4227932
Complete genome (Accession number NC_008277)	UDP-N-acetylmuramate dehydrogenase	624795	625706	-	303	111115427	4227933
Complete genome (Accession number NC_008277)	cysteinyl-tRNA synthetase	625758	627200	+	480	111115428	4227934
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0632	627097	627240	+	47	111115429	4227935
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0633	627204	628760	+	518	111115430	4227936
Complete genome (Accession number NC_008277)	serine hydroxymethyltransferase	628760	630013	+	417	111115431	4227937
Complete genome (Accession number NC_008277)	DnaJ domain containing protein	630040	630792	+	250	111115432	4227938
Complete genome (Accession number	membrane-associated protein p66	630853	632712	-	619	111115433	4227939

NC_008277)							
Complete genome (Accession number NC_008277)	L-lactate permease	632951	634453	-	500	111115434	4227940
Complete genome (Accession number NC_008277)	serine-type D-Ala-D-Ala carboxypeptidase	634538	635743	+	401	111115435	4227941
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0639	635760	636251	+	163	111115436	4227942
Complete genome (Accession number NC_008277)	rep helicase, single-stranded DNA-dependent ATPase	636254	638233	+	659	111115437	4227943
Complete genome (Accession number NC_008277)	aminoacyl-histidine dipeptidase	638346	639776	+	476	111115438	4227944
Complete genome (Accession number NC_008277)	trigger factor	640354	641712	+	452	111115439	4227232
Complete genome (Accession number NC_008277)	ATP-dependent Clp protease proteolytic component	641718	642311	+	197	111115440	4227233
Complete genome (Accession number NC_008277)	ATP-dependent protease ATP-binding subunit	642336	643628	+	430	111115441	4227234
Complete genome (Accession number NC_008277)	ATP-dependent protease LA	643597	646005	+	802	111115442	4227235
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0650	646045	646197	+	50	111115443	4227236
Complete genome (Accession number	hypothetical protein BAPKO_0651	646142	646249	+	35	111115444	4227237

NC_008277)							
Complete genome (Accession number NC_008277)	30S ribosomal protein S4	646261	646887	-	208	111115445	4227238
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0654	647064	648425	-	453	111115446	4227240
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0655	648546	648914	+	122	111115447	4227241
Complete genome (Accession number NC_008277)	cytidine deaminase	648937	649377	-	146	111115448	4227242
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0657	649497	650459	+	320	111115449	4227243
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0658	650437	652032	-	531	111115450	4227244
Complete genome (Accession number NC_008277)	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein	652331	652885	+	184	111115451	4227246
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0661	652882	652974	+	30	111115452	4227247
Complete genome (Accession number NC_008277)	acetate kinase	652947	654128	-	393	111115453	4227248
Complete genome (Accession number NC_008277)	transcription-repair coupling factor	654189	657563	-	1124	111115454	4227249
Complete genome (Accession	hypothetical protein BAPKO_0664	657660	658622	+	320	111115455	4227250

number NC_008277)							
Complete genome (Accession number NC_008277)	N-acetylmuramoyl-L-alanine amidase, putative	658636	660678	+	680	111115456	4227251
Complete genome (Accession number NC_008277)	small primase-like protein	660772	661317	-	181	111115457	4227253
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0668	661286	661336	-	16	111115458	4227353
Complete genome (Accession number NC_008277)	putative aminopeptidase 2	661320	662591	-	423	111115459	4227354
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0670	662676	663401	+	241	111115460	4227355
Complete genome (Accession number NC_008277)	PTS system, fructose-specific IIABC component	663429	665294	-	621	111115461	4227356
Complete genome (Accession number NC_008277)	1-phosphofructokinase	665384	666307	+	307	111115462	4227357
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0673	666356	666673	-	105	111115463	4227358
Complete genome (Accession number NC_008277)	exodeoxyribonuclease V, alpha chain	666937	668769	-	610	111115464	4227360
Complete genome (Accession number NC_008277)	exodeoxyribonuclease V, beta chain	668766	672278	-	1170	111115465	4227361
Complete genome (Accession number NC_008277)	exodeoxyribonuclease V, gamma chain	672284	675523	-	1079	111115466	4227362
Complete genome (Accession number							

NC_008277)							
Complete genome (Accession number NC_008277)	nicotinate phosphoribosyltransferase	675527	676972	-	481	111115467	4227363
Complete genome (Accession number NC_008277)	glucose-6-phosphate 1-dehydrogenase	677105	678541	+	478	111115468	4227364
Complete genome (Accession number NC_008277)	Na+/H+ antiporter	678842	680185	+	447	111115469	4227365
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0681	680133	680219	-	28	111115470	4227848
Complete genome (Accession number NC_008277)	Na+/H+ antiporter	680285	681640	+	451	111115471	4227849
Complete genome (Accession number NC_008277)	spermidine/putrescine ABC transporter, binding periplasmic protein	681686	682732	-	348	111115472	4227850
Complete genome (Accession number NC_008277)	spermidine/putrescine ABC transporter, permease protein	682752	683543	-	263	111115473	4227851
Complete genome (Accession number NC_008277)	spermidine/putrescine ABC transporter, permease protein	683547	684356	-	269	111115474	4227852
Complete genome (Accession number NC_008277)	spermidine/putrescine ABC transporter, ATP- binding protein	684356	685399	-	347	111115475	4227853
Complete genome (Accession number NC_008277)	ribosomal biogenesis GTPase	685478	686284	-	268	111115476	4227854
Complete genome (Accession	N-acetylmannosamine-6-	686488	687186	+	232	111115477	4227855

number NC_008277)	phosphate 2-epimerase						
Complete genome (Accession number NC_008277)	PTS system, glucose-specific IIBC component	687235	688779	+	514	111115478	4227856
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0690	688805	689788	-	327	111115479	4227857
Complete genome (Accession number NC_008277)	ferric uptake regulation protein	689785	690312	-	175	111115480	4227858
Complete genome (Accession number NC_008277)	serine/threonine kinase, putative	690412	692100	-	562	111115481	4227859
Complete genome (Accession number NC_008277)	chaperonin GroEL	692291	693928	+	545	111115482	4227860
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0694	693995	694291	+	98	111115483	4227861
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0695	694304	694618	+	104	111115484	4227862
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecD	694684	696444	+	586	111115485	4227863
Complete genome (Accession number NC_008277)	preprotein translocase subunit SecF	696428	697327	+	299	111115486	4227864
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0698	697354	698496	+	380	111115487	4227865
Complete genome (Accession number	heat shock protein	698493	699323	-	276	111115488	4227866

NC_008277)							
Complete genome (Accession number NC_008277)	HemN-related protein	699432	700565	+	377	111115489	4227867
Complete genome (Accession number NC_008277)	ribose 5-phosphate isomerase	700552	701238	-	228	111115490	4227648
Complete genome (Accession number NC_008277)	phosphoglycerate mutase	701383	702129	+	248	111115491	4227649
Complete genome (Accession number NC_008277)	lysyl-tRNA synthetase	702199	703764	-	521	111115492	4227650
Complete genome (Accession number NC_008277)	GTP-binding protein Era	703837	704709	-	290	111115493	4227651
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0705	704816	705172	+	118	111115494	4227652
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0706	705182	705592	+	136	111115495	4227653
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0707	705612	706061	+	149	111115496	4227654
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0708	706070	706759	-	229	111115497	4227655
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0709	706802	707761	+	319	111115498	4227656
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0710	707745	708752	+	335	111115499	4227657

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0711	708742	709293	+	183	111115500	4227658
Complete genome (Accession number NC_008277)	flagellar filament outer layer protein	709376	710401	+	341	111115501	4227659
Complete genome (Accession number NC_008277)	chemotaxis histidine kinase	710476	713070	+	864	111115502	4227660
Complete genome (Accession number NC_008277)	purine-binding chemotaxis protein	713078	714478	+	466	111115503	4227661
Complete genome (Accession number NC_008277)	chemotaxis operon protein	714490	714975	+	161	111115504	4227662
Complete genome (Accession number NC_008277)	chemotaxis response regulator	715015	715455	+	146	111115505	4227663
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0717	715504	716010	-	168	111115506	4227664
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0718	716007	717053	-	348	111115507	4227665
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0719	717047	717910	-	287	111115508	4227666
Complete genome (Accession number NC_008277)	phosphoglycolate phosphatase	717907	718569	-	220	111115509	4227962
Complete genome (Accession number NC_008277)	ribose/galactose ABC transporter, ATP-binding protein	718812	720422	+	536	111115510	4227963

Complete genome (Accession number NC_008277)	ribose/galactose ABC transporter, permease protein	720423	721574	+	383	111115511	4227964
Complete genome (Accession number NC_008277)	ribose/galactose ABC transporter, permease protein	721546	722472	+	308	111115512	4227965
Complete genome (Accession number NC_008277)	methyl-accepting chemotaxis protein	722629	724890	+	753	111115513	4227966
Complete genome (Accession number NC_008277)	methyl-accepting chemotaxis protein	724921	726822	+	633	111115514	4227967
Complete genome (Accession number NC_008277)	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	726864	727931	-	355	111115515	4227968
Complete genome (Accession number NC_008277)	3-hydroxy-3-methylglutaryl-CoA synthase	728027	729250	+	407	111115516	4227969
Complete genome (Accession number NC_008277)	isopentenyl pyrophosphate isomerase	729234	730298	+	354	111115517	4227970
Complete genome (Accession number NC_008277)	3-hydroxy-3-methylglutaryl-CoA reductase	730288	731556	+	422	111115518	4227971
Complete genome (Accession number NC_008277)	mevalonate pyrophosphate decarboxylase	731540	732478	+	312	111115519	4227972
Complete genome (Accession number NC_008277)	phosphomevalonate kinase, putative	732469	733422	+	317	111115520	4227973
Complete genome (Accession number NC_008277)	mevalonate kinase, putative	733416	734309	+	297	111115521	4227974

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0734	734432	734899	-	155	111115522	4227976
Complete genome (Accession number NC_008277)	neutrophil activating protein	734984	735514	+	176	111115523	4227977
Complete genome (Accession number NC_008277)	elongation factor G	735591	737600	+	669	111115524	4227978
Complete genome (Accession number NC_008277)	xylose operon regulatory protein	737879	739087	+	402	111115525	4227107
Complete genome (Accession number NC_008277)	signal recognition particle protein	739150	740484	+	444	111115526	4227074
Complete genome (Accession number NC_008277)	30S ribosomal protein S16	740497	740757	+	86	111115527	4227075
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0740	740758	741006	+	82	111115528	4227076
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0741	741010	741510	+	166	111115529	4227077
Complete genome (Accession number NC_008277)	tRNA (guanine-N(1)-)-methyltransferase	741507	742226	+	239	111115530	4227078
Complete genome (Accession number NC_008277)	50S ribosomal protein L19	742204	742563	+	119	111115531	4227079
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0744	742944	743483	+	179	111115532	4227080

Complete genome (Accession number NC_008277)	lipopolysaccharide biosynthesis-related protein	743485	743976	+	163	111115533	4227081
Complete genome (Accession number NC_008277)	50S ribosomal protein L32	744039	744221	+	60	111115534	4227082
Complete genome (Accession number NC_008277)	acyl carrier protein	744245	744487	+	80	111115535	4227083
Complete genome (Accession number NC_008277)	ribonuclease III	744487	745224	+	245	111115536	4227084
Complete genome (Accession number NC_008277)	polynucleotide adenylyltransferase	745195	746427	-	410	111115537	4227085
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0750	746545	748317	+	590	111115538	4227086
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0751	748323	748646	+	107	111115539	4227087
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0754	749104	750135	+	343	111115540	4227090
Complete genome (Accession number NC_008277)	DNA primase	750141	751922	+	593	111115541	4227091
Complete genome (Accession number NC_008277)	RNA polymerase sigma factor RpoD	751926	753821	+	631	111115542	4227055
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0757	753818	754594	+	258	111115543	4227056

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0758	754999	755967	+	322	111115544	4227057
Complete genome (Accession number NC_008277)	rod shape-determining protein	755942	757027	+	361	111115545	4227058
Complete genome (Accession number NC_008277)	rod shape-determining protein	757031	757876	+	281	111115546	4227059
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0761	757876	758358	+	160	111115547	4227060
Complete genome (Accession number NC_008277)	penicillin-binding protein	758358	760157	+	599	111115548	4227061
Complete genome (Accession number NC_008277)	rod shape-determining protein	760162	761478	+	438	111115549	4227062
Complete genome (Accession number NC_008277)	threonyl-tRNA synthetase	761645	763390	+	581	111115550	4227063
Complete genome (Accession number NC_008277)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	763395	764024	+	209	111115551	4227064
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0766	764011	765456	+	481	111115552	4227065
Complete genome (Accession number NC_008277)	adenylyl cyclase, CyaB-type, putative	765430	765963	-	177	111115553	4227066
Complete genome (Accession number NC_008277)	K+ transport protein	766063	767382	+	439	111115554	4227067

Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0769	767386	768168	+	260	111115555	4227068
Complete genome (Accession number NC_008277)	minD-related ATP-binding protein	768178	769149	+	323	111115556	4227069
Complete genome (Accession number NC_008277)	diphosphate--fructose-6-phosphate 1-phosphotransferase	769180	770523	+	447	111115557	4227070
Complete genome (Accession number NC_008277)	coenzyme A disulfide reductase	770538	771869	-	443	111115558	4227071
Complete genome (Accession number NC_008277)	glutamate transporter	771884	773275	-	463	111115559	4227072
Complete genome (Accession number NC_008277)	glucose-6-phosphate isomerase	773340	774932	-	530	111115560	4227073
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0775	774955	775356	-	133	111115561	4227484
Complete genome (Accession number NC_008277)	penicillin-binding protein	775363	778134	-	923	111115562	4227526
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0777	778429	779214	+	261	111115563	4227527
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0778	779420	780424	-	334	111115564	4227528
Complete genome (Accession number NC_008277)	rare lipoprotein A	780504	781316	+	270	111115565	4227529

Complete genome (Accession number NC_008277)	histidine phosphokinase/ phophatase, putative	781512	782516	+	334	111115566	4227530
Complete genome (Accession number NC_008277)	valyl-tRNA synthetase	782506	785133	+	875	111115567	4227531
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0782	785224	785823	-	199	111115568	4227532
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0783	785897	786244	-	115	111115569	4227533
Complete genome (Accession number NC_008277)	co-chaperonin GroES	786733	787005	-	90	111115570	4227534
Complete genome (Accession number NC_008277)	ABC transporter, ATP-binding protein	787163	788794	+	543	111115571	4227535
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0786	788854	790509	+	551	111115572	4227536
Complete genome (Accession number NC_008277)	antigen, p83/100	790613	792604	+	663	111115573	4227537
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0788	792637	792738	-	33	111115574	4227538
Complete genome (Accession number NC_008277)	endonuclease III	792921	793565	+	214	111115575	4227541
Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, permease protein	793574	794434	-	286	111115576	4227542

Complete genome (Accession number NC_008277)	oligopeptide ABC transporter, permease protein	794434	795414	-	326	111115577	4227632
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0794	795421	795879	-	152	111115578	4227633
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0795	795978	797099	+	373	111115579	4227634
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0796	797334	798347	-	337	111115580	4227635
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0797	798364	799872	-	502	111115581	4227636
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0798	799877	800611	-	244	111115582	4227637
Complete genome (Accession number NC_008277)	ABC transporter, ATP-binding protein	800608	801537	-	309	111115583	4227638
Complete genome (Accession number NC_008277)	ribonuclease Z	801546	802505	-	319	111115584	4227639
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0801	802635	802739	+	34	111115585	4227640
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0802	802675	802788	+	37	111115586	4227868
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0803	802696	803763	-	355	111115587	4227869

Complete genome (Accession number NC_008277)	ATP-dependent Clp protease proteolytic subunit	803962	804558	+	198	111115588	4227870
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0805	804536	805264	+	242	111115589	4227871
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0807	805419	806276	-	285	111115590	4227873
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0808	806316	806645	-	109	111115591	4227874
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0809	806756	807643	+	295	111115592	4227875
Complete genome (Accession number NC_008277)	response regulatory protein	807890	809248	-	452	111115593	4227876
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0811	809251	809646	-	131	111115594	4227877
Complete genome (Accession number NC_008277)	sensory transduction histidine kinase, putative	809639	810400	-	253	111115595	4227878
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0813	810397	811443	-	348	111115596	4227879
Complete genome (Accession number NC_008277)	colicin V production protein, putative	811454	811942	-	162	111115597	4227880
Complete genome (Accession number NC_008277)	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecapr	811939	813030	-	363	111115598	4227881

Complete genome (Accession number NC_008277)	pyridoxal kinase	813208	814002	-	264	111115599	4227882
Complete genome (Accession number NC_008277)	O-sialoglycoprotein endopeptidase	813977	815017	-	346	111115600	4227883
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0818	815014	815895	-	293	111115601	4227884
Complete genome (Accession number NC_008277)	RNA polymerase sigma factor	815946	816746	-	266	111115602	4227885
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0820	816886	817206	-	106	111115603	4227886
Complete genome (Accession number NC_008277)	flagellar basal body P-ring protein	817196	818206	-	336	111115604	4227887
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0822	818380	818943	-	187	111115605	4227888
Complete genome (Accession number NC_008277)	flagellar basal body rod protein FlgG	819014	819811	-	265	111115606	4227889
Complete genome (Accession number NC_008277)	flagellar hook-basal body complex protein	819824	820672	-	282	111115607	4227890
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0825	820921	821481	+	186	111115608	4227891
Complete genome (Accession number NC_008277)	adenine phosphoribosyltransferase	821546	822076	+	176	111115609	4227892

Complete genome (Accession number NC_008277)	50S ribosomal protein L21	822134	822445	+	103	111115610	4227893
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0828	822451	822771	+	106	111115611	4227894
Complete genome (Accession number NC_008277)	50S ribosomal protein L27	822771	823016	+	81	111115612	4227314
Complete genome (Accession number NC_008277)	GTPase ObgE	823058	824044	+	328	111115613	4227315
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0831	824001	824081	+	26	111115614	4227316
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0832	824127	824708	+	193	111115615	4227317
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0833	824705	825889	+	394	111115616	4227318
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0834	825864	826214	+	116	111115617	4227319
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0835	826168	826317	+	49	111115618	4227320
Complete genome (Accession number NC_008277)	regulatory protein SpoVG	826318	826611	+	97	111115619	4227321
Complete genome (Accession number NC_008277)	50S ribosomal protein L25/general stress protein Ctc	826768	827316	+	182	111115620	4227323
Complete genome	peptidyl-tRNA hydrolase	827321	827887	+	188	111115621	4227324

(Accession number NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0840	827887	829209	+	440	111115622	4227325
Complete genome (Accession number NC_008277)	cell division protein	829206	831125	+	639	111115623	4227326
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0842	831131	832615	+	494	111115624	4227327
Complete genome (Accession number NC_008277)	thymidine kinase	832720	833823	+	367	111115625	4227328
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0844	833753	833896	-	47	111115626	4227329
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0845	833820	834437	-	205	111115627	4227330
Complete genome (Accession number NC_008277)	thymidylate kinase	834463	835071	-	202	111115628	4227331
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0847	835157	839560	+	1467	111115629	4227332
Complete genome (Accession number NC_008277)	outer membrane protein	839578	842043	+	821	111115630	4227822
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0849	842064	842597	+	177	111115631	4227823
Complete genome (Accession number	DNA mismatch repair protein	843020	845608	+	862	111115632	4227824

NC_008277)							
Complete genome (Accession number NC_008277)	competence protein F, putative	845610	846227	+	205	111115633	4227825
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0852	846328	846765	+	145	111115634	4227826
Complete genome (Accession number NC_008277)	transcription elongation factor NusA	846779	848227	+	482	111115635	4227827
Complete genome (Accession number NC_008277)	translation initiation factor IF-2	848230	850578	+	782	111115636	4227828
Complete genome (Accession number NC_008277)	ribosome-binding factor A	850601	850963	+	120	111115637	4227016
Complete genome (Accession number NC_008277)	tRNA pseudouridine 55 synthase	850966	851814	+	282	111115638	4227017
Complete genome (Accession number NC_008277)	30S ribosomal protein S15	851990	852256	+	88	111115639	4227018
Complete genome (Accession number NC_008277)	polynucleotide phosphorylase/ polyadenylase	852271	854439	+	722	111115640	4227019
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0859	854446	855987	+	513	111115641	4227020
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0860	855962	857251	+	429	111115642	4227021
Complete genome (Accession number	hypothetical protein BAPKO_0861	857248	858315	+	355	111115643	4227022

NC_008277)							
Complete genome (Accession number NC_008277)	tRNA-guanine transglycosylase	858347	859474	+	375	111115644	4227023
Complete genome (Accession number NC_008277)	virulence factor mviN protein	859467	860987	+	506	111115645	4227024
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0864	860984	862390	+	468	111115646	4227025
Complete genome (Accession number NC_008277)	pantothenate metabolism flavoprotein	862415	863476	-	353	111115647	4227026
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0866	863730	863834	-	34	111115648	4227027
Complete genome (Accession number NC_008277)	sodium/panthothenate symporter	863916	865250	+	444	111115649	4227144
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0868	865263	866210	+	315	111115650	4227145
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0869	866179	867126	+	315	111115651	4227146
Complete genome (Accession number NC_008277)	UDP-N-acetylmuramate--L-alanine ligase	867116	868522	+	468	111115652	4227147
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0871	868533	869399	+	288	111115653	4227148
Complete genome (Accession number	cytidylate kinase	869396	869932	+	178	111115654	4227149

NC_008277)							
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0873	869972	870172	+	66	111115655	4227150
Complete genome (Accession number NC_008277)	2-methylthio-N6-isopentyladenosine tRNA modification enzyme	870159	871061	+	300	111115656	4227151
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0875	871083	871178	+	31	111115657	4227152
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0876	871222	871593	-	123	111115658	4227153
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0877	871674	872219	+	181	111115659	4227154
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0878	872212	872994	-	260	111115660	4227155
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0879	872987	873502	-	171	111115661	4227156
Complete genome (Accession number NC_008277)	ATP-dependent helicase	873629	876100	-	823	111115662	4227157
Complete genome (Accession number NC_008277)	DNA topoisomerase I	876103	878652	-	849	111115663	4227158
Complete genome (Accession number NC_008277)	exonuclease SbcD	878728	879969	+	413	111115664	4227159
Complete genome (Accession number	exonuclease SbcC	879956	882796	+	946	111115665	4227160

NC_008277)							
Complete genome (Accession number NC_008277)	xylose operon regulatory protein	882830	883768	+	312	111115666	4227161
Complete genome (Accession number NC_008277)	lipoprotein, putative	883782	884621	-	279	111115667	4227162
Complete genome (Accession number NC_008277)	isoleucyl-tRNA synthetase	884615	887743	-	1042	111115668	4227163
Complete genome (Accession number NC_008277)	ATP-dependent Clp protease, subunit C	887764	889911	-	715	111115669	4227543
Complete genome (Accession number NC_008277)	phosphomanno mutase	890006	891715	-	569	111115670	4227544
Complete genome (Accession number NC_008277)	excinuclease ABC subunit B	891858	893852	+	664	111115671	4227545
Complete genome (Accession number NC_008277)	excinuclease ABC, subunit A	893869	896721	+	950	111115672	4227546
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0891	896724	900125	+	1133	111115673	4227547
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0892	900091	900477	+	128	111115674	4227548
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0893	900135	900674	-	179	111115675	4227549
Complete genome (Accession number NC_008277)	hypothetical protein BAPKO_0894	900652	901251	-	199	111115676	4227550

Complete genome (Accession number NC_008277)	lipoprotein, putative	901261	902847	-	528	111115677	4227551
Complete genome (Accession number NC_008277)	arginine deiminase	903057	904286	+	409	111115678	4227552
Complete genome (Accession number NC_008277)	ornithine carbamoyltransferase, catabolic	904351	905337	+	328	111115679	4227553

Fig. 29. Borrelia garinii

Plasmid or genome	Product Name	Start	End	Strand	Length	Gi	GeneID
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB01	45	326	+	93	51038598	2942824
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB02	310	756	-	148	51038599	2942818
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB03	844	2193	-	449	51038600	2942810
Plasmid cp26 (Accession number NC_006128)	PTS system, cellobiose-specific IIC component	2471	3802	-	443	51038601	2942815
Plasmid cp26 (Accession number NC_006128)	PTS system, cellobiose-specific IIA	3993	4340	+	115	51038602	2942820
Plasmid cp26 (Accession number NC_006128)	PTS system, cellobiose-specific IIB component	4349	4666	+	105	51038603	2942809
Plasmid cp26 (Accession number NC_006128)	outer surface protein, putative	4678	5775	+	365	51038604	2942806
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB08	5796	6428	-	210	51038605	2942805
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB09	6570	7613	+	347	51038606	2942823

Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB10	7729	8673	+	314	51038607	2942821
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB11	8663	9181	+	172	51038608	2942826
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB12	9157	9918	+	253	51038609	2942807
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB13	9986	10534	+	182	51038610	2942822
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB14	10804	11319	-	171	51038611	2942814
Plasmid cp26 (Accession number NC_006128)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	12545	14146	+	533	51038612	2942812
Plasmid cp26 (Accession number NC_006128)	inositol-5-monophosphate dehydrogenase	14482	15696	-	404	51038613	2942827
Plasmid cp26 (Accession number NC_006128)	bifunctional GMP synthase/glutamine amidotransferase protein	15721	17307	-	528	51038614	2942828
Plasmid cp26 (Accession number NC_006128)	outer surface protein C	17531	18154	+	207	51038615	2942825
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB19	18596	19951	-	451	51038616	2942829

Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB20	20061	21416	-	451	51038617	2942830
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB21	21484	21990	-	168	51038618	2942817
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB22	21965	22450	-	161	51038619	2942819
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB23	22524	23219	+	231	51038620	2942813
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB24	23229	23780	-	183	51038621	2942816
Plasmid cp26 (Accession number NC_006128)	hypothetical protein BGB25	24096	25136	+	346	51038622	2942811
Plasmid cp26 (Accession number NC_006128)	PTS system, maltose and glucose-specific IIABC component	25437	27065	+	542	51038623	2942808
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA01	1024	1509	+	161	51038625	2942865
Plasmid lp54 (Accession number NC_006129)	outer membrane protein	1825	2343	+	172	51038626	2942881
Plasmid lp54 (Accession number NC_006129)	antigen, S2	2434	3255	-	273	51038627	2942890
Plasmid lp54 (Accession number NC_006129)	antigen, S1	3380	4573	-	397	51038628	2942835
Plasmid lp54 (Accession number	chpAI protein, putative	4982	5455	-	157	51038629	2942880

NC_006129)							
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA06	5599	5961	+	120	51038630	2942838
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA07	6163	6351	+	62	51038631	2942867
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA08	6606	6812	+	68	51038632	2942892
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA09	6825	7430	+	201	51038633	2942894
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA10	7885	8547	+	220	51038634	2942871
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA11	8640	8750	+	36	51038635	2942802
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA12	8747	9106	+	119	51038636	2942874
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA13	9302	9649	+	115	51038637	2942833
Plasmid lp54 (Accession number NC_006129)	outer surface protein A	9700	10521	+	273	51038638	2942836
Plasmid lp54 (Accession number NC_006129)	outer surface protein B	10531	11415	+	294	51038639	2942852
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA16	11967	13166	+	399	51038640	2942854
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA17	13172	13795	+	207	51038641	2942853

Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA18	13771	14523	+	250	51038642	2942834
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA19	14524	15096	+	190	51038643	2942855
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA20	15991	16314	+	107	51038644	2942841
Plasmid lp54 (Accession number NC_006129)	decorin binding protein A	16429	16956	-	175	51038645	2942886
Plasmid lp54 (Accession number NC_006129)	decorin binding protein B	17077	17631	-	184	51038646	2942878
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA23	18024	18335	-	103	51038647	2942885
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA24	19210	19773	+	187	51038648	2942831
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA25	19900	20406	+	168	51038649	2942803
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA26	20749	21120	+	123	51038650	2942839
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA27	21685	22152	+	155	51038651	2942897
Plasmid lp54 (Accession number NC_006129)	oligopeptide ABC transporter, periplasmic	22316	23902	-	528	51038652	2942887
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA29	23865	24053	+	62	51038653	2942844

Plasmid lp54 (Accession number NC_006129)	lipoprotein	24377	25060	+	227	51038654	2942896
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA31	25181	25789	+	202	51038655	2942895
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA32	26382	26540	+	52	51038656	2942891
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA33	26718	27389	+	223	51038657	2942866
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA34	27401	27928	+	175	51038658	2942889
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA35	28057	28188	+	43	51038659	2942883
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA36	28188	28520	+	110	51038660	2942868
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA37	28551	29495	+	314	51038661	2942856
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA38	29499	29840	+	113	51038662	2942857
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA39	29956	30330	+	124	51038663	2942872
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA40	30416	30700	+	94	51038664	2942875
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA41	30681	30851	+	56	51038665	2942832

Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA42	31004	31228	+	74	51038666	2942899
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA43	31264	31494	+	76	51038667	2942876
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA44	31501	31971	+	156	51038668	2942860
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA45	32334	32756	+	140	51038669	2942870
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA46	32799	33290	+	163	51038670	2942862
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA47	33515	34081	+	188	51038671	2942848
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA48	34103	34834	+	243	51038672	2942849
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA49	34923	35078	+	51	51038673	2942884
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA50	35263	35487	+	74	51038674	2942847
Plasmid lp54 (Accession number NC_006129)	outer membrane protein	35526	36293	+	255	51038675	2942843
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA52	36438	36668	+	76	51038676	2942846
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA53	36707	36970	+	87	51038677	2942804

Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA54	37048	37251	+	67	51038678	2942893
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA55	37254	38015	+	253	51038679	2942901
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA56	37997	38344	+	115	51038680	2942879
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA57	38392	38547	+	51	51038681	2942873
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA58	38600	39739	-	379	51038682	2942851
Plasmid lp54 (Accession number NC_006129)	lipoprotein	40298	40510	-	70	51038683	2942877
Plasmid lp54 (Accession number NC_006129)	surface lipoprotein P27	40610	41443	-	277	51038684	2942842
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA61	41798	42421	-	207	51038685	2942869
Plasmid lp54 (Accession number NC_006129)	lipoprotein	42689	42847	+	52	51038686	2942863
Plasmid lp54 (Accession number NC_006129)	antigen, P35	43007	43963	-	318	51038687	2942861
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA64	44130	44960	-	276	51038688	2942859
Plasmid lp54 (Accession number NC_006129)	antigen, P35, putative	45129	46403	-	424	51038689	2942900
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA66	46747	47499	-	250	51038690	2942882

Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA67	47824	48606	-	260	51038691	2942898
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA68	48839	49546	-	235	51038692	2942845
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA69	49872	50075	-	67	51038693	2942837
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA70	50205	50573	-	122	51038694	2942850
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA71	50845	51600	-	251	51038695	2942864
Plasmid lp54 (Accession number NC_006129)	hypothetical protein BGA72	51911	52684	-	257	51038696	2942858
Plasmid lp54 (Accession number NC_006129)	antigen, P35, putative	52835	53692	-	285	51038697	2942888
Plasmid lp54 (Accession number NC_006129)	outer membrane porin	54230	55003	+	257	51038698	2942840
Complete genome (Accession number NC_006156)	hypothetical protein BG0001	443	526	-	27	51598264	2957747
Complete genome (Accession number NC_006156)	beta-N-acetylhexosaminidase, putative	629	1648	-	339	51598265	2957836
Complete genome (Accession number NC_006156)	hypothetical protein BG0003	1636	3114	-	492	51598266	2957388
Complete genome (Accession number NC_006156)	phosphoglucomutase	3254	5041	+	595	51598267	2957341

Complete genome (Accession number NC_006156)	tryptophanyl-tRNA synthetase	5126	6163	-	345	51598268	2957736
Complete genome (Accession number NC_006156)	hypothetical protein BG0006	6166	7254	-	362	51598269	2957926
Complete genome (Accession number NC_006156)	hypothetical protein BG0007	7308	8168	-	286	51598270	2957823
Complete genome (Accession number NC_006156)	hypothetical protein BG0008	8277	9047	+	256	51598271	2957719
Complete genome (Accession number NC_006156)	hypothetical protein BG0009	9052	10056	+	334	51598272	2957763
Complete genome (Accession number NC_006156)	holo-acyl-carrier protein synthase, putative	10053	10427	+	124	51598273	2957930
Complete genome (Accession number NC_006156)	hypothetical protein BG0011	10431	11270	+	279	51598274	2958006
Complete genome (Accession number NC_006156)	tRNA pseudouridine synthase A	11271	12011	+	246	51598275	2957468
Complete genome (Accession number NC_006156)	hypothetical protein BG0013	12004	12594	+	196	51598276	2957813
Complete genome (Accession number NC_006156)	primosomal protein N	12587	14569	+	660	51598277	2957928
Complete genome (Accession number NC_006156)	uridine kinase	14566	15186	-	206	51598278	2957927

Complete genome (Accession number NC_006156)	glpE protein	15186	15467	-	93	51598279	2957998
Complete genome (Accession number NC_006156)	hypothetical protein BG0017	15690	16655	+	321	51598280	2957916
Complete genome (Accession number NC_006156)	hypothetical protein BG0018	16652	17635	-	327	51598281	2957605
Complete genome (Accession number NC_006156)	hypothetical protein BG0019	17637	18149	-	170	51598282	2957659
Complete genome (Accession number NC_006156)	diphosphate--fructose-6-phosphate 1-phosphotransferase	18157	19827	-	556	51598283	2957509
Complete genome (Accession number NC_006156)	S-adenosylmethionine: tRNA ribosyltransferase-isomerase	19905	20945	-	346	51598284	2957477
Complete genome (Accession number NC_006156)	Holliday junction DNA helicase B	20920	21963	-	347	51598285	2957993
Complete genome (Accession number NC_006156)	Holliday junction DNA helicase	22008	22598	-	196	51598286	2957957
Complete genome (Accession number NC_006156)	hypothetical protein BG0024	22668	23807	+	379	51598287	2957981
Complete genome (Accession number	hypothetical protein BG0025	23822	24553	-	243	51598288	2957984

NC_006156)							
Complete genome (Accession number NC_006156)	methylenetetrahydrofolate dehydrogenase	24554	25459	-	301	51598289	2957612
Complete genome (Accession number NC_006156)	hypothetical protein BG0027	25610	26248	+	212	51598290	2957660
Complete genome (Accession number NC_006156)	lipoprotein, putative	26256	27305	+	349	51598291	2957613
Complete genome (Accession number NC_006156)	hypothetical protein BG0029	27291	27722	-	143	51598292	2957982
Complete genome (Accession number NC_006156)	signal peptidase I	27712	28347	-	211	51598293	2957611
Complete genome (Accession number NC_006156)	signal peptidase I	28349	29329	-	326	51598294	2957616
Complete genome (Accession number NC_006156)	hypothetical protein BG0032	29400	30863	+	487	51598295	2957950
Complete genome (Accession number NC_006156)	SsrA-binding protein	30875	31327	+	150	51598296	2957961
Complete genome (Accession number NC_006156)	hypothetical protein BG0034	31401	31934	-	177	51598297	2957962
Complete genome (Accession number NC_006156)	DNA topoisomerase IV subunit A	32002	33882	-	626	51598298	2957933

Complete genome (Accession number NC_006156)	DNA topoisomerase IV subunit B	33882	35681	-	599	51598299	2957619
Complete genome (Accession number NC_006156)	1-acyl-sn-glycerol-3-phosphate acyltransferase	35702	36439	-	245	51598300	2957945
Complete genome (Accession number NC_006156)	hypothetical protein BG0038	36448	37986	-	512	51598301	2957952
Complete genome (Accession number NC_006156)	hypothetical protein BG0039	37998	39500	-	500	51598302	2957938
Complete genome (Accession number NC_006156)	chemotaxis protein methyltransferase	39692	40543	+	283	51598303	2957656
Complete genome (Accession number NC_006156)	phosphate transport system regulatory protein	40626	41297	-	223	51598304	2957623
Complete genome (Accession number NC_006156)	hypothetical protein BG0042	41308	42342	-	344	51598305	2957939
Complete genome (Accession number NC_006156)	hypothetical protein BG0043	42339	42740	-	133	51598306	2957624
Complete genome (Accession number NC_006156)	P115 protein	42766	45213	-	815	51598307	2957969
Complete genome (Accession number NC_006156)	ribonuclease H	45306	45851	+	181	51598308	2957615

Complete genome (Accession number NC_006156)	hypothetical protein BG0046	45866	46228	-	120	51598309	2957992
Complete genome (Accession number NC_006156)	hypothetical protein BG0048	46765	46884	-	39	51598310	2957882
Complete genome (Accession number NC_006156)	hypothetical protein BG0049	47007	47681	+	224	51598311	2957860
Complete genome (Accession number NC_006156)	hypothetical protein BG0050	47758	48447	+	229	51598312	2957631
Complete genome (Accession number NC_006156)	spoU protein	48444	49100	-	218	51598313	2957632
Complete genome (Accession number NC_006156)	uracil-DNA glycosylase	49183	49854	+	223	51598314	2957874
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecG	49952	50314	-	120	51598315	2957870
Complete genome (Accession number NC_006156)	triosephosphate isomerase	50330	51091	-	253	51598316	2957633
Complete genome (Accession number NC_006156)	phosphoglycerate kinase	51093	52274	-	393	51598317	2957894
Complete genome (Accession number NC_006156)	glyceraldehyde 3-phosphate dehydrogenase	52300	53307	-	335	51598318	2957866
Complete genome (Accession number	hypothetical protein BG0057	53382	55352	-	656	51598319	2957635

NC_006156)							
Complete genome (Accession number NC_006156)	hemolysin	55349	56128	-	259	51598320	2957634
Complete genome (Accession number NC_006156)	hypothetical protein BG0059	56129	56587	-	152	51598321	2957642
Complete genome (Accession number NC_006156)	thioredoxin	56676	57029	-	117	51598322	2957639
Complete genome (Accession number NC_006156)	hypothetical protein BG0061	57103	57819	+	238	51598323	2957637
Complete genome (Accession number NC_006156)	hypothetical protein BG0062	57871	58815	-	314	51598324	2957640
Complete genome (Accession number NC_006156)	methionyl-tRNA formyltransferase	58928	59875	-	315	51598325	2957645
Complete genome (Accession number NC_006156)	polypeptide deformylase	59872	60432	-	186	51598326	2957647
Complete genome (Accession number NC_006156)	hypothetical protein BG0065	60405	61091	-	228	51598327	2957646
Complete genome (Accession number NC_006156)	peptidase, putative	61088	62866	-	592	51598328	2957644
Complete genome (Accession number NC_006156)	hypothetical protein BG0067	62979	63869	+	296	51598329	2957641
Complete genome	aminopeptidase II	63870	65108	+	412	51598330	2957650

(Accession number NC_006156)							
Complete genome (Accession number NC_006156)	hypothetical protein BG0069	65123	65584	+	153	51598331	2957684
Complete genome (Accession number NC_006156)	hypothetical protein BG0070	65601	67073	+	490	51598332	2957655
Complete genome (Accession number NC_006156)	hypothetical protein BG0071	67081	69399	+	772	51598333	2957685
Complete genome (Accession number NC_006156)	hypothetical protein BG0072	69396	69956	+	186	51598334	2957667
Complete genome (Accession number NC_006156)	peptide chain release factor 2	69997	71049	+	350	51598335	2957657
Complete genome (Accession number NC_006156)	hypothetical protein BG0074	71031	72440	+	469	51598336	2957675
Complete genome (Accession number NC_006156)	signal recognition particle-docking protein FtsY	72477	73322	+	281	51598337	2957669
Complete genome (Accession number NC_006156)	hypothetical protein BG0076	73319	74347	+	342	51598338	2957700
Complete genome (Accession number NC_006156)	hypothetical protein BG0077	74348	75601	+	417	51598339	2957676
Complete genome (Accession number NC_006156)	ABC transporter, ATP-binding protein	75603	76283	+	226	51598340	2957668

Complete genome (Accession number NC_006156)	hypothetical protein BG0079	76280	77533	+	417	51598341	2957671
Complete genome (Accession number NC_006156)	hypothetical protein BG0080	77545	78843	-	432	51598342	2957670
Complete genome (Accession number NC_006156)	hypothetical protein BG0081	78836	79156	-	106	51598343	2957673
Complete genome (Accession number NC_006156)	nifS protein	79339	80607	+	422	51598344	2957672
Complete genome (Accession number NC_006156)	hypothetical protein BG0083	80538	80690	-	50	51598345	2957677
Complete genome (Accession number NC_006156)	hypothetical protein BG0084	80811	81239	+	142	51598346	2957674
Complete genome (Accession number NC_006156)	hypothetical protein BG0085	81232	81492	-	86	51598347	2957678
Complete genome (Accession number NC_006156)	hypothetical protein BG0086	81551	82342	+	263	51598348	2957680
Complete genome (Accession number NC_006156)	hypothetical protein BG0087	82379	82771	+	130	51598349	2957679
Complete genome (Accession number NC_006156)	L-lactate dehydrogenase	82801	83751	-	316	51598350	2957681
Complete genome (Accession number NC_006156)	GTP-binding protein LepA	83874	85679	-	601	51598351	2957827

Complete genome (Accession number NC_006156)	hypothetical protein BG0090	85713	86699	-	328	51598352	2957845
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit K	86759	87193	-	144	51598353	2957887
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit I	87210	89036	-	608	51598354	2957465
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit D	89047	89643	-	198	51598355	2957466
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit B	89646	90950	-	434	51598356	2957463
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit A	90972	92699	-	575	51598357	2957476
Complete genome (Accession number NC_006156)	hypothetical protein BG0096	92713	93258	-	181	51598358	2957174
Complete genome (Accession number NC_006156)	V-type ATP synthase subunit E	93268	93867	-	199	51598359	2957175
Complete genome (Accession number NC_006156)	hypothetical protein BG0098	94053	94439	-	128	51598360	2957472
Complete genome (Accession number NC_006156)	recombination and DNA strand exchange inhibitor protein	94445	96781	-	778	51598361	2957607

Complete genome (Accession number NC_006156)	hypothetical protein BG0100	96771	97694	-	307	51598362	2957453
Complete genome (Accession number NC_006156)	glutamate racemase	97691	98473	-	260	51598363	2957454
Complete genome (Accession number NC_006156)	asparaginyl-tRNA synthetase	98636	100024	+	462	51598364	2957176
Complete genome (Accession number NC_006156)	hypothetical protein BG0103	100039	100560	+	173	51598365	2957386
Complete genome (Accession number NC_006156)	hypothetical protein BG0104	100557	101153	-	198	51598366	2957447
Complete genome (Accession number NC_006156)	periplasmic serine protease DO	101341	102765	-	474	51598367	2957448
Complete genome (Accession number NC_006156)	methionine aminopeptidase	102836	103591	-	251	51598368	2957271
Complete genome (Accession number NC_006156)	hypothetical protein BG0107	103584	105251	-	555	51598369	2957464
Complete genome (Accession number NC_006156)	transcription antitermination protein NusB	105238	105666	-	142	51598370	2957181
Complete genome (Accession number NC_006156)	basic membrane protein	105704	106714	-	336	51598371	2957182
Complete genome (Accession number NC_006156)	acetyl-CoA C-acetyltransferase	106794	107987	-	397	51598372	2957180

Complete genome (Accession number NC_006156)	hypothetical protein BG0111	108130	109494	+	454	51598373	2957457
Complete genome (Accession number NC_006156)	replicative DNA helicase	109505	110872	-	455	51598374	2957189
Complete genome (Accession number NC_006156)	50S ribosomal protein L9	110897	111397	-	166	51598375	2957190
Complete genome (Accession number NC_006156)	30S ribosomal protein S18	111414	111704	-	96	51598376	2957348
Complete genome (Accession number NC_006156)	single-stranded DNA-binding protein	111719	112168	-	149	51598377	2957347
Complete genome (Accession number NC_006156)	30S ribosomal protein S6	112180	112599	-	139	51598378	2957314
Complete genome (Accession number NC_006156)	PTS system, maltose and glucose-specific IIABC component	112743	114437	-	564	51598379	2957315
Complete genome (Accession number NC_006156)	hemolysin III	114639	115340	+	233	51598380	2957387
Complete genome (Accession number NC_006156)	zinc protease, putative	115337	116638	-	433	51598381	2957585
Complete genome (Accession number NC_006156)	phosphatidate cytidylyltransferase	116660	117517	-	285	51598382	2957185

Complete genome (Accession number NC_006156)	undecaprenyl diphosphate synthase	117507	118199	-	230	51598383	2957186
Complete genome (Accession number NC_006156)	ribosome releasing factor	118204	118758	-	184	51598384	2957318
Complete genome (Accession number NC_006156)	elongation factor Ts	118796	119635	-	279	51598385	2957433
Complete genome (Accession number NC_006156)	30S ribosomal protein S2	119632	120420	-	262	51598386	2957197
Complete genome (Accession number NC_006156)	hypothetical protein BG0125	120640	120918	-	92	51598387	2957198
Complete genome (Accession number NC_006156)	hypothetical protein BG0126	120824	120937	-	37	51598388	2957431
Complete genome (Accession number NC_006156)	hypothetical protein BG0127	120938	121720	-	260	51598389	2957536
Complete genome (Accession number NC_006156)	hypothetical protein BG0128	121722	122333	-	203	51598390	2957195
Complete genome (Accession number NC_006156)	30S ribosomal protein S1	122333	123988	-	551	51598391	2957196
Complete genome (Accession number NC_006156)	cytidylate kinase	123991	124656	-	221	51598392	2957248
Complete genome (Accession number NC_006156)	hypothetical protein BG0131	124640	125389	-	249	51598393	2957455

Complete genome (Accession number NC_006156)	hypothetical protein BG0132	125376	126125	-	249	51598394	2957512
Complete genome (Accession number NC_006156)	recombinase A	126149	127237	-	362	51598395	2957513
Complete genome (Accession number NC_006156)	transcript cleavage factor/unknown domain fusion protein	127251	129953	-	900	51598396	2957425
Complete genome (Accession number NC_006156)	hypothetical protein BG0135	129990	130934	-	314	51598397	2957531
Complete genome (Accession number NC_006156)	hypothetical protein BG0136	131119	132246	+	375	51598398	2957206
Complete genome (Accession number NC_006156)	histidyl-tRNA synthetase	132293	133663	-	456	51598399	2957207
Complete genome (Accession number NC_006156)	penicillin-binding protein	133796	135685	+	629	51598400	2957421
Complete genome (Accession number NC_006156)	long-chain-fatty-acid CoA ligase	135686	137578	-	630	51598401	2957519
Complete genome (Accession number NC_006156)	hypothetical protein BG0140	138021	138329	-	102	51598402	2957440
Complete genome (Accession number NC_006156)	acriflavine resistance protein	138331	141543	-	1070	51598403	2957441
Complete genome (Accession number NC_006156)	membrane fusion protein	141562	142515	-	317	51598404	2957414
Complete genome (Accession							

number NC_006156)							
Complete genome (Accession number NC_006156)	hypothetical protein BG0143	142527	143762	-	411	51598405	2957479
Complete genome (Accession number NC_006156)	glycine betaine, L-proline ABC transporter, binding protein	144170	145054	-	294	51598406	2957481
Complete genome (Accession number NC_006156)	glycine betaine, L-proline ABC transporter, permease protein	145069	145968	-	299	51598407	2957482
Complete genome (Accession number NC_006156)	glycine betaine, L-proline ABC transporter, ATP-binding protein	145975	147093	-	372	51598408	2957400
Complete genome (Accession number NC_006156)	flagellin	147245	148255	-	336	51598409	2957384
Complete genome (Accession number NC_006156)	flagellar hook-associated protein FliD	148382	150379	-	665	51598410	2957361
Complete genome (Accession number NC_006156)	N-acetylglucosamine-6-phosphate deacetylase	150550	151755	+	401	51598411	2957362

Complete genome (Accession number NC_006156)	glucosamine-6-phosphate deaminase	151782	152588	+	268	51598412	2957532
Complete genome (Accession number NC_006156)	superoxide dismutase	152655	153266	-	203	51598413	2957282
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecA	153281	155980	-	899	51598414	2957227
Complete genome (Accession number NC_006156)	lipoprotein, putative	156049	157182	+	377	51598415	2957228
Complete genome (Accession number NC_006156)	hypothetical protein BG0154	157214	157642	+	142	51598416	2957377
Complete genome (Accession number NC_006156)	hypothetical protein BG0155	157646	158062	+	138	51598417	2957373
Complete genome (Accession number NC_006156)	antigen, S2, putative	158208	158945	+	245	51598418	2957237
Complete genome (Accession number NC_006156)	antigen S2-related protein	158969	159643	+	224	51598419	2957238
Complete genome (Accession number NC_006156)	alanine racemase	159709	160809	+	366	51598420	2957370
Complete genome (Accession number NC_006156)	hypothetical protein BG0159	160801	162402	-	533	51598421	2957252
Complete genome (Accession number	hypothetical protein BG0160	162479	162646	+	55	51598422	2957217

NC_006156)							
Complete genome (Accession number NC_006156)	hypothetical protein BG0161	162673	164421	-	582	51598423	2957218
Complete genome (Accession number NC_006156)	Na+/Ca+ exchange protein, putative	164502	165488	-	328	51598424	2957357
Complete genome (Accession number NC_006156)	hypothetical protein BG0163	165516	167360	-	614	51598425	2957349
Complete genome (Accession number NC_006156)	4-alpha-glucanotransferase	167472	168992	-	506	51598426	2957578
Complete genome (Accession number NC_006156)	outer membrane protein	169134	170303	+	389	51598427	2957579
Complete genome (Accession number NC_006156)	hypothetical protein BG0166	170305	170370	-	21	51598428	2957296
Complete genome (Accession number NC_006156)	dnaK suppressor, putative	170315	170692	-	125	51598429	2957329
Complete genome (Accession number NC_006156)	translation initiation factor IF-1	170858	171079	+	73	51598430	2957208
Complete genome (Accession number NC_006156)	hypothetical protein BG0169	171126	173177	-	683	51598431	2957209
Complete genome (Accession number NC_006156)	hypothetical protein BG0170	173126	173713	-	195	51598432	2957331

Complete genome (Accession number NC_006156)	hypothetical protein BG0171	173695	174681	-	328	51598433	2957326
Complete genome (Accession number NC_006156)	hypothetical protein BG0172	174678	175679	-	333	51598434	2957266
Complete genome (Accession number NC_006156)	hypothetical protein BG0173	175666	176565	-	299	51598435	2957267
Complete genome (Accession number NC_006156)	hypothetical protein BG0174	176572	177444	-	290	51598436	2957269
Complete genome (Accession number NC_006156)	MoxR-related protein	177462	178454	-	330	51598437	2957444
Complete genome (Accession number NC_006156)	glucose inhibited division protein B	178511	179137	-	208	51598438	2957279
Complete genome (Accession number NC_006156)	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	179134	180999	-	621	51598439	2957280
Complete genome (Accession number NC_006156)	tRNA modification GTPase TrmE	181002	182396	-	464	51598440	2957300
Complete genome (Accession number NC_006156)	flagellar protein, putative	182479	182973	+	164	51598441	2957214
Complete genome (Accession number NC_006156)	flagellar hook-associated protein FlgK	182985	184868	+	627	51598442	2957159

Complete genome (Accession number NC_006156)	flagellar hook-associated protein FlgL	184871	186145	+	424	51598443	2957160
Complete genome (Accession number NC_006156)	flagellar assembly protein FliW	186147	186539	+	130	51598444	2957533
Complete genome (Accession number NC_006156)	carbon storage regulator	186542	186787	+	81	51598445	2957289
Complete genome (Accession number NC_006156)	hypothetical protein BG0184	186771	187424	-	217	51598446	2957285
Complete genome (Accession number NC_006156)	hypothetical protein BG0185	187417	187830	-	137	51598447	2957286
Complete genome (Accession number NC_006156)	hypothetical protein BG0186	187827	188087	-	86	51598448	2957262
Complete genome (Accession number NC_006156)	50S ribosomal protein L20	188301	188648	-	115	51598449	2957298
Complete genome (Accession number NC_006156)	50S ribosomal protein L35	188669	188869	-	66	51598450	2957283
Complete genome (Accession number NC_006156)	translation initiation factor IF-3	188892	189452	-	186	51598451	2957284
Complete genome (Accession number NC_006156)	hypothetical protein BG0190	190055	190297	-	80	51598452	2957529
Complete genome (Accession number NC_006156)	lipoprotein, putative	190318	191058	+	246	51598453	2957272

Complete genome (Accession number NC_006156)	hypothetical protein BG0192	191111	191920	-	269	51598454	2957287
Complete genome (Accession number NC_006156)	hypothetical protein BG0193	191917	193056	-	379	51598455	2957288
Complete genome (Accession number NC_006156)	peptide chain release factor 1	193392	194465	+	357	51598456	2957534
Complete genome (Accession number NC_006156)	HemK family methylase, putative	194468	195289	+	273	51598457	2957216
Complete genome (Accession number NC_006156)	guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	195286	197289	+	667	51598458	2957301
Complete genome (Accession number NC_006156)	hypothetical protein BG0197	197279	199543	+	754	51598459	2957302
Complete genome (Accession number NC_006156)	hypothetical protein BG0198	199488	199592	-	34	51598460	2957167
Complete genome (Accession number NC_006156)	D-alanine--D-alanine ligase	199540	200625	-	361	51598461	2957253
Complete genome (Accession number NC_006156)	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	200627	202153	-	508	51598462	2957178
Complete genome (Accession	hemolysin, putative	202426	203664	+	412	51598463	2957244

number NC_006156)							
Complete genome (Accession number NC_006156)	Lambda CII stability-governing protein	203717	204652	+	311	51598464	2957245
Complete genome (Accession number NC_006156)	Lambda CII stability-governing protein	204653	205624	+	323	51598465	2957303
Complete genome (Accession number NC_006156)	hypothetical protein BG0207	206124	207701	+	525	51598466	2957310
Complete genome (Accession number NC_006156)	hypothetical protein BG0208	207679	208218	-	179	51598467	2957304
Complete genome (Accession number NC_006156)	UTP--glucose-1-phosphate uridylyltransferase	208304	209140	+	278	51598468	2957219
Complete genome (Accession number NC_006156)	hypothetical protein BG0210	209127	210875	+	582	51598469	2957164
Complete genome (Accession number NC_006156)	hypothetical protein BG0211	210902	211657	+	251	51598470	2957165
Complete genome (Accession number NC_006156)	surface-located membrane protein 1	211650	214370	+	906	51598471	2957308
Complete genome (Accession number NC_006156)	DNA mismatch repair protein	214377	216212	+	611	51598472	2957412
Complete genome (Accession number NC_006156)	hypothetical protein BG0214	216231	217262	+	343	51598473	2957306

Complete genome (Accession number NC_006156)	lipoprotein, putative	217345	217998	-	217	51598474	2957183
Complete genome (Accession number NC_006156)	translation elongation factor P	218006	218584	-	192	51598475	2957184
Complete genome (Accession number NC_006156)	phosphate ABC transporter, periplasmic phosphate-binding protein	218750	219586	+	278	51598476	2957320
Complete genome (Accession number NC_006156)	phosphate ABC transporter, permease protein	219676	220584	+	302	51598477	2957311
Complete genome (Accession number NC_006156)	phosphate ABC transporter, permease protein	220755	222125	+	456	51598478	2957324
Complete genome (Accession number NC_006156)	phosphate ABC transporter, ATP-binding protein	222126	222908	+	260	51598479	2957325
Complete genome (Accession number NC_006156)	gufA protein	222911	223732	-	273	51598480	2957265
Complete genome (Accession number NC_006156)	alanyl-tRNA synthetase	223767	225551	-	594	51598481	2957270
Complete genome (Accession number NC_006156)	flagellar motor switch protein	225551	226768	-	405	51598482	2957169

Complete genome (Accession number NC_006156)	6-phosphogluconolactonase	226755	227462	-	235	51598483	2957170
Complete genome (Accession number NC_006156)	hypothetical protein BG0226	227601	227747	-	48	51598484	2957249
Complete genome (Accession number NC_006156)	lipoprotein, putative	227865	228092	-	75	51598485	2957435
Complete genome (Accession number NC_006156)	tRNA-dihydrouridine synthase A	228169	229170	+	333	51598486	2957514
Complete genome (Accession number NC_006156)	seryl-tRNA synthetase	229160	230437	-	425	51598487	2957515
Complete genome (Accession number NC_006156)	hypothetical protein BG0230	230567	231268	+	233	51598488	2957401
Complete genome (Accession number NC_006156)	hypothetical protein BG0231	231284	234202	+	972	51598489	2957330
Complete genome (Accession number NC_006156)	50S ribosomal protein L31 type B	234238	234483	-	81	51598490	2957332
Complete genome (Accession number NC_006156)	transcription termination factor Rho	234544	236091	-	515	51598491	2957333
Complete genome (Accession number NC_006156)	hypothetical protein BG0234	236171	236578	-	135	51598492	2957268
Complete genome (Accession number NC_006156)	hbbU protein	236579	236905	-	108	51598493	2957489

Complete genome (Accession number NC_006156)	30S ribosomal protein S20	236918	237175	-	85	51598494	2957260
Complete genome (Accession number NC_006156)	hypothetical protein BG0237	237246	238073	-	275	51598495	2957261
Complete genome (Accession number NC_006156)	translation-associated GTPase	238088	239194	-	368	51598496	2957275
Complete genome (Accession number NC_006156)	hypothetical protein BG0239	239224	241230	-	668	51598497	2957254
Complete genome (Accession number NC_006156)	apolipoprotein N-acyltransferase	241377	242942	+	521	51598498	2957352
Complete genome (Accession number NC_006156)	hypothetical protein BG0241	242882	243652	-	256	51598499	2957353
Complete genome (Accession number NC_006156)	deoxyguanosine/deoxyadenosine kinase(I) subunit 2	243717	244319	-	200	51598500	2957355
Complete genome (Accession number NC_006156)	glycerol uptake facilitator	244731	245495	+	254	51598501	2957340
Complete genome (Accession number NC_006156)	glycerol kinase	245534	247039	+	501	51598502	2957503
Complete genome (Accession number NC_006156)	glycerol-3-phosphate dehydrogenase, anaerobic	247316	248884	+	522	51598503	2957504

Complete genome (Accession number NC_006156)	hypothetical protein BG0246	248971	249465	-	164	51598504	2957259
Complete genome (Accession number NC_006156)	hypothetical protein BG0247	249452	250006	-	184	51598505	2957356
Complete genome (Accession number NC_006156)	hypothetical protein BG0248	250007	251032	-	341	51598506	2957473
Complete genome (Accession number NC_006156)	hypothetical protein BG0249	251229	251834	+	201	51598507	2957474
Complete genome (Accession number NC_006156)	oligoendopeptidase F	251955	253727	+	590	51598508	2957490
Complete genome (Accession number NC_006156)	phosphatidyltransferase	253741	254445	+	234	51598509	2957246
Complete genome (Accession number NC_006156)	dedA protein	254442	255056	+	204	51598510	2957359
Complete genome (Accession number NC_006156)	leucyl-tRNA synthetase	255253	257775	+	840	51598511	2957256
Complete genome (Accession number NC_006156)	hypothetical protein BG0255	257790	260090	+	766	51598512	2957257
Complete genome (Accession number NC_006156)	ATP-dependent protease LA	260087	262507	-	806	51598513	2957369

Complete genome (Accession number NC_006156)	single-stranded-DNA-specific exonuclease	262784	264910	+	708	51598514	2957309
Complete genome (Accession number NC_006156)	hypothetical protein BG0258	264903	265847	+	314	51598515	2957415
Complete genome (Accession number NC_006156)	30S ribosomal protein S21	265862	266071	+	69	51598516	2957416
Complete genome (Accession number NC_006156)	cell division protein, putative	266107	268458	-	783	51598517	2957488
Complete genome (Accession number NC_006156)	undecaprenyl pyrophosphate phosphatase	268455	269255	-	266	51598518	2957365
Complete genome (Accession number NC_006156)	hypothetical protein BG0262	269270	271417	-	715	51598519	2957242
Complete genome (Accession number NC_006156)	hypothetical protein BG0263	271410	272426	-	338	51598520	2957243
Complete genome (Accession number NC_006156)	hypothetical protein BG0264	272630	274012	+	460	51598521	2957297
Complete genome (Accession number NC_006156)	hypothetical protein BG0265	274019	275272	-	417	51598522	2957291
Complete genome (Accession number NC_006156)	signal peptidase I	275448	275840	+	130	51598523	2957336
Complete genome (Accession number NC_006156)	heat shock protein 70	275865	277334	-	489	51598524	2957337
Complete genome (Accession							

number NC_006156)							
Complete genome (Accession number NC_006156)	hypothetical protein BG0268	277312	277833	-	173	51598525	2957344
Complete genome (Accession number NC_006156)	hypothetical protein BG0269	277853	278155	-	100	51598526	2957234
Complete genome (Accession number NC_006156)	hypothetical protein BG0270	278182	280086	-	634	51598527	2957350
Complete genome (Accession number NC_006156)	hypothetical protein BG0271	280089	280568	-	159	51598528	2957351
Complete genome (Accession number NC_006156)	minD-related ATP-binding protein	280578	281465	-	295	51598529	2957478
Complete genome (Accession number NC_006156)	flagellar biosynthesis regulator FlhF	281477	282643	-	388	51598530	2957354
Complete genome (Accession number NC_006156)	flagellar biosynthesis protein A	282648	284738	-	696	51598531	2957235
Complete genome (Accession number NC_006156)	flagellar biosynthesis protein FlhB	284750	285868	-	372	51598532	2957236
Complete genome (Accession number NC_006156)	flagellar biosynthesis protein	285868	286656	-	262	51598533	2957430
Complete genome (Accession number NC_006156)	flagellar biosynthesis protein	286692	286955	-	87	51598534	2957371

Complete genome (Accession number NC_006156)	flagellar biosynthesis protein FliP	286964	287728	-	254	51598535	2957451
Complete genome (Accession number NC_006156)	flagellar biosynthesis protein	287739	288365	-	208	51598536	2957452
Complete genome (Accession number NC_006156)	flagellar motor switch protein	288358	288699	-	113	51598537	2957233
Complete genome (Accession number NC_006156)	flagellar motor switch protein FliM	288745	289803	-	352	51598538	2957229
Complete genome (Accession number NC_006156)	flagellar basal body-associated protein FliL	289828	290364	-	178	51598539	2957375
Complete genome (Accession number NC_006156)	flagellar motor protein MotB	290412	291194	-	260	51598540	2957376
Complete genome (Accession number NC_006156)	flagellar motor rotation protein A	291194	291976	-	260	51598541	2957338
Complete genome (Accession number NC_006156)	flagellar protein	291973	292197	-	74	51598542	2957417
Complete genome (Accession number NC_006156)	flagellar hook protein FlgE	292219	293547	-	442	51598543	2957199
Complete genome (Accession number NC_006156)	flagellar basal body rod modification protein	293552	293995	-	147	51598544	2957200
Complete genome (Accession	flagellar protein	294009	295196	-	395	51598545	2957379

number NC_006156)							
Complete genome (Accession number NC_006156)	flagellar protein	295204	295782	-	192	51598546	2957255
Complete genome (Accession number NC_006156)	flagellar protein	295814	296245	-	143	51598547	2957381
Complete genome (Accession number NC_006156)	flagellum-specific ATP synthase	296242	297552	-	436	51598548	2957382
Complete genome (Accession number NC_006156)	flagellar assembly protein H	297571	298491	-	306	51598549	2957396
Complete genome (Accession number NC_006156)	flagellar motor switch protein G	298506	299540	-	344	51598550	2957172
Complete genome (Accession number NC_006156)	flagellar MS-ring protein	299556	301265	-	569	51598551	2957154
Complete genome (Accession number NC_006156)	flagellar hook-basal body protein FliE	301280	301615	-	111	51598552	2957155
Complete genome (Accession number NC_006156)	flagellar basal body rod protein FlgC	301627	302085	-	152	51598553	2957191
Complete genome (Accession number NC_006156)	flagellar basal body rod protein FlgB	302109	302516	-	135	51598554	2957391

Complete genome (Accession number NC_006156)	ATP-dependent protease ATP-binding subunit	302550	303896	-	448	51598555	2957193
Complete genome (Accession number NC_006156)	ATP-dependent protease peptidase subunit	303889	304437	-	182	51598556	2957194
Complete genome (Accession number NC_006156)	hypothetical protein BG0300	304447	304563	-	38	51598557	2957398
Complete genome (Accession number NC_006156)	smg protein	304538	305395	-	285	51598558	2957406
Complete genome (Accession number NC_006156)	hypothetical protein BG0302	305402	306094	-	230	51598559	2957404
Complete genome (Accession number NC_006156)	cell division protein FtsZ	306095	307294	-	399	51598560	2957405
Complete genome (Accession number NC_006156)	cell division protein	307316	308557	-	413	51598561	2957222
Complete genome (Accession number NC_006156)	cell division protein	308557	309300	-	247	51598562	2957399
Complete genome (Accession number NC_006156)	cell division protein	309336	310394	-	352	51598563	2957520

Complete genome (Accession number NC_006156)	phospho-N-acetylmuramoyl-pentapeptide-transferase	310437	311492	-	351	51598564	2957521
Complete genome (Accession number NC_006156)	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanine ligase	311510	312901	-	463	51598565	2957545
Complete genome (Accession number NC_006156)	hypothetical protein BG0309	312923	313204	-	93	51598566	2957403
Complete genome (Accession number NC_006156)	hypothetical protein BG0310	313201	314091	-	296	51598567	2957410
Complete genome (Accession number NC_006156)	hypothetical protein BG0311	314084	314920	-	278	51598568	2957411
Complete genome (Accession number NC_006156)	hypothetical protein BG0312	314917	315993	-	358	51598569	2957168
Complete genome (Accession number NC_006156)	hypothetical protein BG0313	316022	316780	-	252	51598570	2957456
Complete genome (Accession number NC_006156)	hypothetical protein BG0314	317096	317935	-	279	51598571	2957418
Complete genome (Accession number NC_006156)	purine-binding chemotaxis protein	317925	318455	-	176	51598572	2957419

Complete genome (Accession number NC_006156)	cell division protein	318501	319079	-	192	51598573	2957413
Complete genome (Accession number NC_006156)	octaprenyl-diphosphate synthase	319130	320173	+	347	51598574	2957201
Complete genome (Accession number NC_006156)	hypothetical protein BG0318	320173	320856	+	227	51598575	2957203
Complete genome (Accession number NC_006156)	hypothetical protein BG0319	320858	321664	-	268	51598576	2957204
Complete genome (Accession number NC_006156)	hypothetical protein BG0320	321665	322597	-	310	51598577	2957526
Complete genome (Accession number NC_006156)	methylgalactoside ABC transporter, ATP-binding protein	322594	324054	-	486	51598578	2957527
Complete genome (Accession number NC_006156)	exported protein	324054	325106	-	350	51598579	2957140
Complete genome (Accession number NC_006156)	hypothetical protein BG0323	325524	326564	-	346	51598580	2957141
Complete genome (Accession number NC_006156)	hypothetical protein BG0324	326853	327983	+	376	51598581	2957205
Complete genome (Accession number NC_006156)	hypothetical protein BG0325	328078	328443	+	121	51598582	2957220

Complete genome (Accession number NC_006156)	hypothetical protein BG0326	328450	329559	-	369	51598583	2957423
Complete genome (Accession number NC_006156)	hypothetical protein BG0327	329610	332414	-	934	51598584	2957424
Complete genome (Accession number NC_006156)	glycerol-3-phosphate O-acyltransferase, putative	332438	333331	-	297	51598585	2957420
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	333722	335293	+	523	51598586	2957449
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	335391	336974	+	527	51598587	2957540
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	337116	338741	+	541	51598588	2957541
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, permease protein	339078	339998	+	306	51598589	2957496

Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, permease protein	340011	341060	+	349	51598590	2957142
Complete genome (Accession number NC_006156)	hypothetical protein BG0334	341068	341115	+	15	51598591	2957427
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, ATP-binding protein	341072	341944	+	290	51598592	2957428
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, ATP-binding protein	341945	342916	+	323	51598593	2957537
Complete genome (Accession number NC_006156)	P26	342930	343685	-	251	51598594	2957439
Complete genome (Accession number NC_006156)	enolase	343804	345120	+	438	51598595	2957276
Complete genome (Accession number NC_006156)	30S ribosomal protein S9	345172	345582	-	136	51598596	2957277
Complete genome (Accession number NC_006156)	50S ribosomal protein L13	345579	346043	-	154	51598597	2957528
Complete genome (Accession number NC_006156)	hypothetical protein BG0341	346096	346932	-	278	51598598	2957443
Complete genome (Accession number NC_006156)	aspartyl/glutamyl-tRNA amidotransferase subunit B	346898	348355	-	485	51598599	2957239

Complete genome (Accession number NC_006156)	Glu-tRNA(Gln) amidotransferase, subunit A	348345	349790	-	481	51598600	2957240
Complete genome (Accession number NC_006156)	aspartyl/glutamyl-tRNA amidotransferase subunit C	349801	350076	-	91	51598601	2957436
Complete genome (Accession number NC_006156)	DNA helicase	350086	352182	-	698	51598602	2957535
Complete genome (Accession number NC_006156)	hypothetical protein BG0346	352185	353384	-	399	51598603	2957393
Complete genome (Accession number NC_006156)	hypothetical protein BG0347	353395	354045	-	216	51598604	2957394
Complete genome (Accession number NC_006156)	fibronectin/fibrinogen-binding protein, putative	354239	355657	+	472	51598605	2957187
Complete genome (Accession number NC_006156)	pyruvate kinase	355755	357188	+	477	51598606	2957437
Complete genome (Accession number NC_006156)	hypothetical protein BG0350	357206	357946	+	246	51598607	2957442
Complete genome (Accession number NC_006156)	50S ribosomal protein L28	357965	358243	-	92	51598608	2957273
Complete genome (Accession number NC_006156)	hypothetical protein BG0352	358265	359827	-	520	51598609	2957274

Complete genome (Accession number NC_006156)	hypothetical protein BG0353	359950	361071	+	373	51598610	2957480
Complete genome (Accession number NC_006156)	hypothetical protein BG0354	361068	362867	-	599	51598611	2957471
Complete genome (Accession number NC_006156)	hypothetical protein BG0355	362880	363830	-	316	51598612	2957334
Complete genome (Accession number NC_006156)	transcription factor, putative	363864	364352	-	162	51598613	2957499
Complete genome (Accession number NC_006156)	hypothetical protein BG0357	364392	364985	-	197	51598614	2957500
Complete genome (Accession number NC_006156)	hypothetical protein BG0358	364978	365709	-	243	51598615	2957475
Complete genome (Accession number NC_006156)	carboxyl-terminal protease	365713	367143	-	476	51598616	2957226
Complete genome (Accession number NC_006156)	minD-related ATP-binding protein	367637	368779	+	380	51598617	2957450
Complete genome (Accession number NC_006156)	prolipoprotein diacylglyceryl transferase	368779	369765	+	328	51598618	2957263
Complete genome (Accession number NC_006156)	periplasmic protein	369786	371798	+	670	51598619	2957264
Complete genome (Accession number	methylglyoxal synthase	371893	372273	+	126	51598620	2957171

NC_006156)							
Complete genome (Accession number NC_006156)	lipoprotein LA7	372327	372914	-	195	51598621	2957422
Complete genome (Accession number NC_006156)	putative aminopeptidase 1	373038	374414	+	458	51598622	2957317
Complete genome (Accession number NC_006156)	hypothetical protein BG0366	374421	374699	+	92	51598623	2957445
Complete genome (Accession number NC_006156)	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	374725	375780	-	351	51598624	2957213
Complete genome (Accession number NC_006156)	ATP-dependent Clp protease, subunit A	375798	378065	-	755	51598625	2957467
Complete genome (Accession number NC_006156)	tyrosyl-tRNA synthetase	378103	379320	-	405	51598626	2957409
Complete genome (Accession number NC_006156)	glycyl-tRNA synthetase	379317	380654	-	445	51598627	2957156
Complete genome (Accession number NC_006156)	glutamyl-tRNA synthetase	380672	382144	-	490	51598628	2957485
Complete genome (Accession number NC_006156)	hypothetical protein BG0372	382157	382924	-	255	51598629	2957511

Complete genome (Accession number NC_006156)	hypothetical protein BG0373	383050	384186	+	378	51598630	2957544
Complete genome (Accession number NC_006156)	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative	384209	384922	+	237	51598631	2957392
Complete genome (Accession number NC_006156)	S-adenosylmethionine synthetase	384919	386097	+	392	51598632	2957498
Complete genome (Accession number NC_006156)	S-ribosylhomocysteinase	386094	386567	+	157	51598633	2957157
Complete genome (Accession number NC_006156)	hypothetical protein BG0377	386578	387237	-	219	51598634	2957158
Complete genome (Accession number NC_006156)	protein kinase C1 inhibitor	387264	387683	-	139	51598635	2957225
Complete genome (Accession number NC_006156)	Mg2+ transport protein	387734	389098	-	454	51598636	2957364
Complete genome (Accession number NC_006156)	hypothetical protein BG0380	389152	390576	-	474	51598637	2957374
Complete genome (Accession number NC_006156)	basic membrane protein B	390689	391714	-	341	51598638	2957152

Complete genome (Accession number NC_006156)	basic membrane protein A	391811	392824	-	337	51598639	2957497
Complete genome (Accession number NC_006156)	basic membrane protein A	393689	394702	-	337	51598640	2957518
Complete genome (Accession number NC_006156)	basic membrane protein C	394743	395804	-	353	51598641	2957339
Complete genome (Accession number NC_006156)	basic membrane protein D	396127	397152	-	341	51598642	2957188
Complete genome (Accession number NC_006156)	30S ribosomal protein S7	397254	397727	-	157	51598643	2957395
Complete genome (Accession number NC_006156)	30S ribosomal protein S12	397752	398126	-	124	51598644	2957507
Complete genome (Accession number NC_006156)	DNA-directed RNA polymerase subunit beta'	398192	402325	-	1377	51598645	2957150
Complete genome (Accession number NC_006156)	DNA-directed RNA polymerase subunit beta	402341	405808	-	1155	51598646	2957177
Complete genome (Accession number NC_006156)	50S ribosomal protein L7/L12	405891	406265	-	124	51598647	2957147
Complete genome (Accession number NC_006156)	50S ribosomal protein L10	406336	406824	-	162	51598648	2957161

Complete genome (Accession number NC_006156)	50S ribosomal protein L1	406829	407509	-	226	51598649	2957163
Complete genome (Accession number NC_006156)	50S ribosomal protein L11	407509	407940	-	143	51598650	2957510
Complete genome (Accession number NC_006156)	transcription antitermination factor	407992	408546	-	184	51598651	2957539
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecE	408570	408740	-	56	51598652	2957517
Complete genome (Accession number NC_006156)	50S ribosomal protein L33	408848	409027	-	59	51598653	2957146
Complete genome (Accession number NC_006156)	hypothetical protein BG0400	409192	410049	-	285	51598654	2957293
Complete genome (Accession number NC_006156)	lipoprotein, putative	410063	411094	-	343	51598655	2957294
Complete genome (Accession number NC_006156)	hypothetical protein BG0402	411418	412077	+	219	51598656	2957148
Complete genome (Accession number NC_006156)	hypothetical protein BG0403	412087	413610	-	507	51598657	2957144
Complete genome (Accession number NC_006156)	glutamate transporter, putative	413744	414946	+	400	51598658	2957524
Complete genome (Accession number NC_006156)	prolyl-tRNA synthetase	414958	416424	-	488	51598659	2957143

Complete genome (Accession number NC_006156)	hypothetical protein BG0406	416477	417046	-	189	51598660	2957880
Complete genome (Accession number NC_006156)	hypothetical protein BG0407	417734	418345	+	203	51598661	2957426
Complete genome (Accession number NC_006156)	hypothetical protein BG0408	418356	418967	+	203	51598662	2957865
Complete genome (Accession number NC_006156)	mannose-6-phosphate isomerase	419020	420135	-	371	51598663	2957881
Complete genome (Accession number NC_006156)	PTS system, fructose-specific IIABC component	420132	422009	-	625	51598664	2957530
Complete genome (Accession number NC_006156)	hypothetical protein BG0411	422179	422808	+	209	51598665	2957868
Complete genome (Accession number NC_006156)	endonuclease precursor	422805	423686	+	293	51598666	2957869
Complete genome (Accession number NC_006156)	hypothetical protein BG0413	423683	424462	+	259	51598667	2957542
Complete genome (Accession number NC_006156)	hypothetical protein BG0414	424450	425070	-	206	51598668	2957543
Complete genome (Accession number NC_006156)	hypothetical protein BG0415	425063	425125	-	20	51598669	2957871

Complete genome (Accession number NC_006156)	chemotaxis protein methyltransferase	425317	426174	+	285	51598670	2957886
Complete genome (Accession number NC_006156)	hypothetical protein BG0417	426110	426193	+	27	51598671	2957385
Complete genome (Accession number NC_006156)	protein-glutamate methylesterase	426207	427334	+	375	51598672	2957875
Complete genome (Accession number NC_006156)	pheromone shutdown protein	427358	428572	+	404	51598673	2957888
Complete genome (Accession number NC_006156)	adenylate kinase	428611	429246	+	211	51598674	2957295
Complete genome (Accession number NC_006156)	hypothetical protein BG0421	429269	430312	+	347	51598675	2957892
Complete genome (Accession number NC_006156)	response regulatory protein	430331	431254	-	307	51598676	2957915
Complete genome (Accession number NC_006156)	sensory transduction histidine kinase/response regulator	431257	435747	-	1496	51598677	2957342
Complete genome (Accession number NC_006156)	hydrolase	442357	443196	-	279	51598678	2957895
Complete genome (Accession number NC_006156)	3-methyladenine DNA glycosylase	443330	443890	-	186	51598679	2957903

Complete genome (Accession number NC_006156)	hypothetical protein BG0431	445610	445708	-	32	51598680	2957893
Complete genome (Accession number NC_006156)	hypothetical protein BG0434	448522	449070	-	182	51598681	2957912
Complete genome (Accession number NC_006156)	hypothetical protein BG0435	449165	449839	-	224	51598682	2957995
Complete genome (Accession number NC_006156)	hypothetical protein BG0436	450048	450365	+	105	51598683	2957890
Complete genome (Accession number NC_006156)	hypothetical protein BG0437	450395	450784	-	129	51598684	2957891
Complete genome (Accession number NC_006156)	hypothetical protein BG0438	450902	451507	+	201	51598685	2957564
Complete genome (Accession number NC_006156)	chromosome segregation protein, putative	451616	452368	+	250	51598686	2957996
Complete genome (Accession number NC_006156)	hypothetical protein BG0440	452371	453084	+	237	51598687	2957994
Complete genome (Accession number NC_006156)	stage 0 sporulation protein J	453353	454135	-	260	51598688	2957565
Complete genome (Accession number NC_006156)	DNA gyrase, subunit A	454254	456686	-	810	51598689	2957946
Complete genome (Accession number NC_006156)	DNA gyrase, subunit B	456698	458602	-	634	51598690	2957949

Complete genome (Accession number NC_006156)	chromosomal replication initiator protein	458789	460243	+	484	51598691	2957604
Complete genome (Accession number NC_006156)	DNA polymerase III, subunit beta	460484	461644	+	386	51598692	2957989
Complete genome (Accession number NC_006156)	hypothetical protein BG0446	461737	462036	+	99	51598693	2957944
Complete genome (Accession number NC_006156)	50S ribosomal protein L34	462128	462283	+	51	51598694	2957566
Complete genome (Accession number NC_006156)	ribonuclease P protein component	462264	462599	+	111	51598695	2957951
Complete genome (Accession number NC_006156)	putative inner membrane protein translocase component YidC	462610	464244	+	544	51598696	2957947
Complete genome (Accession number NC_006156)	spoIIIJ-associated protein	464257	464985	+	242	51598697	2957586
Complete genome (Accession number NC_006156)	hypothetical protein BG0451	464912	465016	+	34	51598698	2957948
Complete genome (Accession number NC_006156)	nucleotide sugar epimerase	465031	466098	+	355	51598699	2957941
Complete genome (Accession number NC_006156)	fructose-bisphosphate aldolase	466260	467339	+	359	51598700	2957942

Complete genome (Accession number NC_006156)	aspartyl-tRNA synthetase	467793	469553	-	586	51598701	2957979
Complete genome (Accession number NC_006156)	Na+/H+ antiporter	469557	471662	-	701	51598702	2957954
Complete genome (Accession number NC_006156)	phosphocarrier protein HPr	471677	471940	-	87	51598703	2957583
Complete genome (Accession number NC_006156)	hypothetical protein BG0457	471953	472246	-	97	51598704	2957970
Complete genome (Accession number NC_006156)	RNA polymerase sigma-54 factor	472236	473393	-	385	51598705	2957971
Complete genome (Accession number NC_006156)	chromate transport protein, putative	473498	474031	-	177	51598706	2957588
Complete genome (Accession number NC_006156)	hypothetical protein BG0460	474028	474621	-	197	51598707	2957589
Complete genome (Accession number NC_006156)	hypothetical protein BG0461	474590	474709	-	39	51598708	2957953
Complete genome (Accession number NC_006156)	hypothetical protein BG0462	474840	475682	+	280	51598709	2957983
Complete genome (Accession number NC_006156)	lipopolysaccharide biosynthesis-related protein	475679	476827	-	382	51598710	2957584
Complete genome (Accession number NC_006156)	hypothetical protein BG0464	476884	477873	+	329	51598711	2957976

Complete genome (Accession number NC_006156)	hypothetical protein BG0465	477940	478518	+	192	51598712	2957937
Complete genome (Accession number NC_006156)	excinuclease ABC, subunit C	478590	480332	-	580	51598713	2957594
Complete genome (Accession number NC_006156)	hypothetical protein BG0467	480523	482040	+	505	51598714	2957988
Complete genome (Accession number NC_006156)	hypothetical protein BG0468	482033	483352	+	439	51598715	2957977
Complete genome (Accession number NC_006156)	lipoprotein, putative	483664	484368	-	234	51598716	2957602
Complete genome (Accession number NC_006156)	DNA polymerase III subunits gamma and tau	484951	486633	+	560	51598717	2957980
Complete genome (Accession number NC_006156)	hypothetical protein BG0475	486638	486937	+	99	51598718	2957965
Complete genome (Accession number NC_006156)	nucleoside-diphosphate kinase	487109	487618	+	169	51598719	2957595
Complete genome (Accession number NC_006156)	hypothetical protein BG0477	487889	488431	+	180	51598720	2957975
Complete genome (Accession number NC_006156)	hypothetical protein BG0478	488428	489123	+	231	51598721	2957972

Complete genome (Accession number NC_006156)	ABC transporter, ATP-binding protein	489092	489892	+	266	51598722	2957603
Complete genome (Accession number NC_006156)	hypothetical protein BG0480	489889	490578	+	229	51598723	2957955
Complete genome (Accession number NC_006156)	hypothetical protein BG0481	490580	491326	+	248	51598724	2957973
Complete genome (Accession number NC_006156)	signal peptidase II	491337	491849	+	170	51598725	2957974
Complete genome (Accession number NC_006156)	hypothetical protein BG0483	492085	492915	+	276	51598726	2957967
Complete genome (Accession number NC_006156)	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	493043	494326	+	427	51598727	2957968
Complete genome (Accession number NC_006156)	hypothetical protein BG0485	494922	496280	+	452	51598728	2957600
Complete genome (Accession number NC_006156)	lipoprotein, putative	496574	496705	-	43	51598729	2957601
Complete genome (Accession number NC_006156)	elongation factor Tu	497347	498531	+	394	51598730	2957964
Complete genome (Accession number NC_006156)	30S ribosomal protein S10	498583	498894	+	103	51598731	2957963
Complete genome (Accession	50S ribosomal protein L3	498935	499555	+	206	51598732	2957609

number NC_006156)							
Complete genome (Accession number NC_006156)	50S ribosomal protein L4	499565	500194	+	209	51598733	2957966
Complete genome (Accession number NC_006156)	hypothetical protein BG0491	500184	500228	+	14	51598734	2957960
Complete genome (Accession number NC_006156)	50S ribosomal protein L23	500215	500511	+	98	51598735	2957617
Complete genome (Accession number NC_006156)	50S ribosomal protein L2	500533	501366	+	277	51598736	2957956
Complete genome (Accession number NC_006156)	30S ribosomal protein S19	501376	501654	+	92	51598737	2957742
Complete genome (Accession number NC_006156)	50S ribosomal protein L22	501623	502024	+	133	51598738	2957745
Complete genome (Accession number NC_006156)	30S ribosomal protein S3	502028	502906	+	292	51598739	2957824
Complete genome (Accession number NC_006156)	50S ribosomal protein L16	502911	503327	+	138	51598740	2957904
Complete genome (Accession number NC_006156)	50S ribosomal protein L29	503330	503530	+	66	51598741	2957898
Complete genome (Accession number NC_006156)	30S ribosomal protein S17	503533	503787	+	84	51598742	2957877

Complete genome (Accession number NC_006156)	50S ribosomal protein L14	503815	504183	+	122	51598743	2957221
Complete genome (Accession number NC_006156)	50S ribosomal protein L24	504198	504503	+	101	51598744	2957343
Complete genome (Accession number NC_006156)	50S ribosomal protein L5	504509	505057	+	182	51598745	2957434
Complete genome (Accession number NC_006156)	30S ribosomal protein S14	505075	505260	+	61	51598746	2957162
Complete genome (Accession number NC_006156)	30S ribosomal protein S8	505270	505668	+	132	51598747	2957577
Complete genome (Accession number NC_006156)	50S ribosomal protein L6	505686	506228	+	180	51598748	2957438
Complete genome (Accession number NC_006156)	50S ribosomal protein L18	506246	506605	+	119	51598749	2957548
Complete genome (Accession number NC_006156)	30S ribosomal protein S5	506618	507118	+	166	51598750	2957487
Complete genome (Accession number NC_006156)	ribosomal protein L30	507122	507433	+	103	51598751	2957321
Complete genome (Accession number NC_006156)	50S ribosomal protein L15	507426	507863	+	145	51598752	2957597
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecY	507876	509180	+	434	51598753	2957590

Complete genome (Accession number NC_006156)	50S ribosomal protein L36	509193	509306	+	37	51598754	2957550
Complete genome (Accession number NC_006156)	30S ribosomal protein S13	509324	509701	+	125	51598755	2957560
Complete genome (Accession number NC_006156)	30S ribosomal protein S11	509729	510121	+	130	51598756	2957610
Complete genome (Accession number NC_006156)	DNA-directed RNA polymerase subunit alpha	510137	511171	+	344	51598757	2957563
Complete genome (Accession number NC_006156)	50S ribosomal protein L17	511193	511564	+	123	51598758	2957618
Complete genome (Accession number NC_006156)	hypothetical protein BG0516	511634	513166	+	510	51598759	2957599
Complete genome (Accession number NC_006156)	hypothetical protein BG0517	513156	513944	+	262	51598760	2957627
Complete genome (Accession number NC_006156)	hemolysin	513997	514716	+	239	51598761	2957662
Complete genome (Accession number NC_006156)	hypothetical protein BG0519	514713	515459	-	248	51598762	2957653
Complete genome (Accession number NC_006156)	GTP-binding protein EngA	515546	516847	+	433	51598763	2957651

Complete genome (Accession number NC_006156)	hypothetical protein BG0521	516844	518103	+	419	51598764	2957690
Complete genome (Accession number NC_006156)	hypothetical protein BG0522	518100	518786	+	228	51598765	2957691
Complete genome (Accession number NC_006156)	hypothetical protein BG0523	518806	525294	+	2162	51598766	2957710
Complete genome (Accession number NC_006156)	phenylalanyl-tRNA synthetase subunit alpha	525306	526868	+	520	51598767	2957709
Complete genome (Accession number NC_006156)	phenylalanyl-tRNA synthetase subunit beta	526856	528556	+	566	51598768	2957705
Complete genome (Accession number NC_006156)	thioredoxin reductase	528627	529607	+	326	51598769	2957706
Complete genome (Accession number NC_006156)	rRNA methylase	529657	530397	-	246	51598770	2957718
Complete genome (Accession number NC_006156)	heat shock protein	530400	531494	-	364	51598771	2957722
Complete genome (Accession number NC_006156)	molecular chaperone DnaK	531494	533401	-	635	51598772	2957753
Complete genome (Accession number NC_006156)	grpE protein	533425	533988	-	187	51598773	2957794
Complete genome (Accession number NC_006156)	NH(3)-dependent NAD+ synthetase	534365	535903	+	512	51598774	2957720

Complete genome (Accession number NC_006156)	hypothetical protein BG0532	536747	536842	+	31	51598775	2957783
Complete genome (Accession number NC_006156)	inositol monophosphatase	537167	537343	+	58	51598776	2957767
Complete genome (Accession number NC_006156)	hypothetical protein BG0534	537370	537786	-	138	51598777	2957768
Complete genome (Accession number NC_006156)	hypothetical protein BG0535	537927	539708	+	593	51598778	2957782
Complete genome (Accession number NC_006156)	pantothenate kinase	539701	540489	+	262	51598779	2957785
Complete genome (Accession number NC_006156)	aldose reductase, putative	540511	541458	-	315	51598780	2957784
Complete genome (Accession number NC_006156)	hypothetical protein BG0538	541547	542356	-	269	51598781	2957786
Complete genome (Accession number NC_006156)	hypothetical protein BG0539	542340	542954	-	204	51598782	2957788
Complete genome (Accession number NC_006156)	hypothetical protein BG0540	542957	544252	-	431	51598783	2957789
Complete genome (Accession number NC_006156)	phnP protein	544446	545207	+	253	51598784	2957787
Complete genome (Accession number NC_006156)	exodeoxyribonuclease III	545228	545995	+	255	51598785	2957798

Complete genome (Accession number NC_006156)	hypothetical protein BG0543	546011	546784	+	257	51598786	2957793
Complete genome (Accession number NC_006156)	zinc protease, putative	546765	549566	+	933	51598787	2957799
Complete genome (Accession number NC_006156)	hypothetical protein BG0547	549999	550643	-	214	51598788	2957837
Complete genome (Accession number NC_006156)	hypothetical protein BG0548	550640	550996	-	118	51598789	2957809
Complete genome (Accession number NC_006156)	hypothetical protein BG0549	551081	551779	-	232	51598790	2957812
Complete genome (Accession number NC_006156)	elongation factor G	551802	553883	-	693	51598791	2957985
Complete genome (Accession number NC_006156)	hypothetical protein BG0551	554195	554422	+	75	51598792	2957990
Complete genome (Accession number NC_006156)	hypothetical protein BG0552	554653	555180	+	175	51598793	2957991
Complete genome (Accession number NC_006156)	hypothetical protein BG0553	555289	555939	+	216	51598794	2957935
Complete genome (Accession number NC_006156)	phosphoribosylpyrophosphate synthetase	556145	557365	+	406	51598795	2957913
Complete genome (Accession number NC_006156)	xylulokinase	557369	558736	+	455	51598796	2957906

Complete genome (Accession number NC_006156)	hypothetical protein BG0556	558719	559402	-	227	51598797	2957909
Complete genome (Accession number NC_006156)	dephospho-CoA kinase	559386	560003	-	205	51598798	2957910
Complete genome (Accession number NC_006156)	DNA polymerase I	559985	562714	-	909	51598799	2957902
Complete genome (Accession number NC_006156)	hypothetical protein BG0559	562711	563115	-	134	51598800	2957900
Complete genome (Accession number NC_006156)	flagellar protein	563105	563524	-	139	51598801	2957889
Complete genome (Accession number NC_006156)	chemotaxis response regulator	563533	563913	-	126	51598802	2957899
Complete genome (Accession number NC_006156)	DNA ligase	564160	566142	+	660	51598803	2957884
Complete genome (Accession number NC_006156)	hypothetical protein BG0563	566167	567654	-	495	51598804	2957872
Complete genome (Accession number NC_006156)	hypothetical protein BG0564	567938	569800	+	620	51598805	2957873
Complete genome (Accession number NC_006156)	hypothetical protein BG0565	569787	570254	+	155	51598806	2957151
Complete genome (Accession number NC_006156)	hypothetical protein BG0566	570247	571116	+	289	51598807	2957145

Complete genome (Accession number NC_006156)	phosphocarrier protein HPr	571254	571514	+	86	51598808	2957328
Complete genome (Accession number NC_006156)	phosphoenolpyruvate-protein phosphatase	571535	573256	+	573	51598809	2957389
Complete genome (Accession number NC_006156)	glucose-specific PTS system component	573259	573828	+	189	51598810	2957390
Complete genome (Accession number NC_006156)	heat shock protein 90	573866	575716	-	616	51598811	2957327
Complete genome (Accession number NC_006156)	6-phosphogluconate dehydrogenase	575829	577223	+	464	51598812	2957345
Complete genome (Accession number NC_006156)	hypothetical protein BG0572	577254	577793	-	179	51598813	2957549
Complete genome (Accession number NC_006156)	hypothetical protein BG0573	577947	578465	-	172	51598814	2957570
Complete genome (Accession number NC_006156)	hypothetical protein BG0574	578547	579131	-	194	51598815	2957322
Complete genome (Accession number NC_006156)	purine-binding chemotaxis protein	579337	579879	+	180	51598816	2957323
Complete genome (Accession number NC_006156)	hypothetical protein BG0576	579891	580202	+	103	51598817	2957551

Complete genome (Accession number NC_006156)	chemotaxis histidine kinase	580218	582359	+	713	51598818	2957620
Complete genome (Accession number NC_006156)	protein-glutamate methylesterase	582415	583572	+	385	51598819	2957569
Complete genome (Accession number NC_006156)	hypothetical protein BG0579	583575	585347	+	590	51598820	2957652
Complete genome (Accession number NC_006156)	chemotaxis response regulator	585388	585762	+	124	51598821	2957571
Complete genome (Accession number NC_006156)	uridylate kinase	586119	586808	-	229	51598822	2957643
Complete genome (Accession number NC_006156)	glycosyl transferase	587026	588090	+	354	51598823	2957701
Complete genome (Accession number NC_006156)	ABC transporter, ATP-binding protein	588153	588959	+	268	51598824	2957614
Complete genome (Accession number NC_006156)	hypothetical protein BG0585	588966	589817	+	283	51598825	2957694
Complete genome (Accession number NC_006156)	CTP synthetase	590007	591608	+	533	51598826	2957695
Complete genome (Accession number NC_006156)	hypothetical protein BG0587	591625	592149	-	174	51598827	2957689
Complete genome (Accession number NC_006156)	hypothetical protein BG0588	592285	592875	+	196	51598828	2957725

Complete genome (Accession number NC_006156)	hypothetical protein BG0589	593107	593169	+	20	51598829	2957687
Complete genome (Accession number NC_006156)	methyl-accepting chemotaxis protein	593123	594295	+	390	51598830	2957726
Complete genome (Accession number NC_006156)	DNA polymerase III subunit alpha	594425	597868	+	1147	51598831	2957727
Complete genome (Accession number NC_006156)	hypothetical protein BG0592	597877	598458	+	193	51598832	2957724
Complete genome (Accession number NC_006156)	DNA recombinase	598468	600528	+	686	51598833	2957735
Complete genome (Accession number NC_006156)	carboxypeptidase, putative	600525	601211	-	228	51598834	2957732
Complete genome (Accession number NC_006156)	MATE efflux family protein	601450	602787	+	445	51598835	2957728
Complete genome (Accession number NC_006156)	hypothetical protein BG0596	602800	602997	+	65	51598836	2957733
Complete genome (Accession number NC_006156)	hypothetical protein BG0597	602966	604321	+	451	51598837	2957734
Complete genome (Accession number NC_006156)	UDP-N-acetylmuramoylalanine--D-glutamate ligase	604334	605689	+	451	51598838	2957769
Complete genome (Accession number	femA protein	605686	606729	-	347	51598839	2957744

NC_006156)							
Complete genome (Accession number NC_006156)	methionyl-tRNA synthetase	606739	608913	-	724	51598840	2957737
Complete genome (Accession number NC_006156)	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase, putative	609072	609866	+	264	51598841	2957358
Complete genome (Accession number NC_006156)	phosphate acetyltransferase	609978	611015	+	345	51598842	2957781
Complete genome (Accession number NC_006156)	dimethyladenosine transferase	610998	611843	-	281	51598843	2957791
Complete genome (Accession number NC_006156)	competence locus E, putative	612518	613132	-	204	51598844	2957792
Complete genome (Accession number NC_006156)	hypothetical protein BG0605	613249	613962	+	237	51598845	2957750
Complete genome (Accession number NC_006156)	long-chain-fatty-acid CoA ligase	613988	615925	+	645	51598846	2957801
Complete genome (Accession number NC_006156)	arginyl-tRNA synthetase	615954	617711	-	585	51598847	2957800
Complete genome (Accession number NC_006156)	hypothetical protein BG0608	617777	618073	+	98	51598848	2957806

Complete genome (Accession number NC_006156)	methyl-accepting chemotaxis protein	618325	620472	-	715	51598849	2957807
Complete genome (Accession number NC_006156)	methyl-accepting chemotaxis protein	620741	622948	+	735	51598850	2957808
Complete genome (Accession number NC_006156)	UDP-N-acetylmuramate dehydrogenase	622945	623865	-	306	51598851	2957815
Complete genome (Accession number NC_006156)	cysteinyl-tRNA synthetase	623917	625359	+	480	51598852	2957814
Complete genome (Accession number NC_006156)	hypothetical protein BG0613	625363	626934	+	523	51598853	2957817
Complete genome (Accession number NC_006156)	serine hydroxymethyltransferase	626934	628187	+	417	51598854	2957830
Complete genome (Accession number NC_006156)	DnaJ domain containing protein	628214	628966	+	250	51598855	2957828
Complete genome (Accession number NC_006156)	membrane-associated protein p66	629026	630891	-	621	51598856	2957829
Complete genome (Accession number NC_006156)	L-lactate permease	631139	632647	-	502	51598857	2957833
Complete genome (Accession number NC_006156)	serine-type D-Ala-D-Ala carboxypeptidase	632719	633924	+	401	51598858	2957825
Complete genome (Accession number NC_006156)	hypothetical protein BG0619	633941	634432	+	163	51598859	2957839

Complete genome (Accession number NC_006156)	rep helicase, single-stranded DNA-dependent ATPase	634435	636411	+	658	51598860	2957835
Complete genome (Accession number NC_006156)	aminoacyl-histidine dipeptidase	636526	637956	+	476	51598861	2957834
Complete genome (Accession number NC_006156)	trigger factor	638527	639885	+	452	51598862	2957844
Complete genome (Accession number NC_006156)	ATP-dependent Clp protease proteolytic component	639900	640484	+	194	51598863	2957855
Complete genome (Accession number NC_006156)	ATP-dependent protease ATP-binding subunit	640493	641800	+	435	51598864	2957854
Complete genome (Accession number NC_006156)	ATP-dependent protease LA	641769	644177	+	802	51598865	2957856
Complete genome (Accession number NC_006156)	hypothetical protein BG0630	644211	644363	+	50	51598866	2957852
Complete genome (Accession number NC_006156)	hypothetical protein BG0631	644293	644400	+	35	51598867	2957858
Complete genome (Accession number NC_006156)	30S ribosomal protein S4	644425	645051	-	208	51598868	2957863

Complete genome (Accession number NC_006156)	hypothetical protein BG0634	645228	646589	-	453	51598869	2957843
Complete genome (Accession number NC_006156)	hypothetical protein BG0635	646710	647078	+	122	51598870	2957846
Complete genome (Accession number NC_006156)	cytidine deaminase	647101	647541	-	146	51598871	2957847
Complete genome (Accession number NC_006156)	hypothetical protein BG0637	647662	648624	+	320	51598872	2957816
Complete genome (Accession number NC_006156)	beta-glucosidase, putative	648602	650197	-	531	51598873	2957848
Complete genome (Accession number NC_006156)	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein	650496	651050	+	184	51598874	2957822
Complete genome (Accession number NC_006156)	acetate kinase	651105	652322	-	405	51598875	2957780
Complete genome (Accession number NC_006156)	transcription-repair coupling factor	652347	655721	-	1124	51598876	2957821
Complete genome (Accession number NC_006156)	hypothetical protein BG0643	655818	656780	+	320	51598877	2957795

Complete genome (Accession number NC_006156)	N-acetylmuramoyl-L-alanine amidase, putative	656749	658836	+	695	51598878	2957778
Complete genome (Accession number NC_006156)	small primase-like protein	658919	659467	-	182	51598879	2957779
Complete genome (Accession number NC_006156)	hypothetical protein BG0647	659436	659486	-	16	51598880	2957746
Complete genome (Accession number NC_006156)	putative aminopeptidase 2	659470	660741	-	423	51598881	2957290
Complete genome (Accession number NC_006156)	hypothetical protein BG0649	660825	661553	+	242	51598882	2957501
Complete genome (Accession number NC_006156)	PTS system, fructose-specific IIABC component	661581	663446	-	621	51598883	2957502
Complete genome (Accession number NC_006156)	1-phosphofructokinase	663536	664459	+	307	51598884	2957749
Complete genome (Accession number NC_006156)	hypothetical protein BG0652	664534	664848	-	104	51598885	2957372
Complete genome (Accession number NC_006156)	exodeoxyribonuclease V, alpha chain	665116	666948	-	610	51598886	2957522
Complete genome (Accession number NC_006156)	exodeoxyribonuclease V, beta chain	666945	670451	-	1168	51598887	2957523

Complete genome (Accession number NC_006156)	exodeoxyribonuclease V, gamma chain	670457	673696	-	1079	51598888	2957299
Complete genome (Accession number NC_006156)	nicotinate phosphoribosyltransferase	673700	675145	-	481	51598889	2957368
Complete genome (Accession number NC_006156)	glucose-6-phosphate 1-dehydrogenase	675258	676694	+	478	51598890	2957173
Complete genome (Accession number NC_006156)	Na+/H+ antiporter	676956	678299	+	447	51598891	2957305
Complete genome (Accession number NC_006156)	hypothetical protein BG0660	678247	678333	-	28	51598892	2957483
Complete genome (Accession number NC_006156)	Na+/H+ antiporter	678399	679754	+	451	51598893	2957484
Complete genome (Accession number NC_006156)	spermidine/putrescine ABC transporter, binding periplasmic protein	679803	680849	-	348	51598894	2957462
Complete genome (Accession number NC_006156)	spermidine/putrescine ABC transporter, permease protein	680869	681660	-	263	51598895	2957491
Complete genome (Accession number NC_006156)	spermidine/putrescine ABC transporter, permease protein	681663	682472	-	269	51598896	2957380

Complete genome (Accession number NC_006156)	spermidine/putrescine ABC transporter, ATP-binding protein	682472	683515	-	347	51598897	2957525
Complete genome (Accession number NC_006156)	ribosomal biogenesis GTPase	683594	684433	-	279	1,62E+08	2957366
Complete genome (Accession number NC_006156)	N-acetylmannosamine-6-phosphate 2-epimerase	684598	685296	+	232	51598899	2957774
Complete genome (Accession number NC_006156)	PTS system, glucose-specific IIBC component	685344	686888	+	514	51598900	2957775
Complete genome (Accession number NC_006156)	hydrolase, alpha/beta fold family	686916	687899	-	327	51598901	2957711
Complete genome (Accession number NC_006156)	ferric uptake regulation protein	687896	688423	-	175	51598902	2957776
Complete genome (Accession number NC_006156)	serine/threonine kinase, putative	688521	690209	-	562	51598903	2957224
Complete genome (Accession number NC_006156)	chaperonin GroEL	690400	692037	+	545	51598904	2957762
Complete genome (Accession number NC_006156)	hypothetical protein BG0673	692105	692401	+	98	51598905	2957765

Complete genome (Accession number NC_006156)	hypothetical protein BG0674	692416	692730	+	104	51598906	2957766
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecD	692808	694568	+	586	1,62E+08	2957759
Complete genome (Accession number NC_006156)	preprotein translocase subunit SecF	694552	695451	+	299	51598908	2957773
Complete genome (Accession number NC_006156)	hypothetical protein BG0677	695477	696619	+	380	51598909	2957755
Complete genome (Accession number NC_006156)	heat shock protein	696616	697446	-	276	51598910	2957721
Complete genome (Accession number NC_006156)	HemN-related protein	697555	698688	+	377	51598911	2957760
Complete genome (Accession number NC_006156)	ribose 5-phosphate isomerase	698675	699361	-	228	51598912	2957761
Complete genome (Accession number NC_006156)	phosphoglycerate mutase	699508	700254	+	248	51598913	2957699
Complete genome (Accession number NC_006156)	lysyl-tRNA synthetase	700321	701886	-	521	51598914	2957658
Complete genome (Accession number NC_006156)	GTP-binding protein Era	701959	702831	-	290	51598915	2957697
Complete genome (Accession number NC_006156)	hypothetical protein BG0684	702937	703293	+	118	51598916	2957688

Complete genome (Accession number NC_006156)	hypothetical protein BG0685	703303	703713	+	136	51598917	2957665
Complete genome (Accession number NC_006156)	hypothetical protein BG0686	703775	704182	+	135	51598918	2957666
Complete genome (Accession number NC_006156)	hypothetical protein BG0687	704191	704880	-	229	51598919	2957664
Complete genome (Accession number NC_006156)	hypothetical protein BG0688	704923	705882	+	319	51598920	2957661
Complete genome (Accession number NC_006156)	hypothetical protein BG0689	705866	706873	+	335	51598921	2957698
Complete genome (Accession number NC_006156)	hypothetical protein BG0690	706863	707414	+	183	51598922	2958007
Complete genome (Accession number NC_006156)	flagellar filament outer layer protein	707492	708517	+	341	51598923	2958008
Complete genome (Accession number NC_006156)	chemotaxis histidine kinase	708560	711181	+	873	51598924	2957663
Complete genome (Accession number NC_006156)	purine-binding chemotaxis protein	711189	712592	+	467	51598925	2957408
Complete genome (Accession number NC_006156)	chemotaxis operon protein	712604	713089	+	161	51598926	2957625
Complete genome (Accession number NC_006156)	chemotaxis response regulator	713131	713571	+	146	51598927	2957598

Complete genome (Accession number NC_006156)	hypothetical protein BG0696	713611	714123	-	170	51598928	2958001
Complete genome (Accession number NC_006156)	hypothetical protein BG0697	714120	715166	-	348	51598929	2958002
Complete genome (Accession number NC_006156)	hypothetical protein BG0698	715160	716023	-	287	51598930	2958003
Complete genome (Accession number NC_006156)	phosphoglycolate phosphatase	716020	716682	-	220	51598931	2958004
Complete genome (Accession number NC_006156)	ribose/galactose ABC transporter, ATP-binding protein	716930	718540	+	536	51598932	2958005
Complete genome (Accession number NC_006156)	ribose/galactose ABC transporter, permease protein	718541	719692	+	383	51598933	2957921
Complete genome (Accession number NC_006156)	ribose/galactose ABC transporter, permease protein	719664	720590	+	308	51598934	2957925
Complete genome (Accession number NC_006156)	methyl-accepting chemotaxis protein	720747	723008	+	753	51598935	2957919
Complete genome (Accession number NC_006156)	methyl-accepting chemotaxis protein	723038	724939	+	633	51598936	2957999

Complete genome (Accession number NC_006156)	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	724982	726049	-	355	51598937	2958000
Complete genome (Accession number NC_006156)	3-hydroxy-3-methylglutaryl-CoA synthase	726143	727366	+	407	51598938	2957920
Complete genome (Accession number NC_006156)	isopentenyl pyrophosphate isomerase	727350	728414	+	354	51598939	2957917
Complete genome (Accession number NC_006156)	3-hydroxy-3-methylglutaryl-CoA reductase	728404	729678	+	424	51598940	2957918
Complete genome (Accession number NC_006156)	mevalonate pyrophosphate decarboxylase	729656	730594	+	312	51598941	2957923
Complete genome (Accession number NC_006156)	phosphomevalonate kinase, putative	730585	731538	+	317	51598942	2957924
Complete genome (Accession number NC_006156)	mevalonate kinase, putative	731532	732425	+	297	51598943	2957929
Complete genome (Accession number NC_006156)	hypothetical protein BG0713	732549	733016	-	155	51598944	2957757
Complete genome (Accession number NC_006156)	neutrophil activating protein	733101	733631	+	176	51598945	2957758
Complete genome (Accession	elongation factor G	733712	735721	+	669	51598946	2957723

number NC_006156)							
Complete genome (Accession number NC_006156)	xylose operon regulatory protein	735998	737206	+	402	51598947	2957756
Complete genome (Accession number NC_006156)	signal recognition particle protein	737269	738603	+	444	51598948	2957764
Complete genome (Accession number NC_006156)	30S ribosomal protein S16	738616	738876	+	86	51598949	2957378
Complete genome (Accession number NC_006156)	hypothetical protein BG0719	738877	739125	+	82	51598950	2957460
Complete genome (Accession number NC_006156)	hypothetical protein BG0720	739129	739629	+	166	51598951	2957461
Complete genome (Accession number NC_006156)	tRNA (guanine-N(1)-)-methyltransferase	739626	740345	+	239	51598952	2957212
Complete genome (Accession number NC_006156)	50S ribosomal protein L19	740323	740688	+	121	51598953	2957247
Complete genome (Accession number NC_006156)	hypothetical protein BG0723	741039	741578	+	179	51598954	2957166
Complete genome (Accession number NC_006156)	lipopolysaccharide biosynthesis-related protein	741580	742071	+	163	51598955	2957752
Complete genome (Accession number NC_006156)	50S ribosomal protein L32	742134	742316	+	60	51598956	2957446

Complete genome (Accession number NC_006156)	acyl carrier protein	742340	742582	+	80	51598957	2957804
Complete genome (Accession number NC_006156)	ribonuclease III	742582	743319	+	245	51598958	2957805
Complete genome (Accession number NC_006156)	polynucleotide adenylyltransferase	743290	744522	-	410	51598959	2957818
Complete genome (Accession number NC_006156)	hypothetical protein BG0729	744639	746411	+	590	51598960	2957849
Complete genome (Accession number NC_006156)	hypothetical protein BG0730	746417	746740	+	107	51598961	2957853
Complete genome (Accession number NC_006156)	hypothetical protein BG0732	747199	748230	+	343	51598962	2957851
Complete genome (Accession number NC_006156)	DNA primase	748236	750017	+	593	51598963	2957838
Complete genome (Accession number NC_006156)	RNA polymerase sigma factor RpoD	750021	751916	+	631	51598964	2957841
Complete genome (Accession number NC_006156)	hypothetical protein BG0735	751930	752688	+	252	51598965	2957826
Complete genome (Accession number NC_006156)	hypothetical protein BG0736	753093	754061	+	322	51598966	2957819
Complete genome (Accession number NC_006156)	rod shape-determining protein	754078	755121	+	347	51598967	2957820

Complete genome (Accession number NC_006156)	rod shape-determining protein	755125	755970	+	281	51598968	2957810
Complete genome (Accession number NC_006156)	hypothetical protein BG0739	755970	756452	+	160	51598969	2957802
Complete genome (Accession number NC_006156)	penicillin-binding protein	756452	758251	+	599	51598970	2957790
Complete genome (Accession number NC_006156)	rod shape-determining protein	758256	759572	+	438	51598971	2957748
Complete genome (Accession number NC_006156)	threonyl-tRNA synthetase	759739	761487	+	582	51598972	2957754
Complete genome (Accession number NC_006156)	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	761489	762118	+	209	51598973	2957730
Complete genome (Accession number NC_006156)	hypothetical protein BG0744	762105	763550	+	481	51598974	2957731
Complete genome (Accession number NC_006156)	adenylyl cyclase, CyaB-type, putative	763524	764054	-	176	51598975	2957714
Complete genome (Accession number NC_006156)	K+ transport protein	764154	765473	+	439	51598976	2957704
Complete genome (Accession number NC_006156)	hypothetical protein BG0747	765470	766261	+	263	51598977	2957654

Complete genome (Accession number NC_006156)	minD-related ATP-binding protein	766271	767242	+	323	51598978	2957648
Complete genome (Accession number NC_006156)	diphosphate--fructose-6-phosphate 1-phosphotransferase	767273	768616	+	447	51598979	2957649
Complete genome (Accession number NC_006156)	coenzyme A disulfide reductase	768633	769964	-	443	51598980	2957553
Complete genome (Accession number NC_006156)	glutamate transporter	769979	771370	-	463	51598981	2957580
Complete genome (Accession number NC_006156)	glucose-6-phosphate isomerase	771437	773029	-	530	51598982	2957575
Complete genome (Accession number NC_006156)	hypothetical protein BG0753	773052	773453	-	133	51598983	2957508
Complete genome (Accession number NC_006156)	penicillin-binding protein	773460	776246	-	928	51598984	2957538
Complete genome (Accession number NC_006156)	hypothetical protein BG0755	776543	777328	+	261	51598985	2957505
Complete genome (Accession number NC_006156)	hypothetical protein BG0756	777535	778548	-	337	51598986	2957506
Complete genome (Accession number NC_006156)	rare lipoprotein A	778658	779446	+	262	51598987	2957494

Complete genome (Accession number NC_006156)	histidine phosphokinase/phosphatase, putative	779639	780628	+	329	51598988	2957335
Complete genome (Accession number NC_006156)	valyl-tRNA synthetase	780633	783260	+	875	51598989	2957319
Complete genome (Accession number NC_006156)	hypothetical protein BG0760	783354	783950	-	198	51598990	2957281
Complete genome (Accession number NC_006156)	hypothetical protein BG0761	784028	784705	-	225	51598991	2957231
Complete genome (Accession number NC_006156)	co-chaperonin GroES	785024	785296	-	90	51598992	2957232
Complete genome (Accession number NC_006156)	ABC transporter, ATP-binding protein	785440	787071	+	543	51598993	2957883
Complete genome (Accession number NC_006156)	hypothetical protein BG0764	787131	788786	+	551	51598994	2957862
Complete genome (Accession number NC_006156)	antigen, p83/100	788892	790973	+	693	51598995	2957934
Complete genome (Accession number NC_006156)	endonuclease III	791299	791916	+	205	51598996	2957958
Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, permease protein	791926	792786	-	286	51598997	2957959

Complete genome (Accession number NC_006156)	oligopeptide ABC transporter, permease protein	792786	793766	-	326	51598998	2957987
Complete genome (Accession number NC_006156)	hypothetical protein BG0771	793772	794230	-	152	51598999	2957936
Complete genome (Accession number NC_006156)	hypothetical protein BG0772	794329	795480	+	383	51599000	2957911
Complete genome (Accession number NC_006156)	hypothetical protein BG0773	795725	796738	-	337	51599001	2957907
Complete genome (Accession number NC_006156)	hypothetical protein BG0774	796755	798263	-	502	51599002	2957908
Complete genome (Accession number NC_006156)	membrane spanning protein, putative	798268	799002	-	244	51599003	2957932
Complete genome (Accession number NC_006156)	ABC transporter, ATP-binding protein	799005	799928	-	307	51599004	2957905
Complete genome (Accession number NC_006156)	ribonuclease Z	799937	800896	-	319	51599005	2957857
Complete genome (Accession number NC_006156)	hypothetical protein BG0778	801087	802154	-	355	51599006	2957878
Complete genome (Accession number NC_006156)	ATP-dependent Clp protease proteolytic subunit	802353	802949	+	198	51599007	2957879

Complete genome (Accession number NC_006156)	hypothetical protein BG0780	803027	803404	+	125	51599008	2957885
Complete genome (Accession number NC_006156)	lipoprotein, putative	803374	803661	+	95	51599009	2957867
Complete genome (Accession number NC_006156)	hypothetical protein BG0783	803824	804678	-	284	51599010	2957258
Complete genome (Accession number NC_006156)	hypothetical protein BG0784	804718	805047	-	109	51599011	2957192
Complete genome (Accession number NC_006156)	hypothetical protein BG0785	805159	806043	+	294	51599012	2957876
Complete genome (Accession number NC_006156)	response regulatory protein	806288	807646	-	452	51599013	2957250
Complete genome (Accession number NC_006156)	sensory transduction histidine kinase, putative	807649	808797	-	382	51599014	2957251
Complete genome (Accession number NC_006156)	hypothetical protein BG0788	808794	809840	-	348	51599015	2957241
Complete genome (Accession number NC_006156)	colicin V production protein, putative	809851	810339	-	162	51599016	2957210

Complete genome (Accession number NC_006156)	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	810336	811427	-	363	51599017	2957493
Complete genome (Accession number NC_006156)	pyridoxal kinase	811580	812374	-	264	51599018	2957223
Complete genome (Accession number NC_006156)	O-sialoglycoprotein endopeptidase	812374	813390	-	338	51599019	2957312
Complete genome (Accession number NC_006156)	hypothetical protein BG0793	813387	814253	-	288	51599020	2957313
Complete genome (Accession number NC_006156)	RNA polymerase sigma factor	814304	815104	-	266	51599021	2957292
Complete genome (Accession number NC_006156)	hypothetical protein BG0795	815249	815569	-	106	51599022	2957316
Complete genome (Accession number NC_006156)	flagellar basal body P-ring protein	815559	816554	-	331	51599023	2957211
Complete genome (Accession number NC_006156)	hypothetical protein BG0797	816724	817158	-	144	51599024	2957383

Complete genome (Accession number NC_006156)	flagellar basal body rod protein FlgG	817358	818155	-	265	51599025	2957469
Complete genome (Accession number NC_006156)	flagellar hook-basal body complex protein	818168	819016	-	282	51599026	2957470
Complete genome (Accession number NC_006156)	hypothetical protein BG0800	819271	819831	+	186	51599027	2957346
Complete genome (Accession number NC_006156)	adenine phosphoribosyltransferase	819893	820423	+	176	51599028	2957397
Complete genome (Accession number NC_006156)	50S ribosomal protein L21	820481	820792	+	103	51599029	2957581
Complete genome (Accession number NC_006156)	hypothetical protein BG0803	820798	821118	+	106	51599030	2957402
Complete genome (Accession number NC_006156)	50S ribosomal protein L27	821118	821363	+	81	51599031	2957486
Complete genome (Accession number NC_006156)	GTPase ObgE	821408	822397	+	329	51599032	2957458
Complete genome (Accession number NC_006156)	hypothetical protein BG0806	822484	823077	+	197	51599033	2957459
Complete genome (Accession number NC_006156)	hypothetical protein BG0807	823062	824246	+	394	51599034	2957429
Complete genome (Accession number	hypothetical protein BG0808	824221	824571	+	116	51599035	2957407

NC_006156)							
Complete genome (Accession number NC_006156)	regulatory protein SpoVG	824675	824968	+	97	51599036	2957432
Complete genome (Accession number NC_006156)	50S ribosomal protein L25/general stress protein Ctc	825125	825673	+	182	51599037	2957552
Complete genome (Accession number NC_006156)	peptidyl-tRNA hydrolase	825687	826244	+	185	51599038	2957492
Complete genome (Accession number NC_006156)	hypothetical protein BG0813	826244	827566	+	440	51599039	2957363
Complete genome (Accession number NC_006156)	cell division protein	827563	829482	+	639	51599040	2957561
Complete genome (Accession number NC_006156)	hypothetical protein BG0815	829495	830976	+	493	51599041	2957562
Complete genome (Accession number NC_006156)	thymidine kinase	831084	832187	+	367	51599042	2957555
Complete genome (Accession number NC_006156)	hypothetical protein BG0817	832117	832209	-	30	51599043	2957556
Complete genome (Accession number NC_006156)	hypothetical protein BG0818	832184	832813	-	209	51599044	2957554
Complete genome (Accession number	thymidylate kinase	832827	833435	-	202	51599045	2957587

NC_006156)							
Complete genome (Accession number NC_006156)	hypothetical protein BG0820	833541	837941	+	1466	51599046	2957557
Complete genome (Accession number NC_006156)	outer membrane protein	837959	840424	+	821	51599047	2957558
Complete genome (Accession number NC_006156)	hypothetical protein BG0822	840446	840979	+	177	51599048	2957546
Complete genome (Accession number NC_006156)	DNA mismatch repair protein	841169	843757	+	862	51599049	2957568
Complete genome (Accession number NC_006156)	competence protein F, putative	843791	844303	+	170	51599050	2957559
Complete genome (Accession number NC_006156)	hypothetical protein BG0825	844476	844913	+	145	51599051	2957572
Complete genome (Accession number NC_006156)	transcription elongation factor NusA	844927	846375	+	482	51599052	2957573
Complete genome (Accession number NC_006156)	translation initiation factor IF-2	846378	849029	+	883	51599053	2957567
Complete genome (Accession number NC_006156)	ribosome-binding factor A	849053	849415	+	120	51599054	2957574
Complete genome (Accession number NC_006156)	tRNA pseudouridine 55 synthase	849418	850266	+	282	51599055	2957576

Complete genome (Accession number NC_006156)	30S ribosomal protein S15	850436	850702	+	88	51599056	2957593
Complete genome (Accession number NC_006156)	polynucleotide phosphorylase/polyadenylase	850735	852882	+	715	51599057	2957582
Complete genome (Accession number NC_006156)	hypothetical protein BG0832	852854	854401	+	515	51599058	2957591
Complete genome (Accession number NC_006156)	hypothetical protein BG0833	854376	855665	+	429	51599059	2957592
Complete genome (Accession number NC_006156)	hypothetical protein BG0834	855662	856729	+	355	51599060	2957621
Complete genome (Accession number NC_006156)	tRNA-guanine transglycosylase	856759	857886	+	375	51599061	2957596
Complete genome (Accession number NC_006156)	virulence factor mviN protein	857879	859399	+	506	51599062	2957608
Complete genome (Accession number NC_006156)	hypothetical protein BG0837	859396	860802	+	468	51599063	2957606
Complete genome (Accession number NC_006156)	pantothenate metabolism flavoprotein	860828	861889	-	353	51599064	2957628
Complete genome (Accession number NC_006156)	sodium/panthothenate symporter	862327	863661	+	444	51599065	2957629

Complete genome (Accession number NC_006156)	hypothetical protein BG0840	863674	864621	+	315	51599066	2957622
Complete genome (Accession number NC_006156)	hypothetical protein BG0841	864596	865537	+	313	51599067	2957630
Complete genome (Accession number NC_006156)	UDP-N-acetylmuramate--L-alanine ligase	865527	866933	+	468	51599068	2957638
Complete genome (Accession number NC_006156)	hypothetical protein BG0843	866944	867813	+	289	51599069	2957686
Complete genome (Accession number NC_006156)	cytidylate kinase	867810	868346	+	178	51599070	2957682
Complete genome (Accession number NC_006156)	hypothetical protein BG0845	868386	868586	+	66	51599071	2957683
Complete genome (Accession number NC_006156)	2-methylthio-N6-isopentyladenosine tRNA modification enzyme	868573	869493	+	306	51599072	2957636
Complete genome (Accession number NC_006156)	hypothetical protein BG0847	869635	870006	-	123	51599073	2957696
Complete genome (Accession number NC_006156)	hypothetical protein BG0848	870087	870632	+	181	51599074	2957707
Complete genome (Accession number NC_006156)	hypothetical protein BG0849	870625	871272	-	215	51599075	2957702

Complete genome (Accession number NC_006156)	hypothetical protein BG0850	871331	871453	+	40	51599076	2957703
Complete genome (Accession number NC_006156)	hypothetical protein BG0851	871400	871810	-	136	51599077	2957693
Complete genome (Accession number NC_006156)	ATP-dependent helicase	872044	874518	-	824	51599078	2957708
Complete genome (Accession number NC_006156)	DNA topoisomerase I	874521	877070	-	849	51599079	2957712
Complete genome (Accession number NC_006156)	exonuclease SbcD	877145	878386	+	413	51599080	2957717
Complete genome (Accession number NC_006156)	exonuclease SbcC	878373	881219	+	948	51599081	2957715
Complete genome (Accession number NC_006156)	xylose operon regulatory protein	881253	882188	+	311	51599082	2957716
Complete genome (Accession number NC_006156)	lipoprotein, putative	882208	883032	-	274	51599083	2957713
Complete genome (Accession number NC_006156)	isoleucyl-tRNA synthetase	883026	886154	-	1042	51599084	2957738
Complete genome (Accession number NC_006156)	ATP-dependent Clp protease, subunit C	886169	888388	-	739	51599085	2957740
Complete genome (Accession number NC_006156)	phosphomannomutase	888411	890120	-	569	51599086	2957729

Complete genome (Accession number NC_006156)	excinuclease ABC subunit B	890270	892264	+	664	51599087	2957739
Complete genome (Accession number NC_006156)	excinuclease ABC, subunit A	892281	895133	+	950	51599088	2957772
Complete genome (Accession number NC_006156)	hypothetical protein BG0863	895136	898537	+	1133	51599089	2957770
Complete genome (Accession number NC_006156)	hypothetical protein BG0864	898503	898559	+	18	51599090	2957771
Complete genome (Accession number NC_006156)	hypothetical protein BG0865	898546	899091	-	181	51599091	2957741
Complete genome (Accession number NC_006156)	hypothetical protein BG0866	899069	899668	-	199	51599092	2957743
Complete genome (Accession number NC_006156)	lipoprotein, putative	899678	901300	-	540	51599093	2957796
Complete genome (Accession number NC_006156)	arginine deiminase	901481	902710	+	409	51599094	2957797
Complete genome (Accession number NC_006156)	ornithine carbamoyltransferase, catabolic	902782	903765	+	327	51599095	2957777
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP227	431	874	+	147	56561105	3189711
Variable plasmid segment G1a19c04.r1 (Accession number	hypothetical protein BGP228	1203	1631	-	142	56561106	3189707

NT_108239)							
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP229	1600	1689	-	29	56561107	3189708
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP230	1690	2106	-	138	56561108	3189710
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP231	2116	2316	-	66	56561109	3189714
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP232	2304	2771	-	155	56561110	3189704
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP233	2966	3055	-	29	56561111	3189705
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP234	3742	3858	-	38	56561112	3189709
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP235	3946	4299	-	117	56561113	3189706
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP236	4312	4710	-	132	56561114	3189715
Variable plasmid segment G1a19c04.r1 (Accession	hypothetical protein BGP237	4921	5076	-	51	56561115	3189713

number NT_108239)							
Variable plasmid segment G1a19c04.r1 (Accession number NT_108239)	hypothetical protein BGP238	5037	5762	-	241	56561116	3189712
Variable plasmid segment G11a15f12.s1 (Accession number NT_108263)	hypothetical protein BGP334	74	286	+	70	56561236	3189985
Variable plasmid segment G11a15f12.s1 (Accession number NT_108263)	hypothetical protein BGP335	635	1195	-	186	56561237	3189987
Variable plasmid segment G11a15f12.s1 (Accession number NT_108263)	hypothetical protein BGP336	1210	1695	-	161	56561238	3189986
Variable plasmid segment G11a15f12.s1 (Accession number NT_108263)	hypothetical protein BGP337	1902	1970	-	22	56561239	3189984
Variable plasmid segment G1M1b11b03.s1(Accession number NT_108262)	hypothetical protein BGP332	1	365	-	122	56561233	3189982
Variable plasmid segment G1M1b11b03.s1(Accession number NT_108262)	hypothetical protein BGP333	795	1928	+	377	56561234	3189983
Variable plasmid segment G1M1b15c06.r1 (Accession number NT_108261)	hypothetical protein BGP329	3	488	+	161	56561229	3189981
Variable plasmid segment G1M1b15c06.r1 (Accession	hypothetical protein BGP330	1652	1984	+	110	56561230	3189979

number NT_108261)							
Variable plasmid segment G1M1b15c06.r1 (Accession number NT_108261)	hypothetical protein BGP331	2120	2242	+	40	56561231	3189980
Variable plasmid segment G11a14d08.s1 (Accession number NT_108260)	hypothetical protein BGP326	1	852	-	284	56561225	3189978
Variable plasmid segment G11a14d08.s1 (Accession number NT_108260)	hypothetical protein BGP327	849	1415	-	188	56561226	3189977
Variable plasmid segment G11a14d08.s1 (Accession number NT_108260)	hypothetical protein BGP328	1604	1858	-	84	56561227	3189976
Variable plasmid segment PBil1a03e01.s1 (Accession number NT_108259)	hypothetical protein BGP325	845	1096	+	83	56561223	3189975
Variable plasmid segment G1a13d03.r1 (Accession number NT_108258)	hypothetical protein BGP321	1	203	-	67	56561218	3189973
Variable plasmid segment G1a13d03.r1 (Accession number NT_108258)	hypothetical protein BGP322	370	990	-	206	56561219	3189974
Variable plasmid segment G1a13d03.r1 (Accession number NT_108258)	hypothetical protein BGP323	1088	1843	-	251	56561220	3189972
Variable plasmid segment G1a13d03.r1 (Accession	hypothetical protein BGP324	1816	1986	-	56	56561221	3189971

number NT_108258)							
Variable plasmid segment G1Mb19g09.r1 (Accession number NT_108257)	hypothetical protein BGP320	1700	1819	+	39	56561216	3189970
Variable plasmid segment G11a19d04.r1 (Accession number NT_108256)	hypothetical protein BGP317	531	644	+	37	56561212	3189967
Variable plasmid segment G11a19d04.r1 (Accession number NT_108256)	hypothetical protein BGP318	960	1049	+	29	56561213	3189968
Variable plasmid segment G11a19d04.r1 (Accession number NT_108256)	hypothetical protein BGP319	2065	2438	+	124	56561214	3189969
Variable plasmid segment G1a13d06.s1 (Accession number NT_108255)	hypothetical protein BGP316	1	2417	-	806	56561210	3189966
Variable plasmid segment G1a18e10.s1 (Accession number NT_108254)	hypothetical protein BGP312	60	719	+	219	56561205	3189965
Variable plasmid segment G1a18e10.s1 (Accession number NT_108254)	hypothetical protein BGP313	759	1280	+	173	56561206	3189962
Variable plasmid segment G1a18e10.s1 (Accession number NT_108254)	hypothetical protein BGP314	1292	1693	+	133	56561207	3189964
Variable plasmid segment G1a18e10.s1 (Accession	hypothetical protein BGP315	2408	2543	+	45	56561208	3189963

number NT_108254)							
Variable plasmid segment G1a22b07.r1 (Accession number NT_108253)	hypothetical protein BGP309	123	239	+	38	56561201	3189960
Variable plasmid segment G1a22b07.r1 (Accession number NT_108253)	hypothetical protein BGP310	695	1249	-	184	56561202	3189961
Variable plasmid segment G1a22b07.r1 (Accession number NT_108253)	hypothetical protein BGP311	1559	2380	+	273	56561203	3189959
Variable plasmid segment G11a15h12.r1 (Accession number NT_108252)	hypothetical protein BGP303	405	1022	-	205	56561194	3189958
Variable plasmid segment G11a15h12.r1 (Accession number NT_108252)	hypothetical protein BGP304	1035	1544	-	169	56561195	3189957
Variable plasmid segment G11a15h12.r1 (Accession number NT_108252)	hypothetical protein BGP305	2190	2342	-	50	56561196	3189953
Variable plasmid segment G11a15h12.r1 (Accession number NT_108252)	hypothetical protein BGP306	2348	2509	-	53	56561197	3189954
Variable plasmid segment G11a15h12.r1 (Accession number NT_108252)	hypothetical protein BGP307	2532	2705	-	57	56561198	3189955
Variable plasmid segment G11a15h12.r1 (Accession	hypothetical protein BGP308	3059	3140	-	26	56561199	3189956

number NT_108252)							
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP296	237	359	+	40	56561186	3189951
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP297	389	811	+	140	56561187	3189949
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP298	774	1088	+	104	56561188	3189788
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP299	1098	1511	+	137	56561189	3189948
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP300	1630	2370	+	246	56561190	3189787
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP301	2411	2953	+	180	56561191	3189950
Variable plasmid segment G1a18d09.s1 (Accession number NT_108251)	hypothetical protein BGP302	2966	3140	+	58	56561192	3189952
Variable plasmid segment G1a07g11.r1 (Accession number NT_108250)	hypothetical protein BGP294	435	2342	-	635	56561183	3189786
Variable plasmid segment G1a07g11.r1 (Accession	hypothetical protein BGP295	2580	3029	-	149	56561184	3189785

number NT_108250)							
Variable plasmid segment G1Mb28a10.r1 (Accession number NT_108249)	hypothetical protein BGP291	320	946	+	208	56561179	3189784
Variable plasmid segment G1Mb28a10.r1 (Accession number NT_108249)	hypothetical protein BGP292	1023	1970	-	315	56561180	3189782
Variable plasmid segment G1Mb28a10.r1 (Accession number NT_108249)	hypothetical protein BGP293	2358	3380	+	341	56561181	3189783
Variable plasmid segment G1a23g09.r1 (Accession number NT_108248)	hypothetical protein BGP287	226	777	+	183	56561174	3189780
Variable plasmid segment G1a23g09.r1 (Accession number NT_108248)	hypothetical protein BGP288	1065	1388	-	107	56561175	3189781
Variable plasmid segment G1a23g09.r1 (Accession number NT_108248)	hypothetical protein BGP289	2136	2675	-	179	56561176	3189779
Variable plasmid segment G1a23g09.r1 (Accession number NT_108248)	hypothetical protein BGP290	3009	3236	-	75	56561177	3189778
Variable plasmid segment PBilM1b05c04.r1 (Accession number NT_108247)	hypothetical protein BGP283	392	547	+	51	56561169	3189763
Variable plasmid segment PBilM1b05c04.r1 (Accession	hypothetical protein BGP284	630	1139	+	169	56561170	3189762

number NT_108247)							
Variable plasmid segment PBilM1b05c04.r1 (Accession number NT_108247)	hypothetical protein BGP285	2210	2392	-	60	56561171	3189761
Variable plasmid segment PBilM1b05c04.r1 (Accession number NT_108247)	hypothetical protein BGP286	2699	2860	+	53	56561172	3189760
Variable plasmid segment G1M1b09a03.r1 (Accession number NT_108246)	hypothetical protein BGP278	1	187	-	62	56561163	3189759
Variable plasmid segment G1M1b09a03.r1 (Accession number NT_108246)	hypothetical protein BGP279	191	388	-	65	56561164	3189758
Variable plasmid segment G1M1b09a03.r1 (Accession number NT_108246)	hypothetical protein BGP280	731	1276	-	181	56561165	3189756
Variable plasmid segment G1M1b09a03.r1 (Accession number NT_108246)	hypothetical protein BGP281	1286	1594	-	102	56561166	3189755
Variable plasmid segment G1M1b09a03.r1 (Accession number NT_108246)	hypothetical protein BGP282	1563	2039	-	158	56561167	3189757
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP277	1	72	+	23	56561152	3189745
Variable plasmid segment G1a10e03.r1 (Accession	hypothetical protein BGP276	38	682	-	214	56561153	3189752

number NT_108245)							
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP275	1246	1410	+	54	56561154	3189749
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP274	1420	1548	+	42	56561155	3189747
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP273	2070	2186	+	38	56561156	3189754
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP272	2137	2280	-	47	56561157	3189750
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP271	2228	2662	-	144	56561158	3189753
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP270	2824	3306	+	160	56561159	3189746
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP269	3592	3798	-	68	56561160	3189748
Variable plasmid segment G1a10e03.r1 (Accession number NT_108245)	hypothetical protein BGP268	3791	4050	-	85	56561161	3189751
Variable plasmid segment G1Mb12b07.s1 (Accession	hypothetical protein BGP262	98	433	+	111	56561145	3189742

number NT_108244)							
Variable plasmid segment G1Mb12b07.s1 (Accession number NT_108244)	hypothetical protein BGP263	417	1067	+	216	56561146	3189739
Variable plasmid segment G1Mb12b07.s1 (Accession number NT_108244)	hypothetical protein BGP264	1356	1541	-	61	56561147	3189743
Variable plasmid segment G1Mb12b07.s1 (Accession number NT_108244)	hypothetical protein BGP265	1959	2210	+	83	56561148	3189744
Variable plasmid segment G1Mb12b07.s1 (Accession number NT_108244)	hypothetical protein BGP266	2367	2861	+	164	56561149	3189741
Variable plasmid segment G1Mb12b07.s1 (Accession number NT_108244)	hypothetical protein BGP267	3835	4017	-	60	56561150	3189740
Variable plasmid segment G1a25a05.r1 (Accession number NT_108243)	hypothetical protein BGP257	84	1193	+	369	56561139	3189737
Variable plasmid segment G1a25a05.r1 (Accession number NT_108243)	hypothetical protein BGP258	1246	1671	+	141	56561140	3189738
Variable plasmid segment G1a25a05.r1 (Accession number NT_108243)	hypothetical protein BGP259	1677	2453	-	258	56561141	3189734
Variable plasmid segment G1a25a05.r1 (Accession	hypothetical protein BGP260	2885	3568	+	227	56561142	3189735

number NT_108243)							
Variable plasmid segment G1a25a05.r1 (Accession number NT_108243)	hypothetical protein BGP261	3620	4649	+	343	56561143	3189736
Variable plasmid segment G11a16g12.s1 (Accession number NT_108242)	hypothetical protein BGP253	3193	3768	-	191	56561134	3189731
Variable plasmid segment G11a16g12.s1 (Accession number NT_108242)	hypothetical protein BGP254	3791	4549	-	252	56561135	3189730
Variable plasmid segment G11a16g12.s1 (Accession number NT_108242)	hypothetical protein BGP255	4525	4821	-	98	56561136	3189733
Variable plasmid segment G11a16g12.s1 (Accession number NT_108242)	hypothetical protein BGP256	5002	5088	-	28	56561137	3189732
Variable plasmid segment G11a14a06.r1 (Accession number NT_108241)	hypothetical protein BGP247	242	322	-	26	56561127	3189726
Variable plasmid segment G11a14a06.r1 (Accession number NT_108241)	hypothetical protein BGP248	1108	1905	+	265	56561128	3189724
Variable plasmid segment G11a14a06.r1 (Accession number NT_108241)	hypothetical protein BGP249	2017	2244	+	75	56561129	3189728
Variable plasmid segment G11a14a06.r1 (Accession	hypothetical protein BGP250	2989	3123	-	44	56561130	3189729

number NT_108241)							
Variable plasmid segment G11a14a06.r1 (Accession number NT_108241)	hypothetical protein BGP251	3473	4315	-	280	56561131	3189725
Variable plasmid segment G11a14a06.r1 (Accession number NT_108241)	hypothetical protein BGP252	5334	5558	+	74	56561132	3189727
Variable plasmid segment G1Mb03b12.r1 (Accession number NT_108238)	hypothetical protein BGP223	236	3274	+	1012	56561100	3189703
Variable plasmid segment G1Mb03b12.r1 (Accession number NT_108238)	hypothetical protein BGP224	3315	4643	+	442	56561101	3189700
Variable plasmid segment G1Mb03b12.r1 (Accession number NT_108238)	hypothetical protein BGP225	4633	4965	+	110	56561102	3189701
Variable plasmid segment G1Mb03b12.r1 (Accession number NT_108238)	hypothetical protein BGP226	4943	5982	+	347	56561103	3189702
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP216	108	1019	+	303	56561092	3189697
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP217	1029	1583	+	184	56561093	3189699
Variable plasmid segment G11a16d07.r1 (Accession	hypothetical protein BGP218	1559	2311	+	250	56561094	3189694

number NT_108237)							
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP219	2370	2939	+	189	56561095	3189693
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP220	3806	4621	-	271	56561096	3189696
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP221	5841	5978	-	45	56561097	3189695
Variable plasmid segment G11a16d07.r1 (Accession number NT_108237)	hypothetical protein BGP222	6089	6265	-	58	56561098	3189698
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP207	69	530	-	153	56561082	3189685
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP208	686	1012	-	108	56561083	3189688
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP209	1081	1257	+	58	56561084	3189686
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP210	1164	2117	-	317	56561085	3189687
Variable plasmid segment G1a09h07.r1 (Accession	hypothetical protein BGP211	2345	2923	+	192	56561086	3189684

number NT_108236)							
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP212	3069	3752	-	227	56561087	3189690
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP213	4580	5242	-	220	56561088	3189689
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP214	6192	6932	+	246	56561089	3189691
Variable plasmid segment G1a09h07.r1 (Accession number NT_108236)	hypothetical protein BGP215	6923	7198	+	91	56561090	3189692
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP195	41	181	+	46	56561069	3189677
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP196	181	303	+	40	56561070	3189678
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP197	506	778	+	90	56561071	3189865
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP198	726	953	+	75	56561072	3189675
Variable plasmid segment G1a07d05.r1 (Accession	hypothetical protein BGP199	2140	5724	-	1194	56561073	3189683

number NT_108235)							
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP200	5840	6196	-	118	56561074	3190011
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP201	6141	6332	-	63	56561075	3189674
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP202	6811	7422	-	203	56561076	3189682
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP203	7403	7480	-	25	56561077	3189681
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP204	8141	8314	-	57	56561078	3189679
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP205	8337	8864	+	175	56561079	3189676
Variable plasmid segment G1a07d05.r1 (Accession number NT_108235)	hypothetical protein BGP206	8857	9174	+	106	56561080	3189680
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP175	39	734	+	231	56561048	3189849
Variable plasmid segment G1M1b07c12.s1 (Accession	hypothetical protein BGP176	1588	1974	+	128	56561049	3189864

number NT_108234)							
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP177	1971	2540	+	189	56561050	3189863
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP178	2521	2841	+	106	56561051	3189854
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP179	2870	3217	+	115	56561052	3189853
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP180	3241	3876	+	211	56561053	3189851
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP181	3880	4827	+	315	56561054	3189850
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP182	4839	5384	+	181	56561055	3189862
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP183	5414	5614	+	66	56561056	3189858
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP184	5745	6623	+	292	56561057	3189847
Variable plasmid segment G1M1b07c12.s1 (Accession	hypothetical protein BGP185	6626	7225	+	199	56561058	3189856

number NT_108234)							
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP186	7242	7292	+	16	56561059	3189860
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP187	7302	8057	+	251	56561060	3189848
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP188	8132	8326	+	64	56561061	3189852
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP189	8330	8668	+	112	56561062	3189861
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP190	8668	9003	+	111	56561063	3189859
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP191	8996	9349	+	117	56561064	3189855
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP192	9546	10184	+	212	56561065	3189846
Variable plasmid segment G1M1b07c12.s1 (Accession number NT_108234)	hypothetical protein BGP193	10287	11189	-	300	56561066	3189845
Variable plasmid segment G1M1b07c12.s1 (Accession	hypothetical protein BGP194	11562	11868	+	102	56561067	3189857

number NT_108234)							
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP157	1	721	-	240	56561029	3189837
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP158	731	1336	-	201	56561030	3189844
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP159	1346	2221	-	291	56561031	3189830
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP160	2218	2550	-	110	56561032	3189836
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP161	2580	3125	-	181	56561033	3189842
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP162	3150	4091	-	313	56561034	3189835
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP163	4095	4778	-	227	56561035	3189839
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP164	4800	6110	-	436	56561036	3189838
Variable plasmid segment G11a15e03.s1 (Accession	hypothetical protein BGP165	6118	6354	-	78	56561037	3189833

number NT_108233)							
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP166	6351	6806	-	151	56561038	3189827
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP167	6822	7151	-	109	56561039	3189828
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP168	7264	8376	-	370	56561040	3189841
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP169	8357	8926	-	189	56561041	3189834
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP170	8923	9312	-	129	56561042	3189832
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP171	9300	9683	-	127	56561043	3189829
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP172	9683	10138	-	151	56561044	3189843
Variable plasmid segment G11a15e03.s1 (Accession number NT_108233)	hypothetical protein BGP173	10158	11117	-	319	56561045	3189831
Variable plasmid segment G11a15e03.s1 (Accession	hypothetical protein BGP174	11139	11648	-	169	56561046	3189840

number NT_108233)							
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP338	1	306	+	101	56561002	3189814
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP132	383	646	-	87	56561003	3189812
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP133	726	980	-	84	56561004	3189806
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP134	1203	2081	-	292	56561005	3189817
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP135	2501	2617	+	38	56561006	3189821
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP136	3506	3682	+	58	56561007	3189825
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP137	3691	3897	+	68	56561008	3189803
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP138	4472	5548	+	358	56561009	3189801
Variable plasmid segment G1M1b09g01.s1 (Accession	hypothetical protein BGP139	6229	6387	+	52	56561010	3189805

number NT_108232)							
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP140	6428	6529	+	33	56561011	3189807
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP141	6456	6905	-	149	56561012	3189804
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP142	6902	7105	-	67	56561013	3189816
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP143	7102	7434	-	110	56561014	3189813
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP144	7701	7937	+	78	56561015	3189802
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP145	8062	9087	+	341	56561016	3189820
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP146	9157	9294	+	45	56561017	3189810
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP147	9312	9443	+	43	56561018	3189811
Variable plasmid segment G1M1b09g01.s1 (Accession	hypothetical protein BGP148	9584	9799	+	71	56561019	3189808

number NT_108232)							
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP149	9880	10008	+	42	56561020	3189826
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP150	10020	10112	+	30	56561021	3189823
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP151	10869	11063	-	64	56561022	3189809
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP152	11076	11501	-	141	56561023	3189819
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP153	11507	11836	-	109	56561024	3189818
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP154	12022	12168	+	48	56561025	3189824
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP155	12327	12728	+	133	56561026	3189822
Variable plasmid segment G1M1b09g01.s1 (Accession number NT_108232)	hypothetical protein BGP156	12794	13081	-	95	56561027	3189815
Variable plasmid segment G1a34h09.s1 (Accession	hypothetical protein BGP109	1	572	-	190	56560978	3189793

number NT_108231)							
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP110	683	1504	-	273	56560979	3189940
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP111	1563	1754	-	63	56560980	3189944
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP112	1736	2113	-	125	56560981	3189799
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP113	2269	2481	-	70	56560982	3189945
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP114	2548	3318	+	256	56560983	3189792
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP115	3329	3676	+	115	56560984	3189789
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP116	3673	4683	+	336	56560985	3189798
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP117	4680	4865	+	61	56560986	3189942
Variable plasmid segment G1a34h09.s1 (Accession	hypothetical protein BGP118	4876	5073	+	65	56560987	3189790

number NT_108231)							
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP119	5127	5903	+	258	56560988	3189791
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP120	5940	6488	+	182	56560989	3189794
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP121	6489	6998	+	169	56560990	3189937
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP122	7034	7864	+	276	56560991	3189800
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP123	7880	8218	+	112	56560992	3189946
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP124	8234	8626	+	130	56560993	3189943
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP125	8623	9066	+	147	56560994	3189796
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP126	9056	9874	+	272	56560995	3189939
Variable plasmid segment G1a34h09.s1 (Accession	hypothetical protein BGP127	9884	10312	+	142	56560996	3189938

number NT_108231)							
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP128	10402	10599	+	65	56560997	3189936
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP129	10596	12584	+	662	56560998	3189941
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP130	12644	13846	+	400	56560999	3189797
Variable plasmid segment G1a34h09.s1 (Accession number NT_108231)	hypothetical protein BGP131	14167	14531	+	121	56561000	3189795
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP085	117	590	-	157	56560953	3189927
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP086	916	1065	-	49	56560954	3189931
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP087	1076	1807	-	243	56560955	3189921
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP088	2048	3022	+	324	56560956	3189925
Variable plasmid segment G1a08d08.s1 (Accession	hypothetical protein BGP089	3398	3535	+	45	56560957	3189920

number NT_108230)							
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP090	3453	3644	-	63	56560958	3189923
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP091	3664	3849	+	61	56560959	3189913
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP092	3926	4060	-	44	56560960	3189928
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP093	4358	4960	+	200	56560961	3189933
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP094	5333	5482	-	49	56560962	3189915
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP095	5569	5709	-	46	56560963	3189929
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP096	5773	6714	+	313	56560964	3189922
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP097	7435	7521	-	28	56560965	3189926
Variable plasmid segment G1a08d08.s1 (Accession	hypothetical protein BGP098	7737	7904	+	55	56560966	3189935

number NT_108230)							
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP099	8066	8536	+	156	56560967	3189918
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP100	9297	10361	+	354	56560968	3189934
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP101	10715	10783	-	22	56560969	3189932
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP102	11124	11264	-	46	56560970	3189912
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP103	11266	11451	-	61	56560971	3189919
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP104	11475	11837	-	120	56560972	3189930
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP105	12397	12570	+	57	56560973	3189917
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP106	12967	13152	+	61	56560974	3189924
Variable plasmid segment G1a08d08.s1 (Accession	hypothetical protein BGP107	13796	14089	+	97	56560975	3189916

number NT_108230)							
Variable plasmid segment G1a08d08.s1 (Accession number NT_108230)	hypothetical protein BGP108	15520	16067	-	181	56560976	3189914
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP056	56	478	+	140	56560923	3189894
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP057	495	1190	+	231	56560924	3189906
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP058	1202	1765	+	187	56560925	3189910
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP059	1785	2744	+	319	56560926	3189907
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP060	2763	3215	+	150	56560927	3189889
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP061	3215	3598	+	127	56560928	3189902
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP062	3586	3972	+	128	56560929	3189898
Variable plasmid segment G1M1b13a11.r1 (Accession	hypothetical protein BGP063	3975	4538	+	187	56560930	3189890

number NT_108229)							
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP064	4519	5640	+	373	56560931	3189911
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP065	5654	6082	+	142	56560932	3189900
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP066	6098	6553	+	151	56560933	3189909
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP067	6550	6786	+	78	56560934	3189896
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP068	6794	7042	+	82	56560935	3189908
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP069	7096	7875	+	259	56560936	3189888
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP070	7888	8076	-	62	56560937	3189891
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP071	8110	8796	+	228	56560938	3189883
Variable plasmid segment G1M1b13a11.r1 (Accession	hypothetical protein BGP072	8800	9789	+	329	56560939	3189886

number NT_108229)							
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP073	9786	10331	+	181	56560940	3189884
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP074	10361	10693	+	110	56560941	3189892
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP075	10690	11568	+	292	56560942	3189904
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP076	11573	12175	+	200	56560943	3189903
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP077	12185	12997	+	270	56560944	3189895
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP078	13070	13267	+	65	56560945	3189893
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP079	13271	13507	+	78	56560946	3189901
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP080	13608	13943	+	111	56560947	3189897
Variable plasmid segment G1M1b13a11.r1 (Accession	hypothetical protein BGP081	13936	14289	+	117	56560948	3189885

number NT_108229)							
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP082	14542	14976	+	144	56560949	3189905
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP083	14998	15426	+	142	56560950	3189899
Variable plasmid segment G1M1b13a11.r1 (Accession number NT_108229)	hypothetical protein BGP084	15467	16033	-	188	56560951	3189887
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP033	360	458	-	32	56560899	3189874
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP034	680	853	-	57	56560900	3189867
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP035	1425	2240	-	271	56560901	3189773
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP036	2594	3760	+	388	56560902	3189873
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP037	5389	5583	-	64	56560903	3189878
Variable plasmid segment G11a17h03.s1 (Accession	hypothetical protein BGP038	5974	6075	-	33	56560904	3189880

number NT_108228)							
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP039	6075	6530	-	151	56560905	3189882
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP040	6549	7508	-	319	56560906	3189876
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP041	7530	8099	-	189	56560907	3189777
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP042	8114	8884	-	256	56560908	3189875
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP043	8892	9449	-	185	56560909	3189775
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP044	9461	10150	-	229	56560910	3189879
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP045	10167	11390	-	407	56560911	3189871
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP046	11456	12808	-	450	56560912	3189869
Variable plasmid segment G11a17h03.s1 (Accession	hypothetical protein BGP047	12805	13371	-	188	56560913	3189881

number NT_108228)							
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP048	13586	13831	+	81	56560914	3189866
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP049	13930	14991	-	353	56560915	3189872
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP050	15429	15635	+	68	56560916	3189870
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP051	15713	16204	+	163	56560917	3189877
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP052	16210	16635	-	141	56560918	3190010
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP053	16693	16872	-	59	56560919	3189776
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP054	16854	16970	-	38	56560920	3189774
Variable plasmid segment G11a17h03.s1 (Accession number NT_108228)	hypothetical protein BGP055	17191	17640	-	149	56560921	3189868
Variable plasmid segment Gla19d06.s1 (Accession	hypothetical protein BGP001	427	1122	-	231	56560866	3189995

number NT_108227)							
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP002	1181	1732	-	183	56560867	3190009
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP003	1872	2129	-	85	56560868	3189991
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP004	2192	2353	+	53	56560869	3189765
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP005	2350	2445	-	31	56560870	3189993
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP006	2442	3857	-	471	56560871	3189992
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP007	3981	4133	+	50	56560872	3189772
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP008	4232	4645	+	137	56560873	3189996
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP009	4638	5330	+	230	56560874	3189990
Variable plasmid segment Gla19d06.s1 (Accession	hypothetical protein BGP010	5330	5701	+	123	56560875	3189947

number NT_108227)							
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP011	5704	6090	+	128	56560876	3189988
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP012	6102	8726	+	874	56560877	3189989
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP013	8727	9509	+	260	56560878	3190001
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP014	9522	10292	+	256	56560879	3189770
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP015	10303	10650	+	115	56560880	3189768
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP016	10647	11837	+	396	56560881	3190004
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP017	11849	12877	+	342	56560882	3189997
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP018	12911	13459	+	182	56560883	3189769
Variable plasmid segment Gla19d06.s1 (Accession	hypothetical protein BGP019	13460	13969	+	169	56560884	3189998

number NT_108227)							
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP020	14005	14835	+	276	56560885	3189999
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP021	14851	15189	+	112	56560886	3190002
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP022	15205	15597	+	130	56560887	3190007
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP023	15594	16037	+	147	56560888	3190005
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP024	16027	16845	+	272	56560889	3189771
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP025	16855	17283	+	142	56560890	3189994
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP026	17373	17570	+	65	56560891	3189766
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP027	17567	20812	+	1081	56560892	3189767
Variable plasmid segment Gla19d06.s1 (Accession	hypothetical protein BGP028	21133	22245	+	370	56560893	3190003

number NT_108227)							
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP029	22199	22252	+	17	56560894	3189764
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP030	22255	22815	+	186	56560895	3190006
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP031	22791	23555	+	254	56560896	3190008
Variable plasmid segment Gla19d06.s1 (Accession number NT_108227)	hypothetical protein BGP032	23897	24163	+	88	56560897	3190000

Fig. 30.

Antigen designation	Amino acid sequence
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31 SEQ ID NO 1	MNKILLLILLESIVFLSCSGKGSLGSEIPKVSLIIDGTFDDKSFNESALNGVKKVKEEFK IELVLKESSSNSYLSDLEGLKDAGSDLIWLIGYRFSDVAKVAALQNPDMKYAIIDPIYS NDPIPANLVGMTFRAQEGAFLTGYIAAKLSKTGKIGFLGGIEGEIVDAFRYGYEAGAK YANKDIKISTQYIGSFADLEAGRSVATRMYSDEIDIIHHAAGLGGIGAIEVAKELGSGH YIIGVDEDQAYLAPDNVITSTTKDVGRALNIFTSNHLKTNTFEGGKLINYGLKEGVVG FVRNPKMISFELEKEIDNLSSKIINKEIIVPSNKESYEKFLKEFI
NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31 SEQ ID NO 2	MRIVIFIFGILLTSCFSRNGIESSSKKIKISMLVDGVLDDKSFNSSANEALLRLKKDFPE NIEEVFSCAISGVYSSYVSDLDNLKRNGSDLIWLVGYMLTDASLLVSSENPKISYGII DPIYGDDVQIPENLIAVVFRVEQGAFLAGYIAAKKSFSGKIGFIGGMKGNIVDAFRYG YESGAKYANKDIEIISEYSNSFSDVDIGRTIASKMYSKGIDVIHFAAGLAGIGVIETAKN LGDGYYVIGADQDQSYLAPKNFITSVIKNIGDALYLITGEYIKNNNVWEGGKVVQMG LRDGVIGLPNANEFEYIKVLERKIINKEIIVPCNQEEYEIFIKQILKL
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31 SEQ ID NO 3	MFKRFIFITLSLLVFACFKSNKKSIKSDKVVVGVLAHGSFYDKGYNQSVHDGVVKLR DNFGIKLITKSLRPYPIEGKRLLTVDEAMTEDAYEVQKNPLNLFWLIGYRFSDLSVKL SYERPDIYYGIIDAFDYGDIQVPKNSLAIKFRNEEAAFLAGYIAAKMSRKEKIGFLTGP MSEHVKDFKFGFKAGIFYANPKLRLVSKKAPSLFDKEKGKAMALFMYKEDKVGVIF PIAGITGLGVYDAAKELGPKYYVIGLNQDQSYIAPQNVITSIIKDIGKVIYSISSEYINNR VFKGGIIIDRGLKEGVIEIVKDPDVLNNRLVDEVIDLENKIISGEIIVPDSEYAFDLFKSK L
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31 SEQ ID NO 4	MDNYYEIYFLYFFIKSKEDIFMLKKVYYFLIFLFIVACSSSDDGKSEAKTVSLIVDGAF DDKGFNESSSKAIRKLKADLNINIIEKASTGNSYLGDIANLEDGNSNLIWGIGFRLSDI LFQRASENVSVNYAIIEGVYDEIQIPKNLLNISFRSEEVAFLAGYFASKASKTGKIGFV GGVRGKVLESFMYGYEAGAKYANSNIKVVSQYVGTFGDFGLGRSTASNMYRDGV DIIFAAAGLSGIGVIEAAKELGPDHYIIGVDQDQSYLAPNNVIVSAVKKVDSLMYSLTK KYLETGVLDGGKTMFLGLKEDGLGLVLNENLKSNYSEIYNKSLKIGQSIMNGIIKVPY DKVSYFVLQMEN
AAC70056.1 Decorin binding protein A; DbpA [Borrelia afzelii SEQ ID NO 5	MIKYNKIILTLTLLASLLAACSLTGKARLESSVKDITNEIEKAIKEAEDAGVKTDAFTET QTGGKVGGSQIRAAKIRVADLTIKFLEATEEETITFKENGAGEEDFSGIYDLILNAAKA VEKIGMQGMKQAVEEAAKEKPKTTADGIIAIVKVMKAKVENIKEKQTKNQK
AAC70057.1 Decorin binding protein A; DbpA [Borrelia garinii] SEQ ID NO 6	MIKYNKILLKLSLIVSLLVACGLTGETKIRLESSAQEIKDEINKIKANAKKEGVKFEAFT NTQTGSKISEKPEFILKAKIKAIQVAERFVKAIKEEAEKLKKSGSSGAFSAMYDLMIDV SKPLEEIGIQKMTGTVTKEAEKTPPTTADGIIAIAQAMEEKLNNVNKKQHDALKNLEE KANTAATTT
AAC70021.1 Decorin binding protein B; DbpB [Borrelia burgdorferi] SEQ ID NO 7	SIVIALFFKLLVACSIGLVERTNAALESSSKDLKNKILKIKKEATGKGVLFEAFTGLKTG SKVTSGGLALREAKVQAIVETGKFLKIIEEEALKLKETGNSGQFLAMFDLMLEVVESL EDVGIIGLKARVLEESKNNPINTAERLLAAKAQIENQLKVVKEKQNIENGGEKKNNKS KKKK
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31] SEQ ID NO 8	MILIFYFKQIALFIIFRLCYIIKKVKIKLKRKSCMKKQFDTEVNDLLYLIIHSLYSHKEIFLR ELISNASDAIDKLKFLSLTNEKFKNIALEPKIEISFDDKSILIKDNGIGMDEQDLTNHLG VIAKSGTKEFINNLKQDEKKSASLIGQFGVGFYSAFIVSEKVEVTSKKALESDAYIWS SDGKTGYEIEKAKKEESGTEIKLYLNKEGLEYANKWKIQEIIKKYSNHINYPIYIKYSE PIMKDGKQEGIEEKEEKLNETTALWTKNKSEIKAEEYNEFYKNTTFDYENPLMHIHT KAEGNLEYTNLFYVPSKAPYDLYYPNTKPGVKLFINRIFITDSEGSLLPNYLRFIKGIID CQDLPLNVSREILQQNKILSKIKSSSVKKILSELEKLSKKNPEKFSEFSKEFGRCIKEG VYSDFENREKLISLIRFKSSSVDGFVSFKEYKERMNESQKSIYYITGGKENILKENPIV AAYKEKGFEILIMDDELDEAILNLIPEYEGLKLKAINKNETSNELKDENFKKIEEEFKDT LTKVKEILKDHIKEVNLSATLIKEPSAIIIDSNDPTYQMQKIMLSMGQEVKEIKPILELNP

	NNKIVQNLKNLEPEKLEKISILLFEEAMLTSGMPSKNPGKFINIINEFIEKDFL
CAA44492.1| Outer surface protein A [Borrelia burgdorferi] SEQ ID NO 9	MKKYLLGIGLILALIACKQNVSTLDEKNSVSVDLPGGMTELVSKEKDKDGKYSLEAT VDKLELKGTSDKNNGSGTLEGEKTDKSKVKLTIADDLSQTKFEIFKEDAKTLVSKKV TLKDKSSTEEKFNEKGETSEKTIVRANGTRLEYTDIKSDGSGKAKEVLKDFTLEGTL AADGKTTLKVTEGTVVLSKNILKSGEITVALDDSDTTQATKKTGKWDSKTSTLTISVN SQKTKNLVFTKEDTITVQKYDSAGTNLEGKAVEITTLKELKNALK
|BAA22351.1| Outer surface protein B [Borrelia garinii] SEQ ID NO 10	MKKYLLGFALVLALIACGQKGAEPKHNDQEVEDSKKDQKDASKKDLPLVTEDTVKL FNDTKIFISKEKNKDGKYELRATVDTVELKGVADKNDGSGGKLEGVKSDQSKVTMS ITDDLNTITVETYDSSNTKVASKVFKKQGSLTEETEETYKTGKLSTKKITRTNGTTLE YSDMTNDENATKAVETLKNGIMLEGNLVGGKTSVEIKEGTVTLKKEIEKAGTVKLFL DDTSSGSTKKTAVWSDTSNTLTVSADSKKIKDFVFLTDGTITVQNYDTAGTKLAGTA TEIKDLEALKAALK
AAM22469.1| Outer surface protein C [Borrelia afzelii] SEQ ID NO 11	MKKNTLSAILMTLFLFISCNNSGKGGDSASTNPADESAKGPNLTEISKKITDSNAFVL AVKEVETLVSSIDELANKAIGKKIQQNGLGAEANRNESLLAGVHEISTLITEKLSKLKN SGELKAKIEDAKKCSEEFTNKLRVSHADLGKQGVNDDDAKKAILKTNADKTKGAEE LGKLFKSVEGLVKAAQEALTNSVKELTSPVVAESPKKP
AAC62927.1| OspE-related lipoprotein [Borrelia garinii] SEQ ID NO 12	MNKKMKMFIICAVFVLISSCGNFRSSLSDQGSLSDQGSLSDQGSLSDQGGLSGQA SSDTIKFSEFTVNIKNKKDNNGDWSNLGTLVIRKEQDGVETGLNVIGTINGQLRGHS ATFFCIEEAEVNNFVKAMTNVGSFKTSLYYGYKEEQSSTNGIKGKEITTKIETINNSE HITFSGDKI
CAA57806.1| Outer surface protein G [Borrelia burgdorferi] SEQ ID NO 13	MNKKMKNLIICAVFVLIISCKIDASSEDLKQNVKEKVEGFLDKELMQGDDPNNSLFNP PPVLPASSHDNTPVLKAVQAKDGGQQEGKEEKEKEIQELKDKIDKRKKELEEARKK FQEFKEQVESATGESTEKVKKQGNIGQKALKYAKELGVNGSYSVNDGTNTNDFVK KVIDDALKNIEEELEKLAEPQNIEDKK
AAC44770.1| FlaA protein (Borrelia burgdorferi) SEQ ID NO 14	MKRKAKSILFFLLSTVLFAQETDGLAEGSKRAEPGELVLDFAELARDPSSTRLDLTN YVDYVYSGASGIVKPEDMVVDLGINNWSVLLTPSARLQAYVKNSVVAPAVVKSESK RYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLIDNIKTMKEIKV SVYSLGYEIDLEVLFEDMNGMEYAYSMGTLKFKGWADLIWSNPNYIPNISSRIIKDD VPNYPLASSKMRFKAFRVSKSHSSKVKNFIFYVKDLRVLYDKLSVSIDSDIDSESVFK VYETSGTESLRKLKAHETFKRVLKLREKISIAEGSFQNFVEKIESEKPEESSPKN
BAD18055.1 FlaB protein [Borrelia garinii] SEQ ID NO 15	NTSKAINFIQTTEGNLNEVEKVLVRMKELAVQSGNGTYSDADRGSIQIEIEQLTDEIN RIADQAQYNQMHMLSNKSASQNVRTAEELGMQPAKINTPASLSGSQASWTLRVHV GANQDEAIAVNIYAANVANLFSGEGAQAAQTAPVQEGVQQEGAQQPAPATAPSQG GVNSPVNVTTTVDANTSLAKIENAIRMISDQ
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi] SEQ ID NO 16	MIINHNTSAINASRNNSINAANLSKTQEKLSSGYRINRASDDAAGMGVSGKINAQIRG LSQASRNTSKAINFIQTTEGNLNEVEKVLVRMKELAVQSGNGTYSDADRGSIQIEIE QLTDEINRIADQAQYNQMHMLSNKSASQNVRTAEELGMQPAKINTPASLSGSQAS WTLRVHVGANQDEAIAVNIYAANVANLFSGEGSQAAQTAPVQEGAQQEGAQQPA PATAPSQGGVNSPVNVTTTVDANTSLAKIENAIRMISDQRANLGAFQNRLESIKDST EYAIENLKASYAQIKDATMTDEVVASTTNSILTQSAMAMIAQANQVPQYVLSLLR
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen VlsE1 Of Borrelia Burgdorferi SEQ ID NO 17	MRGSHHHHHHGSSQVADKDDPTNKFYQSVIQLGNGFLDVFTSFGGLVAEAFGFKS DPKKSDVKTYFTTVAAKLEKTKTDLNSLPKEKSDISSTTGKPDSTGSVGTAVEGAIK EVSELLDKLVKAVKTAEGASSGTAAIGEVVADADAAKVADKASVKGIAKGIKEIVEAA GGSEKLKAVAAAKGENNKGAGKLFGKAGAAAHGDSEAASKAAGAVSAVSGEQILS AIVTAADAAEQDGKKPEEAKNPIAAAIGDKDGGAEFGQDEXKKDDQIAAAIALRGXA KDGKFAVKDGEKEKAEGAIKGAAESAVRKVLGAITGLIGDAVSSGLRKVGDSVKAA SKETPPALNK
CAA57807.1 Associated protein A	MKKISLLIFLFLFVVSLSANIEENYTETKRAFSKEDFNLINKRLDNYDFKNEYEKSHVF SDAPRIRGDLRKIGIKEKSVFLDALEAIEYLIKIKISTDSIFLSEDMIRLIGSYPDSIFNYLI QLNSDKIDYAEKYGDNARNNFKKDYSEDKANTVKQILKQILADLPKD

(BapA)[Borrelia burgdorferi] SEQ ID NO 18	
AAL25643.1, P37-47 [Borrelia burgdorferi] SEQ ID NO 19	MCAFLLLNLVNCKFDSLNLSTKSVDDKNNSIAKLLQHLSKSEDQANKTSTSEDQKEL EITENKEQEHEKLSQVAQHAPNSKIEKVKSDGKPVPGDKILSSNKDIYNSYIPEVKEE IVYEILEEVIIPETKIPEITEEVIMPIPQTIDFYIEPRPISSFLTQGTSPSITSTIKSYKELAK EKINNGLNIVQKITQNIDNITENLNSKETPKEISGKEVEEKITHPIFDHITGSGNNPGQD SISNTWGEGLEIGGDSNFFTNLEEVRSSIRTKIKVSDGTEQTKDKVEIDEIIEDLQKLK EFLEKLKKYLKDTNNLSAIEESVKGLS
NP_212481.1| fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31] SEQ ID NO 20	MIKMSLNYTEINTLIKEIPFTNSLITKIIQPDYKSLVLEIYNKIDNKKFKILICLNPNTTRFH ITKKNFKKNALKLRFSDFLKSKIQNGKIIKAFQMKNERIISLEILQKDMIILFIKLWPSSP NIIATNSNFKILDAYYRRPKIKETTGEIFLKAKEIHESNKMSDKKIMELKEEYNNTSYTS YSEFLENYYESLNDQIKKTNIKELLIEKYKKELIVLEKRIDSLKQQIKLLENIENEKEKG ELILLNINKIQKGIKEINLLNYKEEKIKISLNQSLSPKENALQYFKAYKKGKNSFKTIQN QLKDNLDKFNLIQSKITMLKVENLIPEEEYNQEKTAIKEKEKTPKIGLHFTYCGFEILIG RNAKENDKLLRHCVKGNDYWLHTRDYPGAYVFIKNQKNKTPSLDVLLGAGNLCVF YTKLAKKSGKADLYYTQVKNLRRVKNKKLGLVIPKAEKNLHIKLDENLIKKIKNQT
AAC44656.1| P30 Borrelia burgdorferi SEQ ID NO 21	MKLQRSLSLIIFSLTVLCCDNKERKEGVSTKISLGAEPRSLDPQLAEDNVASKMIDTL YRGIVTGDPNTGGHKPGLAKGWETSSDGTAYPFYLRDNLTWSDGVAITAEGIRKSY LRILNKETGSTYVDMVKSIIKNGQEYFDGQVTDSELGIRAIDSKTLEITLASPKPYFIDL LVHQSFIPVPVHVTDKYGQNWTSPENMVTSGPFKLKERIPSEKYVFEKDNKYYDSN EVELEEITFYTTNDSSTAYKMYVNEELDAILVPYPQI
NP_045619.1| immunogenic protein P37, putative [Borrelia burgdorferi B31] SEQ ID NO 22	MNLINKLFILTILFSSVISCKLYKKITYNADQVIDKLKSNNGSFNTLKSNDDSKRSGRK PRSVDNTYMDQDTGKKPLMADMQPDMQNDNSSSNHTLQVNIQDNEASEARNIMT EIESSKEEYNRINEDLAKVKASLDKIKSLLSTAKSYLEQTRRGVGSSKANLALLPSLE EAIAKVKSNHASADTHCNDAIAALKRAKNDFEYAQRKADRALEEALSNSNASRHES YYYAGYHQFMADAKASMSSTKSLLEVAKNKQKELNENMTKTNKDFQELNDIYKKL QDMDSR
NP_212281.1| flagellin [Borrelia burgdorferi B31] SEQ ID NO 23	MIINHNTSAINASRNNGINAANLSKTQEKLSSGYRINRASDDAAGMGVSGKINAQIR GLSQASRNTSKAINFIQTTEGNLNEVEKVLVRMKELAVQSGNGTYSDADRGSIQIEI EQLTDEINRIADQAQYNQMHMLSNKSASQNVRTAEELGMQPAKINTPASLSGSQAS WTLRVHVGANQDEAIAVNIYAANVANLFSGEGAQTAQAAPVQEGVQQEGAQQPA PATAPSQGGVNSPVNVTTTVDANTSLAKIENAIRMISDQRANLGAFQNRLESIKNST EYAIENLKASYAQIKDATMTDEVVAATTNSILTQSAMAMIAQANQVPQYVLSLLR
NP_212463.1| oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) [Borrelia burgdorferi B31] SEQ ID NO 24	MKLQRSLFLIIFFLTFLCCNNKERKEGVSFKISLGAEPSSLDPQLAEDNVASKMIDTM FRGIVTGDPNTGGNKPGLAKGWDISSDGTVYTFNLREKITWSDGVAITAEGIRKSYL RILNKETGSKYVEMVKSVIKNGQKYFDGQVTDSELGIRAIDEKTLEITLESPKPYFID MLVHQSFIPVPVHVTEKYGQNWTSPENMVTSGPFKLKERIPNEKYVFEKNNKYYDS NEVELEEITFYTTNDSSTAYKMYENEELDAIFGSIPPDLIKNLKLRSDYYSSAVNAIYF YAFNTHIKPLDNVKIRKALTLAIDRETLTYKVLDNGTTPTRRATPNFSSYSYAKSLELF NPEIAKTLLAEAGYPNGNGFPILKLKYNTNEANKKICEFIQNQWKKNLNIDVELENEE WTTYLNTKANGNYEIARAGWIGDYADPLTFLSIFTQGYTQFSSHNYSNPEYNELIKK SDLELDPIKRQDILRQAEEIIIEKDFPIAPIYIYGNSYLFRNDKWTGWNTNILERFDLSQ LKLKNK
AAC44381.1| outer membrane porin protein Oms28 precursor SEQ ID NO 25	MTKIFSNLIINGLLFGFVSLNVFADSNNANILKPQSNVLEHSDQKDNKKLDQKDQVN QALDTINKVTEDVSSKLEGVRESSLELVESNDAGVVKKFVGSMSLMSDVAKGTVVA SQEATIVAKCSGMVAEGANKVVEMSKKAVQETQKAVSVAGEATFLIEKQIMLNKSP NNKELELTKEEFAKVDEVKETLMASERALDETVQEAQKVLNMVNGLNPSNKDQVL AKKDVRKAISNVVKVAQGARDLTKVMAISLYMR
CAA49829.1| p93 [Borrelia burgdorferi] SEQ ID NO 26	MKKMLLIFSFFLIFLNGFPLNARKVDKEKLKDFVNMDLEFVNYKGPYDSTNTYEQIV GIGEFLARPLTNSNSNSSYYGKYFINRFIDDQDKKASVDVFSISSKSELDSILNLRRIL TGYIIKSFDYDRSSAELIAKVITIYNAVYRGDLDYYKGFYIEPALKSLTKENAGLSRVY SQWAGKTQIFIPLKKDILSGNIESDIDIDSLVTDKVIAALLSENEAGVNFARDITDIQGE THKADQDKIDTELDNIHESDSNITETIENLRDQLEKATDEEHKKEIESQVDAKKKEKE ELDKKAINLDKAQQKLDSAEDNLDVQRDTVREKIQEDINEINKEKNLPKPGDVSSPK VDKQLQIKESLEDLQEQLKEAGDENQKREIEKQIEIKKRDEELLKSKDGKVSKDYEA

	LDLDRELSKASSKEKSKVKEEEITKGKSRASLGDLNNDKNLMLPEDQKLPEDKKLD SKLDGKKEFKPVSEVEKLDKISKSNNNEVGKLSPLDKPSYDDIDSKEEVDNKAINLQ KIDPKVKDQTTSLNEDLDKDLTTMSIDSSSPVFLEVIDPITNLGTLQLIDLNTGVRLKE STQQGIQRYGIYEREKDLVVIKMDSGKAKLQILNKLENLKVVSESNFEINKNSSLYVD SKMILAAVRDKDDSNAWRLAKFSPKNLDEFILSENKILPFTSFSVRKNFIYLQDELKN LVILDVNTLKKVK
NP_212375.1| glycerol kinase (glpK) [Borrelia burgdorferi B31] SEQ ID NO 27	MKYILSIDQGTTSSRAMVFDKNANIKGFAQKEFTQIYPQPSWVEHDPTEIWGSQLG VITEAMANARILPNEIDAIGITNQRETTVIWEKNTGKPIYNAIVWQDRRTAKICDQLKK EGKDKIILEKTGLVLDSYFSGTKIMWILDNVEGARQRAENGELCFGTIDTWILWNLTQ KKEHATDYSNASRTLLLNIKTLEWDDELLSILNVPRAILPELKESSTIYGKTDKALFGA EIPIAGIAGDQFAATFGQACLKKGMAKNTYGTGCFLTVNIGKEPIISHDKLLTSIAWG RKKSVTYVLEGSVFIGGAVIQWLRDGLEFFRKSSDAEALASSVSDNGGVYFVPAFV GLGAPHWDSYARGTIIGITRGSTKAHITRAALESIAFQSFDILNTMKKSIPNFEIQELR VDGGASQNNLLMQFQADLLECKVVRPKITETTALGAAYLAGLATGYWQSAEEIVSL WQVDKIFEPSMPKNQKEKLLENWNKAVGKAKSWIQNSHSS
NP_212342.1| hypothetical protein BB0208 [Borrelia burgdorferi B31] SEQ ID NO 28	MKTIKKDSEFYDSLATLKKHINKYIEEKVLKYSISSQLYKLEKPEIIELIKISNDYEKEKN AFNTSLEECYYKNTQNEAIKKWILEIVRNKNFIQISKEANLNTKKLGTTYKLKSSNFLK LIEIQNSPYYSQEKKDIYKQIILNFSSNINIDSLEQTIDILVAVRNRNKIKILNILNKNLKY RPENQKVFKSSLTNKESRLIKLKRMLILTYWPVGCLSKNIFIKILIKXYKYLEEEILALK YNEILNYLRALKTLSLNEIFYKGSSKNISFNYFFSDFTQYAPKDFQDTLKCYLYVIEKT ITKKYLTWFFKDKISNNWESFIDALEYIEKHKLINIKEKIKEIITAKFQTEDFFISFDKTNF NPYESSIFKERYIKSAFLEIIMHYVKKNSQNIETYGWIAFYIYADNKDKKIFCQRMKEF FKSKTFEIQNQIFVYFLSFYPNIEYKHFKFISDILLYLDENKITIPKKIIKIQKINPNQLDY QKSYLLIKSLKTRSRILKIIIKNIRFNLIEKLEDENEKKLLPAMCYLIYCENLVELKNNRKI KSNEKNSLLEFISFFKTKLKQKINFKKELMKSKGI
NP_045482.1| hypothetical protein BBG22 [Borrelia burgdorferi B31] SEQ ID NO 29	MITQQDYTEIKKKLENTKTRIQFRNGNKIDSLGYQGSLGEPILLKDKLTFSICDGKNID NRKEYEITKNAPSLDSLIEYLEHMILFFLEKTPVGTLTAKFAMEGSILTRSKLIQAFTN TNKFCIPDGRSLPSNCYAYKVLGISSAPKLSGRFLRHYDSGGSTDSDGTRSLGHTQ EDSYKNHDHDLDFSRINFKGKLVKRMTMIYRSADTWYTWYWAEEIMSPFITGYSYE EIDPEYLLPPFTSQSGSKETKPKNTCYISFYRYDL
NP_212885.1| hypothetical protein BB0751 [Borrelia burgdorferi B31] SEQ ID NO 30	MDLLDLLEKEKQINKNKGVFMTKPKIFSINKEKIKILIIVVLTSTFLLGIIFSNENKVARIL EEKFFDFDFNLISKIETELEGTLTKLGKDWILTYNKQNIPVDNKKVNSLIKALDELQKN KLVSRDQKKHKELGIGENPSFKLFDNNNKLLTEIFVGKSGEGDSRLAYIKGSDENVY LTKNIFLSYKGNSYNTFSDTTLFQEKNTKLENLSFKIIRKLNKENENNINNNYEIISKD GLYFLNNQKMTKERPLNIIAEFKADGLEIDKSKIDDYNLQYKIEVKWSNKSVNNIEVY FNKNEENDKDILIKKDKDEYYYTTSKWTFFDVFDLEKKLTEKDDISSNDNQEDHHEH HNNAD
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31] SEQ ID NO 31	MKKLIIIFTLFLSQACNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAK EYAIKLGENRTITHTLFGTTPMQRIHKYDQSFNLTREILASGIELNRVVNAWLNSPSH KEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRKYKN
NP_045709.1| lipoprotein BBA36[Borrelia burgdorferi B31] SEQ ID NO 32	MMQRISILLMLLAVFSCKQFGDVKSLTEIDSGNGIPLVVSDVVKDLIPKEISLTPEEAE KLESLKVFLKDAMSVNGREEALKAEYEKSYKEFFDWLSKDVNRQKEFISSFDNISSI VSKAVDASKKRRPTEQQSLGFKEYVCYKIKNSKGEALSLFFQKVVDAFGADPYKKD NDESVQKPVKCNEEIFKVIKKVLTESESNNELKNLKNYGNV
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi] SEQ ID NO 33	MKRISILSILLLLLLFSCKQYGDVKSLTEVATDLEDDNSFASGSVESKDQIIEKGPVLT SEEFERLEALKTFLKDAMGVNGREGDTKAEYEKSYKEFFDWLSKDVNRQKEFVSF FNNICGIITKAVDASKKRYNSNPKSLGFNEYVCYDIKTRTGDDLSLFFQKVADAFGT QEYKNKDEDDENNQKPEKCNEEIFKVIKRVFTESENNNELANLKNLNSYNLNSNNK
NP_045739.1| BBA66 antigen,	MKIKPLIQLKLLGLFLFSCTIDANLNEDYKNKVKGILNKAADDQETTSADTNSNAAKNI PIADNDKVAAELKKQSQAAKTVAAAPNKGSQNQPQTTPNKGSQNQQAAPSPQLQ

P35, putative [Borrelia burgdorferi B31]SEQ ID NO 34	SLSFSADLSNLPKTTAARAASLTKQRIPIQAVTTVPGNTRTFNSRNSGLPTFALNYSF SQPTRQQTNSSSAVQTTTSSGSKLQTLKNELIRAISEEKNKTQNNFGFRETYDQFK MKDSAFELLDVISSAKVYDRSYAPQLNSNTPEAENERNKFYALMDFDQYKIEQFGSI MEALYNENQNHSLIRELMISGLGTQISFELALEEINKKIEIFNQDYLNAKINSFDFTMK LKELKSKLNQILDKRKEWSRQADGLIANASSNSSLSDSKSLAEYIKKRYLDNMQNAR QSVLEAYISIM
AAT93824.1|BBA 66 antigen, P35, putative [Borrelia garinii PBi] SEQ ID NO 35	MSSCTIDANLNKDYKNKVEELLNSSTDDQAKISINTGSNATKNKTNIKVAGLQKNTQ SKKNNNLQGLNPANQVNPGNPMQIANQANQANQANQANQANQASQASQASQVA SSASQASPVASPATNVQATPPKQIASAQAIQTVPNNTSTPNQSIIKPQQYTFSSSFS QPTSQTNFNNSQSNNVLTNYRHQTQPSFVVPVYSGNSPLQKLKNNLLRRIAEEKNK THNHGFRETYDQFKMKDSAFTLLDVISNISVFDRGSAPQLSSNTPEAESERNRLYA MMDFDQAKTTEFGSIMNILYQENQNHSLIRSLIISGLGIQISLESTLEEIEKKIESFNTQ YLNTIINSYTFKDKLKELESKLNSILAEKKEWLNYADAIITNTSSNSKRNDPQSLGQYI KNKYLDKMQDARQSALDLYLNITEIR
NP_045742.1| hypothetical protein BBA69 [Borrelia burgdorferi B31] SEQ ID NO 36	MKKAKLNIIKINIITMILTLICISCAPFNKINPKANENTKLKKNTRLKKPANPGENIQNFK DKSGDLGASDEKFMGTTASELKAIGKELEDRKNQYDIQIAKITNEESNLLDTYIRAYE LANENEKMLLKRFLLSSLDYKKENIETLKEILEKLINNYENDPKIAANFLYRIALDIQLK LEKHLKSINEKLDTLSKENSKEDLEALLEQVKSALQLQEKFKKTLNKTLEDYRKNTN NIQENKVLAEHFNKYYKDSDSLQSAFY
AAT93826.1| conserved hypothetical protein BBA69[Borrelia garinii PBi] SEQ ID NO 37	MKKTKLNIIKLNILTTTLTLICISCAVNKIDPEPKSKTNKKENIKNFVNKFQDLEPSKKQ NKDLEPLREKYPEATASKLETTLKILEAQKEKENIEIAKIDNTQIDFLKTFKTDPHDSL PEDEKMQMKKIIYSSLNYETEKIKILQEILEKLDKNLQHKKIAKNFIYDIPIIIQSRLDIISK VIKNPIKDELQILNQKEIEELLMRIESELKIKENFKKALNKTIDAYNQDSENIKTSAEQL EKHINENYKEFNSLKPIY
NP_045573.1| hypothetical protein BBI42 [Borrelia burgdorferi B31] SEQ ID NO 38	MRILVGVCIIALALLGCYLPDNQEQAVQTFFENSESSDMGSDEIVTEGIFSSLKLYAS EHRLLVEIKKTLISLKDPNYRGVVLPVSDYNEEYFNKFFLDLGSEQSKDLIKLFIMVK NEQNNNKFMRIVRWLYSCIEELYSPDIKYSGEEGSPEYYRNMPRPTAYQQYLKVKR YDYNRPVPILPT
NP_051318.1| revA protein[Borrelia burgdorferi B31] SEQ ID NO 39	MRNKNIFKLFFASMLFVMACKAYVEEKKEIDSLMEDVLALVNDSSGGKFKDYKDKIN ELKENLKDIGNAELKEKLLNLQNSFQDKLAAKLAALKAAKNTIENITDKDQDISKRKI WSEAKLVGVTVPLLGSNTSGNGDKMSKNAVEQIDKVIKFLEEGTN
NP_045737.1| BBA64 antigen, P35 [Borrelia burgdorferi B31] SEQ ID NO 40	MKDNILKNNKLIAIFLLHVLTVLILISCSLEVKDSNESKKHKKEKRKGKVENLLVAINNL KNPTKPAAGKNKANSKASKQKNNPNANANNAPKKILDPEVAKLIQKILDRSENIIQIS EMDSSRGEPNDQFGMRAEIFSKIFFNANSTVHFDSHEYTEERRMLYTSLNFNEGKI FNLGQILSKLSQDSNYRGLVKETLINRGFSIQLAMEEISAKILNVKDKLQQLNKPNLE TLYNDFEKLTSLKEKWLKDTDDLIDEYNTNPDLQTDVSKLNDTLRSKNSRAQFANIH DIILDLVNTTTNILAPIQ
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi] SEQ ID NO 41	MKNNKLIAIFLLHILTGLILLSCSLEVNQDDNQEKQKKAKTKTSKSENNSSKMKKLSK NAKNKKPTVDNLLVAINTLKNPPKTAGKNKSNSAAALKQPNNANALKQIDPEAKELI QKILERSEDIVQISEIDANKGEPDDQFEMKAEIFSKIFFNAGSTVTFDDNEYVNERRIL YTSLNFNENKILNLGKILSKLSQDSNYRSLVKEILINRGFSIQLAIEEISLRTLNVKDKIQ HLNKPNLKTLYHDFNKLIPLKEKWLKDVDDIIKDYNANPELRTDISKLNDYIISKNSKA QFTDIHNIILNLINTTTNILAPIQ
AAL84596.1| BBK32 [Borrelia burgdorferi] SEQ ID NO 42	MKKVKSKYLALGLLFGFISCDLFIRYEMKEESPGLFDKGNSILETSEESIKKPMNKKG KGKIARKKGKSKVSRKEPYIHSLKRDSANKSNFLQKNVILEEESLKTELLKEQSETR KEKIQKQQDEYKGMTQGSLNSLSGESGELKETIESNEIDITIDSDLRPKSSLQDIAGS NSISYTDEIEEEDYARYYLDEDDEDDEYYEDDYEEIRLSNRYQSYLEGVKYNVDSAI NTINKIYDTYTLFSTKLTQMYSTRLDNLAKAKAKEEAAKFTKEDLEKNFKTLLNYIQV SVKTAANFVYINDTHAKRKLENIEAEIKTLIAKIKEQSNLYEAYKAIVTSILLMRDSLKE

	VQGIIDKNGVWY
AAL84590.1| BBK32 [Borrelia afzelii] SEQ ID NO 43	MKIKSKCLALGLLFGFISCDLFIRDEIKEKSLGLCDEESSILETGDKSVKKSLNKKGKD KVARKKVEGNAVKKDPFNHHVKRESVNNSNLSQKNVISEEEILKTKLLRERPETRK EEIQKQQDEHKRMLQGSLSFLSGESGELKDTIESNEIDFTIDSDLRLKSDLQAISGSN SISYTDEIEEEDYDQYSLEEDYYYDGETRLSNRYESYLEGVKYNVSSAIKTIVKIYDN YTLLSTKQTQMYSTRLDNLAKAKAREEAKKFTKEELEKDLKTLLNYIQVSARTATNF VYAREIYSKRKLDAIETEIKNLILKIKGQSDLYEAYKAIVRSILLMKDSLKIIEIVIDKNGV WY	
AAL84595.1| BBK32 [Borrelia garinii] SEQ ID NO 44	MKKVKSKYLALGLLFGFISCDLFIRYEMKEESPGLFDKGNSILETSEESIKKPMNKKG KGKIARKNGKSKVSGKEPFIHSFKRDAANKSNFLQKNVMLEEESLKTELLKEQSET RKEKIQKQQDEYKGMTKGSLNSLSGESGELKETIESNEIDITIDSDLRPKSSLQDIAG SNSISYTDEIEEEDYARYYLDEDDEDDEYYEDDYEEIRLSNRYQSYLEGVKYNVDSA INTINKIYDTYTLFSTKLTQMYSTRLDNLAKAKAKEEAAKFTKEDLEKNFKTLLNYIQV SVKTATNFVYINEMHAKRKLENIEAKIKTLIAKIKEKSNLYSAYKAIVSSILLMRDSLKE VQYAIDKNGIWY	

Fig. 31.

Antigen designation	Class I Antigen peptide sequences SEQ ID NO/sequences
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31	SEQ ID NO 45-1366/ 8 mers: MNKILLLI; NKILLLIL; KILLLILL; ILLLILLE; LLLILLES; LLILLESI; LILLESIV; ILLESIVF; LLESIVFL; LESIVFLS; ESIVFLSC; SIVFLSCS; IVFLSCSG; VFLSCSGK; FLSCSGKG; LSCSGKGS; SCSGKGSL; CSGKGSLG; SGKGSLGS; GKGSLGSE; KGSLGSEI; GSLGSEIP; SLGSEIPK; LGSEIPKV; GSEIPKVS; SEIPKVSL; EIPKVSLI; IPKVSLII; PKVSLIID; KVSLIIDG; VSLIIDGT; SLIIDGTF; LIIDGTFD; IIDGTFDD; IDGTFDDK; DGTFDDKS; GTFDDKSF; TFDDKSFN; FDDKSFNE; DDKSFNES; DKSFNESA; KSFNESAL; SFNESALN; FNESALNG; NESALNGV; ESALNGVK; SALNGVKK; ALNGVKKV; LNGVKKVK; NGVKKVKE; GVKKVKEE; VKKVKEEF; KKVKEEFK; KVKEEFKI; VKEEFKIE; KEEFKIEL; EEFKIELV; EFKIELVL; FKIELVLK; KIELVLKE; IELVLKES; ELVLKESS; LVLKESSS; VLKESSSN; LKESSSNS; KESSSNSY; ESSSNSYL; SSSNSYLS; SSNSYLSD; SNSYLSDL; NSYLSDLE; SYLSDLEG; YLSDLEGL; LSDLEGLK; SDLEGLKD; DLEGLKDA; LEGLKDAG; EGLKDAGS; GLKDAGSD; LKDAGSDL; KDAGSDLI; DAGSDLIW; AGSDLIWL; GSDLIWLI; SDLIWLIG; DLIWLIGY; LIWLIGYR; IWLIGYRF; WLIGYRFS; LIGYRFSD; IGYRFSDV; GYRFSDVA; YRFSDVAK; RFSDVAKV; FSDVAKVA; SDVAKVAA; DVAKVAAL; VAKVAALQ; AKVAALQN; KVAALQNP; VAALQNPD; AALQNPDM; ALQNPDMK; LQNPDMKY; QNPDMKYA; NPDMKYAI; PDMKYAII; DMKYAIID; MKYAIIDP; KYAIIDPI; YAIIDPIY; AIIDPIYS; IIDPIYSN; IDPIYSND; DPIYSNDP; PIYSNDPI; IYSNDPIP; YSNDPIPA; SNDPIPAN; NDPIPANL; DPIPANLV; PIPANLVG; IPANLVGM; PANLVGMT; ANLVGMTF; NLVGMTFR; LVGMTFRA; VGMTFRAQ; GMTFRAQE; MTFRAQEG; TFRAQEGA; FRAQEGAF; RAQEGAFL; AQEGAFLT; QEGAFLTG; EGAFLTGY; GAFLTGYI; AFLTGYIA; FLTGYIAA; LTGYIAAK; TGYIAAKL; GYIAAKLS; YIAAKLSK; IAAKLSKT; AAKLSKTG; AKLSKTGK; KLSKTGKI; LSKTGKIG; SKTGKIGF; KTGKIGFL; TGKIGFLG; GKIGFLGG; KIGFLGGI; IGFLGGIE; GFLGGIEG; FLGGIEGE; LGGIEGEI; GGIEGEIV; GIEGEIVD; IEGEIVDA; EGEIVDAF; GEIVDAFR; EIVDAFRY; IVDAFRYG; VDAFRYGY; DAFRYGYE; AFRYGYEA; FRYGYEAG; RYGYEAGA; YGYEAGAK; GYEAGAKY; YEAGAKYA; EAGAKYAN; AGAKYANK; GAKYANKD; AKYANKDI; KYANKDIK; YANKDIKI; ANKDIKIS; NKDIKIST; KDIKISTQ; DIKISTQY; IKISTQYI; KISTQYIG; ISTQYIGS; STQYIGSF; TQYIGSFA; QYIGSFAD; YIGSFADL; IGSFADLE; GSFADLEA; SFADLEAG; FADLEAGR; ADLEAGRS; DLEAGRSV; LEAGRSVA; EAGRSVAT; AGRSVATR; GRSVATRM; RSVATRMY; SVATRMYS; VATRMYSD; ATRMYSDE; TRMYSDEI; RMYSDEID; MYSDEIDI; YSDEIDII; SDEIDIIH; DEIDIIHH; EIDIIHHA; IDIIHHAA; DIIHHAAG; IIHHAAGL; IHHAAGLG; HHAAGLGG; HAAGLGGI; AAGLGGIG; AGLGGIGA; GLGGIGAI; LGGIGAIE; GGIGAIEV; GIGAIEVA; IGAIEVAK; GAIEVAKE; AIEVAKEL; IEVAKELG; EVAKELGS; VAKELGSG; AKELGSGH; KELGSGHY; ELGSGHYI; LGSGHYII; GSGHYIIG; SGHYIIGV; GHYIIGVD; HYIIGVDE; YIIGVDED; IIGVDEDQ; IGVDEDQA; GVDEDQAY; VDEDQAYL; DEDQAYLA; EDQAYLAP; DQAYLAPD; QAYLAPDN; AYLAPDNV; YLAPDNVI; LAPDNVIT; APDNVITS; PDNVITST; DNVITSTT; NVITSTTK; VITSTTKD; ITSTTKDV; TSTTKDVG; STTKDVGR; TTKDVGRA; TKDVGRAL; KDVGRALN; DVGRALNI; VGRALNIF; GRALNIFT; RALNIFTS; ALNIFTSN; LNIFTSNH; NIFTSNHL; IFTSNHLK; FTSNHLKT; TSNHLKTN; SNHLKTNT; NHLKTNTF; HLKTNTFE; LKTNTFEG; KTNTFEGG; TNTFEGGK; NTFEGGKL; TFEGGKLI; FEGGKLIN; EGGKLINY; GGKLINYG; GKLINYGL; KLINYGLK; LINYGLKE; INYGLKEG; NYGLKEGV; YGLKEGVV; GLKEGVVG; LKEGVVGF; KEGVVGFV; EGVVGFVR; GVVGFVRN; VVGFVRNP; VGFVRNPK; GFVRNPKM; FVRNPKMI; VRNPKMIS; RNPKMISF; NPKMISFE; PKMISFEL; KMISFELE;

MISFELEK; ISFELEKE; SFELEKEI; FELEKEID; ELEKEIDN; LEKEIDNL; EKEIDNLS; KEIDNLSS; EIDNLSSK; IDNLSSKI; DNLSSKII; NLSSKIIN; LSSKIINK; SSKIINKE; SKIINKEI; KIINKEII; IINKEIIV; INKEIIVP; NKEIIVPS; KEIIVPSN; EIIVPSNK; IIVPSNKE; IVPSNKES; VPSNKESY; PSNKESYE; SNKESYEK; NKESYEKF; KESYEKFL; ESYEKFLK; SYEKFLKE; YEKFLKEF; EKFLKEFI;

9 mers:
MNKILLLIL; NKILLLILL; KILLLILLE; ILLLILLES; LLLILLESI; LLILLESIV; LILLESIVF; ILLESIVFL; LLESIVFLS; LESIVFLSC; ESIVFLSCS; SIVFLSCSG; IVFLSCSGK; VFLSCSGKG; FLSCSGKGS; LSCSGKGSL; SCSGKGSLG; CSGKGSLGS; SGKGSLGSE; GKGSLGSEI; KGSLGSEIP; GSLGSEIPK; SLGSEIPKV; LGSEIPKVS; GSEIPKVSL; SEIPKVSLI; EIPKVSLII; IPKVSLIID; PKVSLIIDG; KVSLIIDGT; VSLIIDGTF; SLIIDGTFD; LIIDGTFDD; IIDGTFDDK; IDGTFDDKS; DGTFDDKSF; GTFDDKSFN; TFDDKSFNE; FDDKSFNES; DDKSFNESA; DKSFNESAL; KSFNESALN; SFNESALNG; FNESALNGV; NESALNGVK; ESALNGVKK; SALNGVKKV; ALNGVKKVK; LNGVKKVKE; NGVKKVKEE; GVKKVKEEF; VKKVKEEFK; KKVKEEFKI; KVKEEFKIE; VKEEFKIEL; KEEFKIELV; EEFKIELVL; EFKIELVLK; FKIELVLKE; KIELVLKES; IELVLKESS; ELVLKESSS; LVLKESSSN; VLKESSSNS; LKESSSNSY; KESSSNSYL; ESSSNSYLS; SSSNSYLSD; SSNSYLSDL; SNSYLSDLE; NSYLSDLEG; SYLSDLEGL; YLSDLEGLK; LSDLEGLKD; SDLEGLKDA; DLEGLKDAG; LEGLKDAGS; EGLKDAGSD; GLKDAGSDL; LKDAGSDLI; KDAGSDLIW; DAGSDLIWL; AGSDLIWLI; GSDLIWLIG; SDLIWLIGY; DLIWLIGYR; LIWLIGYRF; IWLIGYRFS; WLIGYRFSD; LIGYRFSDV; IGYRFSDVA; GYRFSDVAK; YRFSDVAKV; RFSDVAKVA; FSDVAKVAA; SDVAKVAAL; DVAKVAALQ; VAKVAALQN; AKVAALQNP; KVAALQNPD; VAALQNPDM; AALQNPDMK; ALQNPDMKY; LQNPDMKYA; QNPDMKYAI; NPDMKYAII; PDMKYAIID; DMKYAIIDP; MKYAIIDPI; KYAIIDPIY; YAIIDPIYS; AIIDPIYSN; IIDPIYSND; IDPIYSNDP; DPIYSNDPI; PIYSNDPIP; IYSNDPIPA; YSNDPIPAN; SNDPIPANL; NDPIPANLV; DPIPANLVG; PIPANLVGM; IPANLVGMT; PANLVGMTF; ANLVGMTFR; NLVGMTFRA; LVGMTFRAQ; VGMTFRAQE; GMTFRAQEG; MTFRAQEGA; TFRAQEGAF; FRAQEGAFL; RAQEGAFLT; AQEGAFLTG; QEGAFLTGY; EGAFLTGYI; GAFLTGYIA; AFLTGYIAA; FLTGYIAAK; LTGYIAAKL; TGYIAAKLS; GYIAAKLSK; YIAAKLSKT; IAAKLSKTG; AAKLSKTGK; AKLSKTGKI; KLSKTGKIG; LSKTGKIGF; SKTGKIGFL; KTGKIGFLG; TGKIGFLGG; GKIGFLGGI; KIGFLGGIE; IGFLGGIEG; GFLGGIEGE; FLGGIEGEI; LGGIEGEIV; GGIEGEIVD; GIEGEIVDA; IEGEIVDAF; EGEIVDAFR; GEIVDAFRY; EIVDAFRYG; IVDAFRYGY; VDAFRYGYE; DAFRYGYEA; AFRYGYEAG; FRYGYEAGA; RYGYEAGAK; YGYEAGAKY; GYEAGAKYA; YEAGAKYAN; EAGAKYANK; AGAKYANKD; GAKYANKDI; AKYANKDIK; KYANKDIKI; YANKDIKIS; ANKDIKIST; NKDIKISTQ; KDIKISTQY; DIKISTQYI; IKISTQYIG; KISTQYIGS; ISTQYIGSF; STQYIGSFA; TQYIGSFAD; QYIGSFADL; YIGSFADLE; IGSFADLEA; GSFADLEAG; SFADLEAGR; FADLEAGRS; ADLEAGRSV; DLEAGRSVA; LEAGRSVAT; EAGRSVATR; AGRSVATRM; GRSVATRMY; RSVATRMYS; SVATRMYSD; VATRMYSDE; ATRMYSDEI; TRMYSDEID; RMYSDEIDI; MYSDEIDII; YSDEIDIIH; SDEIDIIHH; DEIDIIHHA; EIDIIHHAA; IDIIHHAAG; DIIHHAAGL; IIHHAAGLG; IHHAAGLGG; HHAAGLGGI; HAAGLGGIG; AAGLGGIGA; AGLGGIGAI; GLGGIGAIE; LGGIGAIEV; GGIGAIEVA; GIGAIEVAK; IGAIEVAKE; GAIEVAKEL; AIEVAKELG; IEVAKELGS; EVAKELGSG; VAKELGSGH; AKELGSGHY; KELGSGHYI; ELGSGHYII; LGSGHYIIG; GSGHYIIGV; SGHYIIGVD; GHYIIGVDE; HYIIGVDED; YIIGVDEDQ; IIGVDEDQA; IGVDEDQAY; GVDEDQAYL; VDEDQAYLA; DEDQAYLAP; EDQAYLAPD; DQAYLAPDN; QAYLAPDNV;

AYLAPDNVI; YLAPDNVIT; LAPDNVITS; APDNVITST; PDNVITSTT;
DNVITSTTK; NVITSTTKD; VITSTTKDV; ITSTTKDVG; TSTTKDVGR;
STTKDVGRA; TTKDVGRAL; TKDVGRALN; KDVGRALNI; DVGRALNIF;
VGRALNIFT; GRALNIFTS; RALNIFTSN; ALNIFTSNH; LNIFTSNHL;
NIFTSNHLK; IFTSNHLKT; FTSNHLKTN; TSNHLKTNT; SNHLKTNTF;
NHLKTNTFE; HLKTNTFEG; LKTNTFEGG; KTNTFEGGK; TNTFEGGKL;
NTFEGGKLI; TFEGGKLIN; FEGGKLINY; EGGKLINYG; GGKLINYGL;
GKLINYGLK; KLINYGLKE; LINYGLKEG; INYGLKEGV; NYGLKEGVV;
YGLKEGVVG; GLKEGVVGF; LKEGVVGFV; KEGVVGFVR; EGVVGFVRN;
GVVGFVRNP; VVGFVRNPK; VGFVRNPKM; GFVRNPKMI; FVRNPKMIS;
VRNPKMISF; RNPKMISFE; NPKMISFEL; PKMISFELE; KMISFELEK;
MISFELEKE; ISFELEKEI; SFELEKEID; FELEKEIDN; ELEKEIDNL;
LEKEIDNLS; EKEIDNLSS; KEIDNLSSK; EIDNLSSKI; IDNLSSKII;
DNLSSKIIN; NLSSKIINK; LSSKIINKE; SSKIINKEI; SKIINKEII;
KIINKEIIV; IINKEIIVP; INKEIIVPS; NKEIIVPSN; KEIIVPSNK;
EIIVPSNKE; IIVPSNKES; IVPSNKESY; VPSNKESYE; PSNKESYEK;
SNKESYEKF; NKESYEKFL; KESYEKFLK; ESYEKFLKE; SYEKFLKEF;
YEKFLKEFI;

10 mers:
MNKILLLILL; NKILLLILLE; KILLLILLES; ILLLILLESI; LLLILLESIV;
LLILLESIVF; LILLESIVFL; ILLESIVFLS; LLESIVFLSC; LESIVFLSCS;
ESIVFLSCSG; SIVFLSCSGK; IVFLSCSGKG; VFLSCSGKGS; FLSCSGKGSL;
LSCSGKGSLG; SCSGKGSLGS; CSGKGSLGSE; SGKGSLGSEI; GKGSLGSEIP;
KGSLGSEIPK; GSLGSEIPKV; SLGSEIPKVS; LGSEIPKVSL; GSEIPKVSLI;
SEIPKVSLII; EIPKVSLIID; IPKVSLIIDG; PKVSLIIDGT; KVSLIIDGTF;
VSLIIDGTFD; SLIIDGTFDD; LIIDGTFDDK; IIDGTFDDKS; IDGTFDDKSF;
DGTFDDKSFN; GTFDDKSFNE; TFDDKSFNES; FDDKSFNESA; DDKSFNESAL;
DKSFNESALN; KSFNESALNG; SFNESALNGV; FNESALNGVK; NESALNGVKK;
ESALNGVKKV; SALNGVKKVK; ALNGVKKVKE; LNGVKKVKEE; NGVKKVKEEF;
GVKKVKEEFK; VKKVKEEFKI; KKVKEEFKIE; KVKEEFKIEL; VKEEFKIELV;
KEEFKIELVL; EEFKIELVLK; EFKIELVLKE; FKIELVLKES; KIELVLKESS;
IELVLKESSS; ELVLKESSSN; LVLKESSSNS; VLKESSSNSY; LKESSSNSYL;
KESSSNSYLS; ESSSNSYLSD; SSSNSYLSDL; SSNSYLSDLE; SNSYLSDLEG;
NSYLSDLEGL; SYLSDLEGLK; YLSDLEGLKD; LSDLEGLKDA; SDLEGLKDAG;
DLEGLKDAGS; LEGLKDAGSD; EGLKDAGSDL; GLKDAGSDLI; LKDAGSDLIW;
KDAGSDLIWL; DAGSDLIWLI; AGSDLIWLIG; GSDLIWLIGY; SDLIWLIGYR;
DLIWLIGYRF; LIWLIGYRFS; IWLIGYRFSD; WLIGYRFSDV; LIGYRFSDVA;
IGYRFSDVAK; GYRFSDVAKV; YRFSDVAKVA; RFSDVAKVAA; FSDVAKVAAL;
SDVAKVAALQ; DVAKVAALQN; VAKVAALQNP; AKVAALQNPD; KVAALQNPDM;
VAALQNPDMK; AALQNPDMKY; ALQNPDMKYA; LQNPDMKYAI; QNPDMKYAII;
NPDMKYAIID; PDMKYAIIDP; DMKYAIIDPI; MKYAIIDPIY; KYAIIDPIYS;
YAIIDPIYSN; AIIDPIYSND; IIDPIYSNDP; IDPIYSNDPI; DPIYSNDPIP;
PIYSNDPIPA; IYSNDPIPAN; YSNDPIPANL; SNDPIPANLV; NDPIPANLVG;
DPIPANLVGM; PIPANLVGMT; IPANLVGMTF; PANLVGMTFR; ANLVGMTFRA;
NLVGMTFRAQ; LVGMTFRAQE; VGMTFRAQEG; GMTFRAQEGA; MTFRAQEGAF;
TFRAQEGAFL; FRAQEGAFLT; RAQEGAFLTG; AQEGAFLTGY; QEGAFLTGYI;
EGAFLTGYIA; GAFLTGYIAA; AFLTGYIAAK; FLTGYIAAKL; LTGYIAAKLS;
TGYIAAKLSK; GYIAAKLSKT; YIAAKLSKTG; IAAKLSKTGK; AAKLSKTGKI;
AKLSKTGKIG; KLSKTGKIGF; LSKTGKIGFL; SKTGKIGFLG; KTGKIGFLGG;
TGKIGFLGGI; GKIGFLGGIE; KIGFLGGIEG; IGFLGGIEGE; GFLGGIEGEI;
FLGGIEGEIV; LGGIEGEIVD; GGIEGEIVDA; GIEGEIVDAF; IEGEIVDAFR;
EGEIVDAFRY; GEIVDAFRYG; EIVDAFRYGY; IVDAFRYGYE; VDAFRYGYEA;
DAFRYGYEAG; AFRYGYEAGA; FRYGYEAGAK; RYGYEAGAKY; YGYEAGAKYA;
GYEAGAKYAN; YEAGAKYANK; EAGAKYANKD; AGAKYANKDI; GAKYANKDIK;
AKYANKDIKI; KYANKDIKIS; YANKDIKIST; ANKDIKISTQ; NKDIKISTQY;
KDIKISTQYI; DIKISTQYIG; IKISTQYIGS; KISTQYIGSF; ISTQYIGSFA;

STQYIGSFAD; TQYIGSFADL; QYIGSFADLE; YIGSFADLEA; IGSFADLEAG;
GSFADLEAGR; SFADLEAGRS; FADLEAGRSV; ADLEAGRSVA; DLEAGRSVAT;
LEAGRSVATR; EAGRSVATRM; AGRSVATRMY; GRSVATRMYS; RSVATRMYSD;
SVATRMYSDE; VATRMYSDEI; ATRMYSDEID; TRMYSDEIDI; RMYSDEIDII;
MYSDEIDIIH; YSDEIDIIHH; SDEIDIIHHA; DEIDIIHHAA; EIDIIHHAAG;
IDIIHHAAGL; DIIHHAAGLG; IIHHAAGLGG; IHHAAGLGGI; HHAAGLGGIG;
HAAGLGGIGA; AAGLGGIGAI; AGLGGIGAIE; GLGGIGAIEV; LGGIGAIEVA;
GGIGAIEVAK; GIGAIEVAKE; IGAIEVAKEL; GAIEVAKELG; AIEVAKELGS;
IEVAKELGSG; EVAKELGSGH; VAKELGSGHY; AKELGSGHYI; KELGSGHYII;
ELGSGHYIIG; LGSGHYIIGV; GSGHYIIGVD; SGHYIIGVDE; GHYIIGVDED;
HYIIGVDEDQ; YIIGVDEDQA; IIGVDEDQAY; IGVDEDQAYL; GVDEDQAYLA;
VDEDQAYLAP; DEDQAYLAPD; EDQAYLAPDN; DQAYLAPDNV; QAYLAPDNVI;
AYLAPDNVIT; YLAPDNVITS; LAPDNVITST; APDNVITSTT; PDNVITSTTK;
DNVITSTTKD; NVITSTTKDV; VITSTTKDVG; ITSTTKDVGR; TSTTKDVGRA;
STTKDVGRAL; TTKDVGRALN; TKDVGRALNI; KDVGRALNIF; DVGRALNIFT;
VGRALNIFTS; GRALNIFTSN; RALNIFTSNH; ALNIFTSNHL; LNIFTSNHLK;
NIFTSNHLKT; IFTSNHLKTN; FTSNHLKTNT; TSNHLKTNTF; SNHLKTNTFE;
NHLKTNTFEG; HLKTNTFEGG; LKTNTFEGGK; KTNTFEGGKL; TNTFEGGKLI;
NTFEGGKLIN; TFEGGKLINY; FEGGKLINYG; EGGKLINYGL; GGKLINYGLK;
GKLINYGLKE; KLINYGLKEG; LINYGLKEGV; INYGLKEGVV; NYGLKEGVVG;
YGLKEGVVGF; GLKEGVVGFV; LKEGVVGFVR; KEGVVGFVRN; EGVVGFVRNP;
GVVGFVRNPK; VVGFVRNPKM; VGFVRNPKMI; GFVRNPKMIS; FVRNPKMISF;
VRNPKMISFE; RNPKMISFEL; NPKMISFELE; PKMISFELEK; KMISFELEKE;
MISFELEKEI; ISFELEKEID; SFELEKEIDN; FELEKEIDNL; ELEKEIDNLS;
LEKEIDNLSS; EKEIDNLSSK; KEIDNLSSKI; EIDNLSSKII; IDNLSSKIIN;
DNLSSKIINK; NLSSKIINKE; LSSKIINKEI; SSKIINKEII; SKIINKEIIV;
KIINKEIIVP; IINKEIIVPS; INKEIIVPSN; NKEIIVPSNK; KEIIVPSNKE;
EIIVPSNKES; IIVPSNKESY; IVPSNKESYE; VPSNKESYEK; PSNKESYEKF;
SNKESYEKFL; NKESYEKFLK; KESYEKFLKE; ESYEKFLKEF; SYEKFLKEFI;

11 mers:
MNKILLLILLE; NKILLLILLES; KILLLILLESI; ILLLILLESIV;
LLLILLESIVF; LLILLESIVFL; LILLESIVFLS; ILLESIVFLSC;
LLESIVFLSCS; LESIVFLSCSG; ESIVFLSCSGK; SIVFLSCSGKG;
IVFLSCSGKGS; VFLSCSGKGSL; FLSCSGKGSLG; LSCSGKGSLGS;
SCSGKGSLGSE; CSGKGSLGSEI; SGKGSLGSEIP; GKGSLGSEIPK;
KGSLGSEIPKV; GSLGSEIPKVS; SLGSEIPKVSL; LGSEIPKVSLI;
GSEIPKVSLII; SEIPKVSLIID; EIPKVSLIIDG; IPKVSLIIDGT;
PKVSLIIDGTF; KVSLIIDGTFD; VSLIIDGTFDD; SLIIDGTFDDK;
LIIDGTFDDKS; IIDGTFDDKSF; IDGTFDDKSFN; DGTFDDKSFNE;
GTFDDKSFNES; TFDDKSFNESA; FDDKSFNESAL; DDKSFNESALN;
DKSFNESALNG; KSFNESALNGV; SFNESALNGVK; FNESALNGVKK;
NESALNGVKKV; ESALNGVKKVK; SALNGVKKVKE; ALNGVKKVKEE;
LNGVKKVKEEF; NGVKKVKEEFK; GVKKVKEEFKI; VKKVKEEFKIE;
KKVKEEFKIEL; KVKEEFKIELV; VKEEFKIELVL; KEEFKIELVLK;
EEFKIELVLKE; EFKIELVLKES; FKIELVLKESS; KIELVLKESSS;
IELVLKESSSN; ELVLKESSSNS; LVLKESSSNSY; VLKESSSNSYL;
LKESSSNSYLS; KESSSNSYLSD; ESSSNSYLSDL; SSSNSYLSDLE;
SSNSYLSDLEG; SNSYLSDLEGL; NSYLSDLEGLK; SYLSDLEGLKD;
YLSDLEGLKDA; LSDLEGLKDAG; SDLEGLKDAGS; DLEGLKDAGSD;
LEGLKDAGSDL; EGLKDAGSDLI; GLKDAGSDLIW; LKDAGSDLIWL;
KDAGSDLIWLI; DAGSDLIWLIG; AGSDLIWLIGY; GSDLIWLIGYR;
SDLIWLIGYRF; DLIWLIGYRFS; LIWLIGYRFSD; IWLIGYRFSDV;
WLIGYRFSDVA; LIGYRFSDVAK; IGYRFSDVAKV; GYRFSDVAKVA;
YRFSDVAKVAA; RFSDVAKVAAL; FSDVAKVAALQ; SDVAKVAALQN;
DVAKVAALQNP; VAKVAALQNPD; AKVAALQNPDM; KVAALQNPDMK;
VAALQNPDMKY; AALQNPDMKYA; ALQNPDMKYAI; LQNPDMKYAII;

	QNPDMKYAIID; NPDMKYAIIDP; PDMKYAIIDPI; DMKYAIIDPIY; MKYAIIDPIYS; KYAIIDPIYSN; YAIIDPIYSND; AIIDPIYSNDP; IIDPIYSNDPI; IDPIYSNDPIP; DPIYSNDPIPA; PIYSNDPIPAN; IYSNDPIPANL; YSNDPIPANLV; SNDPIPANLVG; NDPIPANLVGM; DPIPANLVGMT; PIPANLVGMTF; IPANLVGMTFR; PANLVGMTFRA; ANLVGMTFRAQ; NLVGMTFRAQE; LVGMTFRAQEG; VGMTFRAQEGA; GMTFRAQEGAF; MTFRAQEGAFL; TFRAQEGAFLT; FRAQEGAFLTG; RAQEGAFLTGY; AQEGAFLTGYI; QEGAFLTGYIA; EGAFLTGYIAA; GAFLTGYIAAK; AFLTGYIAAKL; FLTGYIAAKLS; LTGYIAAKLSK; TGYIAAKLSKT; GYIAAKLSKTG; YIAAKLSKTGK; IAAKLSKTGKI; AAKLSKTGKIG; AKLSKTGKIGF; KLSKTGKIGFL; LSKTGKIGFLG; SKTGKIGFLGG; KTGKIGFLGGI; TGKIGFLGGIE; GKIGFLGGIEG; KIGFLGGIEGE; IGFLGGIEGEI; GFLGGIEGEIV; FLGGIEGEIVD; LGGIEGEIVDA; GGIEGEIVDAF; GIEGEIVDAFR; IEGEIVDAFRY; EGEIVDAFRYG; GEIVDAFRYGY; EIVDAFRYGYE; IVDAFRYGYEA; VDAFRYGYEAG; DAFRYGYEAGA; AFRYGYEAGAK; FRYGYEAGAKY; RYGYEAGAKYA; YGYEAGAKYAN; GYEAGAKYANK; YEAGAKYANKD; EAGAKYANKDI; AGAKYANKDIK; GAKYANKDIKI; AKYANKDIKIS; KYANKDIKIST; YANKDIKISTQ; ANKDIKISTQY; NKDIKISTQYI; KDIKISTQYIG; DIKISTQYIGS; IKISTQYIGSF; KISTQYIGSFA; ISTQYIGSFAD; STQYIGSFADL; TQYIGSFADLE; QYIGSFADLEA; YIGSFADLEAG; IGSFADLEAGR; GSFADLEAGRS; SFADLEAGRSV; FADLEAGRSVA; ADLEAGRSVAT; DLEAGRSVATR; LEAGRSVATRM; EAGRSVATRMY; AGRSVATRMYS; GRSVATRMYSD; RSVATRMYSDE; SVATRMYSDEI; VATRMYSDEID; ATRMYSDEIDI; TRMYSDEIDII; RMYSDEIDIIH; MYSDEIDIIHH; YSDEIDIIHHA; SDEIDIIHHAA; DEIDIIHHAAG; EIDIIHHAAGL; IDIIHHAAGLG; DIIHHAAGLGG; IIHHAAGLGGI; IHHAAGLGGIG; HHAAGLGGIGA; HAAGLGGIGAI; AAGLGGIGAIE; AGLGGIGAIEV; GLGGIGAIEVA; LGGIGAIEVAK; GGIGAIEVAKE; GIGAIEVAKEL; IGAIEVAKELG; GAIEVAKELGS; AIEVAKELGSG; IEVAKELGSGH; EVAKELGSGHY; VAKELGSGHYI; AKELGSGHYII; KELGSGHYIIG; ELGSGHYIIGV; LGSGHYIIGVD; GSGHYIIGVDE; SGHYIIGVDED; GHYIIGVDEDQ; HYIIGVDEDQA; YIIGVDEDQAY; IIGVDEDQAYL; IGVDEDQAYLA; GVDEDQAYLAP; VDEDQAYLAPD; DEDQAYLAPDN; EDQAYLAPDNV; DQAYLAPDNVI; QAYLAPDNVIT; AYLAPDNVITS; YLAPDNVITST; LAPDNVITSTT; APDNVITSTTK; PDNVITSTTKD; DNVITSTTKDV; NVITSTTKDVG; VITSTTKDVGR; ITSTTKDVGRA; TSTTKDVGRAL; STTKDVGRALN; TTKDVGRALNI; TKDVGRALNIF; KDVGRALNIFT; DVGRALNIFTS; VGRALNIFTSN; GRALNIFTSNH; RALNIFTSNHL; ALNIFTSNHLK; LNIFTSNHLKT; NIFTSNHLKTN; IFTSNHLKTNT; FTSNHLKTNTF; TSNHLKTNTFE; SNHLKTNTFEG; NHLKTNTFEGG; HLKTNTFEGGK; LKTNTFEGGKL; KTNTFEGGKLI; TNTFEGGKLIN; NTFEGGKLINY; TFEGGKLINYG; FEGGKLINYGL; EGGKLINYGLK; GGKLINYGLKE; GKLINYGLKEG; KLINYGLKEGV; LINYGLKEGVV; INYGLKEGVVG; NYGLKEGVVGF; YGLKEGVVGFV; GLKEGVVGFVR; LKEGVVGFVRN; KEGVVGFVRNP; EGVVGFVRNPK; GVVGFVRNPKM; VVGFVRNPKMI; VGFVRNPKMIS; GFVRNPKMISF; FVRNPKMISFE; VRNPKMISFEL; RNPKMISFELE; NPKMISFELEK; PKMISFELEKE; KMISFELEKEI; MISFELEKEID; ISFELEKEIDN; SFELEKEIDNL; FELEKEIDNLS; ELEKEIDNLSS; LEKEIDNLSSK; EKEIDNLSSKI; KEIDNLSSKII; EIDNLSSKIIN; IDNLSSKIINK; DNLSSKIINKE; NLSSKIINKEI; LSSKIINKEII; SSKIINKEIIV; SKIINKEIIVP; KIINKEIIVPS; IINKEIIVPSN; INKEIIVPSNK; NKEIIVPSNKE; KEIIVPSNKES; EIIVPSNKESY; IIVPSNKESYE; IVPSNKESYEK; VPSNKESYEKF; PSNKESYEKFL; SNKESYEKFLK; NKESYEKFLKE; KESYEKFLKEF; ESYEKFLKEFI;

NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31	SEQ ID NO 1367-2696/ 8 mers: MRIVIFIF; RIVIFIFG; IVIFIFGI; VIFIFGIL; IFIFGILL; FIFGILLT; IFGILLTS; FGILLTSC; GILLTSCF; ILLTSCFS; LLTSCFSR; LTSCFSRN; TSCFSRNG; SCFSRNGI; CFSRNGIE; FSRNGIES; SRNGIESS; RNGIESSS; NGIESSSK; GIESSSKK; IESSSKKI; ESSSKKIK; SSSKKIKI; SSKKIKIS; SKKIKISM; KKIKISML; KIKISMLV; IKISMLVD; KISMLVDG; ISMLVDGV; SMLVDGVL; MLVDGVLD; LVDGVLDD; VDGVLDDK; DGVLDDKS; GVLDDKSF; VLDDKSFN; LDDKSFNS; DDKSFNSS; DKSFNSSA; KSFNSSAN; SFNSSANE; FNSSANEA; NSSANEAL; SSANEALL; SANEALLR; ANEALLRL; NEALLRLK; EALLRLKK; ALLRLKKD; LLRLKKDF; LRLKKDFP; RLKKDFPE; LKKDFPEN; KKDFPENI; KDFPENIE; DFPENIEE; FPENIEEV; PENIEEVF; ENIEEVFS; NIEEVFSC; IEEVFSCA; EEVFSCAI; EVFSCAIS; VFSCAISG; FSCAISGV; SCAISGVY; CAISGVYS; AISGVYSS; ISGVYSSY; SGVYSSYV; GVYSSYVS; VYSSYVSD; YSSYVSDL; SSYVSDLD; SYVSDLDN; YVSDLDNL; VSDLDNLK; SDLDNLKR; DLDNLKRN; LDNLKRNG; DNLKRNGS; NLKRNGSD; LKRNGSDL; KRNGSDLI; RNGSDLIW; NGSDLIWL; GSDLIWLV; SDLIWLVG; DLIWLVGY; LIWLVGYM; IWLVGYML; WLVGYMLT; LVGYMLTD; VGYMLTDA; GYMLTDAS; YMLTDASL; MLTDASLL; LTDASLLV; TDASLLVS; DASLLVSS; ASLLVSSE; SLLVSSEN; LLVSSENP; LVSSENPK; VSSENPKI; SSENPKIS; SENPKISY; ENPKISYG; NPKISYGI; PKISYGII; KISYGIID; ISYGIIDP; SYGIIDPI; YGIIDPIY; GIIDPIYG; IIDPIYGD; IDPIYGDD; DPIYGDDV; PIYGDDVQ; IYGDDVQI; YGDDVQIP; GDDVQIPE; DDVQIPEN; DVQIPENL; VQIPENLI; QIPENLIA; IPENLIAV; PENLIAVV; ENLIAVVF; NLIAVVFR; LIAVVFRV; IAVVFRVE; AVVFRVEQ; VVFRVEQG; VFRVEQGA; FRVEQGAF; RVEQGAFL; VEQGAFLA; EQGAFLAG; QGAFLAGY; GAFLAGYI; AFLAGYIA; FLAGYIAA; LAGYIAAK; AGYIAAKK; GYIAAKKS; YIAAKKSF; IAAKKSFS; AAKKSFSG; AKKSFSGK; KKSFSGKI; KSFSGKIG; SFSGKIGF; FSGKIGFI; SGKIGFIG; GKIGFIGG; KIGFIGGM; IGFIGGMK; GFIGGMKG; FIGGMKGN; IGGMKGNI; GGMKGNIV; GMKGNIVD; MKGNIVDA; KGNIVDAF; GNIVDAFR; NIVDAFRY; IVDAFRYG; VDAFRYGY; DAFRYGYE; AFRYGYES; FRYGYESG; RYGYESGA; YGYESGAK; GYESGAKY; YESGAKYA; ESGAKYAN; SGAKYANK; GAKYANKD; AKYANKDI; KYANKDIE; YANKDIEI; ANKDIEII; NKDIEIIS; KDIEIISE; DIEIISEY; IEIISEYS; EIISEYSN; IISEYSNS; ISEYSNSF; SEYSNSFS; EYSNSFSD; YSNSFSDV; SNSFSDVD; NSFSDVDI; SFSDVDIG; FSDVDIGR; SDVDIGRT; DVDIGRTI; VDIGRTIA; DIGRTIAS; IGRTIASK; GRTIASKM; RTIASKMY; TIASKMYS; IASKMYSK; ASKMYSKG; SKMYSKGI; KMYSKGID; MYSKGIDV; YSKGIDVI; SKGIDVIH; KGIDVIHF; GIDVIHFA; IDVIHFAA; DVIHFAAG; VIHFAAGL; IHFAAGLA; HFAAGLAG; FAAGLAGI; AAGLAGIG; AGLAGIGV; GLAGIGVI; LAGIGVIE; AGIGVIET; GIGVIETA; IGVIETAK; GVIETAKN; VIETAKNL; IETAKNLG; ETAKNLGD; TAKNLGDG; AKNLGDGY; KNLGDGYY; NLGDGYYV; LGDGYYVI; GDGYYVIG; DGYYVIGA; GYYVIGAD; YYVIGADQ; YVIGADQD; VIGADQDQ; IGADQDQS; GADQDQSY; ADQDQSYL; DQDQSYLA; QDQSYLAP; DQSYLAPK; QSYLAPKN; SYLAPKNF; YLAPKNFI; LAPKNFIT; APKNFITS; PKNFITSV; KNFITSVI; NFITSVIK; FITSVIKN; ITSVIKNI; TSVIKNIG; SVIKNIGD; VIKNIGDA; IKNIGDAL; KNIGDALY; NIGDALYL; IGDALYLI; GDALYLIT; DALYLITG; ALYLITGE; LYLITGEY; YLITGEYI; LITGEYIK; ITGEYIKN; TGEYIKNN; GEYIKNNN; EYIKNNNV; YIKNNNVW; IKNNNVWE; KNNNVWEG; NNNVWEGG; NNVWEGGK; NVWEGGKV; VWEGGKVV; WEGGKVVQ; EGGKVVQM; GGKVVQMG; GKVVQMGL; KVVQMGLR; VVQMGLRD; VQMGLRDG; QMGLRDGV; MGLRDGVI; GLRDGVIG; LRDGVIGL; RDGVIGLP; DGVIGLPN; GVIGLPNA; VIGLPNAN; IGLPNANE; GLPNANEF; LPNANEFE; PNANEFEY; NANEFEYI; ANEFEYIK; NEFEYIKV; EFEYIKVL; FEYIKVLE; EYIKVLER; YIKVLERK; IKVLERKI; KVLERKII; VLERKIIN; LERKIINK; ERKIINKE; RKIINKEI; KIINKEII; IINKEIIV; INKEIIVP; NKEIIVPC; KEIIVPCN; EIIVPCNQ; IIVPCNQE; IVPCNQEE; VPCNQEEY;

PCNQEEYE; CNQEEYEI; NQEEYEIF; QEEYEIFI; EEYEIFIK; EYEIFIKQ;
YEIFIKQI; EIFIKQIL; IFIKQILK; FIKQILKL;

9 mers:
MRIVIFIFG; RIVIFIFGI; IVIFIFGIL; VIFIFGILL; IFIFGILLT;
FIFGILLTS; IFGILLTSC; FGILLTSCF; GILLTSCFS; ILLTSCFSR;
LLTSCFSRN; LTSCFSRNG; TSCFSRNGI; SCFSRNGIE; CFSRNGIES;
FSRNGIESS; SRNGIESSS; RNGIESSSK; NGIESSSKK; GIESSSKKI;
IESSSKKIK; ESSSKKIKI; SSSKKIKIS; SSKKIKISM; SKKIKISML;
KKIKISMLV; KIKISMLVD; IKISMLVDG; KISMLVDGV; ISMLVDGVL;
SMLVDGVLD; MLVDGVLDD; LVDGVLDDK; VDGVLDDKS; DGVLDDKSF;
GVLDDKSFN; VLDDKSFNS; LDDKSFNSS; DDKSFNSSA; DKSFNSSAN;
KSFNSSANE; SFNSSANEA; FNSSANEAL; NSSANEALL; SSANEALLR;
SANEALLRL; ANEALLRLK; NEALLRLKK; EALLRLKKD; ALLRLKKDF;
LLRLKKDFP; LRLKKDFPE; RLKKDFPEN; LKKDFPENI; KKDFPENIE;
KDFPENIEE; DFPENIEEV; FPENIEEVF; PENIEEVFS; ENIEEVFSC;
NIEEVFSCA; IEEVFSCAI; EEVFSCAIS; EVFSCAISG; VFSCAISGV;
FSCAISGVY; SCAISGVYS; CAISGVYSS; AISGVYSSY; ISGVYSSYV;
SGVYSSYVS; GVYSSYVSD; VYSSYVSDL; YSSYVSDLD; SSYVSDLDN;
SYVSDLDNL; YVSDLDNLK; VSDLDNLKR; SDLDNLKRN; DLDNLKRNG;
LDNLKRNGS; DNLKRNGSD; NLKRNGSDL; LKRNGSDLI; KRNGSDLIW;
RNGSDLIWL; NGSDLIWLV; GSDLIWLVG; SDLIWLVGY; DLIWLVGYM;
LIWLVGYML; IWLVGYMLT; WLVGYMLTD; LVGYMLTDA; VGYMLTDAS;
GYMLTDASL; YMLTDASLL; MLTDASLLV; LTDASLLVS; TDASLLVSS;
DASLLVSSE; ASLLVSSEN; SLLVSSENP; LLVSSENPK; LVSSENPKI;
VSSENPKIS; SSENPKISY; SENPKISYG; ENPKISYGI; NPKISYGII;
PKISYGIID; KISYGIIDP; ISYGIIDPI; SYGIIDPIY; YGIIDPIYG;
GIIDPIYGD; IIDPIYGDD; IDPIYGDDV; DPIYGDDVQ; PIYGDDVQI;
IYGDDVQIP; YGDDVQIPE; GDDVQIPEN; DDVQIPENL; DVQIPENLI;
VQIPENLIA; QIPENLIAV; IPENLIAVV; PENLIAVVF; ENLIAVVFR;
NLIAVVFRV; LIAVVFRVE; IAVVFRVEQ; AVVFRVEQG; VVFRVEQGA;
VFRVEQGAF; FRVEQGAFL; RVEQGAFLA; VEQGAFLAG; EQGAFLAGY;
QGAFLAGYI; GAFLAGYIA; AFLAGYIAA; FLAGYIAAK; LAGYIAAKK;
AGYIAAKKS; GYIAAKKSF; YIAAKKSFS; IAAKKSFSG; AAKKSFSGK;
AKKSFSGKI; KKSFSGKIG; KSFSGKIGF; SFSGKIGFI; FSGKIGFIG;
SGKIGFIGG; GKIGFIGGM; KIGFIGGMK; IGFIGGMKG; GFIGGMKGN;
FIGGMKGNI; IGGMKGNIV; GGMKGNIVD; GMKGNIVDA; MKGNIVDAF;
KGNIVDAFR; GNIVDAFRY; NIVDAFRYG; IVDAFRYGY; VDAFRYGYE;
DAFRYGYES; AFRYGYESG; FRYGYESGA; RYGYESGAK; YGYESGAKY;
GYESGAKYA; YESGAKYAN; ESGAKYANK; SGAKYANKD; GAKYANKDI;
AKYANKDIE; KYANKDIEI; YANKDIEII; ANKDIEIIS; NKDIEIISE;
KDIEIISEY; DIEIISEYS; IEIISEYSN; EIISEYSNS; IISEYSNSF;
ISEYSNSFS; SEYSNSFSD; EYSNSFSDV; YSNSFSDVD; SNSFSDVDI;
NSFSDVDIG; SFSDVDIGR; FSDVDIGRT; SDVDIGRTI; DVDIGRTIA;
VDIGRTIAS; DIGRTIASK; IGRTIASKM; GRTIASKMY; RTIASKMYS;
TIASKMYSK; IASKMYSKG; ASKMYSKGI; SKMYSKGID; KMYSKGIDV;
MYSKGIDVI; YSKGIDVIH; SKGIDVIHF; KGIDVIHFA; GIDVIHFAA;
IDVIHFAAG; DVIHFAAGL; VIHFAAGLA; IHFAAGLAG; HFAAGLAGI;
FAAGLAGIG; AAGLAGIGV; AGLAGIGVI; GLAGIGVIE; LAGIGVIET;
AGIGVIETA; GIGVIETAK; IGVIETAKN; GVIETAKNL; VIETAKNLG;
IETAKNLGD; ETAKNLGDG; TAKNLGDGY; AKNLGDGYY; KNLGDGYYV;
NLGDGYYVI; LGDGYYVIG; GDGYYVIGA; DGYYVIGAD; GYYVIGADQ;
YYVIGADQD; YVIGADQDQ; VIGADQDQS; IGADQDQSY; GADQDQSYL;
ADQDQSYLA; DQDQSYLAP; QDQSYLAPK; DQSYLAPKN; QSYLAPKNF;
SYLAPKNFI; YLAPKNFIT; LAPKNFITS; APKNFITSV; PKNFITSVI;
KNFITSVIK; NFITSVIKN; FITSVIKNI; ITSVIKNIG; TSVIKNIGD;
SVIKNIGDA; VIKNIGDAL; IKNIGDALY; KNIGDALYL; NIGDALYLI;

IGDALYLIT; GDALYLITG; DALYLITGE; ALYLITGEY; LYLITGEYI;
YLITGEYIK; LITGEYIKN; ITGEYIKNN; TGEYIKNNN; GEYIKNNNV;
EYIKNNNVW; YIKNNNVWE; IKNNNVWEG; KNNNVWEGG; NNNVWEGGK;
NNVWEGGKV; NVWEGGKVV; VWEGGKVVQ; WEGGKVVQM; EGGKVVQMG;
GGKVVQMGL; GKVVQMGLR; KVVQMGLRD; VVQMGLRDG; VQMGLRDGV;
QMGLRDGVI; MGLRDGVIG; GLRDGVIGL; LRDGVIGLP; RDGVIGLPN;
DGVIGLPNA; GVIGLPNAN; VIGLPNANE; IGLPNANEF; GLPNANEFE;
LPNANEFEY; PNANEFEYI; NANEFEYIK; ANEFEYIKV; NEFEYIKVL;
EFEYIKVLE; FEYIKVLER; EYIKVLERK; YIKVLERKI; IKVLERKII;
KVLERKIIN; VLERKIINK; LERKIINKE; ERKIINKEI; RKIINKEII;
KIINKEIIV; IINKEIIVP; INKEIIVPC; NKEIIVPCN; KEIIVPCNQ;
EIIVPCNQE; IIVPCNQEE; IVPCNQEEY; VPCNQEEYE; PCNQEEYEI;
CNQEEYEIF; NQEEYEIFI; QEEYEIFIK; EEYEIFIKQ; EYEIFIKQI;
YEIFIKQIL; EIFIKQILK; IFIKQILKL;

10 mers:
MRIVIFIFGI; RIVIFIFGIL; IVIFIFGILL; VIFIFGILLT; IFIFGILLTS;
FIFGILLTSC; IFGILLTSCF; FGILLTSCFS; GILLTSCFSR; ILLTSCFSRN;
LLTSCFSRNG; LTSCFSRNGI; TSCFSRNGIE; SCFSRNGIES; CFSRNGIESS;
FSRNGIESSS; SRNGIESSSK; RNGIESSSKK; NGIESSSKKI; GIESSSKKIK;
IESSSKKIKI; ESSSKKIKIS; SSSKKIKISM; SSKKIKISML; SKKIKISMLV;
KKIKISMLVD; KIKISMLVDG; IKISMLVDGV; KISMLVDGVL; ISMLVDGVLD;
SMLVDGVLDD; MLVDGVLDDK; LVDGVLDDKS; VDGVLDDKSF; DGVLDDKSFN;
GVLDDKSFNS; VLDDKSFNSS; LDDKSFNSSA; DDKSFNSSAN; DKSFNSSANE;
KSFNSSANEA; SFNSSANEAL; FNSSANEALL; NSSANEALLR; SSANEALLRL;
SANEALLRLK; ANEALLRLKK; NEALLRLKKD; EALLRLKKDF; ALLRLKKDFP;
LLRLKKDFPE; LRLKKDFPEN; RLKKDFPENI; LKKDFPENIE; KKDFPENIEE;
KDFPENIEEV; DFPENIEEVF; FPENIEEVFS; PENIEEVFSC; ENIEEVFSCA;
NIEEVFSCAI; IEEVFSCAIS; EEVFSCAISG; EVFSCAISGV; VFSCAISGVY;
FSCAISGVYS; SCAISGVYSS; CAISGVYSSY; AISGVYSSYV; ISGVYSSYVS;
SGVYSSYVSD; GVYSSYVSDL; VYSSYVSDLD; YSSYVSDLDN; SSYVSDLDNL;
SYVSDLDNLK; YVSDLDNLKR; VSDLDNLKRN; SDLDNLKRNG; DLDNLKRNGS;
LDNLKRNGSD; DNLKRNGSDL; NLKRNGSDLI; LKRNGSDLIW; KRNGSDLIWL;
RNGSDLIWLV; NGSDLIWLVG; GSDLIWLVGY; SDLIWLVGYM; DLIWLVGYML;
LIWLVGYMLT; IWLVGYMLTD; WLVGYMLTDA; LVGYMLTDAS; VGYMLTDASL;
GYMLTDASLL; YMLTDASLLV; MLTDASLLVS; LTDASLLVSS; TDASLLVSSE;
DASLLVSSEN; ASLLVSSENP; SLLVSSENPK; LLVSSENPKI; LVSSENPKIS;
VSSENPKISY; SSENPKISYG; SENPKISYGI; ENPKISYGII; NPKISYGIID;
PKISYGIIDP; KISYGIIDPI; ISYGIIDPIY; SYGIIDPIYG; YGIIDPIYGD;
GIIDPIYGDD; IIDPIYGDDV; IDPIYGDDVQ; DPIYGDDVQI; PIYGDDVQIP;
IYGDDVQIPE; YGDDVQIPEN; GDDVQIPENL; DDVQIPENLI; DVQIPENLIA;
VQIPENLIAV; QIPENLIAVV; IPENLIAVVF; PENLIAVVFR; ENLIAVVFRV;
NLIAVVFRVE; LIAVVFRVEQ; IAVVFRVEQG; AVVFRVEQGA; VVFRVEQGAF;
VFRVEQGAFL; FRVEQGAFLA; RVEQGAFLAG; VEQGAFLAGY; EQGAFLAGYI;
QGAFLAGYIA; GAFLAGYIAA; AFLAGYIAAK; FLAGYIAAKK; LAGYIAAKKS;
AGYIAAKKSF; GYIAAKKSFS; YIAAKKSFSG; IAAKKSFSGK; AAKKSFSGKI;
AKKSFSGKIG; KKSFSGKIGF; KSFSGKIGFI; SFSGKIGFIG; FSGKIGFIGG;
SGKIGFIGGM; GKIGFIGGMK; KIGFIGGMKG; IGFIGGMKGN; GFIGGMKGNI;
FIGGMKGNIV; IGGMKGNIVD; GGMKGNIVDA; GMKGNIVDAF; MKGNIVDAFR;
KGNIVDAFRY; GNIVDAFRYG; NIVDAFRYGY; IVDAFRYGYE; VDAFRYGYES;
DAFRYGYESG; AFRYGYESGA; FRYGYESGAK; RYGYESGAKY; YGYESGAKYA;
GYESGAKYAN; YESGAKYANK; ESGAKYANKD; SGAKYANKDI; GAKYANKDIE;
AKYANKDIEI; KYANKDIEII; YANKDIEIIS; ANKDIEIISE; NKDIEIISEY;
KDIEIISEYS; DIEIISEYSN; IEIISEYSNS; EIISEYSNSF; IISEYSNSFS;
ISEYSNSFSD; SEYSNSFSDV; EYSNSFSDVD; YSNSFSDVDI; SNSFSDVDIG;
NSFSDVDIGR; SFSDVDIGRT; FSDVDIGRTI; SDVDIGRTIA; DVDIGRTIAS;
VDIGRTIASK; DIGRTIASKM; IGRTIASKMY; GRTIASKMYS; RTIASKMYSK;

TIASKMYSKG; IASKMYSKGI; ASKMYSKGID; SKMYSKGIDV; KMYSKGIDVI; MYSKGIDVIH; YSKGIDVIHF; SKGIDVIHFA; KGIDVIHFAA; GIDVIHFAAG; IDVIHFAAGL; DVIHFAAGLA; VIHFAAGLAG; IHFAAGLAGI; HFAAGLAGIG; FAAGLAGIGV; AAGLAGIGVI; AGLAGIGVIE; GLAGIGVIET; LAGIGVIETA; AGIGVIETAK; GIGVIETAKN; IGVIETAKNL; GVIETAKNLG; VIETAKNLGD; IETAKNLGDG; ETAKNLGDGY; TAKNLGDGYY; AKNLGDGYYV; KNLGDGYYVI; NLGDGYYVIG; LGDGYYVIGA; GDGYYVIGAD; DGYYVIGADQ; GYYVIGADQD; YYVIGADQDQ; YVIGADQDQS; VIGADQDQSY; IGADQDQSYL; GADQDQSYLA; ADQDQSYLAP; DQDQSYLAPK; QDQSYLAPKN; DQSYLAPKNF; QSYLAPKNFI; SYLAPKNFIT; YLAPKNFITS; LAPKNFITSV; APKNFITSVI; PKNFITSVIK; KNFITSVIKN; NFITSVIKNI; FITSVIKNIG; ITSVIKNIGD; TSVIKNIGDA; SVIKNIGDAL; VIKNIGDALY; IKNIGDALYL; KNIGDALYLI; NIGDALYLIT; IGDALYLITG; GDALYLITGE; DALYLITGEY; ALYLITGEYI; LYLITGEYIK; YLITGEYIKN; LITGEYIKNN; ITGEYIKNNN; TGEYIKNNNV; GEYIKNNNVW; EYIKNNNVWE; YIKNNNVWEG; IKNNNVWEGG; KNNNVWEGGK; NNNVWEGGKV; NNVWEGGKVV; NVWEGGKVVQ; VWEGGKVVQM; WEGGKVVQMG; EGGKVVQMGL; GGKVVQMGLR; GKVVQMGLRD; KVVQMGLRDG; VVQMGLRDGV; VQMGLRDGVI; QMGLRDGVIG; MGLRDGVIGL; GLRDGVIGLP; LRDGVIGLPN; RDGVIGLPNA; DGVIGLPNAN; GVIGLPNANE; VIGLPNANEF; IGLPNANEFE; GLPNANEFEY; LPNANEFEYI; PNANEFEYIK; NANEFEYIKV; ANEFEYIKVL; NEFEYIKVLE; EFEYIKVLER; FEYIKVLERK; EYIKVLERKI; YIKVLERKII; IKVLERKIIN; KVLERKIINK; VLERKIINKE; LERKIINKEI; ERKIINKEII; RKIINKEIIV; KIINKEIIVP; IINKEIIVPC; INKEIIVPCN; NKEIIVPCNQ; KEIIVPCNQE; EIIVPCNQEE; IIVPCNQEEY; IVPCNQEEYE; VPCNQEEYEI; PCNQEEYEIF; CNQEEYEIFI; NQEEYEIFIK; QEEYEIFIKQ; EEYEIFIKQI; EYEIFIKQIL; YEIFIKQILK; EIFIKQILKL;

11 mers:
MRIVIFIFGIL; RIVIFIFGILL; IVIFIFGILLT; VIFIFGILLTS; IFIFGILLTSC; FIFGILLTSCF; IFGILLTSCFS; FGILLTSCFSR; GILLTSCFSRN; ILLTSCFSRNG; LLTSCFSRNGI; LTSCFSRNGIE; TSCFSRNGIES; SCFSRNGIESS; CFSRNGIESSS; FSRNGIESSSK; SRNGIESSSKK; RNGIESSSKKI; NGIESSSKKIK; GIESSSKKIKI; IESSSKKIKIS; ESSSKKIKISM; SSSKKIKISML; SSKKIKISMLV; SKKIKISMLVD; KKIKISMLVDG; KIKISMLVDGV; IKISMLVDGVL; KISMLVDGVLD; ISMLVDGVLDD; SMLVDGVLDDK; MLVDGVLDDKS; LVDGVLDDKSF; VDGVLDDKSFN; DGVLDDKSFNS; GVLDDKSFNSS; VLDDKSFNSSA; LDDKSFNSSAN; DDKSFNSSANE; DKSFNSSANEA; KSFNSSANEAL; SFNSSANEALL; FNSSANEALLR; NSSANEALLRL; SSANEALLRLK; SANEALLRLKK; ANEALLRLKKD; NEALLRLKKDF; EALLRLKKDFP; ALLRLKKDFPE; LLRLKKDFPEN; LRLKKDFPENI; RLKKDFPENIE; LKKDFPENIEE; KKDFPENIEEV; KDFPENIEEVF; DFPENIEEVFS; FPENIEEVFSC; PENIEEVFSCA; ENIEEVFSCAI; NIEEVFSCAIS; IEEVFSCAISG; EEVFSCAISGV; EVFSCAISGVY; VFSCAISGVYS; FSCAISGVYSS; SCAISGVYSSY; CAISGVYSSYV; AISGVYSSYVS; ISGVYSSYVSD; SGVYSSYVSDL; GVYSSYVSDLD; VYSSYVSDLDN; YSSYVSDLDNL; SSYVSDLDNLK; SYVSDLDNLKR; YVSDLDNLKRN; VSDLDNLKRNG; SDLDNLKRNGS; DLDNLKRNGSD; LDNLKRNGSDL; DNLKRNGSDLI; NLKRNGSDLIW; LKRNGSDLIWL; KRNGSDLIWLV; RNGSDLIWLVG; NGSDLIWLVGY; GSDLIWLVGYM; SDLIWLVGYML; DLIWLVGYMLT; LIWLVGYMLTD; IWLVGYMLTDA; WLVGYMLTDAS; LVGYMLTDASL; VGYMLTDASLL; GYMLTDASLLV; YMLTDASLLVS; MLTDASLLVSS; LTDASLLVSSE; TDASLLVSSEN; DASLLVSSENP; ASLLVSSENPK; SLLVSSENPKI; LLVSSENPKIS; LVSSENPKISY; VSSENPKISYG; SSENPKISYGI; SENPKISYGII; ENPKISYGIID; NPKISYGIIDP; PKISYGIIDPI; KISYGIIDPIY; ISYGIIDPIYG; SYGIIDPIYGD; YGIIDPIYGDD; GIIDPIYGDDV;

	IIDPIYGDDVQ; IDPIYGDDVQI; DPIYGDDVQIP; PIYGDDVQIPE; IYGDDVQIPEN; YGDDVQIPENL; GDDVQIPENLI; DDVQIPENLIA; DVQIPENLIAV; VQIPENLIAVV; QIPENLIAVVF; IPENLIAVVFR; PENLIAVVFRV; ENLIAVVFRVE; NLIAVVFRVEQ; LIAVVFRVEQG; IAVVFRVEQGA; AVVFRVEQGAF; VVFRVEQGAFL; VFRVEQGAFLA; FRVEQGAFLAG; RVEQGAFLAGY; VEQGAFLAGYI; EQGAFLAGYIA; QGAFLAGYIAA; GAFLAGYIAAK; AFLAGYIAAKK; FLAGYIAAKKS; LAGYIAAKKSF; AGYIAAKKSFS; GYIAAKKSFSG; YIAAKKSFSGK; IAAKKSFSGKI; AAKKSFSGKIG; AKKSFSGKIGF; KKSFSGKIGFI; KSFSGKIGFIG; SFSGKIGFIGG; FSGKIGFIGGM; SGKIGFIGGMK; GKIGFIGGMKG; KIGFIGGMKGN; IGFIGGMKGNI; GFIGGMKGNIV; FIGGMKGNIVD; IGGMKGNIVDA; GGMKGNIVDAF; GMKGNIVDAFR; MKGNIVDAFRY; KGNIVDAFRYG; GNIVDAFRYGY; NIVDAFRYGYE; IVDAFRYGYES; VDAFRYGYESG; DAFRYGYESGA; AFRYGYESGAK; FRYGYESGAKY; RYGYESGAKYA; YGYESGAKYAN; GYESGAKYANK; YESGAKYANKD; ESGAKYANKDI; SGAKYANKDIE; GAKYANKDIEI; AKYANKDIEII; KYANKDIEIIS; YANKDIEIISE; ANKDIEIISEY; NKDIEIISEYS; KDIEIISEYSN; DIEIISEYSNS; IEIISEYSNSF; EIISEYSNSFS; IISEYSNSFSD; ISEYSNSFSDV; SEYSNSFSDVD; EYSNSFSDVDI; YSNSFSDVDIG; SNSFSDVDIGR; NSFSDVDIGRT; SFSDVDIGRTI; FSDVDIGRTIA; SDVDIGRTIAS; DVDIGRTIASK; VDIGRTIASKM; DIGRTIASKMY; IGRTIASKMYS; GRTIASKMYSK; RTIASKMYSKG; TIASKMYSKGI; IASKMYSKGID; ASKMYSKGIDV; SKMYSKGIDVI; KMYSKGIDVIH; MYSKGIDVIHF; YSKGIDVIHFA; SKGIDVIHFAA; KGIDVIHFAAG; GIDVIHFAAGL; IDVIHFAAGLA; DVIHFAAGLAG; VIHFAAGLAGI; IHFAAGLAGIG; HFAAGLAGIGV; FAAGLAGIGVI; AAGLAGIGVIE; AGLAGIGVIET; GLAGIGVIETA; LAGIGVIETAK; AGIGVIETAKN; GIGVIETAKNL; IGVIETAKNLG; GVIETAKNLGD; VIETAKNLGDG; IETAKNLGDGY; ETAKNLGDGYY; TAKNLGDGYYV; AKNLGDGYYVI; KNLGDGYYVIG; NLGDGYYVIGA; LGDGYYVIGAD; GDGYYVIGADQ; DGYYVIGADQD; GYYVIGADQDQ; YYVIGADQDQS; YVIGADQDQSY; VIGADQDQSYL; IGADQDQSYLA; GADQDQSYLAP; ADQDQSYLAPK; DQDQSYLAPKN; QDQSYLAPKNF; DQSYLAPKNFI; QSYLAPKNFIT; SYLAPKNFITS; YLAPKNFITSV; LAPKNFITSVI; APKNFITSVIK; PKNFITSVIKN; KNFITSVIKNI; NFITSVIKNIG; FITSVIKNIGD; ITSVIKNIGDA; TSVIKNIGDAL; SVIKNIGDALY; VIKNIGDALYL; IKNIGDALYLI; KNIGDALYLIT; NIGDALYLITG; IGDALYLITGE; GDALYLITGEY; DALYLITGEYI; ALYLITGEYIK; LYLITGEYIKN; YLITGEYIKNN; LITGEYIKNNN; ITGEYIKNNNV; TGEYIKNNNVW; GEYIKNNNVWE; EYIKNNNVWEG; YIKNNNVWEGG; IKNNNVWEGGK; KNNNVWEGGKV; NNNVWEGGKVV; NNVWEGGKVVQ; NVWEGGKVVQM; VWEGGKVVQMG; WEGGKVVQMGL; EGGKVVQMGLR; GGKVVQMGLRD; GKVVQMGLRDG; KVVQMGLRDGV; VVQMGLRDGVI; VQMGLRDGVIG; QMGLRDGVIGL; MGLRDGVIGLP; GLRDGVIGLPN; LRDGVIGLPNA; RDGVIGLPNAN; DGVIGLPNANE; GVIGLPNANEF; VIGLPNANEFE; IGLPNANEFEY; GLPNANEFEYI; LPNANEFEYIK; PNANEFEYIKV; NANEFEYIKVL; ANEFEYIKVLE; NEFEYIKVLER; EFEYIKVLERK; FEYIKVLERKI; EYIKVLERKII; YIKVLERKIIN; IKVLERKIINK; KVLERKIINKE; VLERKIINKEI; LERKIINKEII; ERKIINKEIIV; RKIINKEIIVP; KIINKEIIVPC; IINKEIIVPCN; INKEIIVPCNQ; NKEIIVPCNQE; KEIIVPCNQEE; EIIVPCNQEEY; IIVPCNQEEYE; IVPCNQEEYEI; VPCNQEEYEIF; PCNQEEYEIFI; CNQEEYEIFIK; NQEEYEIFIKQ; QEEYEIFIKQI; EEYEIFIKQIL; EYEIFIKQILK; YEIFIKQILKL;
NP_212518.1 Basic membrane	SEQ ID NO 2697-4074/ 8 mers:

protein C (bmpC) [Borrelia burgdorferi B31	MFKRFIFI; FKRFIFIT; KRFIFITL; RFIFITLS; FIFITLSL; IFITLSLL; FITLSLLV; ITLSLLVF; TLSLLVFA; LSLLVFAC; SLLVFACF; LLVFACFK; LVFACFKS; VFACFKSN; FACFKSNK; ACFKSNKK; CFKSNKKS; FKSNKKSI; KSNKKSIK; SNKKSIKS; NKKSIKSD; KKSIKSDK; KSIKSDKV; SIKSDKVV; IKSDKVVV; KSDKVVVG; SDKVVVGV; DKVVVGVL; KVVVGVLA; VVVGVLAH; VVGVLAHG; VGVLAHGS; GVLAHGSF; VLAHGSFY; LAHGSFYD; AHGSFYDK; HGSFYDKG; GSFYDKGY; SFYDKGYN; FYDKGYNQ; YDKGYNQS; DKGYNQSV; KGYNQSVH; GYNQSVHD; YNQSVHDG; NQSVHDGV; QSVHDGVV; SVHDGVVK; VHDGVVKL; HDGVVKLR; DGVVKLRD; GVVKLRDN; VVKLRDNF; VKLRDNFG; KLRDNFGI; LRDNFGIK; RDNFGIKL; DNFGIKLI; NFGIKLIT; FGIKLITK; GIKLITKS; IKLITKSL; KLITKSLR; LITKSLRP; ITKSLRPY; TKSLRPYP; KSLRPYPI; SLRPYPIE; LRPYPIEG; RPYPIEGK; PYPIEGKR; YPIEGKRL; PIEGKRLL; IEGKRLLT; EGKRLLTV; GKRLLTVD; KRLLTVDE; RLLTVDEA; LLTVDEAM; LTVDEAMT; TVDEAMTE; VDEAMTED; DEAMTEDA; EAMTEDAY; AMTEDAYE; MTEDAYEV; TEDAYEVQ; EDAYEVQK; DAYEVQKN; AYEVQKNP; YEVQKNPL; EVQKNPLN; VQKNPLNL; QKNPLNLF; KNPLNLFW; NPLNLFWL; PLNLFWLI; LNLFWLIG; NLFWLIGY; LFWLIGYR; FWLIGYRF; WLIGYRFS; LIGYRFSD; IGYRFSDL; GYRFSDLS; YRFSDLSV; RFSDLSVK; FSDLSVKL; SDLSVKLS; DLSVKLSY; LSVKLSYE; SVKLSYER; VKLSYERP; KLSYERPD; LSYERPDI; SYERPDIY; YERPDIYY; ERPDIYYG; RPDIYYGI; PDIYYGII; DIYYGIID; IYYGIIDA; YYGIIDAF; YGIIDAFD; GIIDAFDY; IIDAFDYG; IDAFDYGD; DAFDYGDI; AFDYGDIQ; FDYGDIQV; DYGDIQVP; YGDIQVPK; GDIQVPKN; DIQVPKNS; IQVPKNSL; QVPKNSLA; VPKNSLAI; PKNSLAIK; KNSLAIKF; NSLAIKFR; SLAIKFRN; LAIKFRNE; AIKFRNEE; IKFRNEEA; KFRNEEAA; FRNEEAAF; RNEEAAFL; NEEAAFLA; EEAAFLAG; EAAFLAGY; AAFLAGYI; AFLAGYIA; FLAGYIAA; LAGYIAAK; AGYIAAKM; GYIAAKMS; YIAAKMSR; IAAKMSRK; AAKMSRKE; AKMSRKEK; KMSRKEKI; MSRKEKIG; SRKEKIGF; RKEKIGFL; KEKIGFLT; EKIGFLTG; KIGFLTGP; IGFLTGPM; GFLTGPMS; FLTGPMSE; LTGPMSEH; TGPMSEHV; GPMSEHVK; PMSEHVKD; MSEHVKDF; SEHVKDFK; EHVKDFKF; HVKDFKFG; VKDFKFGF; KDFKFGFK; DFKFGFKA; FKFGFKAG; KFGFKAGI; FGFKAGIF; GFKAGIFY; FKAGIFYA; KAGIFYAN; AGIFYANP; GIFYANPK; IFYANPKL; FYANPKLR; YANPKLRL; ANPKLRLV; NPKLRLVS; PKLRLVSK; KLRLVSKK; LRLVSKKA; RLVSKKAP; LVSKKAPS; VSKKAPSL; SKKAPSLF; KKAPSLFD; KAPSLFDK; APSLFDKE; PSLFDKEK; SLFDKEKG; LFDKEKGK; FDKEKGKA; DKEKGKAM; KEKGKAMA; EKGKAMAL; KGKAMALF; GKAMALFM; KAMALFMY; AMALFMYK; MALFMYKE; ALFMYKED; LFMYKEDK; FMYKEDKV; MYKEDKVG; YKEDKVGV; KEDKVGVI; EDKVGVIF; DKVGVIFP; KVGVIFPI; VGVIFPIA; GVIFPIAG; VIFPIAGI; IFPIAGIT; FPIAGITG; PIAGITGL; IAGITGLG; AGITGLGV; GITGLGVY; ITGLGVYD; TGLGVYDA; GLGVYDAA; LGVYDAAK; GVYDAAKE; VYDAAKEL; YDAAKELG; DAAKELGP; AAKELGPK; AKELGPKY; KELGPKYY; ELGPKYYV; LGPKYYVI; GPKYYVIG; PKYYVIGL; KYYVIGLN; YYVIGLNQ; YVIGLNQD; VIGLNQDQ; IGLNQDQS; GLNQDQSY; LNQDQSYI; NQDQSYIA; QDQSYIAP; DQSYIAPQ; QSYIAPQN; SYIAPQNV; YIAPQNVI; IAPQNVIT; APQNVITS; PQNVITSI; QNVITSII; NVITSIIK; VITSIIKD; ITSIIKDI; TSIIKDIG; SIIKDIGK; IIKDIGKV; IKDIGKVI; KDIGKVIY; DIGKVIYS; IGKVIYSI; GKVIYSIS; KVIYSISS; VIYSISSE; IYSISSEY; YSISSEYI; SISSEYIN; ISSEYINN; SSEYINNR; SEYINNRV; EYINNRVF; YINNRVFK; INNRVFKG; NNRVFKGG; NRVFKGGI; RVFKGGII; VFKGGIII; FKGGIIID; KGGIIIDR; GGIIIDRG; GIIIDRGL; IIIDRGLK; IIDRGLKE; IDRGLKEG; DRGLKEGV; RGLKEGVI; GLKEGVIE; LKEGVIEI; KEGVIEIV; EGVIEIVK; GVIEIVKD; VIEIVKDP; IEIVKDPD; EIVKDPDV; IVKDPDVL; VKDPDVLN; KDPDVLNN; DPDVLNNR; PDVLNNRL; DVLNNRLV; VLNNRLVD; LNNRLVDE; NNRLVDEV; NRLVDEVI; RLVDEVID; LVDEVIDL; VDEVIDLE; DEVIDLEN; EVIDLENK; VIDLENKI; IDLENKII; DLENKIIS; LENKIISG; ENKIISGE; NKIISGEI; KIISGEII; IISGEIIV; ISGEIIVP; SGEIIVPD; GEIIVPDS; EIIVPDSE; IIVPDSEY; IVPDSEYA; VPDSEYAF; PDSEYAFD; DSEYAFDL; SEYAFDLF;

EYAFDLFK; YAFDLFKS; AFDLFKSK; FDLFKSKL;

9 mers:
MFKRFIFIT; FKRFIFITL; KRFIFITLS; RFIFITLSL; FIFITLSLL;
IFITLSLLV; FITLSLLVF; ITLSLLVFA; TLSLLVFAC; LSLLVFACF;
SLLVFACFK; LLVFACFKS; LVFACFKSN; VFACFKSNK; FACFKSNKK;
ACFKSNKKS; CFKSNKKSI; FKSNKKSIK; KSNKKSIKS; SNKKSIKSD;
NKKSIKSDK; KKSIKSDKV; KSIKSDKVV; SIKSDKVVV; IKSDKVVVG;
KSDKVVVGV; SDKVVVGVL; DKVVVGVLA; KVVVGVLAH; VVVGVLAHG;
VVGVLAHGS; VGVLAHGSF; GVLAHGSFY; VLAHGSFYD; LAHGSFYDK;
AHGSFYDKG; HGSFYDKGY; GSFYDKGYN; SFYDKGYNQ; FYDKGYNQS;
YDKGYNQSV; DKGYNQSVH; KGYNQSVHD; GYNQSVHDG; YNQSVHDGV;
NQSVHDGVV; QSVHDGVVK; SVHDGVVKL; VHDGVVKLR; HDGVVKLRD;
DGVVKLRDN; GVVKLRDNF; VVKLRDNFG; VKLRDNFGI; KLRDNFGIK;
LRDNFGIKL; RDNFGIKLI; DNFGIKLIT; NFGIKLITK; FGIKLITKS;
GIKLITKSL; IKLITKSLR; KLITKSLRP; LITKSLRPY; ITKSLRPYP;
TKSLRPYPI; KSLRPYPIE; SLRPYPIEG; LRPYPIEGK; RPYPIEGKR;
PYPIEGKRL; YPIEGKRLL; PIEGKRLLT; IEGKRLLTV; EGKRLLTVD;
GKRLLTVDE; KRLLTVDEA; RLLTVDEAM; LLTVDEAMT; LTVDEAMTE;
TVDEAMTED; VDEAMTEDA; DEAMTEDAY; EAMTEDAYE; AMTEDAYEV;
MTEDAYEVQ; TEDAYEVQK; EDAYEVQKN; DAYEVQKNP; AYEVQKNPL;
YEVQKNPLN; EVQKNPLNL; VQKNPLNLF; QKNPLNLFW; KNPLNLFWL;
NPLNLFWLI; PLNLFWLIG; LNLFWLIGY; NLFWLIGYR; LFWLIGYRF;
FWLIGYRFS; WLIGYRFSD; LIGYRFSDL; IGYRFSDLS; GYRFSDLSV;
YRFSDLSVK; RFSDLSVKL; FSDLSVKLS; SDLSVKLSY; DLSVKLSYE;
LSVKLSYER; SVKLSYERP; VKLSYERPD; KLSYERPDI; LSYERPDIY;
SYERPDIYY; YERPDIYYG; ERPDIYYGI; RPDIYYGII; PDIYYGIID;
DIYYGIIDA; IYYGIIDAF; YYGIIDAFD; YGIIDAFDY; GIIDAFDYG;
IIDAFDYGD; IDAFDYGDI; DAFDYGDIQ; AFDYGDIQV; FDYGDIQVP;
DYGDIQVPK; YGDIQVPKN; GDIQVPKNS; DIQVPKNSL; IQVPKNSLA;
QVPKNSLAI; VPKNSLAIK; PKNSLAIKF; KNSLAIKFR; NSLAIKFRN;
SLAIKFRNE; LAIKFRNEE; AIKFRNEEA; IKFRNEEAA; KFRNEEAAF;
FRNEEAAFL; RNEEAAFLA; NEEAAFLAG; EEAAFLAGY; EAAFLAGYI;
AAFLAGYIA; AFLAGYIAA; FLAGYIAAK; LAGYIAAKM; AGYIAAKMS;
GYIAAKMSR; YIAAKMSRK; IAAKMSRKE; AAKMSRKEK; AKMSRKEKI;
KMSRKEKIG; MSRKEKIGF; SRKEKIGFL; RKEKIGFLT; KEKIGFLTG;
EKIGFLTGP; KIGFLTGPM; IGFLTGPMS; GFLTGPMSE; FLTGPMSEH;
LTGPMSEHV; TGPMSEHVK; GPMSEHVKD; PMSEHVKDF; MSEHVKDFK;
SEHVKDFKF; EHVKDFKFG; HVKDFKFGF; VKDFKFGFK; KDFKFGFKA;
DFKFGFKAG; FKFGFKAGI; KFGFKAGIF; FGFKAGIFY; GFKAGIFYA;
FKAGIFYAN; KAGIFYANP; AGIFYANPK; GIFYANPKL; IFYANPKLR;
FYANPKLRL; YANPKLRLV; ANPKLRLVS; NPKLRLVSK; PKLRLVSKK;
KLRLVSKKA; LRLVSKKAP; RLVSKKAPS; LVSKKAPSL; VSKKAPSLF;
SKKAPSLFD; KKAPSLFDK; KAPSLFDKE; APSLFDKEK; PSLFDKEKG;
SLFDKEKGK; LFDKEKGKA; FDKEKGKAM; DKEKGKAMA; KEKGKAMAL;
EKGKAMALF; KGKAMALFM; GKAMALFMY; KAMALFMYK; AMALFMYKE;
MALFMYKED; ALFMYKEDK; LFMYKEDKV; FMYKEDKVG; MYKEDKVGV;
YKEDKVGVI; KEDKVGVIF; EDKVGVIFP; DKVGVIFPI; KVGVIFPIA;
VGVIFPIAG; GVIFPIAGI; VIFPIAGIT; IFPIAGITG; FPIAGITGL;
PIAGITGLG; IAGITGLGV; AGITGLGVY; GITGLGVYD; ITGLGVYDA;
TGLGVYDAA; GLGVYDAAK; LGVYDAAKE; GVYDAAKEL; VYDAAKELG;
YDAAKELGP; DAAKELGPK; AAKELGPKY; AKELGPKYY; KELGPKYYV;
ELGPKYYVI; LGPKYYVIG; GPKYYVIGL; PKYYVIGLN; KYYVIGLNQ;
YYVIGLNQD; YVIGLNQDQ; VIGLNQDQS; IGLNQDQSY; GLNQDQSYI;
LNQDQSYIA; NQDQSYIAP; QDQSYIAPQ; DQSYIAPQN; QSYIAPQNV;
SYIAPQNVI; YIAPQNVIT; IAPQNVITS; APQNVITSI; PQNVITSII;
QNVITSIIK; NVITSIIKD; VITSIIKDI; ITSIIKDIG; TSIIKDIGK;

SIIKDIGKV; IIKDIGKVI; IKDIGKVIY; KDIGKVIYS; DIGKVIYSI;
IGKVIYSIS; GKVIYSISS; KVIYSISSE; VIYSISSEY; IYSISSEYI;
YSISSEYIN; SISSEYINN; ISSEYINNR; SSEYINNRV; SEYINNRVF;
EYINNRVFK; YINNRVFKG; INNRVFKGG; NNRVFKGGI; NRVFKGGII;
RVFKGGIII; VFKGGIIID; FKGGIIIDR; KGGIIIDRG; GGIIIDRGL;
GIIIDRGLK; IIIDRGLKE; IIDRGLKEG; IDRGLKEGV; DRGLKEGVI;
RGLKEGVIE; GLKEGVIEI; LKEGVIEIV; KEGVIEIVK; EGVIEIVKD;
GVIEIVKDP; VIEIVKDPD; IEIVKDPDV; EIVKDPDVL; IVKDPDVLN;
VKDPDVLNN; KDPDVLNNR; DPDVLNNRL; PDVLNNRLV; DVLNNRLVD;
VLNNRLVDE; LNNRLVDEV; NNRLVDEVI; NRLVDEVID; RLVDEVIDL;
LVDEVIDLE; VDEVIDLEN; DEVIDLENK; EVIDLENKI; VIDLENKII;
IDLENKIIS; DLENKIISG; LENKIISGE; ENKIISGEI; NKIISGEII;
KIISGEIIV; IISGEIIVP; ISGEIIVPD; SGEIIVPDS; GEIIVPDSE;
EIIVPDSEY; IIVPDSEYA; IVPDSEYAF; VPDSEYAFD; PDSEYAFDL;
DSEYAFDLF; SEYAFDLFK; EYAFDLFKS; YAFDLFKSK; AFDLFKSKL;

10 mers:
MFKRFIFITL; FKRFIFITLS; KRFIFITLSL; RFIFITLSLL; FIFITLSLLV;
IFITLSLLVF; FITLSLLVFA; ITLSLLVFAC; TLSLLVFACF; LSLLVFACFK;
SLLVFACFKS; LLVFACFKSN; LVFACFKSNK; VFACFKSNKK; FACFKSNKKS;
ACFKSNKKSI; CFKSNKKSIK; FKSNKKSIKS; KSNKKSIKSD; SNKKSIKSDK;
NKKSIKSDKV; KKSIKSDKVV; KSIKSDKVVV; SIKSDKVVVG; IKSDKVVVGV;
KSDKVVVGVL; SDKVVVGVLA; DKVVVGVLAH; KVVVGVLAHG; VVVGVLAHGS;
VVGVLAHGSF; VGVLAHGSFY; GVLAHGSFYD; VLAHGSFYDK; LAHGSFYDKG;
AHGSFYDKGY; HGSFYDKGYN; GSFYDKGYNQ; SFYDKGYNQS; FYDKGYNQSV;
YDKGYNQSVH; DKGYNQSVHD; KGYNQSVHDG; GYNQSVHDGV; YNQSVHDGVV;
NQSVHDGVVK; QSVHDGVVKL; SVHDGVVKLR; VHDGVVKLRD; HDGVVKLRDN;
DGVVKLRDNF; GVVKLRDNFG; VVKLRDNFGI; VKLRDNFGIK; KLRDNFGIKL;
LRDNFGIKLI; RDNFGIKLIT; DNFGIKLITK; NFGIKLITKS; FGIKLITKSL;
GIKLITKSLR; IKLITKSLRP; KLITKSLRPY; LITKSLRPYP; ITKSLRPYPI;
TKSLRPYPIE; KSLRPYPIEG; SLRPYPIEGK; LRPYPIEGKR; RPYPIEGKRL;
PYPIEGKRLL; YPIEGKRLLT; PIEGKRLLTV; IEGKRLLTVD; EGKRLLTVDE;
GKRLLTVDEA; KRLLTVDEAM; RLLTVDEAMT; LLTVDEAMTE; LTVDEAMTED;
TVDEAMTEDA; VDEAMTEDAY; DEAMTEDAYE; EAMTEDAYEV; AMTEDAYEVQ;
MTEDAYEVQK; TEDAYEVQKN; EDAYEVQKNP; DAYEVQKNPL; AYEVQKNPLN;
YEVQKNPLNL; EVQKNPLNLF; VQKNPLNLFW; QKNPLNLFWL; KNPLNLFWLI;
NPLNLFWLIG; PLNLFWLIGY; LNLFWLIGYR; NLFWLIGYRF; LFWLIGYRFS;
FWLIGYRFSD; WLIGYRFSDL; LIGYRFSDLS; IGYRFSDLSV; GYRFSDLSVK;
YRFSDLSVKL; RFSDLSVKLS; FSDLSVKLSY; SDLSVKLSYE; DLSVKLSYER;
LSVKLSYERP; SVKLSYERPD; VKLSYERPDI; KLSYERPDIY; LSYERPDIYY;
SYERPDIYYG; YERPDIYYGI; ERPDIYYGII; RPDIYYGIID; PDIYYGIIDA;
DIYYGIIDAF; IYYGIIDAFD; YYGIIDAFDY; YGIIDAFDYG; GIIDAFDYGD;
IIDAFDYGDI; IDAFDYGDIQ; DAFDYGDIQV; AFDYGDIQVP; FDYGDIQVPK;
DYGDIQVPKN; YGDIQVPKNS; GDIQVPKNSL; DIQVPKNSLA; IQVPKNSLAI;
QVPKNSLAIK; VPKNSLAIKF; PKNSLAIKFR; KNSLAIKFRN; NSLAIKFRNE;
SLAIKFRNEE; LAIKFRNEEA; AIKFRNEEAA; IKFRNEEAAF; KFRNEEAAFL;
FRNEEAAFLA; RNEEAAFLAG; NEEAAFLAGY; EEAAFLAGYI; EAAFLAGYIA;
AAFLAGYIAA; AFLAGYIAAK; FLAGYIAAKM; LAGYIAAKMS; AGYIAAKMSR;
GYIAAKMSRK; YIAAKMSRKE; IAAKMSRKEK; AAKMSRKEKI; AKMSRKEKIG;
KMSRKEKIGF; MSRKEKIGFL; SRKEKIGFLT; RKEKIGFLTG; KEKIGFLTGP;
EKIGFLTGPM; KIGFLTGPMS; IGFLTGPMSE; GFLTGPMSEH; FLTGPMSEHV;
LTGPMSEHVK; TGPMSEHVKD; GPMSEHVKDF; PMSEHVKDFK; MSEHVKDFKF;
SEHVKDFKFG; EHVKDFKFGF; HVKDFKFGFK; VKDFKFGFKA; KDFKFGFKAG;
DFKFGFKAGI; FKFGFKAGIF; KFGFKAGIFY; FGFKAGIFYA; GFKAGIFYAN;
FKAGIFYANP; KAGIFYANPK; AGIFYANPKL; GIFYANPKLR; IFYANPKLRL;
FYANPKLRLV; YANPKLRLVS; ANPKLRLVSK; NPKLRLVSKK; PKLRLVSKKA;
KLRLVSKKAP; LRLVSKKAPS; RLVSKKAPSL; LVSKKAPSLF; VSKKAPSLFD;

SKKAPSLFDK; KKAPSLFDKE; KAPSLFDKEK; APSLFDKEKG; PSLFDKEKGK;
SLFDKEKGKA; LFDKEKGKAM; FDKEKGKAMA; DKEKGKAMAL; KEKGKAMALF;
EKGKAMALFM; KGKAMALFMY; GKAMALFMYK; KAMALFMYKE; AMALFMYKED;
MALFMYKEDK; ALFMYKEDKV; LFMYKEDKVG; FMYKEDKVGV; MYKEDKVGVI;
YKEDKVGVIF; KEDKVGVIFP; EDKVGVIFPI; DKVGVIFPIA; KVGVIFPIAG;
VGVIFPIAGI; GVIFPIAGIT; VIFPIAGITG; IFPIAGITGL; FPIAGITGLG;
PIAGITGLGV; IAGITGLGVY; AGITGLGVYD; GITGLGVYDA; ITGLGVYDAA;
TGLGVYDAAK; GLGVYDAAKE; LGVYDAAKEL; GVYDAAKELG; VYDAAKELGP;
YDAAKELGPK; DAAKELGPKY; AAKELGPKYY; AKELGPKYYV; KELGPKYYVI;
ELGPKYYVIG; LGPKYYVIGL; GPKYYVIGLN; PKYYVIGLNQ; KYYVIGLNQD;
YYVIGLNQDQ; YVIGLNQDQS; VIGLNQDQSY; IGLNQDQSYI; GLNQDQSYIA;
LNQDQSYIAP; NQDQSYIAPQ; QDQSYIAPQN; DQSYIAPQNV; QSYIAPQNVI;
SYIAPQNVIT; YIAPQNVITS; IAPQNVITSI; APQNVITSII; PQNVITSIIK;
QNVITSIIKD; NVITSIIKDI; VITSIIKDIG; ITSIIKDIGK; TSIIKDIGKV;
SIIKDIGKVI; IIKDIGKVIY; IKDIGKVIYS; KDIGKVIYSI; DIGKVIYSIS;
IGKVIYSISS; GKVIYSISSE; KVIYSISSEY; VIYSISSEYI; IYSISSEYIN;
YSISSEYINN; SISSEYINNR; ISSEYINNRV; SSEYINNRVF; SEYINNRVFK;
EYINNRVFKG; YINNRVFKGG; INNRVFKGGI; NNRVFKGGII; NRVFKGGIII;
RVFKGGIIID; VFKGGIIIDR; FKGGIIIDRG; KGGIIIDRGL; GGIIIDRGLK;
GIIIDRGLKE; IIIDRGLKEG; IIDRGLKEGV; IDRGLKEGVI; DRGLKEGVIE;
RGLKEGVIEI; GLKEGVIEIV; LKEGVIEIVK; KEGVIEIVKD; EGVIEIVKDP;
GVIEIVKDPD; VIEIVKDPDV; IEIVKDPDVL; EIVKDPDVLN; IVKDPDVLNN;
VKDPDVLNNR; KDPDVLNNRL; DPDVLNNRLV; PDVLNNRLVD; DVLNNRLVDE;
VLNNRLVDEV; LNNRLVDEVI; NNRLVDEVID; NRLVDEVIDL; RLVDEVIDLE;
LVDEVIDLEN; VDEVIDLENK; DEVIDLENKI; EVIDLENKII; VIDLENKIIS;
IDLENKIISG; DLENKIISGE; LENKIISGEI; ENKIISGEII; NKIISGEIIV;
KIISGEIIVP; IISGEIIVPD; ISGEIIVPDS; SGEIIVPDSE; GEIIVPDSEY;
EIIVPDSEYA; IIVPDSEYAF; IVPDSEYAFD; VPDSEYAFDL; PDSEYAFDLF;
DSEYAFDLFK; SEYAFDLFKS; EYAFDLFKSK; YAFDLFKSKL;

11 mers:
MFKRFIFITLS; FKRFIFITLSL; KRFIFITLSLL; RFIFITLSLLV;
FIFITLSLLVF; IFITLSLLVFA; FITLSLLVFAC; ITLSLLVFACF;
TLSLLVFACFK; LSLLVFACFKS; SLLVFACFKSN; LLVFACFKSNK;
LVFACFKSNKK; VFACFKSNKKS; FACFKSNKKSI; ACFKSNKKSIK;
CFKSNKKSIKS; FKSNKKSIKSD; KSNKKSIKSDK; SNKKSIKSDKV;
NKKSIKSDKVV; KKSIKSDKVVV; KSIKSDKVVVG; SIKSDKVVVGV;
IKSDKVVVGVL; KSDKVVVGVLA; SDKVVVGVLAH; DKVVVGVLAHG;
KVVVGVLAHGS; VVVGVLAHGSF; VVGVLAHGSFY; VGVLAHGSFYD;
GVLAHGSFYDK; VLAHGSFYDKG; LAHGSFYDKGY; AHGSFYDKGYN;
HGSFYDKGYNQ; GSFYDKGYNQS; SFYDKGYNQSV; FYDKGYNQSVH;
YDKGYNQSVHD; DKGYNQSVHDG; KGYNQSVHDGV; GYNQSVHDGVV;
YNQSVHDGVVK; NQSVHDGVVKL; QSVHDGVVKLR; SVHDGVVKLRD;
VHDGVVKLRDN; HDGVVKLRDNF; DGVVKLRDNFG; GVVKLRDNFGI;
VVKLRDNFGIK; VKLRDNFGIKL; KLRDNFGIKLI; LRDNFGIKLIT;
RDNFGIKLITK; DNFGIKLITKS; NFGIKLITKSL; FGIKLITKSLR;
GIKLITKSLRP; IKLITKSLRPY; KLITKSLRPYP; LITKSLRPYPI;
ITKSLRPYPIE; TKSLRPYPIEG; KSLRPYPIEGK; SLRPYPIEGKR;
LRPYPIEGKRL; RPYPIEGKRLL; PYPIEGKRLLT; YPIEGKRLLTV;
PIEGKRLLTVD; IEGKRLLTVDE; EGKRLLTVDEA; GKRLLTVDEAM;
KRLLTVDEAMT; RLLTVDEAMTE; LLTVDEAMTED; LTVDEAMTEDA;
TVDEAMTEDAY; VDEAMTEDAYE; DEAMTEDAYEV; EAMTEDAYEVQ;
AMTEDAYEVQK; MTEDAYEVQKN; TEDAYEVQKNP; EDAYEVQKNPL;
DAYEVQKNPLN; AYEVQKNPLNL; YEVQKNPLNLF; EVQKNPLNLFW;
VQKNPLNLFWL; QKNPLNLFWLI; KNPLNLFWLIG; NPLNLFWLIGY;
PLNLFWLIGYR; LNLFWLIGYRF; NLFWLIGYRFS; LFWLIGYRFSD;
FWLIGYRFSDL; WLIGYRFSDLS; LIGYRFSDLSV; IGYRFSDLSVK;

	GYRFSDLSVKL; YRFSDLSVKLS; RFSDLSVKLSY; FSDLSVKLSYE; SDLSVKLSYER; DLSVKLSYERP; LSVKLSYERPD; SVKLSYERPDI; VKLSYERPDIY; KLSYERPDIYY; LSYERPDIYYG; SYERPDIYYGI; YERPDIYYGII; ERPDIYYGIID; RPDIYYGIIDA; PDIYYGIIDAF; DIYYGIIDAFD; IYYGIIDAFDY; YYGIIDAFDYG; YGIIDAFDYGD; GIIDAFDYGDI; IIDAFDYGDIQ; IDAFDYGDIQV; DAFDYGDIQVP; AFDYGDIQVPK; FDYGDIQVPKN; DYGDIQVPKNS; YGDIQVPKNSL; GDIQVPKNSLA; DIQVPKNSLAI; IQVPKNSLAIK; QVPKNSLAIKF; VPKNSLAIKFR; PKNSLAIKFRN; KNSLAIKFRNE; NSLAIKFRNEE; SLAIKFRNEEA; LAIKFRNEEAA; AIKFRNEEAAF; IKFRNEEAAFL; KFRNEEAAFLA; FRNEEAAFLAG; RNEEAAFLAGY; NEEAAFLAGYI; EEAAFLAGYIA; EAAFLAGYIAA; AAFLAGYIAAK; AFLAGYIAAKM; FLAGYIAAKMS; LAGYIAAKMSR; AGYIAAKMSRK; GYIAAKMSRKE; YIAAKMSRKEK; IAAKMSRKEKI; AAKMSRKEKIG; AKMSRKEKIGF; KMSRKEKIGFL; MSRKEKIGFLT; SRKEKIGFLTG; RKEKIGFLTGP; KEKIGFLTGPM; EKIGFLTGPMS; KIGFLTGPMSE; IGFLTGPMSEH; GFLTGPMSEHV; FLTGPMSEHVK; LTGPMSEHVKD; TGPMSEHVKDF; GPMSEHVKDFK; PMSEHVKDFKF; MSEHVKDFKFG; SEHVKDFKFGF; EHVKDFKFGFK; HVKDFKFGFKA; VKDFKFGFKAG; KDFKFGFKAGI; DFKFGFKAGIF; FKFGFKAGIFY; KFGFKAGIFYA; FGFKAGIFYAN; GFKAGIFYANP; FKAGIFYANPK; KAGIFYANPKL; AGIFYANPKLR; GIFYANPKLRL; IFYANPKLRLV; FYANPKLRLVS; YANPKLRLVSK; ANPKLRLVSKK; NPKLRLVSKKA; PKLRLVSKKAP; KLRLVSKKAPS; LRLVSKKAPSL; RLVSKKAPSLF; LVSKKAPSLFD; VSKKAPSLFDK; SKKAPSLFDKE; KKAPSLFDKEK; KAPSLFDKEKG; APSLFDKEKGK; PSLFDKEKGKA; SLFDKEKGKAM; LFDKEKGKAMA; FDKEKGKAMAL; DKEKGKAMALF; KEKGKAMALFM; EKGKAMALFMY; KGKAMALFMYK; GKAMALFMYKE; KAMALFMYKED; AMALFMYKEDK; MALFMYKEDKV; ALFMYKEDKVG; LFMYKEDKVGV; FMYKEDKVGVI; MYKEDKVGVIF; YKEDKVGVIFP; KEDKVGVIFPI; EDKVGVIFPIA; DKVGVIFPIAG; KVGVIFPIAGI; VGVIFPIAGIT; GVIFPIAGITG; VIFPIAGITGL; IFPIAGITGLG; FPIAGITGLGV; PIAGITGLGVY; IAGITGLGVYD; AGITGLGVYDA; GITGLGVYDAA; ITGLGVYDAAK; TGLGVYDAAKE; GLGVYDAAKEL; LGVYDAAKELG; GVYDAAKELGP; VYDAAKELGPK; YDAAKELGPKY; DAAKELGPKYY; AAKELGPKYYV; AKELGPKYYVI; KELGPKYYVIG; ELGPKYYVIGL; LGPKYYVIGLN; GPKYYVIGLNQ; PKYYVIGLNQD; KYYVIGLNQDQ; YYVIGLNQDQS; YVIGLNQDQSY; VIGLNQDQSYI; IGLNQDQSYIA; GLNQDQSYIAP; LNQDQSYIAPQ; NQDQSYIAPQN; QDQSYIAPQNV; DQSYIAPQNVI; QSYIAPQNVIT; SYIAPQNVITS; YIAPQNVITSI; IAPQNVITSII; APQNVITSIIK; PQNVITSIIKD; QNVITSIIKDI; NVITSIIKDIG; VITSIIKDIGK; ITSIIKDIGKV; TSIIKDIGKVI; SIIKDIGKVIY; IIKDIGKVIYS; IKDIGKVIYSI; KDIGKVIYSIS; DIGKVIYSISS; IGKVIYSISSE; GKVIYSISSEY; KVIYSISSEYI; VIYSISSEYIN; IYSISSEYINN; YSISSEYINNR; SISSEYINNRV; ISSEYINNRVF; SSEYINNRVFK; SEYINNRVFKG; EYINNRVFKGG; YINNRVFKGGI; INNRVFKGGII; NNRVFKGGIII; NRVFKGGIIID; RVFKGGIIIDR; VFKGGIIIDRG; FKGGIIIDRGL; KGGIIIDRGLK; GGIIIDRGLKE; GIIIDRGLKEG; IIIDRGLKEGV; IIDRGLKEGVI; IDRGLKEGVIE; DRGLKEGVIEI; RGLKEGVIEIV; GLKEGVIEIVK; LKEGVIEIVKD; KEGVIEIVKDP; EGVIEIVKDPD; GVIEIVKDPDV; VIEIVKDPDVL; IEIVKDPDVLN; EIVKDPDVLNN; IVKDPDVLNNR; VKDPDVLNNRL; KDPDVLNNRLV; DPDVLNNRLVD; PDVLNNRLVDE; DVLNNRLVDEV; VLNNRLVDEVI; LNNRLVDEVID; NNRLVDEVIDL; NRLVDEVIDLE; RLVDEVIDLEN; LVDEVIDLENK; VDEVIDLENKI; DEVIDLENKII; EVIDLENKIIS; VIDLENKIISG; IDLENKIISGE; DLENKIISGEI; LENKIISGEII; ENKIISGEIIV; NKIISGEIIVP; KIISGEIIVPD; IISGEIIVPDS;

	ISGEIIVPDSE; SGEIIVPDSEY; GEIIVPDSEYA; EIIVPDSEYAF; IIVPDSEYAFD; IVPDSEYAFDL; VPDSEYAFDLF; PDSEYAFDLFK; DSEYAFDLFKS; SEYAFDLFKSK; EYAFDLFKSKL;
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31	SEQ ID NO 4075-5480/ 8 mers: MDNYYEIY; DNYYEIYF; NYYEIYFL; YYEIYFLY; YEIYFLYF; EIYFLYFF; IYFLYFFI; YFLYFFIK; FLYFFIKS; LYFFIKSK; YFFIKSKE; FFIKSKED; FIKSKEDI; IKSKEDIF; KSKEDIFM; SKEDIFML; KEDIFMLK; EDIFMLKK; DIFMLKKV; IFMLKKVY; FMLKKVYY; MLKKVYYF; LKKVYYFL; KKVYYFLI; KVYYFLIF; VYYFLIFL; YYFLIFLF; YFLIFLFI; FLIFLFIV; LIFLFIVA; IFLFIVAC; FLFIVACS; LFIVACSS; FIVACSSS; IVACSSSD; VACSSSDD; ACSSSDDG; CSSSDDGK; SSSDDGKS; SSDDGKSE; SDDGKSEA; DDGKSEAK; DGKSEAKT; GKSEAKTV; KSEAKTVS; SEAKTVSL; EAKTVSLI; AKTVSLIV; KTVSLIVD; TVSLIVDG; VSLIVDGA; SLIVDGAF; LIVDGAFD; IVDGAFDD; VDGAFDDK; DGAFDDKG; GAFDDKGF; AFDDKGFN; FDDKGFNE; DDKGFNES; DKGFNESS; KGFNESSS; GFNESSSK; FNESSSKA; NESSSKAI; ESSSKAIR; SSSKAIRK; SSKAIRKL; SKAIRKLK; KAIRKLKA; AIRKLKAD; IRKLKADL; RKLKADLN; KLKADLNI; LKADLNIN; KADLNINI; ADLNINII; DLNINIIE; LNINIIEK; NINIIEKA; INIIEKAS; NIIEKAST; IIEKASTG; IEKASTGN; EKASTGNS; KASTGNSY; ASTGNSYL; STGNSYLG; TGNSYLGD; GNSYLGDI; NSYLGDIA; SYLGDIAN; YLGDIANL; LGDIANLE; GDIANLED; DIANLEDG; IANLEDGN; ANLEDGNS; NLEDGNSN; LEDGNSNL; EDGNSNLI; DGNSNLIW; GNSNLIWG; NSNLIWGI; SNLIWGIG; NLIWGIGF; LIWGIGFR; IWGIGFRL; WGIGFRLS; GIGFRLSD; IGFRLSDI; GFRLSDIL; FRLSDILF; RLSDILFQ; LSDILFQR; SDILFQRA; DILFQRAS; ILFQRASE; LFQRASEN; FQRASENV; QRASENVS; RASENVSV; ASENVSVN; SENVSVNY; ENVSVNYA; NVSVNYAI; VSVNYAII; SVNYAIIE; VNYAIIEG; NYAIIEGV; YAIIEGVY; AIIEGVYD; IIEGVYDE; IEGVYDEI; EGVYDEIQ; GVYDEIQI; VYDEIQIP; YDEIQIPK; DEIQIPKN; EIQIPKNL; IQIPKNLL; QIPKNLLN; IPKNLLNI; PKNLLNIS; KNLLNISF; NLLNISFR; LLNISFRS; LNISFRSE; NISFRSEE; ISFRSEEV; SFRSEEVA; FRSEEVAF; RSEEVAFL; SEEVAFLA; EEVAFLAG; EVAFLAGY; VAFLAGYF; AFLAGYFA; FLAGYFAS; LAGYFASK; AGYFASKA; GYFASKAS; YFASKASK; FASKASKT; ASKASKTG; SKASKTGK; KASKTGKI; ASKTGKIG; SKTGKIGF; KTGKIGFV; TGKIGFVG; GKIGFVGG; KIGFVGGV; IGFVGGVR; GFVGGVRG; FVGGVRGK; VGGVRGKV; GGVRGKVL; GVRGKVLE; VRGKVLES; RGKVLESF; GKVLESFM; KVLESFMY; VLESFMYG; LESFMYGY; ESFMYGYE; SFMYGYEA; FMYGYEAG; MYGYEAGA; YGYEAGAK; GYEAGAKY; YEAGAKYA; EAGAKYAN; AGAKYANS; GAKYANSN; AKYANSNI; KYANSNIK; YANSNIKV; ANSNIKVV; NSNIKVVS; SNIKVVSQ; NIKVVSQY; IKVVSQYV; KVVSQYVG; VVSQYVGT; VSQYVGTF; SQYVGTFG; QYVGTFGD; YVGTFGDF; VGTFGDFG; GTFGDFGL; TFGDFGLG; FGDFGLGR; GDFGLGRS; DFGLGRST; FGLGRSTA; GLGRSTAS; LGRSTASN; GRSTASNM; RSTASNMY; STASNMYR; TASNMYRD; ASNMYRDG; SNMYRDGV; NMYRDGVD; MYRDGVDI; YRDGVDII; RDGVDIIF; DGVDIIFA; GVDIIFAA; VDIIFAAA; DIIFAAAG; IIFAAAGL; IFAAAGLS; FAAAGLSG; AAAGLSGI; AAGLSGIG; AGLSGIGV; GLSGIGVI; LSGIGVIE; SGIGVIEA; GIGVIEAA; IGVIEAAK; GVIEAAKE; VIEAAKEL; IEAAKELG; EAAKELGP; AAKELGPD; AKELGPDH; KELGPDHY; ELGPDHYI; LGPDHYII; GPDHYIIG; PDHYIIGV; DHYIIGVD; HYIIGVDQ; YIIGVDQD; IIGVDQDQ; IGVDQDQS; GVDQDQSY; VDQDQSYL; DQDQSYLA; QDQSYLAP; DQSYLAPN; QSYLAPNN; SYLAPNNV; YLAPNNVI; LAPNNVIV; APNNVIVS; PNNVIVSA; NNVIVSAV; NVIVSAVK; VIVSAVKK; IVSAVKKV; VSAVKKVD; SAVKKVDS; AVKKVDSL; VKKVDSLM; KKVDSLMY; KVDSLMYS; VDSLMYSL; DSLMYSLT; SLMYSLTK; LMYSLTKK; MYSLTKKY; YSLTKKYL; SLTKKYLE; LTKKYLET; TKKYLETG; KKYLETGV; KYLETGVL; YLETGVLD; LETGVLDG; ETGVLDGG; TGVLDGGK; GVLDGGKT; VLDGGKTM; LDGGKTMF; DGGKTMFL; GGKTMFLG; GKTMFLGL; KTMFLGLK; TMFLGLKE; MFLGLKED; FLGLKEDG; LGLKEDGL;

GLKEDGLG; LKEDGLGL; KEDGLGLV; EDGLGLVL; DGLGLVLN; GLGLVLNE; LGLVLNEN; GLVLNENL; LVLNENLK; VLNENLKS; LNENLKSN; NENLKSNY; ENLKSNYS; NLKSNYSE; LKSNYSEI; KSNYSEIY; SNYSEIYN; NYSEIYNK; YSEIYNKS; SEIYNKSL; EIYNKSLK; IYNKSLKI; YNKSLKIG; NKSLKIGQ; KSLKIGQS; SLKIGQSI; LKIGQSIM; KIGQSIMN; IGQSIMNG; GQSIMNGI; QSIMNGII; SIMNGIIK; IMNGIIKV; MNGIIKVP; NGIIKVPY; GIIKVPYD; IIKVPYDK; IKVPYDKV; KVPYDKVS; VPYDKVSY; PYDKVSYF; YDKVSYFV; DKVSYFVL; KVSYFVLQ; VSYFVLQM; SYFVLQME; YFVLQMEN;

9 mers:
MDNYYEIYF; DNYYEIYFL; NYYEIYFLY; YYEIYFLYF; YEIYFLYFF; EIYFLYFFI; IYFLYFFIK; YFLYFFIKS; FLYFFIKSK; LYFFIKSKE; YFFIKSKED; FFIKSKEDI; FIKSKEDIF; IKSKEDIFM; KSKEDIFML; SKEDIFMLK; KEDIFMLKK; EDIFMLKKV; DIFMLKKVY; IFMLKKVYY; FMLKKVYYF; MLKKVYYFL; LKKVYYFLI; KKVYYFLIF; KVYYFLIFL; VYYFLIFLF; YYFLIFLFI; YFLIFLFIV; FLIFLFIVA; LIFLFIVAC; IFLFIVACS; FLFIVACSS; LFIVACSSS; FIVACSSSD; IVACSSSDD; VACSSSDDG; ACSSSDDGK; CSSSDDGKS; SSSDDGKSE; SSDDGKSEA; SDDGKSEAK; DDGKSEAKT; DGKSEAKTV; GKSEAKTVS; KSEAKTVSL; SEAKTVSLI; EAKTVSLIV; AKTVSLIVD; KTVSLIVDG; TVSLIVDGA; VSLIVDGAF; SLIVDGAFD; LIVDGAFDD; IVDGAFDDK; VDGAFDDKG; DGAFDDKGF; GAFDDKGFN; AFDDKGFNE; FDDKGFNES; DDKGFNESS; DKGFNESSS; KGFNESSSK; GFNESSSKA; FNESSSKAI; NESSSKAIR; ESSSKAIRK; SSSKAIRKL; SSKAIRKLK; SKAIRKLKA; KAIRKLKAD; AIRKLKADL; IRKLKADLN; RKLKADLNI; KLKADLNIN; LKADLNINI; KADLNINII; ADLNINIIE; DLNINIIEK; LNINIIEKA; NINIIEKAS; INIIEKAST; NIIEKASTG; IIEKASTGN; IEKASTGNS; EKASTGNSY; KASTGNSYL; ASTGNSYLG; STGNSYLGD; TGNSYLGDI; GNSYLGDIA; NSYLGDIAN; SYLGDIANL; YLGDIANLE; LGDIANLED; GDIANLEDG; DIANLEDGN; IANLEDGNS; ANLEDGNSN; NLEDGNSNL; LEDGNSNLI; EDGNSNLIW; DGNSNLIWG; GNSNLIWGI; NSNLIWGIG; SNLIWGIGF; NLIWGIGFR; LIWGIGFRL; IWGIGFRLS; WGIGFRLSD; GIGFRLSDI; IGFRLSDIL; GFRLSDILF; FRLSDILFQ; RLSDILFQR; LSDILFQRA; SDILFQRAS; DILFQRASE; ILFQRASEN; LFQRASENV; FQRASENVS; QRASENVSV; RASENVSVN; ASENVSVNY; SENVSVNYA; ENVSVNYAI; NVSVNYAII; VSVNYAIIE; SVNYAIIEG; VNYAIIEGV; NYAIIEGVY; YAIIEGVYD; AIIEGVYDE; IIEGVYDEI; IEGVYDEIQ; EGVYDEIQI; GVYDEIQIP; VYDEIQIPK; YDEIQIPKN; DEIQIPKNL; EIQIPKNLL; IQIPKNLLN; QIPKNLLNI; IPKNLLNIS; PKNLLNISF; KNLLNISFR; NLLNISFRS; LLNISFRSE; LNISFRSEE; NISFRSEEV; ISFRSEEVA; SFRSEEVAF; FRSEEVAFL; RSEEVAFLA; SEEVAFLAG; EEVAFLAGY; EVAFLAGYF; VAFLAGYFA; AFLAGYFAS; FLAGYFASK; LAGYFASKA; AGYFASKAS; GYFASKASK; YFASKASKT; FASKASKTG; ASKASKTGK; SKASKTGKI; KASKTGKIG; ASKTGKIGF; SKTGKIGFV; KTGKIGFVG; TGKIGFVGG; GKIGFVGGV; KIGFVGGVR; IGFVGGVRG; GFVGGVRGK; FVGGVRGKV; VGGVRGKVL; GGVRGKVLE; GVRGKVLES; VRGKVLESF; RGKVLESFM; GKVLESFMY; KVLESFMYG; VLESFMYGY; LESFMYGYE; ESFMYGYEA; SFMYGYEAG; FMYGYEAGA; MYGYEAGAK; YGYEAGAKY; GYEAGAKYA; YEAGAKYAN; EAGAKYANS; AGAKYANSN; GAKYANSNI; AKYANSNIK; KYANSNIKV; YANSNIKVV; ANSNIKVVS; NSNIKVVSQ; SNIKVVSQY; NIKVVSQYV; IKVVSQYVG; KVVSQYVGT; VVSQYVGTF; VSQYVGTFG; SQYVGTFGD; QYVGTFGDF; YVGTFGDFG; VGTFGDFGL; GTFGDFGLG; TFGDFGLGR; FGDFGLGRS; GDFGLGRST; DFGLGRSTA; FGLGRSTAS; GLGRSTASN; LGRSTASNM; GRSTASNMY; RSTASNMYR; STASNMYRD; TASNMYRDG; ASNMYRDGV; SNMYRDGVD; NMYRDGVDI; MYRDGVDII; YRDGVDIIF; RDGVDIIFA; DGVDIIFAA; GVDIIFAAA; VDIIFAAAG; DIIFAAAGL; IIFAAAGLS; IFAAAGLSG; FAAAGLSGI;

AAAGLSGIG; AAGLSGIGV; AGLSGIGVI; GLSGIGVIE; LSGIGVIEA;
SGIGVIEAA; GIGVIEAAK; IGVIEAAKE; GVIEAAKEL; VIEAAKELG;
IEAAKELGP; EAAKELGPD; AAKELGPDH; AKELGPDHY; KELGPDHYI;
ELGPDHYII; LGPDHYIIG; GPDHYIIGV; PDHYIIGVD; DHYIIGVDQ;
HYIIGVDQD; YIIGVDQDQ; IIGVDQDQS; IGVDQDQSY; GVDQDQSYL;
VDQDQSYLA; DQDQSYLAP; QDQSYLAPN; DQSYLAPNN; QSYLAPNNV;
SYLAPNNVI; YLAPNNVIV; LAPNNVIVS; APNNVIVSA; PNNVIVSAV;
NNVIVSAVK; NVIVSAVKK; VIVSAVKKV; IVSAVKKVD; VSAVKKVDS;
SAVKKVDSL; AVKKVDSLM; VKKVDSLMY; KKVDSLMYS; KVDSLMYSL;
VDSLMYSLT; DSLMYSLTK; SLMYSLTKK; LMYSLTKKY; MYSLTKKYL;
YSLTKKYLE; SLTKKYLET; LTKKYLETG; TKKYLETGV; KKYLETGVL;
KYLETGVLD; YLETGVLDG; LETGVLDGG; ETGVLDGGK; TGVLDGGKT;
GVLDGGKTM; VLDGGKTMF; LDGGKTMFL; DGGKTMFLG; GGKTMFLGL;
GKTMFLGLK; KTMFLGLKE; TMFLGLKED; MFLGLKEDG; FLGLKEDGL;
LGLKEDGLG; GLKEDGLGL; LKEDGLGLV; KEDGLGLVL; EDGLGLVLN;
DGLGLVLNE; GLGLVLNEN; LGLVLNENL; GLVLNENLK; LVLNENLKS;
VLNENLKSN; LNENLKSNY; NENLKSNYS; ENLKSNYSE; NLKSNYSEI;
LKSNYSEIY; KSNYSEIYN; SNYSEIYNK; NYSEIYNKS; YSEIYNKSL;
SEIYNKSLK; EIYNKSLKI; IYNKSLKIG; YNKSLKIGQ; NKSLKIGQS;
KSLKIGQSI; SLKIGQSIM; LKIGQSIMN; KIGQSIMNG; IGQSIMNGI;
GQSIMNGII; QSIMNGIIK; SIMNGIIKV; IMNGIIKVP; MNGIIKVPY;
NGIIKVPYD; GIIKVPYDK; IIKVPYDKV; IKVPYDKVS; KVPYDKVSY;
VPYDKVSYF; PYDKVSYFV; YDKVSYFVL; DKVSYFVLQ; KVSYFVLQM;
VSYFVLQME; SYFVLQMEN;

10 mers:
MDNYYEIYFL; DNYYEIYFLY; NYYEIYFLYF; YYEIYFLYFF; YEIYFLYFFI;
EIYFLYFFIK; IYFLYFFIKS; YFLYFFIKSK; FLYFFIKSKE; LYFFIKSKED;
YFFIKSKEDI; FFIKSKEDIF; FIKSKEDIFM; IKSKEDIFML; KSKEDIFMLK;
SKEDIFMLKK; KEDIFMLKKV; EDIFMLKKVY; DIFMLKKVYY; IFMLKKVYYF;
FMLKKVYYFL; MLKKVYYFLI; LKKVYYFLIF; KKVYYFLIFL; KVYYFLIFLF;
VYYFLIFLFI; YYFLIFLFIV; YFLIFLFIVA; FLIFLFIVAC; LIFLFIVACS;
IFLFIVACSS; FLFIVACSSS; LFIVACSSSD; FIVACSSSDD; IVACSSSDDG;
VACSSSDDGK; ACSSSDDGKS; CSSSDDGKSE; SSSDDGKSEA; SSDDGKSEAK;
SDDGKSEAKT; DDGKSEAKTV; DGKSEAKTVS; GKSEAKTVSL; KSEAKTVSLI;
SEAKTVSLIV; EAKTVSLIVD; AKTVSLIVDG; KTVSLIVDGA; TVSLIVDGAF;
VSLIVDGAFD; SLIVDGAFDD; LIVDGAFDDK; IVDGAFDDKG; VDGAFDDKGF;
DGAFDDKGFN; GAFDDKGFNE; AFDDKGFNES; FDDKGFNESS; DDKGFNESSS;
DKGFNESSSK; KGFNESSSKA; GFNESSSKAI; FNESSSKAIR; NESSSKAIRK;
ESSSKAIRKL; SSSKAIRKLK; SSKAIRKLKA; SKAIRKLKAD; KAIRKLKADL;
AIRKLKADLN; IRKLKADLNI; RKLKADLNIN; KLKADLNINI; LKADLNINII;
KADLNINIIE; ADLNINIIEK; DLNINIIEKA; LNINIIEKAS; NINIIEKAST;
INIIEKASTG; NIIEKASTGN; IIEKASTGNS; IEKASTGNSY; EKASTGNSYL;
KASTGNSYLG; ASTGNSYLGD; STGNSYLGDI; TGNSYLGDIA; GNSYLGDIAN;
NSYLGDIANL; SYLGDIANLE; YLGDIANLED; LGDIANLEDG; GDIANLEDGN;
DIANLEDGNS; IANLEDGNSN; ANLEDGNSNL; NLEDGNSNLI; LEDGNSNLIW;
EDGNSNLIWG; DGNSNLIWGI; GNSNLIWGIG; NSNLIWGIGF; SNLIWGIGFR;
NLIWGIGFRL; LIWGIGFRLS; IWGIGFRLSD; WGIGFRLSDI; GIGFRLSDIL;
IGFRLSDILF; GFRLSDILFQ; FRLSDILFQR; RLSDILFQRA; LSDILFQRAS;
SDILFQRASE; DILFQRASEN; ILFQRASENV; LFQRASENVS; FQRASENVSV;
QRASENVSVN; RASENVSVNY; ASENVSVNYA; SENVSVNYAI; ENVSVNYAII;
NVSVNYAIIE; VSVNYAIIEG; SVNYAIIEGV; VNYAIIEGVY; NYAIIEGVYD;
YAIIEGVYDE; AIIEGVYDEI; IIEGVYDEIQ; IEGVYDEIQI; EGVYDEIQIP;
GVYDEIQIPK; VYDEIQIPKN; YDEIQIPKNL; DEIQIPKNLL; EIQIPKNLLN;
IQIPKNLLNI; QIPKNLLNIS; IPKNLLNISF; PKNLLNISFR; KNLLNISFRS;
NLLNISFRSE; LLNISFRSEE; LNISFRSEEV; NISFRSEEVA; ISFRSEEVAF;
SFRSEEVAFL; FRSEEVAFLA; RSEEVAFLAG; SEEVAFLAGY; EEVAFLAGYF;

EVAFLAGYFA; VAFLAGYFAS; AFLAGYFASK; FLAGYFASKA; LAGYFASKAS; AGYFASKASK; GYFASKASKT; YFASKASKTG; FASKASKTGK; ASKASKTGKI; SKASKTGKIG; KASKTGKIGF; ASKTGKIGFV; SKTGKIGFVG; KTGKIGFVGG; TGKIGFVGGV; GKIGFVGGVR; KIGFVGGVRG; IGFVGGVRGK; GFVGGVRGKV; FVGGVRGKVL; VGGVRGKVLE; GGVRGKVLES; GVRGKVLESF; VRGKVLESFM; RGKVLESFMY; GKVLESFMYG; KVLESFMYGY; VLESFMYGYE; LESFMYGYEA; ESFMYGYEAG; SFMYGYEAGA; FMYGYEAGAK; MYGYEAGAKY; YGYEAGAKYA; GYEAGAKYAN; YEAGAKYANS; EAGAKYANSN; AGAKYANSNI; GAKYANSNIK; AKYANSNIKV; KYANSNIKVV; YANSNIKVVS; ANSNIKVVSQ; NSNIKVVSQY; SNIKVVSQYV; NIKVVSQYVG; IKVVSQYVGT; KVVSQYVGTF; VVSQYVGTFG; VSQYVGTFGD; SQYVGTFGDF; QYVGTFGDFG; YVGTFGDFGL; VGTFGDFGLG; GTFGDFGLGR; TFGDFGLGRS; FGDFGLGRST; GDFGLGRSTA; DFGLGRSTAS; FGLGRSTASN; GLGRSTASNM; LGRSTASNMY; GRSTASNMYR; RSTASNMYRD; STASNMYRDG; TASNMYRDGV; ASNMYRDGVD; SNMYRDGVDI; NMYRDGVDII; MYRDGVDIIF; YRDGVDIIFA; RDGVDIIFAA; DGVDIIFAAA; GVDIIFAAAG; VDIIFAAAGL; DIIFAAAGLS; IIFAAAGLSG; IFAAAGLSGI; FAAAGLSGIG; AAAGLSGIGV; AAGLSGIGVI; AGLSGIGVIE; GLSGIGVIEA; LSGIGVIEAA; SGIGVIEAAK; GIGVIEAAKE; IGVIEAAKEL; GVIEAAKELG; VIEAAKELGP; IEAAKELGPD; EAAKELGPDH; AAKELGPDHY; AKELGPDHYI; KELGPDHYII; ELGPDHYIIG; LGPDHYIIGV; GPDHYIIGVD; PDHYIIGVDQ; DHYIIGVDQD; HYIIGVDQDQ; YIIGVDQDQS; IIGVDQDQSY; IGVDQDQSYL; GVDQDQSYLA; VDQDQSYLAP; DQDQSYLAPN; QDQSYLAPNN; DQSYLAPNNV; QSYLAPNNVI; SYLAPNNVIV; YLAPNNVIVS; LAPNNVIVSA; APNNVIVSAV; PNNVIVSAVK; NNVIVSAVKK; NVIVSAVKKV; VIVSAVKKVD; IVSAVKKVDS; VSAVKKVDSL; SAVKKVDSLM; AVKKVDSLMY; VKKVDSLMYS; KKVDSLMYSL; KVDSLMYSLT; VDSLMYSLTK; DSLMYSLTKK; SLMYSLTKKY; LMYSLTKKYL; MYSLTKKYLE; YSLTKKYLET; SLTKKYLETG; LTKKYLETGV; TKKYLETGVL; KKYLETGVLD; KYLETGVLDG; YLETGVLDGG; LETGVLDGGK; ETGVLDGGKT; TGVLDGGKTM; GVLDGGKTMF; VLDGGKTMFL; LDGGKTMFLG; DGGKTMFLGL; GGKTMFLGLK; GKTMFLGLKE; KTMFLGLKED; TMFLGLKEDG; MFLGLKEDGL; FLGLKEDGLG; LGLKEDGLGL; GLKEDGLGLV; LKEDGLGLVL; KEDGLGLVLN; EDGLGLVLNE; DGLGLVLNEN; GLGLVLNENL; LGLVLNENLK; GLVLNENLKS; LVLNENLKSN; VLNENLKSNY; LNENLKSNYS; NENLKSNYSE; ENLKSNYSEI; NLKSNYSEIY; LKSNYSEIYN; KSNYSEIYNK; SNYSEIYNKS; NYSEIYNKSL; YSEIYNKSLK; SEIYNKSLKI; EIYNKSLKIG; IYNKSLKIGQ; YNKSLKIGQS; NKSLKIGQSI; KSLKIGQSIM; SLKIGQSIMN; LKIGQSIMNG; KIGQSIMNGI; IGQSIMNGII; GQSIMNGIIK; QSIMNGIIKV; SIMNGIIKVP; IMNGIIKVPY; MNGIIKVPYD; NGIIKVPYDK; GIIKVPYDKV; IIKVPYDKVS; IKVPYDKVSY; KVPYDKVSYF; VPYDKVSYFV; PYDKVSYFVL; YDKVSYFVLQ; DKVSYFVLQM; KVSYFVLQME; VSYFVLQMEN;

11 mers:
MDNYYEIYFLY; DNYYEIYFLYF; NYYEIYFLYFF; YYEIYFLYFFI; YEIYFLYFFIK; EIYFLYFFIKS; IYFLYFFIKSK; YFLYFFIKSKE; FLYFFIKSKED; LYFFIKSKEDI; YFFIKSKEDIF; FFIKSKEDIFM; FIKSKEDIFML; IKSKEDIFMLK; KSKEDIFMLKK; SKEDIFMLKKV; KEDIFMLKKVY; EDIFMLKKVYY; DIFMLKKVYYF; IFMLKKVYYFL; FMLKKVYYFLI; MLKKVYYFLIF; LKKVYYFLIFL; KKVYYFLIFLF; KVYYFLIFLFI; VYYFLIFLFIV; YYFLIFLFIVA; YFLIFLFIVAC; FLIFLFIVACS; LIFLFIVACSS; IFLFIVACSSS; FLFIVACSSSD; LFIVACSSSDD; FIVACSSSDDG; IVACSSSDDGK; VACSSSDDGKS; ACSSSDDGKSE; CSSSDDGKSEA; SSSDDGKSEAK; SSDDGKSEAKT; SDDGKSEAKTV; DDGKSEAKTVS; DGKSEAKTVSL; GKSEAKTVSLI; KSEAKTVSLIV; SEAKTVSLIVD; EAKTVSLIVDG; AKTVSLIVDGA; KTVSLIVDGAF; TVSLIVDGAFD; VSLIVDGAFDD; SLIVDGAFDDK; LIVDGAFDDKG; IVDGAFDDKGF; VDGAFDDKGFN; DGAFDDKGFNE; GAFDDKGFNES; AFDDKGFNESS; FDDKGFNESSS; DDKGFNESSSK;

	DKGFNESSSKA; KGFNESSSKAI; GFNESSSKAIR; FNESSSKAIRK; NESSSKAIRKL; ESSSKAIRKLK; SSSKAIRKLKA; SSKAIRKLKAD; SKAIRKLKADL; KAIRKLKADLN; AIRKLKADLNI; IRKLKADLNIN; RKLKADLNINI; KLKADLNINII; LKADLNINIIE; KADLNINIIEK; ADLNINIIEKA; DLNINIIEKAS; LNINIIEKAST; NINIIEKASTG; INIIEKASTGN; NIIEKASTGNS; IIEKASTGNSY; IEKASTGNSYL; EKASTGNSYLG; KASTGNSYLGD; ASTGNSYLGDI; STGNSYLGDIA; TGNSYLGDIAN; GNSYLGDIANL; NSYLGDIANLE; SYLGDIANLED; YLGDIANLEDG; LGDIANLEDGN; GDIANLEDGNS; DIANLEDGNSN; IANLEDGNSNL; ANLEDGNSNLI; NLEDGNSNLIW; LEDGNSNLIWG; EDGNSNLIWGI; DGNSNLIWGIG; GNSNLIWGIGF; NSNLIWGIGFR; SNLIWGIGFRL; NLIWGIGFRLS; LIWGIGFRLSD; IWGIGFRLSDI; WGIGFRLSDIL; GIGFRLSDILF; IGFRLSDILFQ; GFRLSDILFQR; FRLSDILFQRA; RLSDILFQRAS; LSDILFQRASE; SDILFQRASEN; DILFQRASENV; ILFQRASENVS; LFQRASENVSV; FQRASENVSVN; QRASENVSVNY; RASENVSVNYA; ASENVSVNYAI; SENVSVNYAII; ENVSVNYAIIE; NVSVNYAIIEG; VSVNYAIIEGV; SVNYAIIEGVY; VNYAIIEGVYD; NYAIIEGVYDE; YAIIEGVYDEI; AIIEGVYDEIQ; IIEGVYDEIQI; IEGVYDEIQIP; EGVYDEIQIPK; GVYDEIQIPKN; VYDEIQIPKNL; YDEIQIPKNLL; DEIQIPKNLLN; EIQIPKNLLNI; IQIPKNLLNIS; QIPKNLLNISF; IPKNLLNISFR; PKNLLNISFRS; KNLLNISFRSE; NLLNISFRSEE; LLNISFRSEEV; LNISFRSEEVA; NISFRSEEVAF; ISFRSEEVAFL; SFRSEEVAFLA; FRSEEVAFLAG; RSEEVAFLAGY; SEEVAFLAGYF; EEVAFLAGYFA; EVAFLAGYFAS; VAFLAGYFASK; AFLAGYFASKA; FLAGYFASKAS; LAGYFASKASK; AGYFASKASKT; GYFASKASKTG; YFASKASKTGK; FASKASKTGKI; ASKASKTGKIG; SKASKTGKIGF; KASKTGKIGFV; ASKTGKIGFVG; SKTGKIGFVGG; KTGKIGFVGGV; TGKIGFVGGVR; GKIGFVGGVRG; KIGFVGGVRGK; IGFVGGVRGKV; GFVGGVRGKVL; FVGGVRGKVLE; VGGVRGKVLES; GGVRGKVLESF; GVRGKVLESFM; VRGKVLESFMY; RGKVLESFMYG; GKVLESFMYGY; KVLESFMYGYE; VLESFMYGYEA; LESFMYGYEAG; ESFMYGYEAGA; SFMYGYEAGAK; FMYGYEAGAKY; MYGYEAGAKYA; YGYEAGAKYAN; GYEAGAKYANS; YEAGAKYANSN; EAGAKYANSNI; AGAKYANSNIK; GAKYANSNIKV; AKYANSNIKVV; KYANSNIKVVS; YANSNIKVVSQ; ANSNIKVVSQY; NSNIKVVSQYV; SNIKVVSQYVG; NIKVVSQYVGT; IKVVSQYVGTF; KVVSQYVGTFG; VVSQYVGTFGD; VSQYVGTFGDF; SQYVGTFGDFG; QYVGTFGDFGL; YVGTFGDFGLG; VGTFGDFGLGR; GTFGDFGLGRS; TFGDFGLGRST; FGDFGLGRSTA; GDFGLGRSTAS; DFGLGRSTASN; FGLGRSTASNM; GLGRSTASNMY; LGRSTASNMYR; GRSTASNMYRD; RSTASNMYRDG; STASNMYRDGV; TASNMYRDGVD; ASNMYRDGVDI; SNMYRDGVDII; NMYRDGVDIIF; MYRDGVDIIFA; YRDGVDIIFAA; RDGVDIIFAAA; DGVDIIFAAAG; GVDIIFAAAGL; VDIIFAAAGLS; DIIFAAAGLSG; IIFAAAGLSGI; IFAAAGLSGIG; FAAAGLSGIGV; AAAGLSGIGVI; AAGLSGIGVIE; AGLSGIGVIEA; GLSGIGVIEAA; LSGIGVIEAAK; SGIGVIEAAKE; GIGVIEAAKEL; IGVIEAAKELG; GVIEAAKELGP; VIEAAKELGPD; IEAAKELGPDH; EAAKELGPDHY; AAKELGPDHYI; AKELGPDHYII; KELGPDHYIIG; ELGPDHYIIGV; LGPDHYIIGVD; GPDHYIIGVDQ; PDHYIIGVDQD; DHYIIGVDQDQ; HYIIGVDQDQS; YIIGVDQDQSY; IIGVDQDQSYL; IGVDQDQSYLA; GVDQDQSYLAP; VDQDQSYLAPN; DQDQSYLAPNN; QDQSYLAPNNV; DQSYLAPNNVI; QSYLAPNNVIV; SYLAPNNVIVS; YLAPNNVIVSA; LAPNNVIVSAV; APNNVIVSAVK; PNNVIVSAVKK; NNVIVSAVKKV; NVIVSAVKKVD; VIVSAVKKVDS; IVSAVKKVDSL; VSAVKKVDSLM; SAVKKVDSLMY; AVKKVDSLMYS; VKKVDSLMYSL; KKVDSLMYSLT; KVDSLMYSLTK; VDSLMYSLTKK; DSLMYSLTKKY; SLMYSLTKKYL; LMYSLTKKYLE; MYSLTKKYLET; YSLTKKYLETG; SLTKKYLETGV; LTKKYLETGVL;

	TKKYLETGVLD; KKYLETGVLDG; KYLETGVLDGG; YLETGVLDGGK; LETGVLDGGKT; ETGVLDGGKTM; TGVLDGGKTMF; GVLDGGKTMFL; VLDGGKTMFLG; LDGGKTMFLGL; DGGKTMFLGLK; GGKTMFLGLKE; GKTMFLGLKED; KTMFLGLKEDG; TMFLGLKEDGL; MFLGLKEDGLG; FLGLKEDGLGL; LGLKEDGLGLV; GLKEDGLGLVL; LKEDGLGLVLN; KEDGLGLVLNE; EDGLGLVLNEN; DGLGLVLNENL; GLGLVLNENLK; LGLVLNENLKS; GLVLNENLKSN; LVLNENLKSNY; VLNENLKSNYS; LNENLKSNYSE; NENLKSNYSEI; ENLKSNYSEIY; NLKSNYSEIYN; LKSNYSEIYNK; KSNYSEIYNKS; SNYSEIYNKSL; NYSEIYNKSLK; YSEIYNKSLKI; SEIYNKSLKIG; EIYNKSLKIGQ; IYNKSLKIGQS; YNKSLKIGQSI; NKSLKIGQSIM; KSLKIGQSIMN; SLKIGQSIMNG; LKIGQSIMNGI; KIGQSIMNGII; IGQSIMNGIIK; GQSIMNGIIKV; QSIMNGIIKVP; SIMNGIIKVPY; IMNGIIKVPYD; MNGIIKVPYDK; NGIIKVPYDKV; GIIKVPYDKVS; IIKVPYDKVSY; IKVPYDKVSYF; KVPYDKVSYFV; VPYDKVSYFVL; PYDKVSYFVLQ; YDKVSYFVLQM; DKVSYFVLQME; KVSYFVLQMEN;
AAC70056.1 Decorin binding protein A; DbpA [Borrelia afzelii	SEQ ID NO 5481-6126/ 8 mers: MIKYNKII; IKYNKIIL; KYNKIILT; YNKIILTL; NKIILTLT; KIILTLTL; IILTLTLL; ILTLTLLA; LTLTLLAS; TLTLLASL; LTLLASLL; TLLASLLA; LLASLLAA; LASLLAAC; ASLLAACS; SLLAACSL; LLAACSLT; LAACSLTG; AACSLTGK; ACSLTGKA; CSLTGKAR; SLTGKARL; LTGKARLE; TGKARLES; GKARLESS; KARLESSV; ARLESSVK; RLESSVKD; LESSVKDI; ESSVKDIT; SSVKDITN; SVKDITNE; VKDITNEI; KDITNEIE; DITNEIEK; ITNEIEKA; TNEIEKAI; NEIEKAIK; EIEKAIKE; IEKAIKEA; EKAIKEAE; KAIKEAED; AIKEAEDA; IKEAEDAG; KEAEDAGV; EAEDAGVK; AEDAGVKT; EDAGVKTD; DAGVKTDA; AGVKTDAF; GVKTDAFT; VKTDAFTE; KTDAFTET; TDAFTETQ; DAFTETQT; AFTETQTG; FTETQTGG; TETQTGGK; ETQTGGKV; TQTGGKVG; QTGGKVGG; TGGKVGGS; GGKVGGSQ; GKVGGSQI; KVGGSQIR; VGGSQIRA; GGSQIRAA; GSQIRAAK; SQIRAAKI; QIRAAKIR; IRAAKIRV; RAAKIRVA; AAKIRVAD; AKIRVADL; KIRVADLT; IRVADLTI; RVADLTIK; VADLTIKF; ADLTIKFL; DLTIKFLE; LTIKFLEA; TIKFLEAT; IKFLEATE; KFLEATEE; FLEATEEE; LEATEEET; EATEEETI; ATEEETIT; TEEETITF; EEETITFK; EETITFKE; ETITFKEN; TITFKENG; ITFKENGA; TFKENGAG; FKENGAGE; KENGAGEE; ENGAGEED; NGAGEEDF; GAGEEDFS; AGEEDFSG; GEEDFSGI; EEDFSGIY; EDFSGIYD; DFSGIYDL; FSGIYDLI; SGIYDLIL; GIYDLILN; IYDLILNA; YDLILNAA; DLILNAAK; LILNAAKA; ILNAAKAV; LNAAKAVE; NAAKAVEK; AAKAVEKI; AKAVEKIG; KAVEKIGM; AVEKIGMQ; VEKIGMQG; EKIGMQGM; KIGMQGMK; IGMQGMKQ; GMQGMKQA; MQGMKQAV; QGMKQAVE; GMKQAVEE; MKQAVEEA; KQAVEEAA; QAVEEAAK; AVEEAAKE; VEEAAKEK; EEAAKEKP; EAAKEKPK; AAKEKPKT; AKEKPKTT; KEKPKTTA; EKPKTTAD; KPKTTADG; PKTTADGI; KTTADGII; TTADGIIA; TADGIIAI; ADGIIAIV; DGIIAIVK; GIIAIVKV; IIAIVKVM; IAIVKVMK; AIVKVMKA; IVKVMKAK; VKVMKAKV; KVMKAKVE; VMKAKVEN; MKAKVENI; KAKVENIK; AKVENIKE; KVENIKEK; VENIKEKQ; ENIKEKQT; NIKEKQTK; IKEKQTKN; KEKQTKNQ; EKQTKNQK; 9 mers: MIKYNKIIL; IKYNKIILT; KYNKIILTL; YNKIILTLT; NKIILTLTL; KIILTLTLL; IILTLTLLA; ILTLTLLAS; LTLTLLASL; TLTLLASLL; LTLLASLLA; TLLASLLAA; LLASLLAAC; LASLLAACS; ASLLAACSL; SLLAACSLT; LLAACSLTG; LAACSLTGK; AACSLTGKA; ACSLTGKAR; CSLTGKARL; SLTGKARLE; LTGKARLES; TGKARLESS; GKARLESSV; KARLESSVK; ARLESSVKD; RLESSVKDI; LESSVKDIT; ESSVKDITN; SSVKDITNE; SVKDITNEI; VKDITNEIE; KDITNEIEK; DITNEIEKA; ITNEIEKAI; TNEIEKAIK; NEIEKAIKE; EIEKAIKEA; IEKAIKEAE;

EKAIKEAED; KAIKEAEDA; AIKEAEDAG; IKEAEDAGV; KEAEDAGVK;
EAEDAGVKT; AEDAGVKTD; EDAGVKTDA; DAGVKTDAF; AGVKTDAFT;
GVKTDAFTE; VKTDAFTET; KTDAFTETQ; TDAFTETQT; DAFTETQTG;
AFTETQTGG; FTETQTGGK; TETQTGGKV; ETQTGGKVG; TQTGGKVGG;
QTGGKVGGS; TGGKVGGSQ; GGKVGGSQI; GKVGGSQIR; KVGGSQIRA;
VGGSQIRAA; GGSQIRAAK; GSQIRAAKI; SQIRAAKIR; QIRAAKIRV;
IRAAKIRVA; RAAKIRVAD; AAKIRVADL; AKIRVADLT; KIRVADLTI;
IRVADLTIK; RVADLTIKF; VADLTIKFL; ADLTIKFLE; DLTIKFLEA;
LTIKFLEAT; TIKFLEATE; IKFLEATEE; KFLEATEEE; FLEATEEET;
LEATEEETI; EATEEETIT; ATEEETITF; TEEETITFK; EEETITFKE;
EETITFKEN; ETITFKENG; TITFKENGA; ITFKENGAG; TFKENGAGE;
FKENGAGEE; KENGAGEED; ENGAGEEDF; NGAGEEDFS; GAGEEDFSG;
AGEEDFSGI; GEEDFSGIY; EEDFSGIYD; EDFSGIYDL; DFSGIYDLI;
FSGIYDLIL; SGIYDLILN; GIYDLILNA; IYDLILNAA; YDLILNAAK;
DLILNAAKA; LILNAAKAV; ILNAAKAVE; LNAAKAVEK; NAAKAVEKI;
AAKAVEKIG; AKAVEKIGM; KAVEKIGMQ; AVEKIGMQG; VEKIGMQGM;
EKIGMQGMK; KIGMQGMKQ; IGMQGMKQA; GMQGMKQAV; MQGMKQAVE;
QGMKQAVEE; GMKQAVEEA; MKQAVEEAA; KQAVEEAAK; QAVEEAAKE;
AVEEAAKEK; VEEAAKEKP; EEAAKEKPK; EAAKEKPKT; AAKEKPKTT;
AKEKPKTTA; KEKPKTTAD; EKPKTTADG; KPKTTADGI; PKTTADGII;
KTTADGIIA; TTADGIIAI; TADGIIAIV; ADGIIAIVK; DGIIAIVKV;
GIIAIVKVM; IIAIVKVMK; IAIVKVMKA; AIVKVMKAK; IVKVMKAKV;
VKVMKAKVE; KVMKAKVEN; VMKAKVENI; MKAKVENIK; KAKVENIKE;
AKVENIKEK; KVENIKEKQ; VENIKEKQT; ENIKEKQTK; NIKEKQTKN;
IKEKQTKNQ; KEKQTKNQK;

10 mers:
MIKYNKIILT; IKYNKIILTL; KYNKIILTLT; YNKIILTLTL; NKIILTLTLL;
KIILTLTLLA; IILTLTLLAS; ILTLTLLASL; LTLTLLASLL; TLTLLASLLA;
LTLLASLLAA; TLLASLLAAC; LLASLLAACS; LASLLAACSL; ASLLAACSLT;
SLLAACSLTG; LLAACSLTGK; LAACSLTGKA; AACSLTGKAR; ACSLTGKARL;
CSLTGKARLE; SLTGKARLES; LTGKARLESS; TGKARLESSV; GKARLESSVK;
KARLESSVKD; ARLESSVKDI; RLESSVKDIT; LESSVKDITN; ESSVKDITNE;
SSVKDITNEI; SVKDITNEIE; VKDITNEIEK; KDITNEIEKA; DITNEIEKAI;
ITNEIEKAIK; TNEIEKAIKE; NEIEKAIKEA; EIEKAIKEAE; IEKAIKEAED;
EKAIKEAEDA; KAIKEAEDAG; AIKEAEDAGV; IKEAEDAGVK; KEAEDAGVKT;
EAEDAGVKTD; AEDAGVKTDA; EDAGVKTDAF; DAGVKTDAFT; AGVKTDAFTE;
GVKTDAFTET; VKTDAFTETQ; KTDAFTETQT; TDAFTETQTG; DAFTETQTGG;
AFTETQTGGK; FTETQTGGKV; TETQTGGKVG; ETQTGGKVGG; TQTGGKVGGS;
QTGGKVGGSQ; TGGKVGGSQI; GGKVGGSQIR; GKVGGSQIRA; KVGGSQIRAA;
VGGSQIRAAK; GGSQIRAAKI; GSQIRAAKIR; SQIRAAKIRV; QIRAAKIRVA;
IRAAKIRVAD; RAAKIRVADL; AAKIRVADLT; AKIRVADLTI; KIRVADLTIK;
IRVADLTIKF; RVADLTIKFL; VADLTIKFLE; ADLTIKFLEA; DLTIKFLEAT;
LTIKFLEATE; TIKFLEATEE; IKFLEATEEE; KFLEATEEET; FLEATEEETI;
LEATEEETIT; EATEEETITF; ATEEETITFK; TEEETITFKE; EEETITFKEN;
EETITFKENG; ETITFKENGA; TITFKENGAG; ITFKENGAGE; TFKENGAGEE;
FKENGAGEED; KENGAGEEDF; ENGAGEEDFS; NGAGEEDFSG; GAGEEDFSGI;
AGEEDFSGIY; GEEDFSGIYD; EEDFSGIYDL; EDFSGIYDLI; DFSGIYDLIL;
FSGIYDLILN; SGIYDLILNA; GIYDLILNAA; IYDLILNAAK; YDLILNAAKA;
DLILNAAKAV; LILNAAKAVE; ILNAAKAVEK; LNAAKAVEKI; NAAKAVEKIG;
AAKAVEKIGM; AKAVEKIGMQ; KAVEKIGMQG; AVEKIGMQGM; VEKIGMQGMK;
EKIGMQGMKQ; KIGMQGMKQA; IGMQGMKQAV; GMQGMKQAVE; MQGMKQAVEE;
QGMKQAVEEA; GMKQAVEEAA; MKQAVEEAAK; KQAVEEAAKE; QAVEEAAKEK;
AVEEAAKEKP; VEEAAKEKPK; EEAAKEKPKT; EAAKEKPKTT; AAKEKPKTTA;
AKEKPKTTAD; KEKPKTTADG; EKPKTTADGI; KPKTTADGII; PKTTADGIIA;
KTTADGIIAI; TTADGIIAIV; TADGIIAIVK; ADGIIAIVKV; DGIIAIVKVM;
GIIAIVKVMK; IIAIVKVMKA; IAIVKVMKAK; AIVKVMKAKV; IVKVMKAKVE;

	VKVMKAKVEN; KVMKAKVENI; VMKAKVENIK; MKAKVENIKE; KAKVENIKEK; AKVENIKEKQ; KVENIKEKQT; VENIKEKQTK; ENIKEKQTKN; NIKEKQTKNQ; IKEKQTKNQK; 11 mers: MIKYNKIILTL; IKYNKIILTLT; KYNKIILTLTL; YNKIILTLTLL; NKIILTLTLLA; KIILTLTLLAS; IILTLTLLASL; ILTLTLLASLL; LTLTLLASLLA; TLTLLASLLAA; LTLLASLLAAC; TLLASLLAACS; LLASLLAACSL; LASLLAACSLT; ASLLAACSLTG; SLLAACSLTGK; LLAACSLTGKA; LAACSLTGKAR; AACSLTGKARL; ACSLTGKARLE; CSLTGKARLES; SLTGKARLESS; LTGKARLESSV; TGKARLESSVK; GKARLESSVKD; KARLESSVKDI; ARLESSVKDIT; RLESSVKDITN; LESSVKDITNE; ESSVKDITNEI; SSVKDITNEIE; SVKDITNEIEK; VKDITNEIEKA; KDITNEIEKAI; DITNEIEKAIK; ITNEIEKAIKE; TNEIEKAIKEA; NEIEKAIKEAE; EIEKAIKEAED; IEKAIKEAEDA; EKAIKEAEDAG; KAIKEAEDAGV; AIKEAEDAGVK; IKEAEDAGVKT; KEAEDAGVKTD; EAEDAGVKTDA; AEDAGVKTDAF; EDAGVKTDAFT; DAGVKTDAFTE; AGVKTDAFTET; GVKTDAFTETQ; VKTDAFTETQT; KTDAFTETQTG; TDAFTETQTGG; DAFTETQTGGK; AFTETQTGGKV; FTETQTGGKVG; TETQTGGKVGG; ETQTGGKVGGS; TQTGGKVGGSQ; QTGGKVGGSQI; TGGKVGGSQIR; GGKVGGSQIRA; GKVGGSQIRAA; KVGGSQIRAAK; VGGSQIRAAKI; GGSQIRAAKIR; GSQIRAAKIRV; SQIRAAKIRVA; QIRAAKIRVAD; IRAAKIRVADL; RAAKIRVADLT; AAKIRVADLTI; AKIRVADLTIK; KIRVADLTIKF; IRVADLTIKFL; RVADLTIKFLE; VADLTIKFLEA; ADLTIKFLEAT; DLTIKFLEATE; LTIKFLEATEE; TIKFLEATEEE; IKFLEATEEET; KFLEATEEETI; FLEATEEETIT; LEATEEETITF; EATEEETITFK; ATEEETITFKE; TEEETITFKEN; EEETITFKENG; EETITFKENGA; ETITFKENGAG; TITFKENGAGE; ITFKENGAGEE; TFKENGAGEED; FKENGAGEEDF; KENGAGEEDFS; ENGAGEEDFSG; NGAGEEDFSGI; GAGEEDFSGIY; AGEEDFSGIYD; GEEDFSGIYDL; EEDFSGIYDLI; EDFSGIYDLIL; DFSGIYDLILN; FSGIYDLILNA; SGIYDLILNAA; GIYDLILNAAK; IYDLILNAAKA; YDLILNAAKAV; DLILNAAKAVE; LILNAAKAVEK; ILNAAKAVEKI; LNAAKAVEKIG; NAAKAVEKIGM; AAKAVEKIGMQ; AKAVEKIGMQG; KAVEKIGMQGM; AVEKIGMQGMK; VEKIGMQGMKQ; EKIGMQGMKQA; KIGMQGMKQAV; IGMQGMKQAVE; GMQGMKQAVEE; MQGMKQAVEEA; QGMKQAVEEAA; GMKQAVEEAAK; MKQAVEEAAKE; KQAVEEAAKEK; QAVEEAAKEKP; AVEEAAKEKPK; VEEAAKEKPKT; EEAAKEKPKTT; EAAKEKPKTTA; AAKEKPKTTAD; AKEKPKTTADG; KEKPKTTADGI; EKPKTTADGII; KPKTTADGIIA; PKTTADGIIAI; KTTADGIIAIV; TTADGIIAIVK; TADGIIAIVKV; ADGIIAIVKVM; DGIIAIVKVMK; GIIAIVKVMKA; IIAIVKVMKAK; IAIVKVMKAKV; AIVKVMKAKVE; IVKVMKAKVEN; VKVMKAKVENI; KVMKAKVENIK; VMKAKVENIKE; MKAKVENIKEK; KAKVENIKEKQ; AKVENIKEKQT; KVENIKEKQTK; VENIKEKQTKN; ENIKEKQTKNQ; NIKEKQTKNQK;
AAC70057.1 Decorin binding protein A; DbpA [Borrelia garinii]	SEQ ID NO 6127-6836/ 8 mers: MIKYNKIL; IKYNKILL; KYNKILLK; YNKILLKL; NKILLKLS; KILLKLSL; ILLKLSLI; LLKLSLIV; LKLSLIVS; KLSLIVSL; LSLIVSLL; SLIVSLLV; LIVSLLVA; IVSLLVAC; VSLLVACG; SLLVACGL; LLVACGLT; LVACGLTG; VACGLTGE; ACGLTGET; CGLTGETK; GLTGETKI; LTGETKIR; TGETKIRL; GETKIRLE; ETKIRLES; TKIRLESS; KIRLESSA; IRLESSAQ; RLESSAQE; LESSAQEI; ESSAQEIK; SSAQEIKD; SAQEIKDE; AQEIKDEI; QEIKDEIN; EIKDEINK; IKDEINKI; KDEINKIK; DEINKIKA; EINKIKAN; INKIKANA; NKIKANAK; KIKANAKK; IKANAKKE; KANAKKEG; ANAKKEGV; NAKKEGVK; AKKEGVKF; KKEGVKFE; KEGVKFEA; EGVKFEAF; GVKFEAFT; VKFEAFTN;

KFEAFTNT; FEAFTNTQ; EAFTNTQT; AFTNTQTG; FTNTQTGS; TNTQTGSK; NTQTGSKI; TQTGSKIS; QTGSKISE; TGSKISEK; GSKISEKP; SKISEKPE; KISEKPEF; ISEKPEFI; SEKPEFIL; EKPEFILK; KPEFILKA; PEFILKAK; EFILKAKI; FILKAKIK; ILKAKIKA; LKAKIKAI; KAKIKAIQ; AKIKAIQV; KIKAIQVA; IKAIQVAE; KAIQVAER; AIQVAERF; IQVAERFV; QVAERFVK; VAERFVKA; AERFVKAI; ERFVKAIK; RFVKAIKE; FVKAIKEE; VKAIKEEA; KAIKEEAE; AIKEEAEK; IKEEAEKL; KEEAEKLK; EEAEKLKK; EAEKLKKS; AEKLKKSG; EKLKKSGS; KLKKSGSS; LKKSGSSG; KKSGSSGA; KSGSSGAF; SGSSGAFS; GSSGAFSA; SSGAFSAM; SGAFSAMY; GAFSAMYD; AFSAMYDL; FSAMYDLM; SAMYDLMI; AMYDLMID; MYDLMIDV; YDLMIDVS; DLMIDVSK; LMIDVSKP; MIDVSKPL; IDVSKPLE; DVSKPLEE; VSKPLEEI; SKPLEEIG; KPLEEIGI; PLEEIGIQ; LEEIGIQK; EEIGIQKM; EIGIQKMT; IGIQKMTG; GIQKMTGT; IQKMTGTV; QKMTGTVT; KMTGTVTK; MTGTVTKE; TGTVTKEA; GTVTKEAE; TVTKEAEK; VTKEAEKT; TKEAEKTP; KEAEKTPP; EAEKTPPT; AEKTPPTT; EKTPPTTA; KTPPTTAD; TPPTTADG; PPTTADGI; PTTADGII; TTADGIIA; TADGIIAI; ADGIIAIA; DGIIAIAQ; GIIAIAQA; IIAIAQAM; IAIAQAME; AIAQAMEE; IAQAMEEK; AQAMEEKL; QAMEEKLN; AMEEKLNN; MEEKLNNV; EEKLNNVN; EKLNNVNK; KLNNVNKK; LNNVNKKQ; NNVNKKQH; NVNKKQHD; VNKKQHDA; NKKQHDAL; KKQHDALK; KQHDALKN; QHDALKNL; HDALKNLE; DALKNLEE; ALKNLEEK; LKNLEEKA; KNLEEKAN; NLEEKANT; LEEKANTA; EEKANTAA; EKANTAAT; KANTAATT; ANTAATTT;

9 mers:
MIKYNKILL; IKYNKILLK; KYNKILLKL; YNKILLKLS; NKILLKLSL; KILLKLSLI; ILLKLSLIV; LLKLSLIVS; LKLSLIVSL; KLSLIVSLL; LSLIVSLLV; SLIVSLLVA; LIVSLLVAC; IVSLLVACG; VSLLVACGL; SLLVACGLT; LLVACGLTG; LVACGLTGE; VACGLTGET; ACGLTGETK; CGLTGETKI; GLTGETKIR; LTGETKIRL; TGETKIRLE; GETKIRLES; ETKIRLESS; TKIRLESSA; KIRLESSAQ; IRLESSAQE; RLESSAQEI; LESSAQEIK; ESSAQEIKD; SSAQEIKDE; SAQEIKDEI; AQEIKDEIN; QEIKDEINK; EIKDEINKI; IKDEINKIK; KDEINKIKA; DEINKIKAN; EINKIKANA; INKIKANAK; NKIKANAKK; KIKANAKKE; IKANAKKEG; KANAKKEGV; ANAKKEGVK; NAKKEGVKF; AKKEGVKFE; KKEGVKFEA; KEGVKFEAF; EGVKFEAFT; GVKFEAFTN; VKFEAFTNT; KFEAFTNTQ; FEAFTNTQT; EAFTNTQTG; AFTNTQTGS; FTNTQTGSK; TNTQTGSKI; NTQTGSKIS; TQTGSKISE; QTGSKISEK; TGSKISEKP; GSKISEKPE; SKISEKPEF; KISEKPEFI; ISEKPEFIL; SEKPEFILK; EKPEFILKA; KPEFILKAK; PEFILKAKI; EFILKAKIK; FILKAKIKA; ILKAKIKAI; LKAKIKAIQ; KAKIKAIQV; AKIKAIQVA; KIKAIQVAE; IKAIQVAER; KAIQVAERF; AIQVAERFV; IQVAERFVK; QVAERFVKA; VAERFVKAI; AERFVKAIK; ERFVKAIKE; RFVKAIKEE; FVKAIKEEA; VKAIKEEAE; KAIKEEAEK; AIKEEAEKL; IKEEAEKLK; KEEAEKLKK; EEAEKLKKS; EAEKLKKSG; AEKLKKSGS; EKLKKSGSS; KLKKSGSSG; LKKSGSSGA; KKSGSSGAF; KSGSSGAFS; SGSSGAFSA; GSSGAFSAM; SSGAFSAMY; SGAFSAMYD; GAFSAMYDL; AFSAMYDLM; FSAMYDLMI; SAMYDLMID; AMYDLMIDV; MYDLMIDVS; YDLMIDVSK; DLMIDVSKP; LMIDVSKPL; MIDVSKPLE; IDVSKPLEE; DVSKPLEEI; VSKPLEEIG; SKPLEEIGI; KPLEEIGIQ; PLEEIGIQK; LEEIGIQKM; EEIGIQKMT; EIGIQKMTG; IGIQKMTGT; GIQKMTGTV; IQKMTGTVT; QKMTGTVTK; KMTGTVTKE; MTGTVTKEA; TGTVTKEAE; GTVTKEAEK; TVTKEAEKT; VTKEAEKTP; TKEAEKTPP; KEAEKTPPT; EAEKTPPTT; AEKTPPTTA; EKTPPTTAD; KTPPTTADG; TPPTTADGI; PPTTADGII; PTTADGIIA; TTADGIIAI; TADGIIAIA; ADGIIAIAQ; DGIIAIAQA; GIIAIAQAM; IIAIAQAME; IAIAQAMEE; AIAQAMEEK; IAQAMEEKL; AQAMEEKLN; QAMEEKLNN; AMEEKLNNV; MEEKLNNVN; EEKLNNVNK; EKLNNVNKK; KLNNVNKKQ; LNNVNKKQH; NNVNKKQHD; NVNKKQHDA; VNKKQHDAL; NKKQHDALK; KKQHDALKN; KQHDALKNL; QHDALKNLE; HDALKNLEE; DALKNLEEK;

ALKNLEEKA; LKNLEEKAN; KNLEEKANT; NLEEKANTA; LEEKANTAA; EEKANTAAT; EKANTAATT; KANTAATTT;

10 mers:
MIKYNKILLK; IKYNKILLKL; KYNKILLKLS; YNKILLKLSL; NKILLKLSLI; KILLKLSLIV; ILLKLSLIVS; LLKLSLIVSL; LKLSLIVSLL; KLSLIVSLLV; LSLIVSLLVA; SLIVSLLVAC; LIVSLLVACG; IVSLLVACGL; VSLLVACGLT; SLLVACGLTG; LLVACGLTGE; LVACGLTGET; VACGLTGETK; ACGLTGETKI; CGLTGETKIR; GLTGETKIRL; LTGETKIRLE; TGETKIRLES; GETKIRLESS; ETKIRLESSA; TKIRLESSAQ; KIRLESSAQE; IRLESSAQEI; RLESSAQEIK; LESSAQEIKD; ESSAQEIKDE; SSAQEIKDEI; SAQEIKDEIN; AQEIKDEINK; QEIKDEINKI; EIKDEINKIK; IKDEINKIKA; KDEINKIKAN; DEINKIKANA; EINKIKANAK; INKIKANAKK; NKIKANAKKE; KIKANAKKEG; IKANAKKEGV; KANAKKEGVK; ANAKKEGVKF; NAKKEGVKFE; AKKEGVKFEA; KKEGVKFEAF; KEGVKFEAFT; EGVKFEAFTN; GVKFEAFTNT; VKFEAFTNTQ; KFEAFTNTQT; FEAFTNTQTG; EAFTNTQTGS; AFTNTQTGSK; FTNTQTGSKI; TNTQTGSKIS; NTQTGSKISE; TQTGSKISEK; QTGSKISEKP; TGSKISEKPE; GSKISEKPEF; SKISEKPEFI; KISEKPEFIL; ISEKPEFILK; SEKPEFILKA; EKPEFILKAK; KPEFILKAKI; PEFILKAKIK; EFILKAKIKA; FILKAKIKAI; ILKAKIKAIQ; LKAKIKAIQV; KAKIKAIQVA; AKIKAIQVAE; KIKAIQVAER; IKAIQVAERF; KAIQVAERFV; AIQVAERFVK; IQVAERFVKA; QVAERFVKAI; VAERFVKAIK; AERFVKAIKE; ERFVKAIKEE; RFVKAIKEEA; FVKAIKEEAE; VKAIKEEAEK; KAIKEEAEKL; AIKEEAEKLK; IKEEAEKLKK; KEEAEKLKKS; EEAEKLKKSG; EAEKLKKSGS; AEKLKKSGSS; EKLKKSGSSG; KLKKSGSSGA; LKKSGSSGAF; KKSGSSGAFS; KSGSSGAFSA; SGSSGAFSAM; GSSGAFSAMY; SSGAFSAMYD; SGAFSAMYDL; GAFSAMYDLM; AFSAMYDLMI; FSAMYDLMID; SAMYDLMIDV; AMYDLMIDVS; MYDLMIDVSK; YDLMIDVSKP; DLMIDVSKPL; LMIDVSKPLE; MIDVSKPLEE; IDVSKPLEEI; DVSKPLEEIG; VSKPLEEIGI; SKPLEEIGIQ; KPLEEIGIQK; PLEEIGIQKM; LEEIGIQKMT; EEIGIQKMTG; EIGIQKMTGT; IGIQKMTGTV; GIQKMTGTVT; IQKMTGTVTK; QKMTGTVTKE; KMTGTVTKEA; MTGTVTKEAE; TGTVTKEAEK; GTVTKEAEKT; TVTKEAEKTP; VTKEAEKTPP; TKEAEKTPPT; KEAEKTPPTT; EAEKTPPTTA; AEKTPPTTAD; EKTPPTTADG; KTPPTTADGI; TPPTTADGII; PPTTADGIIA; PTTADGIIAI; TTADGIIAIA; TADGIIAIAQ; ADGIIAIAQA; DGIIAIAQAM; GIIAIAQAME; IIAIAQAMEE; IAIAQAMEEK; AIAQAMEEKL; IAQAMEEKLN; AQAMEEKLNN; QAMEEKLNNV; AMEEKLNNVN; MEEKLNNVNK; EEKLNNVNKK; EKLNNVNKKQ; KLNNVNKKQH; LNNVNKKQHD; NNVNKKQHDA; NVNKKQHDAL; VNKKQHDALK; NKKQHDALKN; KKQHDALKNL; KQHDALKNLE; QHDALKNLEE; HDALKNLEEK; DALKNLEEKA; ALKNLEEKAN; LKNLEEKANT; KNLEEKANTA; NLEEKANTAA; LEEKANTAAT; EEKANTAATT; EKANTAATTT;

11 mers:
MIKYNKILLKL; IKYNKILLKLS; KYNKILLKLSL; YNKILLKLSLI; NKILLKLSLIV; KILLKLSLIVS; ILLKLSLIVSL; LLKLSLIVSLL; LKLSLIVSLLV; KLSLIVSLLVA; LSLIVSLLVAC; SLIVSLLVACG; LIVSLLVACGL; IVSLLVACGLT; VSLLVACGLTG; SLLVACGLTGE; LLVACGLTGET; LVACGLTGETK; VACGLTGETKI; ACGLTGETKIR; CGLTGETKIRL; GLTGETKIRLE; LTGETKIRLES; TGETKIRLESS; GETKIRLESSA; ETKIRLESSAQ; TKIRLESSAQE; KIRLESSAQEI; IRLESSAQEIK; RLESSAQEIKD; LESSAQEIKDE; ESSAQEIKDEI; SSAQEIKDEIN; SAQEIKDEINK; AQEIKDEINKI; QEIKDEINKIK; EIKDEINKIKA; IKDEINKIKAN; KDEINKIKANA; DEINKIKANAK; EINKIKANAKK; INKIKANAKKE; NKIKANAKKEG; KIKANAKKEGV; IKANAKKEGVK; KANAKKEGVKF; ANAKKEGVKFE; NAKKEGVKFEA; AKKEGVKFEAF; KKEGVKFEAFT; KEGVKFEAFTN; EGVKFEAFTNT; GVKFEAFTNTQ; VKFEAFTNTQT; KFEAFTNTQTG; FEAFTNTQTGS; EAFTNTQTGSK; AFTNTQTGSKI; FTNTQTGSKIS; TNTQTGSKISE;

	NTQTGSKISEK; TQTGSKISEKP; QTGSKISEKPE; TGSKISEKPEF; GSKISEKPEFI; SKISEKPEFIL; KISEKPEFILK; ISEKPEFILKA; SEKPEFILKAK; EKPEFILKAKI; KPEFILKAKIK; PEFILKAKIKA; EFILKAKIKAI; FILKAKIKAIQ; ILKAKIKAIQV; LKAKIKAIQVA; KAKIKAIQVAE; AKIKAIQVAER; KIKAIQVAERF; IKAIQVAERFV; KAIQVAERFVK; AIQVAERFVKA; IQVAERFVKAI; QVAERFVKAIK; VAERFVKAIKE; AERFVKAIKEE; ERFVKAIKEEA; RFVKAIKEEAE; FVKAIKEEAEK; VKAIKEEAEKL; KAIKEEAEKLK; AIKEEAEKLKK; IKEEAEKLKKS; KEEAEKLKKSG; EEAEKLKKSGS; EAEKLKKSGSS; AEKLKKSGSSG; EKLKKSGSSGA; KLKKSGSSGAF; LKKSGSSGAFS; KKSGSSGAFSA; KSGSSGAFSAM; SGSSGAFSAMY; GSSGAFSAMYD; SSGAFSAMYDL; SGAFSAMYDLM; GAFSAMYDLMI; AFSAMYDLMID; FSAMYDLMIDV; SAMYDLMIDVS; AMYDLMIDVSK; MYDLMIDVSKP; YDLMIDVSKPL; DLMIDVSKPLE; LMIDVSKPLEE; MIDVSKPLEEI; IDVSKPLEEIG; DVSKPLEEIGI; VSKPLEEIGIQ; SKPLEEIGIQK; KPLEEIGIQKM; PLEEIGIQKMT; LEEIGIQKMTG; EEIGIQKMTGT; EIGIQKMTGTV; IGIQKMTGTVT; GIQKMTGTVTK; IQKMTGTVTKE; QKMTGTVTKEA; KMTGTVTKEAE; MTGTVTKEAEK; TGTVTKEAEKT; GTVTKEAEKTP; TVTKEAEKTPP; VTKEAEKTPPT; TKEAEKTPPTT; KEAEKTPPTTA; EAEKTPPTTAD; AEKTPPTTADG; EKTPPTTADGI; KTPPTTADGII; TPPTTADGIIA; PPTTADGIIAI; PTTADGIIAIA; TTADGIIAIAQ; TADGIIAIAQA; ADGIIAIAQAM; DGIIAIAQAME; GIIAIAQAMEE; IIAIAQAMEEK; IAIAQAMEEKL; AIAQAMEEKLN; IAQAMEEKLNN; AQAMEEKLNNV; QAMEEKLNNVN; AMEEKLNNVNK; MEEKLNNVNKK; EEKLNNVNKKQ; EKLNNVNKKQH; KLNNVNKKQHD; LNNVNKKQHDA; NNVNKKQHDAL; NVNKKQHDALK; VNKKQHDALKN; NKKQHDALKNL; KKQHDALKNLE; KQHDALKNLEE; QHDALKNLEEK; HDALKNLEEKA; DALKNLEEKAN; ALKNLEEKANT; LKNLEEKANTA; KNLEEKANTAA; NLEEKANTAAT; LEEKANTAATT; EEKANTAATTT;
AAC70021.1 Decorin binding protein B; DbpB [Borrelia burgdorferi]	SEQ ID NO 6837-7522/ 8 mers: SIVIALFF; IVIALFFK; VIALFFKL; IALFFKLL; ALFFKLLV; LFFKLLVA; FFKLLVAC; FKLLVACS; KLLVACSI; LLVACSIG; LVACSIGL; VACSIGLV; ACSIGLVE; CSIGLVER; SIGLVERT; IGLVERTN; GLVERTNA; LVERTNAA; VERTNAAL; ERTNAALE; RTNAALES; TNAALESS; NAALESSS; AALESSSK; ALESSSKD; LESSSKDL; ESSSKDLK; SSSKDLKN; SSKDLKNK; SKDLKNKI; KDLKNKIL; DLKNKILK; LKNKILKI; KNKILKIK; NKILKIKK; KILKIKKE; ILKIKKEA; LKIKKEAT; KIKKEATG; IKKEATGK; KKEATGKG; KEATGKGV; EATGKGVL; ATGKGVLF; TGKGVLFE; GKGVLFEA; KGVLFEAF; GVLFEAFT; VLFEAFTG; LFEAFTGL; FEAFTGLK; EAFTGLKT; AFTGLKTG; FTGLKTGS; TGLKTGSK; GLKTGSKV; LKTGSKVT; KTGSKVTS; TGSKVTSG; GSKVTSGG; SKVTSGGL; KVTSGGLA; VTSGGLAL; TSGGLALR; SGGLALRE; GGLALREA; GLALREAK; LALREAKV; ALREAKVQ; LREAKVQA; REAKVQAI; EAKVQAIV; AKVQAIVE; KVQAIVET; VQAIVETG; QAIVETGK; AIVETGKF; IVETGKFL; VETGKFLK; ETGKFLKI; TGKFLKII; GKFLKIIE; KFLKIIEE; FLKIIEEE; LKIIEEEA; KIIEEEAL; IIEEEALK; IEEEALKL; EEEALKLK; EEALKLKE; EALKLKET; ALKLKETG; LKLKETGN; KLKETGNS; LKETGNSG; KETGNSGQ; ETGNSGQF; TGNSGQFL; GNSGQFLA; NSGQFLAM; SGQFLAMF; GQFLAMFD; QFLAMFDL; FLAMFDLM; LAMFDLML; AMFDLMLE; MFDLMLEV; FDLMLEVV; DLMLEVVE; LMLEVVES; MLEVVESL; LEVVESLE; EVVESLED; VVESLEDV; VESLEDVG; ESLEDVGI; SLEDVGII; LEDVGIIG; EDVGIIGL; DVGIIGLK; VGIIGLKA; GIIGLKAR; IIGLKARV; IGLKARVL; GLKARVLE; LKARVLEE; KARVLEES; ARVLEESK; RVLEESKN; VLEESKNN; LEESKNNP; EESKNNPI; ESKNNPIN; SKNNPINT; KNNPINTA; NNPINTAE; NPINTAER; PINTAERL; INTAERLL; NTAERLLA; TAERLLAA; AERLLAAK; ERLLAAKA; RLLAAKAQ; LLAAKAQI; LAAKAQIE; AAKAQIEN; AKAQIENQ; KAQIENQL; AQIENQLK;

	QIENQLKV; IENQLKVV; ENQLKVVK; NQLKVVKE; QLKVVKEK; LKVVKEKQ; KVVKEKQN; VVKEKQNI; VKEKQNIE; KEKQNIEN; EKQNIENG; KQNIENGG; QNIENGGE; NIENGGEK; IENGGEKK; ENGGEKKN; NGGEKKNN; GGEKKNNK; GEKKNNKS; EKKNNKSK; KKNNKSKK; KNNKSKKK; NNKSKKKK; 9 mers: SIVIALFFK; IVIALFFKL; VIALFFKLL; IALFFKLLV; ALFFKLLVA; LFFKLLVAC; FFKLLVACS; FKLLVACSI; KLLVACSIG; LLVACSIGL; LVACSIGLV; VACSIGLVE; ACSIGLVER; CSIGLVERT; SIGLVERTN; IGLVERTNA; GLVERTNAA; LVERTNAAL; VERTNAALE; ERTNAALES; RTNAALESS; TNAALESSS; NAALESSSK; AALESSSKD; ALESSSKDL; LESSSKDLK; ESSSKDLKN; SSSKDLKNK; SSKDLKNKI; SKDLKNKIL; KDLKNKILK; DLKNKILKI; LKNKILKIK; KNKILKIKK; NKILKIKKE; KILKIKKEA; ILKIKKEAT; LKIKKEATG; KIKKEATGK; IKKEATGKG; KKEATGKGV; KEATGKGVL; EATGKGVLF; ATGKGVLFE; TGKGVLFEA; GKGVLFEAF; KGVLFEAFT; GVLFEAFTG; VLFEAFTGL; LFEAFTGLK; FEAFTGLKT; EAFTGLKTG; AFTGLKTGS; FTGLKTGSK; TGLKTGSKV; GLKTGSKVT; LKTGSKVTS; KTGSKVTSG; TGSKVTSGG; GSKVTSGGL; SKVTSGGLA; KVTSGGLAL; VTSGGLALR; TSGGLALRE; SGGLALREA; GGLALREAK; GLALREAKV; LALREAKVQ; ALREAKVQA; LREAKVQAI; REAKVQAIV; EAKVQAIVE; AKVQAIVET; KVQAIVETG; VQAIVETGK; QAIVETGKF; AIVETGKFL; IVETGKFLK; VETGKFLKI; ETGKFLKII; TGKFLKIIE; GKFLKIIEE; KFLKIIEEE; FLKIIEEEA; LKIIEEEAL; KIIEEEALK; IIEEEALKL; IEEEALKLK; EEEALKLKE; EEALKLKET; EALKLKETG; ALKLKETGN; LKLKETGNS; KLKETGNSG; LKETGNSGQ; KETGNSGQF; ETGNSGQFL; TGNSGQFLA; GNSGQFLAM; NSGQFLAMF; SGQFLAMFD; GQFLAMFDL; QFLAMFDLM; FLAMFDLML; LAMFDLMLE; AMFDLMLEV; MFDLMLEVV; FDLMLEVVE; DLMLEVVES; LMLEVVESL; MLEVVESLE; LEVVESLED; EVVESLEDV; VVESLEDVG; VESLEDVGI; ESLEDVGII; SLEDVGIIG; LEDVGIIGL; EDVGIIGLK; DVGIIGLKA; VGIIGLKAR; GIIGLKARV; IIGLKARVL; IGLKARVLE; GLKARVLEE; LKARVLEES; KARVLEESK; ARVLEESKN; RVLEESKNN; VLEESKNNP; LEESKNNPI; EESKNNPIN; ESKNNPINT; SKNNPINTA; KNNPINTAE; NNPINTAER; NPINTAERL; PINTAERLL; INTAERLLA; NTAERLLAA; TAERLLAAK; AERLLAAKA; ERLLAAKAQ; RLLAAKAQI; LLAAKAQIE; LAAKAQIEN; AAKAQIENQ; AKAQIENQL; KAQIENQLK; AQIENQLKV; QIENQLKVV; IENQLKVVK; ENQLKVVKE; NQLKVVKEK; QLKVVKEKQ; LKVVKEKQN; KVVKEKQNI; VVKEKQNIE; VKEKQNIEN; KEKQNIENG; EKQNIENGG; KQNIENGGE; QNIENGGEK; NIENGGEKK; IENGGEKKN; ENGGEKKNN; NGGEKKNNK; GGEKKNNKS; GEKKNNKSK; EKKNNKSKK; KKNNKSKKK; KNNKSKKKK; 10 mers: SIVIALFFKL; IVIALFFKLL; VIALFFKLLV; IALFFKLLVA; ALFFKLLVAC; LFFKLLVACS; FFKLLVACSI; FKLLVACSIG; KLLVACSIGL; LLVACSIGLV; LVACSIGLVE; VACSIGLVER; ACSIGLVERT; CSIGLVERTN; SIGLVERTNA; IGLVERTNAA; GLVERTNAAL; LVERTNAALE; VERTNAALES; ERTNAALESS; RTNAALESSS; TNAALESSSK; NAALESSSKD; AALESSSKDL; ALESSSKDLK; LESSSKDLKN; ESSSKDLKNK; SSSKDLKNKI; SSKDLKNKIL; SKDLKNKILK; KDLKNKILKI; DLKNKILKIK; LKNKILKIKK; KNKILKIKKE; NKILKIKKEA; KILKIKKEAT; ILKIKKEATG; LKIKKEATGK; KIKKEATGKG; IKKEATGKGV; KKEATGKGVL; KEATGKGVLF; EATGKGVLFE; ATGKGVLFEA; TGKGVLFEAF; GKGVLFEAFT; KGVLFEAFTG; GVLFEAFTGL; VLFEAFTGLK; LFEAFTGLKT; FEAFTGLKTG; EAFTGLKTGS; AFTGLKTGSK; FTGLKTGSKV; TGLKTGSKVT; GLKTGSKVTS; LKTGSKVTSG; KTGSKVTSGG; TGSKVTSGGL; GSKVTSGGLA; SKVTSGGLAL; KVTSGGLALR; VTSGGLALRE; TSGGLALREA; SGGLALREAK; GGLALREAKV; GLALREAKVQ; LALREAKVQA; ALREAKVQAI; LREAKVQAIV;

REAKVQAIVE; EAKVQAIVET; AKVQAIVETG; KVQAIVETGK; VQAIVETGKF; QAIVETGKFL; AIVETGKFLK; IVETGKFLKI; VETGKFLKII; ETGKFLKIIE; TGKFLKIIEE; GKFLKIIEEE; KFLKIIEEEA; FLKIIEEEAL; LKIIEEEALK; KIIEEEALKL; IIEEEALKLK; IEEEALKLKE; EEEALKLKET; EEALKLKETG; EALKLKETGN; ALKLKETGNS; LKLKETGNSG; KLKETGNSGQ; LKETGNSGQF; KETGNSGQFL; ETGNSGQFLA; TGNSGQFLAM; GNSGQFLAMF; NSGQFLAMFD; SGQFLAMFDL; GQFLAMFDLM; QFLAMFDLML; FLAMFDLMLE; LAMFDLMLEV; AMFDLMLEVV; MFDLMLEVVE; FDLMLEVVES; DLMLEVVESL; LMLEVVESLE; MLEVVESLED; LEVVESLEDV; EVVESLEDVG; VVESLEDVGI; VESLEDVGII; ESLEDVGIIG; SLEDVGIIGL; LEDVGIIGLK; EDVGIIGLKA; DVGIIGLKAR; VGIIGLKARV; GIIGLKARVL; IIGLKARVLE; IGLKARVLEE; GLKARVLEES; LKARVLEESK; KARVLEESKN; ARVLEESKNN; RVLEESKNNP; VLEESKNNPI; LEESKNNPIN; EESKNNPINT; ESKNNPINTA; SKNNPINTAE; KNNPINTAER; NNPINTAERL; NPINTAERLL; PINTAERLLA; INTAERLLAA; NTAERLLAAK; TAERLLAAKA; AERLLAAKAQ; ERLLAAKAQI; RLLAAKAQIE; LLAAKAQIEN; LAAKAQIENQ; AAKAQIENQL; AKAQIENQLK; KAQIENQLKV; AQIENQLKVV; QIENQLKVVK; IENQLKVVKE; ENQLKVVKEK; NQLKVVKEKQ; QLKVVKEKQN; LKVVKEKQNI; KVVKEKQNIE; VVKEKQNIEN; VKEKQNIENG; KEKQNIENGG; EKQNIENGGE; KQNIENGGEK; QNIENGGEKK; NIENGGEKKN; IENGGEKKNN; ENGGEKKNNK; NGGEKKNNKS; GGEKKNNKSK; GEKKNNKSKK; EKKNNKSKKK; KKNNKSKKKK;

11 mers:
SIVIALFFKLL; IVIALFFKLLV; VIALFFKLLVA; IALFFKLLVAC; ALFFKLLVACS; LFFKLLVACSI; FFKLLVACSIG; FKLLVACSIGL; KLLVACSIGLV; LLVACSIGLVE; LVACSIGLVER; VACSIGLVERT; ACSIGLVERTN; CSIGLVERTNA; SIGLVERTNAA; IGLVERTNAAL; GLVERTNAALE; LVERTNAALES; VERTNAALESS; ERTNAALESSS; RTNAALESSSK; TNAALESSSKD; NAALESSSKDL; AALESSSKDLK; ALESSSKDLKN; LESSSKDLKNK; ESSSKDLKNKI; SSSKDLKNKIL; SSKDLKNKILK; SKDLKNKILKI; KDLKNKILKIK; DLKNKILKIKK; LKNKILKIKKE; KNKILKIKKEA; NKILKIKKEAT; KILKIKKEATG; ILKIKKEATGK; LKIKKEATGKG; KIKKEATGKGV; IKKEATGKGVL; KKEATGKGVLF; KEATGKGVLFE; EATGKGVLFEA; ATGKGVLFEAF; TGKGVLFEAFT; GKGVLFEAFTG; KGVLFEAFTGL; GVLFEAFTGLK; VLFEAFTGLKT; LFEAFTGLKTG; FEAFTGLKTGS; EAFTGLKTGSK; AFTGLKTGSKV; FTGLKTGSKVT; TGLKTGSKVTS; GLKTGSKVTSG; LKTGSKVTSGG; KTGSKVTSGGL; TGSKVTSGGLA; GSKVTSGGLAL; SKVTSGGLALR; KVTSGGLALRE; VTSGGLALREA; TSGGLALREAK; SGGLALREAKV; GGLALREAKVQ; GLALREAKVQA; LALREAKVQAI; ALREAKVQAIV; LREAKVQAIVE; REAKVQAIVET; EAKVQAIVETG; AKVQAIVETGK; KVQAIVETGKF; VQAIVETGKFL; QAIVETGKFLK; AIVETGKFLKI; IVETGKFLKII; VETGKFLKIIE; ETGKFLKIIEE; TGKFLKIIEEE; GKFLKIIEEEA; KFLKIIEEEAL; FLKIIEEEALK; LKIIEEEALKL; KIIEEEALKLK; IIEEEALKLKE; IEEEALKLKET; EEEALKLKETG; EEALKLKETGN; EALKLKETGNS; ALKLKETGNSG; LKLKETGNSGQ; KLKETGNSGQF; LKETGNSGQFL; KETGNSGQFLA; ETGNSGQFLAM; TGNSGQFLAMF; GNSGQFLAMFD; NSGQFLAMFDL; SGQFLAMFDLM; GQFLAMFDLML; QFLAMFDLMLE; FLAMFDLMLEV; LAMFDLMLEVV; AMFDLMLEVVE; MFDLMLEVVES; FDLMLEVVESL; DLMLEVVESLE; LMLEVVESLED; MLEVVESLEDV; LEVVESLEDVG; EVVESLEDVGI; VVESLEDVGII; VESLEDVGIIG; ESLEDVGIIGL; SLEDVGIIGLK; LEDVGIIGLKA; EDVGIIGLKAR; DVGIIGLKARV; VGIIGLKARVL; GIIGLKARVLE; IIGLKARVLEE; IGLKARVLEES; GLKARVLEESK; LKARVLEESKN; KARVLEESKNN; ARVLEESKNNP; RVLEESKNNPI; VLEESKNNPIN; LEESKNNPINT; EESKNNPINTA; ESKNNPINTAE; SKNNPINTAER; KNNPINTAERL; NNPINTAERLL;

	NPINTAERLLA; PINTAERLLAA; INTAERLLAAK; NTAERLLAAKA; TAERLLAAKAQ; AERLLAAKAQI; ERLLAAKAQIE; RLLAAKAQIEN; LLAAKAQIENQ; LAAKAQIENQL; AAKAQIENQLK; AKAQIENQLKV; KAQIENQLKVV; AQIENQLKVVK; QIENQLKVVKE; IENQLKVVKEK; ENQLKVVKEKQ; NQLKVVKEKQN; QLKVVKEKQNI; LKVVKEKQNIE; KVVKEKQNIEN; VVKEKQNIENG; VKEKQNIENGG; KEKQNIENGGE; EKQNIENGGEK; KQNIENGGEKK; QNIENGGEKKN; NIENGGEKKNN; IENGGEKKNNK; ENGGEKKNNKS; NGGEKKNNKSK; GGEKKNNKSKK; GEKKNNKSKKK; EKKNNKSKKKK;
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31]	SEQ ID NO 7523-10087/ 8 mers: MILIFYFK; ILIFYFKQ; LIFYFKQI; IFYFKQIA; FYFKQIAL; YFKQIALF; FKQIALFI; KQIALFII; QIALFIIF; IALFIIFR; ALFIIFRL; LFIIFRLC; FIIFRLCY; IIFRLCYI; IFRLCYII; FRLCYIIK; RLCYIIKK; LCYIIKKV; CYIIKKVK; YIIKKVKI; IIKKVKIK; IKKVKIKL; KKVKIKLK; KVKIKLKR; VKIKLKRK; KIKLKRKS; IKLKRKSC; KLKRKSCM; LKRKSCMK; KRKSCMKK; RKSCMKKQ; KSCMKKQF; SCMKKQFD; CMKKQFDT; MKKQFDTE; KKQFDTEV; KQFDTEVN; QFDTEVND; FDTEVNDL; DTEVNDLL; TEVNDLLY; EVNDLLYL; VNDLLYLI; NDLLYLII; DLLYLIIH; LLYLIIHS; LYLIIHSL; YLIIHSLY; LIIHSLYS; IIHSLYSH; IHSLYSHK; HSLYSHKE; SLYSHKEI; LYSHKEIF; YSHKEIFL; SHKEIFLR; HKEIFLRE; KEIFLREL; EIFLRELI; IFLRELIS; FLRELISN; LRELISNA; RELISNAS; ELISNASD; LISNASDA; ISNASDAI; SNASDAID; NASDAIDK; ASDAIDKL; SDAIDKLK; DAIDKLKF; AIDKLKFL; IDKLKFLS; DKLKFLSL; KLKFLSLT; LKFLSLTN; KFLSLTNE; FLSLTNEK; LSLTNEKF; SLTNEKFK; LTNEKFKN; TNEKFKNI; NEKFKNIA; EKFKNIAL; KFKNIALE; FKNIALEP; KNIALEPK; NIALEPKI; IALEPKIE; ALEPKIEI; LEPKIEIS; EPKIEISF; PKIEISFD; KIEISFDD; IEISFDDK; EISFDDKS; ISFDDKSI; SFDDKSIL; FDDKSILI; DDKSILIK; DKSILIKD; KSILIKDN; SILIKDNG; ILIKDNGI; LIKDNGIG; IKDNGIGM; KDNGIGMD; DNGIGMDE; NGIGMDEQ; GIGMDEQD; IGMDEQDL; GMDEQDLT; MDEQDLTN; DEQDLTNH; EQDLTNHL; QDLTNHLG; DLTNHLGV; LTNHLGVI; TNHLGVIA; NHLGVIAK; HLGVIAKS; LGVIAKSG; GVIAKSGT; VIAKSGTK; IAKSGTKE; AKSGTKEF; KSGTKEFI; SGTKEFIN; GTKEFINN; TKEFINNL; KEFINNLK; EFINNLKQ; FINNLKQD; INNLKQDE; NNLKQDEK; NLKQDEKK; LKQDEKKS; KQDEKKSA; QDEKKSAS; DEKKSASL; EKKSASLI; KKSASLIG; KSASLIGQ; SASLIGQF; ASLIGQFG; SLIGQFGV; LIGQFGVG; IGQFGVGF; GQFGVGFY; QFGVGFYS; FGVGFYSA; GVGFYSAF; VGFYSAFI; GFYSAFIV; FYSAFIVS; YSAFIVSE; SAFIVSEK; AFIVSEKV; FIVSEKVE; IVSEKVEV; VSEKVEVT; SEKVEVTS; EKVEVTSK; KVEVTSKK; VEVTSKKA; EVTSKKAL; VTSKKALE; TSKKALES; SKKALESD; KKALESDA; KALESDAY; ALESDAYI; LESDAYIW; ESDAYIWS; SDAYIWSS; DAYIWSSD; AYIWSSDG; YIWSSDGK; IWSSDGKT; WSSDGKTG; SSDGKTGY; SDGKTGYE; DGKTGYEI; GKTGYEIE; KTGYEIEK; TGYEIEKA; GYEIEKAK; YEIEKAKK; EIEKAKKE; IEKAKKEE; EKAKKEES; KAKKEESG; AKKEESGT; KKEESGTE; KEESGTEI; EESGTEIK; ESGTEIKL; SGTEIKLY; GTEIKLYL; TEIKLYLN; EIKLYLNK; IKLYLNKE; KLYLNKEG; LYLNKEGL; YLNKEGLE; LNKEGLEY; NKEGLEYA; KEGLEYAN; EGLEYANK; GLEYANKW; LEYANKWK; EYANKWKI; YANKWKIQ; ANKWKIQE; NKWKIQEI; KWKIQEII; WKIQEIIK; KIQEIIKK; IQEIIKKY; QEIIKKYS; EIIKKYSN; IIKKYSNH; IKKYSNHI; KKYSNHIN; KYSNHINY; YSNHINYP; SNHINYPI; NHINYPIY; HINYPIYI; INYPIYIK; NYPIYIKY; YPIYIKYS; PIYIKYSE; IYIKYSEP; YIKYSEPI; IKYSEPIM; KYSEPIMK; YSEPIMKD; SEPIMKDG; EPIMKDGK; PIMKDGKQ; IMKDGKQE; MKDGKQEG; KDGKQEGI; DGKQEGIE; GKQEGIEE; KQEGIEEK; QEGIEEKE; EGIEEKEE; GIEEKEEK; IEEKEEKL; EEKEEKLN; EKEEKLNE; KEEKLNET; EEKLNETT; EKLNETTA; KLNETTAL; LNETTALW; NETTALWT; ETTALWTK; TTALWTKN; TALWTKNK; ALWTKNKS; LWTKNKSE; WTKNKSEI; TKNKSEIK; KNKSEIKA; NKSEIKAE; KSEIKAEE; SEIKAEEY;

	EIKAEEYN; IKAEEYNE; KAEEYNEF; AEEYNEFY; EEYNEFYK; EYNEFYKN; YNEFYKNT; NEFYKNTT; EFYKNTTF; FYKNTTFD; YKNTTFDY; KNTTFDYE; NTTFDYEN; TTFDYENP; TFDYENPL; FDYENPLM; DYENPLMH; YENPLMHI; ENPLMHIH; NPLMHIHT; PLMHIHTK; LMHIHTKA; MHIHTKAE; HIHTKAEG; IHTKAEGN; HTKAEGNL; TKAEGNLE; KAEGNLEY; AEGNLEYT; EGNLEYTN; GNLEYTNL; NLEYTNLF; LEYTNLFY; EYTNLFYV; YTNLFYVP; TNLFYVPS; NLFYVPSK; LFYVPSKA; FYVPSKAP; YVPSKAPY; VPSKAPYD; PSKAPYDL; SKAPYDLY; KAPYDLYY; APYDLYYP; PYDLYYPN; YDLYYPNT; DLYYPNTK; LYYPNTKP; YYPNTKPG; YPNTKPGV; PNTKPGVK; NTKPGVKL; TKPGVKLF; KPGVKLFI; PGVKLFIN; GVKLFINR; VKLFINRI; KLFINRIF; LFINRIFI; FINRIFIT; INRIFITD; NRIFITDS; RIFITDSE; IFITDSEG; FITDSEGS; ITDSEGSL; TDSEGSLL; DSEGSLLP; SEGSLLPN; EGSLLPNY; GSLLPNYL; SLLPNYLR; LLPNYLRF; LPNYLRFI; PNYLRFIK; NYLRFIKG; YLRFIKGI; LRFIKGII; RFIKGIID; FIKGIIDC; IKGIIDCQ; KGIIDCQD; GIIDCQDL; IIDCQDLP; IDCQDLPL; DCQDLPLN; CQDLPLNV; QDLPLNVS; DLPLNVSR; LPLNVSRE; PLNVSREI; LNVSREIL; NVSREILQ; VSREILQQ; SREILQQN; REILQQNK; EILQQNKI; ILQQNKIL; LQQNKILS; QQNKILSK; QNKILSKI; NKILSKIK; KILSKIKS; ILSKIKSS; LSKIKSSS; SKIKSSSV; KIKSSSVK; IKSSSVKK; KSSSVKKI; SSSVKKIL; SSVKKILS; SVKKILSE; VKKILSEL; KKILSELE; KILSELEK; ILSELEKL; LSELEKLS; SELEKLSK; ELEKLSKK; LEKLSKKN; EKLSKKNP; KLSKKNPE; LSKKNPEK; SKKNPEKF; KKNPEKFS; KNPEKFSE; NPEKFSEF; PEKFSEFS; EKFSEFSK; KFSEFSKE; FSEFSKEF; SEFSKEFG; EFSKEFGR; FSKEFGRC; SKEFGRCI; KEFGRCIK; EFGRCIKE; FGRCIKEG; GRCIKEGV; RCIKEGVY; CIKEGVYS; IKEGVYSD; KEGVYSDF; EGVYSDFE; GVYSDFEN; VYSDFENR; YSDFENRE; SDFENREK; DFENREKL; FENREKLI; ENREKLIS; NREKLISL; REKLISLI; EKLISLIR; KLISLIRF; LISLIRFK; ISLIRFKS; SLIRFKSS; LIRFKSSS; IRFKSSSV; RFKSSSVD; FKSSSVDG; KSSSVDGF; SSSVDGFV; SSVDGFVS; SVDGFVSF; VDGFVSFK; DGFVSFKE; GFVSFKEY; FVSFKEYK; VSFKEYKE; SFKEYKER; FKEYKERM; KEYKERMN; EYKERMNE; YKERMNES; KERMNESQ; ERMNESQK; RMNESQKS; MNESQKSI; NESQKSIY; ESQKSIYY; SQKSIYYI; QKSIYYIT; KSIYYITG; SIYYITGG; IYYITGGK; YYITGGKE; YITGGKEN; ITGGKENI; TGGKENIL; GGKENILK; GKENILKE; KENILKEN; ENILKENP; NILKENPI; ILKENPIV; LKENPIVA; KENPIVAA; ENPIVAAY; NPIVAAYK; PIVAAYKE; IVAAYKEK; VAAYKEKG; AAYKEKGF; AYKEKGFE; YKEKGFEI; KEKGFEIL; EKGFEILI; KGFEILIM; GFEILIMD; FEILIMDD; EILIMDDE; ILIMDDEL; LIMDDELD; IMDDELDE; MDDELDEA; DDELDEAI; DELDEAIL; ELDEAILN; LDEAILNL; DEAILNLI; EAILNLIP; AILNLIPE; ILNLIPEY; LNLIPEYE; NLIPEYEG; LIPEYEGL; IPEYEGLK; PEYEGLKL; EYEGLKLK; YEGLKLKA; EGLKLKAI; GLKLKAIN; LKLKAINK; KLKAINKN; LKAINKNE; KAINKNET; AINKNETS; INKNETSN; NKNETSNE; KNETSNEL; NETSNELK; ETSNELKD; TSNELKDE; SNELKDEN; NELKDENF; ELKDENFK; LKDENFKK; KDENFKKI; DENFKKIE; ENFKKIEE; NFKKIEEE; FKKIEEEF; KKIEEEFK; KIEEEFKD; IEEEFKDT; EEEFKDTL; EEFKDTLT; EFKDTLTK; FKDTLTKV; KDTLTKVK; DTLTKVKE; TLTKVKEI; LTKVKEIL; TKVKEILK; KVKEILKD; VKEILKDH; KEILKDHI; EILKDHIK; ILKDHIKE; LKDHIKEV; KDHIKEVN; DHIKEVNL; HIKEVNLS; IKEVNLSA; KEVNLSAT; EVNLSATL; VNLSATLI; NLSATLIK; LSATLIKE; SATLIKEP; ATLIKEPS; TLIKEPSA; LIKEPSAI; IKEPSAII; KEPSAIII; EPSAIIID; PSAIIIDS; SAIIIDSN; AIIIDSND; IIIDSNDP; IIDSNDPT; IDSNDPTY; DSNDPTYQ; SNDPTYQM; NDPTYQMQ; DPTYQMQK; PTYQMQKI; TYQMQKIM; YQMQKIML; QMQKIMLS; MQKIMLSM; QKIMLSMG; KIMLSMGQ; IMLSMGQE; MLSMGQEV; LSMGQEVK; SMGQEVKE; MGQEVKEI; GQEVKEIK; QEVKEIKP; EVKEIKPI; VKEIKPIL; KEIKPILE; EIKPILEL; IKPILELN; KPILELNP; PILELNPN; ILELNPNN; LELNPNNK; ELNPNNKI; LNPNNKIV; NPNNKIVQ; PNNKIVQN; NNKIVQNL; NKIVQNLK; KIVQNLKN; IVQNLKNL; VQNLKNLE; QNLKNLEP; NLKNLEPE; LKNLEPEK; KNLEPEKL; NLEPEKLE; LEPEKLEK; EPEKLEKI; PEKLEKIS; EKLEKISI; KLEKISIL; LEKISILL;

EKISILLF; KISILLFE; ISILLFEE; SILLFEEA; ILLFEEAM; LLFEEAML; LFEEAMLT; FEEAMLTS; EEAMLTSG; EAMLTSGM; AMLTSGMP; MLTSGMPS; LTSGMPSK; TSGMPSKN; SGMPSKNP; GMPSKNPG; MPSKNPGK; PSKNPGKF; SKNPGKFI; KNPGKFIN; NPGKFINI; PGKFINII; GKFINIIN; KFINIINE; FINIINEF; INIINEFI; NIINEFIE; IINEFIEK; INEFIEKD; NEFIEKDF; EFIEKDFL;

9 mers:
MILIFYFKQ; ILIFYFKQI; LIFYFKQIA; IFYFKQIAL; FYFKQIALF; YFKQIALFI; FKQIALFII; KQIALFIIF; QIALFIIFR; IALFIIFRL; ALFIIFRLC; LFIIFRLCY; FIIFRLCYI; IIFRLCYII; IFRLCYIIK; FRLCYIIKK; RLCYIIKKV; LCYIIKKVK; CYIIKKVKI; YIIKKVKIK; IIKKVKIKL; IKKVKIKLK; KKVKIKLKR; KVKIKLKRK; VKIKLKRKS; KIKLKRKSC; IKLKRKSCM; KLKRKSCMK; LKRKSCMKK; KRKSCMKKQ; RKSCMKKQF; KSCMKKQFD; SCMKKQFDT; CMKKQFDTE; MKKQFDTEV; KKQFDTEVN; KQFDTEVND; QFDTEVNDL; FDTEVNDLL; DTEVNDLLY; TEVNDLLYL; EVNDLLYLI; VNDLLYLII; NDLLYLIIH; DLLYLIIHS; LLYLIIHSL; LYLIIHSLY; YLIIHSLYS; LIIHSLYSH; IIHSLYSHK; IHSLYSHKE; HSLYSHKEI; SLYSHKEIF; LYSHKEIFL; YSHKEIFLR; SHKEIFLRE; HKEIFLREL; KEIFLRELI; EIFLRELIS; IFLRELISN; FLRELISNA; LRELISNAS; RELISNASD; ELISNASDA; LISNASDAI; ISNASDAID; SNASDAIDK; NASDAIDKL; ASDAIDKLK; SDAIDKLKF; DAIDKLKFL; AIDKLKFLS; IDKLKFLSL; DKLKFLSLT; KLKFLSLTN; LKFLSLTNE; KFLSLTNEK; FLSLTNEKF; LSLTNEKFK; SLTNEKFKN; LTNEKFKNI; TNEKFKNIA; NEKFKNIAL; EKFKNIALE; KFKNIALEP; FKNIALEPK; KNIALEPKI; NIALEPKIE; IALEPKIEI; ALEPKIEIS; LEPKIEISF; EPKIEISFD; PKIEISFDD; KIEISFDDK; IEISFDDKS; EISFDDKSI; ISFDDKSIL; SFDDKSILI; FDDKSILIK; DDKSILIKD; DKSILIKDN; KSILIKDNG; SILIKDNGI; ILIKDNGIG; LIKDNGIGM; IKDNGIGMD; KDNGIGMDE; DNGIGMDEQ; NGIGMDEQD; GIGMDEQDL; IGMDEQDLT; GMDEQDLTN; MDEQDLTNH; DEQDLTNHL; EQDLTNHLG; QDLTNHLGV; DLTNHLGVI; LTNHLGVIA; TNHLGVIAK; NHLGVIAKS; HLGVIAKSG; LGVIAKSGT; GVIAKSGTK; VIAKSGTKE; IAKSGTKEF; AKSGTKEFI; KSGTKEFIN; SGTKEFINN; GTKEFINNL; TKEFINNLK; KEFINNLKQ; EFINNLKQD; FINNLKQDE; INNLKQDEK; NNLKQDEKK; NLKQDEKKS; LKQDEKKSA; KQDEKKSAS; QDEKKSASL; DEKKSASLI; EKKSASLIG; KKSASLIGQ; KSASLIGQF; SASLIGQFG; ASLIGQFGV; SLIGQFGVG; LIGQFGVGF; IGQFGVGFY; GQFGVGFYS; QFGVGFYSA; FGVGFYSAF; GVGFYSAFI; VGFYSAFIV; GFYSAFIVS; FYSAFIVSE; YSAFIVSEK; SAFIVSEKV; AFIVSEKVE; FIVSEKVEV; IVSEKVEVT; VSEKVEVTS; SEKVEVTSK; EKVEVTSKK; KVEVTSKKA; VEVTSKKAL; EVTSKKALE; VTSKKALES; TSKKALESD; SKKALESDA; KKALESDAY; KALESDAYI; ALESDAYIW; LESDAYIWS; ESDAYIWSS; SDAYIWSSD; DAYIWSSDG; AYIWSSDGK; YIWSSDGKT; IWSSDGKTG; WSSDGKTGY; SSDGKTGYE; SDGKTGYEI; DGKTGYEIE; GKTGYEIEK; KTGYEIEKA; TGYEIEKAK; GYEIEKAKK; YEIEKAKKE; EIEKAKKEE; IEKAKKEES; EKAKKEESG; KAKKEESGT; AKKEESGTE; KKEESGTEI; KEESGTEIK; EESGTEIKL; ESGTEIKLY; SGTEIKLYL; GTEIKLYLN; TEIKLYLNK; EIKLYLNKE; IKLYLNKEG; KLYLNKEGL; LYLNKEGLE; YLNKEGLEY; LNKEGLEYA; NKEGLEYAN; KEGLEYANK; EGLEYANKW; GLEYANKWK; LEYANKWKI; EYANKWKIQ; YANKWKIQE; ANKWKIQEI; NKWKIQEII; KWKIQEIIK; WKIQEIIKK; KIQEIIKKY; IQEIIKKYS; QEIIKKYSN; EIIKKYSNH; IIKKYSNHI; IKKYSNHIN; KKYSNHINY; KYSNHINYP; YSNHINYPI; SNHINYPIY; NHINYPIYI; HINYPIYIK; INYPIYIKY; NYPIYIKYS; YPIYIKYSE; PIYIKYSEP; IYIKYSEPI; YIKYSEPIM; IKYSEPIMK; KYSEPIMKD; YSEPIMKDG; SEPIMKDGK; EPIMKDGKQ; PIMKDGKQE; IMKDGKQEG; MKDGKQEGI; KDGKQEGIE; DGKQEGIEE;

	GKQEGIEEK; KQEGIEEKE; QEGIEEKEE; EGIEEKEEK; GIEEKEEKL; IEEKEEKLN; EEKEEKLNE; EKEEKLNET; KEEKLNETT; EEKLNETTA; EKLNETTAL; KLNETTALW; LNETTALWT; NETTALWTK; ETTALWTKN; TTALWTKNK; TALWTKNKS; ALWTKNKSE; LWTKNKSEI; WTKNKSEIK; TKNKSEIKA; KNKSEIKAE; NKSEIKAEE; KSEIKAEEY; SEIKAEEYN; EIKAEEYNE; IKAEEYNEF; KAEEYNEFY; AEEYNEFYK; EEYNEFYKN; EYNEFYKNT; YNEFYKNTT; NEFYKNTTF; EFYKNTTFD; FYKNTTFDY; YKNTTFDYE; KNTTFDYEN; NTTFDYENP; TTFDYENPL; TFDYENPLM; FDYENPLMH; DYENPLMHI; YENPLMHIH; ENPLMHIHT; NPLMHIHTK; PLMHIHTKA; LMHIHTKAE; MHIHTKAEG; HIHTKAEGN; IHTKAEGNL; HTKAEGNLE; TKAEGNLEY; KAEGNLEYT; AEGNLEYTN; EGNLEYTNL; GNLEYTNLF; NLEYTNLFY; LEYTNLFYV; EYTNLFYVP; YTNLFYVPS; TNLFYVPSK; NLFYVPSKA; LFYVPSKAP; FYVPSKAPY; YVPSKAPYD; VPSKAPYDL; PSKAPYDLY; SKAPYDLYY; KAPYDLYYP; APYDLYYPN; PYDLYYPNT; YDLYYPNTK; DLYYPNTKP; LYYPNTKPG; YYPNTKPGV; YPNTKPGVK; PNTKPGVKL; NTKPGVKLF; TKPGVKLFI; KPGVKLFIN; PGVKLFINR; GVKLFINRI; VKLFINRIF; KLFINRIFI; LFINRIFIT; FINRIFITD; INRIFITDS; NRIFITDSE; RIFITDSEG; IFITDSEGS; FITDSEGSL; ITDSEGSLL; TDSEGSLLP; DSEGSLLPN; SEGSLLPNY; EGSLLPNYL; GSLLPNYLR; SLLPNYLRF; LLPNYLRFI; LPNYLRFIK; PNYLRFIKG; NYLRFIKGI; YLRFIKGII; LRFIKGIID; RFIKGIIDC; FIKGIIDCQ; IKGIIDCQD; KGIIDCQDL; GIIDCQDLP; IIDCQDLPL; IDCQDLPLN; DCQDLPLNV; CQDLPLNVS; QDLPLNVSR; DLPLNVSRE; LPLNVSREI; PLNVSREIL; LNVSREILQ; NVSREILQQ; VSREILQQN; SREILQQNK; REILQQNKI; EILQQNKIL; ILQQNKILS; LQQNKILSK; QQNKILSKI; QNKILSKIK; NKILSKIKS; KILSKIKSS; ILSKIKSSS; LSKIKSSSV; SKIKSSSVK; KIKSSSVKK; IKSSSVKKI; KSSSVKKIL; SSSVKKILS; SSVKKILSE; SVKKILSEL; VKKILSELE; KKILSELEK; KILSELEKL; ILSELEKLS; LSELEKLSK; SELEKLSKK; ELEKLSKKN; LEKLSKKNP; EKLSKKNPE; KLSKKNPEK; LSKKNPEKF; SKKNPEKFS; KKNPEKFSE; KNPEKFSEF; NPEKFSEFS; PEKFSEFSK; EKFSEFSKE; KFSEFSKEF; FSEFSKEFG; SEFSKEFGR; EFSKEFGRC; FSKEFGRCI; SKEFGRCIK; KEFGRCIKE; EFGRCIKEG; FGRCIKEGV; GRCIKEGVY; RCIKEGVYS; CIKEGVYSD; IKEGVYSDF; KEGVYSDFE; EGVYSDFEN; GVYSDFENR; VYSDFENRE; YSDFENREK; SDFENREKL; DFENREKLI; FENREKLIS; ENREKLISL; NREKLISLI; REKLISLIR; EKLISLIRF; KLISLIRFK; LISLIRFKS; ISLIRFKSS; SLIRFKSSS; LIRFKSSSV; IRFKSSSVD; RFKSSSVDG; FKSSSVDGF; KSSSVDGFV; SSSVDGFVS; SSVDGFVSF; SVDGFVSFK; VDGFVSFKE; DGFVSFKEY; GFVSFKEYK; FVSFKEYKE; VSFKEYKER; SFKEYKERM; FKEYKERMN; KEYKERMNE; EYKERMNES; YKERMNESQ; KERMNESQK; ERMNESQKS; RMNESQKSI; MNESQKSIY; NESQKSIYY; ESQKSIYYI; SQKSIYYIT; QKSIYYITG; KSIYYITGG; SIYYITGGK; IYYITGGKE; YYITGGKEN; YITGGKENI; ITGGKENIL; TGGKENILK; GGKENILKE; GKENILKEN; KENILKENP; ENILKENPI; NILKENPIV; ILKENPIVA; LKENPIVAA; KENPIVAAY; ENPIVAAYK; NPIVAAYKE; PIVAAYKEK; IVAAYKEKG; VAAYKEKGF; AAYKEKGFE; AYKEKGFEI; YKEKGFEIL; KEKGFEILI; EKGFEILIM; KGFEILIMD; GFEILIMDD; FEILIMDDE; EILIMDDEL; ILIMDDELD; LIMDDELDE; IMDDELDEA; MDDELDEAI; DDELDEAIL; DELDEAILN; ELDEAILNL; LDEAILNLI; DEAILNLIP; EAILNLIPE; AILNLIPEY; ILNLIPEYE; LNLIPEYEG; NLIPEYEGL; LIPEYEGLK; IPEYEGLKL; PEYEGLKLK; EYEGLKLKA; YEGLKLKAI; EGLKLKAIN; GLKLKAINK; LKLKAINKN; KLKAINKNE; LKAINKNET; KAINKNETS; AINKNETSN; INKNETSNE; NKNETSNEL; KNETSNELK; NETSNELKD; ETSNELKDE; TSNELKDEN; SNELKDENF; NELKDENFK; ELKDENFKK; LKDENFKKI; KDENFKKIE; DENFKKIEE; ENFKKIEEE; NFKKIEEEF; FKKIEEEFK; KKIEEEFKD; KIEEEFKDT; IEEEFKDTL; EEEFKDTLT; EEFKDTLTK;

EFKDTLTKV; FKDTLTKVK; KDTLTKVKE; DTLTKVKEI; TLTKVKEIL; LTKVKEILK; TKVKEILKD; KVKEILKDH; VKEILKDHI; KEILKDHIK; EILKDHIKE; ILKDHIKEV; LKDHIKEVN; KDHIKEVNL; DHIKEVNLS; HIKEVNLSA; IKEVNLSAT; KEVNLSATL; EVNLSATLI; VNLSATLIK; NLSATLIKE; LSATLIKEP; SATLIKEPS; ATLIKEPSA; TLIKEPSAI; LIKEPSAII; IKEPSAIII; KEPSAIIID; EPSAIIIDS; PSAIIIDSN; SAIIIDSND; AIIIDSNDP; IIIDSNDPT; IIDSNDPTY; IDSNDPTYQ; DSNDPTYQM; SNDPTYQMQ; NDPTYQMQK; DPTYQMQKI; PTYQMQKIM; TYQMQKIML; YQMQKIMLS; QMQKIMLSM; MQKIMLSMG; QKIMLSMGQ; KIMLSMGQE; IMLSMGQEV; MLSMGQEVK; LSMGQEVKE; SMGQEVKEI; MGQEVKEIK; GQEVKEIKP; QEVKEIKPI; EVKEIKPIL; VKEIKPILE; KEIKPILEL; EIKPILELN; IKPILELNP; KPILELNPN; PILELNPNN; ILELNPNNK; LELNPNNKI; ELNPNNKIV; LNPNNKIVQ; NPNNKIVQN; PNNKIVQNL; NNKIVQNLK; NKIVQNLKN; KIVQNLKNL; IVQNLKNLE; VQNLKNLEP; QNLKNLEPE; NLKNLEPEK; LKNLEPEKL; KNLEPEKLE; NLEPEKLEK; LEPEKLEKI; EPEKLEKIS; PEKLEKISI; EKLEKISIL; KLEKISILL; LEKISILLF; EKISILLFE; KISILLFEE; ISILLFEEA; SILLFEEAM; ILLFEEAML; LLFEEAMLT; LFEEAMLTS; FEEAMLTSG; EEAMLTSGM; EAMLTSGMP; AMLTSGMPS; MLTSGMPSK; LTSGMPSKN; TSGMPSKNP; SGMPSKNPG; GMPSKNPGK; MPSKNPGKF; PSKNPGKFI; SKNPGKFIN; KNPGKFINI; NPGKFINII; PGKFINIIN; GKFINIINE; KFINIINEF; FINIINEFI; INIINEFIE; NIINEFIEK; IINEFIEKD; INEFIEKDF;

10 mers:
MILIFYFKQI; ILIFYFKQIA; LIFYFKQIAL; IFYFKQIALF; FYFKQIALFI; YFKQIALFII; FKQIALFIIF; KQIALFIIFR; QIALFIIFRL; IALFIIFRLC; ALFIIFRLCY; LFIIFRLCYI; FIIFRLCYII; IIFRLCYIIK; IFRLCYIIKK; FRLCYIIKKV; RLCYIIKKVK; LCYIIKKVKI; CYIIKKVKIK; YIIKKVKIKL; IIKKVKIKLK; IKKVKIKLKR; KKVKIKLKRK; KVKIKLKRKS; VKIKLKRKSC; KIKLKRKSCM; IKLKRKSCMK; KLKRKSCMKK; LKRKSCMKKQ; KRKSCMKKQF; RKSCMKKQFD; KSCMKKQFDT; SCMKKQFDTE; CMKKQFDTEV; MKKQFDTEVN; KKQFDTEVND; KQFDTEVNDL; QFDTEVNDLL; FDTEVNDLLY; DTEVNDLLYL; TEVNDLLYLI; EVNDLLYLII; VNDLLYLIIH; NDLLYLIIHS; DLLYLIIHSL; LLYLIIHSLY; LYLIIHSLYS; YLIIHSLYSH; LIIHSLYSHK; IIHSLYSHKE; IHSLYSHKEI; HSLYSHKEIF; SLYSHKEIFL; LYSHKEIFLR; YSHKEIFLRE; SHKEIFLREL; HKEIFLRELI; KEIFLRELIS; EIFLRELISN; IFLRELISNA; FLRELISNAS; LRELISNASD; RELISNASDA; ELISNASDAI; LISNASDAID; ISNASDAIDK; SNASDAIDKL; NASDAIDKLK; ASDAIDKLKF; SDAIDKLKFL; DAIDKLKFLS; AIDKLKFLSL; IDKLKFLSLT; DKLKFLSLTN; KLKFLSLTNE; LKFLSLTNEK; KFLSLTNEKF; FLSLTNEKFK; LSLTNEKFKN; SLTNEKFKNI; LTNEKFKNIA; TNEKFKNIAL; NEKFKNIALE; EKFKNIALEP; KFKNIALEPK; FKNIALEPKI; KNIALEPKIE; NIALEPKIEI; IALEPKIEIS; ALEPKIEISF; LEPKIEISFD; EPKIEISFDD; PKIEISFDDK; KIEISFDDKS; IEISFDDKSI; EISFDDKSIL; ISFDDKSILI; SFDDKSILIK; FDDKSILIKD; DDKSILIKDN; DKSILIKDNG; KSILIKDNGI; SILIKDNGIG; ILIKDNGIGM; LIKDNGIGMD; IKDNGIGMDE; KDNGIGMDEQ; DNGIGMDEQD; NGIGMDEQDL; GIGMDEQDLT; IGMDEQDLTN; GMDEQDLTNH; MDEQDLTNHL; DEQDLTNHLG; EQDLTNHLGV; QDLTNHLGVI; DLTNHLGVIA; LTNHLGVIAK; TNHLGVIAKS; NHLGVIAKSG; HLGVIAKSGT; LGVIAKSGTK; GVIAKSGTKE; VIAKSGTKEF; IAKSGTKEFI; AKSGTKEFIN; KSGTKEFINN; SGTKEFINNL; GTKEFINNLK; TKEFINNLKQ; KEFINNLKQD; EFINNLKQDE; FINNLKQDEK; INNLKQDEKK; NNLKQDEKKS; NLKQDEKKSA; LKQDEKKSAS; KQDEKKSASL; QDEKKSASLI; DEKKSASLIG; EKKSASLIGQ; KKSASLIGQF; KSASLIGQFG; SASLIGQFGV; ASLIGQFGVG; SLIGQFGVGF; LIGQFGVGFY; IGQFGVGFYS; GQFGVGFYSA; QFGVGFYSAF; FGVGFYSAFI; GVGFYSAFIV; VGFYSAFIVS; GFYSAFIVSE; FYSAFIVSEK; YSAFIVSEKV; SAFIVSEKVE; AFIVSEKVEV; FIVSEKVEVT; IVSEKVEVTS;

	VSEKVEVTSK; SEKVEVTSKK; EKVEVTSKKA; KVEVTSKKAL; VEVTSKKALE; EVTSKKALES; VTSKKALESD; TSKKALESDA; SKKALESDAY; KKALESDAYI; KALESDAYIW; ALESDAYIWS; LESDAYIWSS; ESDAYIWSSD; SDAYIWSSDG; DAYIWSSDGK; AYIWSSDGKT; YIWSSDGKTG; IWSSDGKTGY; WSSDGKTGYE; SSDGKTGYEI; SDGKTGYEIE; DGKTGYEIEK; GKTGYEIEKA; KTGYEIEKAK; TGYEIEKAKK; GYEIEKAKKE; YEIEKAKKEE; EIEKAKKEES; IEKAKKEESG; EKAKKEESGT; KAKKEESGTE; AKKEESGTEI; KKEESGTEIK; KEESGTEIKL; EESGTEIKLY; ESGTEIKLYL; SGTEIKLYLN; GTEIKLYLNK; TEIKLYLNKE; EIKLYLNKEG; IKLYLNKEGL; KLYLNKEGLE; LYLNKEGLEY; YLNKEGLEYA; LNKEGLEYAN; NKEGLEYANK; KEGLEYANKW; EGLEYANKWK; GLEYANKWKI; LEYANKWKIQ; EYANKWKIQE; YANKWKIQEI; ANKWKIQEII; NKWKIQEIIK; KWKIQEIIKK; WKIQEIIKKY; KIQEIIKKYS; IQEIIKKYSN; QEIIKKYSNH; EIIKKYSNHI; IIKKYSNHIN; IKKYSNHINY; KKYSNHINYP; KYSNHINYPI; YSNHINYPIY; SNHINYPIYI; NHINYPIYIK; HINYPIYIKY; INYPIYIKYS; NYPIYIKYSE; YPIYIKYSEP; PIYIKYSEPI; IYIKYSEPIM; YIKYSEPIMK; IKYSEPIMKD; KYSEPIMKDG; YSEPIMKDGK; SEPIMKDGKQ; EPIMKDGKQE; PIMKDGKQEG; IMKDGKQEGI; MKDGKQEGIE; KDGKQEGIEE; DGKQEGIEEK; GKQEGIEEKE; KQEGIEEKEE; QEGIEEKEEK; EGIEEKEEKL; GIEEKEEKLN; IEEKEEKLNE; EEKEEKLNET; EKEEKLNETT; KEEKLNETTA; EEKLNETTAL; EKLNETTALW; KLNETTALWT; LNETTALWTK; NETTALWTKN; ETTALWTKNK; TTALWTKNKS; TALWTKNKSE; ALWTKNKSEI; LWTKNKSEIK; WTKNKSEIKA; TKNKSEIKAE; KNKSEIKAEE; NKSEIKAEEY; KSEIKAEEYN; SEIKAEEYNE; EIKAEEYNEF; IKAEEYNEFY; KAEEYNEFYK; AEEYNEFYKN; EEYNEFYKNT; EYNEFYKNTT; YNEFYKNTTF; NEFYKNTTFD; EFYKNTTFDY; FYKNTTFDYE; YKNTTFDYEN; KNTTFDYENP; NTTFDYENPL; TTFDYENPLM; TFDYENPLMH; FDYENPLMHI; DYENPLMHIH; YENPLMHIHT; ENPLMHIHTK; NPLMHIHTKA; PLMHIHTKAE; LMHIHTKAEG; MHIHTKAEGN; HIHTKAEGNL; IHTKAEGNLE; HTKAEGNLEY; TKAEGNLEYT; KAEGNLEYTN; AEGNLEYTNL; EGNLEYTNLF; GNLEYTNLFY; NLEYTNLFYV; LEYTNLFYVP; EYTNLFYVPS; YTNLFYVPSK; TNLFYVPSKA; NLFYVPSKAP; LFYVPSKAPY; FYVPSKAPYD; YVPSKAPYDL; VPSKAPYDLY; PSKAPYDLYY; SKAPYDLYYP; KAPYDLYYPN; APYDLYYPNT; PYDLYYPNTK; YDLYYPNTKP; DLYYPNTKPG; LYYPNTKPGV; YYPNTKPGVK; YPNTKPGVKL; PNTKPGVKLF; NTKPGVKLFI; TKPGVKLFIN; KPGVKLFINR; PGVKLFINRI; GVKLFINRIF; VKLFINRIFI; KLFINRIFIT; LFINRIFITD; FINRIFITDS; INRIFITDSE; NRIFITDSEG; RIFITDSEGS; IFITDSEGSL; FITDSEGSLL; ITDSEGSLLP; TDSEGSLLPN; DSEGSLLPNY; SEGSLLPNYL; EGSLLPNYLR; GSLLPNYLRF; SLLPNYLRFI; LLPNYLRFIK; LPNYLRFIKG; PNYLRFIKGI; NYLRFIKGII; YLRFIKGIID; LRFIKGIIDC; RFIKGIIDCQ; FIKGIIDCQD; IKGIIDCQDL; KGIIDCQDLP; GIIDCQDLPL; IIDCQDLPLN; IDCQDLPLNV; DCQDLPLNVS; CQDLPLNVSR; QDLPLNVSRE; DLPLNVSREI; LPLNVSREIL; PLNVSREILQ; LNVSREILQQ; NVSREILQQN; VSREILQQNK; SREILQQNKI; REILQQNKIL; EILQQNKILS; ILQQNKILSK; LQQNKILSKI; QQNKILSKIK; QNKILSKIKS; NKILSKIKSS; KILSKIKSSS; ILSKIKSSSV; LSKIKSSSVK; SKIKSSSVKK; KIKSSSVKKI; IKSSSVKKIL; KSSSVKKILS; SSSVKKILSE; SSVKKILSEL; SVKKILSELE; VKKILSELEK; KKILSELEKL; KILSELEKLS; ILSELEKLSK; LSELEKLSKK; SELEKLSKKN; ELEKLSKKNP; LEKLSKKNPE; EKLSKKNPEK; KLSKKNPEKF; LSKKNPEKFS; SKKNPEKFSE; KKNPEKFSEF; KNPEKFSEFS; NPEKFSEFSK; PEKFSEFSKE; EKFSEFSKEF; KFSEFSKEFG; FSEFSKEFGR; SEFSKEFGRC; EFSKEFGRCI; FSKEFGRCIK; SKEFGRCIKE; KEFGRCIKEG; EFGRCIKEGV; FGRCIKEGVY; GRCIKEGVYS; RCIKEGVYSD; CIKEGVYSDF; IKEGVYSDFE; KEGVYSDFEN; EGVYSDFENR; GVYSDFENRE; VYSDFENREK; YSDFENREKL; SDFENREKLI; DFENREKLIS; FENREKLISL; ENREKLISLI; NREKLISLIR; REKLISLIRF; EKLISLIRFK; KLISLIRFKS; LISLIRFKSS; ISLIRFKSSS; SLIRFKSSSV; LIRFKSSSVD; IRFKSSSVDG; RFKSSSVDGF; FKSSSVDGFV; KSSSVDGFVS; SSSVDGFVSF; SSVDGFVSFK; SVDGFVSFKE; VDGFVSFKEY; DGFVSFKEYK; GFVSFKEYKE; FVSFKEYKER; VSFKEYKERM; SFKEYKERMN; FKEYKERMNE; KEYKERMNES;

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11 mers:
MILIFYFKQIA; ILIFYFKQIAL; LIFYFKQIALF; IFYFKQIALFI; FYFKQIALFII; YFKQIALFIIF; FKQIALFIIFR; KQIALFIIFRL; QIALFIIFRLC; IALFIIFRLCY; ALFIIFRLCYI; LFIIFRLCYII; FIIFRLCYIIK; IIFRLCYIIKK; IFRLCYIIKKV; FRLCYIIKKVK; RLCYIIKKVKI; LCYIIKKVKIK; CYIIKKVKIKL; YIIKKVKIKLK; IIKKVKIKLKR; IKKVKIKLKRK; KKVKIKLKRKS; KVKIKLKRKSC; VKIKLKRKSCM; KIKLKRKSCMK; IKLKRKSCMKK; KLKRKSCMKKQ; LKRKSCMKKQF; KRKSCMKKQFD; RKSCMKKQFDT; KSCMKKQFDTE; SCMKKQFDTEV; CMKKQFDTEVN; MKKQFDTEVND; KKQFDTEVNDL; KQFDTEVNDLL; QFDTEVNDLLY; FDTEVNDLLYL; DTEVNDLLYLI; TEVNDLLYLII; EVNDLLYLIIH; VNDLLYLIIHS; NDLLYLIIHSL; DLLYLIIHSLY; LLYLIIHSLYS; LYLIIHSLYSH; YLIIHSLYSHK; LIIHSLYSHKE; IIHSLYSHKEI; IHSLYSHKEIF; HSLYSHKEIFL; SLYSHKEIFLR; LYSHKEIFLRE; YSHKEIFLREL; SHKEIFLRELI; HKEIFLRELIS; KEIFLRELISN; EIFLRELISNA; IFLRELISNAS;

	FLRELISNASD; LRELISNASDA; RELISNASDAI; ELISNASDAID; LISNASDAIDK; ISNASDAIDKL; SNASDAIDKLK; NASDAIDKLKF; ASDAIDKLKFL; SDAIDKLKFLS; DAIDKLKFLSL; AIDKLKFLSLT; IDKLKFLSLTN; DKLKFLSLTNE; KLKFLSLTNEK; LKFLSLTNEKF; KFLSLTNEKFK; FLSLTNEKFKN; LSLTNEKFKNI; SLTNEKFKNIA; LTNEKFKNIAL; TNEKFKNIALE; NEKFKNIALEP; EKFKNIALEPK; KFKNIALEPKI; FKNIALEPKIE; KNIALEPKIEI; NIALEPKIEIS; IALEPKIEISF; ALEPKIEISFD; LEPKIEISFDD; EPKIEISFDDK; PKIEISFDDKS; KIEISFDDKSI; IEISFDDKSIL; EISFDDKSILI; ISFDDKSILIK; SFDDKSILIKD; FDDKSILIKDN; DDKSILIKDNG; DKSILIKDNGI; KSILIKDNGIG; SILIKDNGIGM; ILIKDNGIGMD; LIKDNGIGMDE; IKDNGIGMDEQ; KDNGIGMDEQD; DNGIGMDEQDL; NGIGMDEQDLT; GIGMDEQDLTN; IGMDEQDLTNH; GMDEQDLTNHL; MDEQDLTNHLG; DEQDLTNHLGV; EQDLTNHLGVI; QDLTNHLGVIA; DLTNHLGVIAK; LTNHLGVIAKS; TNHLGVIAKSG; NHLGVIAKSGT; HLGVIAKSGTK; LGVIAKSGTKE; GVIAKSGTKEF; VIAKSGTKEFI; IAKSGTKEFIN; AKSGTKEFINN; KSGTKEFINNL; SGTKEFINNLK; GTKEFINNLKQ; TKEFINNLKQD; KEFINNLKQDE; EFINNLKQDEK; FINNLKQDEKK; INNLKQDEKKS; NNLKQDEKKSA; NLKQDEKKSAS; LKQDEKKSASL; KQDEKKSASLI; QDEKKSASLIG; DEKKSASLIGQ; EKKSASLIGQF; KKSASLIGQFG; KSASLIGQFGV; SASLIGQFGVG; ASLIGQFGVGF; SLIGQFGVGFY; LIGQFGVGFYS; IGQFGVGFYSA; GQFGVGFYSAF; QFGVGFYSAFI; FGVGFYSAFIV; GVGFYSAFIVS; VGFYSAFIVSE; GFYSAFIVSEK; FYSAFIVSEKV; YSAFIVSEKVE; SAFIVSEKVEV; AFIVSEKVEVT; FIVSEKVEVTS; IVSEKVEVTSK; VSEKVEVTSKK; SEKVEVTSKKA; EKVEVTSKKAL; KVEVTSKKALE; VEVTSKKALES; EVTSKKALESD; VTSKKALESDA; TSKKALESDAY; SKKALESDAYI; KKALESDAYIW; KALESDAYIWS; ALESDAYIWSS; LESDAYIWSSD; ESDAYIWSSDG; SDAYIWSSDGK; DAYIWSSDGKT; AYIWSSDGKTG; YIWSSDGKTGY; IWSSDGKTGYE; WSSDGKTGYEI; SSDGKTGYEIE; SDGKTGYEIEK; DGKTGYEIEKA; GKTGYEIEKAK; KTGYEIEKAKK; TGYEIEKAKKE; GYEIEKAKKEE; YEIEKAKKEES; EIEKAKKEESG; IEKAKKEESGT; EKAKKEESGTE; KAKKEESGTEI; AKKEESGTEIK; KKEESGTEIKL; KEESGTEIKLY; EESGTEIKLYL; ESGTEIKLYLN; SGTEIKLYLNK; GTEIKLYLNKE; TEIKLYLNKEG; EIKLYLNKEGL; IKLYLNKEGLE; KLYLNKEGLEY; LYLNKEGLEYA; YLNKEGLEYAN; LNKEGLEYANK; NKEGLEYANKW; KEGLEYANKWK; EGLEYANKWKI; GLEYANKWKIQ; LEYANKWKIQE; EYANKWKIQEI; YANKWKIQEII; ANKWKIQEIIK; NKWKIQEIIKK; KWKIQEIIKKY; WKIQEIIKKYS; KIQEIIKKYSN; IQEIIKKYSNH; QEIIKKYSNHI; EIIKKYSNHIN; IIKKYSNHINY; IKKYSNHINYP; KKYSNHINYPI; KYSNHINYPIY; YSNHINYPIYI; SNHINYPIYIK; NHINYPIYIKY; HINYPIYIKYS; INYPIYIKYSE; NYPIYIKYSEP; YPIYIKYSEPI; PIYIKYSEPIM; IYIKYSEPIMK; YIKYSEPIMKD; IKYSEPIMKDG; KYSEPIMKDGK; YSEPIMKDGKQ; SEPIMKDGKQE; EPIMKDGKQEG; PIMKDGKQEGI; IMKDGKQEGIE; MKDGKQEGIEE; KDGKQEGIEEK; DGKQEGIEEKE; GKQEGIEEKEE; KQEGIEEKEEK; QEGIEEKEEKL; EGIEEKEEKLN; GIEEKEEKLNE; IEEKEEKLNET; EEKEEKLNETT; EKEEKLNETTA; KEEKLNETTAL; EEKLNETTALW; EKLNETTALWT; KLNETTALWTK; LNETTALWTKN; NETTALWTKNK; ETTALWTKNKS; TTALWTKNKSE; TALWTKNKSEI; ALWTKNKSEIK; LWTKNKSEIKA; WTKNKSEIKAE; TKNKSEIKAEE; KNKSEIKAEEY; NKSEIKAEEYN; KSEIKAEEYNE; SEIKAEEYNEF; EIKAEEYNEFY; IKAEEYNEFYK; KAEEYNEFYKN; AEEYNEFYKNT; EEYNEFYKNTT; EYNEFYKNTTF; YNEFYKNTTFD; NEFYKNTTFDY; EFYKNTTFDYE; FYKNTTFDYEN; YKNTTFDYENP; KNTTFDYENPL; NTTFDYENPLM; TTFDYENPLMH; TFDYENPLMHI; FDYENPLMHIH; DYENPLMHIHT; YENPLMHIHTK;

	ENPLMHIHTKA; NPLMHIHTKAE; PLMHIHTKAEG; LMHIHTKAEGN; MHIHTKAEGNL; HIHTKAEGNLE; IHTKAEGNLEY; HTKAEGNLEYT; TKAEGNLEYTN; KAEGNLEYTNL; AEGNLEYTNLF; EGNLEYTNLFY; GNLEYTNLFYV; NLEYTNLFYVP; LEYTNLFYVPS; EYTNLFYVPSK; YTNLFYVPSKA; TNLFYVPSKAP; NLFYVPSKAPY; LFYVPSKAPYD; FYVPSKAPYDL; YVPSKAPYDLY; VPSKAPYDLYY; PSKAPYDLYYP; SKAPYDLYYPN; KAPYDLYYPNT; APYDLYYPNTK; PYDLYYPNTKP; YDLYYPNTKPG; DLYYPNTKPGV; LYYPNTKPGVK; YYPNTKPGVKL; YPNTKPGVKLF; PNTKPGVKLFI; NTKPGVKLFIN; TKPGVKLFINR; KPGVKLFINRI; PGVKLFINRIF; GVKLFINRIFI; VKLFINRIFIT; KLFINRIFITD; LFINRIFITDS; FINRIFITDSE; INRIFITDSEG; NRIFITDSEGS; RIFITDSEGSL; IFITDSEGSLL; FITDSEGSLLP; ITDSEGSLLPN; TDSEGSLLPNY; DSEGSLLPNYL; SEGSLLPNYLR; EGSLLPNYLRF; GSLLPNYLRFI; SLLPNYLRFIK; LLPNYLRFIKG; LPNYLRFIKGI; PNYLRFIKGII; NYLRFIKGIID; YLRFIKGIIDC; LRFIKGIIDCQ; RFIKGIIDCQD; FIKGIIDCQDL; IKGIIDCQDLP; KGIIDCQDLPL; GIIDCQDLPLN; IIDCQDLPLNV; IDCQDLPLNVS; DCQDLPLNVSR; CQDLPLNVSRE; QDLPLNVSREI; DLPLNVSREIL; LPLNVSREILQ; PLNVSREILQQ; LNVSREILQQN; NVSREILQQNK; VSREILQQNKI; SREILQQNKIL; REILQQNKILS; EILQQNKILSK; ILQQNKILSKI; LQQNKILSKIK; QQNKILSKIKS; QNKILSKIKSS; NKILSKIKSSS; KILSKIKSSSV; ILSKIKSSSVK; LSKIKSSSVKK; SKIKSSSVKKI; KIKSSSVKKIL; IKSSSVKKILS; KSSSVKKILSE; SSSVKKILSEL; SSVKKILSELE; SVKKILSELEK; VKKILSELEKL; KKILSELEKLS; KILSELEKLSK; ILSELEKLSKK; LSELEKLSKKN; SELEKLSKKNP; ELEKLSKKNPE; LEKLSKKNPEK; EKLSKKNPEKF; KLSKKNPEKFS; LSKKNPEKFSE; SKKNPEKFSEF; KKNPEKFSEFS; KNPEKFSEFSK; NPEKFSEFSKE; PEKFSEFSKEF; EKFSEFSKEFG; KFSEFSKEFGR; FSEFSKEFGRC; SEFSKEFGRCI; EFSKEFGRCIK; FSKEFGRCIKE; SKEFGRCIKEG; KEFGRCIKEGV; EFGRCIKEGVY; FGRCIKEGVYS; GRCIKEGVYSD; RCIKEGVYSDF; CIKEGVYSDFE; IKEGVYSDFEN; KEGVYSDFENR; EGVYSDFENRE; GVYSDFENREK; VYSDFENREKL; YSDFENREKLI; SDFENREKLIS; DFENREKLISL; FENREKLISLI; ENREKLISLIR; NREKLISLIRF; REKLISLIRFK; EKLISLIRFKS; KLISLIRFKSS; LISLIRFKSSS; ISLIRFKSSSV; SLIRFKSSSVD; LIRFKSSSVDG; IRFKSSSVDGF; RFKSSSVDGFV; FKSSSVDGFVS; KSSSVDGFVSF; SSSVDGFVSFK; SSVDGFVSFKE; SVDGFVSFKEY; VDGFVSFKEYK; DGFVSFKEYKE; GFVSFKEYKER; FVSFKEYKERM; VSFKEYKERMN; SFKEYKERMNE; FKEYKERMNES; KEYKERMNESQ; EYKERMNESQK; YKERMNESQKS; KERMNESQKSI; ERMNESQKSIY; RMNESQKSIYY; MNESQKSIYYI; NESQKSIYYIT; ESQKSIYYITG; SQKSIYYITGG; QKSIYYITGGK; KSIYYITGGKE; SIYYITGGKEN; IYYITGGKENI; YYITGGKENIL; YITGGKENILK; ITGGKENILKE; TGGKENILKEN; GGKENILKENP; GKENILKENPI; KENILKENPIV; ENILKENPIVA; NILKENPIVAA; ILKENPIVAAY; LKENPIVAAYK; KENPIVAAYKE; ENPIVAAYKEK; NPIVAAYKEKG; PIVAAYKEKGF; IVAAYKEKGFE; VAAYKEKGFEI; AAYKEKGFEIL; AYKEKGFEILI; YKEKGFEILIM; KEKGFEILIMD; EKGFEILIMDD; KGFEILIMDDE; GFEILIMDDEL; FEILIMDDELD; EILIMDDELDE; ILIMDDELDEA; LIMDDELDEAI; IMDDELDEAIL; MDDELDEAILN; DDELDEAILNL; DELDEAILNLI; ELDEAILNLIP; LDEAILNLIPE; DEAILNLIPEY; EAILNLIPEYE; AILNLIPEYEG; ILNLIPEYEGL; LNLIPEYEGLK; NLIPEYEGLKL; LIPEYEGLKLK; IPEYEGLKLKA; PEYEGLKLKAI; EYEGLKLKAIN; YEGLKLKAINK; EGLKLKAINKN; GLKLKAINKNE; LKLKAINKNET; KLKAINKNETS; LKAINKNETSN; KAINKNETSNE; AINKNETSNEL; INKNETSNELK; NKNETSNELKD; KNETSNELKDE; NETSNELKDEN; ETSNELKDENF; TSNELKDENFK;

	SNELKDENFKK; NELKDENFKKI; ELKDENFKKIE; LKDENFKKIEE; KDENFKKIEEE; DENFKKIEEEF; ENFKKIEEEFK; NFKKIEEEFKD; FKKIEEEFKDT; KKIEEEFKDTL; KIEEEFKDTLT; IEEEFKDTLTK; EEEFKDTLTKV; EEFKDTLTKVK; EFKDTLTKVKE; FKDTLTKVKEI; KDTLTKVKEIL; DTLTKVKEILK; TLTKVKEILKD; LTKVKEILKDH; TKVKEILKDHI; KVKEILKDHIK; VKEILKDHIKE; KEILKDHIKEV; EILKDHIKEVN; ILKDHIKEVNL; LKDHIKEVNLS; KDHIKEVNLSA; DHIKEVNLSAT; HIKEVNLSATL; IKEVNLSATLI; KEVNLSATLIK; EVNLSATLIKE; VNLSATLIKEP; NLSATLIKEPS; LSATLIKEPSA; SATLIKEPSAI; ATLIKEPSAII; TLIKEPSAIII; LIKEPSAIIID; IKEPSAIIIDS; KEPSAIIIDSN; EPSAIIIDSND; PSAIIIDSNDP; SAIIIDSNDPT; AIIIDSNDPTY; IIIDSNDPTYQ; IIDSNDPTYQM; IDSNDPTYQMQ; DSNDPTYQMQK; SNDPTYQMQKI; NDPTYQMQKIM; DPTYQMQKIML; PTYQMQKIMLS; TYQMQKIMLSM; YQMQKIMLSMG; QMQKIMLSMGQ; MQKIMLSMGQE; QKIMLSMGQEV; KIMLSMGQEVK; IMLSMGQEVKE; MLSMGQEVKEI; LSMGQEVKEIK; SMGQEVKEIKP; MGQEVKEIKPI; GQEVKEIKPIL; QEVKEIKPILE; EVKEIKPILEL; VKEIKPILELN; KEIKPILELNP; EIKPILELNPN; IKPILELNPNN; KPILELNPNNK; PILELNPNNKI; ILELNPNNKIV; LELNPNNKIVQ; ELNPNNKIVQN; LNPNNKIVQNL; NPNNKIVQNLK; PNNKIVQNLKN; NNKIVQNLKNL; NKIVQNLKNLE; KIVQNLKNLEP; IVQNLKNLEPE; VQNLKNLEPEK; QNLKNLEPEKL; NLKNLEPEKLE; LKNLEPEKLEK; KNLEPEKLEKI; NLEPEKLEKIS; LEPEKLEKISI; EPEKLEKISIL; PEKLEKISILL; EKLEKISILLF; KLEKISILLFE; LEKISILLFEE; EKISILLFEEA; KISILLFEEAM; ISILLFEEAML; SILLFEEAMLT; ILLFEEAMLTS; LLFEEAMLTSG; LFEEAMLTSGM; FEEAMLTSGMP; EEAMLTSGMPS; EAMLTSGMPSK; AMLTSGMPSKN; MLTSGMPSKNP; LTSGMPSKNPG; TSGMPSKNPGK; SGMPSKNPGKF; GMPSKNPGKFI; MPSKNPGKFIN; PSKNPGKFINI; SKNPGKFINII; KNPGKFINIIN; NPGKFINIINE; PGKFINIINEF; GKFINIINEFI; KFINIINEFIE; FINIINEFIEK; INIINEFIEKD; NIINEFIEKDF; IINEFIEKDFL;
CAA44492.1| Outer surface protein A [Borrelia burgdorferi]	SEQ ID NO 10088-11149/ 8 mers: MKKYLLGI; KKYLLGIG; KYLLGIGL; YLLGIGLI; LLGIGLIL; LGIGLILA; GIGLILAL; IGLILALI; GLILALIA; LILALIAC; ILALIACK; LALIACKQ; ALIACKQN; LIACKQNV; IACKQNVS; ACKQNVST; CKQNVSTL; KQNVSTLD; QNVSTLDE; NVSTLDEK; VSTLDEKN; STLDEKNS; TLDEKNSV; LDEKNSVS; DEKNSVSV; EKNSVSVD; KNSVSVDL; NSVSVDLP; SVSVDLPG; VSVDLPGG; SVDLPGGM; VDLPGGMT; DLPGGMTE; LPGGMTEL; PGGMTELV; GGMTELVS; GMTELVSK; MTELVSKE; TELVSKEK; ELVSKEKD; LVSKEKDK; VSKEKDKD; SKEKDKDG; KEKDKDGK; EKDKDGKY; KDKDGKYS; DKDGKYSL; KDGKYSLE; DGKYSLEA; GKYSLEAT; KYSLEATV; YSLEATVD; SLEATVDK; LEATVDKL; EATVDKLE; ATVDKLEL; TVDKLELK; VDKLELKG; DKLELKGT; KLELKGTS; LELKGTSD; ELKGTSDK; LKGTSDKN; KGTSDKNN; GTSDKNNG; TSDKNNGS; SDKNNGSG; DKNNGSGT; KNNGSGTL; NNGSGTLE; NGSGTLEG; GSGTLEGE; SGTLEGEK; GTLEGEKT; TLEGEKTD; LEGEKTDK; EGEKTDKS; GEKTDKSK; EKTDKSKV; KTDKSKVK; TDKSKVKL; DKSKVKLT; KSKVKLTI; SKVKLTIA; KVKLTIAD; VKLTIADD; KLTIADDL; LTIADDLS; TIADDLSQ; IADDLSQT; ADDLSQTK; DDLSQTKF; DLSQTKFE; LSQTKFEI; SQTKFEIF; QTKFEIFK; TKFEIFKE; KFEIFKED; FEIFKEDA; EIFKEDAK; IFKEDAKT; FKEDAKTL; KEDAKTLV; EDAKTLVS; DAKTLVSK; AKTLVSKK; KTLVSKKV; TLVSKKVT; LVSKKVTL; VSKKVTLK; SKKVTLKD; KKVTLKDK; KVTLKDKS; VTLKDKSS; TLKDKSST; LKDKSSTE; KDKSSTEE; DKSSTEEK; KSSTEEKF; SSTEEKFN; STEEKFNE; TEEKFNEK; EEKFNEKG; EKFNEKGE; KFNEKGET; FNEKGETS; NEKGETSE; EKGETSEK; KGETSEKT; GETSEKTI; ETSEKTIV; TSEKTIVR; SEKTIVRA; EKTIVRAN; KTIVRANG; TIVRANGT; IVRANGTR; VRANGTRL;

RANGTRLE; ANGTRLEY; NGTRLEYT; GTRLEYTD; TRLEYTDI; RLEYTDIK;
LEYTDIKS; EYTDIKSD; YTDIKSDG; TDIKSDGS; DIKSDGSG; IKSDGSGK;
KSDGSGKA; SDGSGKAK; DGSGKAKE; GSGKAKEV; SGKAKEVL; GKAKEVLK;
KAKEVLKD; AKEVLKDF; KEVLKDFT; EVLKDFTL; VLKDFTLE; LKDFTLEG;
KDFTLEGT; DFTLEGTL; FTLEGTLA; TLEGTLAA; LEGTLAAD; EGTLAADG;
GTLAADGK; TLAADGKT; LAADGKTT; AADGKTTL; ADGKTTLK; DGKTTLKV;
GKTTLKVT; KTTLKVTE; TTLKVTEG; TLKVTEGT; LKVTEGTV; KVTEGTVV;
VTEGTVVL; TEGTVVLS; EGTVVLSK; GTVVLSKN; TVVLSKNI; VVLSKNIL;
VLSKNILK; LSKNILKS; SKNILKSG; KNILKSGE; NILKSGEI; ILKSGEIT;
LKSGEITV; KSGEITVA; SGEITVAL; GEITVALD; EITVALDD; ITVALDDS;
TVALDDSD; VALDDSDT; ALDDSDTT; LDDSDTTQ; DDSDTTQA; DSDTTQAT;
SDTTQATK; DTTQATKK; TTQATKKT; TQATKKTG; QATKKTGK; ATKKTGKW;
TKKTGKWD; KKTGKWDS; KTGKWDSK; TGKWDSKT; GKWDSKTS; KWDSKTST;
WDSKTSTL; DSKTSTLT; SKTSTLTI; KTSTLTIS; TSTLTISV; STLTISVN;
TLTISVNS; LTISVNSQ; TISVNSQK; ISVNSQKT; SVNSQKTK; VNSQKTKN;
NSQKTKNL; SQKTKNLV; QKTKNLVF; KTKNLVFT; TKNLVFTK; KNLVFTKE;
NLVFTKED; LVFTKEDT; VFTKEDTI; FTKEDTIT; TKEDTITV; KEDTITVQ;
EDTITVQK; DTITVQKY; TITVQKYD; ITVQKYDS; TVQKYDSA; VQKYDSAG;
QKYDSAGT; KYDSAGTN; YDSAGTNL; DSAGTNLE; SAGTNLEG; AGTNLEGK;
GTNLEGKA; TNLEGKAV; NLEGKAVE; LEGKAVEI; EGKAVEIT; GKAVEITT;
KAVEITTL; AVEITTLK; VEITTLKE; EITTLKEL; ITTLKELK; TTLKELKN;
TLKELKNA; LKELKNAL; KELKNALK;

9 mers:
MKKYLLGIG; KKYLLGIGL; KYLLGIGLI; YLLGIGLIL; LLGIGLILA;
LGIGLILAL; GIGLILALI; IGLILALIA; GLILALIAC; LILALIACK;
ILALIACKQ; LALIACKQN; ALIACKQNV; LIACKQNVS; IACKQNVST;
ACKQNVSTL; CKQNVSTLD; KQNVSTLDE; QNVSTLDEK; NVSTLDEKN;
VSTLDEKNS; STLDEKNSV; TLDEKNSVS; LDEKNSVSV; DEKNSVSVD;
EKNSVSVDL; KNSVSVDLP; NSVSVDLPG; SVSVDLPGG; VSVDLPGGM;
SVDLPGGMT; VDLPGGMTE; DLPGGMTEL; LPGGMTELV; PGGMTELVS;
GGMTELVSK; GMTELVSKE; MTELVSKEK; TELVSKEKD; ELVSKEKDK;
LVSKEKDKD; VSKEKDKDG; SKEKDKDGK; KEKDKDGKY; EKDKDGKYS;
KDKDGKYSL; DKDGKYSLE; KDGKYSLEA; DGKYSLEAT; GKYSLEATV;
KYSLEATVD; YSLEATVDK; SLEATVDKL; LEATVDKLE; EATVDKLEL;
ATVDKLELK; TVDKLELKG; VDKLELKGT; DKLELKGTS; KLELKGTSD;
LELKGTSDK; ELKGTSDKN; LKGTSDKNN; KGTSDKNNG; GTSDKNNGS;
TSDKNNGSG; SDKNNGSGT; DKNNGSGTL; KNNGSGTLE; NNGSGTLEG;
NGSGTLEGE; GSGTLEGEK; SGTLEGEKT; GTLEGEKTD; TLEGEKTDK;
LEGEKTDKS; EGEKTDKSK; GEKTDKSKV; EKTDKSKVK; KTDKSKVKL;
TDKSKVKLT; DKSKVKLTI; KSKVKLTIA; SKVKLTIAD; KVKLTIADD;
VKLTIADDL; KLTIADDLS; LTIADDLSQ; TIADDLSQT; IADDLSQTK;
ADDLSQTKF; DDLSQTKFE; DLSQTKFEI; LSQTKFEIF; SQTKFEIFK;
QTKFEIFKE; TKFEIFKED; KFEIFKEDA; FEIFKEDAK; EIFKEDAKT;
IFKEDAKTL; FKEDAKTLV; KEDAKTLVS; EDAKTLVSK; DAKTLVSKK;
AKTLVSKKV; KTLVSKKVT; TLVSKKVTL; LVSKKVTLK; VSKKVTLKD;
SKKVTLKDK; KKVTLKDKS; KVTLKDKSS; VTLKDKSST; TLKDKSSTE;
LKDKSSTEE; KDKSSTEEK; DKSSTEEKF; KSSTEEKFN; SSTEEKFNE;
STEEKFNEK; TEEKFNEKG; EEKFNEKGE; EKFNEKGET; KFNEKGETS;
FNEKGETSE; NEKGETSEK; EKGETSEKT; KGETSEKTI; GETSEKTIV;
ETSEKTIVR; TSEKTIVRA; SEKTIVRAN; EKTIVRANG; KTIVRANGT;
TIVRANGTR; IVRANGTRL; VRANGTRLE; RANGTRLEY; ANGTRLEYT;
NGTRLEYTD; GTRLEYTDI; TRLEYTDIK; RLEYTDIKS; LEYTDIKSD;
EYTDIKSDG; YTDIKSDGS; TDIKSDGSG; DIKSDGSGK; IKSDGSGKA;
KSDGSGKAK; SDGSGKAKE; DGSGKAKEV; GSGKAKEVL; SGKAKEVLK;
GKAKEVLKD; KAKEVLKDF; AKEVLKDFT; KEVLKDFTL; EVLKDFTLE;
VLKDFTLEG; LKDFTLEGT; KDFTLEGTL; DFTLEGTLA; FTLEGTLAA;

TLEGTLAAD; LEGTLAADG; EGTLAADGK; GTLAADGKT; TLAADGKTT; LAADGKTTL; AADGKTTLK; ADGKTTLKV; DGKTTLKVT; GKTTLKVTE; KTTLKVTEG; TTLKVTEGT; TLKVTEGTV; LKVTEGTVV; KVTEGTVVL; VTEGTVVLS; TEGTVVLSK; EGTVVLSKN; GTVVLSKNI; TVVLSKNIL; VVLSKNILK; VLSKNILKS; LSKNILKSG; SKNILKSGE; KNILKSGEI; NILKSGEIT; ILKSGEITV; LKSGEITVA; KSGEITVAL; SGEITVALD; GEITVALDD; EITVALDDS; ITVALDDSD; TVALDDSDT; VALDDSDTT; ALDDSDTTQ; LDDSDTTQA; DDSDTTQAT; DSDTTQATK; SDTTQATKK; DTTQATKKT; TTQATKKTG; TQATKKTGK; QATKKTGKW; ATKKTGKWD; TKKTGKWDS; KKTGKWDSK; KTGKWDSKT; TGKWDSKTS; GKWDSKTST; KWDSKTSTL; WDSKTSTLT; DSKTSTLTI; SKTSTLTIS; KTSTLTISV; TSTLTISVN; STLTISVNS; TLTISVNSQ; LTISVNSQK; TISVNSQKT; ISVNSQKTK; SVNSQKTKN; VNSQKTKNL; NSQKTKNLV; SQKTKNLVF; QKTKNLVFT; KTKNLVFTK; TKNLVFTKE; KNLVFTKED; NLVFTKEDT; LVFTKEDTI; VFTKEDTIT; FTKEDTITV; TKEDTITVQ; KEDTITVQK; EDTITVQKY; DTITVQKYD; TITVQKYDS; ITVQKYDSA; TVQKYDSAG; VQKYDSAGT; QKYDSAGTN; KYDSAGTNL; YDSAGTNLE; DSAGTNLEG; SAGTNLEGK; AGTNLEGKA; GTNLEGKAV; TNLEGKAVE; NLEGKAVEI; LEGKAVEIT; EGKAVEITT; GKAVEITTL; KAVEITTLK; AVEITTLKE; VEITTLKEL; EITTLKELK; ITTLKELKN; TTLKELKNA; TLKELKNAL; LKELKNALK

10 mers:
MKKYLLGIGL; KKYLLGIGLI; KYLLGIGLIL; YLLGIGLILA; LLGIGLILAL; LGIGLILALI; GIGLILALIA; IGLILALIAC; GLILALIACK; LILALIACKQ; ILALIACKQN; LALIACKQNV; ALIACKQNVS; LIACKQNVST; IACKQNVSTL; ACKQNVSTLD; CKQNVSTLDE; KQNVSTLDEK; QNVSTLDEKN; NVSTLDEKNS; VSTLDEKNSV; STLDEKNSVS; TLDEKNSVSV; LDEKNSVSVD; DEKNSVSVDL; EKNSVSVDLP; KNSVSVDLPG; NSVSVDLPGG; SVSVDLPGGM; VSVDLPGGMT; SVDLPGGMTE; VDLPGGMTEL; DLPGGMTELV; LPGGMTELVS; PGGMTELVSK; GGMTELVSKE; GMTELVSKEK; MTELVSKEKD; TELVSKEKDK; ELVSKEKDKD; LVSKEKDKDG; VSKEKDKDGK; SKEKDKDGKY; KEKDKDGKYS; EKDKDGKYSL; KDKDGKYSLE; DKDGKYSLEA; KDGKYSLEAT; DGKYSLEATV; GKYSLEATVD; KYSLEATVDK; YSLEATVDKL; SLEATVDKLE; LEATVDKLEL; EATVDKLELK; ATVDKLELKG; TVDKLELKGT; VDKLELKGTS; DKLELKGTSD; KLELKGTSDK; LELKGTSDKN; ELKGTSDKNN; LKGTSDKNNG; KGTSDKNNGS; GTSDKNNGSG; TSDKNNGSGT; SDKNNGSGTL; DKNNGSGTLE; KNNGSGTLEG; NNGSGTLEGE; NGSGTLEGEK; GSGTLEGEKT; SGTLEGEKTD; GTLEGEKTDK; TLEGEKTDKS; LEGEKTDKSK; EGEKTDKSKV; GEKTDKSKVK; EKTDKSKVKL; KTDKSKVKLT; TDKSKVKLTI; DKSKVKLTIA; KSKVKLTIAD; SKVKLTIADD; KVKLTIADDL; VKLTIADDLS; KLTIADDLSQ; LTIADDLSQT; TIADDLSQTK; IADDLSQTKF; ADDLSQTKFE; DDLSQTKFEI; DLSQTKFEIF; LSQTKFEIFK; SQTKFEIFKE; QTKFEIFKED; TKFEIFKEDA; KFEIFKEDAK; FEIFKEDAKT; EIFKEDAKTL; IFKEDAKTLV; FKEDAKTLVS; KEDAKTLVSK; EDAKTLVSKK; DAKTLVSKKV; AKTLVSKKVT; KTLVSKKVTL; TLVSKKVTLK; LVSKKVTLKD; VSKKVTLKDK; SKKVTLKDKS; KKVTLKDKSS; KVTLKDKSST; VTLKDKSSTE; TLKDKSSTEE; LKDKSSTEEK; KDKSSTEEKF; DKSSTEEKFN; KSSTEEKFNE; SSTEEKFNEK; STEEKFNEKG; TEEKFNEKGE; EEKFNEKGET; EKFNEKGETS; KFNEKGETSE; FNEKGETSEK; NEKGETSEKT; EKGETSEKTI; KGETSEKTIV; GETSEKTIVR; ETSEKTIVRA; TSEKTIVRAN; SEKTIVRANG; EKTIVRANGT; KTIVRANGTR; TIVRANGTRL; IVRANGTRLE; VRANGTRLEY; RANGTRLEYT; ANGTRLEYTD; NGTRLEYTDI; GTRLEYTDIK; TRLEYTDIKS; RLEYTDIKSD; LEYTDIKSDG; EYTDIKSDGS; YTDIKSDGSG; TDIKSDGSGK; DIKSDGSGKA; IKSDGSGKAK; KSDGSGKAKE; SDGSGKAKEV; DGSGKAKEVL; GSGKAKEVLK; SGKAKEVLKD; GKAKEVLKDF; KAKEVLKDFT; AKEVLKDFTL; KEVLKDFTLE; EVLKDFTLEG; VLKDFTLEGT; LKDFTLEGTL; KDFTLEGTLA; DFTLEGTLAA; FTLEGTLAAD; TLEGTLAADG; LEGTLAADGK; EGTLAADGKT; GTLAADGKTT; TLAADGKTTL;

LAADGKTTLK; AADGKTTLKV; ADGKTTLKVT; DGKTTLKVTE; GKTTLKVTEG;
KTTLKVTEGT; TTLKVTEGTV; TLKVTEGTVV; LKVTEGTVVL; KVTEGTVVLS;
VTEGTVVLSK; TEGTVVLSKN; EGTVVLSKNI; GTVVLSKNIL; TVVLSKNILK;
VVLSKNILKS; VLSKNILKSG; LSKNILKSGE; SKNILKSGEI; KNILKSGEIT;
NILKSGEITV; ILKSGEITVA; LKSGEITVAL; KSGEITVALD; SGEITVALDD;
GEITVALDDS; EITVALDDSD; ITVALDDSDT; TVALDDSDTT; VALDDSDTTQ;
ALDDSDTTQA; LDDSDTTQAT; DDSDTTQATK; DSDTTQATKK; SDTTQATKKT;
DTTQATKKTG; TTQATKKTGK; TQATKKTGKW; QATKKTGKWD; ATKKTGKWDS;
TKKTGKWDSK; KKTGKWDSKT; KTGKWDSKTS; TGKWDSKTST; GKWDSKTSTL;
KWDSKTSTLT; WDSKTSTLTI; DSKTSTLTIS; SKTSTLTISV; KTSTLTISVN;
TSTLTISVNS; STLTISVNSQ; TLTISVNSQK; LTISVNSQKT; TISVNSQKTK;
ISVNSQKTKN; SVNSQKTKNL; VNSQKTKNLV; NSQKTKNLVF; SQKTKNLVFT;
QKTKNLVFTK; KTKNLVFTKE; TKNLVFTKED; KNLVFTKEDT; NLVFTKEDTI;
LVFTKEDTIT; VFTKEDTITV; FTKEDTITVQ; TKEDTITVQK; KEDTITVQKY;
EDTITVQKYD; DTITVQKYDS; TITVQKYDSA; ITVQKYDSAG; TVQKYDSAGT;
VQKYDSAGTN; QKYDSAGTNL; KYDSAGTNLE; YDSAGTNLEG; DSAGTNLEGK;
SAGTNLEGKA; AGTNLEGKAV; GTNLEGKAVE; TNLEGKAVEI; NLEGKAVEIT;
LEGKAVEITT; EGKAVEITTL; GKAVEITTLK; KAVEITTLKE; AVEITTLKEL;
VEITTLKELK; EITTLKELKN; ITTLKELKNA; TTLKELKNAL; TLKELKNALK;

11 mers:
MKKYLLGIGLI; KKYLLGIGLIL; KYLLGIGLILA; YLLGIGLILAL;
LLGIGLILALI; LGIGLILALIA; GIGLILALIAC; IGLILALIACK;
GLILALIACKQ; LILALIACKQN; ILALIACKQNV; LALIACKQNVS;
ALIACKQNVST; LIACKQNVSTL; IACKQNVSTLD; ACKQNVSTLDE;
CKQNVSTLDEK; KQNVSTLDEKN; QNVSTLDEKNS; NVSTLDEKNSV;
VSTLDEKNSVS; STLDEKNSVSV; TLDEKNSVSVD; LDEKNSVSVDL;
DEKNSVSVDLP; EKNSVSVDLPG; KNSVSVDLPGG; NSVSVDLPGGM;
SVSVDLPGGMT; VSVDLPGGMTE; SVDLPGGMTEL; VDLPGGMTELV;
DLPGGMTELVS; LPGGMTELVSK; PGGMTELVSKE; GGMTELVSKEK;
GMTELVSKEKD; MTELVSKEKDK; TELVSKEKDKD; ELVSKEKDKDG;
LVSKEKDKDGK; VSKEKDKDGKY; SKEKDKDGKYS; KEKDKDGKYSL;
EKDKDGKYSLE; KDKDGKYSLEA; DKDGKYSLEAT; KDGKYSLEATV;
DGKYSLEATVD; GKYSLEATVDK; KYSLEATVDKL; YSLEATVDKLE;
SLEATVDKLEL; LEATVDKLELK; EATVDKLELKG; ATVDKLELKGT;
TVDKLELKGTS; VDKLELKGTSD; DKLELKGTSDK; KLELKGTSDKN;
LELKGTSDKNN; ELKGTSDKNNG; LKGTSDKNNGS; KGTSDKNNGSG;
GTSDKNNGSGT; TSDKNNGSGTL; SDKNNGSGTLE; DKNNGSGTLEG;
KNNGSGTLEGE; NNGSGTLEGEK; NGSGTLEGEKT; GSGTLEGEKTD;
SGTLEGEKTDK; GTLEGEKTDKS; TLEGEKTDKSK; LEGEKTDKSKV;
EGEKTDKSKVK; GEKTDKSKVKL; EKTDKSKVKLT; KTDKSKVKLTI;
TDKSKVKLTIA; DKSKVKLTIAD; KSKVKLTIADD; SKVKLTIADDL;
KVKLTIADDLS; VKLTIADDLSQ; KLTIADDLSQT; LTIADDLSQTK;
TIADDLSQTKF; IADDLSQTKFE; ADDLSQTKFEI; DDLSQTKFEIF;
DLSQTKFEIFK; LSQTKFEIFKE; SQTKFEIFKED; QTKFEIFKEDA;
TKFEIFKEDAK; KFEIFKEDAKT; FEIFKEDAKTL; EIFKEDAKTLV;
IFKEDAKTLVS; FKEDAKTLVSK; KEDAKTLVSKK; EDAKTLVSKKV;
DAKTLVSKKVT; AKTLVSKKVTL; KTLVSKKVTLK; TLVSKKVTLKD;
LVSKKVTLKDK; VSKKVTLKDKS; SKKVTLKDKSS; KKVTLKDKSST;
KVTLKDKSSTE; VTLKDKSSTEE; TLKDKSSTEEK; LKDKSSTEEKF;
KDKSSTEEKFN; DKSSTEEKFNE; KSSTEEKFNEK; SSTEEKFNEKG;
STEEKFNEKGE; TEEKFNEKGET; EEKFNEKGETS; EKFNEKGETSE;
KFNEKGETSEK; FNEKGETSEKT; NEKGETSEKTI; EKGETSEKTIV;
KGETSEKTIVR; GETSEKTIVRA; ETSEKTIVRAN; TSEKTIVRANG;
SEKTIVRANGT; EKTIVRANGTR; KTIVRANGTRL; TIVRANGTRLE;
IVRANGTRLEY; VRANGTRLEYT; RANGTRLEYTD; ANGTRLEYTDI;
NGTRLEYTDIK; GTRLEYTDIKS; TRLEYTDIKSD; RLEYTDIKSDG;

	LEYTDIKSDGS; EYTDIKSDGSG; YTDIKSDGSGK; TDIKSDGSGKA; DIKSDGSGKAK; IKSDGSGKAKE; KSDGSGKAKEV; SDGSGKAKEVL; DGSGKAKEVLK; GSGKAKEVLKD; SGKAKEVLKDF; GKAKEVLKDFT; KAKEVLKDFTL; AKEVLKDFTLE; KEVLKDFTLEG; EVLKDFTLEGT; VLKDFTLEGTL; LKDFTLEGTLA; KDFTLEGTLAA; DFTLEGTLAAD; FTLEGTLAADG; TLEGTLAADGK; LEGTLAADGKT; EGTLAADGKTT; GTLAADGKTTL; TLAADGKTTLK; LAADGKTTLKV; AADGKTTLKVT; ADGKTTLKVTE; DGKTTLKVTEG; GKTTLKVTEGT; KTTLKVTEGTV; TTLKVTEGTVV; TLKVTEGTVVL; LKVTEGTVVLS; KVTEGTVVLSK; VTEGTVVLSKN; TEGTVVLSKNI; EGTVVLSKNIL; GTVVLSKNILK; TVVLSKNILKS; VVLSKNILKSG; VLSKNILKSGE; LSKNILKSGEI; SKNILKSGEIT; KNILKSGEITV; NILKSGEITVA; ILKSGEITVAL; LKSGEITVALD; KSGEITVALDD; SGEITVALDDS; GEITVALDDSD; EITVALDDSDT; ITVALDDSDTT; TVALDDSDTTQ; VALDDSDTTQA; ALDDSDTTQAT; LDDSDTTQATK; DDSDTTQATKK; DSDTTQATKKT; SDTTQATKKTG; DTTQATKKTGK; TTQATKKTGKW; TQATKKTGKWD; QATKKTGKWDS; ATKKTGKWDSK; TKKTGKWDSKT; KKTGKWDSKTS; KTGKWDSKTST; TGKWDSKTSTL; GKWDSKTSTLT; KWDSKTSTLTI; WDSKTSTLTIS; DSKTSTLTISV; SKTSTLTISVN; KTSTLTISVNS; TSTLTISVNSQ; STLTISVNSQK; TLTISVNSQKT; LTISVNSQKTK; TISVNSQKTKN; ISVNSQKTKNL; SVNSQKTKNLV; VNSQKTKNLVF; NSQKTKNLVFT; SQKTKNLVFTK; QKTKNLVFTKE; KTKNLVFTKED; TKNLVFTKEDT; KNLVFTKEDTI; NLVFTKEDTIT; LVFTKEDTITV; VFTKEDTITVQ; FTKEDTITVQK; TKEDTITVQKY; KEDTITVQKYD; EDTITVQKYDS; DTITVQKYDSA; TITVQKYDSAG; ITVQKYDSAGT; TVQKYDSAGTN; VQKYDSAGTNL; QKYDSAGTNLE; KYDSAGTNLEG; YDSAGTNLEGK; DSAGTNLEGKA; SAGTNLEGKAV; AGTNLEGKAVE; GTNLEGKAVEI; TNLEGKAVEIT; NLEGKAVEITT; LEGKAVEITTL; EGKAVEITTLK; GKAVEITTLKE; KAVEITTLKEL; AVEITTLKELK; VEITTLKELKN; EITTLKELKNA; ITTLKELKNAL; TTLKELKNALK;
|BAA22351.1| Outer surface protein B [Borrelia garinii]	SEQ ID NO 11150-12307/ 8 mers: MKKYLLGF; KKYLLGFA; KYLLGFAL; YLLGFALV; LLGFALVL; LGFALVLA; GFALVLAL; FALVLALI; ALVLALIA; LVLALIAC; VLALIACG; LALIACGQ; ALIACGQK; LIACGQKG; IACGQKGA; ACGQKGAE; CGQKGAEP; GQKGAEPK; QKGAEPKH; KGAEPKHN; GAEPKHND; AEPKHNDQ; EPKHNDQE; PKHNDQEV; KHNDQEVE; HNDQEVED; NDQEVEDS; DQEVEDSK; QEVEDSKK; EVEDSKKD; VEDSKKDQ; EDSKKDQK; DSKKDQKD; SKKDQKDA; KKDQKDAS; KDQKDASK; DQKDASKK; QKDASKKD; KDASKKDL; DASKKDLP; ASKKDLPL; SKKDLPLV; KKDLPLVT; KDLPLVTE; DLPLVTED; LPLVTEDT; PLVTEDTV; LVTEDTVK; VTEDTVKL; TEDTVKLF; EDTVKLFN; DTVKLFND; TVKLFNDT; VKLFNDTK; KLFNDTKI; LFNDTKIF; FNDTKIFI; NDTKIFIS; DTKIFISK; TKIFISKE; KIFISKEK; IFISKEKN; FISKEKNK; ISKEKNKD; SKEKNKDG; KEKNKDGK; EKNKDGKY; KNKDGKYE; NKDGKYEL; KDGKYELR; DGKYELRA; GKYELRAT; KYELRATV; YELRATVD; ELRATVDT; LRATVDTV; RATVDTVE; ATVDTVEL; TVDTVELK; VDTVELKG; DTVELKGV; TVELKGVA; VELKGVAD; ELKGVADK; LKGVADKN; KGVADKND; GVADKNDG; VADKNDGS; ADKNDGSG; DKNDGSGG; KNDGSGGK; NDGSGGKL; DGSGGKLE; GSGGKLEG; SGGKLEGV; GGKLEGVK; GKLEGVKS; KLEGVKSD; LEGVKSDQ; EGVKSDQS; GVKSDQSK; VKSDQSKV; KSDQSKVT; SDQSKVTM; DQSKVTMS; QSKVTMSI; SKVTMSIT; KVTMSITD; VTMSITDD; TMSITDDL; MSITDDLN; SITDDLNT; ITDDLNTI; TDDLNTIT; DDLNTITV; DLNTITVE; LNTITVET; NTITVETY; TITVETYD; ITVETYDS; TVETYDSS; VETYDSSN; ETYDSSNT; TYDSSNTK; YDSSNTKV; DSSNTKVA; SSNTKVAS; SNTKVASK; NTKVASKV; TKVASKVF; KVASKVFK; VASKVFKK; ASKVFKKQ; SKVFKKQG; KVFKKQGS; VFKKQGSL; FKKQGSLT; KKQGSLTE; KQGSLTEE; QGSLTEET; GSLTEETE; SLTEETEE; LTEETEET; TEETEETY;

EETEETYK; ETEETYKT; TEETYKTG; EETYKTGK; ETYKTGKL; TYKTGKLS; YKTGKLST; KTGKLSTK; TGKLSTKK; GKLSTKKI; KLSTKKIT; LSTKKITR; STKKITRT; TKKITRTN; KKITRTNG; KITRTNGT; ITRTNGTT; TRTNGTTL; RTNGTTLE; TNGTTLEY; NGTTLEYS; GTTLEYSD; TTLEYSDM; TLEYSDMT; LEYSDMTN; EYSDMTND; YSDMTNDE; SDMTNDEN; DMTNDENA; MTNDENAT; TNDENATK; NDENATKA; DENATKAV; ENATKAVE; NATKAVET; ATKAVETL; TKAVETLK; KAVETLKN; AVETLKNG; VETLKNGI; ETLKNGIM; TLKNGIML; LKNGIMLE; KNGIMLEG; NGIMLEGN; GIMLEGNL; IMLEGNLV; MLEGNLVG; LEGNLVGG; EGNLVGGK; GNLVGGKT; NLVGGKTS; LVGGKTSV; VGGKTSVE; GGKTSVEI; GKTSVEIK; KTSVEIKE; TSVEIKEG; SVEIKEGT; VEIKEGTV; EIKEGTVT; IKEGTVTL; KEGTVTLK; EGTVTLKK; GTVTLKKE; TVTLKKEI; VTLKKEIE; TLKKEIEK; LKKEIEKA; KKEIEKAG; KEIEKAGT; EIEKAGTV; IEKAGTVK; EKAGTVKL; KAGTVKLF; AGTVKLFL; GTVKLFLD; TVKLFLDD; VKLFLDDT; KLFLDDTS; LFLDDTSS; FLDDTSSG; LDDTSSGS; DDTSSGST; DTSSGSTK; TSSGSTKK; SSGSTKKT; SGSTKKTA; GSTKKTAV; STKKTAVW; TKKTAVWS; KKTAVWSD; KTAVWSDT; TAVWSDTS; AVWSDTSN; VWSDTSNT; WSDTSNTL; SDTSNTLT; DTSNTLTV; TSNTLTVS; SNTLTVSA; NTLTVSAD; TLTVSADS; LTVSADSK; TVSADSKK; VSADSKKI; SADSKKIK; ADSKKIKD; DSKKIKDF; SKKIKDFV; KKIKDFVF; KIKDFVFL; IKDFVFLT; KDFVFLTD; DFVFLTDG; FVFLTDGT; VFLTDGTI; FLTDGTIT; LTDGTITV; TDGTITVQ; DGTITVQN; GTITVQNY; TITVQNYD; ITVQNYDT; TVQNYDTA; VQNYDTAG; QNYDTAGT; NYDTAGTK; YDTAGTKL; DTAGTKLA; TAGTKLAG; AGTKLAGT; GTKLAGTA; TKLAGTAT; KLAGTATE; LAGTATEI; AGTATEIK; GTATEIKD; TATEIKDL; ATEIKDLE; TEIKDLEA; EIKDLEAL; IKDLEALK; KDLEALKA; DLEALKAA; LEALKAAL; EALKAALK

9 mers:
MKKYLLGFA; KKYLLGFAL; KYLLGFALV; YLLGFALVL; LLGFALVLA; LGFALVLAL; GFALVLALI; FALVLALIA; ALVLALIAC; LVLALIACG; VLALIACGQ; LALIACGQK; ALIACGQKG; LIACGQKGA; IACGQKGAE; ACGQKGAEP; CGQKGAEPK; GQKGAEPKH; QKGAEPKHN; KGAEPKHND; GAEPKHNDQ; AEPKHNDQE; EPKHNDQEV; PKHNDQEVE; KHNDQEVED; HNDQEVEDS; NDQEVEDSK; DQEVEDSKK; QEVEDSKKD; EVEDSKKDQ; VEDSKKDQK; EDSKKDQKD; DSKKDQKDA; SKKDQKDAS; KKDQKDASK; KDQKDASKK; DQKDASKKD; QKDASKKDL; KDASKKDLP; DASKKDLPL; ASKKDLPLV; SKKDLPLVT; KKDLPLVTE; KDLPLVTED; DLPLVTEDT; LPLVTEDTV; PLVTEDTVK; LVTEDTVKL; VTEDTVKLF; TEDTVKLFN; EDTVKLFND; DTVKLFNDT; TVKLFNDTK; VKLFNDTKI; KLFNDTKIF; LFNDTKIFI; FNDTKIFIS; NDTKIFISK; DTKIFISKE; TKIFISKEK; KIFISKEKN; IFISKEKNK; FISKEKNKD; ISKEKNKDG; SKEKNKDGK; KEKNKDGKY; EKNKDGKYE; KNKDGKYEL; NKDGKYELR; KDGKYELRA; DGKYELRAT; GKYELRATV; KYELRATVD; YELRATVDT; ELRATVDTV; LRATVDTVE; RATVDTVEL; ATVDTVELK; TVDTVELKG; VDTVELKGV; DTVELKGVA; TVELKGVAD; VELKGVADK; ELKGVADKN; LKGVADKND; KGVADKNDG; GVADKNDGS; VADKNDGSG; ADKNDGSGG; DKNDGSGGK; KNDGSGGKL; NDGSGGKLE; DGSGGKLEG; GSGGKLEGV; SGGKLEGVK; GGKLEGVKS; GKLEGVKSD; KLEGVKSDQ; LEGVKSDQS; EGVKSDQSK; GVKSDQSKV; VKSDQSKVT; KSDQSKVTM; SDQSKVTMS; DQSKVTMSI; QSKVTMSIT; SKVTMSITD; KVTMSITDD; VTMSITDDL; TMSITDDLN; MSITDDLNT; SITDDLNTI; ITDDLNTIT; TDDLNTITV; DDLNTITVE; DLNTITVET; LNTITVETY; NTITVETYD; TITVETYDS; ITVETYDSS; TVETYDSSN; VETYDSSNT; ETYDSSNTK; TYDSSNTKV; YDSSNTKVA; DSSNTKVAS; SSNTKVASK; SNTKVASKV; NTKVASKVF; TKVASKVFK; KVASKVFKK; VASKVFKKQ; ASKVFKKQG; SKVFKKQGS; KVFKKQGSL; VFKKQGSLT; FKKQGSLTE; KKQGSLTEE; KQGSLTEET; QGSLTEETE; GSLTEETEE; SLTEETEET; LTEETEETY; TEETEETYK; EETEETYKT; ETEETYKTG; TEETYKTGK; EETYKTGKL; ETYKTGKLS; TYKTGKLST;

YKTGKLSTK; KTGKLSTKK; TGKLSTKKI; GKLSTKKIT; KLSTKKITR;
LSTKKITRT; STKKITRTN; TKKITRTNG; KKITRTNGT; KITRTNGTT;
ITRTNGTTL; TRTNGTTLE; RTNGTTLEY; TNGTTLEYS; NGTTLEYSD;
GTTLEYSDM; TTLEYSDMT; TLEYSDMTN; LEYSDMTND; EYSDMTNDE;
YSDMTNDEN; SDMTNDENA; DMTNDENAT; MTNDENATK; TNDENATKA;
NDENATKAV; DENATKAVE; ENATKAVET; NATKAVETL; ATKAVETLK;
TKAVETLKN; KAVETLKNG; AVETLKNGI; VETLKNGIM; ETLKNGIML;
TLKNGIMLE; LKNGIMLEG; KNGIMLEGN; NGIMLEGNL; GIMLEGNLV;
IMLEGNLVG; MLEGNLVGG; LEGNLVGGK; EGNLVGGKT; GNLVGGKTS;
NLVGGKTSV; LVGGKTSVE; VGGKTSVEI; GGKTSVEIK; GKTSVEIKE;
KTSVEIKEG; TSVEIKEGT; SVEIKEGTV; VEIKEGTVT; EIKEGTVTL;
IKEGTVTLK; KEGTVTLKK; EGTVTLKKE; GTVTLKKEI; TVTLKKEIE;
VTLKKEIEK; TLKKEIEKA; LKKEIEKAG; KKEIEKAGT; KEIEKAGTV;
EIEKAGTVK; IEKAGTVKL; EKAGTVKLF; KAGTVKLFL; AGTVKLFLD;
GTVKLFLDD; TVKLFLDDT; VKLFLDDTS; KLFLDDTSS; LFLDDTSSG;
FLDDTSSGS; LDDTSSGST; DDTSSGSTK; DTSSGSTKK; TSSGSTKKT;
SSGSTKKTA; SGSTKKTAV; GSTKKTAVW; STKKTAVWS; TKKTAVWSD;
KKTAVWSDT; KTAVWSDTS; TAVWSDTSN; AVWSDTSNT; VWSDTSNTL;
WSDTSNTLT; SDTSNTLTV; DTSNTLTVS; TSNTLTVSA; SNTLTVSAD;
NTLTVSADS; TLTVSADSK; LTVSADSKK; TVSADSKKI; VSADSKKIK;
SADSKKIKD; ADSKKIKDF; DSKKIKDFV; SKKIKDFVF; KKIKDFVFL;
KIKDFVFLT; IKDFVFLTD; KDFVFLTDG; DFVFLTDGT; FVFLTDGTI;
VFLTDGTIT; FLTDGTITV; LTDGTITVQ; TDGTITVQN; DGTITVQNY;
GTITVQNYD; TITVQNYDT; ITVQNYDTA; TVQNYDTAG; VQNYDTAGT;
QNYDTAGTK; NYDTAGTKL; YDTAGTKLA; DTAGTKLAG; TAGTKLAGT;
AGTKLAGTA; GTKLAGTAT; TKLAGTATE; KLAGTATEI; LAGTATEIK;
AGTATEIKD; GTATEIKDL; TATEIKDLE; ATEIKDLEA; TEIKDLEAL;
EIKDLEALK; IKDLEALKA; KDLEALKAA; DLEALKAAL; LEALKAALK;

10 mers:
MKKYLLGFAL; KKYLLGFALV; KYLLGFALVL; YLLGFALVLA; LLGFALVLAL;
LGFALVLALI; GFALVLALIA; FALVLALIAC; ALVLALIACG; LVLALIACGQ;
VLALIACGQK; LALIACGQKG; ALIACGQKGA; LIACGQKGAE; IACGQKGAEP;
ACGQKGAEPK; CGQKGAEPKH; GQKGAEPKHN; QKGAEPKHND; KGAEPKHNDQ;
GAEPKHNDQE; AEPKHNDQEV; EPKHNDQEVE; PKHNDQEVED; KHNDQEVEDS;
HNDQEVEDSK; NDQEVEDSKK; DQEVEDSKKD; QEVEDSKKDQ; EVEDSKKDQK;
VEDSKKDQKD; EDSKKDQKDA; DSKKDQKDAS; SKKDQKDASK; KKDQKDASKK;
KDQKDASKKD; DQKDASKKDL; QKDASKKDLP; KDASKKDLPL; DASKKDLPLV;
ASKKDLPLVT; SKKDLPLVTE; KKDLPLVTED; KDLPLVTEDT; DLPLVTEDTV;
LPLVTEDTVK; PLVTEDTVKL; LVTEDTVKLF; VTEDTVKLFN; TEDTVKLFND;
EDTVKLFNDT; DTVKLFNDTK; TVKLFNDTKI; VKLFNDTKIF; KLFNDTKIFI;
LFNDTKIFIS; FNDTKIFISK; NDTKIFISKE; DTKIFISKEK; TKIFISKEKN;
KIFISKEKNK; IFISKEKNKD; FISKEKNKDG; ISKEKNKDGK; SKEKNKDGKY;
KEKNKDGKYE; EKNKDGKYEL; KNKDGKYELR; NKDGKYELRA; KDGKYELRAT;
DGKYELRATV; GKYELRATVD; KYELRATVDT; YELRATVDTV; ELRATVDTVE;
LRATVDTVEL; RATVDTVELK; ATVDTVELKG; TVDTVELKGV; VDTVELKGVA;
DTVELKGVAD; TVELKGVADK; VELKGVADKN; ELKGVADKND; LKGVADKNDG;
KGVADKNDGS; GVADKNDGSG; VADKNDGSGG; ADKNDGSGGK; DKNDGSGGKL;
KNDGSGGKLE; NDGSGGKLEG; DGSGGKLEGV; GSGGKLEGVK; SGGKLEGVKS;
GGKLEGVKSD; GKLEGVKSDQ; KLEGVKSDQS; LEGVKSDQSK; EGVKSDQSKV;
GVKSDQSKVT; VKSDQSKVTM; KSDQSKVTMS; SDQSKVTMSI; DQSKVTMSIT;
QSKVTMSITD; SKVTMSITDD; KVTMSITDDL; VTMSITDDLN; TMSITDDLNT;
MSITDDLNTI; SITDDLNTIT; ITDDLNTITV; TDDLNTITVE; DDLNTITVET;
DLNTITVETY; LNTITVETYD; NTITVETYDS; TITVETYDSS; ITVETYDSSN;
TVETYDSSNT; VETYDSSNTK; ETYDSSNTKV; TYDSSNTKVA; YDSSNTKVAS;
DSSNTKVASK; SSNTKVASKV; SNTKVASKVF; NTKVASKVFK; TKVASKVFKK;
KVASKVFKKQ; VASKVFKKQG; ASKVFKKQGS; SKVFKKQGSL; KVFKKQGSLT;

VFKKQGSLTE; FKKQGSLTEE; KKQGSLTEET; KQGSLTEETE; QGSLTEETEE;
GSLTEETEET; SLTEETEETY; LTEETEETYK; TEETEETYKT; EETEETYKTG;
ETEETYKTGK; TEETYKTGKL; EETYKTGKLS; ETYKTGKLST; TYKTGKLSTK;
YKTGKLSTKK; KTGKLSTKKI; TGKLSTKKIT; GKLSTKKITR; KLSTKKITRT;
LSTKKITRTN; STKKITRTNG; TKKITRTNGT; KKITRTNGTT; KITRTNGTTL;
ITRTNGTTLE; TRTNGTTLEY; RTNGTTLEYS; TNGTTLEYSD; NGTTLEYSDM;
GTTLEYSDMT; TTLEYSDMTN; TLEYSDMTND; LEYSDMTNDE; EYSDMTNDEN;
YSDMTNDENA; SDMTNDENAT; DMTNDENATK; MTNDENATKA; TNDENATKAV;
NDENATKAVE; DENATKAVET; ENATKAVETL; NATKAVETLK; ATKAVETLKN;
TKAVETLKNG; KAVETLKNGI; AVETLKNGIM; VETLKNGIML; ETLKNGIMLE;
TLKNGIMLEG; LKNGIMLEGN; KNGIMLEGNL; NGIMLEGNLV; GIMLEGNLVG;
IMLEGNLVGG; MLEGNLVGGK; LEGNLVGGKT; EGNLVGGKTS; GNLVGGKTSV;
NLVGGKTSVE; LVGGKTSVEI; VGGKTSVEIK; GGKTSVEIKE; GKTSVEIKEG;
KTSVEIKEGT; TSVEIKEGTV; SVEIKEGTVT; VEIKEGTVTL; EIKEGTVTLK;
IKEGTVTLKK; KEGTVTLKKE; EGTVTLKKEI; GTVTLKKEIE; TVTLKKEIEK;
VTLKKEIEKA; TLKKEIEKAG; LKKEIEKAGT; KKEIEKAGTV; KEIEKAGTVK;
EIEKAGTVKL; IEKAGTVKLF; EKAGTVKLFL; KAGTVKLFLD; AGTVKLFLDD;
GTVKLFLDDT; TVKLFLDDTS; VKLFLDDTSS; KLFLDDTSSG; LFLDDTSSGS;
FLDDTSSGST; LDDTSSGSTK; DDTSSGSTKK; DTSSGSTKKT; TSSGSTKKTA;
SSGSTKKTAV; SGSTKKTAVW; GSTKKTAVWS; STKKTAVWSD; TKKTAVWSDT;
KKTAVWSDTS; KTAVWSDTSN; TAVWSDTSNT; AVWSDTSNTL; VWSDTSNTLT;
WSDTSNTLTV; SDTSNTLTVS; DTSNTLTVSA; TSNTLTVSAD; SNTLTVSADS;
NTLTVSADSK; TLTVSADSKK; LTVSADSKKI; TVSADSKKIK; VSADSKKIKD;
SADSKKIKDF; ADSKKIKDFV; DSKKIKDFVF; SKKIKDFVFL; KKIKDFVFLT;
KIKDFVFLTD; IKDFVFLTDG; KDFVFLTDGT; DFVFLTDGTI; FVFLTDGTIT;
VFLTDGTITV; FLTDGTITVQ; LTDGTITVQN; TDGTITVQNY; DGTITVQNYD;
GTITVQNYDT; TITVQNYDTA; ITVQNYDTAG; TVQNYDTAGT; VQNYDTAGTK;
QNYDTAGTKL; NYDTAGTKLA; YDTAGTKLAG; DTAGTKLAGT; TAGTKLAGTA;
AGTKLAGTAT; GTKLAGTATE; TKLAGTATEI; KLAGTATEIK; LAGTATEIKD;
AGTATEIKDL; GTATEIKDLE; TATEIKDLEA; ATEIKDLEAL; TEIKDLEALK;
EIKDLEALKA; IKDLEALKAA; KDLEALKAAL; DLEALKAALK;

11 mers:
MKKYLLGFALV; KKYLLGFALVL; KYLLGFALVLA; YLLGFALVLAL;
LLGFALVLALI; LGFALVLALIA; GFALVLALIAC; FALVLALIACG;
ALVLALIACGQ; LVLALIACGQK; VLALIACGQKG; LALIACGQKGA;
ALIACGQKGAE; LIACGQKGAEP; IACGQKGAEPK; ACGQKGAEPKH;
CGQKGAEPKHN; GQKGAEPKHND; QKGAEPKHNDQ; KGAEPKHNDQE;
GAEPKHNDQEV; AEPKHNDQEVE; EPKHNDQEVED; PKHNDQEVEDS;
KHNDQEVEDSK; HNDQEVEDSKK; NDQEVEDSKKD; DQEVEDSKKDQ;
QEVEDSKKDQK; EVEDSKKDQKD; VEDSKKDQKDA; EDSKKDQKDAS;
DSKKDQKDASK; SKKDQKDASKK; KKDQKDASKKD; KDQKDASKKDL;
DQKDASKKDLP; QKDASKKDLPL; KDASKKDLPLV; DASKKDLPLVT;
ASKKDLPLVTE; SKKDLPLVTED; KKDLPLVTEDT; KDLPLVTEDTV;
DLPLVTEDTVK; LPLVTEDTVKL; PLVTEDTVKLF; LVTEDTVKLFN;
VTEDTVKLFND; TEDTVKLFNDT; EDTVKLFNDTK; DTVKLFNDTKI;
TVKLFNDTKIF; VKLFNDTKIFI; KLFNDTKIFIS; LFNDTKIFISK;
FNDTKIFISKE; NDTKIFISKEK; DTKIFISKEKN; TKIFISKEKNK;
KIFISKEKNKD; IFISKEKNKDG; FISKEKNKDGK; ISKEKNKDGKY;
SKEKNKDGKYE; KEKNKDGKYEL; EKNKDGKYELR; KNKDGKYELRA;
NKDGKYELRAT; KDGKYELRATV; DGKYELRATVD; GKYELRATVDT;
KYELRATVDTV; YELRATVDTVE; ELRATVDTVEL; LRATVDTVELK;
RATVDTVELKG; ATVDTVELKGV; TVDTVELKGVA; VDTVELKGVAD;
DTVELKGVADK; TVELKGVADKN; VELKGVADKND; ELKGVADKNDG;
LKGVADKNDGS; KGVADKNDGSG; GVADKNDGSGG; VADKNDGSGGK;
ADKNDGSGGKL; DKNDGSGGKLE; KNDGSGGKLEG; NDGSGGKLEGV;
DGSGGKLEGVK; GSGGKLEGVKS; SGGKLEGVKSD; GGKLEGVKSDQ;

	GKLEGVKSDQS; KLEGVKSDQSK; LEGVKSDQSKV; EGVKSDQSKVT; GVKSDQSKVTM; VKSDQSKVTMS; KSDQSKVTMSI; SDQSKVTMSIT; DQSKVTMSITD; QSKVTMSITDD; SKVTMSITDDL; KVTMSITDDLN; VTMSITDDLNT; TMSITDDLNTI; MSITDDLNTIT; SITDDLNTITV; ITDDLNTITVE; TDDLNTITVET; DDLNTITVETY; DLNTITVETYD; LNTITVETYDS; NTITVETYDSS; TITVETYDSSN; ITVETYDSSNT; TVETYDSSNTK; VETYDSSNTKV; ETYDSSNTKVA; TYDSSNTKVAS; YDSSNTKVASK; DSSNTKVASKV; SSNTKVASKVF; SNTKVASKVFK; NTKVASKVFKK; TKVASKVFKKQ; KVASKVFKKQG; VASKVFKKQGS; ASKVFKKQGSL; SKVFKKQGSLT; KVFKKQGSLTE; VFKKQGSLTEE; FKKQGSLTEET; KKQGSLTEETE; KQGSLTEETEE; QGSLTEETEET; GSLTEETEETY; SLTEETEETYK; LTEETEETYKT; TEETEETYKTG; EETEETYKTGK; ETEETYKTGKL; TEETYKTGKLS; EETYKTGKLST; ETYKTGKLSTK; TYKTGKLSTKK; YKTGKLSTKKI; KTGKLSTKKIT; TGKLSTKKITR; GKLSTKKITRT; KLSTKKITRTN; LSTKKITRTNG; STKKITRTNGT; TKKITRTNGTT; KKITRTNGTTL; KITRTNGTTLE; ITRTNGTTLEY; TRTNGTTLEYS; RTNGTTLEYSD; TNGTTLEYSDM; NGTTLEYSDMT; GTTLEYSDMTN; TTLEYSDMTND; TLEYSDMTNDE; LEYSDMTNDEN; EYSDMTNDENA; YSDMTNDENAT; SDMTNDENATK; DMTNDENATKA; MTNDENATKAV; TNDENATKAVE; NDENATKAVET; DENATKAVETL; ENATKAVETLK; NATKAVETLKN; ATKAVETLKNG; TKAVETLKNGI; KAVETLKNGIM; AVETLKNGIML; VETLKNGIMLE; ETLKNGIMLEG; TLKNGIMLEGN; LKNGIMLEGNL; KNGIMLEGNLV; NGIMLEGNLVG; GIMLEGNLVGG; IMLEGNLVGGK; MLEGNLVGGKT; LEGNLVGGKTS; EGNLVGGKTSV; GNLVGGKTSVE; NLVGGKTSVEI; LVGGKTSVEIK; VGGKTSVEIKE; GGKTSVEIKEG; GKTSVEIKEGT; KTSVEIKEGTV; TSVEIKEGTVT; SVEIKEGTVTL; VEIKEGTVTLK; EIKEGTVTLKK; IKEGTVTLKKE; KEGTVTLKKEI; EGTVTLKKEIE; GTVTLKKEIEK; TVTLKKEIEKA; VTLKKEIEKAG; TLKKEIEKAGT; LKKEIEKAGTV; KKEIEKAGTVK; KEIEKAGTVKL; EIEKAGTVKLF; IEKAGTVKLFL; EKAGTVKLFLD; KAGTVKLFLDD; AGTVKLFLDDT; GTVKLFLDDTS; TVKLFLDDTSS; VKLFLDDTSSG; KLFLDDTSSGS; LFLDDTSSGST; FLDDTSSGSTK; LDDTSSGSTKK; DDTSSGSTKKT; DTSSGSTKKTA; TSSGSTKKTAV; SSGSTKKTAVW; SGSTKKTAVWS; GSTKKTAVWSD; STKKTAVWSDT; TKKTAVWSDTS; KKTAVWSDTSN; KTAVWSDTSNT; TAVWSDTSNTL; AVWSDTSNTLT; VWSDTSNTLTV; WSDTSNTLTVS; SDTSNTLTVSA; DTSNTLTVSAD; TSNTLTVSADS; SNTLTVSADSK; NTLTVSADSKK; TLTVSADSKKI; LTVSADSKKIK; TVSADSKKIKD; VSADSKKIKDF; SADSKKIKDFV; ADSKKIKDFVF; DSKKIKDFVFL; SKKIKDFVFLT; KKIKDFVFLTD; KIKDFVFLTDG; IKDFVFLTDGT; KDFVFLTDGTI; DFVFLTDGTIT; FVFLTDGTITV; VFLTDGTITVQ; FLTDGTITVQN; LTDGTITVQNY; TDGTITVQNYD; DGTITVQNYDT; GTITVQNYDTA; TITVQNYDTAG; ITVQNYDTAGT; TVQNYDTAGTK; VQNYDTAGTKL; QNYDTAGTKLA; NYDTAGTKLAG; YDTAGTKLAGT; DTAGTKLAGTA; TAGTKLAGTAT; AGTKLAGTATE; GTKLAGTATEI; TKLAGTATEIK; KLAGTATEIKD; LAGTATEIKDL; AGTATEIKDLE; GTATEIKDLEA; TATEIKDLEAL; ATEIKDLEALK; TEIKDLEALKA; EIKDLEALKAA; IKDLEALKAAL; KDLEALKAALK;
AAM22469.1| Outer surface protein C [Borrelia afzelii]	SEQ ID NO 12308-13117/ 8 mers: MKKNTLSA; KKNTLSAI; KNTLSAIL; NTLSAILM; TLSAILMT; LSAILMTL; SAILMTLF; AILMTLFL; ILMTLFLF; LMTLFLFI; MTLFLFIS; TLFLFISC; LFLFISCN; FLFISCNN; LFISCNNS; FISCNNSG; ISCNNSGK; SCNNSGKG; CNNSGKGG; NNSGKGGD; NSGKGGDS; SGKGGDSA; GKGGDSAS; KGGDSAST; GGDSASTN; GDSASTNP; DSASTNPA; SASTNPAD; ASTNPADE; STNPADES; TNPADESA; NPADESAK; PADESAKG; ADESAKGP; DESAKGPN; ESAKGPNL; SAKGPNLT; AKGPNLTE; KGPNLTEI; GPNLTEIS; PNLTEISK; NLTEISKK;

	LTEISKKI; TEISKKIT; EISKKITD; ISKKITDS; SKKITDSN; KKITDSNA; KITDSNAF; ITDSNAFV; TDSNAFVL; DSNAFVLA; SNAFVLAV; NAFVLAVK; AFVLAVKE; FVLAVKEV; VLAVKEVE; LAVKEVET; AVKEVETL; VKEVETLV; KEVETLVS; EVETLVSS; VETLVSSI; ETLVSSID; TLVSSIDE; LVSSIDEL; VSSIDELA; SSIDELAN; SIDELANK; IDELANKA; DELANKAI; ELANKAIG; LANKAIGK; ANKAIGKK; NKAIGKKI; KAIGKKIQ; AIGKKIQQ; IGKKIQQN; GKKIQQNG; KKIQQNGL; KIQQNGLG; IQQNGLGA; QQNGLGAE; QNGLGAEA; NGLGAEAN; GLGAEANR; LGAEANRN; GAEANRNE; AEANRNES; EANRNESL; ANRNESLL; NRNESLLA; RNESLLAG; NESLLAGV; ESLLAGVH; SLLAGVHE; LLAGVHEI; LAGVHEIS; AGVHEIST; GVHEISTL; VHEISTLI; HEISTLIT; EISTLITE; ISTLITEK; STLITEKL; TLITEKLS; LITEKLSK; ITEKLSKL; TEKLSKLK; EKLSKLKN; KLSKLKNS; LSKLKNSG; SKLKNSGE; KLKNSGEL; LKNSGELK; KNSGELKA; NSGELKAK; SGELKAKI; GELKAKIE; ELKAKIED; LKAKIEDA; KAKIEDAK; AKIEDAKK; KIEDAKKC; IEDAKKCS; EDAKKCSE; DAKKCSEE; AKKCSEEF; KKCSEEFT; KCSEEFTN; CSEEFTNK; SEEFTNKL; EEFTNKLR; EFTNKLRV; FTNKLRVS; TNKLRVSH; NKLRVSHA; KLRVSHAD; LRVSHADL; RVSHADLG; VSHADLGK; SHADLGKQ; HADLGKQG; ADLGKQGV; DLGKQGVN; LGKQGVND; GKQGVNDD; KQGVNDDD; QGVNDDDA; GVNDDDAK; VNDDDAKK; NDDDAKKA; DDDAKKAI; DDAKKAIL; DAKKAILK; AKKAILKT; KKAILKTN; KAILKTNA; AILKTNAD; ILKTNADK; LKTNADKT; KTNADKTK; TNADKTKG; NADKTKGA; ADKTKGAE; DKTKGAEE; KTKGAEEL; TKGAEELG; KGAEELGK; GAEELGKL; AEELGKLF; EELGKLFK; ELGKLFKS; LGKLFKSV; GKLFKSVE; KLFKSVEG; LFKSVEGL; FKSVEGLV; KSVEGLVK; SVEGLVKA; VEGLVKAA; EGLVKAAQ; GLVKAAQE; LVKAAQEA; VKAAQEAL; KAAQEALT; AAQEALTN; AQEALTNS; QEALTNSV; EALTNSVK; ALTNSVKE; LTNSVKEL; TNSVKELT; NSVKELTS; SVKELTSP; VKELTSPV; KELTSPVV; ELTSPVVA; LTSPVVAE; TSPVVAES; SPVVAESP; PVVAESPK; VVAESPKK; VAESPKKP; 9 mers: MKKNTLSAI; KKNTLSAIL; KNTLSAILM; NTLSAILMT; TLSAILMTL; LSAILMTLF; SAILMTLFL; AILMTLFLF; ILMTLFLFI; LMTLFLFIS; MTLFLFISC; TLFLFISCN; LFLFISCNN; FLFISCNNS; LFISCNNSG; FISCNNSGK; ISCNNSGKG; SCNNSGKGG; CNNSGKGGD; NNSGKGGDS; NSGKGGDSA; SGKGGDSAS; GKGGDSAST; KGGDSASTN; GGDSASTNP; GDSASTNPA; DSASTNPAD; SASTNPADE; ASTNPADES; STNPADESA; TNPADESAK; NPADESAKG; PADESAKGP; ADESAKGPN; DESAKGPNL; ESAKGPNLT; SAKGPNLTE; AKGPNLTEI; KGPNLTEIS; GPNLTEISK; PNLTEISKK; NLTEISKKI; LTEISKKIT; TEISKKITD; EISKKITDS; ISKKITDSN; SKKITDSNA; KKITDSNAF; KITDSNAFV; ITDSNAFVL; TDSNAFVLA; DSNAFVLAV; SNAFVLAVK; NAFVLAVKE; AFVLAVKEV; FVLAVKEVE; VLAVKEVET; LAVKEVETL; AVKEVETLV; VKEVETLVS; KEVETLVSS; EVETLVSSI; VETLVSSID; ETLVSSIDE; TLVSSIDEL; LVSSIDELA; VSSIDELAN; SSIDELANK; SIDELANKA; IDELANKAI; DELANKAIG; ELANKAIGK; LANKAIGKK; ANKAIGKKI; NKAIGKKIQ; KAIGKKIQQ; AIGKKIQQN; IGKKIQQNG; GKKIQQNGL; KKIQQNGLG; KIQQNGLGA; IQQNGLGAE; QQNGLGAEA; QNGLGAEAN; NGLGAEANR; GLGAEANRN; LGAEANRNE; GAEANRNES; AEANRNESL; EANRNESLL; ANRNESLLA; NRNESLLAG; RNESLLAGV; NESLLAGVH; ESLLAGVHE; SLLAGVHEI; LLAGVHEIS; LAGVHEIST; AGVHEISTL; GVHEISTLI; VHEISTLIT; HEISTLITE; EISTLITEK; ISTLITEKL; STLITEKLS; TLITEKLSK; LITEKLSKL; ITEKLSKLK; TEKLSKLKN; EKLSKLKNS; KLSKLKNSG; LSKLKNSGE; SKLKNSGEL; KLKNSGELK; LKNSGELKA; KNSGELKAK; NSGELKAKI; SGELKAKIE; GELKAKIED; ELKAKIEDA; LKAKIEDAK; KAKIEDAKK; AKIEDAKKC; KIEDAKKCS; IEDAKKCSE; EDAKKCSEE; DAKKCSEEF; AKKCSEEFT; KKCSEEFTN; KCSEEFTNK; CSEEFTNKL; SEEFTNKLR; EEFTNKLRV; EFTNKLRVS; FTNKLRVSH; TNKLRVSHA; NKLRVSHAD; KLRVSHADL; LRVSHADLG; RVSHADLGK;

VSHADLGKQ; SHADLGKQG; HADLGKQGV; ADLGKQGVN; DLGKQGVND;
LGKQGVNDD; GKQGVNDDD; KQGVNDDDA; QGVNDDDAK; GVNDDDAKK;
VNDDDAKKA; NDDDAKKAI; DDDAKKAIL; DDAKKAILK; DAKKAILKT;
AKKAILKTN; KKAILKTNA; KAILKTNAD; AILKTNADK; ILKTNADKT;
LKTNADKTK; KTNADKTKG; TNADKTKGA; NADKTKGAE; ADKTKGAEE;
DKTKGAEEL; KTKGAEELG; TKGAEELGK; KGAEELGKL; GAEELGKLF;
AEELGKLFK; EELGKLFKS; ELGKLFKSV; LGKLFKSVE; GKLFKSVEG;
KLFKSVEGL; LFKSVEGLV; FKSVEGLVK; KSVEGLVKA; SVEGLVKAA;
VEGLVKAAQ; EGLVKAAQE; GLVKAAQEA; LVKAAQEAL; VKAAQEALT;
KAAQEALTN; AAQEALTNS; AQEALTNSV; QEALTNSVK; EALTNSVKE;
ALTNSVKEL; LTNSVKELT; TNSVKELTS; NSVKELTSP; SVKELTSPV;
VKELTSPVV; KELTSPVVA; ELTSPVVAE; LTSPVVAES; TSPVVAESP;
SPVVAESPK; PVVAESPKK; VVAESPKKP;

10 mers:
MKKNTLSAIL; KKNTLSAILM; KNTLSAILMT; NTLSAILMTL; TLSAILMTLF;
LSAILMTLFL; SAILMTLFLF; AILMTLFLFI; ILMTLFLFIS; LMTLFLFISC;
MTLFLFISCN; TLFLFISCNN; LFLFISCNNS; FLFISCNNSG; LFISCNNSGK;
FISCNNSGKG; ISCNNSGKGG; SCNNSGKGGD; CNNSGKGGDS; NNSGKGGDSA;
NSGKGGDSAS; SGKGGDSAST; GKGGDSASTN; KGGDSASTNP; GGDSASTNPA;
GDSASTNPAD; DSASTNPADE; SASTNPADES; ASTNPADESA; STNPADESAK;
TNPADESAKG; NPADESAKGP; PADESAKGPN; ADESAKGPNL; DESAKGPNLT;
ESAKGPNLTE; SAKGPNLTEI; AKGPNLTEIS; KGPNLTEISK; GPNLTEISKK;
PNLTEISKKI; NLTEISKKIT; LTEISKKITD; TEISKKITDS; EISKKITDSN;
ISKKITDSNA; SKKITDSNAF; KKITDSNAFV; KITDSNAFVL; ITDSNAFVLA;
TDSNAFVLAV; DSNAFVLAVK; SNAFVLAVKE; NAFVLAVKEV; AFVLAVKEVE;
FVLAVKEVET; VLAVKEVETL; LAVKEVETLV; AVKEVETLVS; VKEVETLVSS;
KEVETLVSSI; EVETLVSSID; VETLVSSIDE; ETLVSSIDEL; TLVSSIDELA;
LVSSIDELAN; VSSIDELANK; SSIDELANKA; SIDELANKAI; IDELANKAIG;
DELANKAIGK; ELANKAIGKK; LANKAIGKKI; ANKAIGKKIQ; NKAIGKKIQQ;
KAIGKKIQQN; AIGKKIQQNG; IGKKIQQNGL; GKKIQQNGLG; KKIQQNGLGA;
KIQQNGLGAE; IQQNGLGAEA; QQNGLGAEAN; QNGLGAEANR; NGLGAEANRN;
GLGAEANRNE; LGAEANRNES; GAEANRNESL; AEANRNESLL; EANRNESLLA;
ANRNESLLAG; NRNESLLAGV; RNESLLAGVH; NESLLAGVHE; ESLLAGVHEI;
SLLAGVHEIS; LLAGVHEIST; LAGVHEISTL; AGVHEISTLI; GVHEISTLIT;
VHEISTLITE; HEISTLITEK; EISTLITEKL; ISTLITEKLS; STLITEKLSK;
TLITEKLSKL; LITEKLSKLK; ITEKLSKLKN; TEKLSKLKNS; EKLSKLKNSG;
KLSKLKNSGE; LSKLKNSGEL; SKLKNSGELK; KLKNSGELKA; LKNSGELKAK;
KNSGELKAKI; NSGELKAKIE; SGELKAKIED; GELKAKIEDA; ELKAKIEDAK;
LKAKIEDAKK; KAKIEDAKKC; AKIEDAKKCS; KIEDAKKCSE; IEDAKKCSEE;
EDAKKCSEEF; DAKKCSEEFT; AKKCSEEFTN; KKCSEEFTNK; KCSEEFTNKL;
CSEEFTNKLR; SEEFTNKLRV; EEFTNKLRVS; EFTNKLRVSH; FTNKLRVSHA;
TNKLRVSHAD; NKLRVSHADL; KLRVSHADLG; LRVSHADLGK; RVSHADLGKQ;
VSHADLGKQG; SHADLGKQGV; HADLGKQGVN; ADLGKQGVND; DLGKQGVNDD;
LGKQGVNDDD; GKQGVNDDDA; KQGVNDDDAK; QGVNDDDAKK; GVNDDDAKKA;
VNDDDAKKAI; NDDDAKKAIL; DDDAKKAILK; DDAKKAILKT; DAKKAILKTN;
AKKAILKTNA; KKAILKTNAD; KAILKTNADK; AILKTNADKT; ILKTNADKTK;
LKTNADKTKG; KTNADKTKGA; TNADKTKGAE; NADKTKGAEE; ADKTKGAEEL;
DKTKGAEELG; KTKGAEELGK; TKGAEELGKL; KGAEELGKLF; GAEELGKLFK;
AEELGKLFKS; EELGKLFKSV; ELGKLFKSVE; LGKLFKSVEG; GKLFKSVEGL;
KLFKSVEGLV; LFKSVEGLVK; FKSVEGLVKA; KSVEGLVKAA; SVEGLVKAAQ;
VEGLVKAAQE; EGLVKAAQEA; GLVKAAQEAL; LVKAAQEALT; VKAAQEALTN;
KAAQEALTNS; AAQEALTNSV; AQEALTNSVK; QEALTNSVKE; EALTNSVKEL;
ALTNSVKELT; LTNSVKELTS; TNSVKELTSP; NSVKELTSPV; SVKELTSPVV;
VKELTSPVVA; KELTSPVVAE; ELTSPVVAES; LTSPVVAESP; TSPVVAESPK;
SPVVAESPKK; PVVAESPKKP;

	11 mers: MKKNTLSAILM; KKNTLSAILMT; KNTLSAILMTL; NTLSAILMTLF; TLSAILMTLFL; LSAILMTLFLF; SAILMTLFLFI; AILMTLFLFIS; ILMTLFLFISC; LMTLFLFISCN; MTLFLFISCNN; TLFLFISCNNS; LFLFISCNNSG; FLFISCNNSGK; LFISCNNSGKG; FISCNNSGKGG; ISCNNSGKGGD; SCNNSGKGGDS; CNNSGKGGDSA; NNSGKGGDSAS; NSGKGGDSAST; SGKGGDSASTN; GKGGDSASTNP; KGGDSASTNPA; GGDSASTNPAD; GDSASTNPADE; DSASTNPADES; SASTNPADESA; ASTNPADESAK; STNPADESAKG; TNPADESAKGP; NPADESAKGPN; PADESAKGPNL; ADESAKGPNLT; DESAKGPNLTE; ESAKGPNLTEI; SAKGPNLTEIS; AKGPNLTEISK; KGPNLTEISKK; GPNLTEISKKI; PNLTEISKKIT; NLTEISKKITD; LTEISKKITDS; TEISKKITDSN; EISKKITDSNA; ISKKITDSNAF; SKKITDSNAFV; KKITDSNAFVL; KITDSNAFVLA; ITDSNAFVLAV; TDSNAFVLAVK; DSNAFVLAVKE; SNAFVLAVKEV; NAFVLAVKEVE; AFVLAVKEVET; FVLAVKEVETL; VLAVKEVETLV; LAVKEVETLVS; AVKEVETLVSS; VKEVETLVSSI; KEVETLVSSID; EVETLVSSIDE; VETLVSSIDEL; ETLVSSIDELA; TLVSSIDELAN; LVSSIDELANK; VSSIDELANKA; SSIDELANKAI; SIDELANKAIG; IDELANKAIGK; DELANKAIGKK; ELANKAIGKKI; LANKAIGKKIQ; ANKAIGKKIQQ; NKAIGKKIQQN; KAIGKKIQQNG; AIGKKIQQNGL; IGKKIQQNGLG; GKKIQQNGLGA; KKIQQNGLGAE; KIQQNGLGAEA; IQQNGLGAEAN; QQNGLGAEANR; QNGLGAEANRN; NGLGAEANRNE; GLGAEANRNES; LGAEANRNESL; GAEANRNESLL; AEANRNESLLA; EANRNESLLAG; ANRNESLLAGV; NRNESLLAGVH; RNESLLAGVHE; NESLLAGVHEI; ESLLAGVHEIS; SLLAGVHEIST; LLAGVHEISTL; LAGVHEISTLI; AGVHEISTLIT; GVHEISTLITE; VHEISTLITEK; HEISTLITEKL; EISTLITEKLS; ISTLITEKLSK; STLITEKLSKL; TLITEKLSKLK; LITEKLSKLKN; ITEKLSKLKNS; TEKLSKLKNSG; EKLSKLKNSGE; KLSKLKNSGEL; LSKLKNSGELK; SKLKNSGELKA; KLKNSGELKAK; LKNSGELKAKI; KNSGELKAKIE; NSGELKAKIED; SGELKAKIEDA; GELKAKIEDAK; ELKAKIEDAKK; LKAKIEDAKKC; KAKIEDAKKCS; AKIEDAKKCSE; KIEDAKKCSEE; IEDAKKCSEEF; EDAKKCSEEFT; DAKKCSEEFTN; AKKCSEEFTNK; KKCSEEFTNKL; KCSEEFTNKLR; CSEEFTNKLRV; SEEFTNKLRVS; EEFTNKLRVSH; EFTNKLRVSHA; FTNKLRVSHAD; TNKLRVSHADL; NKLRVSHADLG; KLRVSHADLGK; LRVSHADLGKQ; RVSHADLGKQG; VSHADLGKQGV; SHADLGKQGVN; HADLGKQGVND; ADLGKQGVNDD; DLGKQGVNDDD; LGKQGVNDDDA; GKQGVNDDDAK; KQGVNDDDAKK; QGVNDDDAKKA; GVNDDDAKKAI; VNDDDAKKAIL; NDDDAKKAILK; DDDAKKAILKT; DDAKKAILKTN; DAKKAILKTNA; AKKAILKTNAD; KKAILKTNADK; KAILKTNADKT; AILKTNADKTK; ILKTNADKTKG; LKTNADKTKGA; KTNADKTKGAE; TNADKTKGAEE; NADKTKGAEEL; ADKTKGAEELG; DKTKGAEELGK; KTKGAEELGKL; TKGAEELGKLF; KGAEELGKLFK; GAEELGKLFKS; AEELGKLFKSV; EELGKLFKSVE; ELGKLFKSVEG; LGKLFKSVEGL; GKLFKSVEGLV; KLFKSVEGLVK; LFKSVEGLVKA; FKSVEGLVKAA; KSVEGLVKAAQ; SVEGLVKAAQE; VEGLVKAAQEA; EGLVKAAQEAL; GLVKAAQEALT; LVKAAQEALTN; VKAAQEALTNS; KAAQEALTNSV; AAQEALTNSVK; AQEALTNSVKE; QEALTNSVKEL; EALTNSVKELT; ALTNSVKELTS; LTNSVKELTSP; TNSVKELTSPV; NSVKELTSPVV; SVKELTSPVVA; VKELTSPVVAE; KELTSPVVAES; ELTSPVVAESP; LTSPVVAESPK; TSPVVAESPKK; SPVVAESPKKP;
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]	SEQ ID NO 13118-13799 8 mers: MNKKMKMF; NKKMKMFI; KKMKMFII; KMKMFIIC; MKMFIICA; KMFIICAV; MFIICAVF; FIICAVFV; IICAVFVL; ICAVFVLI; CAVFVLIS; AVFVLISS;

VFVLISSC; FVLISSCG; VLISSCGN; LISSCGNF; ISSCGNFR; SSCGNFRS; SCGNFRSS; CGNFRSSL; GNFRSSLS; NFRSSLSD; FRSSLSDQ; RSSLSDQG; SSLSDQGS; SLSDQGSL; LSDQGSLS; SDQGSLSD; DQGSLSDQ; QGSLSDQG; GSLSDQGS; SLSDQGSL; LSDQGSLS; SDQGSLSD; DQGSLSDQ; QGSLSDQG; GSLSDQGS; SLSDQGSL; LSDQGSLS; SDQGSLSD; DQGSLSDQ; QGSLSDQG; GSLSDQGG; SLSDQGGL; LSDQGGLS; SDQGGLSG; DQGGLSGQ; QGGLSGQA; GGLSGQAS; GLSGQASS; LSGQASSD; SGQASSDT; GQASSDTI; QASSDTIK; ASSDTIKF; SSDTIKFS; SDTIKFSE; DTIKFSEF; TIKFSEFT; IKFSEFTV; KFSEFTVN; FSEFTVNI; SEFTVNIK; EFTVNIKN; FTVNIKNK; TVNIKNKK; VNIKNKKD; NIKNKKDN; IKNKKDNN; KNKKDNNG; NKKDNNGD; KKDNNGDW; KDNNGDWS; DNNGDWSN; NNGDWSNL; NGDWSNLG; GDWSNLGT; DWSNLGTL; WSNLGTLV; SNLGTLVI; NLGTLVIR; LGTLVIRK; GTLVIRKE; TLVIRKEQ; LVIRKEQD; VIRKEQDG; IRKEQDGV; RKEQDGVE; KEQDGVET; EQDGVETG; QDGVETGL; DGVETGLN; GVETGLNV; VETGLNVI; ETGLNVIG; TGLNVIGT; GLNVIGTI; LNVIGTIN; NVIGTING; VIGTINGQ; IGTINGQL; GTINGQLR; TINGQLRG; INGQLRGH; NGQLRGHS; GQLRGHSA; QLRGHSAT; LRGHSATF; RGHSATFF; GHSATFFC; HSATFFCI; SATFFCIE; ATFFCIEE; TFFCIEEA; FFCIEEAE; FCIEEAEV; CIEEAEVN; IEEAEVNN; EEAEVNNF; EAEVNNFV; AEVNNFVK; EVNNFVKA; VNNFVKAM; NNFVKAMT; NFVKAMTN; FVKAMTNV; VKAMTNVG; KAMTNVGS; AMTNVGSF; MTNVGSFK; TNVGSFKT; NVGSFKTS; VGSFKTSL; GSFKTSLY; SFKTSLYY; FKTSLYYG; KTSLYYGY; TSLYYGYK; SLYYGYKE; LYYGYKEE; YYGYKEEQ; YGYKEEQS; GYKEEQSS; YKEEQSST; KEEQSSTN; EEQSSTNG; EQSSTNGI; QSSTNGIK; SSTNGIKG; STNGIKGK; TNGIKGKE; NGIKGKEI; GIKGKEIT; IKGKEITT; KGKEITTK; GKEITTKI; KEITTKIE; EITTKIET; ITTKIETI; TTKIETIN; TKIETINN; KIETINNS; IETINNSE; ETINNSEH; TINNSEHI; INNSEHIT; NNSEHITF; NSEHITFS; SEHITFSG; EHITFSGD; HITFSGDK; ITFSGDKI;

9 mers:
MNKKMKMFI; NKKMKMFII; KKMKMFIIC; KMKMFIICA; MKMFIICAV; KMFIICAVF; MFIICAVFV; FIICAVFVL; IICAVFVLI; ICAVFVLIS; CAVFVLISS; AVFVLISSC; VFVLISSCG; FVLISSCGN; VLISSCGNF; LISSCGNFR; ISSCGNFRS; SSCGNFRSS; SCGNFRSSL; CGNFRSSLS; GNFRSSLSD; NFRSSLSDQ; FRSSLSDQG; RSSLSDQGS; SSLSDQGSL; SLSDQGSLS; LSDQGSLSD; SDQGSLSDQ; DQGSLSDQG; QGSLSDQGS; GSLSDQGSL; SLSDQGSLS; LSDQGSLSD; SDQGSLSDQ; DQGSLSDQG; QGSLSDQGS; GSLSDQGSL; SLSDQGSLS; LSDQGSLSD; SDQGSLSDQ; DQGSLSDQG; QGSLSDQGG; GSLSDQGGL; SLSDQGGLS; LSDQGGLSG; SDQGGLSGQ; DQGGLSGQA; QGGLSGQAS; GGLSGQASS; GLSGQASSD; LSGQASSDT; SGQASSDTI; GQASSDTIK; QASSDTIKF; ASSDTIKFS; SSDTIKFSE; SDTIKFSEF; DTIKFSEFT; TIKFSEFTV; IKFSEFTVN; KFSEFTVNI; FSEFTVNIK; SEFTVNIKN; EFTVNIKNK; FTVNIKNKK; TVNIKNKKD; VNIKNKKDN; NIKNKKDNN; IKNKKDNNG; KNKKDNNGD; NKKDNNGDW; KKDNNGDWS; KDNNGDWSN; DNNGDWSNL; NNGDWSNLG; NGDWSNLGT; GDWSNLGTL; DWSNLGTLV; WSNLGTLVI; SNLGTLVIR; NLGTLVIRK; LGTLVIRKE; GTLVIRKEQ; TLVIRKEQD; LVIRKEQDG; VIRKEQDGV; IRKEQDGVE; RKEQDGVET; KEQDGVETG; EQDGVETGL; QDGVETGLN; DGVETGLNV; GVETGLNVI; VETGLNVIG; ETGLNVIGT; TGLNVIGTI; GLNVIGTIN; LNVIGTING; NVIGTINGQ; VIGTINGQL; IGTINGQLR; GTINGQLRG; TINGQLRGH; INGQLRGHS; NGQLRGHSA; GQLRGHSAT; QLRGHSATF; LRGHSATFF; RGHSATFFC; GHSATFFCI; HSATFFCIE; SATFFCIEE; ATFFCIEEA; TFFCIEEAE; FFCIEEAEV; FCIEEAEVN; CIEEAEVNN; IEEAEVNNF; EEAEVNNFV; EAEVNNFVK; AEVNNFVKA; EVNNFVKAM; VNNFVKAMT; NNFVKAMTN; NFVKAMTNV; FVKAMTNVG; VKAMTNVGS; KAMTNVGSF; AMTNVGSFK; MTNVGSFKT; TNVGSFKTS; NVGSFKTSL; VGSFKTSLY; GSFKTSLYY; SFKTSLYYG; FKTSLYYGY; KTSLYYGYK; TSLYYGYKE; SLYYGYKEE; LYYGYKEEQ;

YYGYKEEQS; YGYKEEQSS; GYKEEQSST; YKEEQSSTN; KEEQSSTNG;
EEQSSTNGI; EQSSTNGIK; QSSTNGIKG; SSTNGIKGK; STNGIKGKE;
TNGIKGKEI; NGIKGKEIT; GIKGKEITT; IKGKEITTK; KGKEITTKI;
GKEITTKIE; KEITTKIET; EITTKIETI; ITTKIETIN; TTKIETINN;
TKIETINNS; KIETINNSE; IETINNSEH; ETINNSEHI; TINNSEHIT;
INNSEHITF; NNSEHITFS; NSEHITFSG; SEHITFSGD; EHITFSGDK;
HITFSGDKI;

10 mers:
MNKKMKMFII; NKKMKMFIIC; KKMKMFIICA; KMKMFIICAV; MKMFIICAVF;
KMFIICAVFV; MFIICAVFVL; FIICAVFVLI; IICAVFVLIS; ICAVFVLISS;
CAVFVLISSC; AVFVLISSCG; VFVLISSCGN; FVLISSCGNF; VLISSCGNFR;
LISSCGNFRS; ISSCGNFRSS; SSCGNFRSSL; SCGNFRSSLS; CGNFRSSLSD;
GNFRSSLSDQ; NFRSSLSDQG; FRSSLSDQGS; RSSLSDQGSL; SSLSDQGSLS;
SLSDQGSLSD; LSDQGSLSDQ; SDQGSLSDQG; DQGSLSDQGS; QGSLSDQGSL;
GSLSDQGSLS; SLSDQGSLSD; LSDQGSLSDQ; SDQGSLSDQG; DQGSLSDQGS;
QGSLSDQGSL; GSLSDQGSLS; SLSDQGSLSD; LSDQGSLSDQ; SDQGSLSDQG;
DQGSLSDQGG; QGSLSDQGGL; GSLSDQGGLS; SLSDQGGLSG; LSDQGGLSGQ;
SDQGGLSGQA; DQGGLSGQAS; QGGLSGQASS; GGLSGQASSD; GLSGQASSDT;
LSGQASSDTI; SGQASSDTIK; GQASSDTIKF; QASSDTIKFS; ASSDTIKFSE;
SSDTIKFSEF; SDTIKFSEFT; DTIKFSEFTV; TIKFSEFTVN; IKFSEFTVNI;
KFSEFTVNIK; FSEFTVNIKN; SEFTVNIKNK; EFTVNIKNKK; FTVNIKNKKD;
TVNIKNKKDN; VNIKNKKDNN; NIKNKKDNNG; IKNKKDNNGD; KNKKDNNGDW;
NKKDNNGDWS; KKDNNGDWSN; KDNNGDWSNL; DNNGDWSNLG; NNGDWSNLGT;
NGDWSNLGTL; GDWSNLGTLV; DWSNLGTLVI; WSNLGTLVIR; SNLGTLVIRK;
NLGTLVIRKE; LGTLVIRKEQ; GTLVIRKEQD; TLVIRKEQDG; LVIRKEQDGV;
VIRKEQDGVE; IRKEQDGVET; RKEQDGVETG; KEQDGVETGL; EQDGVETGLN;
QDGVETGLNV; DGVETGLNVI; GVETGLNVIG; VETGLNVIGT; ETGLNVIGTI;
TGLNVIGTIN; GLNVIGTING; LNVIGTINGQ; NVIGTINGQL; VIGTINGQLR;
IGTINGQLRG; GTINGQLRGH; TINGQLRGHS; INGQLRGHSA; NGQLRGHSAT;
GQLRGHSATF; QLRGHSATFF; LRGHSATFFC; RGHSATFFCI; GHSATFFCIE;
HSATFFCIEE; SATFFCIEEA; ATFFCIEEAE; TFFCIEEAEV; FFCIEEAEVN;
FCIEEAEVNN; CIEEAEVNNF; IEEAEVNNFV; EEAEVNNFVK; EAEVNNFVKA;
AEVNNFVKAM; EVNNFVKAMT; VNNFVKAMTN; NNFVKAMTNV; NFVKAMTNVG;
FVKAMTNVGS; VKAMTNVGSF; KAMTNVGSFK; AMTNVGSFKT; MTNVGSFKTS;
TNVGSFKTSL; NVGSFKTSLY; VGSFKTSLYY; GSFKTSLYYG; SFKTSLYYGY;
FKTSLYYGYK; KTSLYYGYKE; TSLYYGYKEE; SLYYGYKEEQ; LYYGYKEEQS;
YYGYKEEQSS; YGYKEEQSST; GYKEEQSSTN; YKEEQSSTNG; KEEQSSTNGI;
EEQSSTNGIK; EQSSTNGIKG; QSSTNGIKGK; SSTNGIKGKE; STNGIKGKEI;
TNGIKGKEIT; NGIKGKEITT; GIKGKEITTK; IKGKEITTKI; KGKEITTKIE;
GKEITTKIET; KEITTKIETI; EITTKIETIN; ITTKIETINN; TTKIETINNS;
TKIETINNSE; KIETINNSEH; IETINNSEHI; ETINNSEHIT; TINNSEHITF;
INNSEHITFS; NNSEHITFSG; NSEHITFSGD; SEHITFSGDK; EHITFSGDKI;

11 mers:
MNKKMKMFIIC; NKKMKMFIICA; KKMKMFIICAV; KMKMFIICAVF;
MKMFIICAVFV; KMFIICAVFVL; MFIICAVFVLI; FIICAVFVLIS;
IICAVFVLISS; ICAVFVLISSC; CAVFVLISSCG; AVFVLISSCGN;
VFVLISSCGNF; FVLISSCGNFR; VLISSCGNFRS; LISSCGNFRSS;
ISSCGNFRSSL; SSCGNFRSSLS; SCGNFRSSLSD; CGNFRSSLSDQ;
GNFRSSLSDQG; NFRSSLSDQGS; FRSSLSDQGSL; RSSLSDQGSLS;
SSLSDQGSLSD; SLSDQGSLSDQ; LSDQGSLSDQG; SDQGSLSDQGS;
DQGSLSDQGSL; QGSLSDQGSLS; GSLSDQGSLSD; SLSDQGSLSDQ;
LSDQGSLSDQG; SDQGSLSDQGS; DQGSLSDQGSL; QGSLSDQGSLS;
GSLSDQGSLSD; SLSDQGSLSDQ; LSDQGSLSDQG; SDQGSLSDQGG;
DQGSLSDQGGL; QGSLSDQGGLS; GSLSDQGGLSG; SLSDQGGLSGQ;
LSDQGGLSGQA; SDQGGLSGQAS; DQGGLSGQASS; QGGLSGQASSD;

	GGLSGQASSDT; GLSGQASSDTI; LSGQASSDTIK; SGQASSDTIKF; GQASSDTIKFS; QASSDTIKFSE; ASSDTIKFSEF; SSDTIKFSEFT; SDTIKFSEFTV; DTIKFSEFTVN; TIKFSEFTVNI; IKFSEFTVNIK; KFSEFTVNIKN; FSEFTVNIKNK; SEFTVNIKNKK; EFTVNIKNKKD; FTVNIKNKKDN; TVNIKNKKDNN; VNIKNKKDNNG; NIKNKKDNNGD; IKNKKDNNGDW; KNKKDNNGDWS; NKKDNNGDWSN; KKDNNGDWSNL; KDNNGDWSNLG; DNNGDWSNLGT; NNGDWSNLGTL; NGDWSNLGTLV; GDWSNLGTLVI; DWSNLGTLVIR; WSNLGTLVIRK; SNLGTLVIRKE; NLGTLVIRKEQ; LGTLVIRKEQD; GTLVIRKEQDG; TLVIRKEQDGV; LVIRKEQDGVE; VIRKEQDGVET; IRKEQDGVETG; RKEQDGVETGL; KEQDGVETGLN; EQDGVETGLNV; QDGVETGLNVI; DGVETGLNVIG; GVETGLNVIGT; VETGLNVIGTI; ETGLNVIGTIN; TGLNVIGTING; GLNVIGTINGQ; LNVIGTINGQL; NVIGTINGQLR; VIGTINGQLRG; IGTINGQLRGH; GTINGQLRGHS; TINGQLRGHSA; INGQLRGHSAT; NGQLRGHSATF; GQLRGHSATFF; QLRGHSATFFC; LRGHSATFFCI; RGHSATFFCIE; GHSATFFCIEE; HSATFFCIEEA; SATFFCIEEAE; ATFFCIEEAEV; TFFCIEEAEVN; FFCIEEAEVNN; FCIEEAEVNNF; CIEEAEVNNFV; IEEAEVNNFVK; EEAEVNNFVKA; EAEVNNFVKAM; AEVNNFVKAMT; EVNNFVKAMTN; VNNFVKAMTNV; NNFVKAMTNVG; NFVKAMTNVGS; FVKAMTNVGSF; VKAMTNVGSFK; KAMTNVGSFKT; AMTNVGSFKTS; MTNVGSFKTSL; TNVGSFKTSLY; NVGSFKTSLYY; VGSFKTSLYYG; GSFKTSLYYGY; SFKTSLYYGYK; FKTSLYYGYKE; KTSLYYGYKEE; TSLYYGYKEEQ; SLYYGYKEEQS; LYYGYKEEQSS; YYGYKEEQSST; YGYKEEQSSTN; GYKEEQSSTNG; YKEEQSSTNGI; KEEQSSTNGIK; EEQSSTNGIKG; EQSSTNGIKGK; QSSTNGIKGKE; SSTNGIKGKEI; STNGIKGKEIT; TNGIKGKEITT; NGIKGKEITTK; GIKGKEITTKI; IKGKEITTKIE; KGKEITTKIET; GKEITTKIETI; KEITTKIETIN; EITTKIETINN; ITTKIETINNS; TTKIETINNSE; TKIETINNSEH; KIETINNSEHI; IETINNSEHIT; ETINNSEHITF; TINNSEHITFS; INNSEHITFSG; NNSEHITFSGD; NSEHITFSGDK; SEHITFSGDKI
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]	SEQ ID NO 13800-14549/ 8 mers: MNKKMKNL; NKKMKNLI; KKMKNLII; KMKNLIIC; MKNLIICA; KNLIICAV; NLIICAVF; LIICAVFV; IICAVFVL; ICAVFVLI; CAVFVLII; AVFVLIIS; VFVLIISC; FVLIISCK; VLIISCKI; LIISCKID; IISCKIDA; ISCKIDAS; SCKIDASS; CKIDASSE; KIDASSED; IDASSEDL; DASSEDLK; ASSEDLKQ; SSEDLKQN; SEDLKQNV; EDLKQNVK; DLKQNVKE; LKQNVKEK; KQNVKEKV; QNVKEKVE; NVKEKVEG; VKEKVEGF; KEKVEGFL; EKVEGFLD; KVEGFLDK; VEGFLDKE; EGFLDKEL; GFLDKELM; FLDKELMQ; LDKELMQG; DKELMQGD; KELMQGDD; ELMQGDDP; LMQGDDPN; MQGDDPNN; QGDDPNNS; GDDPNNSL; DDPNNSLF; DPNNSLFN; PNNSLFNP; NNSLFNPP; NSLFNPPP; SLFNPPPV; LFNPPPVL; FNPPPVLP; NPPPVLPA; PPPVLPAS; PPVLPASS; PVLPASSH; VLPASSHD; LPASSHDN; PASSHDNT; ASSHDNTP; SSHDNTPV; SHDNTPVL; HDNTPVLK; DNTPVLKA; NTPVLKAV; TPVLKAVQ; PVLKAVQA; VLKAVQAK; LKAVQAKD; KAVQAKDG; AVQAKDGG; VQAKDGGQ; QAKDGGQQ; AKDGGQQE; KDGGQQEG; DGGQQEGK; GGQQEGKE; GQQEGKEE; QQEGKEEK; QEGKEEKE; EGKEEKEK; GKEEKEKE; KEEKEKEI; EEKEKEIQ; EKEKEIQE; KEKEIQEL; EKEIQELK; KEIQELKD; EIQELKDK; IQELKDKI; QELKDKID; ELKDKIDK; LKDKIDKR; KDKIDKRK; DKIDKRKK; KIDKRKKE; IDKRKKEL; DKRKKELE; KRKKELEE; RKKELEEA; KKELEEAR; KELEEARK; ELEEARKK; LEEARKKF; EEARKKFQ; EARKKFQE; ARKKFQEF; RKKFQEFK; KKFQEFKE; KFQEFKEQ; FQEFKEQV; QEFKEQVE; EFKEQVES; FKEQVESA; KEQVESAT; EQVESATG; QVESATGE; VESATGES; ESATGEST; SATGESTE; ATGESTEK; TGESTEKV; GESTEKVK; ESTEKVKK; STEKVKKQ; TEKVKKQG; EKVKKQGN; KVKKQGNI; VKKQGNIG; KKQGNIGQ; KQGNIGQK; QGNIGQKA; GNIGQKAL; NIGQKALK;

IGQKALKY; GQKALKYA; QKALKYAK; KALKYAKE; ALKYAKEL; LKYAKELG; KYAKELGV; YAKELGVN; AKELGVNG; KELGVNGS; ELGVNGSY; LGVNGSYS; GVNGSYSV; VNGSYSVN; NGSYSVND; GSYSVNDG; SYSVNDGT; YSVNDGTN; SVNDGTNT; VNDGTNTN; NDGTNTND; DGTNTNDF; GTNTNDFV; TNTNDFVK; NTNDFVKK; TNDFVKKV; NDFVKKVI; DFVKKVID; FVKKVIDD; VKKVIDDA; KKVIDDAL; KVIDDALK; VIDDALKN; IDDALKNI; DDALKNIE; DALKNIEE; ALKNIEEE; LKNIEEEL; KNIEEELE; NIEEELEK; IEEELEKL; EEELEKLA; EELEKLAE; ELEKLAEP; LEKLAEPQ; EKLAEPQN; KLAEPQNI; LAEPQNIE; AEPQNIED; EPQNIEDK; PQNIEDKK;

9 mers:
MNKKMKNLI; NKKMKNLII; KKMKNLIIC; KMKNLIICA; MKNLIICAV; KNLIICAVF; NLIICAVFV; LIICAVFVL; IICAVFVLI; ICAVFVLII; CAVFVLIIS; AVFVLIISC; VFVLIISCK; FVLIISCKI; VLIISCKID; LIISCKIDA; IISCKIDAS; ISCKIDASS; SCKIDASSE; CKIDASSED; KIDASSEDL; IDASSEDLK; DASSEDLKQ; ASSEDLKQN; SSEDLKQNV; SEDLKQNVK; EDLKQNVKE; DLKQNVKEK; LKQNVKEKV; KQNVKEKVE; QNVKEKVEG; NVKEKVEGF; VKEKVEGFL; KEKVEGFLD; EKVEGFLDK; KVEGFLDKE; VEGFLDKEL; EGFLDKELM; GFLDKELMQ; FLDKELMQG; LDKELMQGD; DKELMQGDD; KELMQGDDP; ELMQGDDPN; LMQGDDPNN; MQGDDPNNS; QGDDPNNSL; GDDPNNSLF; DDPNNSLFN; DPNNSLFNP; PNNSLFNPP; NNSLFNPPP; NSLFNPPPV; SLFNPPPVL; LFNPPPVLP; FNPPPVLPA; NPPPVLPAS; PPPVLPASS; PPVLPASSH; PVLPASSHD; VLPASSHDN; LPASSHDNT; PASSHDNTP; ASSHDNTPV; SSHDNTPVL; SHDNTPVLK; HDNTPVLKA; DNTPVLKAV; NTPVLKAVQ; TPVLKAVQA; PVLKAVQAK; VLKAVQAKD; LKAVQAKDG; KAVQAKDGG; AVQAKDGGQ; VQAKDGGQQ; QAKDGGQQE; AKDGGQQEG; KDGGQQEGK; DGGQQEGKE; GGQQEGKEE; GQQEGKEEK; QQEGKEEKE; QEGKEEKEK; EGKEEKEKE; GKEEKEKEI; KEEKEKEIQ; EEKEKEIQE; EKEKEIQEL; KEKEIQELK; EKEIQELKD; KEIQELKDK; EIQELKDKI; IQELKDKID; QELKDKIDK; ELKDKIDKR; LKDKIDKRK; KDKIDKRKK; DKIDKRKKE; KIDKRKKEL; IDKRKKELE; DKRKKELEE; KRKKELEEA; RKKELEEAR; KKELEEARK; KELEEARKK; ELEEARKKF; LEEARKKFQ; EEARKKFQE; EARKKFQEF; ARKKFQEFK; RKKFQEFKE; KKFQEFKEQ; KFQEFKEQV; FQEFKEQVE; QEFKEQVES; EFKEQVESA; FKEQVESAT; KEQVESATG; EQVESATGE; QVESATGES; VESATGEST; ESATGESTE; SATGESTEK; ATGESTEKV; TGESTEKVK; GESTEKVKK; ESTEKVKKQ; STEKVKKQG; TEKVKKQGN; EKVKKQGNI; KVKKQGNIG; VKKQGNIGQ; KKQGNIGQK; KQGNIGQKA; QGNIGQKAL; GNIGQKALK; NIGQKALKY; IGQKALKYA; GQKALKYAK; QKALKYAKE; KALKYAKEL; ALKYAKELG; LKYAKELGV; KYAKELGVN; YAKELGVNG; AKELGVNGS; KELGVNGSY; ELGVNGSYS; LGVNGSYSV; GVNGSYSVN; VNGSYSVND; NGSYSVNDG; GSYSVNDGT; SYSVNDGTN; YSVNDGTNT; SVNDGTNTN; VNDGTNTND; NDGTNTNDF; DGTNTNDFV; GTNTNDFVK; TNTNDFVKK; NTNDFVKKV; TNDFVKKVI; NDFVKKVID; DFVKKVIDD; FVKKVIDDA; VKKVIDDAL; KKVIDDALK; KVIDDALKN; VIDDALKNI; IDDALKNIE; DDALKNIEE; DALKNIEEE; ALKNIEEEL; LKNIEEELE; KNIEEELEK; NIEEELEKL; IEEELEKLA; EEELEKLAE; EELEKLAEP; ELEKLAEPQ; LEKLAEPQN; EKLAEPQNI; KLAEPQNIE; LAEPQNIED; AEPQNIEDK; EPQNIEDKK;

10 mers:
MNKKMKNLII; NKKMKNLIIC; KKMKNLIICA; KMKNLIICAV; MKNLIICAVF; KNLIICAVFV; NLIICAVFVL; LIICAVFVLI; IICAVFVLII; ICAVFVLIIS; CAVFVLIISC; AVFVLIISCK; VFVLIISCKI; FVLIISCKID; VLIISCKIDA; LIISCKIDAS; IISCKIDASS; ISCKIDASSE; SCKIDASSED; CKIDASSEDL; KIDASSEDLK; IDASSEDLKQ; DASSEDLKQN; ASSEDLKQNV; SSEDLKQNVK; SEDLKQNVKE; EDLKQNVKEK; DLKQNVKEKV; LKQNVKEKVE; KQNVKEKVEG;

QNVKEKVEGF; NVKEKVEGFL; VKEKVEGFLD; KEKVEGFLDK; EKVEGFLDKE;
KVEGFLDKEL; VEGFLDKELM; EGFLDKELMQ; GFLDKELMQG; FLDKELMQGD;
LDKELMQGDD; DKELMQGDDP; KELMQGDDPN; ELMQGDDPNN; LMQGDDPNNS;
MQGDDPNNSL; QGDDPNNSLF; GDDPNNSLFN; DDPNNSLFNP; DPNNSLFNPP;
PNNSLFNPPP; NNSLFNPPPV; NSLFNPPPVL; SLFNPPPVLP; LFNPPPVLPA;
FNPPPVLPAS; NPPPVLPASS; PPPVLPASSH; PPVLPASSHD; PVLPASSHDN;
VLPASSHDNT; LPASSHDNTP; PASSHDNTPV; ASSHDNTPVL; SSHDNTPVLK;
SHDNTPVLKA; HDNTPVLKAV; DNTPVLKAVQ; NTPVLKAVQA; TPVLKAVQAK;
PVLKAVQAKD; VLKAVQAKDG; LKAVQAKDGG; KAVQAKDGGQ; AVQAKDGGQQ;
VQAKDGGQQE; QAKDGGQQEG; AKDGGQQEGK; KDGGQQEGKE; DGGQQEGKEE;
GGQQEGKEEK; GQQEGKEEKE; QQEGKEEKEK; QEGKEEKEKE; EGKEEKEKEI;
GKEEKEKEIQ; KEEKEKEIQE; EEKEKEIQEL; EKEKEIQELK; KEKEIQELKD;
EKEIQELKDK; KEIQELKDKI; EIQELKDKID; IQELKDKIDK; QELKDKIDKR;
ELKDKIDKRK; LKDKIDKRKK; KDKIDKRKKE; DKIDKRKKEL; KIDKRKKELE;
IDKRKKELEE; DKRKKELEEA; KRKKELEEAR; RKKELEEARK; KKELEEARKK;
KELEEARKKF; ELEEARKKFQ; LEEARKKFQE; EEARKKFQEF; EARKKFQEFK;
ARKKFQEFKE; RKKFQEFKEQ; KKFQEFKEQV; KFQEFKEQVE; FQEFKEQVES;
QEFKEQVESA; EFKEQVESAT; FKEQVESATG; KEQVESATGE; EQVESATGES;
QVESATGEST; VESATGESTE; ESATGESTEK; SATGESTEKV; ATGESTEKVK;
TGESTEKVKK; GESTEKVKKQ; ESTEKVKKQG; STEKVKKQGN; TEKVKKQGNI;
EKVKKQGNIG; KVKKQGNIGQ; VKKQGNIGQK; KKQGNIGQKA; KQGNIGQKAL;
QGNIGQKALK; GNIGQKALKY; NIGQKALKYA; IGQKALKYAK; GQKALKYAKE;
QKALKYAKEL; KALKYAKELG; ALKYAKELGV; LKYAKELGVN; KYAKELGVNG;
YAKELGVNGS; AKELGVNGSY; KELGVNGSYS; ELGVNGSYSV; LGVNGSYSVN;
GVNGSYSVND; VNGSYSVNDG; NGSYSVNDGT; GSYSVNDGTN; SYSVNDGTNT;
YSVNDGTNTN; SVNDGTNTND; VNDGTNTNDF; NDGTNTNDFV; DGTNTNDFVK;
GTNTNDFVKK; TNTNDFVKKV; NTNDFVKKVI; TNDFVKKVID; NDFVKKVIDD;
DFVKKVIDDA; FVKKVIDDAL; VKKVIDDALK; KKVIDDALKN; KVIDDALKNI;
VIDDALKNIE; IDDALKNIEE; DDALKNIEEE; DALKNIEEEL; ALKNIEEELE;
LKNIEEELEK; KNIEEELEKL; NIEEELEKLA; IEEELEKLAE; EEELEKLAEP;
EELEKLAEPQ; ELEKLAEPQN; LEKLAEPQNI; EKLAEPQNIE; KLAEPQNIED;
LAEPQNIEDK; AEPQNIEDKK

11 mers:
MNKKMKNLIIC; NKKMKNLIICA; KKMKNLIICAV; KMKNLIICAVF;
MKNLIICAVFV; KNLIICAVFVL; NLIICAVFVLI; LIICAVFVLII;
IICAVFVLIIS; ICAVFVLIISC; CAVFVLIISCK; AVFVLIISCKI;
VFVLIISCKID; FVLIISCKIDA; VLIISCKIDAS; LIISCKIDASS;
IISCKIDASSE; ISCKIDASSED; SCKIDASSEDL; CKIDASSEDLK;
KIDASSEDLKQ; IDASSEDLKQN; DASSEDLKQNV; ASSEDLKQNVK;
SSEDLKQNVKE; SEDLKQNVKEK; EDLKQNVKEKV; DLKQNVKEKVE;
LKQNVKEKVEG; KQNVKEKVEGF; QNVKEKVEGFL; NVKEKVEGFLD;
VKEKVEGFLDK; KEKVEGFLDKE; EKVEGFLDKEL; KVEGFLDKELM;
VEGFLDKELMQ; EGFLDKELMQG; GFLDKELMQGD; FLDKELMQGDD;
LDKELMQGDDP; DKELMQGDDPN; KELMQGDDPNN; ELMQGDDPNNS;
LMQGDDPNNSL; MQGDDPNNSLF; QGDDPNNSLFN; GDDPNNSLFNP;
DDPNNSLFNPP; DPNNSLFNPPP; PNNSLFNPPPV; NNSLFNPPPVL;
NSLFNPPPVLP; SLFNPPPVLPA; LFNPPPVLPAS; FNPPPVLPASS;
NPPPVLPASSH; PPPVLPASSHD; PPVLPASSHDN; PVLPASSHDNT;
VLPASSHDNTP; LPASSHDNTPV; PASSHDNTPVL; ASSHDNTPVLK;
SSHDNTPVLKA; SHDNTPVLKAV; HDNTPVLKAVQ; DNTPVLKAVQA;
NTPVLKAVQAK; TPVLKAVQAKD; PVLKAVQAKDG; VLKAVQAKDGG;
LKAVQAKDGGQ; KAVQAKDGGQQ; AVQAKDGGQQE; VQAKDGGQQEG;
QAKDGGQQEGK; AKDGGQQEGKE; KDGGQQEGKEE; DGGQQEGKEEK;
GGQQEGKEEKE; GQQEGKEEKEK; QQEGKEEKEKE; QEGKEEKEKEI;
EGKEEKEKEIQ; GKEEKEKEIQE; KEEKEKEIQEL; EEKEKEIQELK;
EKEKEIQELKD; KEKEIQELKDK; EKEIQELKDKI; KEIQELKDKID;

	EIQELKDKIDK; IQELKDKIDKR; QELKDKIDKRK; ELKDKIDKRKK; LKDKIDKRKKE; KDKIDKRKKEL; DKIDKRKKELE; KIDKRKKELEE; IDKRKKELEEA; DKRKKELEEAR; KRKKELEEARK; RKKELEEARKK; KKELEEARKKF; KELEEARKKFQ; ELEEARKKFQE; LEEARKKFQEF; EEARKKFQEFK; EARKKFQEFKE; ARKKFQEFKEQ; RKKFQEFKEQV; KKFQEFKEQVE; KFQEFKEQVES; FQEFKEQVESA; QEFKEQVESAT; EFKEQVESATG; FKEQVESATGE; KEQVESATGES; EQVESATGEST; QVESATGESTE; VESATGESTEK; ESATGESTEKV; SATGESTEKVK; ATGESTEKVKK; TGESTEKVKKQ; GESTEKVKKQG; ESTEKVKKQGN; STEKVKKQGNI; TEKVKKQGNIG; EKVKKQGNIGQ; KVKKQGNIGQK; VKKQGNIGQKA; KKQGNIGQKAL; KQGNIGQKALK; QGNIGQKALKY; GNIGQKALKYA; NIGQKALKYAK; IGQKALKYAKE; GQKALKYAKEL; QKALKYAKELG; KALKYAKELGV; ALKYAKELGVN; LKYAKELGVNG; KYAKELGVNGS; YAKELGVNGSY; AKELGVNGSYS; KELGVNGSYSV; ELGVNGSYSVN; LGVNGSYSVND; GVNGSYSVNDG; VNGSYSVNDGT; NGSYSVNDGTN; GSYSVNDGTNT; SYSVNDGTNTN; YSVNDGTNTND; SVNDGTNTNDF; VNDGTNTNDFV; NDGTNTNDFVK; DGTNTNDFVKK; GTNTNDFVKKV; TNTNDFVKKVI; NTNDFVKKVID; TNDFVKKVIDD; NDFVKKVIDDA; DFVKKVIDDAL; FVKKVIDDALK; VKKVIDDALKN; KKVIDDALKNI; KVIDDALKNIE; VIDDALKNIEE; IDDALKNIEEE; DDALKNIEEEL; DALKNIEEELE; ALKNIEEELEK; LKNIEEELEKL; KNIEEELEKLA; NIEEELEKLAE; IEEELEKLAEP; EEELEKLAEPQ; EELEKLAEPQN; ELEKLAEPQNI; LEKLAEPQNIE; EKLAEPQNIED; KLAEPQNIEDK; LAEPQNIEDKK;
AAC44770.1| FlaA protein (Borrelia burgdorferi)	SEQ ID NO 14550-15879/ 8 mers: MKRKAKSI; KRKAKSIL; RKAKSILF; KAKSILFF; AKSILFFL; KSILFFLL; SILFFLLS; ILFFLLST; LFFLLSTV; FFLLSTVL; FLLSTVLF; LLSTVLFA; LSTVLFAQ; STVLFAQE; TVLFAQET; VLFAQETD; LFAQETDG; FAQETDGL; AQETDGLA; QETDGLAE; ETDGLAEG; TDGLAEGS; DGLAEGSK; GLAEGSKR; LAEGSKRA; AEGSKRAE; EGSKRAEP; GSKRAEPG; SKRAEPGE; KRAEPGEL; RAEPGELV; AEPGELVL; EPGELVLD; PGELVLDF; GELVLDFA; ELVLDFAE; LVLDFAEL; VLDFAELA; LDFAELAR; DFAELARD; FAELARDP; AELARDPS; ELARDPSS; LARDPSST; ARDPSSTR; RDPSSTRL; DPSSTRLD; PSSTRLDL; SSTRLDLT; STRLDLTN; TRLDLTNY; RLDLTNYV; LDLTNYVD; DLTNYVDY; LTNYVDYV; TNYVDYVY; NYVDYVYS; YVDYVYSG; VDYVYSGA; DYVYSGAS; YVYSGASG; VYSGASGI; YSGASGIV; SGASGIVK; GASGIVKP; ASGIVKPE; SGIVKPED; GIVKPEDM; IVKPEDMV; VKPEDMVV; KPEDMVVD; PEDMVVDL; EDMVVDLG; DMVVDLGI; MVVDLGIN; VVDLGINN; VDLGINNW; DLGINNWS; LGINNWSV; GINNWSVL; INNWSVLL; NNWSVLLT; NWSVLLTP; WSVLLTPS; SVLLTPSA; VLLTPSAR; LLTPSARL; LTPSARLQ; TPSARLQA; PSARLQAY; SARLQAYV; ARLQAYVK; RLQAYVKN; LQAYVKNS; QAYVKNSV; AYVKNSVV; YVKNSVVA; VKNSVVAP; KNSVVAPA; NSVVAPAV; SVVAPAVV; VVAPAVVK; VAPAVVKS; APAVVKSE; PAVVKSES; AVVKSESK; VVKSESKR; VKSESKRY; KSESKRYA; SESKRYAG; ESKRYAGD; SKRYAGDT; KRYAGDTI; RYAGDTIL; YAGDTILG; AGDTILGV; GDTILGVR; DTILGVRV; TILGVRVL; ILGVRVLF; LGVRVLFP; GVRVLFPS; VRVLFPSY; RVLFPSYS; VLFPSYSQ; LFPSYSQS; FPSYSQSS; PSYSQSSA; SYSQSSAM; YSQSSAMI; SQSSAMIM; QSSAMIMP; SSAMIMPP; SAMIMPPF; AMIMPPFK; MIMPPFKI; IMPPFKIP; MPPFKIPF; PPFKIPFY; PFKIPFYS; FKIPFYSG; KIPFYSGE; IPFYSGES; PFYSGESG; FYSGESGN; YSGESGNQ; SGESGNQF; GESGNQFL; ESGNQFLG; SGNQFLGK; GNQFLGKG; NQFLGKGL; QFLGKGLI; FLGKGLID; LGKGLIDN; GKGLIDNI; KGLIDNIK; GLIDNIKT; LIDNIKTM; IDNIKTMK; DNIKTMKE; NIKTMKEI; IKTMKEIK; KTMKEIKV; TMKEIKVS; MKEIKVSV; KEIKVSVY; EIKVSVYS; IKVSVYSL; KVSVYSLG; VSVYSLGY; SVYSLGYE; VYSLGYEI; YSLGYEID; SLGYEIDL; LGYEIDLE; GYEIDLEV; YEIDLEVL; EIDLEVLF; IDLEVLFE;

DLEVLFED; LEVLFEDM; EVLFEDMN; VLFEDMNG; LFEDMNGM; FEDMNGME; EDMNGMEY; DMNGMEYA; MNGMEYAY; NGMEYAYS; GMEYAYSM; MEYAYSMG; EYAYSMGT; YAYSMGTL; AYSMGTLK; YSMGTLKF; SMGTLKFK; MGTLKFKG; GTLKFKGW; TLKFKGWA; LKFKGWAD; KFKGWADL; FKGWADLI; KGWADLIW; GWADLIWS; WADLIWSN; ADLIWSNP; DLIWSNPN; LIWSNPNY; IWSNPNYI; WSNPNYIP; SNPNYIPN; NPNYIPNI; PNYIPNIS; NYIPNISS; YIPNISSR; IPNISSRI; PNISSRII; NISSRIIK; ISSRIIKD; SSRIIKDD; SRIIKDDV; RIIKDDVP; IIKDDVPN; IKDDVPNY; KDDVPNYP; DDVPNYPL; DVPNYPLA; VPNYPLAS; PNYPLASS; NYPLASSK; YPLASSKM; PLASSKMR; LASSKMRF; ASSKMRFK; SSKMRFKA; SKMRFKAF; KMRFKAFR; MRFKAFRV; RFKAFRVS; FKAFRVSK; KAFRVSKS; AFRVSKSH; FRVSKSHS; RVSKSHSS; VSKSHSSK; SKSHSSKV; KSHSSKVK; SHSSKVKN; HSSKVKNF; SSKVKNFI; SKVKNFIF; KVKNFIFY; VKNFIFYV; KNFIFYVK; NFIFYVKD; FIFYVKDL; IFYVKDLR; FYVKDLRV; YVKDLRVL; VKDLRVLY; KDLRVLYD; DLRVLYDK; LRVLYDKL; RVLYDKLS; VLYDKLSV; LYDKLSVS; YDKLSVSI; DKLSVSID; KLSVSIDS; LSVSIDSD; SVSIDSDI; VSIDSDID; SIDSDIDS; IDSDIDSE; DSDIDSES; SDIDSESV; DIDSESVF; IDSESVFK; DSESVFKV; SESVFKVY; ESVFKVYE; SVFKVYET; VFKVYETS; FKVYETSG; KVYETSGT; VYETSGTE; YETSGTES; ETSGTESL; TSGTESLR; SGTESLRK; GTESLRKL; TESLRKLK; ESLRKLKA; SLRKLKAH; LRKLKAHE; RKLKAHET; KLKAHETF; LKAHETFK; KAHETFKR; AHETFKRV; HETFKRVL; ETFKRVLK; TFKRVLKL; FKRVLKLR; KRVLKLRE; RVLKLREK; VLKLREKI; LKLREKIS; KLREKISI; LREKISIA; REKISIAE; EKISIAEG; KISIAEGS; ISIAEGSF; SIAEGSFQ; IAEGSFQN; AEGSFQNF; EGSFQNFV; GSFQNFVE; SFQNFVEK; FQNFVEKI; QNFVEKIE; NFVEKIES; FVEKIESE; VEKIESEK; EKIESEKP; KIESEKPE; IESEKPEE; ESEKPEES; SEKPEESS; EKPEESSP; KPEESSPK; PEESSPKN

9 mers:
MKRKAKSIL; KRKAKSILF; RKAKSILFF; KAKSILFFL; AKSILFFLL; KSILFFLLS; SILFFLLST; ILFFLLSTV; LFFLLSTVL; FFLLSTVLF; FLLSTVLFA; LLSTVLFAQ; LSTVLFAQE; STVLFAQET; TVLFAQETD; VLFAQETDG; LFAQETDGL; FAQETDGLA; AQETDGLAE; QETDGLAEG; ETDGLAEGS; TDGLAEGSK; DGLAEGSKR; GLAEGSKRA; LAEGSKRAE; AEGSKRAEP; EGSKRAEPG; GSKRAEPGE; SKRAEPGEL; KRAEPGELV; RAEPGELVL; AEPGELVLD; EPGELVLDF; PGELVLDFA; GELVLDFAE; ELVLDFAEL; LVLDFAELA; VLDFAELAR; LDFAELARD; DFAELARDP; FAELARDPS; AELARDPSS; ELARDPSST; LARDPSSTR; ARDPSSTRL; RDPSSTRLD; DPSSTRLDL; PSSTRLDLT; SSTRLDLTN; STRLDLTNY; TRLDLTNYV; RLDLTNYVD; LDLTNYVDY; DLTNYVDYV; LTNYVDYVY; TNYVDYVYS; NYVDYVYSG; YVDYVYSGA; VDYVYSGAS; DYVYSGASG; YVYSGASGI; VYSGASGIV; YSGASGIVK; SGASGIVKP; GASGIVKPE; ASGIVKPED; SGIVKPEDM; GIVKPEDMV; IVKPEDMVV; VKPEDMVVD; KPEDMVVDL; PEDMVVDLG; EDMVVDLGI; DMVVDLGIN; MVVDLGINN; VVDLGINNW; VDLGINNWS; DLGINNWSV; LGINNWSVL; GINNWSVLL; INNWSVLLT; NNWSVLLTP; NWSVLLTPS; WSVLLTPSA; SVLLTPSAR; VLLTPSARL; LLTPSARLQ; LTPSARLQA; TPSARLQAY; PSARLQAYV; SARLQAYVK; ARLQAYVKN; RLQAYVKNS; LQAYVKNSV; QAYVKNSVV; AYVKNSVVA; YVKNSVVAP; VKNSVVAPA; KNSVVAPAV; NSVVAPAVV; SVVAPAVVK; VVAPAVVKS; VAPAVVKSE; APAVVKSES; PAVVKSESK; AVVKSESKR; VVKSESKRY; VKSESKRYA; KSESKRYAG; SESKRYAGD; ESKRYAGDT; SKRYAGDTI; KRYAGDTIL; RYAGDTILG; YAGDTILGV; AGDTILGVR; GDTILGVRV; DTILGVRVL; TILGVRVLF; ILGVRVLFP; LGVRVLFPS; GVRVLFPSY; VRVLFPSYS; RVLFPSYSQ; VLFPSYSQS; LFPSYSQSS; FPSYSQSSA; PSYSQSSAM; SYSQSSAMI; YSQSSAMIM; SQSSAMIMP; QSSAMIMPP; SSAMIMPPF; SAMIMPPFK; AMIMPPFKI; MIMPPFKIP; IMPPFKIPF; MPPFKIPFY; PPFKIPFYS; PFKIPFYSG; FKIPFYSGE; KIPFYSGES; IPFYSGESG; PFYSGESGN; FYSGESGNQ;

YSGESGNQF; SGESGNQFL; GESGNQFLG; ESGNQFLGK; SGNQFLGKG;
GNQFLGKGL; NQFLGKGLI; QFLGKGLID; FLGKGLIDN; LGKGLIDNI;
GKGLIDNIK; KGLIDNIKT; GLIDNIKTM; LIDNIKTMK; IDNIKTMKE;
DNIKTMKEI; NIKTMKEIK; IKTMKEIKV; KTMKEIKVS; TMKEIKVSV;
MKEIKVSVY; KEIKVSVYS; EIKVSVYSL; IKVSVYSLG; KVSVYSLGY;
VSVYSLGYE; SVYSLGYEI; VYSLGYEID; YSLGYEIDL; SLGYEIDLE;
LGYEIDLEV; GYEIDLEVL; YEIDLEVLF; EIDLEVLFE; IDLEVLFED;
DLEVLFEDM; LEVLFEDMN; EVLFEDMNG; VLFEDMNGM; LFEDMNGME;
FEDMNGMEY; EDMNGMEYA; DMNGMEYAY; MNGMEYAYS; NGMEYAYSM;
GMEYAYSMG; MEYAYSMGT; EYAYSMGTL; YAYSMGTLK; AYSMGTLKF;
YSMGTLKFK; SMGTLKFKG; MGTLKFKGW; GTLKFKGWA; TLKFKGWAD;
LKFKGWADL; KFKGWADLI; FKGWADLIW; KGWADLIWS; GWADLIWSN;
WADLIWSNP; ADLIWSNPN; DLIWSNPNY; LIWSNPNYI; IWSNPNYIP;
WSNPNYIPN; SNPNYIPNI; NPNYIPNIS; PNYIPNISS; NYIPNISSR;
YIPNISSRI; IPNISSRII; PNISSRIIK; NISSRIIKD; ISSRIIKDD;
SSRIIKDDV; SRIIKDDVP; RIIKDDVPN; IIKDDVPNY; IKDDVPNYP;
KDDVPNYPL; DDVPNYPLA; DVPNYPLAS; VPNYPLASS; PNYPLASSK;
NYPLASSKM; YPLASSKMR; PLASSKMRF; LASSKMRFK; ASSKMRFKA;
SSKMRFKAF; SKMRFKAFR; KMRFKAFRV; MRFKAFRVS; RFKAFRVSK;
FKAFRVSKS; KAFRVSKSH; AFRVSKSHS; FRVSKSHSS; RVSKSHSSK;
VSKSHSSKV; SKSHSSKVK; KSHSSKVKN; SHSSKVKNF; HSSKVKNFI;
SSKVKNFIF; SKVKNFIFY; KVKNFIFYV; VKNFIFYVK; KNFIFYVKD;
NFIFYVKDL; FIFYVKDLR; IFYVKDLRV; FYVKDLRVL; YVKDLRVLY;
VKDLRVLYD; KDLRVLYDK; DLRVLYDKL; LRVLYDKLS; RVLYDKLSV;
VLYDKLSVS; LYDKLSVSI; YDKLSVSID; DKLSVSIDS; KLSVSIDSD;
LSVSIDSDI; SVSIDSDID; VSIDSDIDS; SIDSDIDSE; IDSDIDSES;
DSDIDSESV; SDIDSESVF; DIDSESVFK; IDSESVFKV; DSESVFKVY;
SESVFKVYE; ESVFKVYET; SVFKVYETS; VFKVYETSG; FKVYETSGT;
KVYETSGTE; VYETSGTES; YETSGTESL; ETSGTESLR; TSGTESLRK;
SGTESLRKL; GTESLRKLK; TESLRKLKA; ESLRKLKAH; SLRKLKAHE;
LRKLKAHET; RKLKAHETF; KLKAHETFK; LKAHETFKR; KAHETFKRV;
AHETFKRVL; HETFKRVLK; ETFKRVLKL; TFKRVLKLR; FKRVLKLRE;
KRVLKLREK; RVLKLREKI; VLKLREKIS; LKLREKISI; KLREKISIA;
LREKISIAE; REKISIAEG; EKISIAEGS; KISIAEGSF; ISIAEGSFQ;
SIAEGSFQN; IAEGSFQNF; AEGSFQNFV; EGSFQNFVE; GSFQNFVEK;
SFQNFVEKI; FQNFVEKIE; QNFVEKIES; NFVEKIESE; FVEKIESEK;
VEKIESEKP; EKIESEKPE; KIESEKPEE; IESEKPEES; ESEKPEESS;
SEKPEESSP; EKPEESSPK; KPEESSPKN;

10 mers:
MKRKAKSILF; KRKAKSILFF; RKAKSILFFL; KAKSILFFLL; AKSILFFLLS;
KSILFFLLST; SILFFLLSTV; ILFFLLSTVL; LFFLLSTVLF; FFLLSTVLFA;
FLLSTVLFAQ; LLSTVLFAQE; LSTVLFAQET; STVLFAQETD; TVLFAQETDG;
VLFAQETDGL; LFAQETDGLA; FAQETDGLAE; AQETDGLAEG; QETDGLAEGS;
ETDGLAEGSK; TDGLAEGSKR; DGLAEGSKRA; GLAEGSKRAE; LAEGSKRAEP;
AEGSKRAEPG; EGSKRAEPGE; GSKRAEPGEL; SKRAEPGELV; KRAEPGELVL;
RAEPGELVLD; AEPGELVLDF; EPGELVLDFA; PGELVLDFAE; GELVLDFAEL;
ELVLDFAELA; LVLDFAELAR; VLDFAELARD; LDFAELARDP; DFAELARDPS;
FAELARDPSS; AELARDPSST; ELARDPSSTR; LARDPSSTRL; ARDPSSTRLD;
RDPSSTRLDL; DPSSTRLDLT; PSSTRLDLTN; SSTRLDLTNY; STRLDLTNYV;
TRLDLTNYVD; RLDLTNYVDY; LDLTNYVDYV; DLTNYVDYVY; LTNYVDYVYS;
TNYVDYVYSG; NYVDYVYSGA; YVDYVYSGAS; VDYVYSGASG; DYVYSGASGI;
YVYSGASGIV; VYSGASGIVK; YSGASGIVKP; SGASGIVKPE; GASGIVKPED;
ASGIVKPEDM; SGIVKPEDMV; GIVKPEDMVV; IVKPEDMVVD; VKPEDMVVDL;
KPEDMVVDLG; PEDMVVDLGI; EDMVVDLGIN; DMVVDLGINN; MVVDLGINNW;
VVDLGINNWS; VDLGINNWSV; DLGINNWSVL; LGINNWSVLL; GINNWSVLLT;
INNWSVLLTP; NNWSVLLTPS; NWSVLLTPSA; WSVLLTPSAR; SVLLTPSARL;

VLLTPSARLQ; LLTPSARLQA; LTPSARLQAY; TPSARLQAYV; PSARLQAYVK;
SARLQAYVKN; ARLQAYVKNS; RLQAYVKNSV; LQAYVKNSVV; QAYVKNSVVA;
AYVKNSVVAP; YVKNSVVAPA; VKNSVVAPAV; KNSVVAPAVV; NSVVAPAVVK;
SVVAPAVVKS; VVAPAVVKSE; VAPAVVKSES; APAVVKSESK; PAVVKSESKR;
AVVKSESKRY; VVKSESKRYA; VKSESKRYAG; KSESKRYAGD; SESKRYAGDT;
ESKRYAGDTI; SKRYAGDTIL; KRYAGDTILG; RYAGDTILGV; YAGDTILGVR;
AGDTILGVRV; GDTILGVRVL; DTILGVRVLF; TILGVRVLFP; ILGVRVLFPS;
LGVRVLFPSY; GVRVLFPSYS; VRVLFPSYSQ; RVLFPSYSQS; VLFPSYSQSS;
LFPSYSQSSA; FPSYSQSSAM; PSYSQSSAMI; SYSQSSAMIM; YSQSSAMIMP;
SQSSAMIMPP; QSSAMIMPPF; SSAMIMPPFK; SAMIMPPFKI; AMIMPPFKIP;
MIMPPFKIPF; IMPPFKIPFY; MPPFKIPFYS; PPFKIPFYSG; PFKIPFYSGE;
FKIPFYSGES; KIPFYSGESG; IPFYSGESGN; PFYSGESGNQ; FYSGESGNQF;
YSGESGNQFL; SGESGNQFLG; GESGNQFLGK; ESGNQFLGKG; SGNQFLGKGL;
GNQFLGKGLI; NQFLGKGLID; QFLGKGLIDN; FLGKGLIDNI; LGKGLIDNIK;
GKGLIDNIKT; KGLIDNIKTM; GLIDNIKTMK; LIDNIKTMKE; IDNIKTMKEI;
DNIKTMKEIK; NIKTMKEIKV; IKTMKEIKVS; KTMKEIKVSV; TMKEIKVSVY;
MKEIKVSVYS; KEIKVSVYSL; EIKVSVYSLG; IKVSVYSLGY; KVSVYSLGYE;
VSVYSLGYEI; SVYSLGYEID; VYSLGYEIDL; YSLGYEIDLE; SLGYEIDLEV;
LGYEIDLEVL; GYEIDLEVLF; YEIDLEVLFE; EIDLEVLFED; IDLEVLFEDM;
DLEVLFEDMN; LEVLFEDMNG; EVLFEDMNGM; VLFEDMNGME; LFEDMNGMEY;
FEDMNGMEYA; EDMNGMEYAY; DMNGMEYAYS; MNGMEYAYSM; NGMEYAYSMG;
GMEYAYSMGT; MEYAYSMGTL; EYAYSMGTLK; YAYSMGTLKF; AYSMGTLKFK;
YSMGTLKFKG; SMGTLKFKGW; MGTLKFKGWA; GTLKFKGWAD; TLKFKGWADL;
LKFKGWADLI; KFKGWADLIW; FKGWADLIWS; KGWADLIWSN; GWADLIWSNP;
WADLIWSNPN; ADLIWSNPNY; DLIWSNPNYI; LIWSNPNYIP; IWSNPNYIPN;
WSNPNYIPNI; SNPNYIPNIS; NPNYIPNISS; PNYIPNISSR; NYIPNISSRI;
YIPNISSRII; IPNISSRIIK; PNISSRIIKD; NISSRIIKDD; ISSRIIKDDV;
SSRIIKDDVP; SRIIKDDVPN; RIIKDDVPNY; IIKDDVPNYP; IKDDVPNYPL;
KDDVPNYPLA; DDVPNYPLAS; DVPNYPLASS; VPNYPLASSK; PNYPLASSKM;
NYPLASSKMR; YPLASSKMRF; PLASSKMRFK; LASSKMRFKA; ASSKMRFKAF;
SSKMRFKAFR; SKMRFKAFRV; KMRFKAFRVS; MRFKAFRVSK; RFKAFRVSKS;
FKAFRVSKSH; KAFRVSKSHS; AFRVSKSHSS; FRVSKSHSSK; RVSKSHSSKV;
VSKSHSSKVK; SKSHSSKVKN; KSHSSKVKNF; SHSSKVKNFI; HSSKVKNFIF;
SSKVKNFIFY; SKVKNFIFYV; KVKNFIFYVK; VKNFIFYVKD; KNFIFYVKDL;
NFIFYVKDLR; FIFYVKDLRV; IFYVKDLRVL; FYVKDLRVLY; YVKDLRVLYD;
VKDLRVLYDK; KDLRVLYDKL; DLRVLYDKLS; LRVLYDKLSV; RVLYDKLSVS;
VLYDKLSVSI; LYDKLSVSID; YDKLSVSIDS; DKLSVSIDSD; KLSVSIDSDI;
LSVSIDSDID; SVSIDSDIDS; VSIDSDIDSE; SIDSDIDSES; IDSDIDSESV;
DSDIDSESVF; SDIDSESVFK; DIDSESVFKV; IDSESVFKVY; DSESVFKVYE;
SESVFKVYET; ESVFKVYETS; SVFKVYETSG; VFKVYETSGT; FKVYETSGTE;
KVYETSGTES; VYETSGTESL; YETSGTESLR; ETSGTESLRK; TSGTESLRKL;
SGTESLRKLK; GTESLRKLKA; TESLRKLKAH; ESLRKLKAHE; SLRKLKAHET;
LRKLKAHETF; RKLKAHETFK; KLKAHETFKR; LKAHETFKRV; KAHETFKRVL;
AHETFKRVLK; HETFKRVLKL; ETFKRVLKLR; TFKRVLKLRE; FKRVLKLREK;
KRVLKLREKI; RVLKLREKIS; VLKLREKISI; LKLREKISIA; KLREKISIAE;
LREKISIAEG; REKISIAEGS; EKISIAEGSF; KISIAEGSFQ; ISIAEGSFQN;
SIAEGSFQNF; IAEGSFQNFV; AEGSFQNFVE; EGSFQNFVEK; GSFQNFVEKI;
SFQNFVEKIE; FQNFVEKIES; QNFVEKIESE; NFVEKIESEK; FVEKIESEKP;
VEKIESEKPE; EKIESEKPEE; KIESEKPEES; IESEKPEESS; ESEKPEESSP;
SEKPEESSPK; EKPEESSPKN;

11 mers:
MKRKAKSILFF; KRKAKSILFFL; RKAKSILFFLL; KAKSILFFLLS;
AKSILFFLLST; KSILFFLLSTV; SILFFLLSTVL; ILFFLLSTVLF;
LFFLLSTVLFA; FFLLSTVLFAQ; FLLSTVLFAQE; LLSTVLFAQET;
LSTVLFAQETD; STVLFAQETDG; TVLFAQETDGL; VLFAQETDGLA;
LFAQETDGLAE; FAQETDGLAEG; AQETDGLAEGS; QETDGLAEGSK;

	ETDGLAEGSKR; TDGLAEGSKRA; DGLAEGSKRAE; GLAEGSKRAEP; LAEGSKRAEPG; AEGSKRAEPGE; EGSKRAEPGEL; GSKRAEPGELV; SKRAEPGELVL; KRAEPGELVLD; RAEPGELVLDF; AEPGELVLDFA; EPGELVLDFAE; PGELVLDFAEL; GELVLDFAELA; ELVLDFAELAR; LVLDFAELARD; VLDFAELARDP; LDFAELARDPS; DFAELARDPSS; FAELARDPSST; AELARDPSSTR; ELARDPSSTRL; LARDPSSTRLD; ARDPSSTRLDL; RDPSSTRLDLT; DPSSTRLDLTN; PSSTRLDLTNY; SSTRLDLTNYV; STRLDLTNYVD; TRLDLTNYVDY; RLDLTNYVDYV; LDLTNYVDYVY; DLTNYVDYVYS; LTNYVDYVYSG; TNYVDYVYSGA; NYVDYVYSGAS; YVDYVYSGASG; VDYVYSGASGI; DYVYSGASGIV; YVYSGASGIVK; VYSGASGIVKP; YSGASGIVKPE; SGASGIVKPED; GASGIVKPEDM; ASGIVKPEDMV; SGIVKPEDMVV; GIVKPEDMVVD; IVKPEDMVVDL; VKPEDMVVDLG; KPEDMVVDLGI; PEDMVVDLGIN; EDMVVDLGINN; DMVVDLGINNW; MVVDLGINNWS; VVDLGINNWSV; VDLGINNWSVL; DLGINNWSVLL; LGINNWSVLLT; GINNWSVLLTP; INNWSVLLTPS; NNWSVLLTPSA; NWSVLLTPSAR; WSVLLTPSARL; SVLLTPSARLQ; VLLTPSARLQA; LLTPSARLQAY; LTPSARLQAYV; TPSARLQAYVK; PSARLQAYVKN; SARLQAYVKNS; ARLQAYVKNSV; RLQAYVKNSVV; LQAYVKNSVVA; QAYVKNSVVAP; AYVKNSVVAPA; YVKNSVVAPAV; VKNSVVAPAVV; KNSVVAPAVVK; NSVVAPAVVKS; SVVAPAVVKSE; VVAPAVVKSES; VAPAVVKSESK; APAVVKSESKR; PAVVKSESKRY; AVVKSESKRYA; VVKSESKRYAG; VKSESKRYAGD; KSESKRYAGDT; SESKRYAGDTI; ESKRYAGDTIL; SKRYAGDTILG; KRYAGDTILGV; RYAGDTILGVR; YAGDTILGVRV; AGDTILGVRVL; GDTILGVRVLF; DTILGVRVLFP; TILGVRVLFPS; ILGVRVLFPSY; LGVRVLFPSYS; GVRVLFPSYSQ; VRVLFPSYSQS; RVLFPSYSQSS; VLFPSYSQSSA; LFPSYSQSSAM; FPSYSQSSAMI; PSYSQSSAMIM; SYSQSSAMIMP; YSQSSAMIMPP; SQSSAMIMPPF; QSSAMIMPPFK; SSAMIMPPFKI; SAMIMPPFKIP; AMIMPPFKIPF; MIMPPFKIPFY; IMPPFKIPFYS; MPPFKIPFYSG; PPFKIPFYSGE; PFKIPFYSGES; FKIPFYSGESG; KIPFYSGESGN; IPFYSGESGNQ; PFYSGESGNQF; FYSGESGNQFL; YSGESGNQFLG; SGESGNQFLGK; GESGNQFLGKG; ESGNQFLGKGL; SGNQFLGKGLI; GNQFLGKGLID; NQFLGKGLIDN; QFLGKGLIDNI; FLGKGLIDNIK; LGKGLIDNIKT; GKGLIDNIKTM; KGLIDNIKTMK; GLIDNIKTMKE; LIDNIKTMKEI; IDNIKTMKEIK; DNIKTMKEIKV; NIKTMKEIKVS; IKTMKEIKVSV; KTMKEIKVSVY; TMKEIKVSVYS; MKEIKVSVYSL; KEIKVSVYSLG; EIKVSVYSLGY; IKVSVYSLGYE; KVSVYSLGYEI; VSVYSLGYEID; SVYSLGYEIDL; VYSLGYEIDLE; YSLGYEIDLEV; SLGYEIDLEVL; LGYEIDLEVLF; GYEIDLEVLFE; YEIDLEVLFED; EIDLEVLFEDM; IDLEVLFEDMN; DLEVLFEDMNG; LEVLFEDMNGM; EVLFEDMNGME; VLFEDMNGMEY; LFEDMNGMEYA; FEDMNGMEYAY; EDMNGMEYAYS; DMNGMEYAYSM; MNGMEYAYSMG; NGMEYAYSMGT; GMEYAYSMGTL; MEYAYSMGTLK; EYAYSMGTLKF; YAYSMGTLKFK; AYSMGTLKFKG; YSMGTLKFKGW; SMGTLKFKGWA; MGTLKFKGWAD; GTLKFKGWADL; TLKFKGWADLI; LKFKGWADLIW; KFKGWADLIWS; FKGWADLIWSN; KGWADLIWSNP; GWADLIWSNPN; WADLIWSNPNY; ADLIWSNPNYI; DLIWSNPNYIP; LIWSNPNYIPN; IWSNPNYIPNI; WSNPNYIPNIS; SNPNYIPNISS; NPNYIPNISSR; PNYIPNISSRI; NYIPNISSRII; YIPNISSRIIK; IPNISSRIIKD; PNISSRIIKDD; NISSRIIKDDV; ISSRIIKDDVP; SSRIIKDDVPN; SRIIKDDVPNY; RIIKDDVPNYP; IIKDDVPNYPL; IKDDVPNYPLA; KDDVPNYPLAS; DDVPNYPLASS; DVPNYPLASSK; VPNYPLASSKM; PNYPLASSKMR; NYPLASSKMRF; YPLASSKMRFK; PLASSKMRFKA; LASSKMRFKAF; ASSKMRFKAFR; SSKMRFKAFRV; SKMRFKAFRVS; KMRFKAFRVSK; MRFKAFRVSKS; RFKAFRVSKSH; FKAFRVSKSHS; KAFRVSKSHSS; AFRVSKSHSSK; FRVSKSHSSKV; RVSKSHSSKVK; VSKSHSSKVKN; SKSHSSKVKNF; KSHSSKVKNFI;

	SHSSKVKNFIF; HSSKVKNFIFY; SSKVKNFIFYV; SKVKNFIFYVK; KVKNFIFYVKD; VKNFIFYVKDL; KNFIFYVKDLR; NFIFYVKDLRV; FIFYVKDLRVL; IFYVKDLRVLY; FYVKDLRVLYD; YVKDLRVLYDK; VKDLRVLYDKL; KDLRVLYDKLS; DLRVLYDKLSV; LRVLYDKLSVS; RVLYDKLSVSI; VLYDKLSVSID; LYDKLSVSIDS; YDKLSVSIDSD; DKLSVSIDSDI; KLSVSIDSDID; LSVSIDSDIDS; SVSIDSDIDSE; VSIDSDIDSES; SIDSDIDSESV; IDSDIDSESVF; DSDIDSESVFK; SDIDSESVFKV; DIDSESVFKVY; IDSESVFKVYE; DSESVFKVYET; SESVFKVYETS; ESVFKVYETSG; SVFKVYETSGT; VFKVYETSGTE; FKVYETSGTES; KVYETSGTESL; VYETSGTESLR; YETSGTESLRK; ETSGTESLRKL; TSGTESLRKLK; SGTESLRKLKA; GTESLRKLKAH; TESLRKLKAHE; ESLRKLKAHET; SLRKLKAHETF; LRKLKAHETFK; RKLKAHETFKR; KLKAHETFKRV; LKAHETFKRVL; KAHETFKRVLK; AHETFKRVLKL; HETFKRVLKLR; ETFKRVLKLRE; TFKRVLKLREK; FKRVLKLREKI; KRVLKLREKIS; RVLKLREKISI; VLKLREKISIA; LKLREKISIAE; KLREKISIAEG; LREKISIAEGS; REKISIAEGSF; EKISIAEGSFQ; KISIAEGSFQN; ISIAEGSFQNF; SIAEGSFQNFV; IAEGSFQNFVE; AEGSFQNFVEK; EGSFQNFVEKI; GSFQNFVEKIE; SFQNFVEKIES; FQNFVEKIESE; QNFVEKIESEK; NFVEKIESEKP; FVEKIESEKPE; VEKIESEKPEE; EKIESEKPEES; KIESEKPEESS; IESEKPEESSP; ESEKPEESSPK; SEKPEESSPKN;
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]	SEQ ID NO 15880-17189/ 8 mers: MIINHNTS; IINHNTSA; INHNTSAI; NHNTSAIN; HNTSAINA; NTSAINAS; TSAINASR; SAINASRN; AINASRNN; INASRNNS; NASRNNSI; ASRNNSIN; SRNNSINA; RNNSINAA; NNSINAAN; NSINAANL; SINAANLS; INAANLSK; NAANLSKT; AANLSKTQ; ANLSKTQE; NLSKTQEK; LSKTQEKL; SKTQEKLS; KTQEKLSS; TQEKLSSG; QEKLSSGY; EKLSSGYR; KLSSGYRI; LSSGYRIN; SSGYRINR; SGYRINRA; GYRINRAS; YRINRASD; RINRASDD; INRASDDA; NRASDDAA; RASDDAAG; ASDDAAGM; SDDAAGMG; DDAAGMGV; DAAGMGVS; AAGMGVSG; AGMGVSGK; GMGVSGKI; MGVSGKIN; GVSGKINA; VSGKINAQ; SGKINAQI; GKINAQIR; KINAQIRG; INAQIRGL; NAQIRGLS; AQIRGLSQ; QIRGLSQA; IRGLSQAS; RGLSQASR; GLSQASRN; LSQASRNT; SQASRNTS; QASRNTSK; ASRNTSKA; SRNTSKAI; RNTSKAIN; NTSKAINF; TSKAINFI; SKAINFIQ; KAINFIQT; AINFIQTT; INFIQTTE; NFIQTTEG; FIQTTEGN; IQTTEGNL; QTTEGNLN; TTEGNLNE; TEGNLNEV; EGNLNEVE; GNLNEVEK; NLNEVEKV; LNEVEKVL; NEVEKVLV; EVEKVLVR; VEKVLVRM; EKVLVRMK; KVLVRMKE; VLVRMKEL; LVRMKELA; VRMKELAV; RMKELAVQ; MKELAVQS; KELAVQSG; ELAVQSGN; LAVQSGNG; AVQSGNGT; VQSGNGTY; QSGNGTYS; SGNGTYSD; GNGTYSDA; NGTYSDAD; GTYSDADR; TYSDADRG; YSDADRGS; SDADRGSI; DADRGSIQ; ADRGSIQI; DRGSIQIE; RGSIQIEI; GSIQIEIE; SIQIEIEQ; IQIEIEQL; QIEIEQLT; IEIEQLTD; EIEQLTDE; IEQLTDEI; EQLTDEIN; QLTDEINR; LTDEINRI; TDEINRIA; DEINRIAD; EINRIADQ; INRIADQA; NRIADQAQ; RIADQAQY; IADQAQYN; ADQAQYNQ; DQAQYNQM; QAQYNQMH; AQYNQMHM; QYNQMHML; YNQMHMLS; NQMHMLSN; QMHMLSNK; MHMLSNKS; HMLSNKSA; MLSNKSAS; LSNKSASQ; SNKSASQN; NKSASQNV; KSASQNVR; SASQNVRT; ASQNVRTA; SQNVRTAE; QNVRTAEE; NVRTAEEL; VRTAEELG; RTAEELGM; TAEELGMQ; AEELGMQP; EELGMQPA; ELGMQPAK; LGMQPAKI; GMQPAKIN; MQPAKINT; QPAKINTP; PAKINTPA; AKINTPAS; KINTPASL; INTPASLS; NTPASLSG; TPASLSGS; PASLSGSQ; ASLSGSQA; SLSGSQAS; LSGSQASW; SGSQASWT; GSQASWTL; SQASWTLR; QASWTLRV; ASWTLRVH; SWTLRVHV; WTLRVHVG; TLRVHVGA; LRVHVGAN; RVHVGANQ; VHVGANQD; HVGANQDE; VGANQDEA; GANQDEAI; ANQDEAIA; NQDEAIAV; QDEAIAVN; DEAIAVNI; EAIAVNIY; AIAVNIYA; IAVNIYAA; AVNIYAAN; VNIYAANV; NIYAANVA; IYAANVAN; YAANVANL; AANVANLF; ANVANLFS; NVANLFSG; VANLFSGE; ANLFSGEG; NLFSGEGS; LFSGEGSQ; FSGEGSQA;

SGEGSQAA; GEGSQAAQ; EGSQAAQT; GSQAAQTA; SQAAQTAP; QAAQTAPV;
AAQTAPVQ; AQTAPVQE; QTAPVQEG; TAPVQEGA; APVQEGAQ; PVQEGAQQ;
VQEGAQQE; QEGAQQEG; EGAQQEGA; GAQQEGAQ; AQQEGAQQ; QQEGAQQP;
QEGAQQPA; EGAQQPAP; GAQQPAPA; AQQPAPAT; QQPAPATA; QPAPATAP;
PAPATAPS; APATAPSQ; PATAPSQG; ATAPSQGG; TAPSQGGV; APSQGGVN;
PSQGGVNS; SQGGVNSP; QGGVNSPV; GGVNSPVN; GVNSPVNV; VNSPVNVT;
NSPVNVTT; SPVNVTTT; PVNVTTTV; VNVTTTVD; NVTTTVDA; VTTTVDAN;
TTTVDANT; TTVDANTS; TVDANTSL; VDANTSLA; DANTSLAK; ANTSLAKI;
NTSLAKIE; TSLAKIEN; SLAKIENA; LAKIENAI; AKIENAIR; KIENAIRM;
IENAIRMI; ENAIRMIS; NAIRMISD; AIRMISDQ; IRMISDQR; RMISDQRA;
MISDQRAN; ISDQRANL; SDQRANLG; DQRANLGA; QRANLGAF; RANLGAFQ;
ANLGAFQN; NLGAFQNR; LGAFQNRL; GAFQNRLE; AFQNRLES; FQNRLESI;
QNRLESIK; NRLESIKD; RLESIKDS; LESIKDST; ESIKDSTE; SIKDSTEY;
IKDSTEYA; KDSTEYAI; DSTEYAIE; STEYAIEN; TEYAIENL; EYAIENLK;
YAIENLKA; AIENLKAS; IENLKASY; ENLKASYA; NLKASYAQ; LKASYAQI;
KASYAQIK; ASYAQIKD; SYAQIKDA; YAQIKDAT; AQIKDATM; QIKDATMT;
IKDATMTD; KDATMTDE; DATMTDEV; ATMTDEVV; TMTDEVVA; MTDEVVAS;
TDEVVAST; DEVVASTT; EVVASTTN; VVASTTNS; VASTTNSI; ASTTNSIL;
STTNSILT; TTNSILTQ; TNSILTQS; NSILTQSA; SILTQSAM; ILTQSAMA;
LTQSAMAM; TQSAMAMI; QSAMAMIA; SAMAMIAQ; AMAMIAQA; MAMIAQAN;
AMIAQANQ; MIAQANQV; IAQANQVP; AQANQVPQ; QANQVPQY; ANQVPQYV;
NQVPQYVL; QVPQYVLS; VPQYVLSL; PQYVLSLL; QYVLSLLR;

9 mers:
MIINHNTSA; IINHNTSAI; INHNTSAIN; NHNTSAINA; HNTSAINAS;
NTSAINASR; TSAINASRN; SAINASRNN; AINASRNNS; INASRNNSI;
NASRNNSIN; ASRNNSINA; SRNNSINAA; RNNSINAAN; NNSINAANL;
NSINAANLS; SINAANLSK; INAANLSKT; NAANLSKTQ; AANLSKTQE;
ANLSKTQEK; NLSKTQEKL; LSKTQEKLS; SKTQEKLSS; KTQEKLSSG;
TQEKLSSGY; QEKLSSGYR; EKLSSGYRI; KLSSGYRIN; LSSGYRINR;
SSGYRINRA; SGYRINRAS; GYRINRASD; YRINRASDD; RINRASDDA;
INRASDDAA; NRASDDAAG; RASDDAAGM; ASDDAAGMG; SDDAAGMGV;
DDAAGMGVS; DAAGMGVSG; AAGMGVSGK; AGMGVSGKI; GMGVSGKIN;
MGVSGKINA; GVSGKINAQ; VSGKINAQI; SGKINAQIR; GKINAQIRG;
KINAQIRGL; INAQIRGLS; NAQIRGLSQ; AQIRGLSQA; QIRGLSQAS;
IRGLSQASR; RGLSQASRN; GLSQASRNT; LSQASRNTS; SQASRNTSK;
QASRNTSKA; ASRNTSKAI; SRNTSKAIN; RNTSKAINF; NTSKAINFI;
TSKAINFIQ; SKAINFIQT; KAINFIQTT; AINFIQTTE; INFIQTTEG;
NFIQTTEGN; FIQTTEGNL; IQTTEGNLN; QTTEGNLNE; TTEGNLNEV;
TEGNLNEVE; EGNLNEVEK; GNLNEVEKV; NLNEVEKVL; LNEVEKVLV;
NEVEKVLVR; EVEKVLVRM; VEKVLVRMK; EKVLVRMKE; KVLVRMKEL;
VLVRMKELA; LVRMKELAV; VRMKELAVQ; RMKELAVQS; MKELAVQSG;
KELAVQSGN; ELAVQSGNG; LAVQSGNGT; AVQSGNGTY; VQSGNGTYS;
QSGNGTYSD; SGNGTYSDA; GNGTYSDAD; NGTYSDADR; GTYSDADRG;
TYSDADRGS; YSDADRGSI; SDADRGSIQ; DADRGSIQI; ADRGSIQIE;
DRGSIQIEI; RGSIQIEIE; GSIQIEIEQ; SIQIEIEQL; IQIEIEQLT;
QIEIEQLTD; IEIEQLTDE; EIEQLTDEI; IEQLTDEIN; EQLTDEINR;
QLTDEINRI; LTDEINRIA; TDEINRIAD; DEINRIADQ; EINRIADQA;
INRIADQAQ; NRIADQAQY; RIADQAQYN; IADQAQYNQ; ADQAQYNQM;
DQAQYNQMH; QAQYNQMHM; AQYNQMHML; QYNQMHMLS; YNQMHMLSN;
NQMHMLSNK; QMHMLSNKS; MHMLSNKSA; HMLSNKSAS; MLSNKSASQ;
LSNKSASQN; SNKSASQNV; NKSASQNVR; KSASQNVRT; SASQNVRTA;
ASQNVRTAE; SQNVRTAEE; QNVRTAEEL; NVRTAEELG; VRTAEELGM;
RTAEELGMQ; TAEELGMQP; AEELGMQPA; EELGMQPAK; ELGMQPAKI;
LGMQPAKIN; GMQPAKINT; MQPAKINTP; QPAKINTPA; PAKINTPAS;
AKINTPASL; KINTPASLS; INTPASLSG; NTPASLSGS; TPASLSGSQ;
PASLSGSQA; ASLSGSQAS; SLSGSQASW; LSGSQASWT; SGSQASWTL;

GSQASWTLR; SQASWTLRV; QASWTLRVH; ASWTLRVHV; SWTLRVHVG;
WTLRVHVGA; TLRVHVGAN; LRVHVGANQ; RVHVGANQD; VHVGANQDE;
HVGANQDEA; VGANQDEAI; GANQDEAIA; ANQDEAIAV; NQDEAIAVN;
QDEAIAVNI; DEAIAVNIY; EAIAVNIYA; AIAVNIYAA; IAVNIYAAN;
AVNIYAANV; VNIYAANVA; NIYAANVAN; IYAANVANL; YAANVANLF;
AANVANLFS; ANVANLFSG; NVANLFSGE; VANLFSGEG; ANLFSGEGS;
NLFSGEGSQ; LFSGEGSQA; FSGEGSQAA; SGEGSQAAQ; GEGSQAAQT;
EGSQAAQTA; GSQAAQTAP; SQAAQTAPV; QAAQTAPVQ; AAQTAPVQE;
AQTAPVQEG; QTAPVQEGA; TAPVQEGAQ; APVQEGAQQ; PVQEGAQQE;
VQEGAQQEG; QEGAQQEGA; EGAQQEGAQ; GAQQEGAQQ; AQQEGAQQP;
QQEGAQQPA; QEGAQQPAP; EGAQQPAPA; GAQQPAPAT; AQQPAPATA;
QQPAPATAP; QPAPATAPS; PAPATAPSQ; APATAPSQG; PATAPSQGG;
ATAPSQGGV; TAPSQGGVN; APSQGGVNS; PSQGGVNSP; SQGGVNSPV;
QGGVNSPVN; GGVNSPVNV; GVNSPVNVT; VNSPVNVTT; NSPVNVTTT;
SPVNVTTTV; PVNVTTTVD; VNVTTTVDA; NVTTTVDAN; VTTTVDANT;
TTTVDANTS; TTVDANTSL; TVDANTSLA; VDANTSLAK; DANTSLAKI;
ANTSLAKIE; NTSLAKIEN; TSLAKIENA; SLAKIENAI; LAKIENAIR;
AKIENAIRM; KIENAIRMI; IENAIRMIS; ENAIRMISD; NAIRMISDQ;
AIRMISDQR; IRMISDQRA; RMISDQRAN; MISDQRANL; ISDQRANLG;
SDQRANLGA; DQRANLGAF; QRANLGAFQ; RANLGAFQN; ANLGAFQNR;
NLGAFQNRL; LGAFQNRLE; GAFQNRLES; AFQNRLESI; FQNRLESIK;
QNRLESIKD; NRLESIKDS; RLESIKDST; LESIKDSTE; ESIKDSTEY;
SIKDSTEYA; IKDSTEYAI; KDSTEYAIE; DSTEYAIEN; STEYAIENL;
TEYAIENLK; EYAIENLKA; YAIENLKAS; AIENLKASY; IENLKASYA;
ENLKASYAQ; NLKASYAQI; LKASYAQIK; KASYAQIKD; ASYAQIKDA;
SYAQIKDAT; YAQIKDATM; AQIKDATMT; QIKDATMTD; IKDATMTDE;
KDATMTDEV; DATMTDEVV; ATMTDEVVA; TMTDEVVAS; MTDEVVAST;
TDEVVASTT; DEVVASTTN; EVVASTTNS; VVASTTNSI; VASTTNSIL;
ASTTNSILT; STTNSILTQ; TTNSILTQS; TNSILTQSA; NSILTQSAM;
SILTQSAMA; ILTQSAMAM; LTQSAMAMI; TQSAMAMIA; QSAMAMIAQ;
SAMAMIAQA; AMAMIAQAN; MAMIAQANQ; AMIAQANQV; MIAQANQVP;
IAQANQVPQ; AQANQVPQY; QANQVPQYV; ANQVPQYVL; NQVPQYVLS;
QVPQYVLSL; VPQYVLSLL; PQYVLSLLR;

10 mers:
MIINHNTSAI; IINHNTSAIN; INHNTSAINA; NHNTSAINAS; HNTSAINASR;
NTSAINASRN; TSAINASRNN; SAINASRNNS; AINASRNNSI; INASRNNSIN;
NASRNNSINA; ASRNNSINAA; SRNNSINAAN; RNNSINAANL; NNSINAANLS;
NSINAANLSK; SINAANLSKT; INAANLSKTQ; NAANLSKTQE; AANLSKTQEK;
ANLSKTQEKL; NLSKTQEKLS; LSKTQEKLSS; SKTQEKLSSG; KTQEKLSSGY;
TQEKLSSGYR; QEKLSSGYRI; EKLSSGYRIN; KLSSGYRINR; LSSGYRINRA;
SSGYRINRAS; SGYRINRASD; GYRINRASDD; YRINRASDDA; RINRASDDAA;
INRASDDAAG; NRASDDAAGM; RASDDAAGMG; ASDDAAGMGV; SDDAAGMGVS;
DDAAGMGVSG; DAAGMGVSGK; AAGMGVSGKI; AGMGVSGKIN; GMGVSGKINA;
MGVSGKINAQ; GVSGKINAQI; VSGKINAQIR; SGKINAQIRG; GKINAQIRGL;
KINAQIRGLS; INAQIRGLSQ; NAQIRGLSQA; AQIRGLSQAS; QIRGLSQASR;
IRGLSQASRN; RGLSQASRNT; GLSQASRNTS; LSQASRNTSK; SQASRNTSKA;
QASRNTSKAI; ASRNTSKAIN; SRNTSKAINF; RNTSKAINFI; NTSKAINFIQ;
TSKAINFIQT; SKAINFIQTT; KAINFIQTTE; AINFIQTTEG; INFIQTTEGN;
NFIQTTEGNL; FIQTTEGNLN; IQTTEGNLNE; QTTEGNLNEV; TTEGNLNEVE;
TEGNLNEVEK; EGNLNEVEKV; GNLNEVEKVL; NLNEVEKVLV; LNEVEKVLVR;
NEVEKVLVRM; EVEKVLVRMK; VEKVLVRMKE; EKVLVRMKEL; KVLVRMKELA;
VLVRMKELAV; LVRMKELAVQ; VRMKELAVQS; RMKELAVQSG; MKELAVQSGN;
KELAVQSGNG; ELAVQSGNGT; LAVQSGNGTY; AVQSGNGTYS; VQSGNGTYSD;
QSGNGTYSDA; SGNGTYSDAD; GNGTYSDADR; NGTYSDADRG; GTYSDADRGS;
TYSDADRGSI; YSDADRGSIQ; SDADRGSIQI; DADRGSIQIE; ADRGSIQIEI;
DRGSIQIEIE; RGSIQIEIEQ; GSIQIEIEQL; SIQIEIEQLT; IQIEIEQLTD;

QIEIEQLTDE; IEIEQLTDEI; EIEQLTDEIN; IEQLTDEINR; EQLTDEINRI;
QLTDEINRIA; LTDEINRIAD; TDEINRIADQ; DEINRIADQA; EINRIADQAQ;
INRIADQAQY; NRIADQAQYN; RIADQAQYNQ; IADQAQYNQM; ADQAQYNQMH;
DQAQYNQMHM; QAQYNQMHML; AQYNQMHMLS; QYNQMHMLSN; YNQMHMLSNK;
NQMHMLSNKS; QMHMLSNKSA; MHMLSNKSAS; HMLSNKSASQ; MLSNKSASQN;
LSNKSASQNV; SNKSASQNVR; NKSASQNVRT; KSASQNVRTA; SASQNVRTAE;
ASQNVRTAEE; SQNVRTAEEL; QNVRTAEELG; NVRTAEELGM; VRTAEELGMQ;
RTAEELGMQP; TAEELGMQPA; AEELGMQPAK; EELGMQPAKI; ELGMQPAKIN;
LGMQPAKINT; GMQPAKINTP; MQPAKINTPA; QPAKINTPAS; PAKINTPASL;
AKINTPASLS; KINTPASLSG; INTPASLSGS; NTPASLSGSQ; TPASLSGSQA;
PASLSGSQAS; ASLSGSQASW; SLSGSQASWT; LSGSQASWTL; SGSQASWTLR;
GSQASWTLRV; SQASWTLRVH; QASWTLRVHV; ASWTLRVHVG; SWTLRVHVGA;
WTLRVHVGAN; TLRVHVGANQ; LRVHVGANQD; RVHVGANQDE; VHVGANQDEA;
HVGANQDEAI; VGANQDEAIA; GANQDEAIAV; ANQDEAIAVN; NQDEAIAVNI;
QDEAIAVNIY; DEAIAVNIYA; EAIAVNIYAA; AIAVNIYAAN; IAVNIYAANV;
AVNIYAANVA; VNIYAANVAN; NIYAANVANL; IYAANVANLF; YAANVANLFS;
AANVANLFSG; ANVANLFSGE; NVANLFSGEG; VANLFSGEGS; ANLFSGEGSQ;
NLFSGEGSQA; LFSGEGSQAA; FSGEGSQAAQ; SGEGSQAAQT; GEGSQAAQTA;
EGSQAAQTAP; GSQAAQTAPV; SQAAQTAPVQ; QAAQTAPVQE; AAQTAPVQEG;
AQTAPVQEGA; QTAPVQEGAQ; TAPVQEGAQQ; APVQEGAQQE; PVQEGAQQEG;
VQEGAQQEGA; QEGAQQEGAQ; EGAQQEGAQQ; GAQQEGAQQP; AQQEGAQQPA;
QQEGAQQPAP; QEGAQQPAPA; EGAQQPAPAT; GAQQPAPATA; AQQPAPATAP;
QQPAPATAPS; QPAPATAPSQ; PAPATAPSQG; APATAPSQGG; PATAPSQGGV;
ATAPSQGGVN; TAPSQGGVNS; APSQGGVNSP; PSQGGVNSPV; SQGGVNSPVN;
QGGVNSPVNV; GGVNSPVNVT; GVNSPVNVTT; VNSPVNVTTT; NSPVNVTTTV;
SPVNVTTTVD; PVNVTTTVDA; VNVTTTVDAN; NVTTTVDANT; VTTTVDANTS;
TTTVDANTSL; TTVDANTSLA; TVDANTSLAK; VDANTSLAKI; DANTSLAKIE;
ANTSLAKIEN; NTSLAKIENA; TSLAKIENAI; SLAKIENAIR; LAKIENAIRM;
AKIENAIRMI; KIENAIRMIS; IENAIRMISD; ENAIRMISDQ; NAIRMISDQR;
AIRMISDQRA; IRMISDQRAN; RMISDQRANL; MISDQRANLG; ISDQRANLGA;
SDQRANLGAF; DQRANLGAFQ; QRANLGAFQN; RANLGAFQNR; ANLGAFQNRL;
NLGAFQNRLE; LGAFQNRLES; GAFQNRLESI; AFQNRLESIK; FQNRLESIKD;
QNRLESIKDS; NRLESIKDST; RLESIKDSTE; LESIKDSTEY; ESIKDSTEYA;
SIKDSTEYAI; IKDSTEYAIE; KDSTEYAIEN; DSTEYAIENL; STEYAIENLK;
TEYAIENLKA; EYAIENLKAS; YAIENLKASY; AIENLKASYA; IENLKASYAQ;
ENLKASYAQI; NLKASYAQIK; LKASYAQIKD; KASYAQIKDA; ASYAQIKDAT;
SYAQIKDATM; YAQIKDATMT; AQIKDATMTD; QIKDATMTDE; IKDATMTDEV;
KDATMTDEVV; DATMTDEVVA; ATMTDEVVAS; TMTDEVVAST; MTDEVVASTT;
TDEVVASTTN; DEVVASTTNS; EVVASTTNSI; VVASTTNSIL; VASTTNSILT;
ASTTNSILTQ; STTNSILTQS; TTNSILTQSA; TNSILTQSAM; NSILTQSAMA;
SILTQSAMAM; ILTQSAMAMI; LTQSAMAMIA; TQSAMAMIAQ; QSAMAMIAQA;
SAMAMIAQAN; AMAMIAQANQ; MAMIAQANQV; AMIAQANQVP; MIAQANQVPQ;
IAQANQVPQY; AQANQVPQYV; QANQVPQYVL; ANQVPQYVLS; NQVPQYVLSL;
QVPQYVLSLL; VPQYVLSLLR;

11 mers:
MIINHNTSAIN; IINHNTSAINA; INHNTSAINAS; NHNTSAINASR;
HNTSAINASRN; NTSAINASRNN; TSAINASRNNS; SAINASRNNSI;
AINASRNNSIN; INASRNNSINA; NASRNNSINAA; ASRNNSINAAN;
SRNNSINAANL; RNNSINAANLS; NNSINAANLSK; NSINAANLSKT;
SINAANLSKTQ; INAANLSKTQE; NAANLSKTQEK; AANLSKTQEKL;
ANLSKTQEKLS; NLSKTQEKLSS; LSKTQEKLSSG; SKTQEKLSSGY;
KTQEKLSSGYR; TQEKLSSGYRI; QEKLSSGYRIN; EKLSSGYRINR;
KLSSGYRINRA; LSSGYRINRAS; SSGYRINRASD; SGYRINRASDD;
GYRINRASDDA; YRINRASDDAA; RINRASDDAAG; INRASDDAAGM;
NRASDDAAGMG; RASDDAAGMGV; ASDDAAGMGVS; SDDAAGMGVSG;
DDAAGMGVSGK; DAAGMGVSGKI; AAGMGVSGKIN; AGMGVSGKINA;

	GMGVSGKINAQ; MGVSGKINAQI; GVSGKINAQIR; VSGKINAQIRG; SGKINAQIRGL; GKINAQIRGLS; KINAQIRGLSQ; INAQIRGLSQA; NAQIRGLSQAS; AQIRGLSQASR; QIRGLSQASRN; IRGLSQASRNT; RGLSQASRNTS; GLSQASRNTSK; LSQASRNTSKA; SQASRNTSKAI; QASRNTSKAIN; ASRNTSKAINF; SRNTSKAINFI; RNTSKAINFIQ; NTSKAINFIQT; TSKAINFIQTT; SKAINFIQTTE; KAINFIQTTEG; AINFIQTTEGN; INFIQTTEGNL; NFIQTTEGNLN; FIQTTEGNLNE; IQTTEGNLNEV; QTTEGNLNEVE; TTEGNLNEVEK; TEGNLNEVEKV; EGNLNEVEKVL; GNLNEVEKVLV; NLNEVEKVLVR; LNEVEKVLVRM; NEVEKVLVRMK; EVEKVLVRMKE; VEKVLVRMKEL; EKVLVRMKELA; KVLVRMKELAV; VLVRMKELAVQ; LVRMKELAVQS; VRMKELAVQSG; RMKELAVQSGN; MKELAVQSGNG; KELAVQSGNGT; ELAVQSGNGTY; LAVQSGNGTYS; AVQSGNGTYSD; VQSGNGTYSDA; QSGNGTYSDAD; SGNGTYSDADR; GNGTYSDADRG; NGTYSDADRGS; GTYSDADRGSI; TYSDADRGSIQ; YSDADRGSIQI; SDADRGSIQIE; DADRGSIQIEI; ADRGSIQIEIE; DRGSIQIEIEQ; RGSIQIEIEQL; GSIQIEIEQLT; SIQIEIEQLTD; IQIEIEQLTDE; QIEIEQLTDEI; IEIEQLTDEIN; EIEQLTDEINR; IEQLTDEINRI; EQLTDEINRIA; QLTDEINRIAD; LTDEINRIADQ; TDEINRIADQA; DEINRIADQAQ; EINRIADQAQY; INRIADQAQYN; NRIADQAQYNQ; RIADQAQYNQM; IADQAQYNQMH; ADQAQYNQMHM; DQAQYNQMHML; QAQYNQMHMLS; AQYNQMHMLSN; QYNQMHMLSNK; YNQMHMLSNKS; NQMHMLSNKSA; QMHMLSNKSAS; MHMLSNKSASQ; HMLSNKSASQN; MLSNKSASQNV; LSNKSASQNVR; SNKSASQNVRT; NKSASQNVRTA; KSASQNVRTAE; SASQNVRTAEE; ASQNVRTAEEL; SQNVRTAEELG; QNVRTAEELGM; NVRTAEELGMQ; VRTAEELGMQP; RTAEELGMQPA; TAEELGMQPAK; AEELGMQPAKI; EELGMQPAKIN; ELGMQPAKINT; LGMQPAKINTP; GMQPAKINTPA; MQPAKINTPAS; QPAKINTPASL; PAKINTPASLS; AKINTPASLSG; KINTPASLSGS; INTPASLSGSQ; NTPASLSGSQA; TPASLSGSQAS; PASLSGSQASW; ASLSGSQASWT; SLSGSQASWTL; LSGSQASWTLR; SGSQASWTLRV; GSQASWTLRVH; SQASWTLRVHV; QASWTLRVHVG; ASWTLRVHVGA; SWTLRVHVGAN; WTLRVHVGANQ; TLRVHVGANQD; LRVHVGANQDE; RVHVGANQDEA; VHVGANQDEAI; HVGANQDEAIA; VGANQDEAIAV; GANQDEAIAVN; ANQDEAIAVNI; NQDEAIAVNIY; QDEAIAVNIYA; DEAIAVNIYAA; EAIAVNIYAAN; AIAVNIYAANV; IAVNIYAANVA; AVNIYAANVAN; VNIYAANVANL; NIYAANVANLF; IYAANVANLFS; YAANVANLFSG; AANVANLFSGE; ANVANLFSGEG; NVANLFSGEGS; VANLFSGEGSQ; ANLFSGEGSQA; NLFSGEGSQAA; LFSGEGSQAAQ; FSGEGSQAAQT; SGEGSQAAQTA; GEGSQAAQTAP; EGSQAAQTAPV; GSQAAQTAPVQ; SQAAQTAPVQE; QAAQTAPVQEG; AAQTAPVQEGA; AQTAPVQEGAQ; QTAPVQEGAQQ; TAPVQEGAQQE; APVQEGAQQEG; PVQEGAQQEGA; VQEGAQQEGAQ; QEGAQQEGAQQ; EGAQQEGAQQP; GAQQEGAQQPA; AQQEGAQQPAP; QQEGAQQPAPA; QEGAQQPAPAT; EGAQQPAPATA; GAQQPAPATAP; AQQPAPATAPS; QQPAPATAPSQ; QPAPATAPSQG; PAPATAPSQGG; APATAPSQGGV; PATAPSQGGVN; ATAPSQGGVNS; TAPSQGGVNSP; APSQGGVNSPV; PSQGGVNSPVN; SQGGVNSPVNV; QGGVNSPVNVT; GGVNSPVNVTT; GVNSPVNVTTT; VNSPVNVTTTV; NSPVNVTTTVD; SPVNVTTTVDA; PVNVTTTVDAN; VNVTTTVDANT; NVTTTVDANTS; VTTTVDANTSL; TTTVDANTSLA; TTVDANTSLAK; TVDANTSLAKI; VDANTSLAKIE; DANTSLAKIEN; ANTSLAKIENA; NTSLAKIENAI; TSLAKIENAIR; SLAKIENAIRM; LAKIENAIRMI; AKIENAIRMIS; KIENAIRMISD; IENAIRMISDQ; ENAIRMISDQR; NAIRMISDQRA; AIRMISDQRAN; IRMISDQRANL; RMISDQRANLG; MISDQRANLGA; ISDQRANLGAF; SDQRANLGAFQ; DQRANLGAFQN; QRANLGAFQNR; RANLGAFQNRL; ANLGAFQNRLE; NLGAFQNRLES; LGAFQNRLESI; GAFQNRLESIK; AFQNRLESIKD; FQNRLESIKDS; QNRLESIKDST; NRLESIKDSTE;

	RLESIKDSTEY; LESIKDSTEYA; ESIKDSTEYAI; SIKDSTEYAIE; IKDSTEYAIEN; KDSTEYAIENL; DSTEYAIENLK; STEYAIENLKA; TEYAIENLKAS; EYAIENLKASY; YAIENLKASYA; AIENLKASYAQ; IENLKASYAQI; ENLKASYAQIK; NLKASYAQIKD; LKASYAQIKDA; KASYAQIKDAT; ASYAQIKDATM; SYAQIKDATMT; YAQIKDATMTD; AQIKDATMTDE; QIKDATMTDEV; IKDATMTDEVV; KDATMTDEVVA; DATMTDEVVAS; ATMTDEVVAST; TMTDEVVASTT; MTDEVVASTTN; TDEVVASTTNS; DEVVASTTNSI; EVVASTTNSIL; VVASTTNSILT; VASTTNSILTQ; ASTTNSILTQS; STTNSILTQSA; TTNSILTQSAM; TNSILTQSAMA; NSILTQSAMAM; SILTQSAMAMI; ILTQSAMAMIA; LTQSAMAMIAQ; TQSAMAMIAQA; QSAMAMIAQAN; SAMAMIAQANQ; AMAMIAQANQV; MAMIAQANQVP; AMIAQANQVPQ; MIAQANQVPQY; IAQANQVPQYV; AQANQVPQYVL; QANQVPQYVLS; ANQVPQYVLSL; NQVPQYVLSLL; QVPQYVLSLLR;
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen Vlse Of Borrelia Burgdorferi	SEQ ID NO 17190-18547/ 8 mers: MRGSHHHH; RGSHHHHH; GSHHHHHH; SHHHHHHG; HHHHHHGS; HHHHHGSS; HHHHGSSQ; HHHGSSQV; HHGSSQVA; HGSSQVAD; GSSQVADK; SSQVADKD; SQVADKDD; QVADKDDP; VADKDDPT; ADKDDPTN; DKDDPTNK; KDDPTNKF; DDPTNKFY; DPTNKFYQ; PTNKFYQS; TNKFYQSV; NKFYQSVI; KFYQSVIQ; FYQSVIQL; YQSVIQLG; QSVIQLGN; SVIQLGNG; VIQLGNGF; IQLGNGFL; QLGNGFLD; LGNGFLDV; GNGFLDVF; NGFLDVFT; GFLDVFTS; FLDVFTSF; LDVFTSFG; DVFTSFGG; VFTSFGGL; FTSFGGLV; TSFGGLVA; SFGGLVAE; FGGLVAEA; GGLVAEAF; GLVAEAFG; LVAEAFGF; VAEAFGFK; AEAFGFKS; EAFGFKSD; AFGFKSDP; FGFKSDPK; GFKSDPKK; FKSDPKKS; KSDPKKSD; SDPKKSDV; DPKKSDVK; PKKSDVKT; KKSDVKTY; KSDVKTYF; SDVKTYFT; DVKTYFTT; VKTYFTTV; KTYFTTVA; TYFTTVAA; YFTTVAAK; FTTVAAKL; TTVAAKLE; TVAAKLEK; VAAKLEKT; AAKLEKTK; AKLEKTKT; KLEKTKTD; LEKTKTDL; EKTKTDLN; KTKTDLNS; TKTDLNSL; KTDLNSLP; TDLNSLPK; DLNSLPKE; LNSLPKEK; NSLPKEKS; SLPKEKSD; LPKEKSDI; PKEKSDIS; KEKSDISS; EKSDISST; KSDISSTT; SDISSTTG; DISSTTGK; ISSTTGKP; SSTTGKPD; STTGKPDS; TTGKPDST; TGKPDSTG; GKPDSTGS; KPDSTGSV; PDSTGSVG; DSTGSVGT; STGSVGTA; TGSVGTAV; GSVGTAVE; SVGTAVEG; VGTAVEGA; GTAVEGAI; TAVEGAIK; AVEGAIKE; VEGAIKEV; EGAIKEVS; GAIKEVSE; AIKEVSEL; IKEVSELL; KEVSELLD; EVSELLDK; VSELLDKL; SELLDKLV; ELLDKLVK; LLDKLVKA; LDKLVKAV; DKLVKAVK; KLVKAVKT; LVKAVKTA; VKAVKTAE; KAVKTAEG; AVKTAEGA; VKTAEGAS; KTAEGASS; TAEGASSG; AEGASSGT; EGASSGTA; GASSGTAA; ASSGTAAI; SSGTAAIG; SGTAAIGE; GTAAIGEV; TAAIGEVV; AAIGEVVA; AIGEVVAD; IGEVVADA; GEVVADAD; EVVADADA; VVADADAA; VADADAAK; ADADAAKV; DADAAKVA; ADAAKVAD; DAAKVADK; AAKVADKA; AKVADKAS; KVADKASV; VADKASVK; ADKASVKG; DKASVKGI; KASVKGIA; ASVKGIAK; SVKGIAKG; VKGIAKGI; KGIAKGIK; GIAKGIKE; IAKGIKEI; AKGIKEIV; KGIKEIVE; GIKEIVEA; IKEIVEAA; KEIVEAAG; EIVEAAGG; IVEAAGGS; VEAAGGSE; EAAGGSEK; AAGGSEKL; AGGSEKLK; GGSEKLKA; GSEKLKAV; SEKLKAVA; EKLKAVAA; KLKAVAAA; LKAVAAAK; KAVAAAKG; AVAAAKGE; VAAAKGEN; AAAKGENN; AAKGENNK; AKGENNKG; KGENNKGA; GENNKGAG; ENNKGAGK; NNKGAGKL; NKGAGKLF; KGAGKLFG; GAGKLFGK; AGKLFGKA; GKLFGKAG; KLFGKAGA; LFGKAGAA; FGKAGAAA; GKAGAAAH; KAGAAAHG; AGAAAHGD; GAAAHGDS; AAAHGDSE; AAHGDSEA; AHGDSEAA; HGDSEAAS; GDSEAASK; DSEAASKA; SEAASKAA; EAASKAAG; AASKAAGA; ASKAAGAV; SKAAGAVS; KAAGAVSA; AAGAVSAV; AGAVSAVS; GAVSAVSG; AVSAVSGE; VSAVSGEQ; SAVSGEQI; AVSGEQIL; VSGEQILS; SGEQILSA; GEQILSAI; EQILSAIV; QILSAIVT; ILSAIVTA; LSAIVTAA; SAIVTAAD; AIVTAADA; IVTAADAA; VTAADAAE; TAADAAEQ; AADAAEQD; ADAAEQDG; DAAEQDGK; AAEQDGKK; AEQDGKKP; EQDGKKPE; QDGKKPEE; DGKKPEEA; GKKPEEAK; KKPEEAKN; KPEEAKNP;

PEEAKNPI; EEAKNPIA; EAKNPIAA; AKNPIAAA; KNPIAAAI; NPIAAAIG;
PIAAAIGD; IAAAIGDK; AAAIGDKD; AAIGDKDG; AIGDKDGG; IGDKDGGA;
GDKDGGAE; DKDGGAEF; KDGGAEFG; DGGAEFGQ; GGAEFGQD; GAEFGQDE;
AEFGQDEX; EFGQDEXK; FGQDEXKK; GQDEXKKD; QDEXKKDD; DEXKKDDQ;
EXKKDDQI; XKKDDQIA; KKDDQIAA; KDDQIAAA; DDQIAAAI; DQIAAAIA;
QIAAAIAL; IAAAIALR; AAAIALRG; AAIALRGX; AIALRGXA; IALRGXAK;
ALRGXAKD; LRGXAKDG; RGXAKDGK; GXAKDGKF; XAKDGKFA; AKDGKFAV;
KDGKFAVK; DGKFAVKD; GKFAVKDG; KFAVKDGE; FAVKDGEK; AVKDGEKE;
VKDGEKEK; KDGEKEKA; DGEKEKAE; GEKEKAEG; EKEKAEGA; KEKAEGAI;
EKAEGAIK; KAEGAIKG; AEGAIKGA; EGAIKGAA; GAIKGAAE; AIKGAAES;
IKGAAESA; KGAAESAV; GAAESAVR; AAESAVRK; AESAVRKV; ESAVRKVL;
SAVRKVLG; AVRKVLGA; VRKVLGAI; RKVLGAIT; KVLGAITG; VLGAITGL;
LGAITGLI; GAITGLIG; AITGLIGD; ITGLIGDA; TGLIGDAV; GLIGDAVS;
LIGDAVSS; IGDAVSSG; GDAVSSGL; DAVSSGLR; AVSSGLRK; VSSGLRKV;
SSGLRKVG; SGLRKVGD; GLRKVGDS; LRKVGDSV; RKVGDSVK; KVGDSVKA;
VGDSVKAA; GDSVKAAS; DSVKAASK; SVKAASKE; VKAASKET; KAASKETP;
AASKETPP; ASKETPPA; SKETPPAL; KETPPALN; ETPPALNK;

9 mers:
MRGSHHHHH; RGSHHHHHH; GSHHHHHHG; SHHHHHHGS; HHHHHHGSS;
HHHHHGSSQ; HHHHGSSQV; HHHGSSQVA; HHGSSQVAD; HGSSQVADK;
GSSQVADKD; SSQVADKDD; SQVADKDDP; QVADKDDPT; VADKDDPTN;
ADKDDPTNK; DKDDPTNKF; KDDPTNKFY; DDPTNKFYQ; DPTNKFYQS;
PTNKFYQSV; TNKFYQSVI; NKFYQSVIQ; KFYQSVIQL; FYQSVIQLG;
YQSVIQLGN; QSVIQLGNG; SVIQLGNGF; VIQLGNGFL; IQLGNGFLD;
QLGNGFLDV; LGNGFLDVF; GNGFLDVFT; NGFLDVFTS; GFLDVFTSF;
FLDVFTSFG; LDVFTSFGG; DVFTSFGGL; VFTSFGGLV; FTSFGGLVA;
TSFGGLVAE; SFGGLVAEA; FGGLVAEAF; GGLVAEAFG; GLVAEAFGF;
LVAEAFGFK; VAEAFGFKS; AEAFGFKSD; EAFGFKSDP; AFGFKSDPK;
FGFKSDPKK; GFKSDPKKS; FKSDPKKSD; KSDPKKSDV; SDPKKSDVK;
DPKKSDVKT; PKKSDVKTY; KKSDVKTYF; KSDVKTYFT; SDVKTYFTT;
DVKTYFTTV; VKTYFTTVA; KTYFTTVAA; TYFTTVAAK; YFTTVAAKL;
FTTVAAKLE; TTVAAKLEK; TVAAKLEKT; VAAKLEKTK; AAKLEKTKT;
AKLEKTKTD; KLEKTKTDL; LEKTKTDLN; EKTKTDLNS; KTKTDLNSL;
TKTDLNSLP; KTDLNSLPK; TDLNSLPKE; DLNSLPKEK; LNSLPKEKS;
NSLPKEKSD; SLPKEKSDI; LPKEKSDIS; PKEKSDISS; KEKSDISST;
EKSDISSTT; KSDISSTTG; SDISSTTGK; DISSTTGKP; ISSTTGKPD;
SSTTGKPDS; STTGKPDST; TTGKPDSTG; TGKPDSTGS; GKPDSTGSV;
KPDSTGSVG; PDSTGSVGT; DSTGSVGTA; STGSVGTAV; TGSVGTAVE;
GSVGTAVEG; SVGTAVEGA; VGTAVEGAI; GTAVEGAIK; TAVEGAIKE;
AVEGAIKEV; VEGAIKEVS; EGAIKEVSE; GAIKEVSEL; AIKEVSELL;
IKEVSELLD; KEVSELLDK; EVSELLDKL; VSELLDKLV; SELLDKLVK;
ELLDKLVKA; LLDKLVKAV; LDKLVKAVK; DKLVKAVKT; KLVKAVKTA;
LVKAVKTAE; VKAVKTAEG; KAVKTAEGA; AVKTAEGAS; VKTAEGASS;
KTAEGASSG; TAEGASSGT; AEGASSGTA; EGASSGTAA; GASSGTAAI;
ASSGTAAIG; SSGTAAIGE; SGTAAIGEV; GTAAIGEVV; TAAIGEVVA;
AAIGEVVAD; AIGEVVADA; IGEVVADAD; GEVVADADA; EVVADADAA;
VVADADAAK; VADADAAKV; ADADAAKVA; DADAAKVAD; ADAAKVADK;
DAAKVADKA; AAKVADKAS; AKVADKASV; KVADKASVK; VADKASVKG;
ADKASVKGI; DKASVKGIA; KASVKGIAK; ASVKGIAKG; SVKGIAKGI;
VKGIAKGIK; KGIAKGIKE; GIAKGIKEI; IAKGIKEIV; AKGIKEIVE;
KGIKEIVEA; GIKEIVEAA; IKEIVEAAG; KEIVEAAGG; EIVEAAGGS;
IVEAAGGSE; VEAAGGSEK; EAAGGSEKL; AAGGSEKLK; AGGSEKLKA;
GGSEKLKAV; GSEKLKAVA; SEKLKAVAA; EKLKAVAAA; KLKAVAAAK;
LKAVAAAKG; KAVAAAKGE; AVAAAKGEN; VAAAKGENN; AAAKGENNK;
AAKGENNKG; AKGENNKGA; KGENNKGAG; GENNKGAGK; ENNKGAGKL;
NNKGAGKLF; NKGAGKLFG; KGAGKLFGK; GAGKLFGKA; AGKLFGKAG;

GKLFGKAGA; KLFGKAGAA; LFGKAGAAA; FGKAGAAAH; GKAGAAAHG;
KAGAAAHGD; AGAAAHGDS; GAAAHGDSE; AAAHGDSEA; AAHGDSEAA;
AHGDSEAAS; HGDSEAASK; GDSEAASKA; DSEAASKAA; SEAASKAAG;
EAASKAAGA; AASKAAGAV; ASKAAGAVS; SKAAGAVSA; KAAGAVSAV;
AAGAVSAVS; AGAVSAVSG; GAVSAVSGE; AVSAVSGEQ; VSAVSGEQI;
SAVSGEQIL; AVSGEQILS; VSGEQILSA; SGEQILSAI; GEQILSAIV;
EQILSAIVT; QILSAIVTA; ILSAIVTAA; LSAIVTAAD; SAIVTAADA;
AIVTAADAA; IVTAADAAE; VTAADAAEQ; TAADAAEQD; AADAAEQDG;
ADAAEQDGK; DAAEQDGKK; AAEQDGKKP; AEQDGKKPE; EQDGKKPEE;
QDGKKPEEA; DGKKPEEAK; GKKPEEAKN; KKPEEAKNP; KPEEAKNPI;
PEEAKNPIA; EEAKNPIAA; EAKNPIAAA; AKNPIAAAI; KNPIAAAIG;
NPIAAAIGD; PIAAAIGDK; IAAAIGDKD; AAAIGDKDG; AAIGDKDGG;
AIGDKDGGA; IGDKDGGAE; GDKDGGAEF; DKDGGAEFG; KDGGAEFGQ;
DGGAEFGQD; GGAEFGQDE; GAEFGQDEX; AEFGQDEXK; EFGQDEXKK;
FGQDEXKKD; GQDEXKKDD; QDEXKKDDQ; DEXKKDDQI; EXKKDDQIA;
XKKDDQIAA; KKDDQIAAA; KDDQIAAAI; DDQIAAAIA; DQIAAAIAL;
QIAAAIALR; IAAAIALRG; AAAIALRGX; AAIALRGXA; AIALRGXAK;
IALRGXAKD; ALRGXAKDG; LRGXAKDGK; RGXAKDGKF; GXAKDGKFA;
XAKDGKFAV; AKDGKFAVK; KDGKFAVKD; DGKFAVKDG; GKFAVKDGE;
KFAVKDGEK; FAVKDGEKE; AVKDGEKEK; VKDGEKEKA; KDGEKEKAE;
DGEKEKAEG; GEKEKAEGA; EKEKAEGAI; KEKAEGAIK; EKAEGAIKG;
KAEGAIKGA; AEGAIKGAA; EGAIKGAAE; GAIKGAAES; AIKGAAESA;
IKGAAESAV; KGAAESAVR; GAAESAVRK; AAESAVRKV; AESAVRKVL;
ESAVRKVLG; SAVRKVLGA; AVRKVLGAI; VRKVLGAIT; RKVLGAITG;
KVLGAITGL; VLGAITGLI; LGAITGLIG; GAITGLIGD; AITGLIGDA;
ITGLIGDAV; TGLIGDAVS; GLIGDAVSS; LIGDAVSSG; IGDAVSSGL;
GDAVSSGLR; DAVSSGLRK; AVSSGLRKV; VSSGLRKVG; SSGLRKVGD;
SGLRKVGDS; GLRKVGDSV; LRKVGDSVK; RKVGDSVKA; KVGDSVKAA;
VGDSVKAAS; GDSVKAASK; DSVKAASKE; SVKAASKET; VKAASKETP;
KAASKETPP; AASKETPPA; ASKETPPAL; SKETPPALN; KETPPALNK

10 mers:
MRGSHHHHHH; RGSHHHHHHG; GSHHHHHHGS; SHHHHHHGSS; HHHHHHGSSQ;
HHHHHGSSQV; HHHHGSSQVA; HHHGSSQVAD; HHGSSQVADK; HGSSQVADKD;
GSSQVADKDD; SSQVADKDDP; SQVADKDDPT; QVADKDDPTN; VADKDDPTNK;
ADKDDPTNKF; DKDDPTNKFY; KDDPTNKFYQ; DDPTNKFYQS; DPTNKFYQSV;
PTNKFYQSVI; TNKFYQSVIQ; NKFYQSVIQL; KFYQSVIQLG; FYQSVIQLGN;
YQSVIQLGNG; QSVIQLGNGF; SVIQLGNGFL; VIQLGNGFLD; IQLGNGFLDV;
QLGNGFLDVF; LGNGFLDVFT; GNGFLDVFTS; NGFLDVFTSF; GFLDVFTSFG;
FLDVFTSFGG; LDVFTSFGGL; DVFTSFGGLV; VFTSFGGLVA; FTSFGGLVAE;
TSFGGLVAEA; SFGGLVAEAF; FGGLVAEAFG; GGLVAEAFGF; GLVAEAFGFK;
LVAEAFGFKS; VAEAFGFKSD; AEAFGFKSDP; EAFGFKSDPK; AFGFKSDPKK;
FGFKSDPKKS; GFKSDPKKSD; FKSDPKKSDV; KSDPKKSDVK; SDPKKSDVKT;
DPKKSDVKTY; PKKSDVKTYF; KKSDVKTYFT; KSDVKTYFTT; SDVKTYFTTV;
DVKTYFTTVA; VKTYFTTVAA; KTYFTTVAAK; TYFTTVAAKL; YFTTVAAKLE;
FTTVAAKLEK; TTVAAKLEKT; TVAAKLEKTK; VAAKLEKTKT; AAKLEKTKTD;
AKLEKTKTDL; KLEKTKTDLN; LEKTKTDLNS; EKTKTDLNSL; KTKTDLNSLP;
TKTDLNSLPK; KTDLNSLPKE; TDLNSLPKEK; DLNSLPKEKS; LNSLPKEKSD;
NSLPKEKSDI; SLPKEKSDIS; LPKEKSDISS; PKEKSDISST; KEKSDISSTT;
EKSDISSTTG; KSDISSTTGK; SDISSTTGKP; DISSTTGKPD; ISSTTGKPDS;
SSTTGKPDST; STTGKPDSTG; TTGKPDSTGS; TGKPDSTGSV; GKPDSTGSVG;
KPDSTGSVGT; PDSTGSVGTA; DSTGSVGTAV; STGSVGTAVE; TGSVGTAVEG;
GSVGTAVEGA; SVGTAVEGAI; VGTAVEGAIK; GTAVEGAIKE; TAVEGAIKEV;
AVEGAIKEVS; VEGAIKEVSE; EGAIKEVSEL; GAIKEVSELL; AIKEVSELLD;
IKEVSELLDK; KEVSELLDKL; EVSELLDKLV; VSELLDKLVK; SELLDKLVKA;
ELLDKLVKAV; LLDKLVKAVK; LDKLVKAVKT; DKLVKAVKTA; KLVKAVKTAE;
LVKAVKTAEG; VKAVKTAEGA; KAVKTAEGAS; AVKTAEGASS; VKTAEGASSG;

KTAEGASSGT; TAEGASSGTA; AEGASSGTAA; EGASSGTAAI; GASSGTAAIG;
ASSGTAAIGE; SSGTAAIGEV; SGTAAIGEVV; GTAAIGEVVA; TAAIGEVVAD;
AAIGEVVADA; AIGEVVADAD; IGEVVADADA; GEVVADADAA; EVVADADAAK;
VVADADAAKV; VADADAAKVA; ADADAAKVAD; DADAAKVADK; ADAAKVADKA;
DAAKVADKAS; AAKVADKASV; AKVADKASVK; KVADKASVKG; VADKASVKGI;
ADKASVKGIA; DKASVKGIAK; KASVKGIAKG; ASVKGIAKGI; SVKGIAKGIK;
VKGIAKGIKE; KGIAKGIKEI; GIAKGIKEIV; IAKGIKEIVE; AKGIKEIVEA;
KGIKEIVEAA; GIKEIVEAAG; IKEIVEAAGG; KEIVEAAGGS; EIVEAAGGSE;
IVEAAGGSEK; VEAAGGSEKL; EAAGGSEKLK; AAGGSEKLKA; AGGSEKLKAV;
GGSEKLKAVA; GSEKLKAVAA; SEKLKAVAAA; EKLKAVAAAK; KLKAVAAAKG;
LKAVAAAKGE; KAVAAAKGEN; AVAAAKGENN; VAAAKGENNK; AAAKGENNKG;
AAKGENNKGA; AKGENNKGAG; KGENNKGAGK; GENNKGAGKL; ENNKGAGKLF;
NNKGAGKLFG; NKGAGKLFGK; KGAGKLFGKA; GAGKLFGKAG; AGKLFGKAGA;
GKLFGKAGAA; KLFGKAGAAA; LFGKAGAAAH; FGKAGAAAHG; GKAGAAAHGD;
KAGAAAHGDS; AGAAAHGDSE; GAAAHGDSEA; AAAHGDSEAA; AAHGDSEAAS;
AHGDSEAASK; HGDSEAASKA; GDSEAASKAA; DSEAASKAAG; SEAASKAAGA;
EAASKAAGAV; AASKAAGAVS; ASKAAGAVSA; SKAAGAVSAV; KAAGAVSAVS;
AAGAVSAVSG; AGAVSAVSGE; GAVSAVSGEQ; AVSAVSGEQI; VSAVSGEQIL;
SAVSGEQILS; AVSGEQILSA; VSGEQILSAI; SGEQILSAIV; GEQILSAIVT;
EQILSAIVTA; QILSAIVTAA; ILSAIVTAAD; LSAIVTAADA; SAIVTAADAA;
AIVTAADAAE; IVTAADAAEQ; VTAADAAEQD; TAADAAEQDG; AADAAEQDGK;
ADAAEQDGKK; DAAEQDGKKP; AAEQDGKKPE; AEQDGKKPEE; EQDGKKPEEA;
QDGKKPEEAK; DGKKPEEAKN; GKKPEEAKNP; KKPEEAKNPI; KPEEAKNPIA;
PEEAKNPIAA; EEAKNPIAAA; EAKNPIAAAI; AKNPIAAAIG; KNPIAAAIGD;
NPIAAAIGDK; PIAAAIGDKD; IAAAIGDKDG; AAAIGDKDGG; AAIGDKDGGA;
AIGDKDGGAE; IGDKDGGAEF; GDKDGGAEFG; DKDGGAEFGQ; KDGGAEFGQD;
DGGAEFGQDE; GGAEFGQDEX; GAEFGQDEXK; AEFGQDEXKK; EFGQDEXKKD;
FGQDEXKKDD; GQDEXKKDDQ; QDEXKKDDQI; DEXKKDDQIA; EXKKDDQIAA;
XKKDDQIAAA; KKDDQIAAAI; KDDQIAAAIA; DDQIAAAIAL; DQIAAAIALR;
QIAAAIALRG; IAAAIALRGX; AAAIALRGXA; AAIALRGXAK; AIALRGXAKD;
IALRGXAKDG; ALRGXAKDGK; LRGXAKDGKF; RGXAKDGKFA; GXAKDGKFAV;
XAKDGKFAVK; AKDGKFAVKD; KDGKFAVKDG; DGKFAVKDGE; GKFAVKDGEK;
KFAVKDGEKE; FAVKDGEKEK; AVKDGEKEKA; VKDGEKEKAE; KDGEKEKAEG;
DGEKEKAEGA; GEKEKAEGAI; EKEKAEGAIK; KEKAEGAIKG; EKAEGAIKGA;
KAEGAIKGAA; AEGAIKGAAE; EGAIKGAAES; GAIKGAAESA; AIKGAAESAV;
IKGAAESAVR; KGAAESAVRK; GAAESAVRKV; AAESAVRKVL; AESAVRKVLG;
ESAVRKVLGA; SAVRKVLGAI; AVRKVLGAIT; VRKVLGAITG; RKVLGAITGL;
KVLGAITGLI; VLGAITGLIG; LGAITGLIGD; GAITGLIGDA; AITGLIGDAV;
ITGLIGDAVS; TGLIGDAVSS; GLIGDAVSSG; LIGDAVSSGL; IGDAVSSGLR;
GDAVSSGLRK; DAVSSGLRKV; AVSSGLRKVG; VSSGLRKVGD; SSGLRKVGDS;
SGLRKVGDSV; GLRKVGDSVK; LRKVGDSVKA; RKVGDSVKAA; KVGDSVKAAS;
VGDSVKAASK; GDSVKAASKE; DSVKAASKET; SVKAASKETP; VKAASKETPP;
KAASKETPPA; AASKETPPAL; ASKETPPALN; SKETPPALNK

11 mers:
MRGSHHHHHHG; RGSHHHHHHGS; GSHHHHHHGSS; SHHHHHHGSSQ;
HHHHHHGSSQV; HHHHHGSSQVA; HHHHGSSQVAD; HHHGSSQVADK;
HHGSSQVADKD; HGSSQVADKDD; GSSQVADKDDP; SSQVADKDDPT;
SQVADKDDPTN; QVADKDDPTNK; VADKDDPTNKF; ADKDDPTNKFY;
DKDDPTNKFYQ; KDDPTNKFYQS; DDPTNKFYQSV; DPTNKFYQSVI;
PTNKFYQSVIQ; TNKFYQSVIQL; NKFYQSVIQLG; KFYQSVIQLGN;
FYQSVIQLGNG; YQSVIQLGNGF; QSVIQLGNGFL; SVIQLGNGFLD;
VIQLGNGFLDV; IQLGNGFLDVF; QLGNGFLDVFT; LGNGFLDVFTS;
GNGFLDVFTSF; NGFLDVFTSFG; GFLDVFTSFGG; FLDVFTSFGGL;
LDVFTSFGGLV; DVFTSFGGLVA; VFTSFGGLVAE; FTSFGGLVAEA;
TSFGGLVAEAF; SFGGLVAEAFG; FGGLVAEAFGF; GGLVAEAFGFK;
GLVAEAFGFKS; LVAEAFGFKSD; VAEAFGFKSDP; AEAFGFKSDPK;

	EAFGFKSDPKK; AFGFKSDPKKS; FGFKSDPKKSD; GFKSDPKKSDV; FKSDPKKSDVK; KSDPKKSDVKT; SDPKKSDVKTY; DPKKSDVKTYF; PKKSDVKTYFT; KKSDVKTYFTT; KSDVKTYFTTV; SDVKTYFTTVA; DVKTYFTTVAA; VKTYFTTVAAK; KTYFTTVAAKL; TYFTTVAAKLE; YFTTVAAKLEK; FTTVAAKLEKT; TTVAAKLEKTK; TVAAKLEKTKT; VAAKLEKTKTD; AAKLEKTKTDL; AKLEKTKTDLN; KLEKTKTDLNS; LEKTKTDLNSL; EKTKTDLNSLP; KTKTDLNSLPK; TKTDLNSLPKE; KTDLNSLPKEK; TDLNSLPKEKS; DLNSLPKEKSD; LNSLPKEKSDI; NSLPKEKSDIS; SLPKEKSDISS; LPKEKSDISST; PKEKSDISSTT; KEKSDISSTTG; EKSDISSTTGK; KSDISSTTGKP; SDISSTTGKPD; DISSTTGKPDS; ISSTTGKPDST; SSTTGKPDSTG; STTGKPDSTGS; TTGKPDSTGSV; TGKPDSTGSVG; GKPDSTGSVGT; KPDSTGSVGTA; PDSTGSVGTAV; DSTGSVGTAVE; STGSVGTAVEG; TGSVGTAVEGA; GSVGTAVEGAI; SVGTAVEGAIK; VGTAVEGAIKE; GTAVEGAIKEV; TAVEGAIKEVS; AVEGAIKEVSE; VEGAIKEVSEL; EGAIKEVSELL; GAIKEVSELLD; AIKEVSELLDK; IKEVSELLDKL; KEVSELLDKLV; EVSELLDKLVK; VSELLDKLVKA; SELLDKLVKAV; ELLDKLVKAVK; LLDKLVKAVKT; LDKLVKAVKTA; DKLVKAVKTAE; KLVKAVKTAEG; LVKAVKTAEGA; VKAVKTAEGAS; KAVKTAEGASS; AVKTAEGASSG; VKTAEGASSGT; KTAEGASSGTA; TAEGASSGTAA; AEGASSGTAAI; EGASSGTAAIG; GASSGTAAIGE; ASSGTAAIGEV; SSGTAAIGEVV; SGTAAIGEVVA; GTAAIGEVVAD; TAAIGEVVADA; AAIGEVVADAD; AIGEVVADADA; IGEVVADADAA; GEVVADADAAK; EVVADADAAKV; VVADADAAKVA; VADADAAKVAD; ADADAAKVADK; DADAAKVADKA; ADAAKVADKAS; DAAKVADKASV; AAKVADKASVK; AKVADKASVKG; KVADKASVKGI; VADKASVKGIA; ADKASVKGIAK; DKASVKGIAKG; KASVKGIAKGI; ASVKGIAKGIK; SVKGIAKGIKE; VKGIAKGIKEI; KGIAKGIKEIV; GIAKGIKEIVE; IAKGIKEIVEA; AKGIKEIVEAA; KGIKEIVEAAG; GIKEIVEAAGG; IKEIVEAAGGS; KEIVEAAGGSE; EIVEAAGGSEK; IVEAAGGSEKL; VEAAGGSEKLK; EAAGGSEKLKA; AAGGSEKLKAV; AGGSEKLKAVA; GGSEKLKAVAA; GSEKLKAVAAA; SEKLKAVAAAK; EKLKAVAAAKG; KLKAVAAAKGE; LKAVAAAKGEN; KAVAAAKGENN; AVAAAKGENNK; VAAAKGENNKG; AAAKGENNKGA; AAKGENNKGAG; AKGENNKGAGK; KGENNKGAGKL; GENNKGAGKLF; ENNKGAGKLFG; NNKGAGKLFGK; NKGAGKLFGKA; KGAGKLFGKAG; GAGKLFGKAGA; AGKLFGKAGAA; GKLFGKAGAAA; KLFGKAGAAAH; LFGKAGAAAHG; FGKAGAAAHGD; GKAGAAAHGDS; KAGAAAHGDSE; AGAAAHGDSEA; GAAAHGDSEAA; AAAHGDSEAAS; AAHGDSEAASK; AHGDSEAASKA; HGDSEAASKAA; GDSEAASKAAG; DSEAASKAAGA; SEAASKAAGAV; EAASKAAGAVS; AASKAAGAVSA; ASKAAGAVSAV; SKAAGAVSAVS; KAAGAVSAVSG; AAGAVSAVSGE; AGAVSAVSGEQ; GAVSAVSGEQI; AVSAVSGEQIL; VSAVSGEQILS; SAVSGEQILSA; AVSGEQILSAI; VSGEQILSAIV; SGEQILSAIVT; GEQILSAIVTA; EQILSAIVTAA; QILSAIVTAAD; ILSAIVTAADA; LSAIVTAADAA; SAIVTAADAAE; AIVTAADAAEQ; IVTAADAAEQD; VTAADAAEQDG; TAADAAEQDGK; AADAAEQDGKK; ADAAEQDGKKP; DAAEQDGKKPE; AAEQDGKKPEE; AEQDGKKPEEA; EQDGKKPEEAK; QDGKKPEEAKN; DGKKPEEAKNP; GKKPEEAKNPI; KKPEEAKNPIA; KPEEAKNPIAA; PEEAKNPIAAA; EEAKNPIAAAI; EAKNPIAAAIG; AKNPIAAAIGD; KNPIAAAIGDK; NPIAAAIGDKD; PIAAAIGDKDG; IAAAIGDKDGG; AAAIGDKDGGA; AAIGDKDGGAE; AIGDKDGGAEF; IGDKDGGAEFG; GDKDGGAEFGQ; DKDGGAEFGQD; KDGGAEFGQDE; DGGAEFGQDEX; GGAEFGQDEXK; GAEFGQDEXKK; AEFGQDEXKKD; EFGQDEXKKDD; FGQDEXKKDDQ; GQDEXKKDDQI; QDEXKKDDQIA; DEXKKDDQIAA; EXKKDDQIAAA; XKKDDQIAAAI; KKDDQIAAAIA; KDDQIAAAIAL; DDQIAAAIALR; DQIAAAIALRG; QIAAAIALRGX; IAAAIALRGXA; AAAIALRGXAK; AAIALRGXAKD; AIALRGXAKDG; IALRGXAKDGK;

	ALRGXAKDGKF; LRGXAKDGKFA; RGXAKDGKFAV; GXAKDGKFAVK; XAKDGKFAVKD; AKDGKFAVKDG; KDGKFAVKDGE; DGKFAVKDGEK; GKFAVKDGEKE; KFAVKDGEKEK; FAVKDGEKEKA; AVKDGEKEKAE; VKDGEKEKAEG; KDGEKEKAEGA; DGEKEKAEGAI; GEKEKAEGAIK; EKEKAEGAIKG; KEKAEGAIKGA; EKAEGAIKGAA; KAEGAIKGAAE; AEGAIKGAAES; EGAIKGAAESA; GAIKGAAESAV; AIKGAAESAVR; IKGAAESAVRK; KGAAESAVRKV; GAAESAVRKVL; AAESAVRKVLG; AESAVRKVLGA; ESAVRKVLGAI; SAVRKVLGAIT; AVRKVLGAITG; VRKVLGAITGL; RKVLGAITGLI; KVLGAITGLIG; VLGAITGLIGD; LGAITGLIGDA; GAITGLIGDAV; AITGLIGDAVS; ITGLIGDAVSS; TGLIGDAVSSG; GLIGDAVSSGL; LIGDAVSSGLR; IGDAVSSGLRK; GDAVSSGLRKV; DAVSSGLRKVG; AVSSGLRKVGD; VSSGLRKVGDS; SSGLRKVGDSV; SGLRKVGDSVK; GLRKVGDSVKA; LRKVGDSVKAA; RKVGDSVKAAS; KVGDSVKAASK; VGDSVKAASKE; GDSVKAASKET; DSVKAASKETP; SVKAASKETPP; VKAASKETPPA; KAASKETPPAL; AASKETPPALN; ASKETPPALNK;
CAA57807.1 Associated protein A (BapA)[Borrelia burgdorferi]	SEQ ID NO 18548-19189/ 8 mers: MKKISLLI; KKISLLIF; KISLLIFL; ISLLIFLF; SLLIFLFL; LLIFLFLF; LIFLFLFV; IFLFLFVV; FLFLFVVS; LFLFVVSL; FLFVVSLS; LFVVSLSA; FVVSLSAN; VVSLSANI; VSLSANIE; SLSANIEE; LSANIEEN; SANIEENY; ANIEENYT; NIEENYTE; IEENYTET; EENYTETK; ENYTETKR; NYTETKRA; YTETKRAF; TETKRAFS; ETKRAFSK; TKRAFSKE; KRAFSKED; RAFSKEDF; AFSKEDFN; FSKEDFNL; SKEDFNLI; KEDFNLIN; EDFNLINK; DFNLINKR; FNLINKRL; NLINKRLD; LINKRLDN; INKRLDNY; NKRLDNYD; KRLDNYDF; RLDNYDFK; LDNYDFKN; DNYDFKNE; NYDFKNEY; YDFKNEYE; DFKNEYEK; FKNEYEKS; KNEYEKSH; NEYEKSHV; EYEKSHVF; YEKSHVFS; EKSHVFSD; KSHVFSDA; SHVFSDAP; HVFSDAPR; VFSDAPRI; FSDAPRIR; SDAPRIRG; DAPRIRGD; APRIRGDL; PRIRGDLR; RIRGDLRK; IRGDLRKI; RGDLRKIG; GDLRKIGI; DLRKIGIK; LRKIGIKE; RKIGIKEK; KIGIKEKS; IGIKEKSV; GIKEKSVF; IKEKSVFL; KEKSVFLD; EKSVFLDA; KSVFLDAL; SVFLDALE; VFLDALEA; FLDALEAI; LDALEAIE; DALEAIEY; ALEAIEYL; LEAIEYLI; EAIEYLIK; AIEYLIKI; IEYLIKIK; EYLIKIKI; YLIKIKIS; LIKIKIST; IKIKISTD; KIKISTDS; IKISTDSI; KISTDSIF; ISTDSIFL; STDSIFLS; TDSIFLSE; DSIFLSED; SIFLSEDM; IFLSEDMI; FLSEDMIR; LSEDMIRL; SEDMIRLI; EDMIRLIG; DMIRLIGS; MIRLIGSY; IRLIGSYP; RLIGSYPD; LIGSYPDS; IGSYPDSI; GSYPDSIF; SYPDSIFN; YPDSIFNY; PDSIFNYL; DSIFNYLI; SIFNYLIQ; IFNYLIQL; FNYLIQLN; NYLIQLNS; YLIQLNSD; LIQLNSDK; IQLNSDKI; QLNSDKID; LNSDKIDY; NSDKIDYA; SDKIDYAE; DKIDYAEK; KIDYAEKY; IDYAEKYG; DYAEKYGD; YAEKYGDN; AEKYGDNA; EKYGDNAR; KYGDNARN; YGDNARNN; GDNARNNF; DNARNNFK; NARNNFKK; ARNNFKKD; RNNFKKDY; NNFKKDYS; NFKKDYSE; FKKDYSED; KKDYSEDK; KDYSEDKA; DYSEDKAN; YSEDKANT; SEDKANTV; EDKANTVK; DKANTVKQ; KANTVKQI; ANTVKQIL; NTVKQILK; TVKQILKQ; VKQILKQI; KQILKQIL; QILKQILA; ILKQILAD; LKQILADL; KQILADLP; QILADLPK; ILADLPKD; 9 mers: MKKISLLIF; KKISLLIFL; KISLLIFLF; ISLLIFLFL; SLLIFLFLF; LLIFLFLFV; LIFLFLFVV; IFLFLFVVS; FLFLFVVSL; LFLFVVSLS; FLFVVSLSA; LFVVSLSAN; FVVSLSANI; VVSLSANIE; VSLSANIEE; SLSANIEEN; LSANIEENY; SANIEENYT; ANIEENYTE; NIEENYTET; IEENYTETK; EENYTETKR; ENYTETKRA; NYTETKRAF; YTETKRAFS; TETKRAFSK; ETKRAFSKE; TKRAFSKED; KRAFSKEDF; RAFSKEDFN; AFSKEDFNL; FSKEDFNLI; SKEDFNLIN; KEDFNLINK; EDFNLINKR; DFNLINKRL; FNLINKRLD; NLINKRLDN; LINKRLDNY; INKRLDNYD; NKRLDNYDF; KRLDNYDFK; RLDNYDFKN; LDNYDFKNE; DNYDFKNEY;

NYDFKNEYE; YDFKNEYEK; DFKNEYEKS; FKNEYEKSH; KNEYEKSHV; NEYEKSHVF; EYEKSHVFS; YEKSHVFSD; EKSHVFSDA; KSHVFSDAP; SHVFSDAPR; HVFSDAPRI; VFSDAPRIR; FSDAPRIRG; SDAPRIRGD; DAPRIRGDL; APRIRGDLR; PRIRGDLRK; RIRGDLRKI; IRGDLRKIG; RGDLRKIGI; GDLRKIGIK; DLRKIGIKE; LRKIGIKEK; RKIGIKEKS; KIGIKEKSV; IGIKEKSVF; GIKEKSVFL; IKEKSVFLD; KEKSVFLDA; EKSVFLDAL; KSVFLDALE; SVFLDALEA; VFLDALEAI; FLDALEAIE; LDALEAIEY; DALEAIEYL; ALEAIEYLI; LEAIEYLIK; EAIEYLIKI; AIEYLIKIK; IEYLIKIKI; EYLIKIKIS; YLIKIKIST; LIKIKISTD; IKIKISTDS; KIKISTDSI; IKISTDSIF; KISTDSIFL; ISTDSIFLS; STDSIFLSE; TDSIFLSED; DSIFLSEDM; SIFLSEDMI; IFLSEDMIR; FLSEDMIRL; LSEDMIRLI; SEDMIRLIG; EDMIRLIGS; DMIRLIGSY; MIRLIGSYP; IRLIGSYPD; RLIGSYPDS; LIGSYPDSI; IGSYPDSIF; GSYPDSIFN; SYPDSIFNY; YPDSIFNYL; PDSIFNYLI; DSIFNYLIQ; SIFNYLIQL; IFNYLIQLN; FNYLIQLNS; NYLIQLNSD; YLIQLNSDK; LIQLNSDKI; IQLNSDKID; QLNSDKIDY; LNSDKIDYA; NSDKIDYAE; SDKIDYAEK; DKIDYAEKY; KIDYAEKYG; IDYAEKYGD; DYAEKYGDN; YAEKYGDNA; AEKYGDNAR; EKYGDNARN; KYGDNARNN; YGDNARNNF; GDNARNNFK; DNARNNFKK; NARNNFKKD; ARNNFKKDY; RNNFKKDYS; NNFKKDYSE; NFKKDYSED; FKKDYSEDK; KKDYSEDKA; KDYSEDKAN; DYSEDKANT; YSEDKANTV; SEDKANTVK; EDKANTVKQ; DKANTVKQI; KANTVKQIL; ANTVKQILK; NTVKQILKQ; TVKQILKQI; VKQILKQIL; KQILKQILA; QILKQILAD; ILKQILADL; LKQILADLP; KQILADLPK; QILADLPKD;

10 mers:
MKKISLLIFL; KKISLLIFLF; KISLLIFLFL; ISLLIFLFLF; SLLIFLFLFV; LLIFLFLFVV; LIFLFLFVVS; IFLFLFVVSL; FLFLFVVSLS; LFLFVVSLSA; FLFVVSLSAN; LFVVSLSANI; FVVSLSANIE; VVSLSANIEE; VSLSANIEEN; SLSANIEENY; LSANIEENYT; SANIEENYTE; ANIEENYTET; NIEENYTETK; IEENYTETKR; EENYTETKRA; ENYTETKRAF; NYTETKRAFS; YTETKRAFSK; TETKRAFSKE; ETKRAFSKED; TKRAFSKEDF; KRAFSKEDFN; RAFSKEDFNL; AFSKEDFNLI; FSKEDFNLIN; SKEDFNLINK; KEDFNLINKR; EDFNLINKRL; DFNLINKRLD; FNLINKRLDN; NLINKRLDNY; LINKRLDNYD; INKRLDNYDF; NKRLDNYDFK; KRLDNYDFKN; RLDNYDFKNE; LDNYDFKNEY; DNYDFKNEYE; NYDFKNEYEK; YDFKNEYEKS; DFKNEYEKSH; FKNEYEKSHV; KNEYEKSHVF; NEYEKSHVFS; EYEKSHVFSD; YEKSHVFSDA; EKSHVFSDAP; KSHVFSDAPR; SHVFSDAPRI; HVFSDAPRIR; VFSDAPRIRG; FSDAPRIRGD; SDAPRIRGDL; DAPRIRGDLR; APRIRGDLRK; PRIRGDLRKI; RIRGDLRKIG; IRGDLRKIGI; RGDLRKIGIK; GDLRKIGIKE; DLRKIGIKEK; LRKIGIKEKS; RKIGIKEKSV; KIGIKEKSVF; IGIKEKSVFL; GIKEKSVFLD; IKEKSVFLDA; KEKSVFLDAL; EKSVFLDALE; KSVFLDALEA; SVFLDALEAI; VFLDALEAIE; FLDALEAIEY; LDALEAIEYL; DALEAIEYLI; ALEAIEYLIK; LEAIEYLIKI; EAIEYLIKIK; AIEYLIKIKI; IEYLIKIKIS; EYLIKIKIST; YLIKIKISTD; LIKIKISTDS; IKIKISTDSI; KIKISTDSIF; IKISTDSIFL; KISTDSIFLS; ISTDSIFLSE; STDSIFLSED; TDSIFLSEDM; DSIFLSEDMI; SIFLSEDMIR; IFLSEDMIRL; FLSEDMIRLI; LSEDMIRLIG; SEDMIRLIGS; EDMIRLIGSY; DMIRLIGSYP; MIRLIGSYPD; IRLIGSYPDS; RLIGSYPDSI; LIGSYPDSIF; IGSYPDSIFN; GSYPDSIFNY; SYPDSIFNYL; YPDSIFNYLI; PDSIFNYLIQ; DSIFNYLIQL; SIFNYLIQLN; IFNYLIQLNS; FNYLIQLNSD; NYLIQLNSDK; YLIQLNSDKI; LIQLNSDKID; IQLNSDKIDY; QLNSDKIDYA; LNSDKIDYAE; NSDKIDYAEK; SDKIDYAEKY; DKIDYAEKYG; KIDYAEKYGD; IDYAEKYGDN; DYAEKYGDNA; YAEKYGDNAR; AEKYGDNARN; EKYGDNARNN; KYGDNARNNF; YGDNARNNFK; GDNARNNFKK; DNARNNFKKD; NARNNFKKDY; ARNNFKKDYS; RNNFKKDYSE; NNFKKDYSED; NFKKDYSEDK; FKKDYSEDKA; KKDYSEDKAN; KDYSEDKANT; DYSEDKANTV; YSEDKANTVK; SEDKANTVKQ; EDKANTVKQI; DKANTVKQIL; KANTVKQILK; ANTVKQILKQ; NTVKQILKQI; TVKQILKQIL; VKQILKQILA;

	KQILKQILAD; QILKQILADL; ILKQILADLP; LKQILADLPK; KQILADLPKD; 11 mers: MKKISLLIFLF; KKISLLIFLFL; KISLLIFLFLF; ISLLIFLFLFV; SLLIFLFLFVV; LLIFLFLFVVS; LIFLFLFVVSL; IFLFLFVVSLS; FLFLFVVSLSA; LFLFVVSLSAN; FLFVVSLSANI; LFVVSLSANIE; FVVSLSANIEE; VVSLSANIEEN; VSLSANIEENY; SLSANIEENYT; LSANIEENYTE; SANIEENYTET; ANIEENYTETK; NIEENYTETKR; IEENYTETKRA; EENYTETKRAF; ENYTETKRAFS; NYTETKRAFSK; YTETKRAFSKE; TETKRAFSKED; ETKRAFSKEDF; TKRAFSKEDFN; KRAFSKEDFNL; RAFSKEDFNLI; AFSKEDFNLIN; FSKEDFNLINK; SKEDFNLINKR; KEDFNLINKRL; EDFNLINKRLD; DFNLINKRLDN; FNLINKRLDNY; NLINKRLDNYD; LINKRLDNYDF; INKRLDNYDFK; NKRLDNYDFKN; KRLDNYDFKNE; RLDNYDFKNEY; LDNYDFKNEYE; DNYDFKNEYEK; NYDFKNEYEKS; YDFKNEYEKSH; DFKNEYEKSHV; FKNEYEKSHVF; KNEYEKSHVFS; NEYEKSHVFSD; EYEKSHVFSDA; YEKSHVFSDAP; EKSHVFSDAPR; KSHVFSDAPRI; SHVFSDAPRIR; HVFSDAPRIRG; VFSDAPRIRGD; FSDAPRIRGDL; SDAPRIRGDLR; DAPRIRGDLRK; APRIRGDLRKI; PRIRGDLRKIG; RIRGDLRKIGI; IRGDLRKIGIK; RGDLRKIGIKE; GDLRKIGIKEK; DLRKIGIKEKS; LRKIGIKEKSV; RKIGIKEKSVF; KIGIKEKSVFL; IGIKEKSVFLD; GIKEKSVFLDA; IKEKSVFLDAL; KEKSVFLDALE; EKSVFLDALEA; KSVFLDALEAI; SVFLDALEAIE; VFLDALEAIEY; FLDALEAIEYL; LDALEAIEYLI; DALEAIEYLIK; ALEAIEYLIKI; LEAIEYLIKIK; EAIEYLIKIKI; AIEYLIKIKIS; IEYLIKIKIST; EYLIKIKISTD; YLIKIKISTDS; LIKIKISTDSI; IKIKISTDSIF; KIKISTDSIFL; IKISTDSIFLS; KISTDSIFLSE; ISTDSIFLSED; STDSIFLSEDM; TDSIFLSEDMI; DSIFLSEDMIR; SIFLSEDMIRL; IFLSEDMIRLI; FLSEDMIRLIG; LSEDMIRLIGS; SEDMIRLIGSY; EDMIRLIGSYP; DMIRLIGSYPD; MIRLIGSYPDS; IRLIGSYPDSI; RLIGSYPDSIF; LIGSYPDSIFN; IGSYPDSIFNY; GSYPDSIFNYL; SYPDSIFNYLI; YPDSIFNYLIQ; PDSIFNYLIQL; DSIFNYLIQLN; SIFNYLIQLNS; IFNYLIQLNSD; FNYLIQLNSDK; NYLIQLNSDKI; YLIQLNSDKID; LIQLNSDKIDY; IQLNSDKIDYA; QLNSDKIDYAE; LNSDKIDYAEK; NSDKIDYAEKY; SDKIDYAEKYG; DKIDYAEKYGD; KIDYAEKYGDN; IDYAEKYGDNA; DYAEKYGDNAR; YAEKYGDNARN; AEKYGDNARNN; EKYGDNARNNF; KYGDNARNNFK; YGDNARNNFKK; GDNARNNFKKD; DNARNNFKKDY; NARNNFKKDYS; ARNNFKKDYSE; RNNFKKDYSED; NNFKKDYSEDK; NFKKDYSEDKA; FKKDYSEDKAN; KKDYSEDKANT; KDYSEDKANTV; DYSEDKANTVK; YSEDKANTVKQ; SEDKANTVKQI; EDKANTVKQIL; DKANTVKQILK; KANTVKQILKQ; ANTVKQILKQI; NTVKQILKQIL; TVKQILKQILA; VKQILKQILAD; KQILKQILADL; QILKQILADLP; ILKQILADLPK; LKQILADLPKD;
Seq19	SEQ ID NO 19190-20455/ 8 mers: MCAFLLLN; CAFLLLNL; AFLLLNLV; FLLLNLVN; LLLNLVNC; LLNLVNCK; LNLVNCKF; NLVNCKFD; LVNCKFDS; VNCKFDSL; NCKFDSLN; CKFDSLNL; KFDSLNLS; FDSLNLST; DSLNLSTK; SLNLSTKS; LNLSTKSV; NLSTKSVD; LSTKSVDD; STKSVDDK; TKSVDDKN; KSVDDKNN; SVDDKNNS; VDDKNNSI; DDKNNSIA; DKNNSIAK; KNNSIAKL; NNSIAKLL; NSIAKLLQ; SIAKLLQH; IAKLLQHL; AKLLQHLS; KLLQHLSK; LLQHLSKS; LQHLSKSE; QHLSKSED; HLSKSEDQ; LSKSEDQA; SKSEDQAN; KSEDQANK; SEDQANKT; EDQANKTS; DQANKTST; QANKTSTS; ANKTSTSE;

	NKTSTSED; KTSTSEDQ; TSTSEDQK; STSEDQKE; TSEDQKEL; SEDQKELE; EDQKELEI; DQKELEIT; QKELEITE; KELEITEN; ELEITENK; LEITENKE; EITENKEQ; ITENKEQE; TENKEQEH; ENKEQEHE; NKEQEHEK; KEQEHEKL; EQEHEKLS; QEHEKLSQ; EHEKLSQV; HEKLSQVA; EKLSQVAQ; KLSQVAQH; LSQVAQHA; SQVAQHAP; QVAQHAPN; VAQHAPNS; AQHAPNSK; QHAPNSKI; HAPNSKIE; APNSKIEK; PNSKIEKV; NSKIEKVK; SKIEKVKS; KIEKVKSD; IEKVKSDG; EKVKSDGK; KVKSDGKP; VKSDGKPV; KSDGKPVP; SDGKPVPG; DGKPVPGD; GKPVPGDK; KPVPGDKI; PVPGDKIL; VPGDKILS; PGDKILSS; GDKILSSN; DKILSSNK; KILSSNKD; ILSSNKDI; LSSNKDIY; SSNKDIYN; SNKDIYNS; NKDIYNSY; KDIYNSYI; DIYNSYIP; IYNSYIPE; YNSYIPEV; NSYIPEVK; SYIPEVKE; YIPEVKEE; IPEVKEEI; PEVKEEIV; EVKEEIVY; VKEEIVYE; KEEIVYEI; EEIVYEIL; EIVYEILE; IVYEILEE; VYEILEEV; YEILEEVI; EILEEVII; ILEEVIIP; LEEVIIPE; EEVIIPET; EVIIPETK; VIIPETKI; IIPETKIP; IPETKIPE; PETKIPEI; ETKIPEIT; TKIPEITE; KIPEITEE; IPEITEEV; PEITEEVI; EITEEVIM; ITEEVIMP; TEEVIMPI; EEVIMPIP; EVIMPIPQ; VIMPIPQT; IMPIPQTI; MPIPQTID; PIPQTIDF; IPQTIDFY; PQTIDFYI; QTIDFYIE; TIDFYIEP; IDFYIEPR; DFYIEPRP; FYIEPRPI; YIEPRPIS; IEPRPISS; EPRPISSF; PRPISSFL; RPISSFLT; PISSFLTQ; ISSFLTQG; SSFLTQGT; SFLTQGTS; FLTQGTSP; LTQGTSPS; TQGTSPSI; QGTSPSIT; GTSPSITS; TSPSITST; SPSITSTI; PSITSTIK; SITSTIKS; ITSTIKSY; TSTIKSYK; STIKSYKE; TIKSYKEL; IKSYKELA; KSYKELAK; SYKELAKE; YKELAKEK; KELAKEKI; ELAKEKIN; LAKEKINN; AKEKINNG; KEKINNGL; EKINNGLN; KINNGLNI; INNGLNIV; NNGLNIVQ; NGLNIVQK; GLNIVQKI; LNIVQKIT; NIVQKITQ; IVQKITQN; VQKITQNI; QKITQNID; KITQNIDN; ITQNIDNI; TQNIDNIT; QNIDNITE; NIDNITEN; IDNITENL; DNITENLN; NITENLNS; ITENLNSK; TENLNSKE; ENLNSKET; NLNSKETP; LNSKETPK; NSKETPKE; SKETPKEI; KETPKEIS; ETPKEISG; TPKEISGK; PKEISGKE; KEISGKEV; EISGKEVE; ISGKEVEE; SGKEVEEK; GKEVEEKI; KEVEEKIT; EVEEKITH; VEEKITHP; EEKITHPI; EKITHPIF; KITHPIFD; ITHPIFDH; THPIFDHI; HPIFDHIT; PIFDHITG; IFDHITGS; FDHITGSG; DHITGSGN; HITGSGNN; ITGSGNNP; TGSGNNPG; GSGNNPGQ; SGNNPGQD; GNNPGQDS; NNPGQDSI; NPGQDSIS; PGQDSISN; GQDSISNT; QDSISNTW; DSISNTWG; SISNTWGE; ISNTWGEG; SNTWGEGL; NTWGEGLE; TWGEGLEI; WGEGLEIG; GEGLEIGG; EGLEIGGD; GLEIGGDS; LEIGGDSN; EIGGDSNF; IGGDSNFF; GGDSNFFT; GDSNFFTN; DSNFFTNL; SNFFTNLE; NFFTNLEE; FFTNLEEV; FTNLEEVR; TNLEEVRS; NLEEVRSS; LEEVRSSI; EEVRSSIR; EVRSSIRT; VRSSIRTK; RSSIRTKI; SSIRTKIK; SIRTKIKV; IRTKIKVS; RTKIKVSD; TKIKVSDG; KIKVSDGT; IKVSDGTE; KVSDGTEQ; VSDGTEQT; SDGTEQTK; DGTEQTKD; GTEQTKDK; TEQTKDKV; EQTKDKVE; QTKDKVEI; TKDKVEID; KDKVEIDE; DKVEIDEI; KVEIDEII; VEIDEIIE; EIDEIIED; IDEIIEDL; DEIIEDLQ; EIIEDLQK; IIEDLQKL; IEDLQKLK; EDLQKLKE; DLQKLKEF; LQKLKEFL; QKLKEFLE; KLKEFLEK; LKEFLEKL; KEFLEKLK; EFLEKLKK; FLEKLKKY;

	LEKLKKYL; EKLKKYLK; KLKKYLKD; LKKYLKDT; KKYLKDTN; KYLKDTNN; YLKDTNNL; LKDTNNLS; KDTNNLSA; DTNNLSAI; TNNLSAIE; NNLSAIEE; NLSAIEES; LSAIEESV; SAIEESVK; AIEESVKG; IEESVKGL; EESVKGLS; 9 mers: MCAFLLLNL; CAFLLLNLV; AFLLLNLVN; FLLLNLVNC; LLLNLVNCK; LLNLVNCKF; LNLVNCKFD; NLVNCKFDS; LVNCKFDSL; VNCKFDSLN; NCKFDSLNL; CKFDSLNLS; KFDSLNLST; FDSLNLSTK; DSLNLSTKS; SLNLSTKSV; LNLSTKSVD; NLSTKSVDD; LSTKSVDDK; STKSVDDKN; TKSVDDKNN; KSVDDKNNS; SVDDKNNSI; VDDKNNSIA; DDKNNSIAK; DKNNSIAKL; KNNSIAKLL; NNSIAKLLQ; NSIAKLLQH; SIAKLLQHL; IAKLLQHLS; AKLLQHLSK; KLLQHLSKS; LLQHLSKSE; LQHLSKSED; QHLSKSEDQ; HLSKSEDQA; LSKSEDQAN; SKSEDQANK; KSEDQANKT; SEDQANKTS; EDQANKTST; DQANKTSTS; QANKTSTSE; ANKTSTSED; NKTSTSEDQ; KTSTSEDQK; TSTSEDQKE; STSEDQKEL; TSEDQKELE; SEDQKELEI; EDQKELEIT; DQKELEITE; QKELEITEN; KELEITENK; ELEITENKE; LEITENKEQ; EITENKEQE; ITENKEQEH; TENKEQEHE; ENKEQEHEK; NKEQEHEKL; KEQEHEKLS; EQEHEKLSQ; QEHEKLSQV; EHEKLSQVA; HEKLSQVAQ; EKLSQVAQH; KLSQVAQHA; LSQVAQHAP; SQVAQHAPN; QVAQHAPNS; VAQHAPNSK; AQHAPNSKI; QHAPNSKIE; HAPNSKIEK; APNSKIEKV; PNSKIEKVK; NSKIEKVKS; SKIEKVKSD; KIEKVKSDG; IEKVKSDGK; EKVKSDGKP; KVKSDGKPV; VKSDGKPVP; KSDGKPVPG; SDGKPVPGD; DGKPVPGDK; GKPVPGDKI; KPVPGDKIL; PVPGDKILS; VPGDKILSS; PGDKILSSN; GDKILSSNK; DKILSSNKD; KILSSNKDI; ILSSNKDIY; LSSNKDIYN; SSNKDIYNS; SNKDIYNSY; NKDIYNSYI; KDIYNSYIP; DIYNSYIPE; IYNSYIPEV; YNSYIPEVK; NSYIPEVKE; SYIPEVKEE; YIPEVKEEI; IPEVKEEIV; PEVKEEIVY; EVKEEIVYE; VKEEIVYEI; KEEIVYEIL; EEIVYEILE; EIVYEILEE; IVYEILEEV; VYEILEEVI; YEILEEVII; EILEEVIIP; ILEEVIIPE; LEEVIIPET; EEVIIPETK; EVIIPETKI; VIIPETKIP; IIPETKIPE; IPETKIPEI; PETKIPEIT; ETKIPEITE; TKIPEITEE; KIPEITEEV; IPEITEEVI; PEITEEVIM; EITEEVIMP; ITEEVIMPI; TEEVIMPIP; EEVIMPIPQ; EVIMPIPQT; VIMPIPQTI; IMPIPQTID; MPIPQTIDF; PIPQTIDFY; IPQTIDFYI; PQTIDFYIE; QTIDFYIEP; TIDFYIEPR; IDFYIEPRP; DFYIEPRPI; FYIEPRPIS; YIEPRPISS; IEPRPISSF; EPRPISSFL; PRPISSFLT; RPISSFLTQ; PISSFLTQG; ISSFLTQGT; SSFLTQGTS; SFLTQGTSP; FLTQGTSPS; LTQGTSPSI; TQGTSPSIT; QGTSPSITS; GTSPSITST; TSPSITSTI; SPSITSTIK; PSITSTIKS; SITSTIKSY; ITSTIKSYK; TSTIKSYKE; STIKSYKEL; TIKSYKELA; IKSYKELAK; KSYKELAKE; SYKELAKEK; YKELAKEKI; KELAKEKIN; ELAKEKINN; LAKEKINNG; AKEKINNGL; KEKINNGLN; EKINNGLNI; KINNGLNIV; INNGLNIVQ; NNGLNIVQK; NGLNIVQKI; GLNIVQKIT; LNIVQKITQ; NIVQKITQN; IVQKITQNI; VQKITQNID; QKITQNIDN; KITQNIDNI; ITQNIDNIT; TQNIDNITE; QNIDNITEN; NIDNITENL; IDNITENLN; DNITENLNS; NITENLNSK; ITENLNSKE; TENLNSKET; ENLNSKETP; NLNSKETPK; LNSKETPKE; NSKETPKEI; SKETPKEIS; KETPKEISG; ETPKEISGK; TPKEISGKE; PKEISGKEV; KEISGKEVE; EISGKEVEE; ISGKEVEEK; SGKEVEEKI; GKEVEEKIT; KEVEEKITH; EVEEKITHP; VEEKITHPI; EEKITHPIF; EKITHPIFD; KITHPIFDH; ITHPIFDHI; THPIFDHIT; HPIFDHITG; PIFDHITGS; IFDHITGSG;

FDHITGSGN; DHITGSGNN; HITGSGNNP; ITGSGNNPG; TGSGNNPGQ;
GSGNNPGQD; SGNNPGQDS; GNNPGQDSI; NNPGQDSIS; NPGQDSISN;
PGQDSISNT; GQDSISNTW; QDSISNTWG; DSISNTWGE; SISNTWGEG;
ISNTWGEGL; SNTWGEGLE; NTWGEGLEI; TWGEGLEIG; WGEGLEIGG;
GEGLEIGGD; EGLEIGGDS; GLEIGGDSN; LEIGGDSNF; EIGGDSNFF;
IGGDSNFFT; GGDSNFFTN; GDSNFFTNL; DSNFFTNLE; SNFFTNLEE;
NFFTNLEEV; FFTNLEEVR; FTNLEEVRS; TNLEEVRSS; NLEEVRSSI;
LEEVRSSIR; EEVRSSIRT; EVRSSIRTK; VRSSIRTKI; RSSIRTKIK;
SSIRTKIKV; SIRTKIKVS; IRTKIKVSD; RTKIKVSDG; TKIKVSDGT;
KIKVSDGTE; IKVSDGTEQ; KVSDGTEQT; VSDGTEQTK; SDGTEQTKD;
DGTEQTKDK; GTEQTKDKV; TEQTKDKVE; EQTKDKVEI; QTKDKVEID;
TKDKVEIDE; KDKVEIDEI; DKVEIDEII; KVEIDEIIE; VEIDEIIED;
EIDEIIEDL; IDEIIEDLQ; DEIIEDLQK; EIIEDLQKL; IIEDLQKLK;
IEDLQKLKE; EDLQKLKEF; DLQKLKEFL; LQKLKEFLE; QKLKEFLEK;
KLKEFLEKL; LKEFLEKLK; KEFLEKLKK; EFLEKLKKY; FLEKLKKYL;
LEKLKKYLK; EKLKKYLKD; KLKKYLKDT; LKKYLKDTN; KKYLKDTNN;
KYLKDTNNL; YLKDTNNLS; LKDTNNLSA; KDTNNLSAI; DTNNLSAIE;
TNNLSAIEE; NNLSAIEES; NLSAIEESV; LSAIEESVK; SAIEESVKG;
AIEESVKGL; IEESVKGLS;

10 mers:
MCAFLLLNLV; CAFLLLNLVN; AFLLLNLVNC; FLLLNLVNCK;
LLLNLVNCKF; LLNLVNCKFD; LNLVNCKFDS; NLVNCKFDSL;
LVNCKFDSLN; VNCKFDSLNL; NCKFDSLNLS; CKFDSLNLST;
KFDSLNLSTK; FDSLNLSTKS; DSLNLSTKSV; SLNLSTKSVD;
LNLSTKSVDD; NLSTKSVDDK; LSTKSVDDKN; STKSVDDKNN;
TKSVDDKNNS; KSVDDKNNSI; SVDDKNNSIA; VDDKNNSIAK;
DDKNNSIAKL; DKNNSIAKLL; KNNSIAKLLQ; NNSIAKLLQH;
NSIAKLLQHL; SIAKLLQHLS; IAKLLQHLSK; AKLLQHLSKS;
KLLQHLSKSE; LLQHLSKSED; LQHLSKSEDQ; QHLSKSEDQA;
HLSKSEDQAN; LSKSEDQANK; SKSEDQANKT; KSEDQANKTS;
SEDQANKTST; EDQANKTSTS; DQANKTSTSE; QANKTSTSED;
ANKTSTSEDQ; NKTSTSEDQK; KTSTSEDQKE; TSTSEDQKEL;
STSEDQKELE; TSEDQKELEI; SEDQKELEIT; EDQKELEITE;
DQKELEITEN; QKELEITENK; KELEITENKE; ELEITENKEQ;
LEITENKEQE; EITENKEQEH; ITENKEQEHE; TENKEQEHEK;
ENKEQEHEKL; NKEQEHEKLS; KEQEHEKLSQ; EQEHEKLSQV;
QEHEKLSQVA; EHEKLSQVAQ; HEKLSQVAQH; EKLSQVAQHA;
KLSQVAQHAP; LSQVAQHAPN; SQVAQHAPNS; QVAQHAPNSK;
VAQHAPNSKI; AQHAPNSKIE; QHAPNSKIEK; HAPNSKIEKV;
APNSKIEKVK; PNSKIEKVKS; NSKIEKVKSD; SKIEKVKSDG;
KIEKVKSDGK; IEKVKSDGKP; EKVKSDGKPV; KVKSDGKPVP;
VKSDGKPVPG; KSDGKPVPGD; SDGKPVPGDK; DGKPVPGDKI;
GKPVPGDKIL; KPVPGDKILS; PVPGDKILSS; VPGDKILSSN;
PGDKILSSNK; GDKILSSNKD; DKILSSNKDI; KILSSNKDIY;
ILSSNKDIYN; LSSNKDIYNS; SSNKDIYNSY; SNKDIYNSYI;
NKDIYNSYIP; KDIYNSYIPE; DIYNSYIPEV; IYNSYIPEVK;
YNSYIPEVKE; NSYIPEVKEE; SYIPEVKEEI; YIPEVKEEIV;
IPEVKEEIVY; PEVKEEIVYE; EVKEEIVYEI; VKEEIVYEIL;
KEEIVYEILE; EEIVYEILEE; EIVYEILEEV; IVYEILEEVI;
VYEILEEVII; YEILEEVIIP; EILEEVIIPE; ILEEVIIPET;

	LEEVIIPETK; EEVIIPETKI; EVIIPETKIP; VIIPETKIPE; IIPETKIPEI; IPETKIPEIT; PETKIPEITE; ETKIPEITEE; TKIPEITEEV; KIPEITEEVI; IPEITEEVIM; PEITEEVIMP; EITEEVIMPI; ITEEVIMPIP; TEEVIMPIPQ; EEVIMPIPQT; EVIMPIPQTI; VIMPIPQTID; IMPIPQTIDF; MPIPQTIDFY; PIPQTIDFYI; IPQTIDFYIE; PQTIDFYIEP; QTIDFYIEPR; TIDFYIEPRP; IDFYIEPRPI; DFYIEPRPIS; FYIEPRPISS; YIEPRPISSF; IEPRPISSFL; EPRPISSFLT; PRPISSFLTQ; RPISSFLTQG; PISSFLTQGT; ISSFLTQGTS; SSFLTQGTSP; SFLTQGTSPS; FLTQGTSPSI; LTQGTSPSIT; TQGTSPSITS; QGTSPSITST; GTSPSITSTI; TSPSITSTIK; SPSITSTIKS; PSITSTIKSY; SITSTIKSYK; ITSTIKSYKE; TSTIKSYKEL; STIKSYKELA; TIKSYKELAK; IKSYKELAKE; KSYKELAKEK; SYKELAKEKI; YKELAKEKIN; KELAKEKINN; ELAKEKINNG; LAKEKINNGL; AKEKINNGLN; KEKINNGLNI; EKINNGLNIV; KINNGLNIVQ; INNGLNIVQK; NNGLNIVQKI; NGLNIVQKIT; GLNIVQKITQ; LNIVQKITQN; NIVQKITQNI; IVQKITQNID; VQKITQNIDN; QKITQNIDNI; KITQNIDNIT; ITQNIDNITE; TQNIDNITEN; QNIDNITENL; NIDNITENLN; IDNITENLNS; DNITENLNSK; NITENLNSKE; ITENLNSKET; TENLNSKETP; ENLNSKETPK; NLNSKETPKE; LNSKETPKEI; NSKETPKEIS; SKETPKEISG; KETPKEISGK; ETPKEISGKE; TPKEISGKEV; PKEISGKEVE; KEISGKEVEE; EISGKEVEEK; ISGKEVEEKI; SGKEVEEKIT; GKEVEEKITH; KEVEEKITHP; EVEEKITHPI; VEEKITHPIF; EEKITHPIFD; EKITHPIFDH; KITHPIFDHI; ITHPIFDHIT; THPIFDHITG; HPIFDHITGS; PIFDHITGSG; IFDHITGSGN; FDHITGSGNN; DHITGSGNNP; HITGSGNNPG; ITGSGNNPGQ; TGSGNNPGQD; GSGNNPGQDS; SGNNPGQDSI; GNNPGQDSIS; NNPGQDSISN; NPGQDSISNT; PGQDSISNTW; GQDSISNTWG; QDSISNTWGE; DSISNTWGEG; SISNTWGEGL; ISNTWGEGLE; SNTWGEGLEI; NTWGEGLEIG; TWGEGLEIGG; WGEGLEIGGD; GEGLEIGGDS; EGLEIGGDSN; GLEIGGDSNF; LEIGGDSNFF; EIGGDSNFFT; IGGDSNFFTN; GGDSNFFTNL; GDSNFFTNLE; DSNFFTNLEE; SNFFTNLEEV; NFFTNLEEVR; FFTNLEEVRS; FTNLEEVRSS; TNLEEVRSSI; NLEEVRSSIR; LEEVRSSIRT; EEVRSSIRTK; EVRSSIRTKI; VRSSIRTKIK; RSSIRTKIKV; SSIRTKIKVS; SIRTKIKVSD; IRTKIKVSDG; RTKIKVSDGT; TKIKVSDGTE; KIKVSDGTEQ; IKVSDGTEQT; KVSDGTEQTK; VSDGTEQTKD; SDGTEQTKDK; DGTEQTKDKV; GTEQTKDKVE; TEQTKDKVEI; EQTKDKVEID; QTKDKVEIDE; TKDKVEIDEI; KDKVEIDEII; DKVEIDEIIE; KVEIDEIIED; VEIDEIIEDL; EIDEIIEDLQ; IDEIIEDLQK; DEIIEDLQKL; EIIEDLQKLK; IIEDLQKLKE; IEDLQKLKEF; EDLQKLKEFL; DLQKLKEFLE; LQKLKEFLEK; QKLKEFLEKL; KLKEFLEKLK; LKEFLEKLKK; KEFLEKLKKY; EFLEKLKKYL; FLEKLKKYLK; LEKLKKYLKD; EKLKKYLKDT; KLKKYLKDTN; LKKYLKDTNN; KKYLKDTNNL; KYLKDTNNLS; YLKDTNNLSA; LKDTNNLSAI; KDTNNLSAIE; DTNNLSAIEE; TNNLSAIEES; NNLSAIEESV; NLSAIEESVK; LSAIEESVKG; SAIEESVKGL; AIEESVKGLS; 11 mers:

	MCAFLLLNLVN; CAFLLLNLVNC; AFLLLNLVNCK; FLLLNLVNCKF; LLLNLVNCKFD; LLNLVNCKFDS; LNLVNCKFDSL; NLVNCKFDSLN; LVNCKFDSLNL; VNCKFDSLNLS; NCKFDSLNLST; CKFDSLNLSTK; KFDSLNLSTKS; FDSLNLSTKSV; DSLNLSTKSVD; SLNLSTKSVDD; LNLSTKSVDDK; NLSTKSVDDKN; LSTKSVDDKNN; STKSVDDKNNS; TKSVDDKNNSI; KSVDDKNNSIA; SVDDKNNSIAK; VDDKNNSIAKL; DDKNNSIAKLL; DKNNSIAKLLQ; KNNSIAKLLQH; NNSIAKLLQHL; NSIAKLLQHLS; SIAKLLQHLSK; IAKLLQHLSKS; AKLLQHLSKSE; KLLQHLSKSED; LLQHLSKSEDQ; LQHLSKSEDQA; QHLSKSEDQAN; HLSKSEDQANK; LSKSEDQANKT; SKSEDQANKTS; KSEDQANKTST; SEDQANKTSTS; EDQANKTSTSE; DQANKTSTSED; QANKTSTSEDQ; ANKTSTSEDQK; NKTSTSEDQKE; KTSTSEDQKEL; TSTSEDQKELE; STSEDQKELEI; TSEDQKELEIT; SEDQKELEITE; EDQKELEITEN; DQKELEITENK; QKELEITENKE; KELEITENKEQ; ELEITENKEQE; LEITENKEQEH; EITENKEQEHE; ITENKEQEHEK; TENKEQEHEKL; ENKEQEHEKLS; NKEQEHEKLSQ; KEQEHEKLSQV; EQEHEKLSQVA; QEHEKLSQVAQ; EHEKLSQVAQH; HEKLSQVAQHA; EKLSQVAQHAP; KLSQVAQHAPN; LSQVAQHAPNS; SQVAQHAPNSK; QVAQHAPNSKI; VAQHAPNSKIE; AQHAPNSKIEK; QHAPNSKIEKV; HAPNSKIEKVK; APNSKIEKVKS; PNSKIEKVKSD; NSKIEKVKSDG; SKIEKVKSDGK; KIEKVKSDGKP; IEKVKSDGKPV; EKVKSDGKPVP; KVKSDGKPVPG; VKSDGKPVPGD; KSDGKPVPGDK; SDGKPVPGDKI; DGKPVPGDKIL; GKPVPGDKILS; KPVPGDKILSS; PVPGDKILSSN; VPGDKILSSNK; PGDKILSSNKD; GDKILSSNKDI; DKILSSNKDIY; KILSSNKDIYN; ILSSNKDIYNS; LSSNKDIYNSY; SSNKDIYNSYI; SNKDIYNSYIP; NKDIYNSYIPE; KDIYNSYIPEV; DIYNSYIPEVK; IYNSYIPEVKE; YNSYIPEVKEE; NSYIPEVKEEI; SYIPEVKEEIV; YIPEVKEEIVY; IPEVKEEIVYE; PEVKEEIVYEI; EVKEEIVYEIL; VKEEIVYEILE; KEEIVYEILEE; EEIVYEILEEV; EIVYEILEEVI; IVYEILEEVII; VYEILEEVIIP; YEILEEVIIPE; EILEEVIIPET; ILEEVIIPETK; LEEVIIPETKI; EEVIIPETKIP; EVIIPETKIPE; VIIPETKIPEI; IIPETKIPEIT; IPETKIPEITE; PETKIPEITEE; ETKIPEITEEV; TKIPEITEEVI; KIPEITEEVIM; IPEITEEVIMP; PEITEEVIMPI; EITEEVIMPIP; ITEEVIMPIPQ; TEEVIMPIPQT; EEVIMPIPQTI; EVIMPIPQTID; VIMPIPQTIDF; IMPIPQTIDFY; MPIPQTIDFYI; PIPQTIDFYIE; IPQTIDFYIEP; PQTIDFYIEPR; QTIDFYIEPRP; TIDFYIEPRPI; IDFYIEPRPIS; DFYIEPRPISS; FYIEPRPISSF; YIEPRPISSFL; IEPRPISSFLT; EPRPISSFLTQ; PRPISSFLTQG; RPISSFLTQGT; PISSFLTQGTS; ISSFLTQGTSP; SSFLTQGTSPS; SFLTQGTSPSI; FLTQGTSPSIT; LTQGTSPSITS; TQGTSPSITST; QGTSPSITSTI; GTSPSITSTIK; TSPSITSTIKS; SPSITSTIKSY; PSITSTIKSYK; SITSTIKSYKE; ITSTIKSYKEL; TSTIKSYKELA; STIKSYKELAK; TIKSYKELAKE; IKSYKELAKEK; KSYKELAKEKI; SYKELAKEKIN; YKELAKEKINN; KELAKEKINNG; ELAKEKINNGL; LAKEKINNGLN; AKEKINNGLNI; KEKINNGLNIV; EKINNGLNIVQ; KINNGLNIVQK; INNGLNIVQKI; NNGLNIVQKIT; NGLNIVQKITQ; GLNIVQKITQN; LNIVQKITQNI; NIVQKITQNID; IVQKITQNIDN; VQKITQNIDNI; QKITQNIDNIT; KITQNIDNITE; ITQNIDNITEN; TQNIDNITENL; QNIDNITENLN; NIDNITENLNS; IDNITENLNSK; DNITENLNSKE; NITENLNSKET; ITENLNSKETP; TENLNSKETPK; ENLNSKETPKE; NLNSKETPKEI; LNSKETPKEIS; NSKETPKEISG;

	SKETPKEISGK; KETPKEISGKE; ETPKEISGKEV; TPKEISGKEVE; PKEISGKEVEE; KEISGKEVEEK; EISGKEVEEKI; ISGKEVEEKIT; SGKEVEEKITH; GKEVEEKITHP; KEVEEKITHPI; EVEEKITHPIF; VEEKITHPIFD; EEKITHPIFDH; EKITHPIFDHI; KITHPIFDHIT; ITHPIFDHITG; THPIFDHITGS; HPIFDHITGSG; PIFDHITGSGN; IFDHITGSGNN; FDHITGSGNNP; DHITGSGNNPG; HITGSGNNPGQ; ITGSGNNPGQD; TGSGNNPGQDS; GSGNNPGQDSI; SGNNPGQDSIS; GNNPGQDSISN; NNPGQDSISNT; NPGQDSISNTW; PGQDSISNTWG; GQDSISNTWGE; QDSISNTWGEG; DSISNTWGEGL; SISNTWGEGLE; ISNTWGEGLEI; SNTWGEGLEIG; NTWGEGLEIGG; TWGEGLEIGGD; WGEGLEIGGDS; GEGLEIGGDSN; EGLEIGGDSNF; GLEIGGDSNFF; LEIGGDSNFFT; EIGGDSNFFTN; IGGDSNFFTNL; GGDSNFFTNLE; GDSNFFTNLEE; DSNFFTNLEEV; SNFFTNLEEVR; NFFTNLEEVRS; FFTNLEEVRSS; FTNLEEVRSSI; TNLEEVRSSIR; NLEEVRSSIRT; LEEVRSSIRTK; EEVRSSIRTKI; EVRSSIRTKIK; VRSSIRTKIKV; RSSIRTKIKVS; SSIRTKIKVSD; SIRTKIKVSDG; IRTKIKVSDGT; RTKIKVSDGTE; TKIKVSDGTEQ; KIKVSDGTEQT; IKVSDGTEQTK; KVSDGTEQTKD; VSDGTEQTKDK; SDGTEQTKDKV; DGTEQTKDKVE; GTEQTKDKVEI; TEQTKDKVEID; EQTKDKVEIDE; QTKDKVEIDEI; TKDKVEIDEII; KDKVEIDEIIE; DKVEIDEIIED; KVEIDEIIEDL; VEIDEIIEDLQ; EIDEIIEDLQK; IDEIIEDLQKL; DEIIEDLQKLK; EIIEDLQKLKE; IIEDLQKLKEF; IEDLQKLKEFL; EDLQKLKEFLE; DLQKLKEFLEK; LQKLKEFLEKL; QKLKEFLEKLK; KLKEFLEKLKK; LKEFLEKLKKY; KEFLEKLKKYL; EFLEKLKKYLK; FLEKLKKYLKD; LEKLKKYLKDT; EKLKKYLKDTN; KLKKYLKDTNN; LKKYLKDTNNL; KKYLKDTNNLS; KYLKDTNNLSA; YLKDTNNLSAI; LKDTNNLSAIE; KDTNNLSAIEE; DTNNLSAIEES; TNNLSAIEESV; NNLSAIEESVK; NLSAIEESVKG; LSAIEESVKGL; SAIEESVKGLS;
Seq 20	SEQ ID NO 20456-22321/ 8 mers: MIKMSLNY; IKMSLNYT; KMSLNYTE; MSLNYTEI; SLNYTEIN; LNYTEINT; NYTEINTL; YTEINTLI; TEINTLIK; EINTLIKE; INTLIKEI; NTLIKEIP; TLIKEIPF; LIKEIPFT; IKEIPFTN; KEIPFTNS; EIPFTNSL; IPFTNSLI; PFTNSLIT; FTNSLITK; TNSLITKI; NSLITKII; SLITKIIQ; LITKIIQP; ITKIIQPD; TKIIQPDY; KIIQPDYK; IIQPDYKS; IQPDYKSL; QPDYKSLV; PDYKSLVL; DYKSLVLE; YKSLVLEI; KSLVLEIY; SLVLEIYN; LVLEIYNK; VLEIYNKI; LEIYNKID; EIYNKIDN; IYNKIDNK; YNKIDNKK; NKIDNKKF; KIDNKKFK; IDNKKFKI; DNKKFKIL; NKKFKILI; KKFKILIC; KFKILICL; FKILICLN; KILICLNP; ILICLNPN; LICLNPNT; ICLNPNTT; CLNPNTTR; LNPNTTRF; NPNTTRFH; PNTTRFHI; NTTRFHIT; TTRFHITK; TRFHITKK; RFHITKKN; FHITKKNF; HITKKNFK; ITKKNFKK; TKKNFKKN; KKNFKKNA; KNFKKNAL; NFKKNALK; FKKNALKL; KKNALKLR; KNALKLRF; NALKLRFS; ALKLRFSD; LKLRFSDF; KLRFSDFL; LRFSDFLK; RFSDFLKS; FSDFLKSK; SDFLKSKI; DFLKSKIQ; FLKSKIQN; LKSKIQNG; KSKIQNGK; SKIQNGKI; KIQNGKII; IQNGKIIK; QNGKIIKA; NGKIIKAF; GKIIKAFQ; KIIKAFQM; IIKAFQMK; IKAFQMKN; KAFQMKNE; AFQMKNER; FQMKNERI;

	QMKNERII; MKNERIIS; KNERIISL; NERIISLE; ERIISLEI; RIISLEIL; IISLEILQ; ISLEILQK; SLEILQKD; LEILQKDM; EILQKDMI; ILQKDMII; LQKDMIIL; QKDMIILF; KDMIILFI; DMIILFIK; MIILFIKL; IILFIKLW; ILFIKLWP; LFIKLWPS; FIKLWPSS; IKLWPSSP; KLWPSSPN; LWPSSPNI; WPSSPNII; PSSPNIIA; SSPNIIAT; SPNIIATN; PNIIATNS; NIIATNSN; IIATNSNF; IATNSNFK; ATNSNFKI; TNSNFKIL; NSNFKILD; SNFKILDA; NFKILDAY; FKILDAYY; KILDAYYR; ILDAYYRR; LDAYYRRP; DAYYRRPK; AYYRRPKI; YYRRPKIK; YRRPKIKE; RRPKIKET; RPKIKETT; PKIKETTG; KIKETTGE; IKETTGEI; KETTGEIF; ETTGEIFL; TTGEIFLK; TGEIFLKA; GEIFLKAK; EIFLKAKE; IFLKAKEI; FLKAKEIH; LKAKEIHE; KAKEIHES; AKEIHESN; KEIHESNK; EIHESNKM; IHESNKMS; HESNKMSD; ESNKMSDK; SNKMSDKK; NKMSDKKI; KMSDKKIM; MSDKKIME; SDKKIMEL; DKKIMELK; KKIMELKE; KIMELKEE; IMELKEEY; MELKEEYN; ELKEEYNN; LKEEYNNT; KEEYNNTS; EEYNNTSY; EYNNTSYT; YNNTSYTS; NNTSYTSY; NTSYTSYS; TSYTSYSE; SYTSYSEF; YTSYSEFL; TSYSEFLE; SYSEFLEN; YSEFLENY; SEFLENYY; EFLENYYE; FLENYYES; LENYYESL; ENYYESLN; NYYESLND; YYESLNDQ; YESLNDQI; ESLNDQIK; SLNDQIKK; LNDQIKKT; NDQIKKTN; DQIKKTNI; QIKKTNIK; IKKTNIKE; KKTNIKEL; KTNIKELL; TNIKELLI; NIKELLIE; IKELLIEK; KELLIEKY; ELLIEKYK; LLIEKYKK; LIEKYKKE; IEKYKKEL; EKYKKELI; KYKKELIV; YKKELIVL; KKELIVLE; KELIVLEK; ELIVLEKR; LIVLEKRI; IVLEKRID; VLEKRIDS; LEKRIDSL; EKRIDSLK; KRIDSLKQ; RIDSLKQQ; IDSLKQQI; DSLKQQIK; SLKQQIKL; LKQQIKLL; KQQIKLLE; QQIKLLEN; QIKLLENI; IKLLENIE; KLLENIEN; LLENIENE; LENIENEK; ENIENEKE; NIENEKEK; IENEKEKG; ENEKEKGE; NEKEKGEL; EKEKGELI; KEKGELIL; EKGELILL; KGELILLN; GELILLNI; ELILLNIN; LILLNINK; ILLNINKI; LLNINKIQ; LNINKIQK; NINKIQKG; INKIQKGI; NKIQKGIK; KIQKGIKE; IQKGIKEI; QKGIKEIN; KGIKEINL; GIKEINLL; IKEINLLN; KEINLLNY; EINLLNYK; INLLNYKE; NLLNYKEE; LLNYKEEK; LNYKEEKI; NYKEEKIK; YKEEKIKI; KEEKIKIS; EEKIKISL; EKIKISLN; KIKISLNQ; IKISLNQS; KISLNQSL; ISLNQSLS; SLNQSLSP; LNQSLSPK; NQSLSPKE; QSLSPKEN; SLSPKENA; LSPKENAL; SPKENALQ; PKENALQY; KENALQYF; ENALQYFK; NALQYFKA; ALQYFKAY; LQYFKAYK; QYFKAYKK; YFKAYKKG; FKAYKKGK; KAYKKGKN; AYKKGKNS; YKKGKNSF; KKGKNSFK; KGKNSFKT; GKNSFKTI; KNSFKTIQ; NSFKTIQN; SFKTIQNQ; FKTIQNQL; KTIQNQLK; TIQNQLKD; IQNQLKDN; QNQLKDNL; NQLKDNLD; QLKDNLDK; LKDNLDKF; KDNLDKFN; DNLDKFNL; NLDKFNLI; LDKFNLIQ; DKFNLIQS; KFNLIQSK; FNLIQSKI; NLIQSKIT; LIQSKITM; IQSKITML; QSKITMLK; SKITMLKV; KITMLKVE; ITMLKVEN; TMLKVENL; MLKVENLI; LKVENLIP; KVENLIPE; VENLIPEE; ENLIPEEE; NLIPEEEY; LIPEEEYN; IPEEEYNQ; PEEEYNQE; EEEYNQEK; EEYNQEKT; EYNQEKTA; YNQEKTAI; NQEKTAIK; QEKTAIKE; EKTAIKEK; KTAIKEKE; TAIKEKEK; AIKEKEKT; IKEKEKTP; KEKEKTPK; EKEKTPKI; KEKTPKIG; EKTPKIGL; KTPKIGLH; TPKIGLHF; PKIGLHFT; KIGLHFTY; IGLHFTYC;

GLHFTYCG; LHFTYCGF; HFTYCGFE; FTYCGFEI; TYCGFEIL;
YCGFEILI; CGFEILIG; GFEILIGR; FEILIGRN; EILIGRNA;
ILIGRNAK; LIGRNAKE; IGRNAKEN; GRNAKEND; RNAKENDK;
NAKENDKL; AKENDKLL; KENDKLLR; ENDKLLRH; NDKLLRHC;
DKLLRHCV; KLLRHCVK; LLRHCVKG; LRHCVKGN; RHCVKGND;
HCVKGNDY; CVKGNDYW; VKGNDYWL; KGNDYWLH; GNDYWLHT;
NDYWLHTR; DYWLHTRD; YWLHTRDY; WLHTRDYP; LHTRDYPG;
HTRDYPGA; TRDYPGAY; RDYPGAYV; DYPGAYVF; YPGAYVFI;
PGAYVFIK; GAYVFIKN; AYVFIKNQ; YVFIKNQK; VFIKNQKN;
FIKNQKNK; IKNQKNKT; KNQKNKTP; NQKNKTPS; QKNKTPSL;
KNKTPSLD; NKTPSLDV; KTPSLDVL; TPSLDVLL; PSLDVLLG;
SLDVLLGA; LDVLLGAG; DVLLGAGN; VLLGAGNL; LLGAGNLC;
LGAGNLCV; GAGNLCVF; AGNLCVFY; GNLCVFYT; NLCVFYTK;
LCVFYTKL; CVFYTKLA; VFYTKLAK; FYTKLAKK; YTKLAKKS;
TKLAKKSG; KLAKKSGK; LAKKSGKA; AKKSGKAD; KKSGKADL;
KSGKADLY; SGKADLYY; GKADLYYT; KADLYYTQ; ADLYYTQV;
DLYYTQVK; LYYTQVKN; YYTQVKNL; YTQVKNLR; TQVKNLRR;
QVKNLRRV; VKNLRRVK; KNLRRVKN; NLRRVKNK; LRRVKNKK;
RRVKNKKL; RVKNKKLG; VKNKKLGL; KNKKLGLV; NKKLGLVI;
KKLGLVIP; KLGLVIPK; LGLVIPKA; GLVIPKAE; LVIPKAEK;
VIPKAEKN; IPKAEKNL; PKAEKNLH; KAEKNLHI; AEKNLHIK;
EKNLHIKL; KNLHIKLD; NLHIKLDE; LHIKLDEN; HIKLDENL;
IKLDENLI; KLDENLIK; LDENLIKK; DENLIKKI; ENLIKKIK;
NLIKKIKN; LIKKIKNQ; IKKIKNQT;

9 mers:
MIKMSLNYT; IKMSLNYTE; KMSLNYTEI; MSLNYTEIN; SLNYTEINT;
LNYTEINTL; NYTEINTLI; YTEINTLIK; TEINTLIKE; EINTLIKEI;
INTLIKEIP; NTLIKEIPF; TLIKEIPFT; LIKEIPFTN; IKEIPFTNS;
KEIPFTNSL; EIPFTNSLI; IPFTNSLIT; PFTNSLITK; FTNSLITKI;
TNSLITKII; NSLITKIIQ; SLITKIIQP; LITKIIQPD; ITKIIQPDY;
TKIIQPDYK; KIIQPDYKS; IIQPDYKSL; IQPDYKSLV; QPDYKSLVL;
PDYKSLVLE; DYKSLVLEI; YKSLVLEIY; KSLVLEIYN; SLVLEIYNK;
LVLEIYNKI; VLEIYNKID; LEIYNKIDN; EIYNKIDNK; IYNKIDNKK;
YNKIDNKKF; NKIDNKKFK; KIDNKKFKI; IDNKKFKIL; DNKKFKILI;
NKKFKILIC; KKFKILICL; KFKILICLN; FKILICLNP; KILICLNPN;
ILICLNPNT; LICLNPNTT; ICLNPNTTR; CLNPNTTRF; LNPNTTRFH;
NPNTTRFHI; PNTTRFHIT; NTTRFHITK; TTRFHITKK; TRFHITKKN;
RFHITKKNF; FHITKKNFK; HITKKNFKK; ITKKNFKKN; TKKNFKKNA;
KKNFKKNAL; KNFKKNALK; NFKKNALKL; FKKNALKLR; KKNALKLRF;
KNALKLRFS; NALKLRFSD; ALKLRFSDF; LKLRFSDFL; KLRFSDFLK;
LRFSDFLKS; RFSDFLKSK; FSDFLKSKI; SDFLKSKIQ; DFLKSKIQN;
FLKSKIQNG; LKSKIQNGK; KSKIQNGKI; SKIQNGKII; KIQNGKIIK;
IQNGKIIKA; QNGKIIKAF; NGKIIKAFQ; GKIIKAFQM; KIIKAFQMK;
IIKAFQMKN; IKAFQMKNE; KAFQMKNER; AFQMKNERI; FQMKNERII;
QMKNERIIS; MKNERIISL; KNERIISLE; NERIISLEI; ERIISLEIL;
RIISLEILQ; IISLEILQK; ISLEILQKD; SLEILQKDM; LEILQKDMI;
EILQKDMII; ILQKDMIIL; LQKDMIILF; QKDMIILFI; KDMIILFIK;
DMIILFIKL; MIILFIKLW; IILFIKLWP; ILFIKLWPS; LFIKLWPSS;
FIKLWPSSP; IKLWPSSPN; KLWPSSPNI; LWPSSPNII; WPSSPNIIA;
PSSPNIIAT; SSPNIIATN; SPNIIATNS; PNIIATNSN; NIIATNSNF;

	IIATNSNFK; IATNSNFKI; ATNSNFKIL; TNSNFKILD; NSNFKILDA; SNFKILDAY; NFKILDAYY; FKILDAYYR; KILDAYYRR; ILDAYYRRP; LDAYYRRPK; DAYYRRPKI; AYYRRPKIK; YYRRPKIKE; YRRPKIKET; RRPKIKETT; RPKIKETTG; PKIKETTGE; KIKETTGEI; IKETTGEIF; KETTGEIFL; ETTGEIFLK; TTGEIFLKA; TGEIFLKAK; GEIFLKAKE; EIFLKAKEI; IFLKAKEIH; FLKAKEIHE; LKAKEIHES; KAKEIHESN; AKEIHESNK; KEIHESNKM; EIHESNKMS; IHESNKMSD; HESNKMSDK; ESNKMSDKK; SNKMSDKKI; NKMSDKKIM; KMSDKKIME; MSDKKIMEL; SDKKIMELK; DKKIMELKE; KKIMELKEE; KIMELKEEY; IMELKEEYN; MELKEEYNN; ELKEEYNNT; LKEEYNNTS; KEEYNNTSY; EEYNNTSYT; EYNNTSYTS; YNNTSYTSY; NNTSYTSYS; NTSYTSYSE; TSYTSYSEF; SYTSYSEFL; YTSYSEFLE; TSYSEFLEN; SYSEFLENY; YSEFLENYY; SEFLENYYE; EFLENYYES; FLENYYESL; LENYYESLN; ENYYESLND; NYYESLNDQ; YYESLNDQI; YESLNDQIK; ESLNDQIKK; SLNDQIKKT; LNDQIKKTN; NDQIKKTNI; DQIKKTNIK; QIKKTNIKE; IKKTNIKEL; KKTNIKELL; KTNIKELLI; TNIKELLIE; NIKELLIEK; IKELLIEKY; KELLIEKYK; ELLIEKYKK; LLIEKYKKE; LIEKYKKEL; IEKYKKELI; EKYKKELIV; KYKKELIVL; YKKELIVLE; KKELIVLEK; KELIVLEKR; ELIVLEKRI; LIVLEKRID; IVLEKRIDS; VLEKRIDSL; LEKRIDSLK; EKRIDSLKQ; KRIDSLKQQ; RIDSLKQQI; IDSLKQQIK; DSLKQQIKL; SLKQQIKLL; LKQQIKLLE; KQQIKLLEN; QQIKLLENI; QIKLLENIE; IKLLENIEN; KLLENIENE; LLENIENEK; LENIENEKE; ENIENEKEK; NIENEKEKG; IENEKEKGE; ENEKEKGEL; NEKEKGELI; EKEKGELIL; KEKGELILL; EKGELILLN; KGELILLNI; GELILLNIN; ELILLNINK; LILLNINKI; ILLNINKIQ; LLNINKIQK; LNINKIQKG; NINKIQKGI; INKIQKGIK; NKIQKGIKE; KIQKGIKEI; IQKGIKEIN; QKGIKEINL; KGIKEINLL; GIKEINLLN; IKEINLLNY; KEINLLNYK; EINLLNYKE; INLLNYKEE; NLLNYKEEK; LLNYKEEKI; LNYKEEKIK; NYKEEKIKI; YKEEKIKIS; KEEKIKISL; EEKIKISLN; EKIKISLNQ; KIKISLNQS; IKISLNQSL; KISLNQSLS; ISLNQSLSP; SLNQSLSPK; LNQSLSPKE; NQSLSPKEN; QSLSPKENA; SLSPKENAL; LSPKENALQ; SPKENALQY; PKENALQYF; KENALQYFK; ENALQYFKA; NALQYFKAY; ALQYFKAYK; LQYFKAYKK; QYFKAYKKG; YFKAYKKGK; FKAYKKGKN; KAYKKGKNS; AYKKGKNSF; YKKGKNSFK; KKGKNSFKT; KGKNSFKTI; GKNSFKTIQ; KNSFKTIQN; NSFKTIQNQ; SFKTIQNQL; FKTIQNQLK; KTIQNQLKD; TIQNQLKDN; IQNQLKDNL; QNQLKDNLD; NQLKDNLDK; QLKDNLDKF; LKDNLDKFN; KDNLDKFNL; DNLDKFNLI; NLDKFNLIQ; LDKFNLIQS; DKFNLIQSK; KFNLIQSKI; FNLIQSKIT; NLIQSKITM; LIQSKITML; IQSKITMLK; QSKITMLKV; SKITMLKVE; KITMLKVEN; ITMLKVENL; TMLKVENLI; MLKVENLIP; LKVENLIPE; KVENLIPEE; VENLIPEEE; ENLIPEEEY; NLIPEEEYN; LIPEEEYNQ; IPEEEYNQE; PEEEYNQEK; EEEYNQEKT; EEYNQEKTA; EYNQEKTAI; YNQEKTAIK; NQEKTAIKE; QEKTAIKEK; EKTAIKEKE; KTAIKEKEK; TAIKEKEKT; AIKEKEKTP; IKEKEKTPK; KEKEKTPKI; EKEKTPKIG; KEKTPKIGL; EKTPKIGLH; KTPKIGLHF; TPKIGLHFT; PKIGLHFTY; KIGLHFTYC; IGLHFTYCG; GLHFTYCGF; LHFTYCGFE; HFTYCGFEI; FTYCGFEIL; TYCGFEILI; YCGFEILIG; CGFEILIGR; GFEILIGRN; FEILIGRNA; EILIGRNAK; ILIGRNAKE; LIGRNAKEN; IGRNAKEND; GRNAKENDK; RNAKENDKL; NAKENDKLL; AKENDKLLR; KENDKLLRH; ENDKLLRHC; NDKLLRHCV; DKLLRHCVK; KLLRHCVKG; LLRHCVKGN; LRHCVKGND; RHCVKGNDY; HCVKGNDYW; CVKGNDYWL; VKGNDYWLH; KGNDYWLHT; GNDYWLHTR;

NDYWLHTRD; DYWLHTRDY; YWLHTRDYP; WLHTRDYPG; LHTRDYPGA; HTRDYPGAY; TRDYPGAYV; RDYPGAYVF; DYPGAYVFI; YPGAYVFIK; PGAYVFIKN; GAYVFIKNQ; AYVFIKNQK; YVFIKNQKN; VFIKNQKNK; FIKNQKNKT; IKNQKNKTP; KNQKNKTPS; NQKNKTPSL; QKNKTPSLD; KNKTPSLDV; NKTPSLDVL; KTPSLDVLL; TPSLDVLLG; PSLDVLLGA; SLDVLLGAG; LDVLLGAGN; DVLLGAGNL; VLLGAGNLC; LLGAGNLCV; LGAGNLCVF; GAGNLCVFY; AGNLCVFYT; GNLCVFYTK; NLCVFYTKL; LCVFYTKLA; CVFYTKLAK; VFYTKLAKK; FYTKLAKKS; YTKLAKKSG; TKLAKKSGK; KLAKKSGKA; LAKKSGKAD; AKKSGKADL; KKSGKADLY; KSGKADLYY; SGKADLYYT; GKADLYYTQ; KADLYYTQV; ADLYYTQVK; DLYYTQVKN; LYYTQVKNL; YYTQVKNLR; YTQVKNLRR; TQVKNLRRV; QVKNLRRVK; VKNLRRVKN; KNLRRVKNK; NLRRVKNKK; LRRVKNKKL; RRVKNKKLG; RVKNKKLGL; VKNKKLGLV; KNKKLGLVI; NKKLGLVIP; KKLGLVIPK; KLGLVIPKA; LGLVIPKAE; GLVIPKAEK; LVIPKAEKN; VIPKAEKNL; IPKAEKNLH; PKAEKNLHI; KAEKNLHIK; AEKNLHIKL; EKNLHIKLD; KNLHIKLDE; NLHIKLDEN; LHIKLDENL; HIKLDENLI; IKLDENLIK; KLDENLIKK; LDENLIKKI; DENLIKKIK; ENLIKKIKN; NLIKKIKNQ; LIKKIKNQT;

10 mers:
MIKMSLNYTE; IKMSLNYTEI; KMSLNYTEIN; MSLNYTEINT; SLNYTEINTL; LNYTEINTLI; NYTEINTLIK; YTEINTLIKE; TEINTLIKEI; EINTLIKEIP; INTLIKEIPF; NTLIKEIPFT; TLIKEIPFTN; LIKEIPFTNS; IKEIPFTNSL; KEIPFTNSLI; EIPFTNSLIT; IPFTNSLITK; PFTNSLITKI; FTNSLITKII; TNSLITKIIQ; NSLITKIIQP; SLITKIIQPD; LITKIIQPDY; ITKIIQPDYK; TKIIQPDYKS; KIIQPDYKSL; IIQPDYKSLV; IQPDYKSLVL; QPDYKSLVLE; PDYKSLVLEI; DYKSLVLEIY; YKSLVLEIYN; KSLVLEIYNK; SLVLEIYNKI; LVLEIYNKID; VLEIYNKIDN; LEIYNKIDNK; EIYNKIDNKK; IYNKIDNKKF; YNKIDNKKFK; NKIDNKKFKI; KIDNKKFKIL; IDNKKFKILI; DNKKFKILIC; NKKFKILICL; KKFKILICLN; KFKILICLNP; FKILICLNPN; KILICLNPNT; ILICLNPNTT; LICLNPNTTR; ICLNPNTTRF; CLNPNTTRFH; LNPNTTRFHI; NPNTTRFHIT; PNTTRFHITK; NTTRFHITKK; TTRFHITKKN; TRFHITKKNF; RFHITKKNFK; FHITKKNFKK; HITKKNFKKN; ITKKNFKKNA; TKKNFKKNAL; KKNFKKNALK; KNFKKNALKL; NFKKNALKLR; FKKNALKLRF; KKNALKLRFS; KNALKLRFSD; NALKLRFSDF; ALKLRFSDFL; LKLRFSDFLK; KLRFSDFLKS; LRFSDFLKSK; RFSDFLKSKI; FSDFLKSKIQ; SDFLKSKIQN; DFLKSKIQNG; FLKSKIQNGK; LKSKIQNGKI; KSKIQNGKII; SKIQNGKIIK; KIQNGKIIKA; IQNGKIIKAF; QNGKIIKAFQ; NGKIIKAFQM; GKIIKAFQMK; KIIKAFQMKN; IIKAFQMKNE; IKAFQMKNER; KAFQMKNERI; AFQMKNERII; FQMKNERIIS; QMKNERIISL; MKNERIISLE; KNERIISLEI; NERIISLEIL; ERIISLEILQ; RIISLEILQK; IISLEILQKD; ISLEILQKDM; SLEILQKDMI; LEILQKDMII; EILQKDMIIL; ILQKDMIILF; LQKDMIILFI; QKDMIILFIK; KDMIILFIKL; DMIILFIKLW; MIILFIKLWP; IILFIKLWPS; ILFIKLWPSS; LFIKLWPSSP; FIKLWPSSPN; IKLWPSSPNI; KLWPSSPNII; LWPSSPNIIA; WPSSPNIIAT; PSSPNIIATN; SSPNIIATNS; SPNIIATNSN; PNIIATNSNF;

	NIIATNSNFK; IIATNSNFKI; IATNSNFKIL; ATNSNFKILD; TNSNFKILDA; NSNFKILDAY; SNFKILDAYY; NFKILDAYYR; FKILDAYYRR; KILDAYYRRP; ILDAYYRRPK; LDAYYRRPKI; DAYYRRPKIK; AYYRRPKIKE; YYRRPKIKET; YRRPKIKETT; RRPKIKETTG; RPKIKETTGE; PKIKETTGEI; KIKETTGEIF; IKETTGEIFL; KETTGEIFLK; ETTGEIFLKA; TTGEIFLKAK; TGEIFLKAKE; GEIFLKAKEI; EIFLKAKEIH; IFLKAKEIHE; FLKAKEIHES; LKAKEIHESN; KAKEIHESNK; AKEIHESNKM; KEIHESNKMS; EIHESNKMSD; IHESNKMSDK; HESNKMSDKK; ESNKMSDKKI; SNKMSDKKIM; NKMSDKKIME; KMSDKKIMEL; MSDKKIMELK; SDKKIMELKE; DKKIMELKEE; KKIMELKEEY; KIMELKEEYN; IMELKEEYNN; MELKEEYNNT; ELKEEYNNTS; LKEEYNNTSY; KEEYNNTSYT; EEYNNTSYTS; EYNNTSYTSY; YNNTSYTSYS; NNTSYTSYSE; NTSYTSYSEF; TSYTSYSEFL; SYTSYSEFLE; YTSYSEFLEN; TSYSEFLENY; SYSEFLENYY; YSEFLENYYE; SEFLENYYES; EFLENYYESL; FLENYYESLN; LENYYESLND; ENYYESLNDQ; NYYESLNDQI; YYESLNDQIK; YESLNDQIKK; ESLNDQIKKT; SLNDQIKKTN; LNDQIKKTNI; NDQIKKTNIK; DQIKKTNIKE; QIKKTNIKEL; IKKTNIKELL; KKTNIKELLI; KTNIKELLIE; TNIKELLIEK; NIKELLIEKY; IKELLIEKYK; KELLIEKYKK; ELLIEKYKKE; LLIEKYKKEL; LIEKYKKELI; IEKYKKELIV; EKYKKELIVL; KYKKELIVLE; YKKELIVLEK; KKELIVLEKR; KELIVLEKRI; ELIVLEKRID; LIVLEKRIDS; IVLEKRIDSL; VLEKRIDSLK; LEKRIDSLKQ; EKRIDSLKQQ; KRIDSLKQQI; RIDSLKQQIK; IDSLKQQIKL; DSLKQQIKLL; SLKQQIKLLE; LKQQIKLLEN; KQQIKLLENI; QQIKLLENIE; QIKLLENIEN; IKLLENIENE; KLLENIENEK; LLENIENEKE; LENIENEKEK; ENIENEKEKG; NIENEKEKGE; IENEKEKGEL; ENEKEKGELI; NEKEKGELIL; EKEKGELILL; KEKGELILLN; EKGELILLNI; KGELILLNIN; GELILLNINK; ELILLNINKI; LILLNINKIQ; ILLNINKIQK; LLNINKIQKG; LNINKIQKGI; NINKIQKGIK; INKIQKGIKE; NKIQKGIKEI; KIQKGIKEIN; IQKGIKEINL; QKGIKEINLL; KGIKEINLLN; GIKEINLLNY; IKEINLLNYK; KEINLLNYKE; EINLLNYKEE; INLLNYKEEK; NLLNYKEEKI; LLNYKEEKIK; LNYKEEKIKI; NYKEEKIKIS; YKEEKIKISL; KEEKIKISLN; EEKIKISLNQ; EKIKISLNQS; KIKISLNQSL; IKISLNQSLS; KISLNQSLSP; ISLNQSLSPK; SLNQSLSPKE; LNQSLSPKEN; NQSLSPKENA; QSLSPKENAL; SLSPKENALQ; LSPKENALQY; SPKENALQYF; PKENALQYFK; KENALQYFKA; ENALQYFKAY; NALQYFKAYK; ALQYFKAYKK; LQYFKAYKKG; QYFKAYKKGK; YFKAYKKGKN; FKAYKKGKNS; KAYKKGKNSF; AYKKGKNSFK; YKKGKNSFKT; KKGKNSFKTI; KGKNSFKTIQ; GKNSFKTIQN; KNSFKTIQNQ; NSFKTIQNQL; SFKTIQNQLK; FKTIQNQLKD; KTIQNQLKDN; TIQNQLKDNL; IQNQLKDNLD; QNQLKDNLDK; NQLKDNLDKF; QLKDNLDKFN; LKDNLDKFNL; KDNLDKFNLI; DNLDKFNLIQ; NLDKFNLIQS; LDKFNLIQSK; DKFNLIQSKI; KFNLIQSKIT; FNLIQSKITM; NLIQSKITML; LIQSKITMLK; IQSKITMLKV; QSKITMLKVE; SKITMLKVEN; KITMLKVENL; ITMLKVENLI; TMLKVENLIP; MLKVENLIPE; LKVENLIPEE; KVENLIPEEE; VENLIPEEEY; ENLIPEEEYN; NLIPEEEYNQ; LIPEEEYNQE;

IPEEEYNQEK; PEEEYNQEKT; EEEYNQEKTA; EEYNQEKTAI;
EYNQEKTAIK; YNQEKTAIKE; NQEKTAIKEK; QEKTAIKEKE;
EKTAIKEKEK; KTAIKEKEKT; TAIKEKEKTP; AIKEKEKTPK;
IKEKEKTPKI; KEKEKTPKIG; EKEKTPKIGL; KEKTPKIGLH;
EKTPKIGLHF; KTPKIGLHFT; TPKIGLHFTY; PKIGLHFTYC;
KIGLHFTYCG; IGLHFTYCGF; GLHFTYCGFE; LHFTYCGFEI;
HFTYCGFEIL; FTYCGFEILI; TYCGFEILIG; YCGFEILIGR;
CGFEILIGRN; GFEILIGRNA; FEILIGRNAK; EILIGRNAKE;
ILIGRNAKEN; LIGRNAKEND; IGRNAKENDK; GRNAKENDKL;
RNAKENDKLL; NAKENDKLLR; AKENDKLLRH; KENDKLLRHC;
ENDKLLRHCV; NDKLLRHCVK; DKLLRHCVKG; KLLRHCVKGN;
LLRHCVKGND; LRHCVKGNDY; RHCVKGNDYW; HCVKGNDYWL;
CVKGNDYWLH; VKGNDYWLHT; KGNDYWLHTR; GNDYWLHTRD;
NDYWLHTRDY; DYWLHTRDYP; YWLHTRDYPG; WLHTRDYPGA;
LHTRDYPGAY; HTRDYPGAYV; TRDYPGAYVF; RDYPGAYVFI;
DYPGAYVFIK; YPGAYVFIKN; PGAYVFIKNQ; GAYVFIKNQK;
AYVFIKNQKN; YVFIKNQKNK; VFIKNQKNKT; FIKNQKNKTP;
IKNQKNKTPS; KNQKNKTPSL; NQKNKTPSLD; QKNKTPSLDV;
KNKTPSLDVL; NKTPSLDVLL; KTPSLDVLLG; TPSLDVLLGA;
PSLDVLLGAG; SLDVLLGAGN; LDVLLGAGNL; DVLLGAGNLC;
VLLGAGNLCV; LLGAGNLCVF; LGAGNLCVFY; GAGNLCVFYT;
AGNLCVFYTK; GNLCVFYTKL; NLCVFYTKLA; LCVFYTKLAK;
CVFYTKLAKK; VFYTKLAKKS; FYTKLAKKSG; YTKLAKKSGK;
TKLAKKSGKA; KLAKKSGKAD; LAKKSGKADL; AKKSGKADLY;
KKSGKADLYY; KSGKADLYYT; SGKADLYYTQ; GKADLYYTQV;
KADLYYTQVK; ADLYYTQVKN; DLYYTQVKNL; LYYTQVKNLR;
YYTQVKNLRR; YTQVKNLRRV; TQVKNLRRVK; QVKNLRRVKN;
VKNLRRVKNK; KNLRRVKNKK; NLRRVKNKKL; LRRVKNKKLG;
RRVKNKKLGL; RVKNKKLGLV; VKNKKLGLVI; KNKKLGLVIP;
NKKLGLVIPK; KKLGLVIPKA; KLGLVIPKAE; LGLVIPKAEK;
GLVIPKAEKN; LVIPKAEKNL; VIPKAEKNLH; IPKAEKNLHI;
PKAEKNLHIK; KAEKNLHIKL; AEKNLHIKLD; EKNLHIKLDE;
KNLHIKLDEN; NLHIKLDENL; LHIKLDENLI; HIKLDENLIK;
IKLDENLIKK; KLDENLIKKI; LDENLIKKIK; DENLIKKIKN;
ENLIKKIKNQ; NLIKKIKNQT;

11 mers:
MIKMSLNYTEI; IKMSLNYTEIN; KMSLNYTEINT; MSLNYTEINTL;
SLNYTEINTLI; LNYTEINTLIK; NYTEINTLIKE; YTEINTLIKEI;
TEINTLIKEIP; EINTLIKEIPF; INTLIKEIPFT; NTLIKEIPFTN;
TLIKEIPFTNS; LIKEIPFTNSL; IKEIPFTNSLI; KEIPFTNSLIT;
EIPFTNSLITK; IPFTNSLITKI; PFTNSLITKII; FTNSLITKIIQ;
TNSLITKIIQP; NSLITKIIQPD; SLITKIIQPDY; LITKIIQPDYK;
ITKIIQPDYKS; TKIIQPDYKSL; KIIQPDYKSLV; IIQPDYKSLVL;
IQPDYKSLVLE; QPDYKSLVLEI; PDYKSLVLEIY; DYKSLVLEIYN;
YKSLVLEIYNK; KSLVLEIYNKI; SLVLEIYNKID; LVLEIYNKIDN;
VLEIYNKIDNK; LEIYNKIDNKK; EIYNKIDNKKF; IYNKIDNKKFK;
YNKIDNKKFKI; NKIDNKKFKIL; KIDNKKFKILI; IDNKKFKILIC;
DNKKFKILICL; NKKFKILICLN; KKFKILICLNP; KFKILICLNPN;
FKILICLNPNT; KILICLNPNTT; ILICLNPNTTR; LICLNPNTTRF;
ICLNPNTTRFH; CLNPNTTRFHI; LNPNTTRFHIT; NPNTTRFHITK;

	PNTTRFHITKK; NTTRFHITKKN; TTRFHITKKNF; TRFHITKKNFK; RFHITKKNFKK; FHITKKNFKKN; HITKKNFKKNA; ITKKNFKKNAL; TKKNFKKNALK; KKNFKKNALKL; KNFKKNALKLR; NFKKNALKLRF; FKKNALKLRFS; KKNALKLRFSD; KNALKLRFSDF; NALKLRFSDFL; ALKLRFSDFLK; LKLRFSDFLKS; KLRFSDFLKSK; LRFSDFLKSKI; RFSDFLKSKIQ; FSDFLKSKIQN; SDFLKSKIQNG; DFLKSKIQNGK; FLKSKIQNGKI; LKSKIQNGKII; KSKIQNGKIIK; SKIQNGKIIKA; KIQNGKIIKAF; IQNGKIIKAFQ; QNGKIIKAFQM; NGKIIKAFQMK; GKIIKAFQMKN; KIIKAFQMKNE; IIKAFQMKNER; IKAFQMKNERI; KAFQMKNERII; AFQMKNERIIS; FQMKNERIISL; QMKNERIISLE; MKNERIISLEI; KNERIISLEIL; NERIISLEILQ; ERIISLEILQK; RIISLEILQKD; IISLEILQKDM; ISLEILQKDMI; SLEILQKDMII; LEILQKDMIIL; EILQKDMIILF; ILQKDMIILFI; LQKDMIILFIK; QKDMIILFIKL; KDMIILFIKLW; DMIILFIKLWP; MIILFIKLWPS; IILFIKLWPSS; ILFIKLWPSSP; LFIKLWPSSPN; FIKLWPSSPNI; IKLWPSSPNII; KLWPSSPNIIA; LWPSSPNIIAT; WPSSPNIIATN; PSSPNIIATNS; SSPNIIATNSN; SPNIIATNSNF; PNIIATNSNFK; NIIATNSNFKI; IIATNSNFKIL; IATNSNFKILD; ATNSNFKILDA; TNSNFKILDAY; NSNFKILDAYY; SNFKILDAYYR; NFKILDAYYRR; FKILDAYYRRP; KILDAYYRRPK; ILDAYYRRPKI; LDAYYRRPKIK; DAYYRRPKIKE; AYYRRPKIKET; YYRRPKIKETT; YRRPKIKETTG; RRPKIKETTGE; RPKIKETTGEI; PKIKETTGEIF; KIKETTGEIFL; IKETTGEIFLK; KETTGEIFLKA; ETTGEIFLKAK; TTGEIFLKAKE; TGEIFLKAKEI; GEIFLKAKEIH; EIFLKAKEIHE; IFLKAKEIHES; FLKAKEIHESN; LKAKEIHESNK; KAKEIHESNKM; AKEIHESNKMS; KEIHESNKMSD; EIHESNKMSDK; IHESNKMSDKK; HESNKMSDKKI; ESNKMSDKKIM; SNKMSDKKIME; NKMSDKKIMEL; KMSDKKIMELK; MSDKKIMELKE; SDKKIMELKEE; DKKIMELKEEY; KKIMELKEEYN; KIMELKEEYNN; IMELKEEYNNT; MELKEEYNNTS; ELKEEYNNTSY; LKEEYNNTSYT; KEEYNNTSYTS; EEYNNTSYTSY; EYNNTSYTSYS; YNNTSYTSYSE; NNTSYTSYSEF; NTSYTSYSEFL; TSYTSYSEFLE; SYTSYSEFLEN; YTSYSEFLENY; TSYSEFLENYY; SYSEFLENYYE; YSEFLENYYES; SEFLENYYESL; EFLENYYESLN; FLENYYESLND; LENYYESLNDQ; ENYYESLNDQI; NYYESLNDQIK; YYESLNDQIKK; YESLNDQIKKT; ESLNDQIKKTN; SLNDQIKKTNI; LNDQIKKTNIK; NDQIKKTNIKE; DQIKKTNIKEL; QIKKTNIKELL; IKKTNIKELLI; KKTNIKELLIE; KTNIKELLIEK; TNIKELLIEKY; NIKELLIEKYK; IKELLIEKYKK; KELLIEKYKKE; ELLIEKYKKEL; LLIEKYKKELI; LIEKYKKELIV; IEKYKKELIVL; EKYKKELIVLE; KYKKELIVLEK; YKKELIVLEKR; KKELIVLEKRI; KELIVLEKRID; ELIVLEKRIDS; LIVLEKRIDSL; IVLEKRIDSLK; VLEKRIDSLKQ; LEKRIDSLKQQ; EKRIDSLKQQI; KRIDSLKQQIK; RIDSLKQQIKL; IDSLKQQIKLL; DSLKQQIKLLE; SLKQQIKLLEN; LKQQIKLLENI; KQQIKLLENIE; QQIKLLENIEN; QIKLLENIENE; IKLLENIENEK; KLLENIENEKE; LLENIENEKEK; LENIENEKEKG; ENIENEKEKGE; NIENEKEKGEL; IENEKEKGELI; ENEKEKGELIL; NEKEKGELILL; EKEKGELILLN; KEKGELILLNI; EKGELILLNIN; KGELILLNINK; GELILLNINKI; ELILLNINKIQ; LILLNINKIQK; ILLNINKIQKG; LLNINKIQKGI; LNINKIQKGIK; NINKIQKGIKE; INKIQKGIKEI; NKIQKGIKEIN; KIQKGIKEINL; IQKGIKEINLL; QKGIKEINLLN; KGIKEINLLNY; GIKEINLLNYK; IKEINLLNYKE; KEINLLNYKEE; EINLLNYKEEK;

	INLLNYKEEKI; NLLNYKEEKIK; LLNYKEEKIKI; LNYKEEKIKIS; NYKEEKIKISL; YKEEKIKISLN; KEEKIKISLNQ; EEKIKISLNQS; EKIKISLNQSL; KIKISLNQSLS; IKISLNQSLSP; KISLNQSLSPK; ISLNQSLSPKE; SLNQSLSPKEN; LNQSLSPKENA; NQSLSPKENAL; QSLSPKENALQ; SLSPKENALQY; LSPKENALQYF; SPKENALQYFK; PKENALQYFKA; KENALQYFKAY; ENALQYFKAYK; NALQYFKAYKK; ALQYFKAYKKG; LQYFKAYKKGK; QYFKAYKKGKN; YFKAYKKGKNS; FKAYKKGKNSF; KAYKKGKNSFK; AYKKGKNSFKT; YKKGKNSFKTI; KKGKNSFKTIQ; KGKNSFKTIQN; GKNSFKTIQNQ; KNSFKTIQNQL; NSFKTIQNQLK; SFKTIQNQLKD; FKTIQNQLKDN; KTIQNQLKDNL; TIQNQLKDNLD; IQNQLKDNLDK; QNQLKDNLDKF; NQLKDNLDKFN; QLKDNLDKFNL; LKDNLDKFNLI; KDNLDKFNLIQ; DNLDKFNLIQS; NLDKFNLIQSK; LDKFNLIQSKI; DKFNLIQSKIT; KFNLIQSKITM; FNLIQSKITML; NLIQSKITMLK; LIQSKITMLKV; IQSKITMLKVE; QSKITMLKVEN; SKITMLKVENL; KITMLKVENLI; ITMLKVENLIP; TMLKVENLIPE; MLKVENLIPEE; LKVENLIPEEE; KVENLIPEEEY; VENLIPEEEYN; ENLIPEEEYNQ; NLIPEEEYNQE; LIPEEEYNQEK; IPEEEYNQEKT; PEEEYNQEKTA; EEEYNQEKTAI; EEYNQEKTAIK; EYNQEKTAIKE; YNQEKTAIKEK; NQEKTAIKEKE; QEKTAIKEKEK; EKTAIKEKEKT; KTAIKEKEKTP; TAIKEKEKTPK; AIKEKEKTPKI; IKEKEKTPKIG; KEKEKTPKIGL; EKEKTPKIGLH; KEKTPKIGLHF; EKTPKIGLHFT; KTPKIGLHFTY; TPKIGLHFTYC; PKIGLHFTYCG; KIGLHFTYCGF; IGLHFTYCGFE; GLHFTYCGFEI; LHFTYCGFEIL; HFTYCGFEILI; FTYCGFEILIG; TYCGFEILIGR; YCGFEILIGRN; CGFEILIGRNA; GFEILIGRNAK; FEILIGRNAKE; EILIGRNAKEN; ILIGRNAKEND; LIGRNAKENDK; IGRNAKENDKL; GRNAKENDKLL; RNAKENDKLLR; NAKENDKLLRH; AKENDKLLRHC; KENDKLLRHCV; ENDKLLRHCVK; NDKLLRHCVKG; DKLLRHCVKGN; KLLRHCVKGND; LLRHCVKGNDY; LRHCVKGNDYW; RHCVKGNDYWL; HCVKGNDYWLH; CVKGNDYWLHT; VKGNDYWLHTR; KGNDYWLHTRD; GNDYWLHTRDY; NDYWLHTRDYP; DYWLHTRDYPG; YWLHTRDYPGA; WLHTRDYPGAY; LHTRDYPGAYV; HTRDYPGAYVF; TRDYPGAYVFI; RDYPGAYVFIK; DYPGAYVFIKN; YPGAYVFIKNQ; PGAYVFIKNQK; GAYVFIKNQKN; AYVFIKNQKNK; YVFIKNQKNKT; VFIKNQKNKTP; FIKNQKNKTPS; IKNQKNKTPSL; KNQKNKTPSLD; NQKNKTPSLDV; QKNKTPSLDVL; KNKTPSLDVLL; NKTPSLDVLLG; KTPSLDVLLGA; TPSLDVLLGAG; PSLDVLLGAGN; SLDVLLGAGNL; LDVLLGAGNLC; DVLLGAGNLCV; VLLGAGNLCVF; LLGAGNLCVFY; LGAGNLCVFYT; GAGNLCVFYTK; AGNLCVFYTKL; GNLCVFYTKLA; NLCVFYTKLAK; LCVFYTKLAKK; CVFYTKLAKKS; VFYTKLAKKSG; FYTKLAKKSGK; YTKLAKKSGKA; TKLAKKSGKAD; KLAKKSGKADL; LAKKSGKADLY; AKKSGKADLYY; KKSGKADLYYT; KSGKADLYYTQ; SGKADLYYTQV; GKADLYYTQVK; KADLYYTQVKN; ADLYYTQVKNL; DLYYTQVKNLR; LYYTQVKNLRR; YYTQVKNLRRV; YTQVKNLRRVK; TQVKNLRRVKN; QVKNLRRVKNK; VKNLRRVKNKK; KNLRRVKNKKL; NLRRVKNKKLG; LRRVKNKKLGL; RRVKNKKLGLV; RVKNKKLGLVI; VKNKKLGLVIP; KNKKLGLVIPK; NKKLGLVIPKA; KKLGLVIPKAE; KLGLVIPKAEK; LGLVIPKAEKN; GLVIPKAEKNL; LVIPKAEKNLH; VIPKAEKNLHI; IPKAEKNLHIK; PKAEKNLHIKL; KAEKNLHIKLD; AEKNLHIKLDE; EKNLHIKLDEN; KNLHIKLDENL; NLHIKLDENLI; LHIKLDENLIK; HIKLDENLIKK; IKLDENLIKKI; KLDENLIKKIK; LDENLIKKIKN; DENLIKKIKNQ;

	ENLIKKIKNQT;
Seq 21	SEQ ID NO 22322-23355/ 8 mers: MKLQRSLS; KLQRSLSL; LQRSLSLI; QRSLSLII; RSLSLIIF; SLSLIIFS; LSLIIFSL; SLIIFSLT; LIIFSLTV; IIFSLTVL; IFSLTVLC; FSLTVLCC; SLTVLCCD; LTVLCCDN; TVLCCDNK; VLCCDNKE; LCCDNKER; CCDNKERK; CDNKERKE; DNKERKEG; NKERKEGV; KERKEGVS; ERKEGVST; RKEGVSTK; KEGVSTKI; EGVSTKIS; GVSTKISL; VSTKISLG; STKISLGA; TKISLGAE; KISLGAEP; ISLGAEPR; SLGAEPRS; LGAEPRSL; GAEPRSLD; AEPRSLDP; EPRSLDPQ; PRSLDPQL; RSLDPQLA; SLDPQLAE; LDPQLAED; DPQLAEDN; PQLAEDNV; QLAEDNVA; LAEDNVAS; AEDNVASK; EDNVASKM; DNVASKMI; NVASKMID; VASKMIDT; ASKMIDTL; SKMIDTLY; KMIDTLYR; MIDTLYRG; IDTLYRGI; DTLYRGIV; TLYRGIVT; LYRGIVTG; YRGIVTGD; RGIVTGDP; GIVTGDPN; IVTGDPNT; VTGDPNTG; TGDPNTGG; GDPNTGGH; DPNTGGHK; PNTGGHKP; NTGGHKPG; TGGHKPGL; GGHKPGLA; GHKPGLAK; HKPGLAKG; KPGLAKGW; PGLAKGWE; GLAKGWET; LAKGWETS; AKGWETSS; KGWETSSD; GWETSSDG; WETSSDGT; ETSSDGTA; TSSDGTAY; SSDGTAYP; SDGTAYPF; DGTAYPFY; GTAYPFYL; TAYPFYLR; AYPFYLRD; YPFYLRDN; PFYLRDNL; FYLRDNLT; YLRDNLTW; LRDNLTWS; RDNLTWSD; DNLTWSDG; NLTWSDGV; LTWSDGVA; TWSDGVAI; WSDGVAIT; SDGVAITA; DGVAITAE; GVAITAEG; VAITAEGI; AITAEGIR; ITAEGIRK; TAEGIRKS; AEGIRKSY; EGIRKSYL; GIRKSYLR; IRKSYLRI; RKSYLRIL; KSYLRILN; SYLRILNK; YLRILNKE; LRILNKET; RILNKETG; ILNKETGS; LNKETGST; NKETGSTY; KETGSTYV; ETGSTYVD; TGSTYVDM; GSTYVDMV; STYVDMVK; TYVDMVKS; YVDMVKSI; VDMVKSII; DMVKSIIK; MVKSIIKN; VKSIIKNG; KSIIKNGQ; SIIKNGQE; IIKNGQEY; IKNGQEYF; KNGQEYFD; NGQEYFDG; GQEYFDGQ; QEYFDGQV; EYFDGQVT; YFDGQVTD; FDGQVTDS; DGQVTDSE; GQVTDSEL; QVTDSELG; VTDSELGI; TDSELGIR; DSELGIRA; SELGIRAI; ELGIRAID; LGIRAIDS; GIRAIDSK; IRAIDSKT; RAIDSKTL; AIDSKTLE; IDSKTLEI; DSKTLEIT; SKTLEITL; KTLEITLA; TLEITLAS; LEITLASP; EITLASPK; ITLASPKP; TLASPKPY; LASPKPYF; ASPKPYFI; SPKPYFID; PKPYFIDL; KPYFIDLL; PYFIDLLV; YFIDLLVH; FIDLLVHQ; IDLLVHQS; DLLVHQSF; LLVHQSFI; LVHQSFIP; VHQSFIPV; HQSFIPVP; QSFIPVPV; SFIPVPVH; FIPVPVHV; IPVPVHVT; PVPVHVTD; VPVHVTDK; PVHVTDKY; VHVTDKYG; HVTDKYGQ; VTDKYGQN; TDKYGQNW; DKYGQNWT; KYGQNWTS; YGQNWTSP; GQNWTSPE; QNWTSPEN; NWTSPENM; WTSPENMV; TSPENMVT; SPENMVTS; PENMVTSG; ENMVTSGP; NMVTSGPF; MVTSGPFK; VTSGPFKL; TSGPFKLK; SGPFKLKE; GPFKLKER; PFKLKERI; FKLKERIP; KLKERIPS; LKERIPSE; KERIPSEK; ERIPSEKY; RIPSEKYV; IPSEKYVF; PSEKYVFE; SEKYVFEK; EKYVFEKD; KYVFEKDN; YVFEKDNK; VFEKDNKY; FEKDNKYY; EKDNKYYD; KDNKYYDS; DNKYYDSN; NKYYDSNE; KYYDSNEV; YYDSNEVE; YDSNEVEL; DSNEVELE; SNEVELEE; NEVELEEI; EVELEEIT; VELEEITF; ELEEITFY; LEEITFYT; EEITFYTT;

	EITFYTTN; ITFYTTND; TFYTTNDS; FYTTNDSS; YTTNDSST; TTNDSSTA; TNDSSTAY; NDSSTAYK; DSSTAYKM; SSTAYKMY; STAYKMYV; TAYKMYVN; AYKMYVNE; YKMYVNEE; KMYVNEEL; MYVNEELD; YVNEELDA; VNEELDAI; NEELDAIL; EELDAILV; ELDAILVP; LDAILVPY; DAILVPYP; AILVPYPQ; ILVPYPQI; 9 mers: MKLQRSLSL; KLQRSLSLI; LQRSLSLII; QRSLSLIIF; RSLSLIIFS; SLSLIIFSL; LSLIIFSLT; SLIIFSLTV; LIIFSLTVL; IIFSLTVLC; IFSLTVLCC; FSLTVLCCD; SLTVLCCDN; LTVLCCDNK; TVLCCDNKE; VLCCDNKER; LCCDNKERK; CCDNKERKE; CDNKERKEG; DNKERKEGV; NKERKEGVS; KERKEGVST; ERKEGVSTK; RKEGVSTKI; KEGVSTKIS; EGVSTKISL; GVSTKISLG; VSTKISLGA; STKISLGAE; TKISLGAEP; KISLGAEPR; ISLGAEPRS; SLGAEPRSL; LGAEPRSLD; GAEPRSLDP; AEPRSLDPQ; EPRSLDPQL; PRSLDPQLA; RSLDPQLAE; SLDPQLAED; LDPQLAEDN; DPQLAEDNV; PQLAEDNVA; QLAEDNVAS; LAEDNVASK; AEDNVASKM; EDNVASKMI; DNVASKMID; NVASKMIDT; VASKMIDTL; ASKMIDTLY; SKMIDTLYR; KMIDTLYRG; MIDTLYRGI; IDTLYRGIV; DTLYRGIVT; TLYRGIVTG; LYRGIVTGD; YRGIVTGDP; RGIVTGDPN; GIVTGDPNT; IVTGDPNTG; VTGDPNTGG; TGDPNTGGH; GDPNTGGHK; DPNTGGHKP; PNTGGHKPG; NTGGHKPGL; TGGHKPGLA; GGHKPGLAK; GHKPGLAKG; HKPGLAKGW; KPGLAKGWE; PGLAKGWET; GLAKGWETS; LAKGWETSS; AKGWETSSD; KGWETSSDG; GWETSSDGT; WETSSDGTA; ETSSDGTAY; TSSDGTAYP; SSDGTAYPF; SDGTAYPFY; DGTAYPFYL; GTAYPFYLR; TAYPFYLRD; AYPFYLRDN; YPFYLRDNL; PFYLRDNLT; FYLRDNLTW; YLRDNLTWS; LRDNLTWSD; RDNLTWSDG; DNLTWSDGV; NLTWSDGVA; LTWSDGVAI; TWSDGVAIT; WSDGVAITA; SDGVAITAE; DGVAITAEG; GVAITAEGI; VAITAEGIR; AITAEGIRK; ITAEGIRKS; TAEGIRKSY; AEGIRKSYL; EGIRKSYLR; GIRKSYLRI; IRKSYLRIL; RKSYLRILN; KSYLRILNK; SYLRILNKE; YLRILNKET; LRILNKETG; RILNKETGS; ILNKETGST; LNKETGSTY; NKETGSTYV; KETGSTYVD; ETGSTYVDM; TGSTYVDMV; GSTYVDMVK; STYVDMVKS; TYVDMVKSI; YVDMVKSII; VDMVKSIIK; DMVKSIIKN; MVKSIIKNG; VKSIIKNGQ; KSIIKNGQE; SIIKNGQEY; IIKNGQEYF; IKNGQEYFD; KNGQEYFDG; NGQEYFDGQ; GQEYFDGQV; QEYFDGQVT; EYFDGQVTD; YFDGQVTDS; FDGQVTDSE; DGQVTDSEL; GQVTDSELG; QVTDSELGI; VTDSELGIR; TDSELGIRA; DSELGIRAI; SELGIRAID; ELGIRAIDS; LGIRAIDSK; GIRAIDSKT; IRAIDSKTL; RAIDSKTLE; AIDSKTLEI; IDSKTLEIT; DSKTLEITL; SKTLEITLA; KTLEITLAS; TLEITLASP; LEITLASPK; EITLASPKP; ITLASPKPY; TLASPKPYF; LASPKPYFI; ASPKPYFID; SPKPYFIDL; PKPYFIDLL; KPYFIDLLV; PYFIDLLVH; YFIDLLVHQ; FIDLLVHQS; IDLLVHQSF; DLLVHQSFI; LLVHQSFIP; LVHQSFIPV; VHQSFIPVP; HQSFIPVPV; QSFIPVPVH; SFIPVPVHV; FIPVPVHVT; IPVPVHVTD; PVPVHVTDK; VPVHVTDKY; PVHVTDKYG; VHVTDKYGQ; HVTDKYGQN; VTDKYGQNW; TDKYGQNWT; DKYGQNWTS; KYGQNWTSP; YGQNWTSPE; GQNWTSPEN; QNWTSPENM; NWTSPENMV; WTSPENMVT; TSPENMVTS; SPENMVTSG; PENMVTSGP; ENMVTSGPF; NMVTSGPFK; MVTSGPFKL; VTSGPFKLK; TSGPFKLKE; SGPFKLKER; GPFKLKERI; PFKLKERIP; FKLKERIPS; KLKERIPSE; LKERIPSEK; KERIPSEKY; ERIPSEKYV; RIPSEKYVF; IPSEKYVFE; PSEKYVFEK; SEKYVFEKD; EKYVFEKDN; KYVFEKDNK; YVFEKDNKY; VFEKDNKYY; FEKDNKYYD;

EKDNKYYDS; KDNKYYDSN; DNKYYDSNE; NKYYDSNEV; KYYDSNEVE;
YYDSNEVEL; YDSNEVELE; DSNEVELEE; SNEVELEEI; NEVELEEIT;
EVELEEITF; VELEEITFY; ELEEITFYT; LEEITFYTT; EEITFYTTN;
EITFYTTND; ITFYTTNDS; TFYTTNDSS; FYTTNDSST; YTTNDSSTA;
TTNDSSTAY; TNDSSTAYK; NDSSTAYKM; DSSTAYKMY; SSTAYKMYV;
STAYKMYVN; TAYKMYVNE; AYKMYVNEE; YKMYVNEEL; KMYVNEELD;
MYVNEELDA; YVNEELDAI; VNEELDAIL; NEELDAILV; EELDAILVP;
ELDAILVPY; LDAILVPYP; DAILVPYPQ; AILVPYPQI;

10 mers:
MKLQRSLSLI; KLQRSLSLII; LQRSLSLIIF; QRSLSLIIFS;
RSLSLIIFSL; SLSLIIFSLT; LSLIIFSLTV; SLIIFSLTVL;
LIIFSLTVLC; IIFSLTVLCC; IFSLTVLCCD; FSLTVLCCDN;
SLTVLCCDNK; LTVLCCDNKE; TVLCCDNKER; VLCCDNKERK;
LCCDNKERKE; CCDNKERKEG; CDNKERKEGV; DNKERKEGVS;
NKERKEGVST; KERKEGVSTK; ERKEGVSTKI; RKEGVSTKIS;
KEGVSTKISL; EGVSTKISLG; GVSTKISLGA; VSTKISLGAE;
STKISLGAEP; TKISLGAEPR; KISLGAEPRS; ISLGAEPRSL;
SLGAEPRSLD; LGAEPRSLDP; GAEPRSLDPQ; AEPRSLDPQL;
EPRSLDPQLA; PRSLDPQLAE; RSLDPQLAED; SLDPQLAEDN;
LDPQLAEDNV; DPQLAEDNVA; PQLAEDNVAS; QLAEDNVASK;
LAEDNVASKM; AEDNVASKMI; EDNVASKMID; DNVASKMIDT;
NVASKMIDTL; VASKMIDTLY; ASKMIDTLYR; SKMIDTLYRG;
KMIDTLYRGI; MIDTLYRGIV; IDTLYRGIVT; DTLYRGIVTG;
TLYRGIVTGD; LYRGIVTGDP; YRGIVTGDPN; RGIVTGDPNT;
GIVTGDPNTG; IVTGDPNTGG; VTGDPNTGGH; TGDPNTGGHK;
GDPNTGGHKP; DPNTGGHKPG; PNTGGHKPGL; NTGGHKPGLA;
TGGHKPGLAK; GGHKPGLAKG; GHKPGLAKGW; HKPGLAKGWE;
KPGLAKGWET; PGLAKGWETS; GLAKGWETSS; LAKGWETSSD;
AKGWETSSDG; KGWETSSDGT; GWETSSDGTA; WETSSDGTAY;
ETSSDGTAYP; TSSDGTAYPF; SSDGTAYPFY; SDGTAYPFYL;
DGTAYPFYLR; GTAYPFYLRD; TAYPFYLRDN; AYPFYLRDNL;
YPFYLRDNLT; PFYLRDNLTW; FYLRDNLTWS; YLRDNLTWSD;
LRDNLTWSDG; RDNLTWSDGV; DNLTWSDGVA; NLTWSDGVAI;
LTWSDGVAIT; TWSDGVAITA; WSDGVAITAE; SDGVAITAEG;
DGVAITAEGI; GVAITAEGIR; VAITAEGIRK; AITAEGIRKS;
ITAEGIRKSY; TAEGIRKSYL; AEGIRKSYLR; EGIRKSYLRI;
GIRKSYLRIL; IRKSYLRILN; RKSYLRILNK; KSYLRILNKE;
SYLRILNKET; YLRILNKETG; LRILNKETGS; RILNKETGST;
ILNKETGSTY; LNKETGSTYV; NKETGSTYVD; KETGSTYVDM;
ETGSTYVDMV; TGSTYVDMVK; GSTYVDMVKS; STYVDMVKSI;
TYVDMVKSII; YVDMVKSIIK; VDMVKSIIKN; DMVKSIIKNG;
MVKSIIKNGQ; VKSIIKNGQE; KSIIKNGQEY; SIIKNGQEYF;
IIKNGQEYFD; IKNGQEYFDG; KNGQEYFDGQ; NGQEYFDGQV;
GQEYFDGQVT; QEYFDGQVTD; EYFDGQVTDS; YFDGQVTDSE;
FDGQVTDSEL; DGQVTDSELG; GQVTDSELGI; QVTDSELGIR;
VTDSELGIRA; TDSELGIRAI; DSELGIRAID; SELGIRAIDS;
ELGIRAIDSK; LGIRAIDSKT; GIRAIDSKTL; IRAIDSKTLE;
RAIDSKTLEI; AIDSKTLEIT; IDSKTLEITL; DSKTLEITLA;
SKTLEITLAS; KTLEITLASP; TLEITLASPK; LEITLASPKP;
EITLASPKPY; ITLASPKPYF; TLASPKPYFI; LASPKPYFID;

ASPKPYFIDL; SPKPYFIDLL; PKPYFIDLLV; KPYFIDLLVH;
PYFIDLLVHQ; YFIDLLVHQS; FIDLLVHQSF; IDLLVHQSFI;
DLLVHQSFIP; LLVHQSFIPV; LVHQSFIPVP; VHQSFIPVPV;
HQSFIPVPVH; QSFIPVPVHV; SFIPVPVHVT; FIPVPVHVTD;
IPVPVHVTDK; PVPVHVTDKY; VPVHVTDKYG; PVHVTDKYGQ;
VHVTDKYGQN; HVTDKYGQNW; VTDKYGQNWT; TDKYGQNWTS;
DKYGQNWTSP; KYGQNWTSPE; YGQNWTSPEN; GQNWTSPENM;
QNWTSPENMV; NWTSPENMVT; WTSPENMVTS; TSPENMVTSG;
SPENMVTSGP; PENMVTSGPF; ENMVTSGPFK; NMVTSGPFKL;
MVTSGPFKLK; VTSGPFKLKE; TSGPFKLKER; SGPFKLKERI;
GPFKLKERIP; PFKLKERIPS; FKLKERIPSE; KLKERIPSEK;
LKERIPSEKY; KERIPSEKYV; ERIPSEKYVF; RIPSEKYVFE;
IPSEKYVFEK; PSEKYVFEKD; SEKYVFEKDN; EKYVFEKDNK;
KYVFEKDNKY; YVFEKDNKYY; VFEKDNKYYD; FEKDNKYYDS;
EKDNKYYDSN; KDNKYYDSNE; DNKYYDSNEV; NKYYDSNEVE;
KYYDSNEVEL; YYDSNEVELE; YDSNEVELEE; DSNEVELEEI;
SNEVELEEIT; NEVELEEITF; EVELEEITFY; VELEEITFYT;
ELEEITFYTT; LEEITFYTTN; EEITFYTTND; EITFYTTNDS;
ITFYTTNDSS; TFYTTNDSST; FYTTNDSSTA; YTTNDSSTAY;
TTNDSSTAYK; TNDSSTAYKM; NDSSTAYKMY; DSSTAYKMYV;
SSTAYKMYVN; STAYKMYVNE; TAYKMYVNEE; AYKMYVNEEL;
YKMYVNEELD; KMYVNEELDA; MYVNEELDAI; YVNEELDAIL;
VNEELDAILV; NEELDAILVP; EELDAILVPY; ELDAILVPYP;
LDAILVPYPQ; DAILVPYPQI;

11 mers:
MKLQRSLSLII; KLQRSLSLIIF; LQRSLSLIIFS; QRSLSLIIFSL;
RSLSLIIFSLT; SLSLIIFSLTV; LSLIIFSLTVL; SLIIFSLTVLC;
LIIFSLTVLCC; IIFSLTVLCCD; IFSLTVLCCDN; FSLTVLCCDNK;
SLTVLCCDNKE; LTVLCCDNKER; TVLCCDNKERK; VLCCDNKERKE;
LCCDNKERKEG; CCDNKERKEGV; CDNKERKEGVS; DNKERKEGVST;
NKERKEGVSTK; KERKEGVSTKI; ERKEGVSTKIS; RKEGVSTKISL;
KEGVSTKISLG; EGVSTKISLGA; GVSTKISLGAE; VSTKISLGAEP;
STKISLGAEPR; TKISLGAEPRS; KISLGAEPRSL; ISLGAEPRSLD;
SLGAEPRSLDP; LGAEPRSLDPQ; GAEPRSLDPQL; AEPRSLDPQLA;
EPRSLDPQLAE; PRSLDPQLAED; RSLDPQLAEDN; SLDPQLAEDNV;
LDPQLAEDNVA; DPQLAEDNVAS; PQLAEDNVASK; QLAEDNVASKM;
LAEDNVASKMI; AEDNVASKMID; EDNVASKMIDT; DNVASKMIDTL;
NVASKMIDTLY; VASKMIDTLYR; ASKMIDTLYRG; SKMIDTLYRGI;
KMIDTLYRGIV; MIDTLYRGIVT; IDTLYRGIVTG; DTLYRGIVTGD;
TLYRGIVTGDP; LYRGIVTGDPN; YRGIVTGDPNT; RGIVTGDPNTG;
GIVTGDPNTGG; IVTGDPNTGGH; VTGDPNTGGHK; TGDPNTGGHKP;
GDPNTGGHKPG; DPNTGGHKPGL; PNTGGHKPGLA; NTGGHKPGLAK;
TGGHKPGLAKG; GGHKPGLAKGW; GHKPGLAKGWE; HKPGLAKGWET;
KPGLAKGWETS; PGLAKGWETSS; GLAKGWETSSD; LAKGWETSSDG;
AKGWETSSDGT; KGWETSSDGTA; GWETSSDGTAY; WETSSDGTAYP;
ETSSDGTAYPF; TSSDGTAYPFY; SSDGTAYPFYL; SDGTAYPFYLR;
DGTAYPFYLRD; GTAYPFYLRDN; TAYPFYLRDNL; AYPFYLRDNLT;
YPFYLRDNLTW; PFYLRDNLTWS; FYLRDNLTWSD; YLRDNLTWSDG;
LRDNLTWSDGV; RDNLTWSDGVA; DNLTWSDGVAI; NLTWSDGVAIT;
LTWSDGVAITA; TWSDGVAITAE; WSDGVAITAEG; SDGVAITAEGI;

	DGVAITAEGIR; GVAITAEGIRK; VAITAEGIRKS; AITAEGIRKSY; ITAEGIRKSYL; TAEGIRKSYLR; AEGIRKSYLRI; EGIRKSYLRIL; GIRKSYLRILN; IRKSYLRILNK; RKSYLRILNKE; KSYLRILNKET; SYLRILNKETG; YLRILNKETGS; LRILNKETGST; RILNKETGSTY; ILNKETGSTYV; LNKETGSTYVD; NKETGSTYVDM; KETGSTYVDMV; ETGSTYVDMVK; TGSTYVDMVKS; GSTYVDMVKSI; STYVDMVKSII; TYVDMVKSIIK; YVDMVKSIIKN; VDMVKSIIKNG; DMVKSIIKNGQ; MVKSIIKNGQE; VKSIIKNGQEY; KSIIKNGQEYF; SIIKNGQEYFD; IIKNGQEYFDG; IKNGQEYFDGQ; KNGQEYFDGQV; NGQEYFDGQVT; GQEYFDGQVTD; QEYFDGQVTDS; EYFDGQVTDSE; YFDGQVTDSEL; FDGQVTDSELG; DGQVTDSELGI; GQVTDSELGIR; QVTDSELGIRA; VTDSELGIRAI; TDSELGIRAID; DSELGIRAIDS; SELGIRAIDSK; ELGIRAIDSKT; LGIRAIDSKTL; GIRAIDSKTLE; IRAIDSKTLEI; RAIDSKTLEIT; AIDSKTLEITL; IDSKTLEITLA; DSKTLEITLAS; SKTLEITLASP; KTLEITLASPK; TLEITLASPKP; LEITLASPKPY; EITLASPKPYF; ITLASPKPYFI; TLASPKPYFID; LASPKPYFIDL; ASPKPYFIDLL; SPKPYFIDLLV; PKPYFIDLLVH; KPYFIDLLVHQ; PYFIDLLVHQS; YFIDLLVHQSF; FIDLLVHQSFI; IDLLVHQSFIP; DLLVHQSFIPV; LLVHQSFIPVP; LVHQSFIPVPV; VHQSFIPVPVH; HQSFIPVPVHV; QSFIPVPVHVT; SFIPVPVHVTD; FIPVPVHVTDK; IPVPVHVTDKY; PVPVHVTDKYG; VPVHVTDKYGQ; PVHVTDKYGQN; VHVTDKYGQNW; HVTDKYGQNWT; VTDKYGQNWTS; TDKYGQNWTSP; DKYGQNWTSPE; KYGQNWTSPEN; YGQNWTSPENM; GQNWTSPENMV; QNWTSPENMVT; NWTSPENMVTS; WTSPENMVTSG; TSPENMVTSGP; SPENMVTSGPF; PENMVTSGPFK; ENMVTSGPFKL; NMVTSGPFKLK; MVTSGPFKLKE; VTSGPFKLKER; TSGPFKLKERI; SGPFKLKERIP; GPFKLKERIPS; PFKLKERIPSE; FKLKERIPSEK; KLKERIPSEKY; LKERIPSEKYV; KERIPSEKYVF; ERIPSEKYVFE; RIPSEKYVFEK; IPSEKYVFEKD; PSEKYVFEKDN; SEKYVFEKDNK; EKYVFEKDNKY; KYVFEKDNKYY; YVFEKDNKYYD; VFEKDNKYYDS; FEKDNKYYDSN; EKDNKYYDSNE; KDNKYYDSNEV; DNKYYDSNEVE; NKYYDSNEVEL; KYYDSNEVELE; YYDSNEVELEE; YDSNEVELEEI; DSNEVELEEIT; SNEVELEEITF; NEVELEEITFY; EVELEEITFYT; VELEEITFYTT; ELEEITFYTTN; LEEITFYTTND; EEITFYTTNDS; EITFYTTNDSS; ITFYTTNDSST; TFYTTNDSSTA; FYTTNDSSTAY; YTTNDSSTAYK; TTNDSSTAYKM; TNDSSTAYKMY; NDSSTAYKMYV; DSSTAYKMYVN; SSTAYKMYVNE; STAYKMYVNEE; TAYKMYVNEEL; AYKMYVNEELD; YKMYVNEELDA; KMYVNEELDAI; MYVNEELDAIL; YVNEELDAILV; VNEELDAILVP; NEELDAILVPY; EELDAILVPYP; ELDAILVPYPQ; LDAILVPYPQI;
Seq 22	SEQ ID NO 23356-24473/ 8 mers: MNLINKLF; NLINKLFI; LINKLFIL; INKLFILT; NKLFILTI; KLFILTIL; LFILTILF; FILTILFS; ILTILFSS; LTILFSSV; TILFSSVI; ILFSSVIS; LFSSVISC; FSSVISCK; SSVISCKL; SVISCKLY; VISCKLYK; ISCKLYKK; SCKLYKKI; CKLYKKIT; KLYKKITY; LYKKITYN; YKKITYNA; KKITYNAD; KITYNADQ; ITYNADQV; TYNADQVI; YNADQVID; NADQVIDK; ADQVIDKL; DQVIDKLK; QVIDKLKS; VIDKLKSN; IDKLKSNN; DKLKSNNG; KLKSNNGS; LKSNNGSF; KSNNGSFN; SNNGSFNT; NNGSFNTL;

	NGSFNTLK; GSFNTLKS; SFNTLKSN; FNTLKSND; NTLKSNDD; TLKSNDDS; LKSNDDSK; KSNDDSKR; SNDDSKRS; NDDSKRSG; DDSKRSGR; DSKRSGRK; SKRSGRKP; KRSGRKPR; RSGRKPRS; SGRKPRSV; GRKPRSVD; RKPRSVDN; KPRSVDNT; PRSVDNTY; RSVDNTYM; SVDNTYMD; VDNTYMDQ; DNTYMDQD; NTYMDQDT; TYMDQDTG; YMDQDTGK; MDQDTGKK; DQDTGKKP; QDTGKKPL; DTGKKPLM; TGKKPLMA; GKKPLMAD; KKPLMADM; KPLMADMQ; PLMADMQP; LMADMQPD; MADMQPDM; ADMQPDMQ; DMQPDMQN; MQPDMQND; QPDMQNDN; PDMQNDNS; DMQNDNSS; MQNDNSSS; QNDNSSSN; NDNSSSNH; DNSSSNHT; NSSSNHTL; SSSNHTLQ; SSNHTLQV; SNHTLQVN; NHTLQVNI; HTLQVNIQ; TLQVNIQD; LQVNIQDN; QVNIQDNE; VNIQDNEA; NIQDNEAS; IQDNEASE; QDNEASEA; DNEASEAR; NEASEARN; EASEARNI; ASEARNIM; SEARNIMT; EARNIMTE; ARNIMTEI; RNIMTEIE; NIMTEIES; IMTEIESS; MTEIESSK; TEIESSKE; EIESSKEE; IESSKEEY; ESSKEEYN; SSKEEYNR; SKEEYNRI; KEEYNRIN; EEYNRINE; EYNRINED; YNRINEDL; NRINEDLA; RINEDLAK; INEDLAKV; NEDLAKVK; EDLAKVKA; DLAKVKAS; LAKVKASL; AKVKASLD; KVKASLDK; VKASLDKI; KASLDKIK; ASLDKIKS; SLDKIKSL; LDKIKSLL; DKIKSLLS; KIKSLLST; IKSLLSTA; KSLLSTAK; SLLSTAKS; LLSTAKSY; LSTAKSYL; STAKSYLE; TAKSYLEQ; AKSYLEQT; KSYLEQTR; SYLEQTRR; YLEQTRRG; LEQTRRGV; EQTRRGVG; QTRRGVGS; TRRGVGSS; RRGVGSSK; RGVGSSKA; GVGSSKAN; VGSSKANL; GSSKANLA; SSKANLAL; SKANLALL; KANLALLP; ANLALLPS; NLALLPSL; LALLPSLE; ALLPSLEE; LLPSLEEA; LPSLEEAI; PSLEEAIA; SLEEAIAK; LEEAIAKV; EEAIAKVK; EAIAKVKS; AIAKVKSN; IAKVKSNH; AKVKSNHA; KVKSNHAS; VKSNHASA; KSNHASAD; SNHASADT; NHASADTH; HASADTHC; ASADTHCN; SADTHCND; ADTHCNDA; DTHCNDAI; THCNDAIA; HCNDAIAA; CNDAIAAL; NDAIAALK; DAIAALKR; AIAALKRA; IAALKRAK; AALKRAKN; ALKRAKND; LKRAKNDF; KRAKNDFE; RAKNDFEY; AKNDFEYA; KNDFEYAQ; NDFEYAQR; DFEYAQRK; FEYAQRKA; EYAQRKAD; YAQRKADR; AQRKADRA; QRKADRAL; RKADRALE; KADRALEE; ADRALEEA; DRALEEAL; RALEEALS; ALEEALSN; LEEALSNS; EEALSNSN; EALSNSNA; ALSNSNAS; LSNSNASR; SNSNASRH; NSNASRHE; SNASRHES; NASRHESY; ASRHESYY; SRHESYYY; RHESYYYA; HESYYYAG; ESYYYAGY; SYYYAGYH; YYYAGYHQ; YYAGYHQF; YAGYHQFM; AGYHQFMA; GYHQFMAD; YHQFMADA; HQFMADAK; QFMADAKA; FMADAKAS; MADAKASM; ADAKASMS; DAKASMSS; AKASMSST; KASMSSTK; ASMSSTKS; SMSSTKSL; MSSTKSLL; SSTKSLLE; STKSLLEV; TKSLLEVA; KSLLEVAK; SLLEVAKN; LLEVAKNK; LEVAKNKQ; EVAKNKQK; VAKNKQKE; AKNKQKEL; KNKQKELN; NKQKELNE; KQKELNEN; QKELNENM; KELNENMT; ELNENMTK; LNENMTKT; NENMTKTN; ENMTKTNK; NMTKTNKD; MTKTNKDF; TKTNKDFQ; KTNKDFQE; TNKDFQEL; NKDFQELN; KDFQELND; DFQELNDI; FQELNDIY; QELNDIYK; ELNDIYKK; LNDIYKKL; NDIYKKLQ; DIYKKLQD; IYKKLQDM; YKKLQDMD; KKLQDMDS; KLQDMDSR; 9 mers:

	MNLINKLFI; NLINKLFIL; LINKLFILT; INKLFILTI; NKLFILTIL; KLFILTILF; LFILTILFS; FILTILFSS; ILTILFSSV; LTILFSSVI; TILFSSVIS; ILFSSVISC; LFSSVISCK; FSSVISCKL; SSVISCKLY; SVISCKLYK; VISCKLYKK; ISCKLYKKI; SCKLYKKIT; CKLYKKITY; KLYKKITYN; LYKKITYNA; YKKITYNAD; KKITYNADQ; KITYNADQV; ITYNADQVI; TYNADQVID; YNADQVIDK; NADQVIDKL; ADQVIDKLK; DQVIDKLKS; QVIDKLKSN; VIDKLKSNN; IDKLKSNNG; DKLKSNNGS; KLKSNNGSF; LKSNNGSFN; KSNNGSFNT; SNNGSFNTL; NNGSFNTLK; NGSFNTLKS; GSFNTLKSN; SFNTLKSND; FNTLKSNDD; NTLKSNDDS; TLKSNDDSK; LKSNDDSKR; KSNDDSKRS; SNDDSKRSG; NDDSKRSGR; DDSKRSGRK; DSKRSGRKP; SKRSGRKPR; KRSGRKPRS; RSGRKPRSV; SGRKPRSVD; GRKPRSVDN; RKPRSVDNT; KPRSVDNTY; PRSVDNTYM; RSVDNTYMD; SVDNTYMDQ; VDNTYMDQD; DNTYMDQDT; NTYMDQDTG; TYMDQDTGK; YMDQDTGKK; MDQDTGKKP; DQDTGKKPL; QDTGKKPLM; DTGKKPLMA; TGKKPLMAD; GKKPLMADM; KKPLMADMQ; KPLMADMQP; PLMADMQPD; LMADMQPDM; MADMQPDMQ; ADMQPDMQN; DMQPDMQND; MQPDMQNDN; QPDMQNDNS; PDMQNDNSS; DMQNDNSSS; MQNDNSSSN; QNDNSSSNH; NDNSSSNHT; DNSSSNHTL; NSSSNHTLQ; SSSNHTLQV; SSNHTLQVN; SNHTLQVNI; NHTLQVNIQ; HTLQVNIQD; TLQVNIQDN; LQVNIQDNE; QVNIQDNEA; VNIQDNEAS; NIQDNEASE; IQDNEASEA; QDNEASEAR; DNEASEARN; NEASEARNI; EASEARNIM; ASEARNIMT; SEARNIMTE; EARNIMTEI; ARNIMTEIE; RNIMTEIES; NIMTEIESS; IMTEIESSK; MTEIESSKE; TEIESSKEE; EIESSKEEY; IESSKEEYN; ESSKEEYNR; SSKEEYNRI; SKEEYNRIN; KEEYNRINE; EEYNRINED; EYNRINEDL; YNRINEDLA; NRINEDLAK; RINEDLAKV; INEDLAKVK; NEDLAKVKA; EDLAKVKAS; DLAKVKASL; LAKVKASLD; AKVKASLDK; KVKASLDKI; VKASLDKIK; KASLDKIKS; ASLDKIKSL; SLDKIKSLL; LDKIKSLLS; DKIKSLLST; KIKSLLSTA; IKSLLSTAK; KSLLSTAKS; SLLSTAKSY; LLSTAKSYL; LSTAKSYLE; STAKSYLEQ; TAKSYLEQT; AKSYLEQTR; KSYLEQTRR; SYLEQTRRG; YLEQTRRGV; LEQTRRGVG; EQTRRGVGS; QTRRGVGSS; TRRGVGSSK; RRGVGSSKA; RGVGSSKAN; GVGSSKANL; VGSSKANLA; GSSKANLAL; SSKANLALL; SKANLALLP; KANLALLPS; ANLALLPSL; NLALLPSLE; LALLPSLEE; ALLPSLEEA; LLPSLEEAI; LPSLEEAIA; PSLEEAIAK; SLEEAIAKV; LEEAIAKVK; EEAIAKVKS; EAIAKVKSN; AIAKVKSNH; IAKVKSNHA; AKVKSNHAS; KVKSNHASA; VKSNHASAD; KSNHASADT; SNHASADTH; NHASADTHC; HASADTHCN; ASADTHCND; SADTHCNDA; ADTHCNDAI; DTHCNDAIA; THCNDAIAA; HCNDAIAAL; CNDAIAALK; NDAIAALKR; DAIAALKRA; AIAALKRAK; IAALKRAKN; AALKRAKND; ALKRAKNDF; LKRAKNDFE; KRAKNDFEY; RAKNDFEYA; AKNDFEYAQ; KNDFEYAQR; NDFEYAQRK; DFEYAQRKA; FEYAQRKAD; EYAQRKADR; YAQRKADRA; AQRKADRAL; QRKADRALE; RKADRALEE; KADRALEEA; ADRALEEAL; DRALEEALS; RALEEALSN; ALEEALSNS; LEEALSNSN; EEALSNSNA; EALSNSNAS; ALSNSNASR; LSNSNASRH; SNSNASRHE; NSNASRHES; SNASRHESY; NASRHESYY; ASRHESYYY; SRHESYYYA; RHESYYYAG; HESYYYAGY; ESYYYAGYH; SYYYAGYHQ; YYYAGYHQF; YYAGYHQFM; YAGYHQFMA; AGYHQFMAD; GYHQFMADA; YHQFMADAK; HQFMADAKA; QFMADAKAS; FMADAKASM; MADAKASMS; ADAKASMSS; DAKASMSST; AKASMSSTK; KASMSSTKS; ASMSSTKSL; SMSSTKSLL; MSSTKSLLE; SSTKSLLEV; STKSLLEVA; TKSLLEVAK; KSLLEVAKN; SLLEVAKNK; LLEVAKNKQ; LEVAKNKQK; EVAKNKQKE; VAKNKQKEL; AKNKQKELN; KNKQKELNE;

	NKQKELNEN; KQKELNENM; QKELNENMT; KELNENMTK; ELNENMTKT; LNENMTKTN; NENMTKTNK; ENMTKTNKD; NMTKTNKDF; MTKTNKDFQ; TKTNKDFQE; KTNKDFQEL; TNKDFQELN; NKDFQELND; KDFQELNDI; DFQELNDIY; FQELNDIYK; QELNDIYKK; ELNDIYKKL; LNDIYKKLQ; NDIYKKLQD; DIYKKLQDM; IYKKLQDMD; YKKLQDMDS; KKLQDMDSR; 10 mers: MNLINKLFIL; NLINKLFILT; LINKLFILTI; INKLFILTIL; NKLFILTILF; KLFILTILFS; LFILTILFSS; FILTILFSSV; ILTILFSSVI; LTILFSSVIS; TILFSSVISC; ILFSSVISCK; LFSSVISCKL; FSSVISCKLY; SSVISCKLYK; SVISCKLYKK; VISCKLYKKI; ISCKLYKKIT; SCKLYKKITY; CKLYKKITYN; KLYKKITYNA; LYKKITYNAD; YKKITYNADQ; KKITYNADQV; KITYNADQVI; ITYNADQVID; TYNADQVIDK; YNADQVIDKL; NADQVIDKLK; ADQVIDKLKS; DQVIDKLKSN; QVIDKLKSNN; VIDKLKSNNG; IDKLKSNNGS; DKLKSNNGSF; KLKSNNGSFN; LKSNNGSFNT; KSNNGSFNTL; SNNGSFNTLK; NNGSFNTLKS; NGSFNTLKSN; GSFNTLKSND; SFNTLKSNDD; FNTLKSNDDS; NTLKSNDDSK; TLKSNDDSKR; LKSNDDSKRS; KSNDDSKRSG; SNDDSKRSGR; NDDSKRSGRK; DDSKRSGRKP; DSKRSGRKPR; SKRSGRKPRS; KRSGRKPRSV; RSGRKPRSVD; SGRKPRSVDN; GRKPRSVDNT; RKPRSVDNTY; KPRSVDNTYM; PRSVDNTYMD; RSVDNTYMDQ; SVDNTYMDQD; VDNTYMDQDT; DNTYMDQDTG; NTYMDQDTGK; TYMDQDTGKK; YMDQDTGKKP; MDQDTGKKPL; DQDTGKKPLM; QDTGKKPLMA; DTGKKPLMAD; TGKKPLMADM; GKKPLMADMQ; KKPLMADMQP; KPLMADMQPD; PLMADMQPDM; LMADMQPDMQ; MADMQPDMQN; ADMQPDMQND; DMQPDMQNDN; MQPDMQNDNS; QPDMQNDNSS; PDMQNDNSSS; DMQNDNSSSN; MQNDNSSSNH; QNDNSSSNHT; NDNSSSNHTL; DNSSSNHTLQ; NSSSNHTLQV; SSSNHTLQVN; SSNHTLQVNI; SNHTLQVNIQ; NHTLQVNIQD; HTLQVNIQDN; TLQVNIQDNE; LQVNIQDNEA; QVNIQDNEAS; VNIQDNEASE; NIQDNEASEA; IQDNEASEAR; QDNEASEARN; DNEASEARNI; NEASEARNIM; EASEARNIMT; ASEARNIMTE; SEARNIMTEI; EARNIMTEIE; ARNIMTEIES; RNIMTEIESS; NIMTEIESSK; IMTEIESSKE; MTEIESSKEE; TEIESSKEEY; EIESSKEEYN; IESSKEEYNR; ESSKEEYNRI; SSKEEYNRIN; SKEEYNRINE; KEEYNRINED; EEYNRINEDL; EYNRINEDLA; YNRINEDLAK; NRINEDLAKV; RINEDLAKVK; INEDLAKVKA; NEDLAKVKAS; EDLAKVKASL; DLAKVKASLD; LAKVKASLDK; AKVKASLDKI; KVKASLDKIK; VKASLDKIKS; KASLDKIKSL; ASLDKIKSLL; SLDKIKSLLS; LDKIKSLLST; DKIKSLLSTA; KIKSLLSTAK; IKSLLSTAKS; KSLLSTAKSY; SLLSTAKSYL; LLSTAKSYLE; LSTAKSYLEQ; STAKSYLEQT; TAKSYLEQTR; AKSYLEQTRR; KSYLEQTRRG; SYLEQTRRGV; YLEQTRRGVG; LEQTRRGVGS; EQTRRGVGSS; QTRRGVGSSK; TRRGVGSSKA; RRGVGSSKAN; RGVGSSKANL; GVGSSKANLA; VGSSKANLAL; GSSKANLALL; SSKANLALLP; SKANLALLPS; KANLALLPSL; ANLALLPSLE; NLALLPSLEE; LALLPSLEEA; ALLPSLEEAI; LLPSLEEAIA; LPSLEEAIAK; PSLEEAIAKV; SLEEAIAKVK; LEEAIAKVKS; EEAIAKVKSN; EAIAKVKSNH; AIAKVKSNHA; IAKVKSNHAS; AKVKSNHASA; KVKSNHASAD;

VKSNHASADT; KSNHASADTH; SNHASADTHC; NHASADTHCN;
HASADTHCND; ASADTHCNDA; SADTHCNDAI; ADTHCNDAIA;
DTHCNDAIAA; THCNDAIAAL; HCNDAIAALK; CNDAIAALKR;
NDAIAALKRA; DAIAALKRAK; AIAALKRAKN; IAALKRAKND;
AALKRAKNDF; ALKRAKNDFE; LKRAKNDFEY; KRAKNDFEYA;
RAKNDFEYAQ; AKNDFEYAQR; KNDFEYAQRK; NDFEYAQRKA;
DFEYAQRKAD; FEYAQRKADR; EYAQRKADRA; YAQRKADRAL;
AQRKADRALE; QRKADRALEE; RKADRALEEA; KADRALEEAL;
ADRALEEALS; DRALEEALSN; RALEEALSNS; ALEEALSNSN;
LEEALSNSNA; EEALSNSNAS; EALSNSNASR; ALSNSNASRH;
LSNSNASRHE; SNSNASRHES; NSNASRHESY; SNASRHESYY;
NASRHESYYY; ASRHESYYYA; SRHESYYYAG; RHESYYYAGY;
HESYYYAGYH; ESYYYAGYHQ; SYYYAGYHQF; YYYAGYHQFM;
YYAGYHQFMA; YAGYHQFMAD; AGYHQFMADA; GYHQFMADAK;
YHQFMADAKA; HQFMADAKAS; QFMADAKASM; FMADAKASMS;
MADAKASMSS; ADAKASMSST; DAKASMSSTK; AKASMSSTKS;
KASMSSTKSL; ASMSSTKSLL; SMSSTKSLLE; MSSTKSLLEV;
SSTKSLLEVA; STKSLLEVAK; TKSLLEVAKN; KSLLEVAKNK;
SLLEVAKNKQ; LLEVAKNKQK; LEVAKNKQKE; EVAKNKQKEL;
VAKNKQKELN; AKNKQKELNE; KNKQKELNEN; NKQKELNENM;
KQKELNENMT; QKELNENMTK; KELNENMTKT; ELNENMTKTN;
LNENMTKTNK; NENMTKTNKD; ENMTKTNKDF; NMTKTNKDFQ;
MTKTNKDFQE; TKTNKDFQEL; KTNKDFQELN; TNKDFQELND;
NKDFQELNDI; KDFQELNDIY; DFQELNDIYK; FQELNDIYKK;
QELNDIYKKL; ELNDIYKKLQ; LNDIYKKLQD; NDIYKKLQDM;
DIYKKLQDMD; IYKKLQDMDS; YKKLQDMDSR;

11 mers:
MNLINKLFILT; NLINKLFILTI; LINKLFILTIL; INKLFILTILF;
NKLFILTILFS; KLFILTILFSS; LFILTILFSSV; FILTILFSSVI;
ILTILFSSVIS; LTILFSSVISC; TILFSSVISCK; ILFSSVISCKL;
LFSSVISCKLY; FSSVISCKLYK; SSVISCKLYKK; SVISCKLYKKI;
VISCKLYKKIT; ISCKLYKKITY; SCKLYKKITYN; CKLYKKITYNA;
KLYKKITYNAD; LYKKITYNADQ; YKKITYNADQV; KKITYNADQVI;
KITYNADQVID; ITYNADQVIDK; TYNADQVIDKL; YNADQVIDKLK;
NADQVIDKLKS; ADQVIDKLKSN; DQVIDKLKSNN; QVIDKLKSNNG;
VIDKLKSNNGS; IDKLKSNNGSF; DKLKSNNGSFN; KLKSNNGSFNT;
LKSNNGSFNTL; KSNNGSFNTLK; SNNGSFNTLKS; NNGSFNTLKSN;
NGSFNTLKSND; GSFNTLKSNDD; SFNTLKSNDDS; FNTLKSNDDSK;
NTLKSNDDSKR; TLKSNDDSKRS; LKSNDDSKRSG; KSNDDSKRSGR;
SNDDSKRSGRK; NDDSKRSGRKP; DDSKRSGRKPR; DSKRSGRKPRS;
SKRSGRKPRSV; KRSGRKPRSVD; RSGRKPRSVDN; SGRKPRSVDNT;
GRKPRSVDNTY; RKPRSVDNTYM; KPRSVDNTYMD; PRSVDNTYMDQ;
RSVDNTYMDQD; SVDNTYMDQDT; VDNTYMDQDTG; DNTYMDQDTGK;
NTYMDQDTGKK; TYMDQDTGKKP; YMDQDTGKKPL; MDQDTGKKPLM;
DQDTGKKPLMA; QDTGKKPLMAD; DTGKKPLMADM; TGKKPLMADMQ;
GKKPLMADMQP; KKPLMADMQPD; KPLMADMQPDM; PLMADMQPDMQ;
LMADMQPDMQN; MADMQPDMQND; ADMQPDMQNDN; DMQPDMQNDNS;
MQPDMQNDNSS; QPDMQNDNSSS; PDMQNDNSSSN; DMQNDNSSSNH;
MQNDNSSSNHT; QNDNSSSNHTL; NDNSSSNHTLQ; DNSSSNHTLQV;
NSSSNHTLQVN; SSSNHTLQVNI; SSNHTLQVNIQ; SNHTLQVNIQD;

	NHTLQVNIQDN; HTLQVNIQDNE; TLQVNIQDNEA; LQVNIQDNEAS; QVNIQDNEASE; VNIQDNEASEA; NIQDNEASEAR; IQDNEASEARN; QDNEASEARNI; DNEASEARNIM; NEASEARNIMT; EASEARNIMTE; ASEARNIMTEI; SEARNIMTEIE; EARNIMTEIES; ARNIMTEIESS; RNIMTEIESSK; NIMTEIESSKE; IMTEIESSKEE; MTEIESSKEEY; TEIESSKEEYN; EIESSKEEYNR; IESSKEEYNRI; ESSKEEYNRIN; SSKEEYNRINE; SKEEYNRINED; KEEYNRINEDL; EEYNRINEDLA; EYNRINEDLAK; YNRINEDLAKV; NRINEDLAKVK; RINEDLAKVKA; INEDLAKVKAS; NEDLAKVKASL; EDLAKVKASLD; DLAKVKASLDK; LAKVKASLDKI; AKVKASLDKIK; KVKASLDKIKS; VKASLDKIKSL; KASLDKIKSLL; ASLDKIKSLLS; SLDKIKSLLST; LDKIKSLLSTA; DKIKSLLSTAK; KIKSLLSTAKS; IKSLLSTAKSY; KSLLSTAKSYL; SLLSTAKSYLE; LLSTAKSYLEQ; LSTAKSYLEQT; STAKSYLEQTR; TAKSYLEQTRR; AKSYLEQTRRG; KSYLEQTRRGV; SYLEQTRRGVG; YLEQTRRGVGS; LEQTRRGVGSS; EQTRRGVGSSK; QTRRGVGSSKA; TRRGVGSSKAN; RRGVGSSKANL; RGVGSSKANLA; GVGSSKANLAL; VGSSKANLALL; GSSKANLALLP; SSKANLALLPS; SKANLALLPSL; KANLALLPSLE; ANLALLPSLEE; NLALLPSLEEA; LALLPSLEEAI; ALLPSLEEAIA; LLPSLEEAIAK; LPSLEEAIAKV; PSLEEAIAKVK; SLEEAIAKVKS; LEEAIAKVKSN; EEAIAKVKSNH; EAIAKVKSNHA; AIAKVKSNHAS; IAKVKSNHASA; AKVKSNHASAD; KVKSNHASADT; VKSNHASADTH; KSNHASADTHC; SNHASADTHCN; NHASADTHCND; HASADTHCNDA; ASADTHCNDAI; SADTHCNDAIA; ADTHCNDAIAA; DTHCNDAIAAL; THCNDAIAALK; HCNDAIAALKR; CNDAIAALKRA; NDAIAALKRAK; DAIAALKRAKN; AIAALKRAKND; IAALKRAKNDF; AALKRAKNDFE; ALKRAKNDFEY; LKRAKNDFEYA; KRAKNDFEYAQ; RAKNDFEYAQR; AKNDFEYAQRK; KNDFEYAQRKA; NDFEYAQRKAD; DFEYAQRKADR; FEYAQRKADRA; EYAQRKADRAL; YAQRKADRALE; AQRKADRALEE; QRKADRALEEA; RKADRALEEAL; KADRALEEALS; ADRALEEALSN; DRALEEALSNS; RALEEALSNSN; ALEEALSNSNA; LEEALSNSNAS; EEALSNSNASR; EALSNSNASRH; ALSNSNASRHE; LSNSNASRHES; SNSNASRHESY; NSNASRHESYY; SNASRHESYYY; NASRHESYYYA; ASRHESYYYAG; SRHESYYYAGY; RHESYYYAGYH; HESYYYAGYHQ; ESYYYAGYHQF; SYYYAGYHQFM; YYYAGYHQFMA; YYAGYHQFMAD; YAGYHQFMADA; AGYHQFMADAK; GYHQFMADAKA; YHQFMADAKAS; HQFMADAKASM; QFMADAKASMS; FMADAKASMSS; MADAKASMSST; ADAKASMSSTK; DAKASMSSTKS; AKASMSSTKSL; KASMSSTKSLL; ASMSSTKSLLE; SMSSTKSLLEV; MSSTKSLLEVA; SSTKSLLEVAK; STKSLLEVAKN; TKSLLEVAKNK; KSLLEVAKNKQ; SLLEVAKNKQK; LLEVAKNKQKE; LEVAKNKQKEL; EVAKNKQKELN; VAKNKQKELNE; AKNKQKELNEN; KNKQKELNENM; NKQKELNENMT; KQKELNENMTK; QKELNENMTKT; KELNENMTKTN; ELNENMTKTNK; LNENMTKTNKD; NENMTKTNKDF; ENMTKTNKDFQ; NMTKTNKDFQE; MTKTNKDFQEL; TKTNKDFQELN; KTNKDFQELND; TNKDFQELNDI; NKDFQELNDIY; KDFQELNDIYK; DFQELNDIYKK; FQELNDIYKKL; QELNDIYKKLQ; ELNDIYKKLQD; LNDIYKKLQDM; NDIYKKLQDMD; DIYKKLQDMDS; IYKKLQDMDSR;
Seq 23	SEQ ID NO 24474-25783/ 8 mers: MIINHNTS; IINHNTSA; INHNTSAI; NHNTSAIN; HNTSAINA;

	NTSAINAS; TSAINASR; SAINASRN; AINASRNN; INASRNNG; NASRNNGI; ASRNNGIN; SRNNGINA; RNNGINAA; NNGINAAN; NGINAANL; GINAANLS; INAANLSK; NAANLSKT; AANLSKTQ; ANLSKTQE; NLSKTQEK; LSKTQEKL; SKTQEKLS; KTQEKLSS; TQEKLSSG; QEKLSSGY; EKLSSGYR; KLSSGYRI; LSSGYRIN; SSGYRINR; SGYRINRA; GYRINRAS; YRINRASD; RINRASDD; INRASDDA; NRASDDAA; RASDDAAG; ASDDAAGM; SDDAAGMG; DDAAGMGV; DAAGMGVS; AAGMGVSG; AGMGVSGK; GMGVSGKI; MGVSGKIN; GVSGKINA; VSGKINAQ; SGKINAQI; GKINAQIR; KINAQIRG; INAQIRGL; NAQIRGLS; AQIRGLSQ; QIRGLSQA; IRGLSQAS; RGLSQASR; GLSQASRN; LSQASRNT; SQASRNTS; QASRNTSK; ASRNTSKA; SRNTSKAI; RNTSKAIN; NTSKAINF; TSKAINFI; SKAINFIQ; KAINFIQT; AINFIQTT; INFIQTTE; NFIQTTEG; FIQTTEGN; IQTTEGNL; QTTEGNLN; TTEGNLNE; TEGNLNEV; EGNLNEVE; GNLNEVEK; NLNEVEKV; LNEVEKVL; NEVEKVLV; EVEKVLVR; VEKVLVRM; EKVLVRMK; KVLVRMKE; VLVRMKEL; LVRMKELA; VRMKELAV; RMKELAVQ; MKELAVQS; KELAVQSG; ELAVQSGN; LAVQSGNG; AVQSGNGT; VQSGNGTY; QSGNGTYS; SGNGTYSD; GNGTYSDA; NGTYSDAD; GTYSDADR; TYSDADRG; YSDADRGS; SDADRGSI; DADRGSIQ; ADRGSIQI; DRGSIQIE; RGSIQIEI; GSIQIEIE; SIQIEIEQ; IQIEIEQL; QIEIEQLT; IEIEQLTD; EIEQLTDE; IEQLTDEI; EQLTDEIN; QLTDEINR; LTDEINRI; TDEINRIA; DEINRIAD; EINRIADQ; INRIADQA; NRIADQAQ; RIADQAQY; IADQAQYN; ADQAQYNQ; DQAQYNQM; QAQYNQMH; AQYNQMHM; QYNQMHML; YNQMHMLS; NQMHMLSN; QMHMLSNK; MHMLSNKS; HMLSNKSA; MLSNKSAS; LSNKSASQ; SNKSASQN; NKSASQNV; KSASQNVR; SASQNVRT; ASQNVRTA; SQNVRTAE; QNVRTAEE; NVRTAEEL; VRTAEELG; RTAEELGM; TAEELGMQ; AEELGMQP; EELGMQPA; ELGMQPAK; LGMQPAKI; GMQPAKIN; MQPAKINT; QPAKINTP; PAKINTPA; AKINTPAS; KINTPASL; INTPASLS; NTPASLSG; TPASLSGS; PASLSGSQ; ASLSGSQA; SLSGSQAS; LSGSQASW; SGSQASWT; GSQASWTL; SQASWTLR; QASWTLRV; ASWTLRVH; SWTLRVHV; WTLRVHVG; TLRVHVGA; LRVHVGAN; RVHVGANQ; VHVGANQD; HVGANQDE; VGANQDEA; GANQDEAI; ANQDEAIA; NQDEAIAV; QDEAIAVN; DEAIAVNI; EAIAVNIY; AIAVNIYA; IAVNIYAA; AVNIYAAN; VNIYAANV; NIYAANVA; IYAANVAN; YAANVANL; AANVANLF; ANVANLFS; NVANLFSG; VANLFSGE; ANLFSGEG; NLFSGEGA; LFSGEGAQ; FSGEGAQT; SGEGAQTA; GEGAQTAQ; EGAQTAQA; GAQTAQAA; AQTAQAAP; QTAQAAPV; TAQAAPVQ; AQAAPVQE; QAAPVQEG; AAPVQEGV; APVQEGVQ; PVQEGVQQ; VQEGVQQE; QEGVQQEG; EGVQQEGA; GVQQEGAQ; VQQEGAQQ; QQEGAQQP; QEGAQQPA; EGAQQPAP; GAQQPAPA; AQQPAPAT; QQPAPATA; QPAPATAP; PAPATAPS; APATAPSQ; PATAPSQG; ATAPSQGG; TAPSQGGV; APSQGGVN; PSQGGVNS; SQGGVNSP; QGGVNSPV; GGVNSPVN; GVNSPVNV; VNSPVNVT; NSPVNVTT; SPVNVTTT; PVNVTTTV; VNVTTTVD; NVTTTVDA; VTTTVDAN; TTTVDANT; TTVDANTS; TVDANTSL; VDANTSLA; DANTSLAK; ANTSLAKI; NTSLAKIE; TSLAKIEN; SLAKIENA; LAKIENAI; AKIENAIR; KIENAIRM; IENAIRMI; ENAIRMIS; NAIRMISD; AIRMISDQ; IRMISDQR; RMISDQRA; MISDQRAN; ISDQRANL;

	SDQRANLG; DQRANLGA; QRANLGAF; RANLGAFQ; ANLGAFQN; NLGAFQNR; LGAFQNRL; GAFQNRLE; AFQNRLES; FQNRLESI; QNRLESIK; NRLESIKN; RLESIKNS; LESIKNST; ESIKNSTE; SIKNSTEY; IKNSTEYA; KNSTEYAI; NSTEYAIE; STEYAIEN; TEYAIENL; EYAIENLK; YAIENLKA; AIENLKAS; IENLKASY; ENLKASYA; NLKASYAQ; LKASYAQI; KASYAQIK; ASYAQIKD; SYAQIKDA; YAQIKDAT; AQIKDATM; QIKDATMT; IKDATMTD; KDATMTDE; DATMTDEV; ATMTDEVV; TMTDEVVA; MTDEVVAA; TDEVVAAT; DEVVAATT; EVVAATTN; VVAATTNS; VAATTNSI; AATTNSIL; ATTNSILT; TTNSILTQ; TNSILTQS; NSILTQSA; SILTQSAM; ILTQSAMA; LTQSAMAM; TQSAMAMI; QSAMAMIA; SAMAMIAQ; AMAMIAQA; MAMIAQAN; AMIAQANQ; MIAQANQV; IAQANQVP; AQANQVPQ; QANQVPQY; ANQVPQYV; NQVPQYVL; QVPQYVLS; VPQYVLSL; PQYVLSLL; QYVLSLLR; 9 mers: MIINHNTSA; IINHNTSAI; INHNTSAIN; NHNTSAINA; HNTSAINAS; NTSAINASR; TSAINASRN; SAINASRNN; AINASRNNG; INASRNNGI; NASRNNGIN; ASRNNGINA; SRNNGINAA; RNNGINAAN; NNGINAANL; NGINAANLS; GINAANLSK; INAANLSKT; NAANLSKTQ; AANLSKTQE; ANLSKTQEK; NLSKTQEKL; LSKTQEKLS; SKTQEKLSS; KTQEKLSSG; TQEKLSSGY; QEKLSSGYR; EKLSSGYRI; KLSSGYRIN; LSSGYRINR; SSGYRINRA; SGYRINRAS; GYRINRASD; YRINRASDD; RINRASDDA; INRASDDAA; NRASDDAAG; RASDDAAGM; ASDDAAGMG; SDDAAGMGV; DDAAGMGVS; DAAGMGVSG; AAGMGVSGK; AGMGVSGKI; GMGVSGKIN; MGVSGKINA; GVSGKINAQ; VSGKINAQI; SGKINAQIR; GKINAQIRG; KINAQIRGL; INAQIRGLS; NAQIRGLSQ; AQIRGLSQA; QIRGLSQAS; IRGLSQASR; RGLSQASRN; GLSQASRNT; LSQASRNTS; SQASRNTSK; QASRNTSKA; ASRNTSKAI; SRNTSKAIN; RNTSKAINF; NTSKAINFI; TSKAINFIQ; SKAINFIQT; KAINFIQTT; AINFIQTTE; INFIQTTEG; NFIQTTEGN; FIQTTEGNL; IQTTEGNLN; QTTEGNLNE; TTEGNLNEV; TEGNLNEVE; EGNLNEVEK; GNLNEVEKV; NLNEVEKVL; LNEVEKVLV; NEVEKVLVR; EVEKVLVRM; VEKVLVRMK; EKVLVRMKE; KVLVRMKEL; VLVRMKELA; LVRMKELAV; VRMKELAVQ; RMKELAVQS; MKELAVQSG; KELAVQSGN; ELAVQSGNG; LAVQSGNGT; AVQSGNGTY; VQSGNGTYS; QSGNGTYSD; SGNGTYSDA; GNGTYSDAD; NGTYSDADR; GTYSDADRG; TYSDADRGS; YSDADRGSI; SDADRGSIQ; DADRGSIQI; ADRGSIQIE; DRGSIQIEI; RGSIQIEIE; GSIQIEIEQ; SIQIEIEQL; IQIEIEQLT; QIEIEQLTD; IEIEQLTDE; EIEQLTDEI; IEQLTDEIN; EQLTDEINR; QLTDEINRI; LTDEINRIA; TDEINRIAD; DEINRIADQ; EINRIADQA; INRIADQAQ; NRIADQAQY; RIADQAQYN; IADQAQYNQ; ADQAQYNQM; DQAQYNQMH; QAQYNQMHM; AQYNQMHML; QYNQMHMLS; YNQMHMLSN; NQMHMLSNK; QMHMLSNKS; MHMLSNKSA; HMLSNKSAS; MLSNKSASQ; LSNKSASQN; SNKSASQNV; NKSASQNVR; KSASQNVRT; SASQNVRTA; ASQNVRTAE; SQNVRTAEE; QNVRTAEEL; NVRTAEELG; VRTAEELGM; RTAEELGMQ; TAEELGMQP; AEELGMQPA; EELGMQPAK; ELGMQPAKI; LGMQPAKIN; GMQPAKINT; MQPAKINTP; QPAKINTPA; PAKINTPAS; AKINTPASL; KINTPASLS; INTPASLSG; NTPASLSGS; TPASLSGSQ; PASLSGSQA; ASLSGSQAS; SLSGSQASW; LSGSQASWT; SGSQASWTL; GSQASWTLR; SQASWTLRV; QASWTLRVH; ASWTLRVHV; SWTLRVHVG; WTLRVHVGA; TLRVHVGAN; LRVHVGANQ; RVHVGANQD; VHVGANQDE;

HVGANQDEA; VGANQDEAI; GANQDEAIA; ANQDEAIAV; NQDEAIAVN; QDEAIAVNI; DEAIAVNIY; EAIAVNIYA; AIAVNIYAA; IAVNIYAAN; AVNIYAANV; VNIYAANVA; NIYAANVAN; IYAANVANL; YAANVANLF; AANVANLFS; ANVANLFSG; NVANLFSGE; VANLFSGEG; ANLFSGEGA; NLFSGEGAQ; LFSGEGAQT; FSGEGAQTA; SGEGAQTAQ; GEGAQTAQA; EGAQTAQAA; GAQTAQAAP; AQTAQAAPV; QTAQAAPVQ; TAQAAPVQE; AQAAPVQEG; QAAPVQEGV; AAPVQEGVQ; APVQEGVQQ; PVQEGVQQE; VQEGVQQEG; QEGVQQEGA; EGVQQEGAQ; GVQQEGAQQ; VQQEGAQQP; QQEGAQQPA; QEGAQQPAP; EGAQQPAPA; GAQQPAPAT; AQQPAPATA; QQPAPATAP; QPAPATAPS; PAPATAPSQ; APATAPSQG; PATAPSQGG; ATAPSQGGV; TAPSQGGVN; APSQGGVNS; PSQGGVNSP; SQGGVNSPV; QGGVNSPVN; GGVNSPVNV; GVNSPVNVT; VNSPVNVTT; NSPVNVTTT; SPVNVTTTV; PVNVTTTVD; VNVTTTVDA; NVTTTVDAN; VTTTVDANT; TTTVDANTS; TTVDANTSL; TVDANTSLA; VDANTSLAK; DANTSLAKI; ANTSLAKIE; NTSLAKIEN; TSLAKIENA; SLAKIENAI; LAKIENAIR; AKIENAIRM; KIENAIRMI; IENAIRMIS; ENAIRMISD; NAIRMISDQ; AIRMISDQR; IRMISDQRA; RMISDQRAN; MISDQRANL; ISDQRANLG; SDQRANLGA; DQRANLGAF; QRANLGAFQ; RANLGAFQN; ANLGAFQNR; NLGAFQNRL; LGAFQNRLE; GAFQNRLES; AFQNRLESI; FQNRLESIK; QNRLESIKN; NRLESIKNS; RLESIKNST; LESIKNSTE; ESIKNSTEY; SIKNSTEYA; IKNSTEYAI; KNSTEYAIE; NSTEYAIEN; STEYAIENL; TEYAIENLK; EYAIENLKA; YAIENLKAS; AIENLKASY; IENLKASYA; ENLKASYAQ; NLKASYAQI; LKASYAQIK; KASYAQIKD; ASYAQIKDA; SYAQIKDAT; YAQIKDATM; AQIKDATMT; QIKDATMTD; IKDATMTDE; KDATMTDEV; DATMTDEVV; ATMTDEVVA; TMTDEVVAA; MTDEVVAAT; TDEVVAATT; DEVVAATTN; EVVAATTNS; VVAATTNSI; VAATTNSIL; AATTNSILT; ATTNSILTQ; TTNSILTQS; TNSILTQSA; NSILTQSAM; SILTQSAMA; ILTQSAMAM; LTQSAMAMI; TQSAMAMIA; QSAMAMIAQ; SAMAMIAQA; AMAMIAQAN; MAMIAQANQ; AMIAQANQV; MIAQANQVP; IAQANQVPQ; AQANQVPQY; QANQVPQYV; ANQVPQYVL; NQVPQYVLS; QVPQYVLSL; VPQYVLSLL; PQYVLSLLR;

10 mers:

MIINHNTSAI; IINHNTSAIN; INHNTSAINA; NHNTSAINAS; HNTSAINASR; NTSAINASRN; TSAINASRNN; SAINASRNNG; AINASRNNGI; INASRNNGIN; NASRNNGINA; ASRNNGINAA; SRNNGINAAN; RNNGINAANL; NNGINAANLS; NGINAANLSK; GINAANLSKT; INAANLSKTQ; NAANLSKTQE; AANLSKTQEK; ANLSKTQEKL; NLSKTQEKLS; LSKTQEKLSS; SKTQEKLSSG; KTQEKLSSGY; TQEKLSSGYR; QEKLSSGYRI; EKLSSGYRIN; KLSSGYRINR; LSSGYRINRA; SSGYRINRAS; SGYRINRASD; GYRINRASDD; YRINRASDDA; RINRASDDAA; INRASDDAAG; NRASDDAAGM; RASDDAAGMG; ASDDAAGMGV; SDDAAGMGVS; DDAAGMGVSG; DAAGMGVSGK; AAGMGVSGKI; AGMGVSGKIN; GMGVSGKINA; MGVSGKINAQ; GVSGKINAQI; VSGKINAQIR; SGKINAQIRG; GKINAQIRGL; KINAQIRGLS; INAQIRGLSQ; NAQIRGLSQA; AQIRGLSQAS; QIRGLSQASR; IRGLSQASRN; RGLSQASRNT; GLSQASRNTS; LSQASRNTSK; SQASRNTSKA; QASRNTSKAI; ASRNTSKAIN; SRNTSKAINF; RNTSKAINFI; NTSKAINFIQ; TSKAINFIQT; SKAINFIQTT; KAINFIQTTE; AINFIQTTEG; INFIQTTEGN; NFIQTTEGNL; FIQTTEGNLN;

	IQTTEGNLNE; QTTEGNLNEV; TTEGNLNEVE; TEGNLNEVEK; EGNLNEVEKV; GNLNEVEKVL; NLNEVEKVLV; LNEVEKVLVR; NEVEKVLVRM; EVEKVLVRMK; VEKVLVRMKE; EKVLVRMKEL; KVLVRMKELA; VLVRMKELAV; LVRMKELAVQ; VRMKELAVQS; RMKELAVQSG; MKELAVQSGN; KELAVQSGNG; ELAVQSGNGT; LAVQSGNGTY; AVQSGNGTYS; VQSGNGTYSD; QSGNGTYSDA; SGNGTYSDAD; GNGTYSDADR; NGTYSDADRG; GTYSDADRGS; TYSDADRGSI; YSDADRGSIQ; SDADRGSIQI; DADRGSIQIE; ADRGSIQIEI; DRGSIQIEIE; RGSIQIEIEQ; GSIQIEIEQL; SIQIEIEQLT; IQIEIEQLTD; QIEIEQLTDE; IEIEQLTDEI; EIEQLTDEIN; IEQLTDEINR; EQLTDEINRI; QLTDEINRIA; LTDEINRIAD; TDEINRIADQ; DEINRIADQA; EINRIADQAQ; INRIADQAQY; NRIADQAQYN; RIADQAQYNQ; IADQAQYNQM; ADQAQYNQMH; DQAQYNQMHM; QAQYNQMHML; AQYNQMHMLS; QYNQMHMLSN; YNQMHMLSNK; NQMHMLSNKS; QMHMLSNKSA; MHMLSNKSAS; HMLSNKSASQ; MLSNKSASQN; LSNKSASQNV; SNKSASQNVR; NKSASQNVRT; KSASQNVRTA; SASQNVRTAE; ASQNVRTAEE; SQNVRTAEEL; QNVRTAEELG; NVRTAEELGM; VRTAEELGMQ; RTAEELGMQP; TAEELGMQPA; AEELGMQPAK; EELGMQPAKI; ELGMQPAKIN; LGMQPAKINT; GMQPAKINTP; MQPAKINTPA; QPAKINTPAS; PAKINTPASL; AKINTPASLS; KINTPASLSG; INTPASLSGS; NTPASLSGSQ; TPASLSGSQA; PASLSGSQAS; ASLSGSQASW; SLSGSQASWT; LSGSQASWTL; SGSQASWTLR; GSQASWTLRV; SQASWTLRVH; QASWTLRVHV; ASWTLRVHVG; SWTLRVHVGA; WTLRVHVGAN; TLRVHVGANQ; LRVHVGANQD; RVHVGANQDE; VHVGANQDEA; HVGANQDEAI; VGANQDEAIA; GANQDEAIAV; ANQDEAIAVN; NQDEAIAVNI; QDEAIAVNIY; DEAIAVNIYA; EAIAVNIYAA; AIAVNIYAAN; IAVNIYAANV; AVNIYAANVA; VNIYAANVAN; NIYAANVANL; IYAANVANLF; YAANVANLFS; AANVANLFSG; ANVANLFSGE; NVANLFSGEG; VANLFSGEGA; ANLFSGEGAQ; NLFSGEGAQT; LFSGEGAQTA; FSGEGAQTAQ; SGEGAQTAQA; GEGAQTAQAA; EGAQTAQAAP; GAQTAQAAPV; AQTAQAAPVQ; QTAQAAPVQE; TAQAAPVQEG; AQAAPVQEGV; QAAPVQEGVQ; AAPVQEGVQQ; APVQEGVQQE; PVQEGVQQEG; VQEGVQQEGA; QEGVQQEGAQ; EGVQQEGAQQ; GVQQEGAQQP; VQQEGAQQPA; QQEGAQQPAP; QEGAQQPAPA; EGAQQPAPAT; GAQQPAPATA; AQQPAPATAP; QQPAPATAPS; QPAPATAPSQ; PAPATAPSQG; APATAPSQGG; PATAPSQGGV; ATAPSQGGVN; TAPSQGGVNS; APSQGGVNSP; PSQGGVNSPV; SQGGVNSPVN; QGGVNSPVNV; GGVNSPVNVT; GVNSPVNVTT; VNSPVNVTTT; NSPVNVTTTV; SPVNVTTTVD; PVNVTTTVDA; VNVTTTVDAN; NVTTTVDANT; VTTTVDANTS; TTTVDANTSL; TTVDANTSLA; TVDANTSLAK; VDANTSLAKI; DANTSLAKIE; ANTSLAKIEN; NTSLAKIENA; TSLAKIENAI; SLAKIENAIR; LAKIENAIRM; AKIENAIRMI; KIENAIRMIS; IENAIRMISD; ENAIRMISDQ; NAIRMISDQR; AIRMISDQRA; IRMISDQRAN; RMISDQRANL; MISDQRANLG; ISDQRANLGA; SDQRANLGAF; DQRANLGAFQ; QRANLGAFQN; RANLGAFQNR; ANLGAFQNRL; NLGAFQNRLE; LGAFQNRLES; GAFQNRLESI; AFQNRLESIK; FQNRLESIKN; QNRLESIKNS; NRLESIKNST; RLESIKNSTE; LESIKNSTEY; ESIKNSTEYA; SIKNSTEYAI;

IKNSTEYAIE; KNSTEYAIEN; NSTEYAIENL; STEYAIENLK;
TEYAIENLKA; EYAIENLKAS; YAIENLKASY; AIENLKASYA;
IENLKASYAQ; ENLKASYAQI; NLKASYAQIK; LKASYAQIKD;
KASYAQIKDA; ASYAQIKDAT; SYAQIKDATM; YAQIKDATMT;
AQIKDATMTD; QIKDATMTDE; IKDATMTDEV; KDATMTDEVV;
DATMTDEVVA; ATMTDEVVAA; TMTDEVVAAT; MTDEVVAATT;
TDEVVAATTN; DEVVAATTNS; EVVAATTNSI; VVAATTNSIL;
VAATTNSILT; AATTNSILTQ; ATTNSILTQS; TTNSILTQSA;
TNSILTQSAM; NSILTQSAMA; SILTQSAMAM; ILTQSAMAMI;
LTQSAMAMIA; TQSAMAMIAQ; QSAMAMIAQA; SAMAMIAQAN;
AMAMIAQANQ; MAMIAQANQV; AMIAQANQVP; MIAQANQVPQ;
IAQANQVPQY; AQANQVPQYV; QANQVPQYVL; ANQVPQYVLS;
NQVPQYVLSL; QVPQYVLSLL; VPQYVLSLLR;

11 mers:
MIINHNTSAIN; IINHNTSAINA; INHNTSAINAS; NHNTSAINASR;
HNTSAINASRN; NTSAINASRNN; TSAINASRNNG; SAINASRNNGI;
AINASRNNGIN; INASRNNGINA; NASRNNGINAA; ASRNNGINAAN;
SRNNGINAANL; RNNGINAANLS; NNGINAANLSK; NGINAANLSKT;
GINAANLSKTQ; INAANLSKTQE; NAANLSKTQEK; AANLSKTQEKL;
ANLSKTQEKLS; NLSKTQEKLSS; LSKTQEKLSSG; SKTQEKLSSGY;
KTQEKLSSGYR; TQEKLSSGYRI; QEKLSSGYRIN; EKLSSGYRINR;
KLSSGYRINRA; LSSGYRINRAS; SSGYRINRASD; SGYRINRASDD;
GYRINRASDDA; YRINRASDDAA; RINRASDDAAG; INRASDDAAGM;
NRASDDAAGMG; RASDDAAGMGV; ASDDAAGMGVS; SDDAAGMGVSG;
DDAAGMGVSGK; DAAGMGVSGKI; AAGMGVSGKIN; AGMGVSGKINA;
GMGVSGKINAQ; MGVSGKINAQI; GVSGKINAQIR; VSGKINAQIRG;
SGKINAQIRGL; GKINAQIRGLS; KINAQIRGLSQ; INAQIRGLSQA;
NAQIRGLSQAS; AQIRGLSQASR; QIRGLSQASRN; IRGLSQASRNT;
RGLSQASRNTS; GLSQASRNTSK; LSQASRNTSKA; SQASRNTSKAI;
QASRNTSKAIN; ASRNTSKAINF; SRNTSKAINFI; RNTSKAINFIQ;
NTSKAINFIQT; TSKAINFIQTT; SKAINFIQTTE; KAINFIQTTEG;
AINFIQTTEGN; INFIQTTEGNL; NFIQTTEGNLN; FIQTTEGNLNE;
IQTTEGNLNEV; QTTEGNLNEVE; TTEGNLNEVEK; TEGNLNEVEKV;
EGNLNEVEKVL; GNLNEVEKVLV; NLNEVEKVLVR; LNEVEKVLVRM;
NEVEKVLVRMK; EVEKVLVRMKE; VEKVLVRMKEL; EKVLVRMKELA;
KVLVRMKELAV; VLVRMKELAVQ; LVRMKELAVQS; VRMKELAVQSG;
RMKELAVQSGN; MKELAVQSGNG; KELAVQSGNGT; ELAVQSGNGTY;
LAVQSGNGTYS; AVQSGNGTYSD; VQSGNGTYSDA; QSGNGTYSDAD;
SGNGTYSDADR; GNGTYSDADRG; NGTYSDADRGS; GTYSDADRGSI;
TYSDADRGSIQ; YSDADRGSIQI; SDADRGSIQIE; DADRGSIQIEI;
ADRGSIQIEIE; DRGSIQIEIEQ; RGSIQIEIEQL; GSIQIEIEQLT;
SIQIEIEQLTD; IQIEIEQLTDE; QIEIEQLTDEI; IEIEQLTDEIN;
EIEQLTDEINR; IEQLTDEINRI; EQLTDEINRIA; QLTDEINRIAD;
LTDEINRIADQ; TDEINRIADQA; DEINRIADQAQ; EINRIADQAQY;
INRIADQAQYN; NRIADQAQYNQ; RIADQAQYNQM; IADQAQYNQMH;
ADQAQYNQMHM; DQAQYNQMHML; QAQYNQMHMLS; AQYNQMHMLSN;
QYNQMHMLSNK; YNQMHMLSNKS; NQMHMLSNKSA; QMHMLSNKSAS;
MHMLSNKSASQ; HMLSNKSASQN; MLSNKSASQNV; LSNKSASQNVR;
SNKSASQNVRT; NKSASQNVRTA; KSASQNVRTAE; SASQNVRTAEE;
ASQNVRTAEEL; SQNVRTAEELG; QNVRTAEELGM; NVRTAEELGMQ;

	VRTAEELGMQP; RTAEELGMQPA; TAEELGMQPAK; AEELGMQPAKI; EELGMQPAKIN; ELGMQPAKINT; LGMQPAKINTP; GMQPAKINTPA; MQPAKINTPAS; QPAKINTPASL; PAKINTPASLS; AKINTPASLSG; KINTPASLSGS; INTPASLSGSQ; NTPASLSGSQA; TPASLSGSQAS; PASLSGSQASW; ASLSGSQASWT; SLSGSQASWTL; LSGSQASWTLR; SGSQASWTLRV; GSQASWTLRVH; SQASWTLRVHV; QASWTLRVHVG; ASWTLRVHVGA; SWTLRVHVGAN; WTLRVHVGANQ; TLRVHVGANQD; LRVHVGANQDE; RVHVGANQDEA; VHVGANQDEAI; HVGANQDEAIA; VGANQDEAIAV; GANQDEAIAVN; ANQDEAIAVNI; NQDEAIAVNIY; QDEAIAVNIYA; DEAIAVNIYAA; EAIAVNIYAAN; AIAVNIYAANV; IAVNIYAANVA; AVNIYAANVAN; VNIYAANVANL; NIYAANVANLF; IYAANVANLFS; YAANVANLFSG; AANVANLFSGE; ANVANLFSGEG; NVANLFSGEGA; VANLFSGEGAQ; ANLFSGEGAQT; NLFSGEGAQTA; LFSGEGAQTAQ; FSGEGAQTAQA; SGEGAQTAQAA; GEGAQTAQAAP; EGAQTAQAAPV; GAQTAQAAPVQ; AQTAQAAPVQE; QTAQAAPVQEG; TAQAAPVQEGV; AQAAPVQEGVQ; QAAPVQEGVQQ; AAPVQEGVQQE; APVQEGVQQEG; PVQEGVQQEGA; VQEGVQQEGAQ; QEGVQQEGAQQ; EGVQQEGAQQP; GVQQEGAQQPA; VQQEGAQQPAP; QQEGAQQPAPA; QEGAQQPAPAT; EGAQQPAPATA; GAQQPAPATAP; AQQPAPATAPS; QQPAPATAPSQ; QPAPATAPSQG; PAPATAPSQGG; APATAPSQGGV; PATAPSQGGVN; ATAPSQGGVNS; TAPSQGGVNSP; APSQGGVNSPV; PSQGGVNSPVN; SQGGVNSPVNV; QGGVNSPVNVT; GGVNSPVNVTT; GVNSPVNVTTT; VNSPVNVTTTV; NSPVNVTTTVD; SPVNVTTTVDA; PVNVTTTVDAN; VNVTTTVDANT; NVTTTVDANTS; VTTTVDANTSL; TTTVDANTSLA; TTVDANTSLAK; TVDANTSLAKI; VDANTSLAKIE; DANTSLAKIEN; ANTSLAKIENA; NTSLAKIENAI; TSLAKIENAIR; SLAKIENAIRM; LAKIENAIRMI; AKIENAIRMIS; KIENAIRMISD; IENAIRMISDQ; ENAIRMISDQR; NAIRMISDQRA; AIRMISDQRAN; IRMISDQRANL; RMISDQRANLG; MISDQRANLGA; ISDQRANLGAF; SDQRANLGAFQ; DQRANLGAFQN; QRANLGAFQNR; RANLGAFQNRL; ANLGAFQNRLE; NLGAFQNRLES; LGAFQNRLESI; GAFQNRLESIK; AFQNRLESIKN; FQNRLESIKNS; QNRLESIKNST; NRLESIKNSTE; RLESIKNSTEY; LESIKNSTEYA; ESIKNSTEYAI; SIKNSTEYAIE; IKNSTEYAIEN; KNSTEYAIENL; NSTEYAIENLK; STEYAIENLKA; TEYAIENLKAS; EYAIENLKASY; YAIENLKASYA; AIENLKASYAQ; IENLKASYAQI; ENLKASYAQIK; NLKASYAQIKD; LKASYAQIKDA; KASYAQIKDAT; ASYAQIKDATM; SYAQIKDATMT; YAQIKDATMTD; AQIKDATMTDE; QIKDATMTDEV; IKDATMTDEVV; KDATMTDEVVA; DATMTDEVVAA; ATMTDEVVAAT; TMTDEVVAATT; MTDEVVAATTN; TDEVVAATTNS; DEVVAATTNSI; EVVAATTNSIL; VVAATTNSILT; VAATTNSILTQ; AATTNSILTQS; ATTNSILTQSA; TTNSILTQSAM; TNSILTQSAMA; NSILTQSAMAM; SILTQSAMAMI; ILTQSAMAMIA; LTQSAMAMIAQ; TQSAMAMIAQA; QSAMAMIAQAN; SAMAMIAQANQ; AMAMIAQANQV; MAMIAQANQVP; AMIAQANQVPQ; MIAQANQVPQY; IAQANQVPQYV; AQANQVPQYVL; QANQVPQYVLS; ANQVPQYVLSL; NQVPQYVLSLL; QVPQYVLSLLR;
Seq 24	SEQ ID NO 25784-27861/ 8 mers: MKLQRSLF; KLQRSLFL; LQRSLFLI; QRSLFLII; RSLFLIIF; SLFLIIFF; LFLIIFFL; FLIIFFLT; LIIFFLTF; IIFFLTFL;

	IFFLTFLC; FFLTFLCC; FLTFLCCN; LTFLCCNN; TFLCCNNK; FLCCNNKE; LCCNNKER; CCNNKERK; CNNKERKE; NNKERKEG; NKERKEGV; KERKEGVS; ERKEGVSF; RKEGVSFK; KEGVSFKI; EGVSFKIS; GVSFKISL; VSFKISLG; SFKISLGA; FKISLGAE; KISLGAEP; ISLGAEPS; SLGAEPSS; LGAEPSSL; GAEPSSLD; AEPSSLDP; EPSSLDPQ; PSSLDPQL; SSLDPQLA; SLDPQLAE; LDPQLAED; DPQLAEDN; PQLAEDNV; QLAEDNVA; LAEDNVAS; AEDNVASK; EDNVASKM; DNVASKMI; NVASKMID; VASKMIDT; ASKMIDTM; SKMIDTMF; KMIDTMFR; MIDTMFRG; IDTMFRGI; DTMFRGIV; TMFRGIVT; MFRGIVTG; FRGIVTGD; RGIVTGDP; GIVTGDPN; IVTGDPNT; VTGDPNTG; TGDPNTGG; GDPNTGGN; DPNTGGNK; PNTGGNKP; NTGGNKPG; TGGNKPGL; GGNKPGLA; GNKPGLAK; NKPGLAKG; KPGLAKGW; PGLAKGWD; GLAKGWDI; LAKGWDIS; AKGWDISS; KGWDISSD; GWDISSDG; WDISSDGT; DISSDGTV; ISSDGTVY; SSDGTVYT; SDGTVYTF; DGTVYTFN; GTVYTFNL; TVYTFNLR; VYTFNLRE; YTFNLREK; TFNLREKI; FNLREKIT; NLREKITW; LREKITWS; REKITWSD; EKITWSDG; KITWSDGV; ITWSDGVA; TWSDGVAI; WSDGVAIT; SDGVAITA; DGVAITAE; GVAITAEG; VAITAEGI; AITAEGIR; ITAEGIRK; TAEGIRKS; AEGIRKSY; EGIRKSYL; GIRKSYLR; IRKSYLRI; RKSYLRIL; KSYLRILN; SYLRILNK; YLRILNKE; LRILNKET; RILNKETG; ILNKETGS; LNKETGSK; NKETGSKY; KETGSKYV; ETGSKYVE; TGSKYVEM; GSKYVEMV; SKYVEMVK; KYVEMVKS; YVEMVKSV; VEMVKSVI; EMVKSVIK; MVKSVIKN; VKSVIKNG; KSVIKNGQ; SVIKNGQK; VIKNGQKY; IKNGQKYF; KNGQKYFD; NGQKYFDG; GQKYFDGQ; QKYFDGQV; KYFDGQVT; YFDGQVTD; FDGQVTDS; DGQVTDSE; GQVTDSEL; QVTDSELG; VTDSELGI; TDSELGIR; DSELGIRA; SELGIRAI; ELGIRAID; LGIRAIDE; GIRAIDEK; IRAIDEKT; RAIDEKTL; AIDEKTLE; IDEKTLEI; DEKTLEIT; EKTLEITL; KTLEITLE; TLEITLES; LEITLESP; EITLESPK; ITLESPKP; TLESPKPY; LESPKPYF; ESPKPYFI; SPKPYFID; PKPYFIDM; KPYFIDML; PYFIDMLV; YFIDMLVH; FIDMLVHQ; IDMLVHQS; DMLVHQSF; MLVHQSFI; LVHQSFIP; VHQSFIPV; HQSFIPVP; QSFIPVPV; SFIPVPVH; FIPVPVHV; IPVPVHVT; PVPVHVTE; VPVHVTEK; PVHVTEKY; VHVTEKYG; HVTEKYGQ; VTEKYGQN; TEKYGQNW; EKYGQNWT; KYGQNWTS; YGQNWTSP; GQNWTSPE; QNWTSPEN; NWTSPENM; WTSPENMV; TSPENMVT; SPENMVTS; PENMVTSG; ENMVTSGP; NMVTSGPF; MVTSGPFK; VTSGPFKL; TSGPFKLK; SGPFKLKE; GPFKLKER; PFKLKERI; FKLKERIP; KLKERIPN; LKERIPNE; KERIPNEK; ERIPNEKY; RIPNEKYV; IPNEKYVF; PNEKYVFE; NEKYVFEK; EKYVFEKN; KYVFEKNN; YVFEKNNK; VFEKNNKY; FEKNNKYY; EKNNKYYD; KNNKYYDS; NNKYYDSN; NKYYDSNE; KYYDSNEV; YYDSNEVE; YDSNEVEL; DSNEVELE; SNEVELEE; NEVELEEI; EVELEEIT; VELEEITF; ELEEITFY; LEEITFYT; EEITFYTT; EITFYTTN; ITFYTTND; TFYTTNDS; FYTTNDSS; YTTNDSST; TTNDSSTA; TNDSSTAY; NDSSTAYK; DSSTAYKM; SSTAYKMY; STAYKMYE; TAYKMYEN; AYKMYENE; YKMYENEE; KMYENEEL; MYENEELD; YENEELDA; ENEELDAI; NEELDAIF; EELDAIFG; ELDAIFGS; LDAIFGSI; DAIFGSIP; AIFGSIPP; IFGSIPPD; FGSIPPDL; GSIPPDLI; SIPPDLIK; IPPDLIKN; PPDLIKNL;

	PDLIKNLK; DLIKNLKL; LIKNLKLR; IKNLKLRS; KNLKLRSD; NLKLRSDY; LKLRSDYY; KLRSDYYS; LRSDYYSS; RSDYYSSA; SDYYSSAV; DYYSSAVN; YYSSAVNA; YSSAVNAI; SSAVNAIY; SAVNAIYF; AVNAIYFY; VNAIYFYA; NAIYFYAF; AIYFYAFN; IYFYAFNT; YFYAFNTH; FYAFNTHI; YAFNTHIK; AFNTHIKP; FNTHIKPL; NTHIKPLD; THIKPLDN; HIKPLDNV; IKPLDNVK; KPLDNVKI; PLDNVKIR; LDNVKIRK; DNVKIRKA; NVKIRKAL; VKIRKALT; KIRKALTL; IRKALTLA; RKALTLAI; KALTLAID; ALTLAIDR; LTLAIDRE; TLAIDRET; LAIDRETL; AIDRETLT; IDRETLTY; DRETLTYK; RETLTYKV; ETLTYKVL; TLTYKVLD; LTYKVLDN; TYKVLDNG; YKVLDNGT; KVLDNGTT; VLDNGTTP; LDNGTTPT; DNGTTPTR; NGTTPTRR; GTTPTRRA; TTPTRRAT; TPTRRATP; PTRRATPN; TRRATPNF; RRATPNFS; RATPNFSS; ATPNFSSY; TPNFSSYS; PNFSSYSY; NFSSYSYA; FSSYSYAK; SSYSYAKS; SYSYAKSL; YSYAKSLE; SYAKSLEL; YAKSLELF; AKSLELFN; KSLELFNP; SLELFNPE; LELFNPEI; ELFNPEIA; LFNPEIAK; FNPEIAKT; NPEIAKTL; PEIAKTLL; EIAKTLLA; IAKTLLAE; AKTLLAEA; KTLLAEAG; TLLAEAGY; LLAEAGYP; LAEAGYPN; AEAGYPNG; EAGYPNGN; AGYPNGNG; GYPNGNGF; YPNGNGFP; PNGNGFPI; NGNGFPIL; GNGFPILK; NGFPILKL; GFPILKLK; FPILKLKY; PILKLKYN; ILKLKYNT; LKLKYNTN; KLKYNTNE; LKYNTNEA; KYNTNEAN; YNTNEANK; NTNEANKK; TNEANKKI; NEANKKIC; EANKKICE; ANKKICEF; NKKICEFI; KKICEFIQ; KICEFIQN; ICEFIQNQ; CEFIQNQW; EFIQNQWK; FIQNQWKK; IQNQWKKN; QNQWKKNL; NQWKKNLN; QWKKNLNI; WKKNLNID; KKNLNIDV; KNLNIDVE; NLNIDVEL; LNIDVELE; NIDVELEN; IDVELENE; DVELENEE; VELENEEW; ELENEEWT; LENEEWTT; ENEEWTTY; NEEWTTYL; EEWTTYLN; EWTTYLNT; WTTYLNTK; TTYLNTKA; TYLNTKAN; YLNTKANG; LNTKANGN; NTKANGNY; TKANGNYE; KANGNYEI; ANGNYEIA; NGNYEIAR; GNYEIARA; NYEIARAG; YEIARAGW; EIARAGWI; IARAGWIG; ARAGWIGD; RAGWIGDY; AGWIGDYA; GWIGDYAD; WIGDYADP; IGDYADPL; GDYADPLT; DYADPLTF; YADPLTFL; ADPLTFLS; DPLTFLSI; PLTFLSIF; LTFLSIFT; TFLSIFTQ; FLSIFTQG; LSIFTQGY; SIFTQGYT; IFTQGYTQ; FTQGYTQF; TQGYTQFS; QGYTQFSS; GYTQFSSH; YTQFSSHN; TQFSSHNY; QFSSHNYS; FSSHNYSN; SSHNYSNP; SHNYSNPE; HNYSNPEY; NYSNPEYN; YSNPEYNE; SNPEYNEL; NPEYNELI; PEYNELIK; EYNELIKK; YNELIKKS; NELIKKSD; ELIKKSDL; LIKKSDLE; IKKSDLEL; KKSDLELD; KSDLELDP; SDLELDPI; DLELDPIK; LELDPIKR; ELDPIKRQ; LDPIKRQD; DPIKRQDI; PIKRQDIL; IKRQDILR; KRQDILRQ; RQDILRQA; QDILRQAE; DILRQAEE; ILRQAEEI; LRQAEEII; RQAEEIII; QAEEIIIE; AEEIIIEK; EEIIIEKD; EIIIEKDF; IIIEKDFP; IIEKDFPI; IEKDFPIA; EKDFPIAP; KDFPIAPI; DFPIAPIY; FPIAPIYI; PIAPIYIY; IAPIYIYG; APIYIYGN; PIYIYGNS; IYIYGNSY; YIYGNSYL; IYGNSYLF; YGNSYLFR; GNSYLFRN; NSYLFRND; SYLFRNDK; YLFRNDKW; LFRNDKWT; FRNDKWTG; RNDKWTGW; NDKWTGWN; DKWTGWNT; KWTGWNTN; WTGWNTNI; TGWNTNIL; GWNTNILE; WNTNILER; NTNILERF; TNILERFD; NILERFDL; ILERFDLS; LERFDLSQ; ERFDLSQL; RFDLSQLK; FDLSQLKL; DLSQLKLK; LSQLKLKN;

SQLKLKNK;

9 mers:
MKLQRSLFL; KLQRSLFLI; LQRSLFLII; QRSLFLIIF; RSLFLIIFF;
SLFLIIFFL; LFLIIFFLT; FLIIFFLTF; LIIFFLTFL; IIFFLTFLC;
IFFLTFLCC; FFLTFLCCN; FLTFLCCNN; LTFLCCNNK; TFLCCNNKE;
FLCCNNKER; LCCNNKERK; CCNNKERKE; CNNKERKEG; NNKERKEGV;
NKERKEGVS; KERKEGVSF; ERKEGVSFK; RKEGVSFKI; KEGVSFKIS;
EGVSFKISL; GVSFKISLG; VSFKISLGA; SFKISLGAE; FKISLGAEP;
KISLGAEPS; ISLGAEPSS; SLGAEPSSL; LGAEPSSLD; GAEPSSLDP;
AEPSSLDPQ; EPSSLDPQL; PSSLDPQLA; SSLDPQLAE; SLDPQLAED;
LDPQLAEDN; DPQLAEDNV; PQLAEDNVA; QLAEDNVAS; LAEDNVASK;
AEDNVASKM; EDNVASKMI; DNVASKMID; NVASKMIDT; VASKMIDTM;
ASKMIDTMF; SKMIDTMFR; KMIDTMFRG; MIDTMFRGI; IDTMFRGIV;
DTMFRGIVT; TMFRGIVTG; MFRGIVTGD; FRGIVTGDP; RGIVTGDPN;
GIVTGDPNT; IVTGDPNTG; VTGDPNTGG; TGDPNTGGN; GDPNTGGNK;
DPNTGGNKP; PNTGGNKPG; NTGGNKPGL; TGGNKPGLA; GGNKPGLAK;
GNKPGLAKG; NKPGLAKGW; KPGLAKGWD; PGLAKGWDI; GLAKGWDIS;
LAKGWDISS; AKGWDISSD; KGWDISSDG; GWDISSDGT; WDISSDGTV;
DISSDGTVY; ISSDGTVYT; SSDGTVYTF; SDGTVYTFN; DGTVYTFNL;
GTVYTFNLR; TVYTFNLRE; VYTFNLREK; YTFNLREKI; TFNLREKIT;
FNLREKITW; NLREKITWS; LREKITWSD; REKITWSDG; EKITWSDGV;
KITWSDGVA; ITWSDGVAI; TWSDGVAIT; WSDGVAITA; SDGVAITAE;
DGVAITAEG; GVAITAEGI; VAITAEGIR; AITAEGIRK; ITAEGIRKS;
TAEGIRKSY; AEGIRKSYL; EGIRKSYLR; GIRKSYLRI; IRKSYLRIL;
RKSYLRILN; KSYLRILNK; SYLRILNKE; YLRILNKET; LRILNKETG;
RILNKETGS; ILNKETGSK; LNKETGSKY; NKETGSKYV; KETGSKYVE;
ETGSKYVEM; TGSKYVEMV; GSKYVEMVK; SKYVEMVKS; KYVEMVKSV;
YVEMVKSVI; VEMVKSVIK; EMVKSVIKN; MVKSVIKNG; VKSVIKNGQ;
KSVIKNGQK; SVIKNGQKY; VIKNGQKYF; IKNGQKYFD; KNGQKYFDG;
NGQKYFDGQ; GQKYFDGQV; QKYFDGQVT; KYFDGQVTD; YFDGQVTDS;
FDGQVTDSE; DGQVTDSEL; GQVTDSELG; QVTDSELGI; VTDSELGIR;
TDSELGIRA; DSELGIRAI; SELGIRAID; ELGIRAIDE; LGIRAIDEK;
GIRAIDEKT; IRAIDEKTL; RAIDEKTLE; AIDEKTLEI; IDEKTLEIT;
DEKTLEITL; EKTLEITLE; KTLEITLES; TLEITLESP; LEITLESPK;
EITLESPKP; ITLESPKPY; TLESPKPYF; LESPKPYFI; ESPKPYFID;
SPKPYFIDM; PKPYFIDML; KPYFIDMLV; PYFIDMLVH; YFIDMLVHQ;
FIDMLVHQS; IDMLVHQSF; DMLVHQSFI; MLVHQSFIP; LVHQSFIPV;
VHQSFIPVP; HQSFIPVPV; QSFIPVPVH; SFIPVPVHV; FIPVPVHVT;
IPVPVHVTE; PVPVHVTEK; VPVHVTEKY; PVHVTEKYG; VHVTEKYGQ;
HVTEKYGQN; VTEKYGQNW; TEKYGQNWT; EKYGQNWTS; KYGQNWTSP;
YGQNWTSPE; GQNWTSPEN; QNWTSPENM; NWTSPENMV; WTSPENMVT;
TSPENMVTS; SPENMVTSG; PENMVTSGP; ENMVTSGPF; NMVTSGPFK;
MVTSGPFKL; VTSGPFKLK; TSGPFKLKE; SGPFKLKER; GPFKLKERI;
PFKLKERIP; FKLKERIPN; KLKERIPNE; LKERIPNEK; KERIPNEKY;
ERIPNEKYV; RIPNEKYVF; IPNEKYVFE; PNEKYVFEK; NEKYVFEKN;
EKYVFEKNN; KYVFEKNNK; YVFEKNNKY; VFEKNNKYY; FEKNNKYYD;
EKNNKYYDS; KNNKYYDSN; NNKYYDSNE; NKYYDSNEV; KYYDSNEVE;
YYDSNEVEL; YDSNEVELE; DSNEVELEE; SNEVELEEI; NEVELEEIT;
EVELEEITF; VELEEITFY; ELEEITFYT; LEEITFYTT; EEITFYTTN;
EITFYTTND; ITFYTTNDS; TFYTTNDSS; FYTTNDSST; YTTNDSSTA;

	TTNDSSTAY; TNDSSTAYK; NDSSTAYKM; DSSTAYKMY; SSTAYKMYE; STAYKMYEN; TAYKMYENE; AYKMYENEE; YKMYENEEL; KMYENEELD; MYENEELDA; YENEELDAI; ENEELDAIF; NEELDAIFG; EELDAIFGS; ELDAIFGSI; LDAIFGSIP; DAIFGSIPP; AIFGSIPPD; IFGSIPPDL; FGSIPPDLI; GSIPPDLIK; SIPPDLIKN; IPPDLIKNL; PPDLIKNLK; PDLIKNLKL; DLIKNLKLR; LIKNLKLRS; IKNLKLRSD; KNLKLRSDY; NLKLRSDYY; LKLRSDYYS; KLRSDYYSS; LRSDYYSSA; RSDYYSSAV; SDYYSSAVN; DYYSSAVNA; YYSSAVNAI; YSSAVNAIY; SSAVNAIYF; SAVNAIYFY; AVNAIYFYA; VNAIYFYAF; NAIYFYAFN; AIYFYAFNT; IYFYAFNTH; YFYAFNTHI; FYAFNTHIK; YAFNTHIKP; AFNTHIKPL; FNTHIKPLD; NTHIKPLDN; THIKPLDNV; HIKPLDNVK; IKPLDNVKI; KPLDNVKIR; PLDNVKIRK; LDNVKIRKA; DNVKIRKAL; NVKIRKALT; VKIRKALTL; KIRKALTLA; IRKALTLAI; RKALTLAID; KALTLAIDR; ALTLAIDRE; LTLAIDRET; TLAIDRETL; LAIDRETLT; AIDRETLTY; IDRETLTYK; DRETLTYKV; RETLTYKVL; ETLTYKVLD; TLTYKVLDN; LTYKVLDNG; TYKVLDNGT; YKVLDNGTT; KVLDNGTTP; VLDNGTTPT; LDNGTTPTR; DNGTTPTRR; NGTTPTRRA; GTTPTRRAT; TTPTRRATP; TPTRRATPN; PTRRATPNF; TRRATPNFS; RRATPNFSS; RATPNFSSY; ATPNFSSYS; TPNFSSYSY; PNFSSYSYA; NFSSYSYAK; FSSYSYAKS; SSYSYAKSL; SYSYAKSLE; YSYAKSLEL; SYAKSLELF; YAKSLELFN; AKSLELFNP; KSLELFNPE; SLELFNPEI; LELFNPEIA; ELFNPEIAK; LFNPEIAKT; FNPEIAKTL; NPEIAKTLL; PEIAKTLLA; EIAKTLLAE; IAKTLLAEA; AKTLLAEAG; KTLLAEAGY; TLLAEAGYP; LLAEAGYPN; LAEAGYPNG; AEAGYPNGN; EAGYPNGNG; AGYPNGNGF; GYPNGNGFP; YPNGNGFPI; PNGNGFPIL; NGNGFPILK; GNGFPILKL; NGFPILKLK; GFPILKLKY; FPILKLKYN; PILKLKYNT; ILKLKYNTN; LKLKYNTNE; KLKYNTNEA; LKYNTNEAN; KYNTNEANK; YNTNEANKK; NTNEANKKI; TNEANKKIC; NEANKKICE; EANKKICEF; ANKKICEFI; NKKICEFIQ; KKICEFIQN; KICEFIQNQ; ICEFIQNQW; CEFIQNQWK; EFIQNQWKK; FIQNQWKKN; IQNQWKKNL; QNQWKKNLN; NQWKKNLNI; QWKKNLNID; WKKNLNIDV; KKNLNIDVE; KNLNIDVEL; NLNIDVELE; LNIDVELEN; NIDVELENE; IDVELENEE; DVELENEEW; VELENEEWT; ELENEEWTT; LENEEWTTY; ENEEWTTYL; NEEWTTYLN; EEWTTYLNT; EWTTYLNTK; WTTYLNTKA; TTYLNTKAN; TYLNTKANG; YLNTKANGN; LNTKANGNY; NTKANGNYE; TKANGNYEI; KANGNYEIA; ANGNYEIAR; NGNYEIARA; GNYEIARAG; NYEIARAGW; YEIARAGWI; EIARAGWIG; IARAGWIGD; ARAGWIGDY; RAGWIGDYA; AGWIGDYAD; GWIGDYADP; WIGDYADPL; IGDYADPLT; GDYADPLTF; DYADPLTFL; YADPLTFLS; ADPLTFLSI; DPLTFLSIF; PLTFLSIFT; LTFLSIFTQ; TFLSIFTQG; FLSIFTQGY; LSIFTQGYT; SIFTQGYTQ; IFTQGYTQF; FTQGYTQFS; TQGYTQFSS; QGYTQFSSH; GYTQFSSHN; YTQFSSHNY; TQFSSHNYS; QFSSHNYSN; FSSHNYSNP; SSHNYSNPE; SHNYSNPEY; HNYSNPEYN; NYSNPEYNE; YSNPEYNEL; SNPEYNELI; NPEYNELIK; PEYNELIKK; EYNELIKKS; YNELIKKSD; NELIKKSDL; ELIKKSDLE; LIKKSDLEL; IKKSDLELD; KKSDLELDP; KSDLELDPI; SDLELDPIK; DLELDPIKR; LELDPIKRQ; ELDPIKRQD; LDPIKRQDI; DPIKRQDIL; PIKRQDILR; IKRQDILRQ; KRQDILRQA; RQDILRQAE; QDILRQAEE; DILRQAEEI; ILRQAEEII; LRQAEEIII; RQAEEIIIE; QAEEIIIEK; AEEIIIEKD; EEIIIEKDF; EIIIEKDFP; IIIEKDFPI; IIEKDFPIA; IEKDFPIAP; EKDFPIAPI; KDFPIAPIY; DFPIAPIYI; FPIAPIYIY; PIAPIYIYG; IAPIYIYGN; APIYIYGNS; PIYIYGNSY; IYIYGNSYL; YIYGNSYLF; IYGNSYLFR;

	YGNSYLFRN; GNSYLFRND; NSYLFRNDK; SYLFRNDKW; YLFRNDKWT; LFRNDKWTG; FRNDKWTGW; RNDKWTGWN; NDKWTGWNT; DKWTGWNTN; KWTGWNTNI; WTGWNTNIL; TGWNTNILE; GWNTNILER; WNTNILERF; NTNILERFD; TNILERFDL; NILERFDLS; ILERFDLSQ; LERFDLSQL; ERFDLSQLK; RFDLSQLKL; FDLSQLKLK; DLSQLKLKN; LSQLKLKNK; 10 mers: MKLQRSLFLI; KLQRSLFLII; LQRSLFLIIF; QRSLFLIIFF; RSLFLIIFFL; SLFLIIFFLT; LFLIIFFLTF; FLIIFFLTFL; LIIFFLTFLC; IIFFLTFLCC; IFFLTFLCCN; FFLTFLCCNN; FLTFLCCNNK; LTFLCCNNKE; TFLCCNNKER; FLCCNNKERK; LCCNNKERKE; CCNNKERKEG; CNNKERKEGV; NNKERKEGVS; NKERKEGVSF; KERKEGVSFK; ERKEGVSFKI; RKEGVSFKIS; KEGVSFKISL; EGVSFKISLG; GVSFKISLGA; VSFKISLGAE; SFKISLGAEP; FKISLGAEPS; KISLGAEPSS; ISLGAEPSSL; SLGAEPSSLD; LGAEPSSLDP; GAEPSSLDPQ; AEPSSLDPQL; EPSSLDPQLA; PSSLDPQLAE; SSLDPQLAED; SLDPQLAEDN; LDPQLAEDNV; DPQLAEDNVA; PQLAEDNVAS; QLAEDNVASK; LAEDNVASKM; AEDNVASKMI; EDNVASKMID; DNVASKMIDT; NVASKMIDTM; VASKMIDTMF; ASKMIDTMFR; SKMIDTMFRG; KMIDTMFRGI; MIDTMFRGIV; IDTMFRGIVT; DTMFRGIVTG; TMFRGIVTGD; MFRGIVTGDP; FRGIVTGDPN; RGIVTGDPNT; GIVTGDPNTG; IVTGDPNTGG; VTGDPNTGGN; TGDPNTGGNK; GDPNTGGNKP; DPNTGGNKPG; PNTGGNKPGL; NTGGNKPGLA; TGGNKPGLAK; GGNKPGLAKG; GNKPGLAKGW; NKPGLAKGWD; KPGLAKGWDI; PGLAKGWDIS; GLAKGWDISS; LAKGWDISSD; AKGWDISSDG; KGWDISSDGT; GWDISSDGTV; WDISSDGTVY; DISSDGTVYT; ISSDGTVYTF; SSDGTVYTFN; SDGTVYTFNL; DGTVYTFNLR; GTVYTFNLRE; TVYTFNLREK; VYTFNLREKI; YTFNLREKIT; TFNLREKITW; FNLREKITWS; NLREKITWSD; LREKITWSDG; REKITWSDGV; EKITWSDGVA; KITWSDGVAI; ITWSDGVAIT; TWSDGVAITA; WSDGVAITAE; SDGVAITAEG; DGVAITAEGI; GVAITAEGIR; VAITAEGIRK; AITAEGIRKS; ITAEGIRKSY; TAEGIRKSYL; AEGIRKSYLR; EGIRKSYLRI; GIRKSYLRIL; IRKSYLRILN; RKSYLRILNK; KSYLRILNKE; SYLRILNKET; YLRILNKETG; LRILNKETGS; RILNKETGSK; ILNKETGSKY; LNKETGSKYV; NKETGSKYVE; KETGSKYVEM; ETGSKYVEMV; TGSKYVEMVK; GSKYVEMVKS; SKYVEMVKSV; KYVEMVKSVI; YVEMVKSVIK; VEMVKSVIKN; EMVKSVIKNG; MVKSVIKNGQ; VKSVIKNGQK; KSVIKNGQKY; SVIKNGQKYF; VIKNGQKYFD; IKNGQKYFDG; KNGQKYFDGQ; NGQKYFDGQV; GQKYFDGQVT; QKYFDGQVTD; KYFDGQVTDS; YFDGQVTDSE; FDGQVTDSEL; DGQVTDSELG; GQVTDSELGI; QVTDSELGIR; VTDSELGIRA; TDSELGIRAI; DSELGIRAID; SELGIRAIDE; ELGIRAIDEK; LGIRAIDEKT; GIRAIDEKTL; IRAIDEKTLE; RAIDEKTLEI; AIDEKTLEIT; IDEKTLEITL; DEKTLEITLE; EKTLEITLES; KTLEITLESP; TLEITLESPK; LEITLESPKP; EITLESPKPY; ITLESPKPYF; TLESPKPYFI; LESPKPYFID; ESPKPYFIDM; SPKPYFIDML; PKPYFIDMLV; KPYFIDMLVH; PYFIDMLVHQ; YFIDMLVHQS; FIDMLVHQSF; IDMLVHQSFI; DMLVHQSFIP; MLVHQSFIPV; LVHQSFIPVP; VHQSFIPVPV;

	HQSFIPVPVH; QSFIPVPVHV; SFIPVPVHVT; FIPVPVHVTE; IPVPVHVTEK; PVPVHVTEKY; VPVHVTEKYG; PVHVTEKYGQ; VHVTEKYGQN; HVTEKYGQNW; VTEKYGQNWT; TEKYGQNWTS; EKYGQNWTSP; KYGQNWTSPE; YGQNWTSPEN; GQNWTSPENM; QNWTSPENMV; NWTSPENMVT; WTSPENMVTS; TSPENMVTSG; SPENMVTSGP; PENMVTSGPF; ENMVTSGPFK; NMVTSGPFKL; MVTSGPFKLK; VTSGPFKLKE; TSGPFKLKER; SGPFKLKERI; GPFKLKERIP; PFKLKERIPN; FKLKERIPNE; KLKERIPNEK; LKERIPNEKY; KERIPNEKYV; ERIPNEKYVF; RIPNEKYVFE; IPNEKYVFEK; PNEKYVFEKN; NEKYVFEKNN; EKYVFEKNNK; KYVFEKNNKY; YVFEKNNKYY; VFEKNNKYYD; FEKNNKYYDS; EKNNKYYDSN; KNNKYYDSNE; NNKYYDSNEV; NKYYDSNEVE; KYYDSNEVEL; YYDSNEVELE; YDSNEVELEE; DSNEVELEEI; SNEVELEEIT; NEVELEEITF; EVELEEITFY; VELEEITFYT; ELEEITFYTT; LEEITFYTTN; EEITFYTTND; EITFYTTNDS; ITFYTTNDSS; TFYTTNDSST; FYTTNDSSTA; YTTNDSSTAY; TTNDSSTAYK; TNDSSTAYKM; NDSSTAYKMY; DSSTAYKMYE; SSTAYKMYEN; STAYKMYENE; TAYKMYENEE; AYKMYENEEL; YKMYENEELD; KMYENEELDA; MYENEELDAI; YENEELDAIF; ENEELDAIFG; NEELDAIFGS; EELDAIFGSI; ELDAIFGSIP; LDAIFGSIPP; DAIFGSIPPD; AIFGSIPPDL; IFGSIPPDLI; FGSIPPDLIK; GSIPPDLIKN; SIPPDLIKNL; IPPDLIKNLK; PPDLIKNLKL; PDLIKNLKLR; DLIKNLKLRS; LIKNLKLRSD; IKNLKLRSDY; KNLKLRSDYY; NLKLRSDYYS; LKLRSDYYSS; KLRSDYYSSA; LRSDYYSSAV; RSDYYSSAVN; SDYYSSAVNA; DYYSSAVNAI; YYSSAVNAIY; YSSAVNAIYF; SSAVNAIYFY; SAVNAIYFYA; AVNAIYFYAF; VNAIYFYAFN; NAIYFYAFNT; AIYFYAFNTH; IYFYAFNTHI; YFYAFNTHIK; FYAFNTHIKP; YAFNTHIKPL; AFNTHIKPLD; FNTHIKPLDN; NTHIKPLDNV; THIKPLDNVK; HIKPLDNVKI; IKPLDNVKIR; KPLDNVKIRK; PLDNVKIRKA; LDNVKIRKAL; DNVKIRKALT; NVKIRKALTL; VKIRKALTLA; KIRKALTLAI; IRKALTLAID; RKALTLAIDR; KALTLAIDRE; ALTLAIDRET; LTLAIDRETL; TLAIDRETLT; LAIDRETLTY; AIDRETLTYK; IDRETLTYKV; DRETLTYKVL; RETLTYKVLD; ETLTYKVLDN; TLTYKVLDNG; LTYKVLDNGT; TYKVLDNGTT; YKVLDNGTTP; KVLDNGTTPT; VLDNGTTPTR; LDNGTTPTRR; DNGTTPTRRA; NGTTPTRRAT; GTTPTRRATP; TTPTRRATPN; TPTRRATPNF; PTRRATPNFS; TRRATPNFSS; RRATPNFSSY; RATPNFSSYS; ATPNFSSYSY; TPNFSSYSYA; PNFSSYSYAK; NFSSYSYAKS; FSSYSYAKSL; SSYSYAKSLE; SYSYAKSLEL; YSYAKSLELF; SYAKSLELFN; YAKSLELFNP; AKSLELFNPE; KSLELFNPEI; SLELFNPEIA; LELFNPEIAK; ELFNPEIAKT; LFNPEIAKTL; FNPEIAKTLL; NPEIAKTLLA; PEIAKTLLAE; EIAKTLLAEA; IAKTLLAEAG; AKTLLAEAGY; KTLLAEAGYP; TLLAEAGYPN; LLAEAGYPNG; LAEAGYPNGN; AEAGYPNGNG; EAGYPNGNGF; AGYPNGNGFP; GYPNGNGFPI; YPNGNGFPIL; PNGNGFPILK; NGNGFPILKL; GNGFPILKLK; NGFPILKLKY; GFPILKLKYN; FPILKLKYNT; PILKLKYNTN; ILKLKYNTNE; LKLKYNTNEA; KLKYNTNEAN; LKYNTNEANK; KYNTNEANKK; YNTNEANKKI; NTNEANKKIC; TNEANKKICE; NEANKKICEF; EANKKICEFI; ANKKICEFIQ; NKKICEFIQN;

KKICEFIQNQ; KICEFIQNQW; ICEFIQNQWK; CEFIQNQWKK;
EFIQNQWKKN; FIQNQWKKNL; IQNQWKKNLN; QNQWKKNLNI;
NQWKKNLNID; QWKKNLNIDV; WKKNLNIDVE; KKNLNIDVEL;
KNLNIDVELE; NLNIDVELEN; LNIDVELENE; NIDVELENEE;
IDVELENEEW; DVELENEEWT; VELENEEWTT; ELENEEWTTY;
LENEEWTTYL; ENEEWTTYLN; NEEWTTYLNT; EEWTTYLNTK;
EWTTYLNTKA; WTTYLNTKAN; TTYLNTKANG; TYLNTKANGN;
YLNTKANGNY; LNTKANGNYE; NTKANGNYEI; TKANGNYEIA;
KANGNYEIAR; ANGNYEIARA; NGNYEIARAG; GNYEIARAGW;
NYEIARAGWI; YEIARAGWIG; EIARAGWIGD; IARAGWIGDY;
ARAGWIGDYA; RAGWIGDYAD; AGWIGDYADP; GWIGDYADPL;
WIGDYADPLT; IGDYADPLTF; GDYADPLTFL; DYADPLTFLS;
YADPLTFLSI; ADPLTFLSIF; DPLTFLSIFT; PLTFLSIFTQ;
LTFLSIFTQG; TFLSIFTQGY; FLSIFTQGYT; LSIFTQGYTQ;
SIFTQGYTQF; IFTQGYTQFS; FTQGYTQFSS; TQGYTQFSSH;
QGYTQFSSHN; GYTQFSSHNY; YTQFSSHNYS; TQFSSHNYSN;
QFSSHNYSNP; FSSHNYSNPE; SSHNYSNPEY; SHNYSNPEYN;
HNYSNPEYNE; NYSNPEYNEL; YSNPEYNELI; SNPEYNELIK;
NPEYNELIKK; PEYNELIKKS; EYNELIKKSD; YNELIKKSDL;
NELIKKSDLE; ELIKKSDLEL; LIKKSDLELD; IKKSDLELDP;
KKSDLELDPI; KSDLELDPIK; SDLELDPIKR; DLELDPIKRQ;
LELDPIKRQD; ELDPIKRQDI; LDPIKRQDIL; DPIKRQDILR;
PIKRQDILRQ; IKRQDILRQA; KRQDILRQAE; RQDILRQAEE;
QDILRQAEEI; DILRQAEEII; ILRQAEEIII; LRQAEEIIIE;
RQAEEIIIEK; QAEEIIIEKD; AEEIIIEKDF; EEIIIEKDFP;
EIIIEKDFPI; IIIEKDFPIA; IIEKDFPIAP; IEKDFPIAPI;
EKDFPIAPIY; KDFPIAPIYI; DFPIAPIYIY; FPIAPIYIYG;
PIAPIYIYGN; IAPIYIYGNS; APIYIYGNSY; PIYIYGNSYL;
IYIYGNSYLF; YIYGNSYLFR; IYGNSYLFRN; YGNSYLFRND;
GNSYLFRNDK; NSYLFRNDKW; SYLFRNDKWT; YLFRNDKWTG;
LFRNDKWTGW; FRNDKWTGWN; RNDKWTGWNT; NDKWTGWNTN;
DKWTGWNTNI; KWTGWNTNIL; WTGWNTNILE; TGWNTNILER;
GWNTNILERF; WNTNILERFD; NTNILERFDL; TNILERFDLS;
NILERFDLSQ; ILERFDLSQL; LERFDLSQLK; ERFDLSQLKL;
RFDLSQLKLK; FDLSQLKLKN; DLSQLKLKNK;

11 mers:
MKLQRSLFLII; KLQRSLFLIIF; LQRSLFLIIFF; QRSLFLIIFFL;
RSLFLIIFFLT; SLFLIIFFLTF; LFLIIFFLTFL; FLIIFFLTFLC;
LIIFFLTFLCC; IIFFLTFLCCN; IFFLTFLCCNN; FFLTFLCCNNK;
FLTFLCCNNKE; LTFLCCNNKER; TFLCCNNKERK; FLCCNNKERKE;
LCCNNKERKEG; CCNNKERKEGV; CNNKERKEGVS; NNKERKEGVSF;
NKERKEGVSFK; KERKEGVSFKI; ERKEGVSFKIS; RKEGVSFKISL;
KEGVSFKISLG; EGVSFKISLGA; GVSFKISLGAE; VSFKISLGAEP;
SFKISLGAEPS; FKISLGAEPSS; KISLGAEPSSL; ISLGAEPSSLD;
SLGAEPSSLDP; LGAEPSSLDPQ; GAEPSSLDPQL; AEPSSLDPQLA;
EPSSLDPQLAE; PSSLDPQLAED; SSLDPQLAEDN; SLDPQLAEDNV;
LDPQLAEDNVA; DPQLAEDNVAS; PQLAEDNVASK; QLAEDNVASKM;
LAEDNVASKMI; AEDNVASKMID; EDNVASKMIDT; DNVASKMIDTM;
NVASKMIDTMF; VASKMIDTMFR; ASKMIDTMFRG; SKMIDTMFRGI;
KMIDTMFRGIV; MIDTMFRGIVT; IDTMFRGIVTG; DTMFRGIVTGD;

	TMFRGIVTGDP; MFRGIVTGDPN; FRGIVTGDPNT; RGIVTGDPNTG; GIVTGDPNTGG; IVTGDPNTGGN; VTGDPNTGGNK; TGDPNTGGNKP; GDPNTGGNKPG; DPNTGGNKPGL; PNTGGNKPGLA; NTGGNKPGLAK; TGGNKPGLAKG; GGNKPGLAKGW; GNKPGLAKGWD; NKPGLAKGWDI; KPGLAKGWDIS; PGLAKGWDISS; GLAKGWDISSD; LAKGWDISSDG; AKGWDISSDGT; KGWDISSDGTV; GWDISSDGTVY; WDISSDGTVYT; DISSDGTVYTF; ISSDGTVYTFN; SSDGTVYTFNL; SDGTVYTFNLR; DGTVYTFNLRE; GTVYTFNLREK; TVYTFNLREKI; VYTFNLREKIT; YTFNLREKITW; TFNLREKITWS; FNLREKITWSD; NLREKITWSDG; LREKITWSDGV; REKITWSDGVA; EKITWSDGVAI; KITWSDGVAIT; ITWSDGVAITA; TWSDGVAITAE; WSDGVAITAEG; SDGVAITAEGI; DGVAITAEGIR; GVAITAEGIRK; VAITAEGIRKS; AITAEGIRKSY; ITAEGIRKSYL; TAEGIRKSYLR; AEGIRKSYLRI; EGIRKSYLRIL; GIRKSYLRILN; IRKSYLRILNK; RKSYLRILNKE; KSYLRILNKET; SYLRILNKETG; YLRILNKETGS; LRILNKETGSK; RILNKETGSKY; ILNKETGSKYV; LNKETGSKYVE; NKETGSKYVEM; KETGSKYVEMV; ETGSKYVEMVK; TGSKYVEMVKS; GSKYVEMVKSV; SKYVEMVKSVI; KYVEMVKSVIK; YVEMVKSVIKN; VEMVKSVIKNG; EMVKSVIKNGQ; MVKSVIKNGQK; VKSVIKNGQKY; KSVIKNGQKYF; SVIKNGQKYFD; VIKNGQKYFDG; IKNGQKYFDGQ; KNGQKYFDGQV; NGQKYFDGQVT; GQKYFDGQVTD; QKYFDGQVTDS; KYFDGQVTDSE; YFDGQVTDSEL; FDGQVTDSELG; DGQVTDSELGI; GQVTDSELGIR; QVTDSELGIRA; VTDSELGIRAI; TDSELGIRAID; DSELGIRAIDE; SELGIRAIDEK; ELGIRAIDEKT; LGIRAIDEKTL; GIRAIDEKTLE; IRAIDEKTLEI; RAIDEKTLEIT; AIDEKTLEITL; IDEKTLEITLE; DEKTLEITLES; EKTLEITLESP; KTLEITLESPK; TLEITLESPKP; LEITLESPKPY; EITLESPKPYF; ITLESPKPYFI; TLESPKPYFID; LESPKPYFIDM; ESPKPYFIDML; SPKPYFIDMLV; PKPYFIDMLVH; KPYFIDMLVHQ; PYFIDMLVHQS; YFIDMLVHQSF; FIDMLVHQSFI; IDMLVHQSFIP; DMLVHQSFIPV; MLVHQSFIPVP; LVHQSFIPVPV; VHQSFIPVPVH; HQSFIPVPVHV; QSFIPVPVHVT; SFIPVPVHVTE; FIPVPVHVTEK; IPVPVHVTEKY; PVPVHVTEKYG; VPVHVTEKYGQ; PVHVTEKYGQN; VHVTEKYGQNW; HVTEKYGQNWT; VTEKYGQNWTS; TEKYGQNWTSP; EKYGQNWTSPE; KYGQNWTSPEN; YGQNWTSPENM; GQNWTSPENMV; QNWTSPENMVT; NWTSPENMVTS; WTSPENMVTSG; TSPENMVTSGP; SPENMVTSGPF; PENMVTSGPFK; ENMVTSGPFKL; NMVTSGPFKLK; MVTSGPFKLKE; VTSGPFKLKER; TSGPFKLKERI; SGPFKLKERIP; GPFKLKERIPN; PFKLKERIPNE; FKLKERIPNEK; KLKERIPNEKY; LKERIPNEKYV; KERIPNEKYVF; ERIPNEKYVFE; RIPNEKYVFEK; IPNEKYVFEKN; PNEKYVFEKNN; NEKYVFEKNNK; EKYVFEKNNKY; KYVFEKNNKYY; YVFEKNNKYYD; VFEKNNKYYDS; FEKNNKYYDSN; EKNNKYYDSNE; KNNKYYDSNEV; NNKYYDSNEVE; NKYYDSNEVEL; KYYDSNEVELE; YYDSNEVELEE; YDSNEVELEEI; DSNEVELEEIT; SNEVELEEITF; NEVELEEITFY; EVELEEITFYT; VELEEITFYTT; ELEEITFYTTN; LEEITFYTTND; EEITFYTTNDS; EITFYTTNDSS; ITFYTTNDSST; TFYTTNDSSTA; FYTTNDSSTAY; YTTNDSSTAYK; TTNDSSTAYKM; TNDSSTAYKMY; NDSSTAYKMYE; DSSTAYKMYEN; SSTAYKMYENE; STAYKMYENEE; TAYKMYENEEL; AYKMYENEELD; YKMYENEELDA; KMYENEELDAI; MYENEELDAIF; YENEELDAIFG; ENEELDAIFGS; NEELDAIFGSI; EELDAIFGSIP; ELDAIFGSIPP; LDAIFGSIPPD; DAIFGSIPPDL; AIFGSIPPDLI; IFGSIPPDLIK;

	FGSIPPDLIKN; GSIPPDLIKNL; SIPPDLIKNLK; IPPDLIKNLKL; PPDLIKNLKLR; PDLIKNLKLRS; DLIKNLKLRSD; LIKNLKLRSDY; IKNLKLRSDYY; KNLKLRSDYYS; NLKLRSDYYSS; LKLRSDYYSSA; KLRSDYYSSAV; LRSDYYSSAVN; RSDYYSSAVNA; SDYYSSAVNAI; DYYSSAVNAIY; YYSSAVNAIYF; YSSAVNAIYFY; SSAVNAIYFYA; SAVNAIYFYAF; AVNAIYFYAFN; VNAIYFYAFNT; NAIYFYAFNTH; AIYFYAFNTHI; IYFYAFNTHIK; YFYAFNTHIKP; FYAFNTHIKPL; YAFNTHIKPLD; AFNTHIKPLDN; FNTHIKPLDNV; NTHIKPLDNVK; THIKPLDNVKI; HIKPLDNVKIR; IKPLDNVKIRK; KPLDNVKIRKA; PLDNVKIRKAL; LDNVKIRKALT; DNVKIRKALTL; NVKIRKALTLA; VKIRKALTLAI; KIRKALTLAID; IRKALTLAIDR; RKALTLAIDRE; KALTLAIDRET; ALTLAIDRETL; LTLAIDRETLT; TLAIDRETLTY; LAIDRETLTYK; AIDRETLTYKV; IDRETLTYKVL; DRETLTYKVLD; RETLTYKVLDN; ETLTYKVLDNG; TLTYKVLDNGT; LTYKVLDNGTT; TYKVLDNGTTP; YKVLDNGTTPT; KVLDNGTTPTR; VLDNGTTPTRR; LDNGTTPTRRA; DNGTTPTRRAT; NGTTPTRRATP; GTTPTRRATPN; TTPTRRATPNF; TPTRRATPNFS; PTRRATPNFSS; TRRATPNFSSY; RRATPNFSSYS; RATPNFSSYSY; ATPNFSSYSYA; TPNFSSYSYAK; PNFSSYSYAKS; NFSSYSYAKSL; FSSYSYAKSLE; SSYSYAKSLEL; SYSYAKSLELF; YSYAKSLELFN; SYAKSLELFNP; YAKSLELFNPE; AKSLELFNPEI; KSLELFNPEIA; SLELFNPEIAK; LELFNPEIAKT; ELFNPEIAKTL; LFNPEIAKTLL; FNPEIAKTLLA; NPEIAKTLLAE; PEIAKTLLAEA; EIAKTLLAEAG; IAKTLLAEAGY; AKTLLAEAGYP; KTLLAEAGYPN; TLLAEAGYPNG; LLAEAGYPNGN; LAEAGYPNGNG; AEAGYPNGNGF; EAGYPNGNGFP; AGYPNGNGFPI; GYPNGNGFPIL; YPNGNGFPILK; PNGNGFPILKL; NGNGFPILKLK; GNGFPILKLKY; NGFPILKLKYN; GFPILKLKYNT; FPILKLKYNTN; PILKLKYNTNE; ILKLKYNTNEA; LKLKYNTNEAN; KLKYNTNEANK; LKYNTNEANKK; KYNTNEANKKI; YNTNEANKKIC; NTNEANKKICE; TNEANKKICEF; NEANKKICEFI; EANKKICEFIQ; ANKKICEFIQN; NKKICEFIQNQ; KKICEFIQNQW; KICEFIQNQWK; ICEFIQNQWKK; CEFIQNQWKKN; EFIQNQWKKNL; FIQNQWKKNLN; IQNQWKKNLNI; QNQWKKNLNID; NQWKKNLNIDV; QWKKNLNIDVE; WKKNLNIDVEL; KKNLNIDVELE; KNLNIDVELEN; NLNIDVELENE; LNIDVELENEE; NIDVELENEEW; IDVELENEEWT; DVELENEEWTT; VELENEEWTTY; ELENEEWTTYL; LENEEWTTYLN; ENEEWTTYLNT; NEEWTTYLNTK; EEWTTYLNTKA; EWTTYLNTKAN; WTTYLNTKANG; TTYLNTKANGN; TYLNTKANGNY; YLNTKANGNYE; LNTKANGNYEI; NTKANGNYEIA; TKANGNYEIAR; KANGNYEIARA; ANGNYEIARAG; NGNYEIARAGW; GNYEIARAGWI; NYEIARAGWIG; YEIARAGWIGD; EIARAGWIGDY; IARAGWIGDYA; ARAGWIGDYAD; RAGWIGDYADP; AGWIGDYADPL; GWIGDYADPLT; WIGDYADPLTF; IGDYADPLTFL; GDYADPLTFLS; DYADPLTFLSI; YADPLTFLSIF; ADPLTFLSIFT; DPLTFLSIFTQ; PLTFLSIFTQG; LTFLSIFTQGY; TFLSIFTQGYT; FLSIFTQGYTQ; LSIFTQGYTQF; SIFTQGYTQFS; IFTQGYTQFSS; FTQGYTQFSSH; TQGYTQFSSHN; QGYTQFSSHNY; GYTQFSSHNYS; YTQFSSHNYSN; TQFSSHNYSNP; QFSSHNYSNPE; FSSHNYSNPEY; SSHNYSNPEYN; SHNYSNPEYNE; HNYSNPEYNEL; NYSNPEYNELI; YSNPEYNELIK; SNPEYNELIKK; NPEYNELIKKS; PEYNELIKKSD; EYNELIKKSDL; YNELIKKSDLE; NELIKKSDLEL; ELIKKSDLELD; LIKKSDLELDP; IKKSDLELDPI; KKSDLELDPIK; KSDLELDPIKR; SDLELDPIKRQ; DLELDPIKRQD;

	LELDPIKRQDI; ELDPIKRQDIL; LDPIKRQDILR; DPIKRQDILRQ; PIKRQDILRQA; IKRQDILRQAE; KRQDILRQAEE; RQDILRQAEEI; QDILRQAEEII; DILRQAEEIII; ILRQAEEIIIE; LRQAEEIIIEK; RQAEEIIIEKD; QAEEIIIEKDF; AEEIIIEKDFP; EEIIIEKDFPI; EIIIEKDFPIA; IIIEKDFPIAP; IIEKDFPIAPI; IEKDFPIAPIY; EKDFPIAPIYI; KDFPIAPIYIY; DFPIAPIYIYG; FPIAPIYIYGN; PIAPIYIYGNS; IAPIYIYGNSY; APIYIYGNSYL; PIYIYGNSYLF; IYIYGNSYLFR; YIYGNSYLFRN; IYGNSYLFRND; YGNSYLFRNDK; GNSYLFRNDKW; NSYLFRNDKWT; SYLFRNDKWTG; YLFRNDKWTGW; LFRNDKWTGWN; FRNDKWTGWNT; RNDKWTGWNTN; NDKWTGWNTNI; DKWTGWNTNIL; KWTGWNTNILE; WTGWNTNILER; TGWNTNILERF; GWNTNILERFD; WNTNILERFDL; NTNILERFDLS; TNILERFDLSQ; NILERFDLSQL; ILERFDLSQLK; LERFDLSQLKL; ERFDLSQLKLK; RFDLSQLKLKN; FDLSQLKLKNK;
Seq 25	SEQ ID NO 27862-28855/ 8 mers: MTKIFSNL; TKIFSNLI; KIFSNLII; IFSNLIIN; FSNLIING; SNLIINGL; NLIINGLL; LIINGLLF; IINGLLFG; INGLLFGF; NGLLFGFV; GLLFGFVS; LLFGFVSL; LFGFVSLN; FGFVSLNV; GFVSLNVF; FVSLNVFA; VSLNVFAD; SLNVFADS; LNVFADSN; NVFADSNN; VFADSNNA; FADSNNAN; ADSNNANI; DSNNANIL; SNNANILK; NNANILKP; NANILKPQ; ANILKPQS; NILKPQSN; ILKPQSNV; LKPQSNVL; KPQSNVLE; PQSNVLEH; QSNVLEHS; SNVLEHSD; NVLEHSDQ; VLEHSDQK; LEHSDQKD; EHSDQKDN; HSDQKDNK; SDQKDNKK; DQKDNKKL; QKDNKKLD; KDNKKLDQ; DNKKLDQK; NKKLDQKD; KKLDQKDQ; KLDQKDQV; LDQKDQVN; DQKDQVNQ; QKDQVNQA; KDQVNQAL; DQVNQALD; QVNQALDT; VNQALDTI; NQALDTIN; QALDTINK; ALDTINKV; LDTINKVT; DTINKVTE; TINKVTED; INKVTEDV; NKVTEDVS; KVTEDVSS; VTEDVSSK; TEDVSSKL; EDVSSKLE; DVSSKLEG; VSSKLEGV; SSKLEGVR; SKLEGVRE; KLEGVRES; LEGVRESS; EGVRESSL; GVRESSLE; VRESSLEL; RESSLELV; ESSLELVE; SSLELVES; SLELVESN; LELVESND; ELVESNDA; LVESNDAG; VESNDAGV; ESNDAGVV; SNDAGVVK; NDAGVVKK; DAGVVKKF; AGVVKKFV; GVVKKFVG; VVKKFVGS; VKKFVGSM; KKFVGSMS; KFVGSMSL; FVGSMSLM; VGSMSLMS; GSMSLMSD; SMSLMSDV; MSLMSDVA; SLMSDVAK; LMSDVAKG; MSDVAKGT; SDVAKGTV; DVAKGTVV; VAKGTVVA; AKGTVVAS; KGTVVASQ; GTVVASQE; TVVASQEA; VVASQEAT; VASQEATI; ASQEATIV; SQEATIVA; QEATIVAK; EATIVAKC; ATIVAKCS; TIVAKCSG; IVAKCSGM; VAKCSGMV; AKCSGMVA; KCSGMVAE; CSGMVAEG; SGMVAEGA; GMVAEGAN; MVAEGANK; VAEGANKV; AEGANKVV; EGANKVVE; GANKVVEM; ANKVVEMS; NKVVEMSK; KVVEMSKK; VVEMSKKA; VEMSKKAV; EMSKKAVQ; MSKKAVQE; SKKAVQET; KKAVQETQ; KAVQETQK; AVQETQKA; VQETQKAV; QETQKAVS; ETQKAVSV; TQKAVSVA; QKAVSVAG; KAVSVAGE; AVSVAGEA; VSVAGEAT; SVAGEATF; VAGEATFL; AGEATFLI; GEATFLIE; EATFLIEK; ATFLIEKQ; TFLIEKQI; FLIEKQIM; LIEKQIML; IEKQIMLN; EKQIMLNK; KQIMLNKS; QIMLNKSP; IMLNKSPN; MLNKSPNN; LNKSPNNK; NKSPNNKE; KSPNNKEL; SPNNKELE; PNNKELEL; NNKELELT;

NKELELTK; KELELTKE; ELELTKEE; LELTKEEF; ELTKEEFA;
LTKEEFAK; TKEEFAKV; KEEFAKVD; EEFAKVDE; EFAKVDEV;
FAKVDEVK; AKVDEVKE; KVDEVKET; VDEVKETL; DEVKETLM;
EVKETLMA; VKETLMAS; KETLMASE; ETLMASER; TLMASERA;
LMASERAL; MASERALD; ASERALDE; SERALDET; ERALDETV;
RALDETVQ; ALDETVQE; LDETVQEA; DETVQEAQ; ETVQEAQK;
TVQEAQKV; VQEAQKVL; QEAQKVLN; EAQKVLNM; AQKVLNMV;
QKVLNMVN; KVLNMVNG; VLNMVNGL; LNMVNGLN; NMVNGLNP;
MVNGLNPS; VNGLNPSN; NGLNPSNK; GLNPSNKD; LNPSNKDQ;
NPSNKDQV; PSNKDQVL; SNKDQVLA; NKDQVLAK; KDQVLAKK;
DQVLAKKD; QVLAKKDV; VLAKKDVR; LAKKDVRK; AKKDVRKA;
KKDVRKAI; KDVRKAIS; DVRKAISN; VRKAISNV; RKAISNVV;
KAISNVVK; AISNVVKV; ISNVVKVA; SNVVKVAQ; NVVKVAQG;
VVKVAQGA; VKVAQGAR; KVAQGARD; VAQGARDL; AQGARDLT;
QGARDLTK; GARDLTKV; ARDLTKVM; RDLTKVMA; DLTKVMAI;
LTKVMAIS; TKVMAISL; KVMAISLY; VMAISLYM; MAISLYMR;

9 mers:
MTKIFSNLI; TKIFSNLII; KIFSNLIIN; IFSNLIING; FSNLIINGL;
SNLIINGLL; NLIINGLLF; LIINGLLFG; IINGLLFGF; INGLLFGFV;
NGLLFGFVS; GLLFGFVSL; LLFGFVSLN; LFGFVSLNV; FGFVSLNVF;
GFVSLNVFA; FVSLNVFAD; VSLNVFADS; SLNVFADSN; LNVFADSNN;
NVFADSNNA; VFADSNNAN; FADSNNANI; ADSNNANIL; DSNNANILK;
SNNANILKP; NNANILKPQ; NANILKPQS; ANILKPQSN; NILKPQSNV;
ILKPQSNVL; LKPQSNVLE; KPQSNVLEH; PQSNVLEHS; QSNVLEHSD;
SNVLEHSDQ; NVLEHSDQK; VLEHSDQKD; LEHSDQKDN; EHSDQKDNK;
HSDQKDNKK; SDQKDNKKL; DQKDNKKLD; QKDNKKLDQ; KDNKKLDQK;
DNKKLDQKD; NKKLDQKDQ; KKLDQKDQV; KLDQKDQVN; LDQKDQVNQ;
DQKDQVNQA; QKDQVNQAL; KDQVNQALD; DQVNQALDT; QVNQALDTI;
VNQALDTIN; NQALDTINK; QALDTINKV; ALDTINKVT; LDTINKVTE;
DTINKVTED; TINKVTEDV; INKVTEDVS; NKVTEDVSS; KVTEDVSSK;
VTEDVSSKL; TEDVSSKLE; EDVSSKLEG; DVSSKLEGV; VSSKLEGVR;
SSKLEGVRE; SKLEGVRES; KLEGVRESS; LEGVRESSL; EGVRESSLE;
GVRESSLEL; VRESSLELV; RESSLELVE; ESSLELVES; SSLELVESN;
SLELVESND; LELVESNDA; ELVESNDAG; LVESNDAGV; VESNDAGVV;
ESNDAGVVK; SNDAGVVKK; NDAGVVKKF; DAGVVKKFV; AGVVKKFVG;
GVVKKFVGS; VVKKFVGSM; VKKFVGSMS; KKFVGSMSL; KFVGSMSLM;
FVGSMSLMS; VGSMSLMSD; GSMSLMSDV; SMSLMSDVA; MSLMSDVAK;
SLMSDVAKG; LMSDVAKGT; MSDVAKGTV; SDVAKGTVV; DVAKGTVVA;
VAKGTVVAS; AKGTVVASQ; KGTVVASQE; GTVVASQEA; TVVASQEAT;
VVASQEATI; VASQEATIV; ASQEATIVA; SQEATIVAK; QEATIVAKC;
EATIVAKCS; ATIVAKCSG; TIVAKCSGM; IVAKCSGMV; VAKCSGMVA;
AKCSGMVAE; KCSGMVAEG; CSGMVAEGA; SGMVAEGAN; GMVAEGANK;
MVAEGANKV; VAEGANKVV; AEGANKVVE; EGANKVVEM; GANKVVEMS;
ANKVVEMSK; NKVVEMSKK; KVVEMSKKA; VVEMSKKAV; VEMSKKAVQ;
EMSKKAVQE; MSKKAVQET; SKKAVQETQ; KKAVQETQK; KAVQETQKA;
AVQETQKAV; VQETQKAVS; QETQKAVSV; ETQKAVSVA; TQKAVSVAG;
QKAVSVAGE; KAVSVAGEA; AVSVAGEAT; VSVAGEATF; SVAGEATFL;
VAGEATFLI; AGEATFLIE; GEATFLIEK; EATFLIEKQ; ATFLIEKQI;
TFLIEKQIM; FLIEKQIML; LIEKQIMLN; IEKQIMLNK; EKQIMLNKS;
KQIMLNKSP; QIMLNKSPN; IMLNKSPNN; MLNKSPNNK; LNKSPNNKE;

NKSPNNKEL; KSPNNKELE; SPNNKELEL; PNNKELELT; NNKELELTK;
NKELELTKE; KELELTKEE; ELELTKEEF; LELTKEEFA; ELTKEEFAK;
LTKEEFAKV; TKEEFAKVD; KEEFAKVDE; EEFAKVDEV; EFAKVDEVK;
FAKVDEVKE; AKVDEVKET; KVDEVKETL; VDEVKETLM; DEVKETLMA;
EVKETLMAS; VKETLMASE; KETLMASER; ETLMASERA; TLMASERAL;
LMASERALD; MASERALDE; ASERALDET; SERALDETV; ERALDETVQ;
RALDETVQE; ALDETVQEA; LDETVQEAQ; DETVQEAQK; ETVQEAQKV;
TVQEAQKVL; VQEAQKVLN; QEAQKVLNM; EAQKVLNMV; AQKVLNMVN;
QKVLNMVNG; KVLNMVNGL; VLNMVNGLN; LNMVNGLNP; NMVNGLNPS;
MVNGLNPSN; VNGLNPSNK; NGLNPSNKD; GLNPSNKDQ; LNPSNKDQV;
NPSNKDQVL; PSNKDQVLA; SNKDQVLAK; NKDQVLAKK; KDQVLAKKD;
DQVLAKKDV; QVLAKKDVR; VLAKKDVRK; LAKKDVRKA; AKKDVRKAI;
KKDVRKAIS; KDVRKAISN; DVRKAISNV; VRKAISNVV; RKAISNVVK;
KAISNVVKV; AISNVVKVA; ISNVVKVAQ; SNVVKVAQG; NVVKVAQGA;
VVKVAQGAR; VKVAQGARD; KVAQGARDL; VAQGARDLT; AQGARDLTK;
QGARDLTKV; GARDLTKVM; ARDLTKVMA; RDLTKVMAI; DLTKVMAIS;
LTKVMAISL; TKVMAISLY; KVMAISLYM; VMAISLYMR;

10 mers:
MTKIFSNLII; TKIFSNLIIN; KIFSNLIING; IFSNLIINGL;
FSNLIINGLL; SNLIINGLLF; NLIINGLLFG; LIINGLLFGF;
IINGLLFGFV; INGLLFGFVS; NGLLFGFVSL; GLLFGFVSLN;
LLFGFVSLNV; LFGFVSLNVF; FGFVSLNVFA; GFVSLNVFAD;
FVSLNVFADS; VSLNVFADSN; SLNVFADSNN; LNVFADSNNA;
NVFADSNNAN; VFADSNNANI; FADSNNANIL; ADSNNANILK;
DSNNANILKP; SNNANILKPQ; NNANILKPQS; NANILKPQSN;
ANILKPQSNV; NILKPQSNVL; ILKPQSNVLE; LKPQSNVLEH;
KPQSNVLEHS; PQSNVLEHSD; QSNVLEHSDQ; SNVLEHSDQK;
NVLEHSDQKD; VLEHSDQKDN; LEHSDQKDNK; EHSDQKDNKK;
HSDQKDNKKL; SDQKDNKKLD; DQKDNKKLDQ; QKDNKKLDQK;
KDNKKLDQKD; DNKKLDQKDQ; NKKLDQKDQV; KKLDQKDQVN;
KLDQKDQVNQ; LDQKDQVNQA; DQKDQVNQAL; QKDQVNQALD;
KDQVNQALDT; DQVNQALDTI; QVNQALDTIN; VNQALDTINK;
NQALDTINKV; QALDTINKVT; ALDTINKVTE; LDTINKVTED;
DTINKVTEDV; TINKVTEDVS; INKVTEDVSS; NKVTEDVSSK;
KVTEDVSSKL; VTEDVSSKLE; TEDVSSKLEG; EDVSSKLEGV;
DVSSKLEGVR; VSSKLEGVRE; SSKLEGVRES; SKLEGVRESS;
KLEGVRESSL; LEGVRESSLE; EGVRESSLEL; GVRESSLELV;
VRESSLELVE; RESSLELVES; ESSLELVESN; SSLELVESND;
SLELVESNDA; LELVESNDAG; ELVESNDAGV; LVESNDAGVV;
VESNDAGVVK; ESNDAGVVKK; SNDAGVVKKF; NDAGVVKKFV;
DAGVVKKFVG; AGVVKKFVGS; GVVKKFVGSM; VVKKFVGSMS;
VKKFVGSMSL; KKFVGSMSLM; KFVGSMSLMS; FVGSMSLMSD;
VGSMSLMSDV; GSMSLMSDVA; SMSLMSDVAK; MSLMSDVAKG;
SLMSDVAKGT; LMSDVAKGTV; MSDVAKGTVV; SDVAKGTVVA;
DVAKGTVVAS; VAKGTVVASQ; AKGTVVASQE; KGTVVASQEA;
GTVVASQEAT; TVVASQEATI; VVASQEATIV; VASQEATIVA;
ASQEATIVAK; SQEATIVAKC; QEATIVAKCS; EATIVAKCSG;
ATIVAKCSGM; TIVAKCSGMV; IVAKCSGMVA; VAKCSGMVAE;
AKCSGMVAEG; KCSGMVAEGA; CSGMVAEGAN; SGMVAEGANK;
GMVAEGANKV; MVAEGANKVV; VAEGANKVVE; AEGANKVVEM;

	EGANKVVEMS; GANKVVEMSK; ANKVVEMSKK; NKVVEMSKKA; KVVEMSKKAV; VVEMSKKAVQ; VEMSKKAVQE; EMSKKAVQET; MSKKAVQETQ; SKKAVQETQK; KKAVQETQKA; KAVQETQKAV; AVQETQKAVS; VQETQKAVSV; QETQKAVSVA; ETQKAVSVAG; TQKAVSVAGE; QKAVSVAGEA; KAVSVAGEAT; AVSVAGEATF; VSVAGEATFL; SVAGEATFLI; VAGEATFLIE; AGEATFLIEK; GEATFLIEKQ; EATFLIEKQI; ATFLIEKQIM; TFLIEKQIML; FLIEKQIMLN; LIEKQIMLNK; IEKQIMLNKS; EKQIMLNKSP; KQIMLNKSPN; QIMLNKSPNN; IMLNKSPNNK; MLNKSPNNKE; LNKSPNNKEL; NKSPNNKELE; KSPNNKELEL; SPNNKELELT; PNNKELELTK; NNKELELTKE; NKELELTKEE; KELELTKEEF; ELELTKEEFA; LELTKEEFAK; ELTKEEFAKV; LTKEEFAKVD; TKEEFAKVDE; KEEFAKVDEV; EEFAKVDEVK; EFAKVDEVKE; FAKVDEVKET; AKVDEVKETL; KVDEVKETLM; VDEVKETLMA; DEVKETLMAS; EVKETLMASE; VKETLMASER; KETLMASERA; ETLMASERAL; TLMASERALD; LMASERALDE; MASERALDET; ASERALDETV; SERALDETVQ; ERALDETVQE; RALDETVQEA; ALDETVQEAQ; LDETVQEAQK; DETVQEAQKV; ETVQEAQKVL; TVQEAQKVLN; VQEAQKVLNM; QEAQKVLNMV; EAQKVLNMVN; AQKVLNMVNG; QKVLNMVNGL; KVLNMVNGLN; VLNMVNGLNP; LNMVNGLNPS; NMVNGLNPSN; MVNGLNPSNK; VNGLNPSNKD; NGLNPSNKDQ; GLNPSNKDQV; LNPSNKDQVL; NPSNKDQVLA; PSNKDQVLAK; SNKDQVLAKK; NKDQVLAKKD; KDQVLAKKDV; DQVLAKKDVR; QVLAKKDVRK; VLAKKDVRKA; LAKKDVRKAI; AKKDVRKAIS; KKDVRKAISN; KDVRKAISNV; DVRKAISNVV; VRKAISNVVK; RKAISNVVKV; KAISNVVKVA; AISNVVKVAQ; ISNVVKVAQG; SNVVKVAQGA; NVVKVAQGAR; VVKVAQGARD; VKVAQGARDL; KVAQGARDLT; VAQGARDLTK; AQGARDLTKV; QGARDLTKVM; GARDLTKVMA; ARDLTKVMAI; RDLTKVMAIS; DLTKVMAISL; LTKVMAISLY; TKVMAISLYM; KVMAISLYMR; 11 mers: MTKIFSNLIIN; TKIFSNLIING; KIFSNLIINGL; IFSNLIINGLL; FSNLIINGLLF; SNLIINGLLFG; NLIINGLLFGF; LIINGLLFGFV; IINGLLFGFVS; INGLLFGFVSL; NGLLFGFVSLN; GLLFGFVSLNV; LLFGFVSLNVF; LFGFVSLNVFA; FGFVSLNVFAD; GFVSLNVFADS; FVSLNVFADSN; VSLNVFADSNN; SLNVFADSNNA; LNVFADSNNAN; NVFADSNNANI; VFADSNNANIL; FADSNNANILK; ADSNNANILKP; DSNNANILKPQ; SNNANILKPQS; NNANILKPQSN; NANILKPQSNV; ANILKPQSNVL; NILKPQSNVLE; ILKPQSNVLEH; LKPQSNVLEHS; KPQSNVLEHSD; PQSNVLEHSDQ; QSNVLEHSDQK; SNVLEHSDQKD; NVLEHSDQKDN; VLEHSDQKDNK; LEHSDQKDNKK; EHSDQKDNKKL; HSDQKDNKKLD; SDQKDNKKLDQ; DQKDNKKLDQK; QKDNKKLDQKD; KDNKKLDQKDQ; DNKKLDQKDQV; NKKLDQKDQVN; KKLDQKDQVNQ; KLDQKDQVNQA; LDQKDQVNQAL; DQKDQVNQALD; QKDQVNQALDT; KDQVNQALDTI; DQVNQALDTIN; QVNQALDTINK; VNQALDTINKV; NQALDTINKVT; QALDTINKVTE; ALDTINKVTED; LDTINKVTEDV; DTINKVTEDVS; TINKVTEDVSS; INKVTEDVSSK; NKVTEDVSSKL; KVTEDVSSKLE; VTEDVSSKLEG; TEDVSSKLEGV; EDVSSKLEGVR; DVSSKLEGVRE; VSSKLEGVRES; SSKLEGVRESS; SKLEGVRESSL; KLEGVRESSLE; LEGVRESSLEL; EGVRESSLELV; GVRESSLELVE;

	VRESSLELVES; RESSLELVESN; ESSLELVESND; SSLELVESNDA; SLELVESNDAG; LELVESNDAGV; ELVESNDAGVV; LVESNDAGVVK; VESNDAGVVKK; ESNDAGVVKKF; SNDAGVVKKFV; NDAGVVKKFVG; DAGVVKKFVGS; AGVVKKFVGSM; GVVKKFVGSMS; VVKKFVGSMSL; VKKFVGSMSLM; KKFVGSMSLMS; KFVGSMSLMSD; FVGSMSLMSDV; VGSMSLMSDVA; GSMSLMSDVAK; SMSLMSDVAKG; MSLMSDVAKGT; SLMSDVAKGTV; LMSDVAKGTVV; MSDVAKGTVVA; SDVAKGTVVAS; DVAKGTVVASQ; VAKGTVVASQE; AKGTVVASQEA; KGTVVASQEAT; GTVVASQEATI; TVVASQEATIV; VVASQEATIVA; VASQEATIVAK; ASQEATIVAKC; SQEATIVAKCS; QEATIVAKCSG; EATIVAKCSGM; ATIVAKCSGMV; TIVAKCSGMVA; IVAKCSGMVAE; VAKCSGMVAEG; AKCSGMVAEGA; KCSGMVAEGAN; CSGMVAEGANK; SGMVAEGANKV; GMVAEGANKVV; MVAEGANKVVE; VAEGANKVVEM; AEGANKVVEMS; EGANKVVEMSK; GANKVVEMSKK; ANKVVEMSKKA; NKVVEMSKKAV; KVVEMSKKAVQ; VVEMSKKAVQE; VEMSKKAVQET; EMSKKAVQETQ; MSKKAVQETQK; SKKAVQETQKA; KKAVQETQKAV; KAVQETQKAVS; AVQETQKAVSV; VQETQKAVSVA; QETQKAVSVAG; ETQKAVSVAGE; TQKAVSVAGEA; QKAVSVAGEAT; KAVSVAGEATF; AVSVAGEATFL; VSVAGEATFLI; SVAGEATFLIE; VAGEATFLIEK; AGEATFLIEKQ; GEATFLIEKQI; EATFLIEKQIM; ATFLIEKQIML; TFLIEKQIMLN; FLIEKQIMLNK; LIEKQIMLNKS; IEKQIMLNKSP; EKQIMLNKSPN; KQIMLNKSPNN; QIMLNKSPNNK; IMLNKSPNNKE; MLNKSPNNKEL; LNKSPNNKELE; NKSPNNKELEL; KSPNNKELELT; SPNNKELELTK; PNNKELELTKE; NNKELELTKEE; NKELELTKEEF; KELELTKEEFA; ELELTKEEFAK; LELTKEEFAKV; ELTKEEFAKVD; LTKEEFAKVDE; TKEEFAKVDEV; KEEFAKVDEVK; EEFAKVDEVKE; EFAKVDEVKET; FAKVDEVKETL; AKVDEVKETLM; KVDEVKETLMA; VDEVKETLMAS; DEVKETLMASE; EVKETLMASER; VKETLMASERA; KETLMASERAL; ETLMASERALD; TLMASERALDE; LMASERALDET; MASERALDETV; ASERALDETVQ; SERALDETVQE; ERALDETVQEA; RALDETVQEAQ; ALDETVQEAQK; LDETVQEAQKV; DETVQEAQKVL; ETVQEAQKVLN; TVQEAQKVLNM; VQEAQKVLNMV; QEAQKVLNMVN; EAQKVLNMVNG; AQKVLNMVNGL; QKVLNMVNGLN; KVLNMVNGLNP; VLNMVNGLNPS; LNMVNGLNPSN; NMVNGLNPSNK; MVNGLNPSNKD; VNGLNPSNKDQ; NGLNPSNKDQV; GLNPSNKDQVL; LNPSNKDQVLA; NPSNKDQVLAK; PSNKDQVLAKK; SNKDQVLAKKD; NKDQVLAKKDV; KDQVLAKKDVR; DQVLAKKDVRK; QVLAKKDVRKA; VLAKKDVRKAI; LAKKDVRKAIS; AKKDVRKAISN; KKDVRKAISNV; KDVRKAISNVV; DVRKAISNVVK; VRKAISNVVKV; RKAISNVVKVA; KAISNVVKVAQ; AISNVVKVAQG; ISNVVKVAQGA; SNVVKVAQGAR; NVVKVAQGARD; VVKVAQGARDL; VKVAQGARDLT; KVAQGARDLTK; VAQGARDLTKV; AQGARDLTKVM; QGARDLTKVMA; GARDLTKVMAI; ARDLTKVMAIS; RDLTKVMAISL; DLTKVMAISLY; LTKVMAISLYM; TKVMAISLYMR;
Seq 26	SEQ ID NO 28856-31653/ 8 mers: MKKMLLIF; KKMLLIFS; KMLLIFSF; MLLIFSFF; LLIFSFFL; LIFSFFLI; IFSFFLIF; FSFFLIFL; SFFLIFLN; FFLIFLNG; FLIFLNGF; LIFLNGFP; IFLNGFPL; FLNGFPLN; LNGFPLNA; NGFPLNAR; GFPLNARK; FPLNARKV; PLNARKVD; LNARKVDK; NARKVDKE; ARKVDKEK; RKVDKEKL; KVDKEKLK; VDKEKLKD;

	DKEKLKDF; KEKLKDFV; EKLKDFVN; KLKDFVNM; LKDFVNMD; KDFVNMDL; DFVNMDLE; FVNMDLEF; VNMDLEFV; NMDLEFVN; MDLEFVNY; DLEFVNYK; LEFVNYKG; EFVNYKGP; FVNYKGPY; VNYKGPYD; NYKGPYDS; YKGPYDST; KGPYDSTN; GPYDSTNT; PYDSTNTY; YDSTNTYE; DSTNTYEQ; STNTYEQI; TNTYEQIV; NTYEQIVG; TYEQIVGI; YEQIVGIG; EQIVGIGE; QIVGIGEF; IVGIGEFL; VGIGEFLA; GIGEFLAR; IGEFLARP; GEFLARPL; EFLARPLT; FLARPLTN; LARPLTNS; ARPLTNSN; RPLTNSNS; PLTNSNSN; LTNSNSNS; TNSNSNSS; NSNSNSSY; SNSNSSYY; NSNSSYYG; SNSSYYGK; NSSYYGKY; SSYYGKYF; SYYGKYFI; YYGKYFIN; YGKYFINR; GKYFINRF; KYFINRFI; YFINRFID; FINRFIDD; INRFIDDQ; NRFIDDQD; RFIDDQDK; FIDDQDKK; IDDQDKKA; DDQDKKAS; DQDKKASV; QDKKASVD; DKKASVDV; KKASVDVF; KASVDVFS; ASVDVFSI; SVDVFSIS; VDVFSISS; DVFSISSK; VFSISSKS; FSISSKSE; SISSKSEL; ISSKSELD; SSKSELDS; SKSELDSI; KSELDSIL; SELDSILN; ELDSILNL; LDSILNLR; DSILNLRR; SILNLRRI; ILNLRRIL; LNLRRILT; NLRRILTG; LRRILTGY; RRILTGYI; RILTGYII; ILTGYIIK; LTGYIIKS; TGYIIKSF; GYIIKSFD; YIIKSFDY; IIKSFDYD; IKSFDYDR; KSFDYDRS; SFDYDRSS; FDYDRSSA; DYDRSSAE; YDRSSAEL; DRSSAELI; RSSAELIA; SSAELIAK; SAELIAKV; AELIAKVI; ELIAKVIT; LIAKVITI; IAKVITIY; AKVITIYN; KVITIYNA; VITIYNAV; ITIYNAVY; TIYNAVYR; IYNAVYRG; YNAVYRGD; NAVYRGDL; AVYRGDLD; VYRGDLDY; YRGDLDYY; RGDLDYYK; GDLDYYKG; DLDYYKGF; LDYYKGFY; DYYKGFYI; YYKGFYIE; YKGFYIEP; KGFYIEPA; GFYIEPAL; FYIEPALK; YIEPALKS; IEPALKSL; EPALKSLT; PALKSLTK; ALKSLTKE; LKSLTKEN; KSLTKENA; SLTKENAG; LTKENAGL; TKENAGLS; KENAGLSR; ENAGLSRV; NAGLSRVY; AGLSRVYS; GLSRVYSQ; LSRVYSQW; SRVYSQWA; RVYSQWAG; VYSQWAGK; YSQWAGKT; SQWAGKTQ; QWAGKTQI; WAGKTQIF; AGKTQIFI; GKTQIFIP; KTQIFIPL; TQIFIPLK; QIFIPLKK; IFIPLKKD; FIPLKKDI; IPLKKDIL; PLKKDILS; LKKDILSG; KKDILSGN; KDILSGNI; DILSGNIE; ILSGNIES; LSGNIESD; SGNIESDI; GNIESDID; NIESDIDI; IESDIDID; ESDIDIDS; SDIDIDSL; DIDIDSLV; IDIDSLVT; DIDSLVTD; IDSLVTDK; DSLVTDKV; SLVTDKVI; LVTDKVIA; VTDKVIAA; TDKVIAAL; DKVIAALL; KVIAALLS; VIAALLSE; IAALLSEN; AALLSENE; ALLSENEA; LLSENEAG; LSENEAGV; SENEAGVN; ENEAGVNF; NEAGVNFA; EAGVNFAR; AGVNFARD; GVNFARDI; VNFARDIT; NFARDITD; FARDITDI; ARDITDIQ; RDITDIQG; DITDIQGE; ITDIQGET; TDIQGETH; DIQGETHK; IQGETHKA; QGETHKAD; GETHKADQ; ETHKADQD; THKADQDK; HKADQDKI; KADQDKID; ADQDKIDT; DQDKIDTE; QDKIDTEL; DKIDTELD; KIDTELDN; IDTELDNI; DTELDNIH; TELDNIHE; ELDNIHES; LDNIHESD; DNIHESDS; NIHESDSN; IHESDSNI; HESDSNIT; ESDSNITE; SDSNITET; DSNITETI; SNITETIE; NITETIEN; ITETIENL; TETIENLR; ETIENLRD; TIENLRDQ; IENLRDQL; ENLRDQLE; NLRDQLEK; LRDQLEKA; RDQLEKAT; DQLEKATD; QLEKATDE; LEKATDEE; EKATDEEH; KATDEEHK; ATDEEHKK; TDEEHKKE; DEEHKKEI; EEHKKEIE; EHKKEIES; HKKEIESQ; KKEIESQV; KEIESQVD; EIESQVDA;

	IESQVDAK; ESQVDAKK; SQVDAKKK; QVDAKKKE; VDAKKKEK; DAKKKEKE; AKKKEKEE; KKKEKEEL; KKEKEELD; KEKEELDK; EKEELDKK; KEELDKKA; EELDKKAI; ELDKKAIN; LDKKAINL; DKKAINLD; KKAINLDK; KAINLDKA; AINLDKAQ; INLDKAQQ; NLDKAQQK; LDKAQQKL; DKAQQKLD; KAQQKLDS; AQQKLDSA; QQKLDSAE; QKLDSAED; KLDSAEDN; LDSAEDNL; DSAEDNLD; SAEDNLDV; AEDNLDVQ; EDNLDVQR; DNLDVQRD; NLDVQRDT; LDVQRDTV; DVQRDTVR; VQRDTVRE; QRDTVREK; RDTVREKI; DTVREKIQ; TVREKIQE; VREKIQED; REKIQEDI; EKIQEDIN; KIQEDINE; IQEDINEI; QEDINEIN; EDINEINK; DINEINKE; INEINKEK; NEINKEKN; EINKEKNL; INKEKNLP; NKEKNLPK; KEKNLPKP; EKNLPKPG; KNLPKPGD; NLPKPGDV; LPKPGDVS; PKPGDVSS; KPGDVSSP; PGDVSSPK; GDVSSPKV; DVSSPKVD; VSSPKVDK; SSPKVDKQ; SPKVDKQL; PKVDKQLQ; KVDKQLQI; VDKQLQIK; DKQLQIKE; KQLQIKES; QLQIKESL; LQIKESLE; QIKESLED; IKESLEDL; KESLEDLQ; ESLEDLQE; SLEDLQEQ; LEDLQEQL; EDLQEQLK; DLQEQLKE; LQEQLKEA; QEQLKEAG; EQLKEAGD; QLKEAGDE; LKEAGDEN; KEAGDENQ; EAGDENQK; AGDENQKR; GDENQKRE; DENQKREI; ENQKREIE; NQKREIEK; QKREIEKQ; KREIEKQI; REIEKQIE; EIEKQIEI; IEKQIEIK; EKQIEIKK; KQIEIKKR; QIEIKKRD; IEIKKRDE; EIKKRDEE; IKKRDEEL; KKRDEELL; KRDEELLK; RDEELLKS; DEELLKSK; EELLKSKD; ELLKSKDG; LLKSKDGK; LKSKDGKV; KSKDGKVS; SKDGKVSK; KDGKVSKD; DGKVSKDY; GKVSKDYE; KVSKDYEA; VSKDYEAL; SKDYEALD; KDYEALDL; DYEALDLD; YEALDLDR; EALDLDRE; ALDLDREL; LDLDRELS; DLDRELSK; LDRELSKA; DRELSKAS; RELSKASS; ELSKASSK; LSKASSKE; SKASSKEK; KASSKEKS; ASSKEKSK; SSKEKSKV; SKEKSKVK; KEKSKVKE; EKSKVKEE; KSKVKEEE; SKVKEEEI; KVKEEEIT; VKEEEITK; KEEEITKG; EEEITKGK; EEITKGKS; EITKGKSR; ITKGKSRA; TKGKSRAS; KGKSRASL; GKSRASLG; KSRASLGD; SRASLGDL; RASLGDLN; ASLGDLNN; SLGDLNND; LGDLNNDK; GDLNNDKN; DLNNDKNL; LNNDKNLM; NNDKNLML; NDKNLMLP; DKNLMLPE; KNLMLPED; NLMLPEDQ; LMLPEDQK; MLPEDQKL; LPEDQKLP; PEDQKLPE; EDQKLPED; DQKLPEDK; QKLPEDKK; KLPEDKKL; LPEDKKLD; PEDKKLDS; EDKKLDSK; DKKLDSKL; KKLDSKLD; KLDSKLDG; LDSKLDGK; DSKLDGKK; SKLDGKKE; KLDGKKEF; LDGKKEFK; DGKKEFKP; GKKEFKPV; KKEFKPVS; KEFKPVSE; EFKPVSEV; FKPVSEVE; KPVSEVEK; PVSEVEKL; VSEVEKLD; SEVEKLDK; EVEKLDKI; VEKLDKIS; EKLDKISK; KLDKISKS; LDKISKSN; DKISKSNN; KISKSNNN; ISKSNNNE; SKSNNNEV; KSNNNEVG; SNNNEVGK; NNNEVGKL; NNEVGKLS; NEVGKLSP; EVGKLSPL; VGKLSPLD; GKLSPLDK; KLSPLDKP; LSPLDKPS; SPLDKPSY; PLDKPSYD; LDKPSYDD; DKPSYDDI; KPSYDDID; PSYDDIDS; SYDDIDSK; YDDIDSKE; DDIDSKEE; DIDSKEEV; IDSKEEVD; DSKEEVDN; SKEEVDNK; KEEVDNKA; EEVDNKAI; EVDNKAIN; VDNKAINL; DNKAINLQ; NKAINLQK; KAINLQKI; AINLQKID; INLQKIDP; NLQKIDPK; LQKIDPKV; QKIDPKVK; KIDPKVKD; IDPKVKDQ; DPKVKDQT; PKVKDQTT; KVKDQTTS; VKDQTTSL; KDQTTSLN; DQTTSLNE; QTTSLNED; TTSLNEDL; TSLNEDLD; SLNEDLDK; LNEDLDKD; NEDLDKDL; EDLDKDLT;

	DLDKDLTT; LDKDLTTM; DKDLTTMS; KDLTTMSI; DLTTMSID; LTTMSIDS; TTMSIDSS; TMSIDSSS; MSIDSSSP; SIDSSSPV; IDSSSPVF; DSSSPVFL; SSSPVFLE; SSPVFLEV; SPVFLEVI; PVFLEVID; VFLEVIDP; FLEVIDPI; LEVIDPIT; EVIDPITN; VIDPITNL; IDPITNLG; DPITNLGT; PITNLGTL; ITNLGTLQ; TNLGTLQL; NLGTLQLI; LGTLQLID; GTLQLIDL; TLQLIDLN; LQLIDLNT; QLIDLNTG; LIDLNTGV; IDLNTGVR; DLNTGVRL; LNTGVRLK; NTGVRLKE; TGVRLKES; GVRLKEST; VRLKESTQ; RLKESTQQ; LKESTQQG; KESTQQGI; ESTQQGIQ; STQQGIQR; TQQGIQRY; QQGIQRYG; QGIQRYGI; GIQRYGIY; IQRYGIYE; QRYGIYER; RYGIYERE; YGIYEREK; GIYEREKD; IYEREKDL; YEREKDLV; EREKDLVV; REKDLVVI; EKDLVVIK; KDLVVIKM; DLVVIKMD; LVVIKMDS; VVIKMDSG; VIKMDSGK; IKMDSGKA; KMDSGKAK; MDSGKAKL; DSGKAKLQ; SGKAKLQI; GKAKLQIL; KAKLQILN; AKLQILNK; KLQILNKL; LQILNKLE; QILNKLEN; ILNKLENL; LNKLENLK; NKLENLKV; KLENLKVV; LENLKVVS; ENLKVVSE; NLKVVSES; LKVVSESN; KVVSESNF; VVSESNFE; VSESNFEI; SESNFEIN; ESNFEINK; SNFEINKN; NFEINKNS; FEINKNSS; EINKNSSL; INKNSSLY; NKNSSLYV; KNSSLYVD; NSSLYVDS; SSLYVDSK; SLYVDSKM; LYVDSKMI; YVDSKMIL; VDSKMILA; DSKMILAA; SKMILAAV; KMILAAVR; MILAAVRD; ILAAVRDK; LAAVRDKD; AAVRDKDD; AVRDKDDS; VRDKDDSN; RDKDDSNA; DKDDSNAW; KDDSNAWR; DDSNAWRL; DSNAWRLA; SNAWRLAK; NAWRLAKF; AWRLAKFS; WRLAKFSP; RLAKFSPK; LAKFSPKN; AKFSPKNL; KFSPKNLD; FSPKNLDE; SPKNLDEF; PKNLDEFI; KNLDEFIL; NLDEFILS; LDEFILSE; DEFILSEN; EFILSENK; FILSENKI; ILSENKIL; LSENKILP; SENKILPF; ENKILPFT; NKILPFTS; KILPFTSF; ILPFTSFS; LPFTSFSV; PFTSFSVR; FTSFSVRK; TSFSVRKN; SFSVRKNF; FSVRKNFI; SVRKNFIY; VRKNFIYL; RKNFIYLQ; KNFIYLQD; NFIYLQDE; FIYLQDEL; IYLQDELK; YLQDELKN; LQDELKNL; QDELKNLV; DELKNLVI; ELKNLVIL; LKNLVILD; KNLVILDV; NLVILDVN; LVILDVNT; VILDVNTL; ILDVNTLK; LDVNTLKK; DVNTLKKV; VNTLKKVK; 9 mers: MKKMLLIFS; KKMLLIFSF; KMLLIFSFF; MLLIFSFFL; LLIFSFFLI; LIFSFFLIF; IFSFFLIFL; FSFFLIFLN; SFFLIFLNG; FFLIFLNGF; FLIFLNGFP; LIFLNGFPL; IFLNGFPLN; FLNGFPLNA; LNGFPLNAR; NGFPLNARK; GFPLNARKV; FPLNARKVD; PLNARKVDK; LNARKVDKE; NARKVDKEK; ARKVDKEKL; RKVDKEKLK; KVDKEKLKD; VDKEKLKDF; DKEKLKDFV; KEKLKDFVN; EKLKDFVNM; KLKDFVNMD; LKDFVNMDL; KDFVNMDLE; DFVNMDLEF; FVNMDLEFV; VNMDLEFVN; NMDLEFVNY; MDLEFVNYK; DLEFVNYKG; LEFVNYKGP; EFVNYKGPY; FVNYKGPYD; VNYKGPYDS; NYKGPYDST; YKGPYDSTN; KGPYDSTNT; GPYDSTNTY; PYDSTNTYE; YDSTNTYEQ; DSTNTYEQI; STNTYEQIV; TNTYEQIVG; NTYEQIVGI; TYEQIVGIG; YEQIVGIGE; EQIVGIGEF; QIVGIGEFL; IVGIGEFLA; VGIGEFLAR; GIGEFLARP; IGEFLARPL; GEFLARPLT; EFLARPLTN; FLARPLTNS; LARPLTNSN; ARPLTNSNS; RPLTNSNSN; PLTNSNSNS; LTNSNSNSS; TNSNSNSSY; NSNSNSSYY; SNSNSSYYG; NSNSSYYGK; SNSSYYGKY; NSSYYGKYF; SSYYGKYFI; SYYGKYFIN;

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	INEINKEKN; NEINKEKNL; EINKEKNLP; INKEKNLPK; NKEKNLPKP; KEKNLPKPG; EKNLPKPGD; KNLPKPGDV; NLPKPGDVS; LPKPGDVSS; PKPGDVSSP; KPGDVSSPK; PGDVSSPKV; GDVSSPKVD; DVSSPKVDK; VSSPKVDKQ; SSPKVDKQL; SPKVDKQLQ; PKVDKQLQI; KVDKQLQIK; VDKQLQIKE; DKQLQIKES; KQLQIKESL; QLQIKESLE; LQIKESLED; QIKESLEDL; IKESLEDLQ; KESLEDLQE; ESLEDLQEQ; SLEDLQEQL; LEDLQEQLK; EDLQEQLKE; DLQEQLKEA; LQEQLKEAG; QEQLKEAGD; EQLKEAGDE; QLKEAGDEN; LKEAGDENQ; KEAGDENQK; EAGDENQKR; AGDENQKRE; GDENQKREI; DENQKREIE; ENQKREIEK; NQKREIEKQ; QKREIEKQI; KREIEKQIE; REIEKQIEI; EIEKQIEIK; IEKQIEIKK; EKQIEIKKR; KQIEIKKRD; QIEIKKRDE; IEIKKRDEE; EIKKRDEEL; IKKRDEELL; KKRDEELLK; KRDEELLKS; RDEELLKSK; DEELLKSKD; EELLKSKDG; ELLKSKDGK; LLKSKDGKV; LKSKDGKVS; KSKDGKVSK; SKDGKVSKD; KDGKVSKDY; DGKVSKDYE; GKVSKDYEA; KVSKDYEAL; VSKDYEALD; SKDYEALDL; KDYEALDLD; DYEALDLDR; YEALDLDRE; EALDLDREL; ALDLDRELS; LDLDRELSK; DLDRELSKA; LDRELSKAS; DRELSKASS; RELSKASSK; ELSKASSKE; LSKASSKEK; SKASSKEKS; KASSKEKSK; ASSKEKSKV; SSKEKSKVK; SKEKSKVKE; KEKSKVKEE; EKSKVKEEE; KSKVKEEEI; SKVKEEEIT; KVKEEEITK; VKEEEITKG; KEEEITKGK; EEEITKGKS; EEITKGKSR; EITKGKSRA; ITKGKSRAS; TKGKSRASL; KGKSRASLG; GKSRASLGD; KSRASLGDL; SRASLGDLN; RASLGDLNN; ASLGDLNND; SLGDLNNDK; LGDLNNDKN; GDLNNDKNL; DLNNDKNLM; LNNDKNLML; NNDKNLMLP; NDKNLMLPE; DKNLMLPED; KNLMLPEDQ; NLMLPEDQK; LMLPEDQKL; MLPEDQKLP; LPEDQKLPE; PEDQKLPED; EDQKLPEDK; DQKLPEDKK; QKLPEDKKL; KLPEDKKLD; LPEDKKLDS; PEDKKLDSK; EDKKLDSKL; DKKLDSKLD; KKLDSKLDG; KLDSKLDGK; LDSKLDGKK; DSKLDGKKE; SKLDGKKEF; KLDGKKEFK; LDGKKEFKP; DGKKEFKPV; GKKEFKPVS; KKEFKPVSE; KEFKPVSEV; EFKPVSEVE; FKPVSEVEK; KPVSEVEKL; PVSEVEKLD; VSEVEKLDK; SEVEKLDKI; EVEKLDKIS; VEKLDKISK; EKLDKISKS; KLDKISKSN; LDKISKSNN; DKISKSNNN; KISKSNNNE; ISKSNNNEV; SKSNNNEVG; KSNNNEVGK; SNNNEVGKL; NNNEVGKLS; NNEVGKLSP; NEVGKLSPL; EVGKLSPLD; VGKLSPLDK; GKLSPLDKP; KLSPLDKPS; LSPLDKPSY; SPLDKPSYD; PLDKPSYDD; LDKPSYDDI; DKPSYDDID; KPSYDDIDS; PSYDDIDSK; SYDDIDSKE; YDDIDSKEE; DDIDSKEEV; DIDSKEEVD; IDSKEEVDN; DSKEEVDNK; SKEEVDNKA; KEEVDNKAI; EEVDNKAIN; EVDNKAINL; VDNKAINLQ; DNKAINLQK; NKAINLQKI; KAINLQKID; AINLQKIDP; INLQKIDPK; NLQKIDPKV; LQKIDPKVK; QKIDPKVKD; KIDPKVKDQ; IDPKVKDQT; DPKVKDQTT; PKVKDQTTS; KVKDQTTSL; VKDQTTSLN; KDQTTSLNE; DQTTSLNED; QTTSLNEDL; TTSLNEDLD; TSLNEDLDK; SLNEDLDKD; LNEDLDKDL; NEDLDKDLT; EDLDKDLTT; DLDKDLTTM; LDKDLTTMS; DKDLTTMSI; KDLTTMSID; DLTTMSIDS; LTTMSIDSS; TTMSIDSSS; TMSIDSSSP; MSIDSSSPV; SIDSSSPVF; IDSSSPVFL; DSSSPVFLE; SSSPVFLEV; SSPVFLEVI; SPVFLEVID; PVFLEVIDP; VFLEVIDPI; FLEVIDPIT; LEVIDPITN; EVIDPITNL; VIDPITNLG; IDPITNLGT; DPITNLGTL; PITNLGTLQ; ITNLGTLQL; TNLGTLQLI; NLGTLQLID; LGTLQLIDL; GTLQLIDLN; TLQLIDLNT; LQLIDLNTG; QLIDLNTGV; LIDLNTGVR; IDLNTGVRL; DLNTGVRLK; LNTGVRLKE; NTGVRLKES; TGVRLKEST; GVRLKESTQ; VRLKESTQQ; RLKESTQQG; LKESTQQGI; KESTQQGIQ; ESTQQGIQR; STQQGIQRY; TQQGIQRYG; QQGIQRYGI; QGIQRYGIY; GIQRYGIYE; IQRYGIYER;

QRYGIYERE; RYGIYEREK; YGIYEREKD; GIYEREKDL; IYEREKDLV;
YEREKDLVV; EREKDLVVI; REKDLVVIK; EKDLVVIKM; KDLVVIKMD;
DLVVIKMDS; LVVIKMDSG; VVIKMDSGK; VIKMDSGKA; IKMDSGKAK;
KMDSGKAKL; MDSGKAKLQ; DSGKAKLQI; SGKAKLQIL; GKAKLQILN;
KAKLQILNK; AKLQILNKL; KLQILNKLE; LQILNKLEN; QILNKLENL;
ILNKLENLK; LNKLENLKV; NKLENLKVV; KLENLKVVS; LENLKVVSE;
ENLKVVSES; NLKVVSESN; LKVVSESNF; KVVSESNFE; VVSESNFEI;
VSESNFEIN; SESNFEINK; ESNFEINKN; SNFEINKNS; NFEINKNSS;
FEINKNSSL; EINKNSSLY; INKNSSLYV; NKNSSLYVD; KNSSLYVDS;
NSSLYVDSK; SSLYVDSKM; SLYVDSKMI; LYVDSKMIL; YVDSKMILA;
VDSKMILAA; DSKMILAAV; SKMILAAVR; KMILAAVRD; MILAAVRDK;
ILAAVRDKD; LAAVRDKDD; AAVRDKDDS; AVRDKDDSN; VRDKDDSNA;
RDKDDSNAW; DKDDSNAWR; KDDSNAWRL; DDSNAWRLA; DSNAWRLAK;
SNAWRLAKF; NAWRLAKFS; AWRLAKFSP; WRLAKFSPK; RLAKFSPKN;
LAKFSPKNL; AKFSPKNLD; KFSPKNLDE; FSPKNLDEF; SPKNLDEFI;
PKNLDEFIL; KNLDEFILS; NLDEFILSE; LDEFILSEN; DEFILSENK;
EFILSENKI; FILSENKIL; ILSENKILP; LSENKILPF; SENKILPFT;
ENKILPFTS; NKILPFTSF; KILPFTSFS; ILPFTSFSV; LPFTSFSVR;
PFTSFSVRK; FTSFSVRKN; TSFSVRKNF; SFSVRKNFI; FSVRKNFIY;
SVRKNFIYL; VRKNFIYLQ; RKNFIYLQD; KNFIYLQDE; NFIYLQDEL;
FIYLQDELK; IYLQDELKN; YLQDELKNL; LQDELKNLV; QDELKNLVI;
DELKNLVIL; ELKNLVILD; LKNLVILDV; KNLVILDVN; NLVILDVNT;
LVILDVNTL; VILDVNTLK; ILDVNTLKK; LDVNTLKKV; DVNTLKKVK;

10 mers:
MKKMLLIFSF; KKMLLIFSFF; KMLLIFSFFL; MLLIFSFFLI;
LLIFSFFLIF; LIFSFFLIFL; IFSFFLIFLN; FSFFLIFLNG;
SFFLIFLNGF; FFLIFLNGFP; FLIFLNGFPL; LIFLNGFPLN;
IFLNGFPLNA; FLNGFPLNAR; LNGFPLNARK; NGFPLNARKV;
GFPLNARKVD; FPLNARKVDK; PLNARKVDKE; LNARKVDKEK;
NARKVDKEKL; ARKVDKEKLK; RKVDKEKLKD; KVDKEKLKDF;
VDKEKLKDFV; DKEKLKDFVN; KEKLKDFVNM; EKLKDFVNMD;
KLKDFVNMDL; LKDFVNMDLE; KDFVNMDLEF; DFVNMDLEFV;
FVNMDLEFVN; VNMDLEFVNY; NMDLEFVNYK; MDLEFVNYKG;
DLEFVNYKGP; LEFVNYKGPY; EFVNYKGPYD; FVNYKGPYDS;
VNYKGPYDST; NYKGPYDSTN; YKGPYDSTNT; KGPYDSTNTY;
GPYDSTNTYE; PYDSTNTYEQ; YDSTNTYEQI; DSTNTYEQIV;
STNTYEQIVG; TNTYEQIVGI; NTYEQIVGIG; TYEQIVGIGE;
YEQIVGIGEF; EQIVGIGEFL; QIVGIGEFLA; IVGIGEFLAR;
VGIGEFLARP; GIGEFLARPL; IGEFLARPLT; GEFLARPLTN;
EFLARPLTNS; FLARPLTNSN; LARPLTNSNS; ARPLTNSNSN;
RPLTNSNSNS; PLTNSNSNSS; LTNSNSNSSY; TNSNSNSSYY;
NSNSNSSYYG; SNSNSSYYGK; NSNSSYYGKY; SNSSYYGKYF;
NSSYYGKYFI; SSYYGKYFIN; SYYGKYFINR; YYGKYFINRF;
YGKYFINRFI; GKYFINRFID; KYFINRFIDD; YFINRFIDDQ;
FINRFIDDQD; INRFIDDQDK; NRFIDDQDKK; RFIDDQDKKA;
FIDDQDKKAS; IDDQDKKASV; DDQDKKASVD; DQDKKASVDV;
QDKKASVDVF; DKKASVDVFS; KKASVDVFSI; KASVDVFSIS;
ASVDVFSISS; SVDVFSISSK; VDVFSISSKS; DVFSISSKSE;
VFSISSKSEL; FSISSKSELD; SISSKSELDS; ISSKSELDSI;
SSKSELDSIL; SKSELDSILN; KSELDSILNL; SELDSILNLR;

	ELDSILNLRR; LDSILNLRRI; DSILNLRRIL; SILNLRRILT; ILNLRRILTG; LNLRRILTGY; NLRRILTGYI; LRRILTGYII; RRILTGYIIK; RILTGYIIKS; ILTGYIIKSF; LTGYIIKSFD; TGYIIKSFDY; GYIIKSFDYD; YIIKSFDYDR; IIKSFDYDRS; IKSFDYDRSS; KSFDYDRSSA; SFDYDRSSAE; FDYDRSSAEL; DYDRSSAELI; YDRSSAELIA; DRSSAELIAK; RSSAELIAKV; SSAELIAKVI; SAELIAKVIT; AELIAKVITI; ELIAKVITIY; LIAKVITIYN; IAKVITIYNA; AKVITIYNAV; KVITIYNAVY; VITIYNAVYR; ITIYNAVYRG; TIYNAVYRGD; IYNAVYRGDL; YNAVYRGDLD; NAVYRGDLDY; AVYRGDLDYY; VYRGDLDYYK; YRGDLDYYKG; RGDLDYYKGF; GDLDYYKGFY; DLDYYKGFYI; LDYYKGFYIE; DYYKGFYIEP; YYKGFYIEPA; YKGFYIEPAL; KGFYIEPALK; GFYIEPALKS; FYIEPALKSL; YIEPALKSLT; IEPALKSLTK; EPALKSLTKE; PALKSLTKEN; ALKSLTKENA; LKSLTKENAG; KSLTKENAGL; SLTKENAGLS; LTKENAGLSR; TKENAGLSRV; KENAGLSRVY; ENAGLSRVYS; NAGLSRVYSQ; AGLSRVYSQW; GLSRVYSQWA; LSRVYSQWAG; SRVYSQWAGK; RVYSQWAGKT; VYSQWAGKTQ; YSQWAGKTQI; SQWAGKTQIF; QWAGKTQIFI; WAGKTQIFIP; AGKTQIFIPL; GKTQIFIPLK; KTQIFIPLKK; TQIFIPLKKD; QIFIPLKKDI; IFIPLKKDIL; FIPLKKDILS; IPLKKDILSG; PLKKDILSGN; LKKDILSGNI; KKDILSGNIE; KDILSGNIES; DILSGNIESD; ILSGNIESDI; LSGNIESDID; SGNIESDIDI; GNIESDIDID; NIESDIDIDS; IESDIDIDSL; ESDIDIDSLV; SDIDIDSLVT; DIDIDSLVTD; IDIDSLVTDK; DIDSLVTDKV; IDSLVTDKVI; DSLVTDKVIA; SLVTDKVIAA; LVTDKVIAAL; VTDKVIAALL; TDKVIAALLS; DKVIAALLSE; KVIAALLSEN; VIAALLSENE; IAALLSENEA; AALLSENEAG; ALLSENEAGV; LLSENEAGVN; LSENEAGVNF; SENEAGVNFA; ENEAGVNFAR; NEAGVNFARD; EAGVNFARDI; AGVNFARDIT; GVNFARDITD; VNFARDITDI; NFARDITDIQ; FARDITDIQG; ARDITDIQGE; RDITDIQGET; DITDIQGETH; ITDIQGETHK; TDIQGETHKA; DIQGETHKAD; IQGETHKADQ; QGETHKADQD; GETHKADQDK; ETHKADQDKI; THKADQDKID; HKADQDKIDT; KADQDKIDTE; ADQDKIDTEL; DQDKIDTELD; QDKIDTELDN; DKIDTELDNI; KIDTELDNIH; IDTELDNIHE; DTELDNIHES; TELDNIHESD; ELDNIHESDS; LDNIHESDSN; DNIHESDSNI; NIHESDSNIT; IHESDSNITE; HESDSNITET; ESDSNITETI; SDSNITETIE; DSNITETIEN; SNITETIENL; NITETIENLR; ITETIENLRD; TETIENLRDQ; ETIENLRDQL; TIENLRDQLE; IENLRDQLEK; ENLRDQLEKA; NLRDQLEKAT; LRDQLEKATD; RDQLEKATDE; DQLEKATDEE; QLEKATDEEH; LEKATDEEHK; EKATDEEHKK; KATDEEHKKE; ATDEEHKKEI; TDEEHKKEIE; DEEHKKEIES; EEHKKEIESQ; EHKKEIESQV; HKKEIESQVD; KKEIESQVDA; KEIESQVDAK; EIESQVDAKK; IESQVDAKKK; ESQVDAKKKE; SQVDAKKKEK; QVDAKKKEKE; VDAKKKEKEE; DAKKKEKEEL; AKKKEKEELD; KKKEKEELDK; KKEKEELDKK; KEKEELDKKA; EKEELDKKAI; KEELDKKAIN; EELDKKAINL; ELDKKAINLD; LDKKAINLDK; DKKAINLDKA; KKAINLDKAQ; KAINLDKAQQ; AINLDKAQQK; INLDKAQQKL; NLDKAQQKLD; LDKAQQKLDS; DKAQQKLDSA; KAQQKLDSAE; AQQKLDSAED; QQKLDSAEDN; QKLDSAEDNL; KLDSAEDNLD;

	LDSAEDNLDV; DSAEDNLDVQ; SAEDNLDVQR; AEDNLDVQRD; EDNLDVQRDT; DNLDVQRDTV; NLDVQRDTVR; LDVQRDTVRE; DVQRDTVREK; VQRDTVREKI; QRDTVREKIQ; RDTVREKIQE; DTVREKIQED; TVREKIQEDI; VREKIQEDIN; REKIQEDINE; EKIQEDINEI; KIQEDINEIN; IQEDINEINK; QEDINEINKE; EDINEINKEK; DINEINKEKN; INEINKEKNL; NEINKEKNLP; EINKEKNLPK; INKEKNLPKP; NKEKNLPKPG; KEKNLPKPGD; EKNLPKPGDV; KNLPKPGDVS; NLPKPGDVSS; LPKPGDVSSP; PKPGDVSSPK; KPGDVSSPKV; PGDVSSPKVD; GDVSSPKVDK; DVSSPKVDKQ; VSSPKVDKQL; SSPKVDKQLQ; SPKVDKQLQI; PKVDKQLQIK; KVDKQLQIKE; VDKQLQIKES; DKQLQIKESL; KQLQIKESLE; QLQIKESLED; LQIKESLEDL; QIKESLEDLQ; IKESLEDLQE; KESLEDLQEQ; ESLEDLQEQL; SLEDLQEQLK; LEDLQEQLKE; EDLQEQLKEA; DLQEQLKEAG; LQEQLKEAGD; QEQLKEAGDE; EQLKEAGDEN; QLKEAGDENQ; LKEAGDENQK; KEAGDENQKR; EAGDENQKRE; AGDENQKREI; GDENQKREIE; DENQKREIEK; ENQKREIEKQ; NQKREIEKQI; QKREIEKQIE; KREIEKQIEI; REIEKQIEIK; EIEKQIEIKK; IEKQIEIKKR; EKQIEIKKRD; KQIEIKKRDE; QIEIKKRDEE; IEIKKRDEEL; EIKKRDEELL; IKKRDEELLK; KKRDEELLKS; KRDEELLKSK; RDEELLKSKD; DEELLKSKDG; EELLKSKDGK; ELLKSKDGKV; LLKSKDGKVS; LKSKDGKVSK; KSKDGKVSKD; SKDGKVSKDY; KDGKVSKDYE; DGKVSKDYEA; GKVSKDYEAL; KVSKDYEALD; VSKDYEALDL; SKDYEALDLD; KDYEALDLDR; DYEALDLDRE; YEALDLDREL; EALDLDRELS; ALDLDRELSK; LDLDRELSKA; DLDRELSKAS; LDRELSKASS; DRELSKASSK; RELSKASSKE; ELSKASSKEK; LSKASSKEKS; SKASSKEKSK; KASSKEKSKV; ASSKEKSKVK; SSKEKSKVKE; SKEKSKVKEE; KEKSKVKEEE; EKSKVKEEEI; KSKVKEEEIT; SKVKEEEITK; KVKEEEITKG; VKEEEITKGK; KEEEITKGKS; EEEITKGKSR; EEITKGKSRA; EITKGKSRAS; ITKGKSRASL; TKGKSRASLG; KGKSRASLGD; GKSRASLGDL; KSRASLGDLN; SRASLGDLNN; RASLGDLNND; ASLGDLNNDK; SLGDLNNDKN; LGDLNNDKNL; GDLNNDKNLM; DLNNDKNLML; LNNDKNLMLP; NNDKNLMLPE; NDKNLMLPED; DKNLMLPEDQ; KNLMLPEDQK; NLMLPEDQKL; LMLPEDQKLP; MLPEDQKLPE; LPEDQKLPED; PEDQKLPEDK; EDQKLPEDKK; DQKLPEDKKL; QKLPEDKKLD; KLPEDKKLDS; LPEDKKLDSK; PEDKKLDSKL; EDKKLDSKLD; DKKLDSKLDG; KKLDSKLDGK; KLDSKLDGKK; LDSKLDGKKE; DSKLDGKKEF; SKLDGKKEFK; KLDGKKEFKP; LDGKKEFKPV; DGKKEFKPVS; GKKEFKPVSE; KKEFKPVSEV; KEFKPVSEVE; EFKPVSEVEK; FKPVSEVEKL; KPVSEVEKLD; PVSEVEKLDK; VSEVEKLDKI; SEVEKLDKIS; EVEKLDKISK; VEKLDKISKS; EKLDKISKSN; KLDKISKSNN; LDKISKSNNN; DKISKSNNNE; KISKSNNNEV; ISKSNNNEVG; SKSNNNEVGK; KSNNNEVGKL; SNNNEVGKLS; NNNEVGKLSP; NNEVGKLSPL; NEVGKLSPLD; EVGKLSPLDK; VGKLSPLDKP; GKLSPLDKPS; KLSPLDKPSY; LSPLDKPSYD; SPLDKPSYDD; PLDKPSYDDI; LDKPSYDDID; DKPSYDDIDS; KPSYDDIDSK; PSYDDIDSKE; SYDDIDSKEE; YDDIDSKEEV; DDIDSKEEVD; DIDSKEEVDN; IDSKEEVDNK; DSKEEVDNKA; SKEEVDNKAI; KEEVDNKAIN; EEVDNKAINL; EVDNKAINLQ; VDNKAINLQK;

	DNKAINLQKI; NKAINLQKID; KAINLQKIDP; AINLQKIDPK; INLQKIDPKV; NLQKIDPKVK; LQKIDPKVKD; QKIDPKVKDQ; KIDPKVKDQT; IDPKVKDQTT; DPKVKDQTTS; PKVKDQTTSL; KVKDQTTSLN; VKDQTTSLNE; KDQTTSLNED; DQTTSLNEDL; QTTSLNEDLD; TTSLNEDLDK; TSLNEDLDKD; SLNEDLDKDL; LNEDLDKDLT; NEDLDKDLTT; EDLDKDLTTM; DLDKDLTTMS; LDKDLTTMSI; DKDLTTMSID; KDLTTMSIDS; DLTTMSIDSS; LTTMSIDSSS; TTMSIDSSSP; TMSIDSSSPV; MSIDSSSPVF; SIDSSSPVFL; IDSSSPVFLE; DSSSPVFLEV; SSSPVFLEVI; SSPVFLEVID; SPVFLEVIDP; PVFLEVIDPI; VFLEVIDPIT; FLEVIDPITN; LEVIDPITNL; EVIDPITNLG; VIDPITNLGT; IDPITNLGTL; DPITNLGTLQ; PITNLGTLQL; ITNLGTLQLI; TNLGTLQLID; NLGTLQLIDL; LGTLQLIDLN; GTLQLIDLNT; TLQLIDLNTG; LQLIDLNTGV; QLIDLNTGVR; LIDLNTGVRL; IDLNTGVRLK; DLNTGVRLKE; LNTGVRLKES; NTGVRLKEST; TGVRLKESTQ; GVRLKESTQQ; VRLKESTQQG; RLKESTQQGI; LKESTQQGIQ; KESTQQGIQR; ESTQQGIQRY; STQQGIQRYG; TQQGIQRYGI; QQGIQRYGIY; QGIQRYGIYE; GIQRYGIYER; IQRYGIYERE; QRYGIYEREK; RYGIYEREKD; YGIYEREKDL; GIYEREKDLV; IYEREKDLVV; YEREKDLVVI; EREKDLVVIK; REKDLVVIKM; EKDLVVIKMD; KDLVVIKMDS; DLVVIKMDSG; LVVIKMDSGK; VVIKMDSGKA; VIKMDSGKAK; IKMDSGKAKL; KMDSGKAKLQ; MDSGKAKLQI; DSGKAKLQIL; SGKAKLQILN; GKAKLQILNK; KAKLQILNKL; AKLQILNKLE; KLQILNKLEN; LQILNKLENL; QILNKLENLK; ILNKLENLKV; LNKLENLKVV; NKLENLKVVS; KLENLKVVSE; LENLKVVSES; ENLKVVSESN; NLKVVSESNF; LKVVSESNFE; KVVSESNFEI; VVSESNFEIN; VSESNFEINK; SESNFEINKN; ESNFEINKNS; SNFEINKNSS; NFEINKNSSL; FEINKNSSLY; EINKNSSLYV; INKNSSLYVD; NKNSSLYVDS; KNSSLYVDSK; NSSLYVDSKM; SSLYVDSKMI; SLYVDSKMIL; LYVDSKMILA; YVDSKMILAA; VDSKMILAAV; DSKMILAAVR; SKMILAAVRD; KMILAAVRDK; MILAAVRDKD; ILAAVRDKDD; LAAVRDKDDS; AAVRDKDDSN; AVRDKDDSNA; VRDKDDSNAW; RDKDDSNAWR; DKDDSNAWRL; KDDSNAWRLA; DDSNAWRLAK; DSNAWRLAKF; SNAWRLAKFS; NAWRLAKFSP; AWRLAKFSPK; WRLAKFSPKN; RLAKFSPKNL; LAKFSPKNLD; AKFSPKNLDE; KFSPKNLDEF; FSPKNLDEFI; SPKNLDEFIL; PKNLDEFILS; KNLDEFILSE; NLDEFILSEN; LDEFILSENK; DEFILSENKI; EFILSENKIL; FILSENKILP; ILSENKILPF; LSENKILPFT; SENKILPFTS; ENKILPFTSF; NKILPFTSFS; KILPFTSFSV; ILPFTSFSVR; LPFTSFSVRK; PFTSFSVRKN; FTSFSVRKNF; TSFSVRKNFI; SFSVRKNFIY; FSVRKNFIYL; SVRKNFIYLQ; VRKNFIYLQD; RKNFIYLQDE; KNFIYLQDEL; NFIYLQDELK; FIYLQDELKN; IYLQDELKNL; YLQDELKNLV; LQDELKNLVI; QDELKNLVIL; DELKNLVILD; ELKNLVILDV; LKNLVILDVN; KNLVILDVNT; NLVILDVNTL; LVILDVNTLK; VILDVNTLKK; ILDVNTLKKV; LDVNTLKKVK; 11 mers: MKKMLLIFSFF; KKMLLIFSFFL; KMLLIFSFFLI; MLLIFSFFLIF; LLIFSFFLIFL; LIFSFFLIFLN; IFSFFLIFLNG; FSFFLIFLNGF;

	SFFLIFLNGFP; FFLIFLNGFPL; FLIFLNGFPLN; LIFLNGFPLNA; IFLNGFPLNAR; FLNGFPLNARK; LNGFPLNARKV; NGFPLNARKVD; GFPLNARKVDK; FPLNARKVDKE; PLNARKVDKEK; LNARKVDKEKL; NARKVDKEKLK; ARKVDKEKLKD; RKVDKEKLKDF; KVDKEKLKDFV; VDKEKLKDFVN; DKEKLKDFVNM; KEKLKDFVNMD; EKLKDFVNMDL; KLKDFVNMDLE; LKDFVNMDLEF; KDFVNMDLEFV; DFVNMDLEFVN; FVNMDLEFVNY; VNMDLEFVNYK; NMDLEFVNYKG; MDLEFVNYKGP; DLEFVNYKGPY; LEFVNYKGPYD; EFVNYKGPYDS; FVNYKGPYDST; VNYKGPYDSTN; NYKGPYDSTNT; YKGPYDSTNTY; KGPYDSTNTYE; GPYDSTNTYEQ; PYDSTNTYEQI; YDSTNTYEQIV; DSTNTYEQIVG; STNTYEQIVGI; TNTYEQIVGIG; NTYEQIVGIGE; TYEQIVGIGEF; YEQIVGIGEFL; EQIVGIGEFLA; QIVGIGEFLAR; IVGIGEFLARP; VGIGEFLARPL; GIGEFLARPLT; IGEFLARPLTN; GEFLARPLTNS; EFLARPLTNSN; FLARPLTNSNS; LARPLTNSNSN; ARPLTNSNSNS; RPLTNSNSNSS; PLTNSNSNSSY; LTNSNSNSSYY; TNSNSNSSYYG; NSNSNSSYYGK; SNSNSSYYGKY; NSNSSYYGKYF; SNSSYYGKYFI; NSSYYGKYFIN; SSYYGKYFINR; SYYGKYFINRF; YYGKYFINRFI; YGKYFINRFID; GKYFINRFIDD; KYFINRFIDDQ; YFINRFIDDQD; FINRFIDDQDK; INRFIDDQDKK; NRFIDDQDKKA; RFIDDQDKKAS; FIDDQDKKASV; IDDQDKKASVD; DDQDKKASVDV; DQDKKASVDVF; QDKKASVDVFS; DKKASVDVFSI; KKASVDVFSIS; KASVDVFSISS; ASVDVFSISSK; SVDVFSISSKS; VDVFSISSKSE; DVFSISSKSEL; VFSISSKSELD; FSISSKSELDS; SISSKSELDSI; ISSKSELDSIL; SSKSELDSILN; SKSELDSILNL; KSELDSILNLR; SELDSILNLRR; ELDSILNLRRI; LDSILNLRRIL; DSILNLRRILT; SILNLRRILTG; ILNLRRILTGY; LNLRRILTGYI; NLRRILTGYII; LRRILTGYIIK; RRILTGYIIKS; RILTGYIIKSF; ILTGYIIKSFD; LTGYIIKSFDY; TGYIIKSFDYD; GYIIKSFDYDR; YIIKSFDYDRS; IIKSFDYDRSS; IKSFDYDRSSA; KSFDYDRSSAE; SFDYDRSSAEL; FDYDRSSAELI; DYDRSSAELIA; YDRSSAELIAK; DRSSAELIAKV; RSSAELIAKVI; SSAELIAKVIT; SAELIAKVITI; AELIAKVITIY; ELIAKVITIYN; LIAKVITIYNA; IAKVITIYNAV; AKVITIYNAVY; KVITIYNAVYR; VITIYNAVYRG; ITIYNAVYRGD; TIYNAVYRGDL; IYNAVYRGDLD; YNAVYRGDLDY; NAVYRGDLDYY; AVYRGDLDYYK; VYRGDLDYYKG; YRGDLDYYKGF; RGDLDYYKGFY; GDLDYYKGFYI; DLDYYKGFYIE; LDYYKGFYIEP; DYYKGFYIEPA; YYKGFYIEPAL; YKGFYIEPALK; KGFYIEPALKS; GFYIEPALKSL; FYIEPALKSLT; YIEPALKSLTK; IEPALKSLTKE; EPALKSLTKEN; PALKSLTKENA; ALKSLTKENAG; LKSLTKENAGL; KSLTKENAGLS; SLTKENAGLSR; LTKENAGLSRV; TKENAGLSRVY; KENAGLSRVYS; ENAGLSRVYSQ; NAGLSRVYSQW; AGLSRVYSQWA; GLSRVYSQWAG; LSRVYSQWAGK; SRVYSQWAGKT; RVYSQWAGKTQ; VYSQWAGKTQI; YSQWAGKTQIF; SQWAGKTQIFI; QWAGKTQIFIP; WAGKTQIFIPL; AGKTQIFIPLK; GKTQIFIPLKK; KTQIFIPLKKD; TQIFIPLKKDI; QIFIPLKKDIL; IFIPLKKDILS; FIPLKKDILSG; IPLKKDILSGN; PLKKDILSGNI; LKKDILSGNIE; KKDILSGNIES; KDILSGNIESD; DILSGNIESDI; ILSGNIESDID; LSGNIESDIDI; SGNIESDIDID; GNIESDIDIDS; NIESDIDIDSL; IESDIDIDSLV; ESDIDIDSLVT; SDIDIDSLVTD; DIDIDSLVTDK; IDIDSLVTDKV; DIDSLVTDKVI; IDSLVTDKVIA; DSLVTDKVIAA; SLVTDKVIAAL; LVTDKVIAALL; VTDKVIAALLS; TDKVIAALLSE; DKVIAALLSEN; KVIAALLSENE; VIAALLSENEA; IAALLSENEAG;

	AALLSENEAGV; ALLSENEAGVN; LLSENEAGVNF; LSENEAGVNFA; SENEAGVNFAR; ENEAGVNFARD; NEAGVNFARDI; EAGVNFARDIT; AGVNFARDITD; GVNFARDITDI; VNFARDITDIQ; NFARDITDIQG; FARDITDIQGE; ARDITDIQGET; RDITDIQGETH; DITDIQGETHK; ITDIQGETHKA; TDIQGETHKAD; DIQGETHKADQ; IQGETHKADQD; QGETHKADQDK; GETHKADQDKI; ETHKADQDKID; THKADQDKIDT; HKADQDKIDTE; KADQDKIDTEL; ADQDKIDTELD; DQDKIDTELDN; QDKIDTELDNI; DKIDTELDNIH; KIDTELDNIHE; IDTELDNIHES; DTELDNIHESD; TELDNIHESDS; ELDNIHESDSN; LDNIHESDSNI; DNIHESDSNIT; NIHESDSNITE; IHESDSNITET; HESDSNITETI; ESDSNITETIE; SDSNITETIEN; DSNITETIENL; SNITETIENLR; NITETIENLRD; ITETIENLRDQ; TETIENLRDQL; ETIENLRDQLE; TIENLRDQLEK; IENLRDQLEKA; ENLRDQLEKAT; NLRDQLEKATD; LRDQLEKATDE; RDQLEKATDEE; DQLEKATDEEH; QLEKATDEEHK; LEKATDEEHKK; EKATDEEHKKE; KATDEEHKKEI; ATDEEHKKEIE; TDEEHKKEIES; DEEHKKEIESQ; EEHKKEIESQV; EHKKEIESQVD; HKKEIESQVDA; KKEIESQVDAK; KEIESQVDAKK; EIESQVDAKKK; IESQVDAKKKE; ESQVDAKKKEK; SQVDAKKKEKE; QVDAKKKEKEE; VDAKKKEKEEL; DAKKKEKEELD; AKKKEKEELDK; KKKEKEELDKK; KKEKEELDKKA; KEKEELDKKAI; EKEELDKKAIN; KEELDKKAINL; EELDKKAINLD; ELDKKAINLDK; LDKKAINLDKA; DKKAINLDKAQ; KKAINLDKAQQ; KAINLDKAQQK; AINLDKAQQKL; INLDKAQQKLD; NLDKAQQKLDS; LDKAQQKLDSA; DKAQQKLDSAE; KAQQKLDSAED; AQQKLDSAEDN; QQKLDSAEDNL; QKLDSAEDNLD; KLDSAEDNLDV; LDSAEDNLDVQ; DSAEDNLDVQR; SAEDNLDVQRD; AEDNLDVQRDT; EDNLDVQRDTV; DNLDVQRDTVR; NLDVQRDTVRE; LDVQRDTVREK; DVQRDTVREKI; VQRDTVREKIQ; QRDTVREKIQE; RDTVREKIQED; DTVREKIQEDI; TVREKIQEDIN; VREKIQEDINE; REKIQEDINEI; EKIQEDINEIN; KIQEDINEINK; IQEDINEINKE; QEDINEINKEK; EDINEINKEKN; DINEINKEKNL; INEINKEKNLP; NEINKEKNLPK; EINKEKNLPKP; INKEKNLPKPG; NKEKNLPKPGD; KEKNLPKPGDV; EKNLPKPGDVS; KNLPKPGDVSS; NLPKPGDVSSP; LPKPGDVSSPK; PKPGDVSSPKV; KPGDVSSPKVD; PGDVSSPKVDK; GDVSSPKVDKQ; DVSSPKVDKQL; VSSPKVDKQLQ; SSPKVDKQLQI; SPKVDKQLQIK; PKVDKQLQIKE; KVDKQLQIKES; VDKQLQIKESL; DKQLQIKESLE; KQLQIKESLED; QLQIKESLEDL; LQIKESLEDLQ; QIKESLEDLQE; IKESLEDLQEQ; KESLEDLQEQL; ESLEDLQEQLK; SLEDLQEQLKE; LEDLQEQLKEA; EDLQEQLKEAG; DLQEQLKEAGD; LQEQLKEAGDE; QEQLKEAGDEN; EQLKEAGDENQ; QLKEAGDENQK; LKEAGDENQKR; KEAGDENQKRE; EAGDENQKREI; AGDENQKREIE; GDENQKREIEK; DENQKREIEKQ; ENQKREIEKQI; NQKREIEKQIE; QKREIEKQIEI; KREIEKQIEIK; REIEKQIEIKK; EIEKQIEIKKR; IEKQIEIKKRD; EKQIEIKKRDE; KQIEIKKRDEE; QIEIKKRDEEL; IEIKKRDEELL; EIKKRDEELLK; IKKRDEELLKS; KKRDEELLKSK; KRDEELLKSKD; RDEELLKSKDG; DEELLKSKDGK; EELLKSKDGKV; ELLKSKDGKVS; LLKSKDGKVSK; LKSKDGKVSKD; KSKDGKVSKDY; SKDGKVSKDYE; KDGKVSKDYEA; DGKVSKDYEAL; GKVSKDYEALD; KVSKDYEALDL; VSKDYEALDLD; SKDYEALDLDR; KDYEALDLDRE; DYEALDLDREL; YEALDLDRELS; EALDLDRELSK; ALDLDRELSKA; LDLDRELSKAS; DLDRELSKASS; LDRELSKASSK; DRELSKASSKE; RELSKASSKEK; ELSKASSKEKS; LSKASSKEKSK; SKASSKEKSKV; KASSKEKSKVK;

	ASSKEKSKVKE; SSKEKSKVKEE; SKEKSKVKEEE; KEKSKVKEEEI; EKSKVKEEEIT; KSKVKEEEITK; SKVKEEEITKG; KVKEEEITKGK; VKEEEITKGKS; KEEEITKGKSR; EEEITKGKSRA; EEITKGKSRAS; EITKGKSRASL; ITKGKSRASLG; TKGKSRASLGD; KGKSRASLGDL; GKSRASLGDLN; KSRASLGDLNN; SRASLGDLNND; RASLGDLNNDK; ASLGDLNNDKN; SLGDLNNDKNL; LGDLNNDKNLM; GDLNNDKNLML; DLNNDKNLMLP; LNNDKNLMLPE; NNDKNLMLPED; NDKNLMLPEDQ; DKNLMLPEDQK; KNLMLPEDQKL; NLMLPEDQKLP; LMLPEDQKLPE; MLPEDQKLPED; LPEDQKLPEDK; PEDQKLPEDKK; EDQKLPEDKKL; DQKLPEDKKLD; QKLPEDKKLDS; KLPEDKKLDSK; LPEDKKLDSKL; PEDKKLDSKLD; EDKKLDSKLDG; DKKLDSKLDGK; KKLDSKLDGKK; KLDSKLDGKKE; LDSKLDGKKEF; DSKLDGKKEFK; SKLDGKKEFKP; KLDGKKEFKPV; LDGKKEFKPVS; DGKKEFKPVSE; GKKEFKPVSEV; KKEFKPVSEVE; KEFKPVSEVEK; EFKPVSEVEKL; FKPVSEVEKLD; KPVSEVEKLDK; PVSEVEKLDKI; VSEVEKLDKIS; SEVEKLDKISK; EVEKLDKISKS; VEKLDKISKSN; EKLDKISKSNN; KLDKISKSNNN; LDKISKSNNNE; DKISKSNNNEV; KISKSNNNEVG; ISKSNNNEVGK; SKSNNNEVGKL; KSNNNEVGKLS; SNNNEVGKLSP; NNNEVGKLSPL; NNEVGKLSPLD; NEVGKLSPLDK; EVGKLSPLDKP; VGKLSPLDKPS; GKLSPLDKPSY; KLSPLDKPSYD; LSPLDKPSYDD; SPLDKPSYDDI; PLDKPSYDDID; LDKPSYDDIDS; DKPSYDDIDSK; KPSYDDIDSKE; PSYDDIDSKEE; SYDDIDSKEEV; YDDIDSKEEVD; DDIDSKEEVDN; DIDSKEEVDNK; IDSKEEVDNKA; DSKEEVDNKAI; SKEEVDNKAIN; KEEVDNKAINL; EEVDNKAINLQ; EVDNKAINLQK; VDNKAINLQKI; DNKAINLQKID; NKAINLQKIDP; KAINLQKIDPK; AINLQKIDPKV; INLQKIDPKVK; NLQKIDPKVKD; LQKIDPKVKDQ; QKIDPKVKDQT; KIDPKVKDQTT; IDPKVKDQTTS; DPKVKDQTTSL; PKVKDQTTSLN; KVKDQTTSLNE; VKDQTTSLNED; KDQTTSLNEDL; DQTTSLNEDLD; QTTSLNEDLDK; TTSLNEDLDKD; TSLNEDLDKDL; SLNEDLDKDLT; LNEDLDKDLTT; NEDLDKDLTTM; EDLDKDLTTMS; DLDKDLTTMSI; LDKDLTTMSID; DKDLTTMSIDS; KDLTTMSIDSS; DLTTMSIDSSS; LTTMSIDSSSP; TTMSIDSSSPV; TMSIDSSSPVF; MSIDSSSPVFL; SIDSSSPVFLE; IDSSSPVFLEV; DSSSPVFLEVI; SSSPVFLEVID; SSPVFLEVIDP; SPVFLEVIDPI; PVFLEVIDPIT; VFLEVIDPITN; FLEVIDPITNL; LEVIDPITNLG; EVIDPITNLGT; VIDPITNLGTL; IDPITNLGTLQ; DPITNLGTLQL; PITNLGTLQLI; ITNLGTLQLID; TNLGTLQLIDL; NLGTLQLIDLN; LGTLQLIDLNT; GTLQLIDLNTG; TLQLIDLNTGV; LQLIDLNTGVR; QLIDLNTGVRL; LIDLNTGVRLK; IDLNTGVRLKE; DLNTGVRLKES; LNTGVRLKEST; NTGVRLKESTQ; TGVRLKESTQQ; GVRLKESTQQG; VRLKESTQQGI; RLKESTQQGIQ; LKESTQQGIQR; KESTQQGIQRY; ESTQQGIQRYG; STQQGIQRYGI; TQQGIQRYGIY; QQGIQRYGIYE; QGIQRYGIYER; GIQRYGIYERE; IQRYGIYEREK; QRYGIYEREKD; RYGIYEREKDL; YGIYEREKDLV; GIYEREKDLVV; IYEREKDLVVI; YEREKDLVVIK; EREKDLVVIKM; REKDLVVIKMD; EKDLVVIKMDS; KDLVVIKMDSG; DLVVIKMDSGK; LVVIKMDSGKA; VVIKMDSGKAK; VIKMDSGKAKL; IKMDSGKAKLQ; KMDSGKAKLQI; MDSGKAKLQIL; DSGKAKLQILN; SGKAKLQILNK; GKAKLQILNKL; KAKLQILNKLE; AKLQILNKLEN; KLQILNKLENL; LQILNKLENLK; QILNKLENLKV; ILNKLENLKVV; LNKLENLKVVS; NKLENLKVVSE; KLENLKVVSES; LENLKVVSESN; ENLKVVSESNF; NLKVVSESNFE; LKVVSESNFEI; KVVSESNFEIN; VVSESNFEINK;

	VSESNFEINKN; SESNFEINKNS; ESNFEINKNSS; SNFEINKNSSL; NFEINKNSSLY; FEINKNSSLYV; EINKNSSLYVD; INKNSSLYVDS; NKNSSLYVDSK; KNSSLYVDSKM; NSSLYVDSKMI; SSLYVDSKMIL; SLYVDSKMILA; LYVDSKMILAA; YVDSKMILAAV; VDSKMILAAVR; DSKMILAAVRD; SKMILAAVRDK; KMILAAVRDKD; MILAAVRDKDD; ILAAVRDKDDS; LAAVRDKDDSN; AAVRDKDDSNA; AVRDKDDSNAW; VRDKDDSNAWR; RDKDDSNAWRL; DKDDSNAWRLA; KDDSNAWRLAK; DDSNAWRLAKF; DSNAWRLAKFS; SNAWRLAKFSP; NAWRLAKFSPK; AWRLAKFSPKN; WRLAKFSPKNL; RLAKFSPKNLD; LAKFSPKNLDE; AKFSPKNLDEF; KFSPKNLDEFI; FSPKNLDEFIL; SPKNLDEFILS; PKNLDEFILSE; KNLDEFILSEN; NLDEFILSENK; LDEFILSENKI; DEFILSENKIL; EFILSENKILP; FILSENKILPF; ILSENKILPFT; LSENKILPFTS; SENKILPFTSF; ENKILPFTSFS; NKILPFTSFSV; KILPFTSFSVR; ILPFTSFSVRK; LPFTSFSVRKN; PFTSFSVRKNF; FTSFSVRKNFI; TSFSVRKNFIY; SFSVRKNFIYL; FSVRKNFIYLQ; SVRKNFIYLQD; VRKNFIYLQDE; RKNFIYLQDEL; KNFIYLQDELK; NFIYLQDELKN; FIYLQDELKNL; IYLQDELKNLV; YLQDELKNLVI; LQDELKNLVIL; QDELKNLVILD; DELKNLVILDV; ELKNLVILDVN; LKNLVILDVNT; KNLVILDVNTL; NLVILDVNTLK; LVILDVNTLKK; VILDVNTLKKV; ILDVNTLKKVK;
Seq 27	SEQ ID NO 31564-33623/ 8 mers: MKYILSID; KYILSIDQ; YILSIDQG; ILSIDQGT; LSIDQGTT; SIDQGTTS; IDQGTTSS; DQGTTSSR; QGTTSSRA; GTTSSRAM; TTSSRAMV; TSSRAMVF; SSRAMVFD; SRAMVFDK; RAMVFDKN; AMVFDKNA; MVFDKNAN; VFDKNANI; FDKNANIK; DKNANIKG; KNANIKGF; NANIKGFA; ANIKGFAQ; NIKGFAQK; IKGFAQKE; KGFAQKEF; GFAQKEFT; FAQKEFTQ; AQKEFTQI; QKEFTQIY; KEFTQIYP; EFTQIYPQ; FTQIYPQP; TQIYPQPS; QIYPQPSW; IYPQPSWV; YPQPSWVE; PQPSWVEH; QPSWVEHD; PSWVEHDP; SWVEHDPT; WVEHDPTE; VEHDPTEI; EHDPTEIW; HDPTEIWG; DPTEIWGS; PTEIWGSQ; TEIWGSQL; EIWGSQLG; IWGSQLGV; WGSQLGVI; GSQLGVIT; SQLGVITE; QLGVITEA; LGVITEAM; GVITEAMA; VITEAMAN; ITEAMANA; TEAMANAR; EAMANARI; AMANARIL; MANARILP; ANARILPN; NARILPNE; ARILPNEI; RILPNEID; ILPNEIDA; LPNEIDAI; PNEIDAIG; NEIDAIGI; EIDAIGIT; IDAIGITN; DAIGITNQ; AIGITNQR; IGITNQRE; GITNQRET; ITNQRETT; TNQRETTV; NQRETTVI; QRETTVIW; RETTVIWE; ETTVIWEK; TTVIWEKN; TVIWEKNT; VIWEKNTG; IWEKNTGK; WEKNTGKP; EKNTGKPI; KNTGKPIY; NTGKPIYN; TGKPIYNA; GKPIYNAI; KPIYNAIV; PIYNAIVW; IYNAIVWQ; YNAIVWQD; NAIVWQDR; AIVWQDRR; IVWQDRRT; VWQDRRTA; WQDRRTAK; QDRRTAKI; DRRTAKIC; RRTAKICD; RTAKICDQ; TAKICDQL; AKICDQLK; KICDQLKK; ICDQLKKE; CDQLKKEG; DQLKKEGK; QLKKEGKD; LKKEGKDK; KKEGKDKI; KEGKDKII; EGKDKIIL; GKDKIILE; KDKIILEK; DKIILEKT; KIILEKTG; IILEKTGL; ILEKTGLV; LEKTGLVL; EKTGLVLD; KTGLVLDS; TGLVLDSY; GLVLDSYF; LVLDSYFS; VLDSYFSG; LDSYFSGT; DSYFSGTK; SYFSGTKI; YFSGTKIM; FSGTKIMW; SGTKIMWI; GTKIMWIL; TKIMWILD; KIMWILDN; IMWILDNV; MWILDNVE;

	WILDNVEG; ILDNVEGA; LDNVEGAR; DNVEGARQ; NVEGARQR; VEGARQRA; EGARQRAE; GARQRAEN; ARQRAENG; RQRAENGE; QRAENGEL; RAENGELC; AENGELCF; ENGELCFG; NGELCFGT; GELCFGTI; ELCFGTID; LCFGTIDT; CFGTIDTW; FGTIDTWI; GTIDTWIL; TIDTWILW; IDTWILWN; DTWILWNL; TWILWNLT; WILWNLTQ; ILWNLTQK; LWNLTQKK; WNLTQKKE; NLTQKKEH; LTQKKEHA; TQKKEHAT; QKKEHATD; KKEHATDY; KEHATDYS; EHATDYSN; HATDYSNA; ATDYSNAS; TDYSNASR; DYSNASRT; YSNASRTL; SNASRTLL; NASRTLLL; ASRTLLLN; SRTLLLNI; RTLLLNIK; TLLLNIKT; LLLNIKTL; LLNIKTLE; LNIKTLEW; NIKTLEWD; IKTLEWDD; KTLEWDDE; TLEWDDEL; LEWDDELL; EWDDELLS; WDDELLSI; DDELLSIL; DELLSILN; ELLSILNV; LLSILNVP; LSILNVPR; SILNVPRA; ILNVPRAI; LNVPRAIL; NVPRAILP; VPRAILPE; PRAILPEL; RAILPELK; AILPELKE; ILPELKES; LPELKESS; PELKESST; ELKESSTI; LKESSTIY; KESSTIYG; ESSTIYGK; SSTIYGKT; STIYGKTD; TIYGKTDK; IYGKTDKA; YGKTDKAL; GKTDKALF; KTDKALFG; TDKALFGA; DKALFGAE; KALFGAEI; ALFGAEIP; LFGAEIPI; FGAEIPIA; GAEIPIAG; AEIPIAGI; EIPIAGIA; IPIAGIAG; PIAGIAGD; IAGIAGDQ; AGIAGDQF; GIAGDQFA; IAGDQFAA; AGDQFAAT; GDQFAATF; DQFAATFG; QFAATFGQ; FAATFGQA; AATFGQAC; ATFGQACL; TFGQACLK; FGQACLKK; GQACLKKG; QACLKKGM; ACLKKGMA; CLKKGMAK; LKKGMAKN; KKGMAKNT; KGMAKNTY; GMAKNTYG; MAKNTYGT; AKNTYGTG; KNTYGTGC; NTYGTGCF; TYGTGCFL; YGTGCFLT; GTGCFLTV; TGCFLTVN; GCFLTVNI; CFLTVNIG; FLTVNIGK; LTVNIGKE; TVNIGKEP; VNIGKEPI; NIGKEPII; IGKEPIIS; GKEPIISH; KEPIISHD; EPIISHDK; PIISHDKL; IISHDKLL; ISHDKLLT; SHDKLLTS; HDKLLTSI; DKLLTSIA; KLLTSIAW; LLTSIAWG; LTSIAWGR; TSIAWGRK; SIAWGRKK; IAWGRKKS; AWGRKKSV; WGRKKSVT; GRKKSVTY; RKKSVTYV; KKSVTYVL; KSVTYVLE; SVTYVLEG; VTYVLEGS; TYVLEGSV; YVLEGSVF; VLEGSVFI; LEGSVFIG; EGSVFIGG; GSVFIGGA; SVFIGGAV; VFIGGAVI; FIGGAVIQ; IGGAVIQW; GGAVIQWL; GAVIQWLR; AVIQWLRD; VIQWLRDG; IQWLRDGL; QWLRDGLE; WLRDGLEF; LRDGLEFF; RDGLEFFR; DGLEFFRK; GLEFFRKS; LEFFRKSS; EFFRKSSD; FFRKSSDA; FRKSSDAE; RKSSDAEA; KSSDAEAL; SSDAEALA; SDAEALAS; DAEALASS; AEALASSV; EALASSVS; ALASSVSD; LASSVSDN; ASSVSDNG; SSVSDNGG; SVSDNGGV; VSDNGGVY; SDNGGVYF; DNGGVYFV; NGGVYFVP; GGVYFVPA; GVYFVPAF; VYFVPAFV; YFVPAFVG; FVPAFVGL; VPAFVGLG; PAFVGLGA; AFVGLGAP; FVGLGAPH; VGLGAPHW; GLGAPHWD; LGAPHWDS; GAPHWDSY; APHWDSYA; PHWDSYAR; HWDSYARG; WDSYARGT; DSYARGTI; SYARGTII; YARGTIIG; ARGTIIGI; RGTIIGIT; GTIIGITR; TIIGITRG; IIGITRGS; IGITRGST; GITRGSTK; ITRGSTKA; TRGSTKAH; RGSTKAHI; GSTKAHIT; STKAHITR; TKAHITRA; KAHITRAA; AHITRAAL; HITRAALE; ITRAALES; TRAALESI; RAALESIA; AALESIAF; ALESIAFQ; LESIAFQS; ESIAFQSF; SIAFQSFD; IAFQSFDI; AFQSFDIL; FQSFDILN; QSFDILNT; SFDILNTM; FDILNTMK; DILNTMKK; ILNTMKKS; LNTMKKSI; NTMKKSIP; TMKKSIPN; MKKSIPNF; KKSIPNFE; KSIPNFEI; SIPNFEIQ;

IPNFEIQE; PNFEIQEL; NFEIQELR; FEIQELRV; EIQELRVD;
IQELRVDG; QELRVDGG; ELRVDGGA; LRVDGGAS; RVDGGASQ;
VDGGASQN; DGGASQNN; GGASQNNL; GASQNNLL; ASQNNLLM;
SQNNLLMQ; QNNLLMQF; NNLLMQFQ; NLLMQFQA; LLMQFQAD;
LMQFQADL; MQFQADLL; QFQADLLE; FQADLLEC; QADLLECK;
ADLLECKV; DLLECKVV; LLECKVVR; LECKVVRP; ECKVVRPK;
CKVVRPKI; KVVRPKIT; VVRPKITE; VRPKITET; RPKITETT;
PKITETTA; KITETTAL; ITETTALG; TETTALGA; ETTALGAA;
TTALGAAY; TALGAAYL; ALGAAYLA; LGAAYLAG; GAAYLAGL;
AAYLAGLA; AYLAGLAT; YLAGLATG; LAGLATGY; AGLATGYW;
GLATGYWQ; LATGYWQS; ATGYWQSA; TGYWQSAE; GYWQSAEE;
YWQSAEEI; WQSAEEIV; QSAEEIVS; SAEEIVSL; AEEIVSLW;
EEIVSLWQ; EIVSLWQV; IVSLWQVD; VSLWQVDK; SLWQVDKI;
LWQVDKIF; WQVDKIFE; QVDKIFEP; VDKIFEPS; DKIFEPSM;
KIFEPSMP; IFEPSMPK; FEPSMPKN; EPSMPKNQ; PSMPKNQK;
SMPKNQKE; MPKNQKEK; PKNQKEKL; KNQKEKLL; NQKEKLLE;
QKEKLLEN; KEKLLENW; EKLLENWN; KLLENWNK; LLENWNKA;
LENWNKAV; ENWNKAVG; NWNKAVGK; WNKAVGKA; NKAVGKAK;
KAVGKAKS; AVGKAKSW; VGKAKSWI; GKAKSWIQ; KAKSWIQN;
AKSWIQNS; KSWIQNSH; SWIQNSHS; WIQNSHSS;

9 mers:
MKYILSIDQ; KYILSIDQG; YILSIDQGT; ILSIDQGTT; LSIDQGTTS;
SIDQGTTSS; IDQGTTSSR; DQGTTSSRA; QGTTSSRAM; GTTSSRAMV;
TTSSRAMVF; TSSRAMVFD; SSRAMVFDK; SRAMVFDKN; RAMVFDKNA;
AMVFDKNAN; MVFDKNANI; VFDKNANIK; FDKNANIKG; DKNANIKGF;
KNANIKGFA; NANIKGFAQ; ANIKGFAQK; NIKGFAQKE; IKGFAQKEF;
KGFAQKEFT; GFAQKEFTQ; FAQKEFTQI; AQKEFTQIY; QKEFTQIYP;
KEFTQIYPQ; EFTQIYPQP; FTQIYPQPS; TQIYPQPSW; QIYPQPSWV;
IYPQPSWVE; YPQPSWVEH; PQPSWVEHD; QPSWVEHDP; PSWVEHDPT;
SWVEHDPTE; WVEHDPTEI; VEHDPTEIW; EHDPTEIWG; HDPTEIWGS;
DPTEIWGSQ; PTEIWGSQL; TEIWGSQLG; EIWGSQLGV; IWGSQLGVI;
WGSQLGVIT; GSQLGVITE; SQLGVITEA; QLGVITEAM; LGVITEAMA;
GVITEAMAN; VITEAMANA; ITEAMANAR; TEAMANARI; EAMANARIL;
AMANARILP; MANARILPN; ANARILPNE; NARILPNEI; ARILPNEID;
RILPNEIDA; ILPNEIDAI; LPNEIDAIG; PNEIDAIGI; NEIDAIGIT;
EIDAIGITN; IDAIGITNQ; DAIGITNQR; AIGITNQRE; IGITNQRET;
GITNQRETT; ITNQRETTV; TNQRETTVI; NQRETTVIW; QRETTVIWE;
RETTVIWEK; ETTVIWEKN; TTVIWEKNT; TVIWEKNTG; VIWEKNTGK;
IWEKNTGKP; WEKNTGKPI; EKNTGKPIY; KNTGKPIYN; NTGKPIYNA;
TGKPIYNAI; GKPIYNAIV; KPIYNAIVW; PIYNAIVWQ; IYNAIVWQD;
YNAIVWQDR; NAIVWQDRR; AIVWQDRRT; IVWQDRRTA; VWQDRRTAK;
WQDRRTAKI; QDRRTAKIC; DRRTAKICD; RRTAKICDQ; RTAKICDQL;
TAKICDQLK; AKICDQLKK; KICDQLKKE; ICDQLKKEG; CDQLKKEGK;
DQLKKEGKD; QLKKEGKDK; LKKEGKDKI; KKEGKDKII; KEGKDKIIL;
EGKDKIILE; GKDKIILEK; KDKIILEKT; DKIILEKTG; KIILEKTGL;
IILEKTGLV; ILEKTGLVL; LEKTGLVLD; EKTGLVLDS; KTGLVLDSY;
TGLVLDSYF; GLVLDSYFS; LVLDSYFSG; VLDSYFSGT; LDSYFSGTK;
DSYFSGTKI; SYFSGTKIM; YFSGTKIMW; FSGTKIMWI; SGTKIMWIL;
GTKIMWILD; TKIMWILDN; KIMWILDNV; IMWILDNVE; MWILDNVEG;
WILDNVEGA; ILDNVEGAR; LDNVEGARQ; DNVEGARQR; NVEGARQRA;

	VEGARQRAE; EGARQRAEN; GARQRAENG; ARQRAENGE; RQRAENGEL; QRAENGELC; RAENGELCF; AENGELCFG; ENGELCFGT; NGELCFGTI; GELCFGTID; ELCFGTIDT; LCFGTIDTW; CFGTIDTWI; FGTIDTWIL; GTIDTWILW; TIDTWILWN; IDTWILWNL; DTWILWNLT; TWILWNLTQ; WILWNLTQK; ILWNLTQKK; LWNLTQKKE; WNLTQKKEH; NLTQKKEHA; LTQKKEHAT; TQKKEHATD; QKKEHATDY; KKEHATDYS; KEHATDYSN; EHATDYSNA; HATDYSNAS; ATDYSNASR; TDYSNASRT; DYSNASRTL; YSNASRTLL; SNASRTLLL; NASRTLLLN; ASRTLLLNI; SRTLLLNIK; RTLLLNIKT; TLLLNIKTL; LLLNIKTLE; LLNIKTLEW; LNIKTLEWD; NIKTLEWDD; IKTLEWDDE; KTLEWDDEL; TLEWDDELL; LEWDDELLS; EWDDELLSI; WDDELLSIL; DDELLSILN; DELLSILNV; ELLSILNVP; LLSILNVPR; LSILNVPRA; SILNVPRAI; ILNVPRAIL; LNVPRAILP; NVPRAILPE; VPRAILPEL; PRAILPELK; RAILPELKE; AILPELKES; ILPELKESS; LPELKESST; PELKESSTI; ELKESSTIY; LKESSTIYG; KESSTIYGK; ESSTIYGKT; SSTIYGKTD; STIYGKTDK; TIYGKTDKA; IYGKTDKAL; YGKTDKALF; GKTDKALFG; KTDKALFGA; TDKALFGAE; DKALFGAEI; KALFGAEIP; ALFGAEIPI; LFGAEIPIA; FGAEIPIAG; GAEIPIAGI; AEIPIAGIA; EIPIAGIAG; IPIAGIAGD; PIAGIAGDQ; IAGIAGDQF; AGIAGDQFA; GIAGDQFAA; IAGDQFAAT; AGDQFAATF; GDQFAATFG; DQFAATFGQ; QFAATFGQA; FAATFGQAC; AATFGQACL; ATFGQACLK; TFGQACLKK; FGQACLKKG; GQACLKKGM; QACLKKGMA; ACLKKGMAK; CLKKGMAKN; LKKGMAKNT; KKGMAKNTY; KGMAKNTYG; GMAKNTYGT; MAKNTYGTG; AKNTYGTGC; KNTYGTGCF; NTYGTGCFL; TYGTGCFLT; YGTGCFLTV; GTGCFLTVN; TGCFLTVNI; GCFLTVNIG; CFLTVNIGK; FLTVNIGKE; LTVNIGKEP; TVNIGKEPI; VNIGKEPII; NIGKEPIIS; IGKEPIISH; GKEPIISHD; KEPIISHDK; EPIISHDKL; PIISHDKLL; IISHDKLLT; ISHDKLLTS; SHDKLLTSI; HDKLLTSIA; DKLLTSIAW; KLLTSIAWG; LLTSIAWGR; LTSIAWGRK; TSIAWGRKK; SIAWGRKKS; IAWGRKKSV; AWGRKKSVT; WGRKKSVTY; GRKKSVTYV; RKKSVTYVL; KKSVTYVLE; KSVTYVLEG; SVTYVLEGS; VTYVLEGSV; TYVLEGSVF; YVLEGSVFI; VLEGSVFIG; LEGSVFIGG; EGSVFIGGA; GSVFIGGAV; SVFIGGAVI; VFIGGAVIQ; FIGGAVIQW; IGGAVIQWL; GGAVIQWLR; GAVIQWLRD; AVIQWLRDG; VIQWLRDGL; IQWLRDGLE; QWLRDGLEF; WLRDGLEFF; LRDGLEFFR; RDGLEFFRK; DGLEFFRKS; GLEFFRKSS; LEFFRKSSD; EFFRKSSDA; FFRKSSDAE; FRKSSDAEA; RKSSDAEAL; KSSDAEALA; SSDAEALAS; SDAEALASS; DAEALASSV; AEALASSVS; EALASSVSD; ALASSVSDN; LASSVSDNG; ASSVSDNGG; SSVSDNGGV; SVSDNGGVY; VSDNGGVYF; SDNGGVYFV; DNGGVYFVP; NGGVYFVPA; GGVYFVPAF; GVYFVPAFV; VYFVPAFVG; YFVPAFVGL; FVPAFVGLG; VPAFVGLGA; PAFVGLGAP; AFVGLGAPH; FVGLGAPHW; VGLGAPHWD; GLGAPHWDS; LGAPHWDSY; GAPHWDSYA; APHWDSYAR; PHWDSYARG; HWDSYARGT; WDSYARGTI; DSYARGTII; SYARGTIIG; YARGTIIGI; ARGTIIGIT; RGTIIGITR; GTIIGITRG; TIIGITRGS; IIGITRGST; IGITRGSTK; GITRGSTKA; ITRGSTKAH; TRGSTKAHI; RGSTKAHIT; GSTKAHITR; STKAHITRA; TKAHITRAA; KAHITRAAL; AHITRAALE; HITRAALES; ITRAALESI; TRAALESIA; RAALESIAF; AALESIAFQ; ALESIAFQS; LESIAFQSF; ESIAFQSFD; SIAFQSFDI; IAFQSFDIL; AFQSFDILN; FQSFDILNT; QSFDILNTM; SFDILNTMK; FDILNTMKK; DILNTMKKS; ILNTMKKSI; LNTMKKSIP; NTMKKSIPN; TMKKSIPNF; MKKSIPNFE; KKSIPNFEI; KSIPNFEIQ; SIPNFEIQE; IPNFEIQEL; PNFEIQELR; NFEIQELRV; FEIQELRVD; EIQELRVDG;

IQELRVDGG; QELRVDGGA; ELRVDGGAS; LRVDGGASQ; RVDGGASQN; VDGGASQNN; DGGASQNNL; GGASQNNLL; GASQNNLLM; ASQNNLLMQ; SQNNLLMQF; QNNLLMQFQ; NNLLMQFQA; NLLMQFQAD; LLMQFQADL; LMQFQADLL; MQFQADLLE; QFQADLLEC; FQADLLECK; QADLLECKV; ADLLECKVV; DLLECKVVR; LLECKVVRP; LECKVVRPK; ECKVVRPKI; CKVVRPKIT; KVVRPKITE; VVRPKITET; VRPKITETT; RPKITETTA; PKITETTAL; KITETTALG; ITETTALGA; TETTALGAA; ETTALGAAY; TTALGAAYL; TALGAAYLA; ALGAAYLAG; LGAAYLAGL; GAAYLAGLA; AAYLAGLAT; AYLAGLATG; YLAGLATGY; LAGLATGYW; AGLATGYWQ; GLATGYWQS; LATGYWQSA; ATGYWQSAE; TGYWQSAEE; GYWQSAEEI; YWQSAEEIV; WQSAEEIVS; QSAEEIVSL; SAEEIVSLW; AEEIVSLWQ; EEIVSLWQV; EIVSLWQVD; IVSLWQVDK; VSLWQVDKI; SLWQVDKIF; LWQVDKIFE; WQVDKIFEP; QVDKIFEPS; VDKIFEPSM; DKIFEPSMP; KIFEPSMPK; IFEPSMPKN; FEPSMPKNQ; EPSMPKNQK; PSMPKNQKE; SMPKNQKEK; MPKNQKEKL; PKNQKEKLL; KNQKEKLLE; NQKEKLLEN; QKEKLLENW; KEKLLENWN; EKLLENWNK; KLLENWNKA; LLENWNKAV; LENWNKAVG; ENWNKAVGK; NWNKAVGKA; WNKAVGKAK; NKAVGKAKS; KAVGKAKSW; AVGKAKSWI; VGKAKSWIQ; GKAKSWIQN; KAKSWIQNS; AKSWIQNSH; KSWIQNSHS; SWIQNSHSS;

10 mers:
MKYILSIDQG; KYILSIDQGT; YILSIDQGTT; ILSIDQGTTS; LSIDQGTTSS; SIDQGTTSSR; IDQGTTSSRA; DQGTTSSRAM; QGTTSSRAMV; GTTSSRAMVF; TTSSRAMVFD; TSSRAMVFDK; SSRAMVFDKN; SRAMVFDKNA; RAMVFDKNAN; AMVFDKNANI; MVFDKNANIK; VFDKNANIKG; FDKNANIKGF; DKNANIKGFA; KNANIKGFAQ; NANIKGFAQK; ANIKGFAQKE; NIKGFAQKEF; IKGFAQKEFT; KGFAQKEFTQ; GFAQKEFTQI; FAQKEFTQIY; AQKEFTQIYP; QKEFTQIYPQ; KEFTQIYPQP; EFTQIYPQPS; FTQIYPQPSW; TQIYPQPSWV; QIYPQPSWVE; IYPQPSWVEH; YPQPSWVEHD; PQPSWVEHDP; QPSWVEHDPT; PSWVEHDPTE; SWVEHDPTEI; WVEHDPTEIW; VEHDPTEIWG; EHDPTEIWGS; HDPTEIWGSQ; DPTEIWGSQL; PTEIWGSQLG; TEIWGSQLGV; EIWGSQLGVI; IWGSQLGVIT; WGSQLGVITE; GSQLGVITEA; SQLGVITEAM; QLGVITEAMA; LGVITEAMAN; GVITEAMANA; VITEAMANAR; ITEAMANARI; TEAMANARIL; EAMANARILP; AMANARILPN; MANARILPNE; ANARILPNEI; NARILPNEID; ARILPNEIDA; RILPNEIDAI; ILPNEIDAIG; LPNEIDAIGI; PNEIDAIGIT; NEIDAIGITN; EIDAIGITNQ; IDAIGITNQR; DAIGITNQRE; AIGITNQRET; IGITNQRETT; GITNQRETTV; ITNQRETTVI; TNQRETTVIW; NQRETTVIWE; QRETTVIWEK; RETTVIWEKN; ETTVIWEKNT; TTVIWEKNTG; TVIWEKNTGK; VIWEKNTGKP; IWEKNTGKPI; WEKNTGKPIY; EKNTGKPIYN; KNTGKPIYNA; NTGKPIYNAI; TGKPIYNAIV; GKPIYNAIVW; KPIYNAIVWQ; PIYNAIVWQD; IYNAIVWQDR; YNAIVWQDRR; NAIVWQDRRT; AIVWQDRRTA; IVWQDRRTAK; VWQDRRTAKI; WQDRRTAKIC; QDRRTAKICD; DRRTAKICDQ; RRTAKICDQL; RTAKICDQLK; TAKICDQLKK; AKICDQLKKE; KICDQLKKEG; ICDQLKKEGK; CDQLKKEGKD; DQLKKEGKDK; QLKKEGKDKI; LKKEGKDKII; KKEGKDKIIL; KEGKDKIILE; EGKDKIILEK; GKDKIILEKT; KDKIILEKTG; DKIILEKTGL; KIILEKTGLV;

	IILEKTGLVL; ILEKTGLVLD; LEKTGLVLDS; EKTGLVLDSY; KTGLVLDSYF; TGLVLDSYFS; GLVLDSYFSG; LVLDSYFSGT; VLDSYFSGTK; LDSYFSGTKI; DSYFSGTKIM; SYFSGTKIMW; YFSGTKIMWI; FSGTKIMWIL; SGTKIMWILD; GTKIMWILDN; TKIMWILDNV; KIMWILDNVE; IMWILDNVEG; MWILDNVEGA; WILDNVEGAR; ILDNVEGARQ; LDNVEGARQR; DNVEGARQRA; NVEGARQRAE; VEGARQRAEN; EGARQRAENG; GARQRAENGE; ARQRAENGEL; RQRAENGELC; QRAENGELCF; RAENGELCFG; AENGELCFGT; ENGELCFGTI; NGELCFGTID; GELCFGTIDT; ELCFGTIDTW; LCFGTIDTWI; CFGTIDTWIL; FGTIDTWILW; GTIDTWILWN; TIDTWILWNL; IDTWILWNLT; DTWILWNLTQ; TWILWNLTQK; WILWNLTQKK; ILWNLTQKKE; LWNLTQKKEH; WNLTQKKEHA; NLTQKKEHAT; LTQKKEHATD; TQKKEHATDY; QKKEHATDYS; KKEHATDYSN; KEHATDYSNA; EHATDYSNAS; HATDYSNASR; ATDYSNASRT; TDYSNASRTL; DYSNASRTLL; YSNASRTLLL; SNASRTLLLN; NASRTLLLNI; ASRTLLLNIK; SRTLLLNIKT; RTLLLNIKTL; TLLLNIKTLE; LLLNIKTLEW; LLNIKTLEWD; LNIKTLEWDD; NIKTLEWDDE; IKTLEWDDEL; KTLEWDDELL; TLEWDDELLS; LEWDDELLSI; EWDDELLSIL; WDDELLSILN; DDELLSILNV; DELLSILNVP; ELLSILNVPR; LLSILNVPRA; LSILNVPRAI; SILNVPRAIL; ILNVPRAILP; LNVPRAILPE; NVPRAILPEL; VPRAILPELK; PRAILPELKE; RAILPELKES; AILPELKESS; ILPELKESST; LPELKESSTI; PELKESSTIY; ELKESSTIYG; LKESSTIYGK; KESSTIYGKT; ESSTIYGKTD; SSTIYGKTDK; STIYGKTDKA; TIYGKTDKAL; IYGKTDKALF; YGKTDKALFG; GKTDKALFGA; KTDKALFGAE; TDKALFGAEI; DKALFGAEIP; KALFGAEIPI; ALFGAEIPIA; LFGAEIPIAG; FGAEIPIAGI; GAEIPIAGIA; AEIPIAGIAG; EIPIAGIAGD; IPIAGIAGDQ; PIAGIAGDQF; IAGIAGDQFA; AGIAGDQFAA; GIAGDQFAAT; IAGDQFAATF; AGDQFAATFG; GDQFAATFGQ; DQFAATFGQA; QFAATFGQAC; FAATFGQACL; AATFGQACLK; ATFGQACLKK; TFGQACLKKG; FGQACLKKGM; GQACLKKGMA; QACLKKGMAK; ACLKKGMAKN; CLKKGMAKNT; LKKGMAKNTY; KKGMAKNTYG; KGMAKNTYGT; GMAKNTYGTG; MAKNTYGTGC; AKNTYGTGCF; KNTYGTGCFL; NTYGTGCFLT; TYGTGCFLTV; YGTGCFLTVN; GTGCFLTVNI; TGCFLTVNIG; GCFLTVNIGK; CFLTVNIGKE; FLTVNIGKEP; LTVNIGKEPI; TVNIGKEPII; VNIGKEPIIS; NIGKEPIISH; IGKEPIISHD; GKEPIISHDK; KEPIISHDKL; EPIISHDKLL; PIISHDKLLT; IISHDKLLTS; ISHDKLLTSI; SHDKLLTSIA; HDKLLTSIAW; DKLLTSIAWG; KLLTSIAWGR; LLTSIAWGRK; LTSIAWGRKK; TSIAWGRKKS; SIAWGRKKSV; IAWGRKKSVT; AWGRKKSVTY; WGRKKSVTYV; GRKKSVTYVL; RKKSVTYVLE; KKSVTYVLEG; KSVTYVLEGS; SVTYVLEGSV; VTYVLEGSVF; TYVLEGSVFI; YVLEGSVFIG; VLEGSVFIGG; LEGSVFIGGA; EGSVFIGGAV; GSVFIGGAVI; SVFIGGAVIQ; VFIGGAVIQW; FIGGAVIQWL; IGGAVIQWLR; GGAVIQWLRD; GAVIQWLRDG; AVIQWLRDGL; VIQWLRDGLE; IQWLRDGLEF; QWLRDGLEFF; WLRDGLEFFR; LRDGLEFFRK; RDGLEFFRKS; DGLEFFRKSS; GLEFFRKSSD; LEFFRKSSDA; EFFRKSSDAE; FFRKSSDAEA; FRKSSDAEAL; RKSSDAEALA; KSSDAEALAS; SSDAEALASS; SDAEALASSV;

DAEALASSVS; AEALASSVSD; EALASSVSDN; ALASSVSDNG;
LASSVSDNGG; ASSVSDNGGV; SSVSDNGGVY; SVSDNGGVYF;
VSDNGGVYFV; SDNGGVYFVP; DNGGVYFVPA; NGGVYFVPAF;
GGVYFVPAFV; GVYFVPAFVG; VYFVPAFVGL; YFVPAFVGLG;
FVPAFVGLGA; VPAFVGLGAP; PAFVGLGAPH; AFVGLGAPHW;
FVGLGAPHWD; VGLGAPHWDS; GLGAPHWDSY; LGAPHWDSYA;
GAPHWDSYAR; APHWDSYARG; PHWDSYARGT; HWDSYARGTI;
WDSYARGTII; DSYARGTIIG; SYARGTIIGI; YARGTIIGIT;
ARGTIIGITR; RGTIIGITRG; GTIIGITRGS; TIIGITRGST;
IIGITRGSTK; IGITRGSTKA; GITRGSTKAH; ITRGSTKAHI;
TRGSTKAHIT; RGSTKAHITR; GSTKAHITRA; STKAHITRAA;
TKAHITRAAL; KAHITRAALE; AHITRAALES; HITRAALESI;
ITRAALESIA; TRAALESIAF; RAALESIAFQ; AALESIAFQS;
ALESIAFQSF; LESIAFQSFD; ESIAFQSFDI; SIAFQSFDIL;
IAFQSFDILN; AFQSFDILNT; FQSFDILNTM; QSFDILNTMK;
SFDILNTMKK; FDILNTMKKS; DILNTMKKSI; ILNTMKKSIP;
LNTMKKSIPN; NTMKKSIPNF; TMKKSIPNFE; MKKSIPNFEI;
KKSIPNFEIQ; KSIPNFEIQE; SIPNFEIQEL; IPNFEIQELR;
PNFEIQELRV; NFEIQELRVD; FEIQELRVDG; EIQELRVDGG;
IQELRVDGGA; QELRVDGGAS; ELRVDGGASQ; LRVDGGASQN;
RVDGGASQNN; VDGGASQNNL; DGGASQNNLL; GGASQNNLLM;
GASQNNLLMQ; ASQNNLLMQF; SQNNLLMQFQ; QNNLLMQFQA;
NNLLMQFQAD; NLLMQFQADL; LLMQFQADLL; LMQFQADLLE;
MQFQADLLEC; QFQADLLECK; FQADLLECKV; QADLLECKVV;
ADLLECKVVR; DLLECKVVRP; LLECKVVRPK; LECKVVRPKI;
ECKVVRPKIT; CKVVRPKITE; KVVRPKITET; VVRPKITETT;
VRPKITETTA; RPKITETTAL; PKITETTALG; KITETTALGA;
ITETTALGAA; TETTALGAAY; ETTALGAAYL; TTALGAAYLA;
TALGAAYLAG; ALGAAYLAGL; LGAAYLAGLA; GAAYLAGLAT;
AAYLAGLATG; AYLAGLATGY; YLAGLATGYW; LAGLATGYWQ;
AGLATGYWQS; GLATGYWQSA; LATGYWQSAE; ATGYWQSAEE;
TGYWQSAEEI; GYWQSAEEIV; YWQSAEEIVS; WQSAEEIVSL;
QSAEEIVSLW; SAEEIVSLWQ; AEEIVSLWQV; EEIVSLWQVD;
EIVSLWQVDK; IVSLWQVDKI; VSLWQVDKIF; SLWQVDKIFE;
LWQVDKIFEP; WQVDKIFEPS; QVDKIFEPSM; VDKIFEPSMP;
DKIFEPSMPK; KIFEPSMPKN; IFEPSMPKNQ; FEPSMPKNQK;
EPSMPKNQKE; PSMPKNQKEK; SMPKNQKEKL; MPKNQKEKLL;
PKNQKEKLLE; KNQKEKLLEN; NQKEKLLENW; QKEKLLENWN;
KEKLLENWNK; EKLLENWNKA; KLLENWNKAV; LLENWNKAVG;
LENWNKAVGK; ENWNKAVGKA; NWNKAVGKAK; WNKAVGKAKS;
NKAVGKAKSW; KAVGKAKSWI; AVGKAKSWIQ; VGKAKSWIQN;
GKAKSWIQNS; KAKSWIQNSH; AKSWIQNSHS; KSWIQNSHSS;

11 mers:
MKYILSIDQGT; KYILSIDQGTT; YILSIDQGTTS; ILSIDQGTTSS;
LSIDQGTTSSR; SIDQGTTSSRA; IDQGTTSSRAM; DQGTTSSRAMV;
QGTTSSRAMVF; GTTSSRAMVFD; TTSSRAMVFDK; TSSRAMVFDKN;
SSRAMVFDKNA; SRAMVFDKNAN; RAMVFDKNANI; AMVFDKNANIK;
MVFDKNANIKG; VFDKNANIKGF; FDKNANIKGFA; DKNANIKGFAQ;
KNANIKGFAQK; NANIKGFAQKE; ANIKGFAQKEF; NIKGFAQKEFT;
IKGFAQKEFTQ; KGFAQKEFTQI; GFAQKEFTQIY; FAQKEFTQIYP;

	AQKEFTQIYPQ; QKEFTQIYPQP; KEFTQIYPQPS; EFTQIYPQPSW; FTQIYPQPSWV; TQIYPQPSWVE; QIYPQPSWVEH; IYPQPSWVEHD; YPQPSWVEHDP; PQPSWVEHDPT; QPSWVEHDPTE; PSWVEHDPTEI; SWVEHDPTEIW; WVEHDPTEIWG; VEHDPTEIWGS; EHDPTEIWGSQ; HDPTEIWGSQL; DPTEIWGSQLG; PTEIWGSQLGV; TEIWGSQLGVI; EIWGSQLGVIT; IWGSQLGVITE; WGSQLGVITEA; GSQLGVITEAM; SQLGVITEAMA; QLGVITEAMAN; LGVITEAMANA; GVITEAMANAR; VITEAMANARI; ITEAMANARIL; TEAMANARILP; EAMANARILPN; AMANARILPNE; MANARILPNEI; ANARILPNEID; NARILPNEIDA; ARILPNEIDAI; RILPNEIDAIG; ILPNEIDAIGI; LPNEIDAIGIT; PNEIDAIGITN; NEIDAIGITNQ; EIDAIGITNQR; IDAIGITNQRE; DAIGITNQRET; AIGITNQRETT; IGITNQRETTV; GITNQRETTVI; ITNQRETTVIW; TNQRETTVIWE; NQRETTVIWEK; QRETTVIWEKN; RETTVIWEKNT; ETTVIWEKNTG; TTVIWEKNTGK; TVIWEKNTGKP; VIWEKNTGKPI; IWEKNTGKPIY; WEKNTGKPIYN; EKNTGKPIYNA; KNTGKPIYNAI; NTGKPIYNAIV; TGKPIYNAIVW; GKPIYNAIVWQ; KPIYNAIVWQD; PIYNAIVWQDR; IYNAIVWQDRR; YNAIVWQDRRT; NAIVWQDRRTA; AIVWQDRRTAK; IVWQDRRTAKI; VWQDRRTAKIC; WQDRRTAKICD; QDRRTAKICDQ; DRRTAKICDQL; RRTAKICDQLK; RTAKICDQLKK; TAKICDQLKKE; AKICDQLKKEG; KICDQLKKEGK; ICDQLKKEGKD; CDQLKKEGKDK; DQLKKEGKDKI; QLKKEGKDKII; LKKEGKDKIIL; KKEGKDKIILE; KEGKDKIILEK; EGKDKIILEKT; GKDKIILEKTG; KDKIILEKTGL; DKIILEKTGLV; KIILEKTGLVL; IILEKTGLVLD; ILEKTGLVLDS; LEKTGLVLDSY; EKTGLVLDSYF; KTGLVLDSYFS; TGLVLDSYFSG; GLVLDSYFSGT; LVLDSYFSGTK; VLDSYFSGTKI; LDSYFSGTKIM; DSYFSGTKIMW; SYFSGTKIMWI; YFSGTKIMWIL; FSGTKIMWILD; SGTKIMWILDN; GTKIMWILDNV; TKIMWILDNVE; KIMWILDNVEG; IMWILDNVEGA; MWILDNVEGAR; WILDNVEGARQ; ILDNVEGARQR; LDNVEGARQRA; DNVEGARQRAE; NVEGARQRAEN; VEGARQRAENG; EGARQRAENGE; GARQRAENGEL; ARQRAENGELC; RQRAENGELCF; QRAENGELCFG; RAENGELCFGT; AENGELCFGTI; ENGELCFGTID; NGELCFGTIDT; GELCFGTIDTW; ELCFGTIDTWI; LCFGTIDTWIL; CFGTIDTWILW; FGTIDTWILWN; GTIDTWILWNL; TIDTWILWNLT; IDTWILWNLTQ; DTWILWNLTQK; TWILWNLTQKK; WILWNLTQKKE; ILWNLTQKKEH; LWNLTQKKEHA; WNLTQKKEHAT; NLTQKKEHATD; LTQKKEHATDY; TQKKEHATDYS; QKKEHATDYSN; KKEHATDYSNA; KEHATDYSNAS; EHATDYSNASR; HATDYSNASRT; ATDYSNASRTL; TDYSNASRTLL; DYSNASRTLLL; YSNASRTLLLN; SNASRTLLLNI; NASRTLLLNIK; ASRTLLLNIKT; SRTLLLNIKTL; RTLLLNIKTLE; TLLLNIKTLEW; LLLNIKTLEWD; LLNIKTLEWDD; LNIKTLEWDDE; NIKTLEWDDEL; IKTLEWDDELL; KTLEWDDELLS; TLEWDDELLSI; LEWDDELLSIL; EWDDELLSILN; WDDELLSILNV; DDELLSILNVP; DELLSILNVPR; ELLSILNVPRA; LLSILNVPRAI; LSILNVPRAIL; SILNVPRAILP; ILNVPRAILPE; LNVPRAILPEL; NVPRAILPELK; VPRAILPELKE; PRAILPELKES; RAILPELKESS; AILPELKESST; ILPELKESSTI; LPELKESSTIY; PELKESSTIYG; ELKESSTIYGK; LKESSTIYGKT; KESSTIYGKTD; ESSTIYGKTDK; SSTIYGKTDKA; STIYGKTDKAL; TIYGKTDKALF; IYGKTDKALFG; YGKTDKALFGA; GKTDKALFGAE; KTDKALFGAEI; TDKALFGAEIP; DKALFGAEIPI; KALFGAEIPIA; ALFGAEIPIAG; LFGAEIPIAGI; FGAEIPIAGIA; GAEIPIAGIAG; AEIPIAGIAGD;

	EIPIAGIAGDQ; IPIAGIAGDQF; PIAGIAGDQFA; IAGIAGDQFAA; AGIAGDQFAAT; GIAGDQFAATF; IAGDQFAATFG; AGDQFAATFGQ; GDQFAATFGQA; DQFAATFGQAC; QFAATFGQACL; FAATFGQACLK; AATFGQACLKK; ATFGQACLKKG; TFGQACLKKGM; FGQACLKKGMA; GQACLKKGMAK; QACLKKGMAKN; ACLKKGMAKNT; CLKKGMAKNTY; LKKGMAKNTYG; KKGMAKNTYGT; KGMAKNTYGTG; GMAKNTYGTGC; MAKNTYGTGCF; AKNTYGTGCFL; KNTYGTGCFLT; NTYGTGCFLTV; TYGTGCFLTVN; YGTGCFLTVNI; GTGCFLTVNIG; TGCFLTVNIGK; GCFLTVNIGKE; CFLTVNIGKEP; FLTVNIGKEPI; LTVNIGKEPII; TVNIGKEPIIS; VNIGKEPIISH; NIGKEPIISHD; IGKEPIISHDK; GKEPIISHDKL; KEPIISHDKLL; EPIISHDKLLT; PIISHDKLLTS; IISHDKLLTSI; ISHDKLLTSIA; SHDKLLTSIAW; HDKLLTSIAWG; DKLLTSIAWGR; KLLTSIAWGRK; LLTSIAWGRKK; LTSIAWGRKKS; TSIAWGRKKSV; SIAWGRKKSVT; IAWGRKKSVTY; AWGRKKSVTYV; WGRKKSVTYVL; GRKKSVTYVLE; RKKSVTYVLEG; KKSVTYVLEGS; KSVTYVLEGSV; SVTYVLEGSVF; VTYVLEGSVFI; TYVLEGSVFIG; YVLEGSVFIGG; VLEGSVFIGGA; LEGSVFIGGAV; EGSVFIGGAVI; GSVFIGGAVIQ; SVFIGGAVIQW; VFIGGAVIQWL; FIGGAVIQWLR; IGGAVIQWLRD; GGAVIQWLRDG; GAVIQWLRDGL; AVIQWLRDGLE; VIQWLRDGLEF; IQWLRDGLEFF; QWLRDGLEFFR; WLRDGLEFFRK; LRDGLEFFRKS; RDGLEFFRKSS; DGLEFFRKSSD; GLEFFRKSSDA; LEFFRKSSDAE; EFFRKSSDAEA; FFRKSSDAEAL; FRKSSDAEALA; RKSSDAEALAS; KSSDAEALASS; SSDAEALASSV; SDAEALASSVS; DAEALASSVSD; AEALASSVSDN; EALASSVSDNG; ALASSVSDNGG; LASSVSDNGGV; ASSVSDNGGVY; SSVSDNGGVYF; SVSDNGGVYFV; VSDNGGVYFVP; SDNGGVYFVPA; DNGGVYFVPAF; NGGVYFVPAFV; GGVYFVPAFVG; GVYFVPAFVGL; VYFVPAFVGLG; YFVPAFVGLGA; FVPAFVGLGAP; VPAFVGLGAPH; PAFVGLGAPHW; AFVGLGAPHWD; FVGLGAPHWDS; VGLGAPHWDSY; GLGAPHWDSYA; LGAPHWDSYAR; GAPHWDSYARG; APHWDSYARGT; PHWDSYARGTI; HWDSYARGTII; WDSYARGTIIG; DSYARGTIIGI; SYARGTIIGIT; YARGTIIGITR; ARGTIIGITRG; RGTIIGITRGS; GTIIGITRGST; TIIGITRGSTK; IIGITRGSTKA; IGITRGSTKAH; GITRGSTKAHI; ITRGSTKAHIT; TRGSTKAHITR; RGSTKAHITRA; GSTKAHITRAA; STKAHITRAAL; TKAHITRAALE; KAHITRAALES; AHITRAALESI; HITRAALESIA; ITRAALESIAF; TRAALESIAFQ; RAALESIAFQS; AALESIAFQSF; ALESIAFQSFD; LESIAFQSFDI; ESIAFQSFDIL; SIAFQSFDILN; IAFQSFDILNT; AFQSFDILNTM; FQSFDILNTMK; QSFDILNTMKK; SFDILNTMKKS; FDILNTMKKSI; DILNTMKKSIP; ILNTMKKSIPN; LNTMKKSIPNF; NTMKKSIPNFE; TMKKSIPNFEI; MKKSIPNFEIQ; KKSIPNFEIQE; KSIPNFEIQEL; SIPNFEIQELR; IPNFEIQELRV; PNFEIQELRVD; NFEIQELRVDG; FEIQELRVDGG; EIQELRVDGGA; IQELRVDGGAS; QELRVDGGASQ; ELRVDGGASQN; LRVDGGASQNN; RVDGGASQNNL; VDGGASQNNLL; DGGASQNNLLM; GGASQNNLLMQ; GASQNNLLMQF; ASQNNLLMQFQ; SQNNLLMQFQA; QNNLLMQFQAD; NNLLMQFQADL; NLLMQFQADLL; LLMQFQADLLE; LMQFQADLLEC; MQFQADLLECK; QFQADLLECKV; FQADLLECKVV; QADLLECKVVR; ADLLECKVVRP; DLLECKVVRPK; LLECKVVRPKI; LECKVVRPKIT; ECKVVRPKITE; CKVVRPKITET; KVVRPKITETT; VVRPKITETTA; VRPKITETTAL; RPKITETTALG; PKITETTALGA; KITETTALGAA; ITETTALGAAY; TETTALGAAYL; ETTALGAAYLA; TTALGAAYLAG;

	TALGAAYLAGL; ALGAAYLAGLA; LGAAYLAGLAT; GAAYLAGLATG; AAYLAGLATGY; AYLAGLATGYW; YLAGLATGYWQ; LAGLATGYWQS; AGLATGYWQSA; GLATGYWQSAE; LATGYWQSAEE; ATGYWQSAEEI; TGYWQSAEEIV; GYWQSAEEIVS; YWQSAEEIVSL; WQSAEEIVSLW; QSAEEIVSLWQ; SAEEIVSLWQV; AEEIVSLWQVD; EEIVSLWQVDK; EIVSLWQVDKI; IVSLWQVDKIF; VSLWQVDKIFE; SLWQVDKIFEP; LWQVDKIFEPS; WQVDKIFEPSM; QVDKIFEPSMP; VDKIFEPSMPK; DKIFEPSMPKN; KIFEPSMPKNQ; IFEPSMPKNQK; FEPSMPKNQKE; EPSMPKNQKEK; PSMPKNQKEKL; SMPKNQKEKLL; MPKNQKEKLLE; PKNQKEKLLEN; KNQKEKLLENW; NQKEKLLENWN; QKEKLLENWNK; KEKLLENWNKA; EKLLENWNKAV; KLLENWNKAVG; LLENWNKAVGK; LENWNKAVGKA; ENWNKAVGKAK; NWNKAVGKAKS; WNKAVGKAKSW; NKAVGKAKSWI; KAVGKAKSWIQ; AVGKAKSWIQN; VGKAKSWIQNS; GKAKSWIQNSH; KAKSWIQNSHS; AKSWIQNSHSS;
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	KILNILNK; ILNILNKN; LNILNKNL; NILNKNLK; ILNKNLKY; LNKNLKYR; NKNLKYRP; KNLKYRPE; NLKYRPEN; LKYRPENQ; KYRPENQK; YRPENQKV; RPENQKVF; PENQKVFK; ENQKVFKS; NQKVFKSS; QKVFKSSL; KVFKSSLT; VFKSSLTN; FKSSLTNK; KSSLTNKE; SSLTNKES; SLTNKESR; LTNKESRL; TNKESRLI; NKESRLIK; KESRLIKL; ESRLIKLK; SRLIKLKR; RLIKLKRM; LIKLKRML; IKLKRMLI; KLKRMLIL; LKRMLILT; KRMLILTY; RMLILTYW; MLILTYWP; LILTYWPV; ILTYWPVG; LTYWPVGC; TYWPVGCL; YWPVGCLS; WPVGCLSK; PVGCLSKN; VGCLSKNI; GCLSKNIF; CLSKNIFI; LSKNIFIK; SKNIFIKI; KNIFIKIL; NIFIKILI; IFIKILIK; FIKILIKX; IKILIKXY; KILIKXYK; ILIKXYKY; LIKXYKYL; IKXYKYLE; KXYKYLEE; XYKYLEEE; YKYLEEEI; KYLEEEIL; YLEEEILA; LEEEILAL; EEEILALK; EEILALKY; EILALKYN; ILALKYNE; LALKYNEI; ALKYNEIL; LKYNEILN; KYNEILNY; YNEILNYL; NEILNYLR; EILNYLRA; ILNYLRAL; LNYLRALK; NYLRALKT; YLRALKTL; LRALKTLS; RALKTLSL; ALKTLSLN; LKTLSLNE; KTLSLNEI; TLSLNEIF; LSLNEIFY; SLNEIFYK; LNEIFYKG; NEIFYKGS; EIFYKGSS; IFYKGSSK; FYKGSSKN; YKGSSKNI; KGSSKNIS; GSSKNISF; SSKNISFN; SKNISFNY; KNISFNYF; NISFNYFF; ISFNYFFS; SFNYFFSD; FNYFFSDF; NYFFSDFT; YFFSDFTQ; FFSDFTQY; FSDFTQYA; SDFTQYAP; DFTQYAPK; FTQYAPKD; TQYAPKDF; QYAPKDFQ; YAPKDFQD; APKDFQDT; PKDFQDTL; KDFQDTLK; DFQDTLKC; FQDTLKCY; QDTLKCYL; DTLKCYLY; TLKCYLYV; LKCYLYVI; KCYLYVIE; CYLYVIEK; YLYVIEKT; LYVIEKTI; YVIEKTIT; VIEKTITK; IEKTITKK; EKTITKKY; KTITKKYL; TITKKYLT; ITKKYLTW; TKKYLTWF; KKYLTWFF; KYLTWFFK; YLTWFFKD; LTWFFKDK; TWFFKDKI; WFFKDKIS; FFKDKISN; FKDKISNN; KDKISNNW; DKISNNWE; KISNNWES; ISNNWESF; SNNWESFI; NNWESFID; NWESFIDA; WESFIDAL; ESFIDALE; SFIDALEY; FIDALEYI; IDALEYIE; DALEYIEK; ALEYIEKH; LEYIEKHK; EYIEKHKL; YIEKHKLI; IEKHKLIN; EKHKLINI; KHKLINIK; HKLINIKE; KLINIKEK; LINIKEKI; INIKEKIK; NIKEKIKE; IKEKIKEI; KEKIKEII; EKIKEIIT; KIKEIITA; IKEIITAK; KEIITAKF; EIITAKFQ; IITAKFQT; ITAKFQTE; TAKFQTED; AKFQTEDF; KFQTEDFF; FQTEDFFI; QTEDFFIS; TEDFFISF; EDFFISFD; DFFISFDK; FFISFDKT; FISFDKTN; ISFDKTNF; SFDKTNFN; FDKTNFNP; DKTNFNPY; KTNFNPYE; TNFNPYES; NFNPYESS; FNPYESSI; NPYESSIF; PYESSIFK; YESSIFKE; ESSIFKER; SSIFKERY; SIFKERYI; IFKERYIK; FKERYIKS; KERYIKSA; ERYIKSAF; RYIKSAFL; YIKSAFLE; IKSAFLEI; KSAFLEII; SAFLEIIM; AFLEIIMH; FLEIIMHY; LEIIMHYV; EIIMHYVK; IIMHYVKK; IMHYVKKN; MHYVKKNS; HYVKKNSQ; YVKKNSQN; VKKNSQNI; KKNSQNIE; KNSQNIET; NSQNIETY; SQNIETYG; QNIETYGW; NIETYGWI; IETYGWIA; ETYGWIAF; TYGWIAFY; YGWIAFYI; GWIAFYIY; WIAFYIYA; IAFYIYAD; AFYIYADN; FYIYADNK; YIYADNKD; IYADNKDK; YADNKDKK; ADNKDKKI; DNKDKKIF; NKDKKIFC; KDKKIFCQ; DKKIFCQR; KKIFCQRM; KIFCQRMK; IFCQRMKE; FCQRMKEF; CQRMKEFF; QRMKEFFK; RMKEFFKS; MKEFFKSK; KEFFKSKT; EFFKSKTF; FFKSKTFE; FKSKTFEI; KSKTFEIQ; SKTFEIQN;

KTFEIQNQ; TFEIQNQI; FEIQNQIF; EIQNQIFV; IQNQIFVY;
QNQIFVYF; NQIFVYFL; QIFVYFLS; IFVYFLSF; FVYFLSFY;
VYFLSFYP; YFLSFYPN; FLSFYPNI; LSFYPNIE; SFYPNIEY;
FYPNIEYK; YPNIEYKH; PNIEYKHF; NIEYKHFK; IEYKHFKF;
EYKHFKFI; YKHFKFIS; KHFKFISD; HFKFISDI; FKFISDIL;
KFISDILL; FISDILLY; ISDILLYL; SDILLYLD; DILLYLDE;
ILLYLDEN; LLYLDENK; LYLDENKI; YLDENKIT; LDENKITI;
DENKITIP; ENKITIPK; NKITIPKK; KITIPKKI; ITIPKKII;
TIPKKIIK; IPKKIIKI; PKKIIKIQ; KKIIKIQK; KIIKIQKI;
IIKIQKIN; IKIQKINP; KIQKINPN; IQKINPNQ; QKINPNQL;
KINPNQLD; INPNQLDY; NPNQLDYQ; PNQLDYQK; NQLDYQKS;
QLDYQKSY; LDYQKSYL; DYQKSYLL; YQKSYLLI; QKSYLLIK;
KSYLLIKS; SYLLIKSL; YLLIKSLK; LLIKSLKT; LIKSLKTR;
IKSLKTRS; KSLKTRSR; SLKTRSRI; LKTRSRIL; KTRSRILK;
TRSRILKI; RSRILKII; SRILKIII; RILKIIIK; ILKIIIKN;
LKIIIKNI; KIIIKNIR; IIIKNIRF; IIKNIRFN; IKNIRFNL;
KNIRFNLI; NIRFNLIE; IRFNLIEK; RFNLIEKL; FNLIEKLE;
NLIEKLED; LIEKLEDE; IEKLEDEN; EKLEDENE; KLEDENEK;
LEDENEKK; EDENEKKL; DENEKKLL; ENEKKLLP; NEKKLLPA;
EKKLLPAM; KKLLPAMC; KLLPAMCY; LLPAMCYL; LPAMCYLI;
PAMCYLIY; AMCYLIYC; MCYLIYCE; CYLIYCEN; YLIYCENL;
LIYCENLV; IYCENLVE; YCENLVEL; CENLVELK; ENLVELKN;
NLVELKNN; LVELKNNR; VELKNNRK; ELKNNRKI; LKNNRKIK;
KNNRKIKS; NNRKIKSN; NRKIKSNE; RKIKSNEK; KIKSNEKN;
IKSNEKNS; KSNEKNSL; SNEKNSLL; NEKNSLLE; EKNSLLEF;
KNSLLEFI; NSLLEFIS; SLLEFISF; LLEFISFF; LEFISFFK;
EFISFFKT; FISFFKTK; ISFFKTKL; SFFKTKLK; FFKTKLKQ;
FKTKLKQK; KTKLKQKI; TKLKQKIN; KLKQKINF; LKQKINFK;
KQKINFKK; QKINFKKE; KINFKKEL; INFKKELM; NFKKELMK;
FKKELMKS; KKELMKSK; KELMKSKG; ELMKSKGI;

9 mers:
MKTIKKDSE; KTIKKDSEF; TIKKDSEFY; IKKDSEFYD; KKDSEFYDS;
KDSEFYDSL; DSEFYDSLA; SEFYDSLAT; EFYDSLATL; FYDSLATLK;
YDSLATLKK; DSLATLKKH; SLATLKKHI; LATLKKHIN; ATLKKHINK;
TLKKHINKY; LKKHINKYI; KKHINKYIE; KHINKYIEE; HINKYIEEK;
INKYIEEKV; NKYIEEKVL; KYIEEKVLK; YIEEKVLKY; IEEKVLKYS;
EEKVLKYSI; EKVLKYSIS; KVLKYSISS; VLKYSISSQ; LKYSISSQL;
KYSISSQLY; YSISSQLYK; SISSQLYKL; ISSQLYKLE; SSQLYKLEK;
SQLYKLEKP; QLYKLEKPE; LYKLEKPEI; YKLEKPEII; KLEKPEIIE;
LEKPEIIEL; EKPEIIELI; KPEIIELIK; PEIIELIKI; EIIELIKIS;
IIELIKISN; IELIKISND; ELIKISNDY; LIKISNDYE; IKISNDYEK;
KISNDYEKE; ISNDYEKEK; SNDYEKEKN; NDYEKEKNA; DYEKEKNAF;
YEKEKNAFN; EKEKNAFNT; KEKNAFNTS; EKNAFNTSL; KNAFNTSLE;
NAFNTSLEE; AFNTSLEEC; FNTSLEECY; NTSLEECYY; TSLEECYYK;
SLEECYYKN; LEECYYKNT; EECYYKNTQ; ECYYKNTQN; CYYKNTQNE;
YYKNTQNEA; YKNTQNEAI; KNTQNEAIK; NTQNEAIKK; TQNEAIKKW;
QNEAIKKWI; NEAIKKWIL; EAIKKWILE; AIKKWILEI; IKKWILEIV;
KKWILEIVR; KWILEIVRN; WILEIVRNK; ILEIVRNKN; LEIVRNKNF;
EIVRNKNFI; IVRNKNFIQ; VRNKNFIQI; RNKNFIQIS; NKNFIQISK;
KNFIQISKE; NFIQISKEA; FIQISKEAN; IQISKEANL; QISKEANLN;

	ISKEANLNT; SKEANLNTK; KEANLNTKK; EANLNTKKL; ANLNTKKLG; NLNTKKLGT; LNTKKLGTT; NTKKLGTTY; TKKLGTTYK; KKLGTTYKL; KLGTTYKLK; LGTTYKLKS; GTTYKLKSS; TTYKLKSSN; TYKLKSSNF; YKLKSSNFL; KLKSSNFLK; LKSSNFLKL; KSSNFLKLI; SSNFLKLIE; SNFLKLIEI; NFLKLIEIQ; FLKLIEIQN; LKLIEIQNS; KLIEIQNSP; LIEIQNSPY; IEIQNSPYY; EIQNSPYYS; IQNSPYYSQ; QNSPYYSQE; NSPYYSQEK; SPYYSQEKK; PYYSQEKKD; YYSQEKKDI; YSQEKKDIY; SQEKKDIYK; QEKKDIYKQ; EKKDIYKQI; KKDIYKQII; KDIYKQIIL; DIYKQIILN; IYKQIILNF; YKQIILNFS; KQIILNFSS; QIILNFSSN; IILNFSSNI; ILNFSSNIN; LNFSSNINI; NFSSNINID; FSSNINIDS; SSNINIDSL; SNINIDSLE; NINIDSLEQ; INIDSLEQT; NIDSLEQTI; IDSLEQTID; DSLEQTIDI; SLEQTIDIL; LEQTIDILV; EQTIDILVA; QTIDILVAV; TIDILVAVR; IDILVAVRN; DILVAVRNR; ILVAVRNRN; LVAVRNRNK; VAVRNRNKI; AVRNRNKIK; VRNRNKIKI; RNRNKIKIL; NRNKIKILN; RNKIKILNI; NKIKILNIL; KIKILNILN; IKILNILNK; KILNILNKN; ILNILNKNL; LNILNKNLK; NILNKNLKY; ILNKNLKYR; LNKNLKYRP; NKNLKYRPE; KNLKYRPEN; NLKYRPENQ; LKYRPENQK; KYRPENQKV; YRPENQKVF; RPENQKVFK; PENQKVFKS; ENQKVFKSS; NQKVFKSSL; QKVFKSSLT; KVFKSSLTN; VFKSSLTNK; FKSSLTNKE; KSSLTNKES; SSLTNKESR; SLTNKESRL; LTNKESRLI; TNKESRLIK; NKESRLIKL; KESRLIKLK; ESRLIKLKR; SRLIKLKRM; RLIKLKRML; LIKLKRMLI; IKLKRMLIL; KLKRMLILT; LKRMLILTY; KRMLILTYW; RMLILTYWP; MLILTYWPV; LILTYWPVG; ILTYWPVGC; LTYWPVGCL; TYWPVGCLS; YWPVGCLSK; WPVGCLSKN; PVGCLSKNI; VGCLSKNIF; GCLSKNIFI; CLSKNIFIK; LSKNIFIKI; SKNIFIKIL; KNIFIKILI; NIFIKILIK; IFIKILIKX; FIKILIKXY; IKILIKXYK; KILIKXYKY; ILIKXYKYL; LIKXYKYLE; IKXYKYLEE; KXYKYLEEE; XYKYLEEEI; YKYLEEEIL; KYLEEEILA; YLEEEILAL; LEEEILALK; EEEILALKY; EEILALKYN; EILALKYNE; ILALKYNEI; LALKYNEIL; ALKYNEILN; LKYNEILNY; KYNEILNYL; YNEILNYLR; NEILNYLRA; EILNYLRAL; ILNYLRALK; LNYLRALKT; NYLRALKTL; YLRALKTLS; LRALKTLSL; RALKTLSLN; ALKTLSLNE; LKTLSLNEI; KTLSLNEIF; TLSLNEIFY; LSLNEIFYK; SLNEIFYKG; LNEIFYKGS; NEIFYKGSS; EIFYKGSSK; IFYKGSSKN; FYKGSSKNI; YKGSSKNIS; KGSSKNISF; GSSKNISFN; SSKNISFNY; SKNISFNYF; KNISFNYFF; NISFNYFFS; ISFNYFFSD; SFNYFFSDF; FNYFFSDFT; NYFFSDFTQ; YFFSDFTQY; FFSDFTQYA; FSDFTQYAP; SDFTQYAPK; DFTQYAPKD; FTQYAPKDF; TQYAPKDFQ; QYAPKDFQD; YAPKDFQDT; APKDFQDTL; PKDFQDTLK; KDFQDTLKC; DFQDTLKCY; FQDTLKCYL; QDTLKCYLY; DTLKCYLYV; TLKCYLYVI; LKCYLYVIE; KCYLYVIEK; CYLYVIEKT; YLYVIEKTI; LYVIEKTIT; YVIEKTITK; VIEKTITKK; IEKTITKKY; EKTITKKYL; KTITKKYLT; TITKKYLTW; ITKKYLTWF; TKKYLTWFF; KKYLTWFFK; KYLTWFFKD; YLTWFFKDK; LTWFFKDKI; TWFFKDKIS; WFFKDKISN; FFKDKISNN; FKDKISNNW; KDKISNNWE; DKISNNWES; KISNNWESF; ISNNWESFI; SNNWESFID; NNWESFIDA; NWESFIDAL; WESFIDALE; ESFIDALEY; SFIDALEYI; FIDALEYIE; IDALEYIEK; DALEYIEKH; ALEYIEKHK; LEYIEKHKL; EYIEKHKLI; YIEKHKLIN; IEKHKLINI; EKHKLINIK; KHKLINIKE; HKLINIKEK; KLINIKEKI; LINIKEKIK; INIKEKIKE; NIKEKIKEI; IKEKIKEII; KEKIKEIIT; EKIKEIITA; KIKEIITAK; IKEIITAKF; KEIITAKFQ; EIITAKFQT; IITAKFQTE; ITAKFQTED; TAKFQTEDF; AKFQTEDFF; KFQTEDFFI; FQTEDFFIS; QTEDFFISF;

	TEDFFISFD; EDFFISFDK; DFFISFDKT; FFISFDKTN; FISFDKTNF; ISFDKTNFN; SFDKTNFNP; FDKTNFNPY; DKTNFNPYE; KTNFNPYES; TNFNPYESS; NFNPYESSI; FNPYESSIF; NPYESSIFK; PYESSIFKE; YESSIFKER; ESSIFKERY; SSIFKERYI; SIFKERYIK; IFKERYIKS; FKERYIKSA; KERYIKSAF; ERYIKSAFL; RYIKSAFLE; YIKSAFLEI; IKSAFLEII; KSAFLEIIM; SAFLEIIMH; AFLEIIMHY; FLEIIMHYV; LEIIMHYVK; EIIMHYVKK; IIMHYVKKN; IMHYVKKNS; MHYVKKNSQ; HYVKKNSQN; YVKKNSQNI; VKKNSQNIE; KKNSQNIET; KNSQNIETY; NSQNIETYG; SQNIETYGW; QNIETYGWI; NIETYGWIA; IETYGWIAF; ETYGWIAFY; TYGWIAFYI; YGWIAFYIY; GWIAFYIYA; WIAFYIYAD; IAFYIYADN; AFYIYADNK; FYIYADNKD; YIYADNKDK; IYADNKDKK; YADNKDKKI; ADNKDKKIF; DNKDKKIFC; NKDKKIFCQ; KDKKIFCQR; DKKIFCQRM; KKIFCQRMK; KIFCQRMKE; IFCQRMKEF; FCQRMKEFF; CQRMKEFFK; QRMKEFFKS; RMKEFFKSK; MKEFFKSKT; KEFFKSKTF; EFFKSKTFE; FFKSKTFEI; FKSKTFEIQ; KSKTFEIQN; SKTFEIQNQ; KTFEIQNQI; TFEIQNQIF; FEIQNQIFV; EIQNQIFVY; IQNQIFVYF; QNQIFVYFL; NQIFVYFLS; QIFVYFLSF; IFVYFLSFY; FVYFLSFYP; VYFLSFYPN; YFLSFYPNI; FLSFYPNIE; LSFYPNIEY; SFYPNIEYK; FYPNIEYKH; YPNIEYKHF; PNIEYKHFK; NIEYKHFKF; IEYKHFKFI; EYKHFKFIS; YKHFKFISD; KHFKFISDI; HFKFISDIL; FKFISDILL; KFISDILLY; FISDILLYL; ISDILLYLD; SDILLYLDE; DILLYLDEN; ILLYLDENK; LLYLDENKI; LYLDENKIT; YLDENKITI; LDENKITIP; DENKITIPK; ENKITIPKK; NKITIPKKI; KITIPKKII; ITIPKKIIK; TIPKKIIKI; IPKKIIKIQ; PKKIIKIQK; KKIIKIQKI; KIIKIQKIN; IIKIQKINP; IKIQKINPN; KIQKINPNQ; IQKINPNQL; QKINPNQLD; KINPNQLDY; INPNQLDYQ; NPNQLDYQK; PNQLDYQKS; NQLDYQKSY; QLDYQKSYL; LDYQKSYLL; DYQKSYLLI; YQKSYLLIK; QKSYLLIKS; KSYLLIKSL; SYLLIKSLK; YLLIKSLKT; LLIKSLKTR; LIKSLKTRS; IKSLKTRSR; KSLKTRSRI; SLKTRSRIL; LKTRSRILK; KTRSRILKI; TRSRILKII; RSRILKIII; SRILKIIIK; RILKIIIKN; ILKIIIKNI; LKIIIKNIR; KIIIKNIRF; IIIKNIRFN; IIKNIRFNL; IKNIRFNLI; KNIRFNLIE; NIRFNLIEK; IRFNLIEKL; RFNLIEKLE; FNLIEKLED; NLIEKLEDE; LIEKLEDEN; IEKLEDENE; EKLEDENEK; KLEDENEKK; LEDENEKKL; EDENEKKLL; DENEKKLLP; ENEKKLLPA; NEKKLLPAM; EKKLLPAMC; KKLLPAMCY; KLLPAMCYL; LLPAMCYLI; LPAMCYLIY; PAMCYLIYC; AMCYLIYCE; MCYLIYCEN; CYLIYCENL; YLIYCENLV; LIYCENLVE; IYCENLVEL; YCENLVELK; CENLVELKN; ENLVELKNN; NLVELKNNR; LVELKNNRK; VELKNNRKI; ELKNNRKIK; LKNNRKIKS; KNNRKIKSN; NNRKIKSNE; NRKIKSNEK; RKIKSNEKN; KIKSNEKNS; IKSNEKNSL; KSNEKNSLL; SNEKNSLLE; NEKNSLLEF; EKNSLLEFI; KNSLLEFIS; NSLLEFISF; SLLEFISFF; LLEFISFFK; LEFISFFKT; EFISFFKTK; FISFFKTKL; ISFFKTKLK; SFFKTKLKQ; FFKTKLKQK; FKTKLKQKI; KTKLKQKIN; TKLKQKINF; KLKQKINFK; LKQKINFKK; KQKINFKKE; QKINFKKEL; KINFKKELM; INFKKELMK; NFKKELMKS; FKKELMKSK; KKELMKSKG; KELMKSKGI; 10 mers: MKTIKKDSEF; KTIKKDSEFY; TIKKDSEFYD; IKKDSEFYDS; KKDSEFYDSL; KDSEFYDSLA; DSEFYDSLAT; SEFYDSLATL; EFYDSLATLK; FYDSLATLKK; YDSLATLKKH; DSLATLKKHI; SLATLKKHIN; LATLKKHINK; ATLKKHINKY; TLKKHINKYI;

	LKKHINKYIE; KKHINKYIEE; KHINKYIEEK; HINKYIEEKV; INKYIEEKVL; NKYIEEKVLK; KYIEEKVLKY; YIEEKVLKYS; IEEKVLKYSI; EEKVLKYSIS; EKVLKYSISS; KVLKYSISSQ; VLKYSISSQL; LKYSISSQLY; KYSISSQLYK; YSISSQLYKL; SISSQLYKLE; ISSQLYKLEK; SSQLYKLEKP; SQLYKLEKPE; QLYKLEKPEI; LYKLEKPEII; YKLEKPEIIE; KLEKPEIIEL; LEKPEIIELI; EKPEIIELIK; KPEIIELIKI; PEIIELIKIS; EIIELIKISN; IIELIKISND; IELIKISNDY; ELIKISNDYE; LIKISNDYEK; IKISNDYEKE; KISNDYEKEK; ISNDYEKEKN; SNDYEKEKNA; NDYEKEKNAF; DYEKEKNAFN; YEKEKNAFNT; EKEKNAFNTS; KEKNAFNTSL; EKNAFNTSLE; KNAFNTSLEE; NAFNTSLEEC; AFNTSLEECY; FNTSLEECYY; NTSLEECYYK; TSLEECYYKN; SLEECYYKNT; LEECYYKNTQ; EECYYKNTQN; ECYYKNTQNE; CYYKNTQNEA; YYKNTQNEAI; YKNTQNEAIK; KNTQNEAIKK; NTQNEAIKKW; TQNEAIKKWI; QNEAIKKWIL; NEAIKKWILE; EAIKKWILEI; AIKKWILEIV; IKKWILEIVR; KKWILEIVRN; KWILEIVRNK; WILEIVRNKN; ILEIVRNKNF; LEIVRNKNFI; EIVRNKNFIQ; IVRNKNFIQI; VRNKNFIQIS; RNKNFIQISK; NKNFIQISKE; KNFIQISKEA; NFIQISKEAN; FIQISKEANL; IQISKEANLN; QISKEANLNT; ISKEANLNTK; SKEANLNTKK; KEANLNTKKL; EANLNTKKLG; ANLNTKKLGT; NLNTKKLGTT; LNTKKLGTTY; NTKKLGTTYK; TKKLGTTYKL; KKLGTTYKLK; KLGTTYKLKS; LGTTYKLKSS; GTTYKLKSSN; TTYKLKSSNF; TYKLKSSNFL; YKLKSSNFLK; KLKSSNFLKL; LKSSNFLKLI; KSSNFLKLIE; SSNFLKLIEI; SNFLKLIEIQ; NFLKLIEIQN; FLKLIEIQNS; LKLIEIQNSP; KLIEIQNSPY; LIEIQNSPYY; IEIQNSPYYS; EIQNSPYYSQ; IQNSPYYSQE; QNSPYYSQEK; NSPYYSQEKK; SPYYSQEKKD; PYYSQEKKDI; YYSQEKKDIY; YSQEKKDIYK; SQEKKDIYKQ; QEKKDIYKQI; EKKDIYKQII; KKDIYKQIIL; KDIYKQIILN; DIYKQIILNF; IYKQIILNFS; YKQIILNFSS; KQIILNFSSN; QIILNFSSNI; IILNFSSNIN; ILNFSSNINI; LNFSSNINID; NFSSNINIDS; FSSNINIDSL; SSNINIDSLE; SNINIDSLEQ; NINIDSLEQT; INIDSLEQTI; NIDSLEQTID; IDSLEQTIDI; DSLEQTIDIL; SLEQTIDILV; LEQTIDILVA; EQTIDILVAV; QTIDILVAVR; TIDILVAVRN; IDILVAVRNR; DILVAVRNRN; ILVAVRNRNK; LVAVRNRNKI; VAVRNRNKIK; AVRNRNKIKI; VRNRNKIKIL; RNRNKIKILN; NRNKIKILNI; RNKIKILNIL; NKIKILNILN; KIKILNILNK; IKILNILNKN; KILNILNKNL; ILNILNKNLK; LNILNKNLKY; NILNKNLKYR; ILNKNLKYRP; LNKNLKYRPE; NKNLKYRPEN; KNLKYRPENQ; NLKYRPENQK; LKYRPENQKV; KYRPENQKVF; YRPENQKVFK; RPENQKVFKS; PENQKVFKSS; ENQKVFKSSL; NQKVFKSSLT; QKVFKSSLTN; KVFKSSLTNK; VFKSSLTNKE; FKSSLTNKES; KSSLTNKESR; SSLTNKESRL; SLTNKESRLI; LTNKESRLIK; TNKESRLIKL; NKESRLIKLK; KESRLIKLKR; ESRLIKLKRM; SRLIKLKRML; RLIKLKRMLI; LIKLKRMLIL; IKLKRMLILT; KLKRMLILTY; LKRMLILTYW; KRMLILTYWP; RMLILTYWPV; MLILTYWPVG; LILTYWPVGC; ILTYWPVGCL; LTYWPVGCLS; TYWPVGCLSK; YWPVGCLSKN; WPVGCLSKNI; PVGCLSKNIF; VGCLSKNIFI; GCLSKNIFIK; CLSKNIFIKI; LSKNIFIKIL; SKNIFIKILI; KNIFIKILIK;

	NIFIKILIKX; IFIKILIKXY; FIKILIKXYK; IKILIKXYKY; KILIKXYKYL; ILIKXYKYLE; LIKXYKYLEE; IKXYKYLEEE; KXYKYLEEEI; XYKYLEEEIL; YKYLEEEILA; KYLEEEILAL; YLEEEILALK; LEEEILALKY; EEEILALKYN; EEILALKYNE; EILALKYNEI; ILALKYNEIL; LALKYNEILN; ALKYNEILNY; LKYNEILNYL; KYNEILNYLR; YNEILNYLRA; NEILNYLRAL; EILNYLRALK; ILNYLRALKT; LNYLRALKTL; NYLRALKTLS; YLRALKTLSL; LRALKTLSLN; RALKTLSLNE; ALKTLSLNEI; LKTLSLNEIF; KTLSLNEIFY; TLSLNEIFYK; LSLNEIFYKG; SLNEIFYKGS; LNEIFYKGSS; NEIFYKGSSK; EIFYKGSSKN; IFYKGSSKNI; FYKGSSKNIS; YKGSSKNISF; KGSSKNISFN; GSSKNISFNY; SSKNISFNYF; SKNISFNYFF; KNISFNYFFS; NISFNYFFSD; ISFNYFFSDF; SFNYFFSDFT; FNYFFSDFTQ; NYFFSDFTQY; YFFSDFTQYA; FFSDFTQYAP; FSDFTQYAPK; SDFTQYAPKD; DFTQYAPKDF; FTQYAPKDFQ; TQYAPKDFQD; QYAPKDFQDT; YAPKDFQDTL; APKDFQDTLK; PKDFQDTLKC; KDFQDTLKCY; DFQDTLKCYL; FQDTLKCYLY; QDTLKCYLYV; DTLKCYLYVI; TLKCYLYVIE; LKCYLYVIEK; KCYLYVIEKT; CYLYVIEKTI; YLYVIEKTIT; LYVIEKTITK; YVIEKTITKK; VIEKTITKKY; IEKTITKKYL; EKTITKKYLT; KTITKKYLTW; TITKKYLTWF; ITKKYLTWFF; TKKYLTWFFK; KKYLTWFFKD; KYLTWFFKDK; YLTWFFKDKI; LTWFFKDKIS; TWFFKDKISN; WFFKDKISNN; FFKDKISNNW; FKDKISNNWE; KDKISNNWES; DKISNNWESF; KISNNWESFI; ISNNWESFID; SNNWESFIDA; NNWESFIDAL; NWESFIDALE; WESFIDALEY; ESFIDALEYI; SFIDALEYIE; FIDALEYIEK; IDALEYIEKH; DALEYIEKHK; ALEYIEKHKL; LEYIEKHKLI; EYIEKHKLIN; YIEKHKLINI; IEKHKLINIK; EKHKLINIKE; KHKLINIKEK; HKLINIKEKI; KLINIKEKIK; LINIKEKIKE; INIKEKIKEI; NIKEKIKEII; IKEKIKEIIT; KEKIKEIITA; EKIKEIITAK; KIKEIITAKF; IKEIITAKFQ; KEIITAKFQT; EIITAKFQTE; IITAKFQTED; ITAKFQTEDF; TAKFQTEDFF; AKFQTEDFFI; KFQTEDFFIS; FQTEDFFISF; QTEDFFISFD; TEDFFISFDK; EDFFISFDKT; DFFISFDKTN; FFISFDKTNF; FISFDKTNFN; ISFDKTNFNP; SFDKTNFNPY; FDKTNFNPYE; DKTNFNPYES; KTNFNPYESS; TNFNPYESSI; NFNPYESSIF; FNPYESSIFK; NPYESSIFKE; PYESSIFKER; YESSIFKERY; ESSIFKERYI; SSIFKERYIK; SIFKERYIKS; IFKERYIKSA; FKERYIKSAF; KERYIKSAFL; ERYIKSAFLE; RYIKSAFLEI; YIKSAFLEII; IKSAFLEIIM; KSAFLEIIMH; SAFLEIIMHY; AFLEIIMHYV; FLEIIMHYVK; LEIIMHYVKK; EIIMHYVKKN; IIMHYVKKNS; IMHYVKKNSQ; MHYVKKNSQN; HYVKKNSQNI; YVKKNSQNIE; VKKNSQNIET; KKNSQNIETY; KNSQNIETYG; NSQNIETYGW; SQNIETYGWI; QNIETYGWIA; NIETYGWIAF; IETYGWIAFY; ETYGWIAFYI; TYGWIAFYIY; YGWIAFYIYA; GWIAFYIYAD; WIAFYIYADN; IAFYIYADNK; AFYIYADNKD; FYIYADNKDK; YIYADNKDKK; IYADNKDKKI; YADNKDKKIF; ADNKDKKIFC; DNKDKKIFCQ; NKDKKIFCQR; KDKKIFCQRM; DKKIFCQRMK; KKIFCQRMKE; KIFCQRMKEF; IFCQRMKEFF; FCQRMKEFFK; CQRMKEFFKS; QRMKEFFKSK; RMKEFFKSKT; MKEFFKSKTF; KEFFKSKTFE; EFFKSKTFEI; FFKSKTFEIQ; FKSKTFEIQN; KSKTFEIQNQ;

SKTFEIQNQI; KTFEIQNQIF; TFEIQNQIFV; FEIQNQIFVY;
EIQNQIFVYF; IQNQIFVYFL; QNQIFVYFLS; NQIFVYFLSF;
QIFVYFLSFY; IFVYFLSFYP; FVYFLSFYPN; VYFLSFYPNI;
YFLSFYPNIE; FLSFYPNIEY; LSFYPNIEYK; SFYPNIEYKH;
FYPNIEYKHF; YPNIEYKHFK; PNIEYKHFKF; NIEYKHFKFI;
IEYKHFKFIS; EYKHFKFISD; YKHFKFISDI; KHFKFISDIL;
HFKFISDILL; FKFISDILLY; KFISDILLYL; FISDILLYLD;
ISDILLYLDE; SDILLYLDEN; DILLYLDENK; ILLYLDENKI;
LLYLDENKIT; LYLDENKITI; YLDENKITIP; LDENKITIPK;
DENKITIPKK; ENKITIPKKI; NKITIPKKII; KITIPKKIIK;
ITIPKKIIKI; TIPKKIIKIQ; IPKKIIKIQK; PKKIIKIQKI;
KKIIKIQKIN; KIIKIQKINP; IIKIQKINPN; IKIQKINPNQ;
KIQKINPNQL; IQKINPNQLD; QKINPNQLDY; KINPNQLDYQ;
INPNQLDYQK; NPNQLDYQKS; PNQLDYQKSY; NQLDYQKSYL;
QLDYQKSYLL; LDYQKSYLLI; DYQKSYLLIK; YQKSYLLIKS;
QKSYLLIKSL; KSYLLIKSLK; SYLLIKSLKT; YLLIKSLKTR;
LLIKSLKTRS; LIKSLKTRSR; IKSLKTRSRI; KSLKTRSRIL;
SLKTRSRILK; LKTRSRILKI; KTRSRILKII; TRSRILKIII;
RSRILKIIIK; SRILKIIIKN; RILKIIIKNI; ILKIIIKNIR;
LKIIIKNIRF; KIIIKNIRFN; IIIKNIRFNL; IIKNIRFNLI;
IKNIRFNLIE; KNIRFNLIEK; NIRFNLIEKL; IRFNLIEKLE;
RFNLIEKLED; FNLIEKLEDE; NLIEKLEDEN; LIEKLEDENE;
IEKLEDENEK; EKLEDENEKK; KLEDENEKKL; LEDENEKKLL;
EDENEKKLLP; DENEKKLLPA; ENEKKLLPAM; NEKKLLPAMC;
EKKLLPAMCY; KKLLPAMCYL; KLLPAMCYLI; LLPAMCYLIY;
LPAMCYLIYC; PAMCYLIYCE; AMCYLIYCEN; MCYLIYCENL;
CYLIYCENLV; YLIYCENLVE; LIYCENLVEL; IYCENLVELK;
YCENLVELKN; CENLVELKNN; ENLVELKNNR; NLVELKNNRK;
LVELKNNRKI; VELKNNRKIK; ELKNNRKIKS; LKNNRKIKSN;
KNNRKIKSNE; NNRKIKSNEK; NRKIKSNEKN; RKIKSNEKNS;
KIKSNEKNSL; IKSNEKNSLL; KSNEKNSLLE; SNEKNSLLEF;
NEKNSLLEFI; EKNSLLEFIS; KNSLLEFISF; NSLLEFISFF;
SLLEFISFFK; LLEFISFFKT; LEFISFFKTK; EFISFFKTKL;
FISFFKTKLK; ISFFKTKLKQ; SFFKTKLKQK; FFKTKLKQKI;
FKTKLKQKIN; KTKLKQKINF; TKLKQKINFK; KLKQKINFKK;
LKQKINFKKE; KQKINFKKEL; QKINFKKELM; KINFKKELMK;
INFKKELMKS; NFKKELMKSK; FKKELMKSKG; KKELMKSKGI;

11 mers:
MKTIKKDSEFY; KTIKKDSEFYD; TIKKDSEFYDS; IKKDSEFYDSL;
KKDSEFYDSLA; KDSEFYDSLAT; DSEFYDSLATL; SEFYDSLATLK;
EFYDSLATLKK; FYDSLATLKKH; YDSLATLKKHI; DSLATLKKHIN;
SLATLKKHINK; LATLKKHINKY; ATLKKHINKYI; TLKKHINKYIE;
LKKHINKYIEE; KKHINKYIEEK; KHINKYIEEKV; HINKYIEEKVL;
INKYIEEKVLK; NKYIEEKVLKY; KYIEEKVLKYS; YIEEKVLKYSI;
IEEKVLKYSIS; EEKVLKYSISS; EKVLKYSISSQ; KVLKYSISSQL;
VLKYSISSQLY; LKYSISSQLYK; KYSISSQLYKL; YSISSQLYKLE;
SISSQLYKLEK; ISSQLYKLEKP; SSQLYKLEKPE; SQLYKLEKPEI;
QLYKLEKPEII; LYKLEKPEIIE; YKLEKPEIIEL; KLEKPEIIELI;
LEKPEIIELIK; EKPEIIELIKI; KPEIIELIKIS; PEIIELIKISN;
EIIELIKISND; IIELIKISNDY; IELIKISNDYE; ELIKISNDYEK;

	LIKISNDYEKE; IKISNDYEKEK; KISNDYEKEKN; ISNDYEKEKNA; SNDYEKEKNAF; NDYEKEKNAFN; DYEKEKNAFNT; YEKEKNAFNTS; EKEKNAFNTSL; KEKNAFNTSLE; EKNAFNTSLEE; KNAFNTSLEEC; NAFNTSLEECY; AFNTSLEECYY; FNTSLEECYYK; NTSLEECYYKN; TSLEECYYKNT; SLEECYYKNTQ; LEECYYKNTQN; EECYYKNTQNE; ECYYKNTQNEA; CYYKNTQNEAI; YYKNTQNEAIK; YKNTQNEAIKK; KNTQNEAIKKW; NTQNEAIKKWI; TQNEAIKKWIL; QNEAIKKWILE; NEAIKKWILEI; EAIKKWILEIV; AIKKWILEIVR; IKKWILEIVRN; KKWILEIVRNK; KWILEIVRNKN; WILEIVRNKNF; ILEIVRNKNFI; LEIVRNKNFIQ; EIVRNKNFIQI; IVRNKNFIQIS; VRNKNFIQISK; RNKNFIQISKE; NKNFIQISKEA; KNFIQISKEAN; NFIQISKEANL; FIQISKEANLN; IQISKEANLNT; QISKEANLNTK; ISKEANLNTKK; SKEANLNTKKL; KEANLNTKKLG; EANLNTKKLGT; ANLNTKKLGTT; NLNTKKLGTTY; LNTKKLGTTYK; NTKKLGTTYKL; TKKLGTTYKLK; KKLGTTYKLKS; KLGTTYKLKSS; LGTTYKLKSSN; GTTYKLKSSNF; TTYKLKSSNFL; TYKLKSSNFLK; YKLKSSNFLKL; KLKSSNFLKLI; LKSSNFLKLIE; KSSNFLKLIEI; SSNFLKLIEIQ; SNFLKLIEIQN; NFLKLIEIQNS; FLKLIEIQNSP; LKLIEIQNSPY; KLIEIQNSPYY; LIEIQNSPYYS; IEIQNSPYYSQ; EIQNSPYYSQE; IQNSPYYSQEK; QNSPYYSQEKK; NSPYYSQEKKD; SPYYSQEKKDI; PYYSQEKKDIY; YYSQEKKDIYK; YSQEKKDIYKQ; SQEKKDIYKQI; QEKKDIYKQII; EKKDIYKQIIL; KKDIYKQIILN; KDIYKQIILNF; DIYKQIILNFS; IYKQIILNFSS; YKQIILNFSSN; KQIILNFSSNI; QIILNFSSNIN; IILNFSSNINI; ILNFSSNINID; LNFSSNINIDS; NFSSNINIDSL; FSSNINIDSLE; SSNINIDSLEQ; SNINIDSLEQT; NINIDSLEQTI; INIDSLEQTID; NIDSLEQTIDI; IDSLEQTIDIL; DSLEQTIDILV; SLEQTIDILVA; LEQTIDILVAV; EQTIDILVAVR; QTIDILVAVRN; TIDILVAVRNR; IDILVAVRNRN; DILVAVRNRNK; ILVAVRNRNKI; LVAVRNRNKIK; VAVRNRNKIKI; AVRNRNKIKIL; VRNRNKIKILN; RNRNKIKILNI; NRNKIKILNIL; RNKIKILNILN; NKIKILNILNK; KIKILNILNKN; IKILNILNKNL; KILNILNKNLK; ILNILNKNLKY; LNILNKNLKYR; NILNKNLKYRP; ILNKNLKYRPE; LNKNLKYRPEN; NKNLKYRPENQ; KNLKYRPENQK; NLKYRPENQKV; LKYRPENQKVF; KYRPENQKVFK; YRPENQKVFKS; RPENQKVFKSS; PENQKVFKSSL; ENQKVFKSSLT; NQKVFKSSLTN; QKVFKSSLTNK; KVFKSSLTNKE; VFKSSLTNKES; FKSSLTNKESR; KSSLTNKESRL; SSLTNKESRLI; SLTNKESRLIK; LTNKESRLIKL; TNKESRLIKLK; NKESRLIKLKR; KESRLIKLKRM; ESRLIKLKRML; SRLIKLKRMLI; RLIKLKRMLIL; LIKLKRMLILT; IKLKRMLILTY; KLKRMLILTYW; LKRMLILTYWP; KRMLILTYWPV; RMLILTYWPVG; MLILTYWPVGC; LILTYWPVGCL; ILTYWPVGCLS; LTYWPVGCLSK; TYWPVGCLSKN; YWPVGCLSKNI; WPVGCLSKNIF; PVGCLSKNIFI; VGCLSKNIFIK; GCLSKNIFIKI; CLSKNIFIKIL; LSKNIFIKILI; SKNIFIKILIK; KNIFIKILIKX; NIFIKILIKXY; IFIKILIKXYK; FIKILIKXYKY; IKILIKXYKYL; KILIKXYKYLE; ILIKXYKYLEE; LIKXYKYLEEE; IKXYKYLEEEI; KXYKYLEEEIL; XYKYLEEEILA; YKYLEEEILAL; KYLEEEILALK; YLEEEILALKY; LEEEILALKYN; EEEILALKYNE; EEILALKYNEI; EILALKYNEIL; ILALKYNEILN; LALKYNEILNY; ALKYNEILNYL; LKYNEILNYLR; KYNEILNYLRA; YNEILNYLRAL; NEILNYLRALK; EILNYLRALKT; ILNYLRALKTL; LNYLRALKTLS; NYLRALKTLSL; YLRALKTLSLN; LRALKTLSLNE; RALKTLSLNEI; ALKTLSLNEIF;

	LKTLSLNEIFY; KTLSLNEIFYK; TLSLNEIFYKG; LSLNEIFYKGS; SLNEIFYKGSS; LNEIFYKGSSK; NEIFYKGSSKN; EIFYKGSSKNI; IFYKGSSKNIS; FYKGSSKNISF; YKGSSKNISFN; KGSSKNISFNY; GSSKNISFNYF; SSKNISFNYFF; SKNISFNYFFS; KNISFNYFFSD; NISFNYFFSDF; ISFNYFFSDFT; SFNYFFSDFTQ; FNYFFSDFTQY; NYFFSDFTQYA; YFFSDFTQYAP; FFSDFTQYAPK; FSDFTQYAPKD; SDFTQYAPKDF; DFTQYAPKDFQ; FTQYAPKDFQD; TQYAPKDFQDT; QYAPKDFQDTL; YAPKDFQDTLK; APKDFQDTLKC; PKDFQDTLKCY; KDFQDTLKCYL; DFQDTLKCYLY; FQDTLKCYLYV; QDTLKCYLYVI; DTLKCYLYVIE; TLKCYLYVIEK; LKCYLYVIEKT; KCYLYVIEKTI; CYLYVIEKTIT; YLYVIEKTITK; LYVIEKTITKK; YVIEKTITKKY; VIEKTITKKYL; IEKTITKKYLT; EKTITKKYLTW; KTITKKYLTWF; TITKKYLTWFF; ITKKYLTWFFK; TKKYLTWFFKD; KKYLTWFFKDK; KYLTWFFKDKI; YLTWFFKDKIS; LTWFFKDKISN; TWFFKDKISNN; WFFKDKISNNW; FFKDKISNNWE; FKDKISNNWES; KDKISNNWESF; DKISNNWESFI; KISNNWESFID; ISNNWESFIDA; SNNWESFIDAL; NNWESFIDALE; NWESFIDALEY; WESFIDALEYI; ESFIDALEYIE; SFIDALEYIEK; FIDALEYIEKH; IDALEYIEKHK; DALEYIEKHKL; ALEYIEKHKLI; LEYIEKHKLIN; EYIEKHKLINI; YIEKHKLINIK; IEKHKLINIKE; EKHKLINIKEK; KHKLINIKEKI; HKLINIKEKIK; KLINIKEKIKE; LINIKEKIKEI; INIKEKIKEII; NIKEKIKEIIT; IKEKIKEIITA; KEKIKEIITAK; EKIKEIITAKF; KIKEIITAKFQ; IKEIITAKFQT; KEIITAKFQTE; EIITAKFQTED; IITAKFQTEDF; ITAKFQTEDFF; TAKFQTEDFFI; AKFQTEDFFIS; KFQTEDFFISF; FQTEDFFISFD; QTEDFFISFDK; TEDFFISFDKT; EDFFISFDKTN; DFFISFDKTNF; FFISFDKTNFN; FISFDKTNFNP; ISFDKTNFNPY; SFDKTNFNPYE; FDKTNFNPYES; DKTNFNPYESS; KTNFNPYESSI; TNFNPYESSIF; NFNPYESSIFK; FNPYESSIFKE; NPYESSIFKER; PYESSIFKERY; YESSIFKERYI; ESSIFKERYIK; SSIFKERYIKS; SIFKERYIKSA; IFKERYIKSAF; FKERYIKSAFL; KERYIKSAFLE; ERYIKSAFLEI; RYIKSAFLEII; YIKSAFLEIIM; IKSAFLEIIMH; KSAFLEIIMHY; SAFLEIIMHYV; AFLEIIMHYVK; FLEIIMHYVKK; LEIIMHYVKKN; EIIMHYVKKNS; IIMHYVKKNSQ; IMHYVKKNSQN; MHYVKKNSQNI; HYVKKNSQNIE; YVKKNSQNIET; VKKNSQNIETY; KKNSQNIETYG; KNSQNIETYGW; NSQNIETYGWI; SQNIETYGWIA; QNIETYGWIAF; NIETYGWIAFY; IETYGWIAFYI; ETYGWIAFYIY; TYGWIAFYIYA; YGWIAFYIYAD; GWIAFYIYADN; WIAFYIYADNK; IAFYIYADNKD; AFYIYADNKDK; FYIYADNKDKK; YIYADNKDKKI; IYADNKDKKIF; YADNKDKKIFC; ADNKDKKIFCQ; DNKDKKIFCQR; NKDKKIFCQRM; KDKKIFCQRMK; DKKIFCQRMKE; KKIFCQRMKEF; KIFCQRMKEFF; IFCQRMKEFFK; FCQRMKEFFKS; CQRMKEFFKSK; QRMKEFFKSKT; RMKEFFKSKTF; MKEFFKSKTFE; KEFFKSKTFEI; EFFKSKTFEIQ; FFKSKTFEIQN; FKSKTFEIQNQ; KSKTFEIQNQI; SKTFEIQNQIF; KTFEIQNQIFV; TFEIQNQIFVY; FEIQNQIFVYF; EIQNQIFVYFL; IQNQIFVYFLS; QNQIFVYFLSF; NQIFVYFLSFY; QIFVYFLSFYP; IFVYFLSFYPN; FVYFLSFYPNI; VYFLSFYPNIE; YFLSFYPNIEY; FLSFYPNIEYK; LSFYPNIEYKH; SFYPNIEYKHF; FYPNIEYKHFK; YPNIEYKHFKF; PNIEYKHFKFI; NIEYKHFKFIS; IEYKHFKFISD; EYKHFKFISDI; YKHFKFISDIL; KHFKFISDILL; HFKFISDILLY; FKFISDILLYL; KFISDILLYLD; FISDILLYLDE; ISDILLYLDEN; SDILLYLDENK; DILLYLDENKI; ILLYLDENKIT;

	LLYLDENKITI; LYLDENKITIP; YLDENKITIPK; LDENKITIPKK; DENKITIPKKI; ENKITIPKKII; NKITIPKKIIK; KITIPKKIIKI; ITIPKKIIKIQ; TIPKKIIKIQK; IPKKIIKIQKI; PKKIIKIQKIN; KKIIKIQKINP; KIIKIQKINPN; IIKIQKINPNQ; IKIQKINPNQL; KIQKINPNQLD; IQKINPNQLDY; QKINPNQLDYQ; KINPNQLDYQK; INPNQLDYQKS; NPNQLDYQKSY; PNQLDYQKSYL; NQLDYQKSYLL; QLDYQKSYLLI; LDYQKSYLLIK; DYQKSYLLIKS; YQKSYLLIKSL; QKSYLLIKSLK; KSYLLIKSLKT; SYLLIKSLKTR; YLLIKSLKTRS; LLIKSLKTRSR; LIKSLKTRSRI; IKSLKTRSRIL; KSLKTRSRILK; SLKTRSRILKI; LKTRSRILKII; KTRSRILKIII; TRSRILKIIIK; RSRILKIIIKN; SRILKIIIKNI; RILKIIIKNIR; ILKIIIKNIRF; LKIIIKNIRFN; KIIIKNIRFNL; IIIKNIRFNLI; IIKNIRFNLIE; IKNIRFNLIEK; KNIRFNLIEKL; NIRFNLIEKLE; IRFNLIEKLED; RFNLIEKLEDE; FNLIEKLEDEN; NLIEKLEDENE; LIEKLEDENEK; IEKLEDENEKK; EKLEDENEKKL; KLEDENEKKLL; LEDENEKKLLP; EDENEKKLLPA; DENEKKLLPAM; ENEKKLLPAMC; NEKKLLPAMCY; EKKLLPAMCYL; KKLLPAMCYLI; KLLPAMCYLIY; LLPAMCYLIYC; LPAMCYLIYCE; PAMCYLIYCEN; AMCYLIYCENL; MCYLIYCENLV; CYLIYCENLVE; YLIYCENLVEL; LIYCENLVELK; IYCENLVELKN; YCENLVELKNN; CENLVELKNNR; ENLVELKNNRK; NLVELKNNRKI; LVELKNNRKIK; VELKNNRKIKS; ELKNNRKIKSN; LKNNRKIKSNE; KNNRKIKSNEK; NNRKIKSNEKN; NRKIKSNEKNS; RKIKSNEKNSL; KIKSNEKNSLL; IKSNEKNSLLE; KSNEKNSLLEF; SNEKNSLLEFI; NEKNSLLEFIS; EKNSLLEFISF; KNSLLEFISFF; NSLLEFISFFK; SLLEFISFFKT; LLEFISFFKTK; LEFISFFKTKL; EFISFFKTKLK; FISFFKTKLKQ; ISFFKTKLKQK; SFFKTKLKQKI; FFKTKLKQKIN; FKTKLKQKINF; KTKLKQKINFK; TKLKQKINFKK; KLKQKINFKKE; LKQKINFKKEL; KQKINFKKELM; QKINFKKELMK; KINFKKELMKS; INFKKELMKSK; NFKKELMKSKG; FKKELMKSKGI;
Seq 29	SEQ ID NO 35914-36939/ 8 mers: MITQQDYT; ITQQDYTE; TQQDYTEI; QQDYTEIK; QDYTEIKK; DYTEIKKK; YTEIKKKL; TEIKKKLE; EIKKKLEN; IKKKLENT; KKKLENTK; KKLENTKT; KLENTKTR; LENTKTRI; ENTKTRIQ; NTKTRIQF; TKTRIQFR; KTRIQFRN; TRIQFRNG; RIQFRNGN; IQFRNGNK; QFRNGNKI; FRNGNKID; RNGNKIDS; NGNKIDSL; GNKIDSLG; NKIDSLGY; KIDSLGYQ; IDSLGYQG; DSLGYQGS; SLGYQGSL; LGYQGSLG; GYQGSLGE; YQGSLGEP; QGSLGEPI; GSLGEPIL; SLGEPILL; LGEPILLK; GEPILLKD; EPILLKDK; PILLKDKL; ILLKDKLT; LLKDKLTF; LKDKLTFS; KDKLTFSI; DKLTFSIC; KLTFSICD; LTFSICDG; TFSICDGK; FSICDGKN; SICDGKNI; ICDGKNID; CDGKNIDN; DGKNIDNR; GKNIDNRK; KNIDNRKE; NIDNRKEY; IDNRKEYE; DNRKEYEI; NRKEYEIT; RKEYEITK; KEYEITKN; EYEITKNA; YEITKNAP; EITKNAPS; ITKNAPSL; TKNAPSLD; KNAPSLDS; NAPSLDSL; APSLDSLI; PSLDSLIE; SLDSLIEY; LDSLIEYL; DSLIEYLE; SLIEYLEH; LIEYLEHM; IEYLEHMI; EYLEHMIL; YLEHMILF; LEHMILFF; EHMILFFL; HMILFFLE; MILFFLEK; ILFFLEKT; LFFLEKTP; FFLEKTPV; FLEKTPVG; LEKTPVGT; EKTPVGTL; KTPVGTLT;

	TPVGTLTA; PVGTLTAK; VGTLTAKF; GTLTAKFA; TLTAKFAM; LTAKFAME; TAKFAMEG; AKFAMEGS; KFAMEGSI; FAMEGSIL; AMEGSILT; MEGSILTR; EGSILTRS; GSILTRSK; SILTRSKL; ILTRSKLI; LTRSKLIQ; TRSKLIQA; RSKLIQAF; SKLIQAFT; KLIQAFTN; LIQAFTNT; IQAFTNTN; QAFTNTNK; AFTNTNKF; FTNTNKFC; TNTNKFCI; NTNKFCIP; TNKFCIPD; NKFCIPDG; KFCIPDGR; FCIPDGRS; CIPDGRSL; IPDGRSLP; PDGRSLPS; DGRSLPSN; GRSLPSNC; RSLPSNCY; SLPSNCYA; LPSNCYAY; PSNCYAYK; SNCYAYKV; NCYAYKVL; CYAYKVLG; YAYKVLGI; AYKVLGIS; YKVLGISS; KVLGISSA; VLGISSAP; LGISSAPK; GISSAPKL; ISSAPKLS; SSAPKLSG; SAPKLSGR; APKLSGRF; PKLSGRFL; KLSGRFLR; LSGRFLRH; SGRFLRHY; GRFLRHYD; RFLRHYDS; FLRHYDSG; LRHYDSGG; RHYDSGGS; HYDSGGST; YDSGGSTD; DSGGSTDS; SGGSTDSD; GGSTDSDG; GSTDSDGT; STDSDGTR; TDSDGTRS; DSDGTRSL; SDGTRSLG; DGTRSLGH; GTRSLGHT; TRSLGHTQ; RSLGHTQE; SLGHTQED; LGHTQEDS; GHTQEDSY; HTQEDSYK; TQEDSYKN; QEDSYKNH; EDSYKNHD; DSYKNHDH; SYKNHDHD; YKNHDHDL; KNHDHDLD; NHDHDLDF; HDHDLDFS; DHDLDFSR; HDLDFSRI; DLDFSRIN; LDFSRINF; DFSRINFK; FSRINFKG; SRINFKGK; RINFKGKL; INFKGKLV; NFKGKLVK; FKGKLVKR; KGKLVKRM; GKLVKRMT; KLVKRMTM; LVKRMTMI; VKRMTMIY; KRMTMIYR; RMTMIYRS; MTMIYRSA; TMIYRSAD; MIYRSADT; IYRSADTW; YRSADTWY; RSADTWYT; SADTWYTW; ADTWYTWY; DTWYTWYW; TWYTWYWA; WYTWYWAE; YTWYWAEE; TWYWAEEI; WYWAEEIM; YWAEEIMS; WAEEIMSP; AEEIMSPF; EEIMSPFI; EIMSPFIT; IMSPFITG; MSPFITGY; SPFITGYS; PFITGYSY; FITGYSYE; ITGYSYEE; TGYSYEEI; GYSYEEID; YSYEEIDP; SYEEIDPE; YEEIDPEY; EEIDPEYL; EIDPEYLL; IDPEYLLP; DPEYLLPP; PEYLLPPF; EYLLPPFT; YLLPPFTS; LLPPFTSQ; LPPFTSQS; PPFTSQSG; PFTSQSGS; FTSQSGSK; TSQSGSKE; SQSGSKET; QSGSKETK; SGSKETKP; GSKETKPK; SKETKPKN; KETKPKNT; ETKPKNTC; TKPKNTCY; KPKNTCYI; PKNTCYIS; KNTCYISF; NTCYISFY; TCYISFYR; CYISFYRY; YISFYRYD; ISFYRYDL; 9 mers: MITQQDYTE; ITQQDYTEI; TQQDYTEIK; QQDYTEIKK; QDYTEIKKK; DYTEIKKKL; YTEIKKKLE; TEIKKKLEN; EIKKKLENT; IKKKLENTK; KKKLENTKT; KKLENTKTR; KLENTKTRI; LENTKTRIQ; ENTKTRIQF; NTKTRIQFR; TKTRIQFRN; KTRIQFRNG; TRIQFRNGN; RIQFRNGNK; IQFRNGNKI; QFRNGNKID; FRNGNKIDS; RNGNKIDSL; NGNKIDSLG; GNKIDSLGY; NKIDSLGYQ; KIDSLGYQG; IDSLGYQGS; DSLGYQGSL; SLGYQGSLG; LGYQGSLGE; GYQGSLGEP; YQGSLGEPI; QGSLGEPIL; GSLGEPILL; SLGEPILLK; LGEPILLKD; GEPILLKDK; EPILLKDKL; PILLKDKLT; ILLKDKLTF; LLKDKLTFS; LKDKLTFSI; KDKLTFSIC; DKLTFSICD; KLTFSICDG; LTFSICDGK; TFSICDGKN; FSICDGKNI; SICDGKNID; ICDGKNIDN; CDGKNIDNR; DGKNIDNRK; GKNIDNRKE; KNIDNRKEY; NIDNRKEYE; IDNRKEYEI; DNRKEYEIT; NRKEYEITK; RKEYEITKN; KEYEITKNA; EYEITKNAP; YEITKNAPS; EITKNAPSL; ITKNAPSLD; TKNAPSLDS; KNAPSLDSL; NAPSLDSLI; APSLDSLIE; PSLDSLIEY; SLDSLIEYL; LDSLIEYLE; DSLIEYLEH; SLIEYLEHM;

LIEYLEHMI; IEYLEHMIL; EYLEHMILF; YLEHMILFF; LEHMILFFL; EHMILFFLE; HMILFFLEK; MILFFLEKT; ILFFLEKTP; LFFLEKTPV; FFLEKTPVG; FLEKTPVGT; LEKTPVGTL; EKTPVGTLT; KTPVGTLTA; TPVGTLTAK; PVGTLTAKF; VGTLTAKFA; GTLTAKFAM; TLTAKFAME; LTAKFAMEG; TAKFAMEGS; AKFAMEGSI; KFAMEGSIL; FAMEGSILT; AMEGSILTR; MEGSILTRS; EGSILTRSK; GSILTRSKL; SILTRSKLI; ILTRSKLIQ; LTRSKLIQA; TRSKLIQAF; RSKLIQAFT; SKLIQAFTN; KLIQAFTNT; LIQAFTNTN; IQAFTNTNK; QAFTNTNKF; AFTNTNKFC; FTNTNKFCI; TNTNKFCIP; NTNKFCIPD; TNKFCIPDG; NKFCIPDGR; KFCIPDGRS; FCIPDGRSL; CIPDGRSLP; IPDGRSLPS; PDGRSLPSN; DGRSLPSNC; GRSLPSNCY; RSLPSNCYA; SLPSNCYAY; LPSNCYAYK; PSNCYAYKV; SNCYAYKVL; NCYAYKVLG; CYAYKVLGI; YAYKVLGIS; AYKVLGISS; YKVLGISSA; KVLGISSAP; VLGISSAPK; LGISSAPKL; GISSAPKLS; ISSAPKLSG; SSAPKLSGR; SAPKLSGRF; APKLSGRFL; PKLSGRFLR; KLSGRFLRH; LSGRFLRHY; SGRFLRHYD; GRFLRHYDS; RFLRHYDSG; FLRHYDSGG; LRHYDSGGS; RHYDSGGST; HYDSGGSTD; YDSGGSTDS; DSGGSTDSD; SGGSTDSDG; GGSTDSDGT; GSTDSDGTR; STDSDGTRS; TDSDGTRSL; DSDGTRSLG; SDGTRSLGH; DGTRSLGHT; GTRSLGHTQ; TRSLGHTQE; RSLGHTQED; SLGHTQEDS; LGHTQEDSY; GHTQEDSYK; HTQEDSYKN; TQEDSYKNH; QEDSYKNHD; EDSYKNHDH; DSYKNHDHD; SYKNHDHDL; YKNHDHDLD; KNHDHDLDF; NHDHDLDFS; HDHDLDFSR; DHDLDFSRI; HDLDFSRIN; DLDFSRINF; LDFSRINFK; DFSRINFKG; FSRINFKGK; SRINFKGKL; RINFKGKLV; INFKGKLVK; NFKGKLVKR; FKGKLVKRM; KGKLVKRMT; GKLVKRMTM; KLVKRMTMI; LVKRMTMIY; VKRMTMIYR; KRMTMIYRS; RMTMIYRSA; MTMIYRSAD; TMIYRSADT; MIYRSADTW; IYRSADTWY; YRSADTWYT; RSADTWYTW; SADTWYTWY; ADTWYTWYW; DTWYTWYWA; TWYTWYWAE; WYTWYWAEE; YTWYWAEEI; TWYWAEEIM; WYWAEEIMS; YWAEEIMSP; WAEEIMSPF; AEEIMSPFI; EEIMSPFIT; EIMSPFITG; IMSPFITGY; MSPFITGYS; SPFITGYSY; PFITGYSYE; FITGYSYEE; ITGYSYEEI; TGYSYEEID; GYSYEEIDP; YSYEEIDPE; SYEEIDPEY; YEEIDPEYL; EEIDPEYLL; EIDPEYLLP; IDPEYLLPP; DPEYLLPPF; PEYLLPPFT; EYLLPPFTS; YLLPPFTSQ; LLPPFTSQS; LPPFTSQSG; PPFTSQSGS; PFTSQSGSK; FTSQSGSKE; TSQSGSKET; SQSGSKETK; QSGSKETKP; SGSKETKPK; GSKETKPKN; SKETKPKNT; KETKPKNTC; ETKPKNTCY; TKPKNTCYI; KPKNTCYIS; PKNTCYISF; KNTCYISFY; NTCYISFYR; TCYISFYRY; CYISFYRYD; YISFYRYDL;

10 mers:
MITQQDYTEI; ITQQDYTEIK; TQQDYTEIKK; QQDYTEIKKK; QDYTEIKKKL; DYTEIKKKLE; YTEIKKKLEN; TEIKKKLENT; EIKKKLENTK; IKKKLENTKT; KKKLENTKTR; KKLENTKTRI; KLENTKTRIQ; LENTKTRIQF; ENTKTRIQFR; NTKTRIQFRN; TKTRIQFRNG; KTRIQFRNGN; TRIQFRNGNK; RIQFRNGNKI; IQFRNGNKID; QFRNGNKIDS; FRNGNKIDSL; RNGNKIDSLG; NGNKIDSLGY; GNKIDSLGYQ; NKIDSLGYQG; KIDSLGYQGS; IDSLGYQGSL; DSLGYQGSLG; SLGYQGSLGE; LGYQGSLGEP; GYQGSLGEPI; YQGSLGEPIL; QGSLGEPILL; GSLGEPILLK; SLGEPILLKD; LGEPILLKDK; GEPILLKDKL; EPILLKDKLT; PILLKDKLTF; ILLKDKLTFS; LLKDKLTFSI; LKDKLTFSIC; KDKLTFSICD; DKLTFSICDG; KLTFSICDGK; LTFSICDGKN;

	TFSICDGKNI; FSICDGKNID; SICDGKNIDN; ICDGKNIDNR; CDGKNIDNRK; DGKNIDNRKE; GKNIDNRKEY; KNIDNRKEYE; NIDNRKEYEI; IDNRKEYEIT; DNRKEYEITK; NRKEYEITKN; RKEYEITKNA; KEYEITKNAP; EYEITKNAPS; YEITKNAPSL; EITKNAPSLD; ITKNAPSLDS; TKNAPSLDSL; KNAPSLDSLI; NAPSLDSLIE; APSLDSLIEY; PSLDSLIEYL; SLDSLIEYLE; LDSLIEYLEH; DSLIEYLEHM; SLIEYLEHMI; LIEYLEHMIL; IEYLEHMILF; EYLEHMILFF; YLEHMILFFL; LEHMILFFLE; EHMILFFLEK; HMILFFLEKT; MILFFLEKTP; ILFFLEKTPV; LFFLEKTPVG; FFLEKTPVGT; FLEKTPVGTL; LEKTPVGTLT; EKTPVGTLTA; KTPVGTLTAK; TPVGTLTAKF; PVGTLTAKFA; VGTLTAKFAM; GTLTAKFAME; TLTAKFAMEG; LTAKFAMEGS; TAKFAMEGSI; AKFAMEGSIL; KFAMEGSILT; FAMEGSILTR; AMEGSILTRS; MEGSILTRSK; EGSILTRSKL; GSILTRSKLI; SILTRSKLIQ; ILTRSKLIQA; LTRSKLIQAF; TRSKLIQAFT; RSKLIQAFTN; SKLIQAFTNT; KLIQAFTNTN; LIQAFTNTNK; IQAFTNTNKF; QAFTNTNKFC; AFTNTNKFCI; FTNTNKFCIP; TNTNKFCIPD; NTNKFCIPDG; TNKFCIPDGR; NKFCIPDGRS; KFCIPDGRSL; FCIPDGRSLP; CIPDGRSLPS; IPDGRSLPSN; PDGRSLPSNC; DGRSLPSNCY; GRSLPSNCYA; RSLPSNCYAY; SLPSNCYAYK; LPSNCYAYKV; PSNCYAYKVL; SNCYAYKVLG; NCYAYKVLGI; CYAYKVLGIS; YAYKVLGISS; AYKVLGISSA; YKVLGISSAP; KVLGISSAPK; VLGISSAPKL; LGISSAPKLS; GISSAPKLSG; ISSAPKLSGR; SSAPKLSGRF; SAPKLSGRFL; APKLSGRFLR; PKLSGRFLRH; KLSGRFLRHY; LSGRFLRHYD; SGRFLRHYDS; GRFLRHYDSG; RFLRHYDSGG; FLRHYDSGGS; LRHYDSGGST; RHYDSGGSTD; HYDSGGSTDS; YDSGGSTDSD; DSGGSTDSDG; SGGSTDSDGT; GGSTDSDGTR; GSTDSDGTRS; STDSDGTRSL; TDSDGTRSLG; DSDGTRSLGH; SDGTRSLGHT; DGTRSLGHTQ; GTRSLGHTQE; TRSLGHTQED; RSLGHTQEDS; SLGHTQEDSY; LGHTQEDSYK; GHTQEDSYKN; HTQEDSYKNH; TQEDSYKNHD; QEDSYKNHDH; EDSYKNHDHD; DSYKNHDHDL; SYKNHDHDLD; YKNHDHDLDF; KNHDHDLDFS; NHDHDLDFSR; HDHDLDFSRI; DHDLDFSRIN; HDLDFSRINF; DLDFSRINFK; LDFSRINFKG; DFSRINFKGK; FSRINFKGKL; SRINFKGKLV; RINFKGKLVK; INFKGKLVKR; NFKGKLVKRM; FKGKLVKRMT; KGKLVKRMTM; GKLVKRMTMI; KLVKRMTMIY; LVKRMTMIYR; VKRMTMIYRS; KRMTMIYRSA; RMTMIYRSAD; MTMIYRSADT; TMIYRSADTW; MIYRSADTWY; IYRSADTWYT; YRSADTWYTW; RSADTWYTWY; SADTWYTWYW; ADTWYTWYWA; DTWYTWYWAE; TWYTWYWAEE; WYTWYWAEEI; YTWYWAEEIM; TWYWAEEIMS; WYWAEEIMSP; YWAEEIMSPF; WAEEIMSPFI; AEEIMSPFIT; EEIMSPFITG; EIMSPFITGY; IMSPFITGYS; MSPFITGYSY; SPFITGYSYE; PFITGYSYEE; FITGYSYEEI; ITGYSYEEID; TGYSYEEIDP; GYSYEEIDPE; YSYEEIDPEY; SYEEIDPEYL; YEEIDPEYLL; EEIDPEYLLP; EIDPEYLLPP; IDPEYLLPPF; DPEYLLPPFT; PEYLLPPFTS; EYLLPPFTSQ; YLLPPFTSQS; LLPPFTSQSG; LPPFTSQSGS; PPFTSQSGSK; PFTSQSGSKE; FTSQSGSKET; TSQSGSKETK; SQSGSKETKP; QSGSKETKPK; SGSKETKPKN; GSKETKPKNT; SKETKPKNTC; KETKPKNTCY; ETKPKNTCYI; TKPKNTCYIS; KPKNTCYISF; PKNTCYISFY;

	KNTCYISFYR; NTCYISFYRY; TCYISFYRYD; CYISFYRYDL; 11 mers: MITQQDYTEIK; ITQQDYTEIKK; TQQDYTEIKKK; QQDYTEIKKKL; QDYTEIKKKLE; DYTEIKKKLEN; YTEIKKKLENT; TEIKKKLENTK; EIKKKLENTKT; IKKKLENTKTR; KKKLENTKTRI; KKLENTKTRIQ; KLENTKTRIQF; LENTKTRIQFR; ENTKTRIQFRN; NTKTRIQFRNG; TKTRIQFRNGN; KTRIQFRNGNK; TRIQFRNGNKI; RIQFRNGNKID; IQFRNGNKIDS; QFRNGNKIDSL; FRNGNKIDSLG; RNGNKIDSLGY; NGNKIDSLGYQ; GNKIDSLGYQG; NKIDSLGYQGS; KIDSLGYQGSL; IDSLGYQGSLG; DSLGYQGSLGE; SLGYQGSLGEP; LGYQGSLGEPI; GYQGSLGEPIL; YQGSLGEPILL; QGSLGEPILLK; GSLGEPILLKD; SLGEPILLKDK; LGEPILLKDKL; GEPILLKDKLT; EPILLKDKLTF; PILLKDKLTFS; ILLKDKLTFSI; LLKDKLTFSIC; LKDKLTFSICD; KDKLTFSICDG; DKLTFSICDGK; KLTFSICDGKN; LTFSICDGKNI; TFSICDGKNID; FSICDGKNIDN; SICDGKNIDNR; ICDGKNIDNRK; CDGKNIDNRKE; DGKNIDNRKEY; GKNIDNRKEYE; KNIDNRKEYEI; NIDNRKEYEIT; IDNRKEYEITK; DNRKEYEITKN; NRKEYEITKNA; RKEYEITKNAP; KEYEITKNAPS; EYEITKNAPSL; YEITKNAPSLD; EITKNAPSLDS; ITKNAPSLDSL; TKNAPSLDSLI; KNAPSLDSLIE; NAPSLDSLIEY; APSLDSLIEYL; PSLDSLIEYLE; SLDSLIEYLEH; LDSLIEYLEHM; DSLIEYLEHMI; SLIEYLEHMIL; LIEYLEHMILF; IEYLEHMILFF; EYLEHMILFFL; YLEHMILFFLE; LEHMILFFLEK; EHMILFFLEKT; HMILFFLEKTP; MILFFLEKTPV; ILFFLEKTPVG; LFFLEKTPVGT; FFLEKTPVGTL; FLEKTPVGTLT; LEKTPVGTLTA; EKTPVGTLTAK; KTPVGTLTAKF; TPVGTLTAKFA; PVGTLTAKFAM; VGTLTAKFAME; GTLTAKFAMEG; TLTAKFAMEGS; LTAKFAMEGSI; TAKFAMEGSIL; AKFAMEGSILT; KFAMEGSILTR; FAMEGSILTRS; AMEGSILTRSK; MEGSILTRSKL; EGSILTRSKLI; GSILTRSKLIQ; SILTRSKLIQA; ILTRSKLIQAF; LTRSKLIQAFT; TRSKLIQAFTN; RSKLIQAFTNT; SKLIQAFTNTN; KLIQAFTNTNK; LIQAFTNTNKF; IQAFTNTNKFC; QAFTNTNKFCI; AFTNTNKFCIP; FTNTNKFCIPD; TNTNKFCIPDG; NTNKFCIPDGR; TNKFCIPDGRS; NKFCIPDGRSL; KFCIPDGRSLP; FCIPDGRSLPS; CIPDGRSLPSN; IPDGRSLPSNC; PDGRSLPSNCY; DGRSLPSNCYA; GRSLPSNCYAY; RSLPSNCYAYK; SLPSNCYAYKV; LPSNCYAYKVL; PSNCYAYKVLG; SNCYAYKVLGI; NCYAYKVLGIS; CYAYKVLGISS; YAYKVLGISSA; AYKVLGISSAP; YKVLGISSAPK; KVLGISSAPKL; VLGISSAPKLS; LGISSAPKLSG; GISSAPKLSGR; ISSAPKLSGRF; SSAPKLSGRFL; SAPKLSGRFLR; APKLSGRFLRH; PKLSGRFLRHY; KLSGRFLRHYD; LSGRFLRHYDS; SGRFLRHYDSG; GRFLRHYDSGG; RFLRHYDSGGS; FLRHYDSGGST; LRHYDSGGSTD; RHYDSGGSTDS; HYDSGGSTDSD; YDSGGSTDSDG; DSGGSTDSDGT; SGGSTDSDGTR; GGSTDSDGTRS; GSTDSDGTRSL; STDSDGTRSLG; TDSDGTRSLGH; DSDGTRSLGHT; SDGTRSLGHTQ; DGTRSLGHTQE; GTRSLGHTQED; TRSLGHTQEDS; RSLGHTQEDSY; SLGHTQEDSYK; LGHTQEDSYKN; GHTQEDSYKNH; HTQEDSYKNHD; TQEDSYKNHDH; QEDSYKNHDHD; EDSYKNHDHDL; DSYKNHDHDLD; SYKNHDHDLDF; YKNHDHDLDFS; KNHDHDLDFSR; NHDHDLDFSRI; HDHDLDFSRIN; DHDLDFSRINF; HDLDFSRINFK; DLDFSRINFKG; LDFSRINFKGK; DFSRINFKGKL; FSRINFKGKLV; SRINFKGKLVK; RINFKGKLVKR; INFKGKLVKRM; NFKGKLVKRMT; FKGKLVKRMTM;

	KGKLVKRMTMI; GKLVKRMTMIY; KLVKRMTMIYR; LVKRMTMIYRS; VKRMTMIYRSA; KRMTMIYRSAD; RMTMIYRSADT; MTMIYRSADTW; TMIYRSADTWY; MIYRSADTWYT; IYRSADTWYTW; YRSADTWYTWY; RSADTWYTWYW; SADTWYTWYWA; ADTWYTWYWAE; DTWYTWYWAEE; TWYTWYWAEEI; WYTWYWAEEIM; YTWYWAEEIMS; TWYWAEEIMSP; WYWAEEIMSPF; YWAEEIMSPFI; WAEEIMSPFIT; AEEIMSPFITG; EEIMSPFITGY; EIMSPFITGYS; IMSPFITGYSY; MSPFITGYSYE; SPFITGYSYEE; PFITGYSYEEI; FITGYSYEEID; ITGYSYEEIDP; TGYSYEEIDPE; GYSYEEIDPEY; YSYEEIDPEYL; SYEEIDPEYLL; YEEIDPEYLLP; EEIDPEYLLPP; EIDPEYLLPPF; IDPEYLLPPFT; DPEYLLPPFTS; PEYLLPPFTSQ; EYLLPPFTSQS; YLLPPFTSQSG; LLPPFTSQSGS; LPPFTSQSGSK; PPFTSQSGSKE; PFTSQSGSKET; FTSQSGSKETK; TSQSGSKETKP; SQSGSKETKPK; QSGSKETKPKN; SGSKETKPKNT; GSKETKPKNTC; SKETKPKNTCY; KETKPKNTCYI; ETKPKNTCYIS; TKPKNTCYISF; KPKNTCYISFY; PKNTCYISFYR; KNTCYISFYRY; NTCYISFYRYD; TCYISFYRYDL;
Seq 30	SEQ ID NO 36940-38333/ 8 mers: MDLLDLLE; DLLDLLEK; LLDLLEKE; LDLLEKEK; DLLEKEKQ; LLEKEKQI; LEKEKQIN; EKEKQINK; KEKQINKN; EKQINKNK; KQINKNKG; QINKNKGV; INKNKGVF; NKNKGVFM; KNKGVFMT; NKGVFMTK; KGVFMTKP; GVFMTKPK; VFMTKPKI; FMTKPKIF; MTKPKIFS; TKPKIFSI; KPKIFSIN; PKIFSINK; KIFSINKE; IFSINKEK; FSINKEKI; SINKEKIK; INKEKIKI; NKEKIKIL; KEKIKILI; EKIKILII; KIKILIIV; IKILIIVV; KILIIVVL; ILIIVVLT; LIIVVLTS; IIVVLTST; IVVLTSTF; VVLTSTFL; VLTSTFLL; LTSTFLLG; TSTFLLGI; STFLLGII; TFLLGIIF; FLLGIIFS; LLGIIFSN; LGIIFSNE; GIIFSNEN; IIFSNENK; IFSNENKV; FSNENKVA; SNENKVAR; NENKVARI; ENKVARIL; NKVARILE; KVARILEE; VARILEEK; ARILEEKF; RILEEKFF; ILEEKFFD; LEEKFFDF; EEKFFDFD; EKFFDFDF; KFFDFDFN; FFDFDFNL; FDFDFNLI; DFDFNLIS; FDFNLISK; DFNLISKI; FNLISKIE; NLISKIET; LISKIETE; ISKIETEL; SKIETELE; KIETELEG; IETELEGT; ETELEGTL; TELEGTLT; ELEGTLTK; LEGTLTKL; EGTLTKLG; GTLTKLGK; TLTKLGKD; LTKLGKDW; TKLGKDWI; KLGKDWIL; LGKDWILT; GKDWILTY; KDWILTYN; DWILTYNK; WILTYNKQ; ILTYNKQN; LTYNKQNI; TYNKQNIP; YNKQNIPV; NKQNIPVD; KQNIPVDN; QNIPVDNK; NIPVDNKK; IPVDNKKV; PVDNKKVN; VDNKKVNS; DNKKVNSL; NKKVNSLI; KKVNSLIK; KVNSLIKA; VNSLIKAL; NSLIKALD; SLIKALDE; LIKALDEL; IKALDELQ; KALDELQK; ALDELQKN; LDELQKNK; DELQKNKL; ELQKNKLV; LQKNKLVS; QKNKLVSR; KNKLVSRD; NKLVSRDQ; KLVSRDQK; LVSRDQKK; VSRDQKKH; SRDQKKHK; RDQKKHKE; DQKKHKEL; QKKHKELG; KKHKELGI; KHKELGIG; HKELGIGE; KELGIGEN; ELGIGENP; LGIGENPS; GIGENPSF; IGENPSFK; GENPSFKL; ENPSFKLF; NPSFKLFD; PSFKLFDN; SFKLFDNN; FKLFDNNN; KLFDNNNK; LFDNNNKL; FDNNNKLL; DNNNKLLT; NNNKLLTE; NNKLLTEI; NKLLTEIF; KLLTEIFV; LLTEIFVG; LTEIFVGK; TEIFVGKS; EIFVGKSG; IFVGKSGE; FVGKSGEG; VGKSGEGD; GKSGEGDS; KSGEGDSR; SGEGDSRL;

GEGDSRLA; EGDSRLAY; GDSRLAYI; DSRLAYIK; SRLAYIKG;
RLAYIKGS; LAYIKGSD; AYIKGSDE; YIKGSDEN; IKGSDENV;
KGSDENVY; GSDENVYL; SDENVYLT; DENVYLTK; ENVYLTKN;
NVYLTKNI; VYLTKNIF; YLTKNIFL; LTKNIFLS; TKNIFLSY;
KNIFLSYK; NIFLSYKG; IFLSYKGN; FLSYKGNS; LSYKGNSY;
SYKGNSYN; YKGNSYNT; KGNSYNTF; GNSYNTFS; NSYNTFSD;
SYNTFSDT; YNTFSDTT; NTFSDTTL; TFSDTTLF; FSDTTLFQ;
SDTTLFQE; DTTLFQEK; TTLFQEKN; TLFQEKNT; LFQEKNTK;
FQEKNTKL; QEKNTKLE; EKNTKLEN; KNTKLENL; NTKLENLS;
TKLENLSF; KLENLSFK; LENLSFKI; ENLSFKII; NLSFKIIR;
LSFKIIRK; SFKIIRKL; FKIIRKLN; KIIRKLNK; IIRKLNKE;
IRKLNKEN; RKLNKENE; KLNKENEN; LNKENENN; NKENENNI;
KENENNIN; ENENNINN; NENNINNN; ENNINNNY; NNINNNYE;
NINNNYEI; INNNYEII; NNNYEIIS; NNYEIISK; NYEIISKD;
YEIISKDG; EIISKDGL; IISKDGLY; ISKDGLYF; SKDGLYFL;
KDGLYFLN; DGLYFLNN; GLYFLNNQ; LYFLNNQK; YFLNNQKM;
FLNNQKMT; LNNQKMTK; NNQKMTKE; NQKMTKER; QKMTKERP;
KMTKERPL; MTKERPLN; TKERPLNI; KERPLNII; ERPLNIIA;
RPLNIIAE; PLNIIAEF; LNIIAEFK; NIIAEFKA; IIAEFKAD;
IAEFKADG; AEFKADGL; EFKADGLE; FKADGLEI; KADGLEID;
ADGLEIDK; DGLEIDKS; GLEIDKSK; LEIDKSKI; EIDKSKID;
IDKSKIDD; DKSKIDDY; KSKIDDYN; SKIDDYNL; KIDDYNLQ;
IDDYNLQY; DDYNLQYK; DYNLQYKI; YNLQYKIE; NLQYKIEV;
LQYKIEVK; QYKIEVKW; YKIEVKWS; KIEVKWSN; IEVKWSNK;
EVKWSNKS; VKWSNKSV; KWSNKSVN; WSNKSVNN; SNKSVNNI;
NKSVNNIE; KSVNNIEV; SVNNIEVY; VNNIEVYF; NNIEVYFN;
NIEVYFNK; IEVYFNKN; EVYFNKNE; VYFNKNEE; YFNKNEEN;
FNKNEEND; NKNEENDK; KNEENDKD; NEENDKDI; EENDKDIL;
ENDKDILI; NDKDILIK; DKDILIKK; KDILIKKD; DILIKKDK;
ILIKKDKD; LIKKDKDE; IKKDKDEY; KKDKDEYY; KDKDEYYY;
DKDEYYYT; KDEYYYTT; DEYYYTTS; EYYYTTSK; YYYTTSKW;
YYTTSKWT; YTTSKWTF; TTSKWTFF; TSKWTFFD; SKWTFFDV;
KWTFFDVF; WTFFDVFD; TFFDVFDL; FFDVFDLE; FDVFDLEK;
DVFDLEKK; VFDLEKKL; FDLEKKLT; DLEKKLTE; LEKKLTEK;
EKKLTEKD; KKLTEKDD; KLTEKDDI; LTEKDDIS; TEKDDISS;
EKDDISSN; KDDISSND; DDISSNDN; DISSNDNQ; ISSNDNQE;
SSNDNQED; SNDNQEDH; NDNQEDHH; DNQEDHHE; NQEDHHEH;
QEDHHEHH; EDHHEHHN; DHHEHHNN; HHEHHNNA; HEHHNNAD;

9 mers:
MDLLDLLEK; DLLDLLEKE; LLDLLEKEK; LDLLEKEKQ; DLLEKEKQI;
LLEKEKQIN; LEKEKQINK; EKEKQINKN; KEKQINKNK; EKQINKNKG;
KQINKNKGV; QINKNKGVF; INKNKGVFM; NKNKGVFMT; KNKGVFMTK;
NKGVFMTKP; KGVFMTKPK; GVFMTKPKI; VFMTKPKIF; FMTKPKIFS;
MTKPKIFSI; TKPKIFSIN; KPKIFSINK; PKIFSINKE; KIFSINKEK;
IFSINKEKI; FSINKEKIK; SINKEKIKI; INKEKIKIL; NKEKIKILI;
KEKIKILII; EKIKILIIV; KIKILIIVV; IKILIIVVL; KILIIVVLT;
ILIIVVLTS; LIIVVLTST; IIVVLTSTF; IVVLTSTFL; VVLTSTFLL;
VLTSTFLLG; LTSTFLLGI; TSTFLLGII; STFLLGIIF; TFLLGIIFS;
FLLGIIFSN; LLGIIFSNE; LGIIFSNEN; GIIFSNENK; IIFSNENKV;
IFSNENKVA; FSNENKVAR; SNENKVARI; NENKVARIL; ENKVARILE;

	NKVARILEE; KVARILEEK; VARILEEKF; ARILEEKFF; RILEEKFFD; ILEEKFFDF; LEEKFFDFD; EEKFFDFDF; EKFFDFDFN; KFFDFDFNL; FFDFDFNLI; FDFDFNLIS; DFDFNLISK; FDFNLISKI; DFNLISKIE; FNLISKIET; NLISKIETE; LISKIETEL; ISKIETELE; SKIETELEG; KIETELEGT; IETELEGTL; ETELEGTLT; TELEGTLTK; ELEGTLTKL; LEGTLTKLG; EGTLTKLGK; GTLTKLGKD; TLTKLGKDW; LTKLGKDWI; TKLGKDWIL; KLGKDWILT; LGKDWILTY; GKDWILTYN; KDWILTYNK; DWILTYNKQ; WILTYNKQN; ILTYNKQNI; LTYNKQNIP; TYNKQNIPV; YNKQNIPVD; NKQNIPVDN; KQNIPVDNK; QNIPVDNKK; NIPVDNKKV; IPVDNKKVN; PVDNKKVNS; VDNKKVNSL; DNKKVNSLI; NKKVNSLIK; KKVNSLIKA; KVNSLIKAL; VNSLIKALD; NSLIKALDE; SLIKALDEL; LIKALDELQ; IKALDELQK; KALDELQKN; ALDELQKNK; LDELQKNKL; DELQKNKLV; ELQKNKLVS; LQKNKLVSR; QKNKLVSRD; KNKLVSRDQ; NKLVSRDQK; KLVSRDQKK; LVSRDQKKH; VSRDQKKHK; SRDQKKHKE; RDQKKHKEL; DQKKHKELG; QKKHKELGI; KKHKELGIG; KHKELGIGE; HKELGIGEN; KELGIGENP; ELGIGENPS; LGIGENPSF; GIGENPSFK; IGENPSFKL; GENPSFKLF; ENPSFKLFD; NPSFKLFDN; PSFKLFDNN; SFKLFDNNN; FKLFDNNNK; KLFDNNNKL; LFDNNNKLL; FDNNNKLLT; DNNNKLLTE; NNNKLLTEI; NNKLLTEIF; NKLLTEIFV; KLLTEIFVG; LLTEIFVGK; LTEIFVGKS; TEIFVGKSG; EIFVGKSGE; IFVGKSGEG; FVGKSGEGD; VGKSGEGDS; GKSGEGDSR; KSGEGDSRL; SGEGDSRLA; GEGDSRLAY; EGDSRLAYI; GDSRLAYIK; DSRLAYIKG; SRLAYIKGS; RLAYIKGSD; LAYIKGSDE; AYIKGSDEN; YIKGSDENV; IKGSDENVY; KGSDENVYL; GSDENVYLT; SDENVYLTK; DENVYLTKN; ENVYLTKNI; NVYLTKNIF; VYLTKNIFL; YLTKNIFLS; LTKNIFLSY; TKNIFLSYK; KNIFLSYKG; NIFLSYKGN; IFLSYKGNS; FLSYKGNSY; LSYKGNSYN; SYKGNSYNT; YKGNSYNTF; KGNSYNTFS; GNSYNTFSD; NSYNTFSDT; SYNTFSDTT; YNTFSDTTL; NTFSDTTLF; TFSDTTLFQ; FSDTTLFQE; SDTTLFQEK; DTTLFQEKN; TTLFQEKNT; TLFQEKNTK; LFQEKNTKL; FQEKNTKLE; QEKNTKLEN; EKNTKLENL; KNTKLENLS; NTKLENLSF; TKLENLSFK; KLENLSFKI; LENLSFKII; ENLSFKIIR; NLSFKIIRK; LSFKIIRKL; SFKIIRKLN; FKIIRKLNK; KIIRKLNKE; IIRKLNKEN; IRKLNKENE; RKLNKENEN; KLNKENENN; LNKENENNI; NKENENNIN; KENENNINN; ENENNININN; NENNININNY; ENNININNYE; NNININNYEI; NININNYEII; ININNYEIIS; NNNYEIISK; NNYEIISKD; NYEIISKDG; YEIISKDGL; EIISKDGLY; IISKDGLYF; ISKDGLYFL; SKDGLYFLN; KDGLYFLNN; DGLYFLNNQ; GLYFLNNQK; LYFLNNQKM; YFLNNQKMT; FLNNQKMTK; LNNQKMTKE; NNQKMTKER; NQKMTKERP; QKMTKERPL; KMTKERPLN; MTKERPLNI; TKERPLNII; KERPLNIIA; ERPLNIIAE; RPLNIIAEF; PLNIIAEFK; LNIIAEFKA; NIIAEFKAD; IIAEFKADG; IAEFKADGL; AEFKADGLE; EFKADGLEI; FKADGLEID; KADGLEIDK; ADGLEIDKS; DGLEIDKSK; GLEIDKSKI; LEIDKSKID; EIDKSKIDD; IDKSKIDDY; DKSKIDDYN; KSKIDDYNL; SKIDDYNLQ; KIDDYNLQY; IDDYNLQYK; DDYNLQYKI; DYNLQYKIE; YNLQYKIEV; NLQYKIEVK; LQYKIEVKW; QYKIEVKWS; YKIEVKWSN; KIEVKWSNK; IEVKWSNKS; EVKWSNKSV; VKWSNKSVN; KWSNKSVNN; WSNKSVNNI; SNKSVNNIE; NKSVNNIEV; KSVNNIEVY; SVNNIEVYF; VNNIEVYFN; NNIEVYFNK; NIEVYFNKN; IEVYFNKNE; EVYFNKNEE; VYFNKNEEN; YFNKNEEND; FNKNEENDK; NKNEENDKD; KNEENDKDI; NEENDKDIL; EENDKDILI; ENDKDILIK; NDKDILIKK; DKDILIKKD; KDILIKKDK; DILIKKDKD; ILIKKDKDE; LIKKDKDEY; IKKDKDEYY; KKDKDEYYY; KDKDEYYYT;

	DKDEYYYTT; KDEYYYTTS; DEYYYTTSK; EYYYTTSKW; YYYTTSKWT; YYTTSKWTF; YTTSKWTFF; TTSKWTFFD; TSKWTFFDV; SKWTFFDVF; KWTFFDVFD; WTFFDVFDL; TFFDVFDLE; FFDVFDLEK; FDVFDLEKK; DVFDLEKKL; VFDLEKKLT; FDLEKKLTE; DLEKKLTEK; LEKKLTEKD; EKKLTEKDD; KKLTEKDDI; KLTEKDDIS; LTEKDDISS; TEKDDISSN; EKDDISSND; KDDISSNDN; DDISSNDNQ; DISSNDNQE; ISSNDNQED; SSNDNQEDH; SNDNQEDHH; NDNQEDHHE; DNQEDHHEH; NQEDHHEHH; QEDHHEHHN; EDHHEHHNN; DHHEHHNNA; HHEHHNNAD; 10 mers: MDLLDLLEKE; DLLDLLEKEK; LLDLLEKEKQ; LDLLEKEKQI; DLLEKEKQIN; LLEKEKQINK; LEKEKQINKN; EKEKQINKNK; KEKQINKNKG; EKQINKNKGV; KQINKNKGVF; QINKNKGVFM; INKNKGVFMT; NKNKGVFMTK; KNKGVFMTKP; NKGVFMTKPK; KGVFMTKPKI; GVFMTKPKIF; VFMTKPKIFS; FMTKPKIFSI; MTKPKIFSIN; TKPKIFSINK; KPKIFSINKE; PKIFSINKEK; KIFSINKEKI; IFSINKEKIK; FSINKEKIKI; SINKEKIKIL; INKEKIKILI; NKEKIKILII; KEKIKILIIV; EKIKILIIVV; KIKILIIVVL; IKILIIVVLT; KILIIVVLTS; ILIIVVLTST; LIIVVLTSTF; IIVVLTSTFL; IVVLTSTFLL; VVLTSTFLLG; VLTSTFLLGI; LTSTFLLGII; TSTFLLGIIF; STFLLGIIFS; TFLLGIIFSN; FLLGIIFSNE; LLGIIFSNEN; LGIIFSNENK; GIIFSNENKV; IIFSNENKVA; IFSNENKVAR; FSNENKVARI; SNENKVARIL; NENKVARILE; ENKVARILEE; NKVARILEEK; KVARILEEKF; VARILEEKFF; ARILEEKFFD; RILEEKFFDF; ILEEKFFDFD; LEEKFFDFDF; EEKFFDFDFN; EKFFDFDFNL; KFFDFDFNLI; FFDFDFNLIS; FDFDFNLISK; DFDFNLISKI; FDFNLISKIE; DFNLISKIET; FNLISKIETE; NLISKIETEL; LISKIETELE; ISKIETELEG; SKIETELEGT; KIETELEGTL; IETELEGTLT; ETELEGTLTK; TELEGTLTKL; ELEGTLTKLG; LEGTLTKLGK; EGTLTKLGKD; GTLTKLGKDW; TLTKLGKDWI; LTKLGKDWIL; TKLGKDWILT; KLGKDWILTY; LGKDWILTYN; GKDWILTYNK; KDWILTYNKQ; DWILTYNKQN; WILTYNKQNI; ILTYNKQNIP; LTYNKQNIPV; TYNKQNIPVD; YNKQNIPVDN; NKQNIPVDNK; KQNIPVDNKK; QNIPVDNKKV; NIPVDNKKVN; IPVDNKKVNS; PVDNKKVNSL; VDNKKVNSLI; DNKKVNSLIK; NKKVNSLIKA; KKVNSLIKAL; KVNSLIKALD; VNSLIKALDE; NSLIKALDEL; SLIKALDELQ; LIKALDELQK; IKALDELQKN; KALDELQKNK; ALDELQKNKL; LDELQKNKLV; DELQKNKLVS; ELQKNKLVSR; LQKNKLVSRD; QKNKLVSRDQ; KNKLVSRDQK; NKLVSRDQKK; KLVSRDQKKH; LVSRDQKKHK; VSRDQKKHKE; SRDQKKHKEL; RDQKKHKELG; DQKKHKELGI; QKKHKELGIG; KKHKELGIGE; KHKELGIGEN; HKELGIGENP; KELGIGENPS; ELGIGENPSF; LGIGENPSFK; GIGENPSFKL; IGENPSFKLF; GENPSFKLFD; ENPSFKLFDN; NPSFKLFDNN; PSFKLFDNNN; SFKLFDNNNK; FKLFDNNNKL; KLFDNNNKLL; LFDNNNKLLT; FDNNNKLLTE; DNNNKLLTEI; NNNKLLTEIF; NNKLLTEIFV; NKLLTEIFVG; KLLTEIFVGK; LLTEIFVGKS; LTEIFVGKSG; TEIFVGKSGE; EIFVGKSGEG; IFVGKSGEGD; FVGKSGEGDS; VGKSGEGDSR; GKSGEGDSRL; KSGEGDSRLA; SGEGDSRLAY;

	GEGDSRLAYI; EGDSRLAYIK; GDSRLAYIKG; DSRLAYIKGS; SRLAYIKGSD; RLAYIKGSDE; LAYIKGSDEN; AYIKGSDENV; YIKGSDENVY; IKGSDENVYL; KGSDENVYLT; GSDENVYLTK; SDENVYLTKN; DENVYLTKNI; ENVYLTKNIF; NVYLTKNIFL; VYLTKNIFLS; YLTKNIFLSY; LTKNIFLSYK; TKNIFLSYKG; KNIFLSYKGN; NIFLSYKGNS; IFLSYKGNSY; FLSYKGNSYN; LSYKGNSYNT; SYKGNSYNTF; YKGNSYNTFS; KGNSYNTFSD; GNSYNTFSDT; NSYNTFSDTT; SYNTFSDTTL; YNTFSDTTLF; NTFSDTTLFQ; TFSDTTLFQE; FSDTTLFQEK; SDTTLFQEKN; DTTLFQEKNT; TTLFQEKNTK; TLFQEKNTKL; LFQEKNTKLE; FQEKNTKLEN; QEKNTKLENL; EKNTKLENLS; KNTKLENLSF; NTKLENLSFK; TKLENLSFKI; KLENLSFKII; LENLSFKIIR; ENLSFKIIRK; NLSFKIIRKL; LSFKIIRKLN; SFKIIRKLNK; FKIIRKLNKE; KIIRKLNKEN; IIRKLNKENE; IRKLNKENEN; RKLNKENENN; KLNKENENNI; LNKENENNIN; NKENENNINN; KENENNINNN; ENENNINNNY; NENNINNNYE; ENNINNNYEI; NNINNNYEII; NINNNYEIIS; INNNYEIISK; NNNYEIISKD; NNYEIISKDG; NYEIISKDGL; YEIISKDGLY; EIISKDGLYF; IISKDGLYFL; ISKDGLYFLN; SKDGLYFLNN; KDGLYFLNNQ; DGLYFLNNQK; GLYFLNNQKM; LYFLNNQKMT; YFLNNQKMTK; FLNNQKMTKE; LNNQKMTKER; NNQKMTKERP; NQKMTKERPL; QKMTKERPLN; KMTKERPLNI; MTKERPLNII; TKERPLNIIA; KERPLNIIAE; ERPLNIIAEF; RPLNIIAEFK; PLNIIAEFKA; LNIIAEFKAD; NIIAEFKADG; IIAEFKADGL; IAEFKADGLE; AEFKADGLEI; EFKADGLEID; FKADGLEIDK; KADGLEIDKS; ADGLEIDKSK; DGLEIDKSKI; GLEIDKSKID; LEIDKSKIDD; EIDKSKIDDY; IDKSKIDDYN; DKSKIDDYNL; KSKIDDYNLQ; SKIDDYNLQY; KIDDYNLQYK; IDDYNLQYKI; DDYNLQYKIE; DYNLQYKIEV; YNLQYKIEVK; NLQYKIEVKW; LQYKIEVKWS; QYKIEVKWSN; YKIEVKWSNK; KIEVKWSNKS; IEVKWSNKSV; EVKWSNKSVN; VKWSNKSVNN; KWSNKSVNNI; WSNKSVNNIE; SNKSVNNIEV; NKSVNNIEVY; KSVNNIEVYF; SVNNIEVYFN; VNNIEVYFNK; NNIEVYFNKN; NIEVYFNKNE; IEVYFNKNEE; EVYFNKNEEN; VYFNKNEEND; YFNKNEENDK; FNKNEENDKD; NKNEENDKDI; KNEENDKDIL; NEENDKDILI; EENDKDILIK; ENDKDILIKK; NDKDILIKKD; DKDILIKKDK; KDILIKKDKD; DILIKKDKDE; ILIKKDKDEY; LIKKDKDEYY; IKKDKDEYYY; KKDKDEYYYT; KDKDEYYYTT; DKDEYYYTTS; KDEYYYTTSK; DEYYYTTSKW; EYYYTTSKWT; YYYTTSKWTF; YYTTSKWTFF; YTTSKWTFFD; TTSKWTFFDV; TSKWTFFDVF; SKWTFFDVFD; KWTFFDVFDL; WTFFDVFDLE; TFFDVFDLEK; FFDVFDLEKK; FDVFDLEKKL; DVFDLEKKLT; VFDLEKKLTE; FDLEKKLTEK; DLEKKLTEKD; LEKKLTEKDD; EKKLTEKDDI; KKLTEKDDIS; KLTEKDDISS; LTEKDDISSN; TEKDDISSND; EKDDISSNDN; KDDISSNDNQ; DDISSNDNQE; DISSNDNQED; ISSNDNQEDH; SSNDNQEDHH; SNDNQEDHHE; NDNQEDHHEH; DNQEDHHEHH; NQEDHHEHHN; QEDHHEHHNN; EDHHEHHNNA; DHHEHHNNAD; 11 mers: MDLLDLLEKEK; DLLDLLEKEKQ; LLDLLEKEKQI; LDLLEKEKQIN; DLLEKEKQINK; LLEKEKQINKN; LEKEKQINKNK; EKEKQINKNKG;

	KEKQINKNKGV; EKQINKNKGVF; KQINKNKGVFM; QINKNKGVFMT; INKNKGVFMTK; NKNKGVFMTKP; KNKGVFMTKPK; NKGVFMTKPKI; KGVFMTKPKIF; GVFMTKPKIFS; VFMTKPKIFSI; FMTKPKIFSIN; MTKPKIFSINK; TKPKIFSINKE; KPKIFSINKEK; PKIFSINKEKI; KIFSINKEKIK; IFSINKEKIKI; FSINKEKIKIL; SINKEKIKILI; INKEKIKILII; NKEKIKILIIV; KEKIKILIIVV; EKIKILIIVVL; KIKILIIVVLT; IKILIIVVLTS; KILIIVVLTST; ILIIVVLTSTF; LIIVVLTSTFL; IIVVLTSTFLL; IVVLTSTFLLG; VVLTSTFLLGI; VLTSTFLLGII; LTSTFLLGIIF; TSTFLLGIIFS; STFLLGIIFSN; TFLLGIIFSNE; FLLGIIFSNEN; LLGIIFSNENK; LGIIFSNENKV; GIIFSNENKVA; IIFSNENKVAR; IFSNENKVARI; FSNENKVARIL; SNENKVARILE; NENKVARILEE; ENKVARILEEK; NKVARILEEKF; KVARILEEKFF; VARILEEKFFD; ARILEEKFFDF; RILEEKFFDFD; ILEEKFFDFDF; LEEKFFDFDFN; EEKFFDFDFNL; EKFFDFDFNLI; KFFDFDFNLIS; FFDFDFNLISK; FDFDFNLISKI; DFDFNLISKIE; FDFNLISKIET; DFNLISKIETE; FNLISKIETEL; NLISKIETELE; LISKIETELEG; ISKIETELEGT; SKIETELEGTL; KIETELEGTLT; IETELEGTLTK; ETELEGTLTKL; TELEGTLTKLG; ELEGTLTKLGK; LEGTLTKLGKD; EGTLTKLGKDW; GTLTKLGKDWI; TLTKLGKDWIL; LTKLGKDWILT; TKLGKDWILTY; KLGKDWILTYN; LGKDWILTYNK; GKDWILTYNKQ; KDWILTYNKQN; DWILTYNKQNI; WILTYNKQNIP; ILTYNKQNIPV; LTYNKQNIPVD; TYNKQNIPVDN; YNKQNIPVDNK; NKQNIPVDNKK; KQNIPVDNKKV; QNIPVDNKKVN; NIPVDNKKVNS; IPVDNKKVNSL; PVDNKKVNSLI; VDNKKVNSLIK; DNKKVNSLIKA; NKKVNSLIKAL; KKVNSLIKALD; KVNSLIKALDE; VNSLIKALDEL; NSLIKALDELQ; SLIKALDELQK; LIKALDELQKN; IKALDELQKNK; KALDELQKNKL; ALDELQKNKLV; LDELQKNKLVS; DELQKNKLVSR; ELQKNKLVSRD; LQKNKLVSRDQ; QKNKLVSRDQK; KNKLVSRDQKK; NKLVSRDQKKH; KLVSRDQKKHK; LVSRDQKKHKE; VSRDQKKHKEL; SRDQKKHKELG; RDQKKHKELGI; DQKKHKELGIG; QKKHKELGIGE; KKHKELGIGEN; KHKELGIGENP; HKELGIGENPS; KELGIGENPSF; ELGIGENPSFK; LGIGENPSFKL; GIGENPSFKLF; IGENPSFKLFD; GENPSFKLFDN; ENPSFKLFDNN; NPSFKLFDNNN; PSFKLFDNNNK; SFKLFDNNNKL; FKLFDNNNKLL; KLFDNNNKLLT; LFDNNNKLLTE; FDNNNKLLTEI; DNNNKLLTEIF; NNNKLLTEIFV; NNKLLTEIFVG; NKLLTEIFVGK; KLLTEIFVGKS; LLTEIFVGKSG; LTEIFVGKSGE; TEIFVGKSGEG; EIFVGKSGEGD; IFVGKSGEGDS; FVGKSGEGDSR; VGKSGEGDSRL; GKSGEGDSRLA; KSGEGDSRLAY; SGEGDSRLAYI; GEGDSRLAYIK; EGDSRLAYIKG; GDSRLAYIKGS; DSRLAYIKGSD; SRLAYIKGSDE; RLAYIKGSDEN; LAYIKGSDENV; AYIKGSDENVY; YIKGSDENVYL; IKGSDENVYLT; KGSDENVYLTK; GSDENVYLTKN; SDENVYLTKNI; DENVYLTKNIF; ENVYLTKNIFL; NVYLTKNIFLS; VYLTKNIFLSY; YLTKNIFLSYK; LTKNIFLSYKG; TKNIFLSYKGN; KNIFLSYKGNS; NIFLSYKGNSY; IFLSYKGNSYN; FLSYKGNSYNT; LSYKGNSYNTF; SYKGNSYNTFS; YKGNSYNTFSD; KGNSYNTFSDT; GNSYNTFSDTT; NSYNTFSDTTL; SYNTFSDTTLF; YNTFSDTTLFQ; NTFSDTTLFQE; TFSDTTLFQEK; FSDTTLFQEKN; SDTTLFQEKNT; DTTLFQEKNTK; TTLFQEKNTKL; TLFQEKNTKLE; LFQEKNTKLEN; FQEKNTKLENL; QEKNTKLENLS; EKNTKLENLSF; KNTKLENLSFK; NTKLENLSFKI; TKLENLSFKII; KLENLSFKIIR; LENLSFKIIRK; ENLSFKIIRKL; NLSFKIIRKLN; LSFKIIRKLNK; SFKIIRKLNKE;

	FKIIRKLNKEN; KIIRKLNKENE; IIRKLNKENEN; IRKLNKENENN; RKLNKENENNI; KLNKENENNIN; LNKENENNINN; NKENENNINNN; KENENNINNNY; ENENNINNNYE; NENNINNNYEI; ENNINNNYEII; NNINNNYEIIS; NINNNYEIISK; INNNYEIISKD; NNNYEIISKDG; NNYEIISKDGL; NYEIISKDGLY; YEIISKDGLYF; EIISKDGLYFL; IISKDGLYFLN; ISKDGLYFLNN; SKDGLYFLNNQ; KDGLYFLNNQK; DGLYFLNNQKM; GLYFLNNQKMT; LYFLNNQKMTK; YFLNNQKMTKE; FLNNQKMTKER; LNNQKMTKERP; NNQKMTKERPL; NQKMTKERPLN; QKMTKERPLNI; KMTKERPLNII; MTKERPLNIIA; TKERPLNIIAE; KERPLNIIAEF; ERPLNIIAEFK; RPLNIIAEFKA; PLNIIAEFKAD; LNIIAEFKADG; NIIAEFKADGL; IIAEFKADGLE; IAEFKADGLEI; AEFKADGLEID; EFKADGLEIDK; FKADGLEIDKS; KADGLEIDKSK; ADGLEIDKSKI; DGLEIDKSKID; GLEIDKSKIDD; LEIDKSKIDDY; EIDKSKIDDYN; IDKSKIDDYNL; DKSKIDDYNLQ; KSKIDDYNLQY; SKIDDYNLQYK; KIDDYNLQYKI; IDDYNLQYKIE; DDYNLQYKIEV; DYNLQYKIEVK; YNLQYKIEVKW; NLQYKIEVKWS; LQYKIEVKWSN; QYKIEVKWSNK; YKIEVKWSNKS; KIEVKWSNKSV; IEVKWSNKSVN; EVKWSNKSVNN; VKWSNKSVNNI; KWSNKSVNNIE; WSNKSVNNIEV; SNKSVNNIEVY; NKSVNNIEVYF; KSVNNIEVYFN; SVNNIEVYFNK; VNNIEVYFNKN; NNIEVYFNKNE; NIEVYFNKNEE; IEVYFNKNEEN; EVYFNKNEEND; VYFNKNEENDK; YFNKNEENDKD; FNKNEENDKDI; NKNEENDKDIL; KNEENDKDILI; NEENDKDILIK; EENDKDILIKK; ENDKDILIKKD; NDKDILIKKDK; DKDILIKKDKD; KDILIKKDKDE; DILIKKDKDEY; ILIKKDKDEYY; LIKKDKDEYYY; IKKDKDEYYYT; KKDKDEYYYTT; KDKDEYYYTTS; DKDEYYYTTSK; KDEYYYTTSKW; DEYYYTTSKWT; EYYYTTSKWTF; YYYTTSKWTFF; YYTTSKWTFFD; YTTSKWTFFDV; TTSKWTFFDVF; TSKWTFFDVFD; SKWTFFDVFDL; KWTFFDVFDLE; WTFFDVFDLEK; TFFDVFDLEKK; FFDVFDLEKKL; FDVFDLEKKLT; DVFDLEKKLTE; VFDLEKKLTEK; FDLEKKLTEKD; DLEKKLTEKDD; LEKKLTEKDDI; EKKLTEKDDIS; KKLTEKDDISS; KLTEKDDISSN; LTEKDDISSND; TEKDDISSNDN; EKDDISSNDNQ; KDDISSNDNQE; DDISSNDNQED; DISSNDNQEDH; ISSNDNQEDHH; SSNDNQEDHHE; SNDNQEDHHEH; NDNQEDHHEHH; DNQEDHHEHHN; NQEDHHEHHNN; QEDHHEHHNNA; EDHHEHHNNAD;
Seq 31	SEQ ID NO 38334-38919/ 8 mers: MKKLIIIF; KKLIIIFT; KLIIIFTL; LIIIFTLF; IIIFTLFL; IIFTLFLS; IFTLFLSQ; FTLFLSQA; TLFLSQAC; LFLSQACN; FLSQACNL; LSQACNLS; SQACNLST; QACNLSTM; ACNLSTMH; CNLSTMHK; NLSTMHKI; LSTMHKID; STMHKIDT; TMHKIDTK; MHKIDTKE; HKIDTKED; KIDTKEDM; IDTKEDMK; DTKEDMKI; TKEDMKIL; KEDMKILY; EDMKILYS; DMKILYSE; MKILYSEI; KILYSEIA; ILYSEIAE; LYSEIAEL; YSEIAELR; SEIAELRK; EIAELRKK; IAELRKKL; AELRKKLN; ELRKKLNL; LRKKLNLN; RKKLNLNH; KKLNLNHL; KLNLNHLE; LNLNHLEI; NLNHLEID; LNHLEIDD; NHLEIDDT; HLEIDDTL; LEIDDTLE; EIDDTLEK; IDDTLEKV; DDTLEKVA; DTLEKVAK; TLEKVAKE; LEKVAKEY; EKVAKEYA; KVAKEYAI; VAKEYAIK; AKEYAIKL; KEYAIKLG; EYAIKLGE; YAIKLGEN; AIKLGENR; IKLGENRT; KLGENRTI; LGENRTIT; GENRTITH; ENRTITHT; NRTITHTL; RTITHTLF;

	TITHTLFG; ITHTLFGT; THTLFGTT; HTLFGTTP; TLFGTTPM; LFGTTPMQ; FGTTPMQR; GTTPMQRI; TTPMQRIH; TPMQRIHK; PMQRIHKY; MQRIHKYD; QRIHKYDQ; RIHKYDQS; IHKYDQSF; HKYDQSFN; KYDQSFNL; YDQSFNLT; DQSFNLTR; QSFNLTRE; SFNLTREI; FNLTREIL; NLTREILA; LTREILAS; TREILASG; REILASGI; EILASGIE; ILASGIEL; LASGIELN; ASGIELNR; SGIELNRV; GIELNRVV; IELNRVVN; ELNRVVNA; LNRVVNAW; NRVVNAWL; RVVNAWLN; VVNAWLNS; VNAWLNSP; NAWLNSPS; AWLNSPSH; WLNSPSHK; LNSPSHKE; NSPSHKEA; SPSHKEAL; PSHKEALI; SHKEALIN; HKEALINT; KEALINTD; EALINTDT; ALINTDTD; LINTDTDK; INTDTDKI; NTDTDKIG; TDTDKIGG; DTDKIGGY; TDKIGGYR; DKIGGYRL; KIGGYRLK; IGGYRLKT; GGYRLKTT; GYRLKTTD; YRLKTTDN; RLKTTDNI; LKTTDNID; KTTDNIDI; TTDNIDIF; TDNIDIFV; DNIDIFVV; NIDIFVVL; IDIFVVLF; DIFVVLFG; IFVVLFGK; FVVLFGKR; VVLFGKRK; VLFGKRKY; LFGKRKYK; FGKRKYKN; 9 mers: MKKLIIIFT; KKLIIIFTL; KLIIIFTLF; LIIIFTLFL; IIIFTLFLS; IIFTLFLSQ; IFTLFLSQA; FTLFLSQAC; TLFLSQACN; LFLSQACNL; FLSQACNLS; LSQACNLST; SQACNLSTM; QACNLSTMH; ACNLSTMHK; CNLSTMHKI; NLSTMHKID; LSTMHKIDT; STMHKIDTK; TMHKIDTKE; MHKIDTKED; HKIDTKEDM; KIDTKEDMK; IDTKEDMKI; DTKEDMKIL; TKEDMKILY; KEDMKILYS; EDMKILYSE; DMKILYSEI; MKILYSEIA; KILYSEIAE; ILYSEIAEL; LYSEIAELR; YSEIAELRK; SEIAELRKK; EIAELRKKL; IAELRKKLN; AELRKKLNL; ELRKKLNLN; LRKKLNLNH; RKKLNLNHL; KKLNLNHLE; KLNLNHLEI; LNLNHLEID; NLNHLEIDD; LNHLEIDDT; NHLEIDDTL; HLEIDDTLE; LEIDDTLEK; EIDDTLEKV; IDDTLEKVA; DDTLEKVAK; DTLEKVAKE; TLEKVAKEY; LEKVAKEYA; EKVAKEYAI; KVAKEYAIK; VAKEYAIKL; AKEYAIKLG; KEYAIKLGE; EYAIKLGEN; YAIKLGENR; AIKLGENRT; IKLGENRTI; KLGENRTIT; LGENRTITH; GENRTITHT; ENRTITHTL; NRTITHTLF; RTITHTLFG; TITHTLFGT; ITHTLFGTT; THTLFGTTP; HTLFGTTPM; TLFGTTPMQ; LFGTTPMQR; FGTTPMQRI; GTTPMQRIH; TTPMQRIHK; TPMQRIHKY; PMQRIHKYD; MQRIHKYDQ; QRIHKYDQS; RIHKYDQSF; IHKYDQSFN; HKYDQSFNL; KYDQSFNLT; YDQSFNLTR; DQSFNLTRE; QSFNLTREI; SFNLTREIL; FNLTREILA; NLTREILAS; LTREILASG; TREILASGI; REILASGIE; EILASGIEL; ILASGIELN; LASGIELNR; ASGIELNRV; SGIELNRVV; GIELNRVVN; IELNRVVNA; ELNRVVNAW; LNRVVNAWL; NRVVNAWLN; RVVNAWLNS; VVNAWLNSP; VNAWLNSPS; NAWLNSPSH; AWLNSPSHK; WLNSPSHKE; LNSPSHKEA; NSPSHKEAL; SPSHKEALI; PSHKEALIN; SHKEALINT; HKEALINTD; KEALINTDT; EALINTDTD; ALINTDTDK; LINTDTDKI; INTDTDKIG; NTDTDKIGG; TDTDKIGGY; DTDKIGGYR; TDKIGGYRL; DKIGGYRLK; KIGGYRLKT; IGGYRLKTT; GGYRLKTTD; GYRLKTTDN; YRLKTTDNI; RLKTTDNID; LKTTDNIDI; KTTDNIDIF; TTDNIDIFV; TDNIDIFVV; DNIDIFVVL; NIDIFVVLF; IDIFVVLFG; DIFVVLFGK; IFVVLFGKR; FVVLFGKRK; VVLFGKRKY; VLFGKRKYK; LFGKRKYKN; 10 mers: MKKLIIIFTL; KKLIIIFTLF; KLIIIFTLFL; LIIIFTLFLS;

	IIIFTLFLSQ; IIFTLFLSQA; IFTLFLSQAC; FTLFLSQACN; TLFLSQACNL; LFLSQACNLS; FLSQACNLST; LSQACNLSTM; SQACNLSTMH; QACNLSTMHK; ACNLSTMHKI; CNLSTMHKID; NLSTMHKIDT; LSTMHKIDTK; STMHKIDTKE; TMHKIDTKED; MHKIDTKEDM; HKIDTKEDMK; KIDTKEDMKI; IDTKEDMKIL; DTKEDMKILY; TKEDMKILYS; KEDMKILYSE; EDMKILYSEI; DMKILYSEIA; MKILYSEIAE; KILYSEIAEL; ILYSEIAELR; LYSEIAELRK; YSEIAELRKK; SEIAELRKKL; EIAELRKKLN; IAELRKKLNL; AELRKKLNLN; ELRKKLNLNH; LRKKLNLNHL; RKKLNLNHLE; KKLNLNHLEI; KLNLNHLEID; LNLNHLEIDD; NLNHLEIDDT; LNHLEIDDTL; NHLEIDDTLE; HLEIDDTLEK; LEIDDTLEKV; EIDDTLEKVA; IDDTLEKVAK; DDTLEKVAKE; DTLEKVAKEY; TLEKVAKEYA; LEKVAKEYAI; EKVAKEYAIK; KVAKEYAIKL; VAKEYAIKLG; AKEYAIKLGE; KEYAIKLGEN; EYAIKLGENR; YAIKLGENRT; AIKLGENRTI; IKLGENRTIT; KLGENRTITH; LGENRTITHT; GENRTITHTL; ENRTITHTLF; NRTITHTLFG; RTITHTLFGT; TITHTLFGTT; ITHTLFGTTP; THTLFGTTPM; HTLFGTTPMQ; TLFGTTPMQR; LFGTTPMQRI; FGTTPMQRIH; GTTPMQRIHK; TTPMQRIHKY; TPMQRIHKYD; PMQRIHKYDQ; MQRIHKYDQS; QRIHKYDQSF; RIHKYDQSFN; IHKYDQSFNL; HKYDQSFNLT; KYDQSFNLTR; YDQSFNLTRE; DQSFNLTREI; QSFNLTREIL; SFNLTREILA; FNLTREILAS; NLTREILASG; LTREILASGI; TREILASGIE; REILASGIEL; EILASGIELN; ILASGIELNR; LASGIELNRV; ASGIELNRVV; SGIELNRVVN; GIELNRVVNA; IELNRVVNAW; ELNRVVNAWL; LNRVVNAWLN; NRVVNAWLNS; RVVNAWLNSP; VVNAWLNSPS; VNAWLNSPSH; NAWLNSPSHK; AWLNSPSHKE; WLNSPSHKEA; LNSPSHKEAL; NSPSHKEALI; SPSHKEALIN; PSHKEALINT; SHKEALINTD; HKEALINTDT; KEALINTDTD; EALINTDTDK; ALINTDTDKI; LINTDTDKIG; INTDTDKIGG; NTDTDKIGGY; TDTDKIGGYR; DTDKIGGYRL; TDKIGGYRLK; DKIGGYRLKT; KIGGYRLKTT; IGGYRLKTTD; GGYRLKTTDN; GYRLKTTDNI; YRLKTTDNID; RLKTTDNIDI; LKTTDNIDIF; KTTDNIDIFV; TTDNIDIFVV; TDNIDIFVVL; DNIDIFVVLF; NIDIFVVLFG; IDIFVVLFGK; DIFVVLFGKR; IFVVLFGKRK; FVVLFGKRKY; VVLFGKRKYK; VLFGKRKYKN; 11 mers: MKKLIIIFTLF; KKLIIIFTLFL; KLIIIFTLFLS; LIIIFTLFLSQ; IIIFTLFLSQA; IIFTLFLSQAC; IFTLFLSQACN; FTLFLSQACNL; TLFLSQACNLS; LFLSQACNLST; FLSQACNLSTM; LSQACNLSTMH; SQACNLSTMHK; QACNLSTMHKI; ACNLSTMHKID; CNLSTMHKIDT; NLSTMHKIDTK; LSTMHKIDTKE; STMHKIDTKED; TMHKIDTKEDM; MHKIDTKEDMK; HKIDTKEDMKI; KIDTKEDMKIL; IDTKEDMKILY; DTKEDMKILYS; TKEDMKILYSE; KEDMKILYSEI; EDMKILYSEIA; DMKILYSEIAE; MKILYSEIAEL; KILYSEIAELR; ILYSEIAELRK; LYSEIAELRKK; YSEIAELRKKL; SEIAELRKKLN; EIAELRKKLNL; IAELRKKLNLN; AELRKKLNLNH; ELRKKLNLNHL; LRKKLNLNHLE; RKKLNLNHLEI; KKLNLNHLEID; KLNLNHLEIDD; LNLNHLEIDDT; NLNHLEIDDTL; LNHLEIDDTLE; NHLEIDDTLEK; HLEIDDTLEKV; LEIDDTLEKVA; EIDDTLEKVAK; IDDTLEKVAKE; DDTLEKVAKEY;

	DTLEKVAKEYA; TLEKVAKEYAI; LEKVAKEYAIK; EKVAKEYAIKL; KVAKEYAIKLG; VAKEYAIKLGE; AKEYAIKLGEN; KEYAIKLGENR; EYAIKLGENRT; YAIKLGENRTI; AIKLGENRTIT; IKLGENRTITH; KLGENRTITHT; LGENRTITHTL; GENRTITHTLF; ENRTITHTLFG; NRTITHTLFGT; RTITHTLFGTT; TITHTLFGTTP; ITHTLFGTTPM; THTLFGTTPMQ; HTLFGTTPMQR; TLFGTTPMQRI; LFGTTPMQRIH; FGTTPMQRIHK; GTTPMQRIHKY; TTPMQRIHKYD; TPMQRIHKYDQ; PMQRIHKYDQS; MQRIHKYDQSF; QRIHKYDQSFN; RIHKYDQSFNL; IHKYDQSFNLT; HKYDQSFNLTR; KYDQSFNLTRE; YDQSFNLTREI; DQSFNLTREIL; QSFNLTREILA; SFNLTREILAS; FNLTREILASG; NLTREILASGI; LTREILASGIE; TREILASGIEL; REILASGIELN; EILASGIELNR; ILASGIELNRV; LASGIELNRVV; ASGIELNRVVN; SGIELNRVVNA; GIELNRVVNAW; IELNRVVNAWL; ELNRVVNAWLN; LNRVVNAWLNS; NRVVNAWLNSP; RVVNAWLNSPS; VVNAWLNSPSH; VNAWLNSPSHK; NAWLNSPSHKE; AWLNSPSHKEA; WLNSPSHKEAL; LNSPSHKEALI; NSPSHKEALIN; SPSHKEALINT; PSHKEALINTD; SHKEALINTDT; HKEALINTDTD; KEALINTDTDK; EALINTDTDKI; ALINTDTDKIG; LINTDTDKIGG; INTDTDKIGGY; NTDTDKIGGYR; TDTDKIGGYRL; DTDKIGGYRLK; TDKIGGYRLKT; DKIGGYRLKTT; KIGGYRLKTTD; IGGYRLKTTDN; GGYRLKTTDNI; GYRLKTTDNID; YRLKTTDNIDI; RLKTTDNIDIF; LKTTDNIDIFV; KTTDNIDIFVV; TTDNIDIFVVL; TDNIDIFVVLF; DNIDIFVVLFG; NIDIFVVLFGK; IDIFVVLFGKR; DIFVVLFGKRK; IFVVLFGKRKY; FVVLFGKRKYK; VVLFGKRKYKN;
Seq 32	SEQ ID NO 38920-39737/ 8 mers: MMQRISIL; MQRISILL; QRISILLM; RISILLML; ISILLMLL; SILLMLLA; ILLMLLAV; LLMLLAVF; LMLLAVFS; MLLAVFSC; LLAVFSCK; LAVFSCKQ; AVFSCKQF; VFSCKQFG; FSCKQFGD; SCKQFGDV; CKQFGDVK; KQFGDVKS; QFGDVKSL; FGDVKSLT; GDVKSLTE; DVKSLTEI; VKSLTEID; KSLTEIDS; SLTEIDSG; LTEIDSGN; TEIDSGNG; EIDSGNGI; IDSGNGIP; DSGNGIPL; SGNGIPLV; GNGIPLVV; NGIPLVVS; GIPLVVSD; IPLVVSDV; PLVVSDVV; LVVSDVVK; VVSDVVKD; VSDVVKDL; SDVVKDLI; DVVKDLIP; VVKDLIPK; VKDLIPKE; KDLIPKEI; DLIPKEIS; LIPKEISL; IPKEISLT; PKEISLTP; KEISLTPE; EISLTPEE; ISLTPEEA; SLTPEEAE; LTPEEAEK; TPEEAEKL; PEEAEKLE; EEAEKLES; EAEKLESL; AEKLESLK; EKLESLKV; KLESLKVF; LESLKVFL; ESLKVFLK; SLKVFLKD; LKVFLKDA; KVFLKDAM; VFLKDAMS; FLKDAMSV; LKDAMSVN; KDAMSVNG; DAMSVNGR; AMSVNGRE; MSVNGREE; SVNGREEA; VNGREEAL; NGREEALK; GREEALKA; REEALKAE; EEALKAEY; EALKAEYE; ALKAEYEK; LKAEYEKS; KAEYEKSY; AEYEKSYK; EYEKSYKE; YEKSYKEF; EKSYKEFF; KSYKEFFD; SYKEFFDW; YKEFFDWL; KEFFDWLS; EFFDWLSK; FFDWLSKD; FDWLSKDV; DWLSKDVN; WLSKDVNR; LSKDVNRQ; SKDVNRQK; KDVNRQKE; DVNRQKEF; VNRQKEFI; NRQKEFIS; RQKEFISS; QKEFISSF; KEFISSFD; EFISSFDN; FISSFDNI; ISSFDNIS; SSFDNISS; SFDNISSI; FDNISSIV; DNISSIVS; NISSIVSK; ISSIVSKA; SSIVSKAV; SIVSKAVD; IVSKAVDA; VSKAVDAS; SKAVDASK; KAVDASKK; AVDASKKR; VDASKKRR; DASKKRRP; ASKKRRPT; SKKRRPTE; KKRRPTEQ;

KRRPTEQQ; RRPTEQQS; RPTEQQSL; PTEQQSLG; TEQQSLGF; EQQSLGFK; QQSLGFKE; QSLGFKEY; SLGFKEYV; LGFKEYVC; GFKEYVCY; FKEYVCYK; KEYVCYKI; EYVCYKIK; YVCYKIKN; VCYKIKNS; CYKIKNSK; YKIKNSKG; KIKNSKGE; IKNSKGEA; KNSKGEAL; NSKGEALS; SKGEALSL; KGEALSLF; GEALSLFF; EALSLFFQ; ALSLFFQK; LSLFFQKV; SLFFQKVV; LFFQKVVD; FFQKVVDA; FQKVVDAF; QKVVDAFG; KVVDAFGA; VVDAFGAD; VDAFGADP; DAFGADPY; AFGADPYK; FGADPYKK; GADPYKKD; ADPYKKDN; DPYKKDND; PYKKDNDE; YKKDNDES; KKDNDESV; KDNDESVQ; DNDESVQK; NDESVQKP; DESVQKPV; ESVQKPVK; SVQKPVKC; VQKPVKCN; QKPVKCNE; KPVKCNEE; PVKCNEEI; VKCNEEIF; KCNEEIFK; CNEEIFKV; NEEIFKVI; EEIFKVIK; EIFKVIKK; IFKVIKKV; FKVIKKVL; KVIKKVLT; VIKKVLTE; IKKVLTES; KKVLTESE; KVLTESES; VLTESESN; LTESESNN; TESESNNE; ESESNNEL; SESNNELK; ESNNELKN; SNNELKNL; NNELKNLK; NELKNLKN; ELKNLKNY; LKNLKNYG; KNLKNYGN; NLKNYGNV;

9 mers:
MMQRISILL; MQRISILLM; QRISILLML; RISILLMLL; ISILLMLLA; SILLMLLAV; ILLMLLAVF; LLMLLAVFS; LMLLAVFSC; MLLAVFSCK; LLAVFSCKQ; LAVFSCKQF; AVFSCKQFG; VFSCKQFGD; FSCKQFGDV; SCKQFGDVK; CKQFGDVKS; KQFGDVKSL; QFGDVKSLT; FGDVKSLTE; GDVKSLTEI; DVKSLTEID; VKSLTEIDS; KSLTEIDSG; SLTEIDSGN; LTEIDSGNG; TEIDSGNGI; EIDSGNGIP; IDSGNGIPL; DSGNGIPLV; SGNGIPLVV; GNGIPLVVS; NGIPLVVSD; GIPLVVSDV; IPLVVSDVV; PLVVSDVVK; LVVSDVVKD; VVSDVVKDL; VSDVVKDLI; SDVVKDLIP; DVVKDLIPK; VVKDLIPKE; VKDLIPKEI; KDLIPKEIS; DLIPKEISL; LIPKEISLT; IPKEISLTP; PKEISLTPE; KEISLTPEE; EISLTPEEA; ISLTPEEAE; SLTPEEAEK; LTPEEAEKL; TPEEAEKLE; PEEAEKLES; EEAEKLESL; EAEKLESLK; AEKLESLKV; EKLESLKVF; KLESLKVFL; LESLKVFLK; ESLKVFLKD; SLKVFLKDA; LKVFLKDAM; KVFLKDAMS; VFLKDAMSV; FLKDAMSVN; LKDAMSVNG; KDAMSVNGR; DAMSVNGRE; AMSVNGREE; MSVNGREEA; SVNGREEAL; VNGREEALK; NGREEALKA; GREEALKAE; REEALKAEY; EEALKAEYE; EALKAEYEK; ALKAEYEKS; LKAEYEKSY; KAEYEKSYK; AEYEKSYKE; EYEKSYKEF; YEKSYKEFF; EKSYKEFFD; KSYKEFFDW; SYKEFFDWL; YKEFFDWLS; KEFFDWLSK; EFFDWLSKD; FFDWLSKDV; FDWLSKDVN; DWLSKDVNR; WLSKDVNRQ; LSKDVNRQK; SKDVNRQKE; KDVNRQKEF; DVNRQKEFI; VNRQKEFIS; NRQKEFISS; RQKEFISSF; QKEFISSFD; KEFISSFDN; EFISSFDNI; FISSFDNIS; ISSFDNISS; SSFDNISSI; SFDNISSIV; FDNISSIVS; DNISSIVSK; NISSIVSKA; ISSIVSKAV; SSIVSKAVD; SIVSKAVDA; IVSKAVDAS; VSKAVDASK; SKAVDASKK; KAVDASKKR; AVDASKKRR; VDASKKRRP; DASKKRRPT; ASKKRRPTE; SKKRRPTEQ; KKRRPTEQQ; KRRPTEQQS; RRPTEQQSL; RPTEQQSLG; PTEQQSLGF; TEQQSLGFK; EQQSLGFKE; QQSLGFKEY; QSLGFKEYV; SLGFKEYVC; LGFKEYVCY; GFKEYVCYK; FKEYVCYKI; KEYVCYKIK; EYVCYKIKN; YVCYKIKNS; VCYKIKNSK; CYKIKNSKG; YKIKNSKGE; KIKNSKGEA; IKNSKGEAL; KNSKGEALS; NSKGEALSL; SKGEALSLF; KGEALSLFF; GEALSLFFQ; EALSLFFQK; ALSLFFQKV; LSLFFQKVV; SLFFQKVVD; LFFQKVVDA; FFQKVVDAF; FQKVVDAFG; QKVVDAFGA; KVVDAFGAD; VVDAFGADP;

	VDAFGADPY; DAFGADPYK; AFGADPYKK; FGADPYKKD; GADPYKKDN; ADPYKKDND; DPYKKDNDE; PYKKDNDES; YKKDNDESV; KKDNDESVQ; KDNDESVQK; DNDESVQKP; NDESVQKPV; DESVQKPVK; ESVQKPVKC; SVQKPVKCN; VQKPVKCNE; QKPVKCNEE; KPVKCNEEI; PVKCNEEIF; VKCNEEIFK; KCNEEIFKV; CNEEIFKVI; NEEIFKVIK; EEIFKVIKK; EIFKVIKKV; IFKVIKKVL; FKVIKKVLT; KVIKKVLTE; VIKKVLTES; IKKVLTESE; KKVLTESES; KVLTESESN; VLTESESNN; LTESESNNE; TESESNNEL; ESESNNELK; SESNNELKN; ESNNELKNL; SNNELKNLK; NNELKNLKN; NELKNLKNY; ELKNLKNYG; LKNLKNYGN; KNLKNYGNV; 10 mers: MMQRISILLM; MQRISILLML; QRISILLMLL; RISILLMLLA; ISILLMLLAV; SILLMLLAVF; ILLMLLAVFS; LLMLLAVFSC; LMLLAVFSCK; MLLAVFSCKQ; LLAVFSCKQF; LAVFSCKQFG; AVFSCKQFGD; VFSCKQFGDV; FSCKQFGDVK; SCKQFGDVKS; CKQFGDVKSL; KQFGDVKSLT; QFGDVKSLTE; FGDVKSLTEI; GDVKSLTEID; DVKSLTEIDS; VKSLTEIDSG; KSLTEIDSGN; SLTEIDSGNG; LTEIDSGNGI; TEIDSGNGIP; EIDSGNGIPL; IDSGNGIPLV; DSGNGIPLVV; SGNGIPLVVS; GNGIPLVVSD; NGIPLVVSDV; GIPLVVSDVV; IPLVVSDVVK; PLVVSDVVKD; LVVSDVVKDL; VVSDVVKDLI; VSDVVKDLIP; SDVVKDLIPK; DVVKDLIPKE; VVKDLIPKEI; VKDLIPKEIS; KDLIPKEISL; DLIPKEISLT; LIPKEISLTP; IPKEISLTPE; PKEISLTPEE; KEISLTPEEA; EISLTPEEAE; ISLTPEEAEK; SLTPEEAEKL; LTPEEAEKLE; TPEEAEKLES; PEEAEKLESL; EEAEKLESLK; EAEKLESLKV; AEKLESLKVF; EKLESLKVFL; KLESLKVFLK; LESLKVFLKD; ESLKVFLKDA; SLKVFLKDAM; LKVFLKDAMS; KVFLKDAMSV; VFLKDAMSVN; FLKDAMSVNG; LKDAMSVNGR; KDAMSVNGRE; DAMSVNGREE; AMSVNGREEA; MSVNGREEAL; SVNGREEALK; VNGREEALKA; NGREEALKAE; GREEALKAEY; REEALKAEYE; EEALKAEYEK; EALKAEYEKS; ALKAEYEKSY; LKAEYEKSYK; KAEYEKSYKE; AEYEKSYKEF; EYEKSYKEFF; YEKSYKEFFD; EKSYKEFFDW; KSYKEFFDWL; SYKEFFDWLS; YKEFFDWLSK; KEFFDWLSKD; EFFDWLSKDV; FFDWLSKDVN; FDWLSKDVNR; DWLSKDVNRQ; WLSKDVNRQK; LSKDVNRQKE; SKDVNRQKEF; KDVNRQKEFI; DVNRQKEFIS; VNRQKEFISS; NRQKEFISSF; RQKEFISSFD; QKEFISSFDN; KEFISSFDNI; EFISSFDNIS; FISSFDNISS; ISSFDNISSI; SSFDNISSIV; SFDNISSIVS; FDNISSIVSK; DNISSIVSKA; NISSIVSKAV; ISSIVSKAVD; SSIVSKAVDA; SIVSKAVDAS; IVSKAVDASK; VSKAVDASKK; SKAVDASKKR; KAVDASKKRR; AVDASKKRRP; VDASKKRRPT; DASKKRRPTE; ASKKRRPTEQ; SKKRRPTEQQ; KKRRPTEQQS; KRRPTEQQSL; RRPTEQQSLG; RPTEQQSLGF; PTEQQSLGFK; TEQQSLGFKE; EQQSLGFKEY; QQSLGFKEYV; QSLGFKEYVC; SLGFKEYVCY; LGFKEYVCYK; GFKEYVCYKI; FKEYVCYKIK; KEYVCYKIKN; EYVCYKIKNS; YVCYKIKNSK; VCYKIKNSKG; CYKIKNSKGE; YKIKNSKGEA; KIKNSKGEAL; IKNSKGEALS; KNSKGEALSL; NSKGEALSLF; SKGEALSLFF; KGEALSLFFQ; GEALSLFFQK; EALSLFFQKV; ALSLFFQKVV; LSLFFQKVVD; SLFFQKVVDA; LFFQKVVDAF; FFQKVVDAFG; FQKVVDAFGA; QKVVDAFGAD; KVVDAFGADP; VVDAFGADPY;

VDAFGADPYK; DAFGADPYKK; AFGADPYKKD; FGADPYKKDN;
GADPYKKDND; ADPYKKDNDE; DPYKKDNDES; PYKKDNDESV;
YKKDNDESVQ; KKDNDESVQK; KDNDESVQKP; DNDESVQKPV;
NDESVQKPVK; DESVQKPVKC; ESVQKPVKCN; SVQKPVKCNE;
VQKPVKCNEE; QKPVKCNEEI; KPVKCNEEIF; PVKCNEEIFK;
VKCNEEIFKV; KCNEEIFKVI; CNEEIFKVIK; NEEIFKVIKK;
EEIFKVIKKV; EIFKVIKKVL; IFKVIKKVLT; FKVIKKVLTE;
KVIKKVLTES; VIKKVLTESE; IKKVLTESES; KKVLTESESN;
KVLTESESNN; VLTESESNNE; LTESESNNEL; TESESNNELK;
ESESNNELKN; SESNNELKNL; ESNNELKNLK; SNNELKNLKN;
NNELKNLKNY; NELKNLKNYG; ELKNLKNYGN; LKNLKNYGNV;

11 mers:
MMQRISILLML; MQRISILLMLL; QRISILLMLLA; RISILLMLLAV;
ISILLMLLAVF; SILLMLLAVFS; ILLMLLAVFSC; LLMLLAVFSCK;
LMLLAVFSCKQ; MLLAVFSCKQF; LLAVFSCKQFG; LAVFSCKQFGD;
AVFSCKQFGDV; VFSCKQFGDVK; FSCKQFGDVKS; SCKQFGDVKSL;
CKQFGDVKSLT; KQFGDVKSLTE; QFGDVKSLTEI; FGDVKSLTEID;
GDVKSLTEIDS; DVKSLTEIDSG; VKSLTEIDSGN; KSLTEIDSGNG;
SLTEIDSGNGI; LTEIDSGNGIP; TEIDSGNGIPL; EIDSGNGIPLV;
IDSGNGIPLVV; DSGNGIPLVVS; SGNGIPLVVSD; GNGIPLVVSDV;
NGIPLVVSDVV; GIPLVVSDVVK; IPLVVSDVVKD; PLVVSDVVKDL;
LVVSDVVKDLI; VVSDVVKDLIP; VSDVVKDLIPK; SDVVKDLIPKE;
DVVKDLIPKEI; VVKDLIPKEIS; VKDLIPKEISL; KDLIPKEISLT;
DLIPKEISLTP; LIPKEISLTPE; IPKEISLTPEE; PKEISLTPEEA;
KEISLTPEEAE; EISLTPEEAEK; ISLTPEEAEKL; SLTPEEAEKLE;
LTPEEAEKLES; TPEEAEKLESL; PEEAEKLESLK; EEAEKLESLKV;
EAEKLESLKVF; AEKLESLKVFL; EKLESLKVFLK; KLESLKVFLKD;
LESLKVFLKDA; ESLKVFLKDAM; SLKVFLKDAMS; LKVFLKDAMSV;
KVFLKDAMSVN; VFLKDAMSVNG; FLKDAMSVNGR; LKDAMSVNGRE;
KDAMSVNGREE; DAMSVNGREEA; AMSVNGREEAL; MSVNGREEALK;
SVNGREEALKA; VNGREEALKAE; NGREEALKAEY; GREEALKAEYE;
REEALKAEYEK; EEALKAEYEKS; EALKAEYEKSY; ALKAEYEKSYK;
LKAEYEKSYKE; KAEYEKSYKEF; AEYEKSYKEFF; EYEKSYKEFFD;
YEKSYKEFFDW; EKSYKEFFDWL; KSYKEFFDWLS; SYKEFFDWLSK;
YKEFFDWLSKD; KEFFDWLSKDV; EFFDWLSKDVN; FFDWLSKDVNR;
FDWLSKDVNRQ; DWLSKDVNRQK; WLSKDVNRQKE; LSKDVNRQKEF;
SKDVNRQKEFI; KDVNRQKEFIS; DVNRQKEFISS; VNRQKEFISSF;
NRQKEFISSFD; RQKEFISSFDN; QKEFISSFDNI; KEFISSFDNIS;
EFISSFDNISS; FISSFDNISSI; ISSFDNISSIV; SSFDNISSIVS;
SFDNISSIVSK; FDNISSIVSKA; DNISSIVSKAV; NISSIVSKAVD;
ISSIVSKAVDA; SSIVSKAVDAS; SIVSKAVDASK; IVSKAVDASKK;
VSKAVDASKKR; SKAVDASKKRR; KAVDASKKRRP; AVDASKKRRPT;
VDASKKRRPTE; DASKKRRPTEQ; ASKKRRPTEQQ; SKKRRPTEQQS;
KKRRPTEQQSL; KRRPTEQQSLG; RRPTEQQSLGF; RPTEQQSLGFK;
PTEQQSLGFKE; TEQQSLGFKEY; EQQSLGFKEYV; QQSLGFKEYVC;
QSLGFKEYVCY; SLGFKEYVCYK; LGFKEYVCYKI; GFKEYVCYKIK;
FKEYVCYKIKN; KEYVCYKIKNS; EYVCYKIKNSK; YVCYKIKNSKG;
VCYKIKNSKGE; CYKIKNSKGEA; YKIKNSKGEAL; KIKNSKGEALS;
IKNSKGEALSL; KNSKGEALSLF; NSKGEALSLFF; SKGEALSLFFQ;
KGEALSLFFQK; GEALSLFFQKV; EALSLFFQKVV; ALSLFFQKVVD;

	LSLFFQKVVDA; SLFFQKVVDAF; LFFQKVVDAFG; FFQKVVDAFGA; FQKVVDAFGAD; QKVVDAFGADP; KVVDAFGADPY; VVDAFGADPYK; VDAFGADPYKK; DAFGADPYKKD; AFGADPYKKDN; FGADPYKKDND; GADPYKKDNDE; ADPYKKDNDES; DPYKKDNDESV; PYKKDNDESVQ; YKKDNDESVQK; KKDNDESVQKP; KDNDESVQKPV; DNDESVQKPVK; NDESVQKPVKC; DESVQKPVKCN; ESVQKPVKCNE; SVQKPVKCNEE; VQKPVKCNEEI; QKPVKCNEEIF; KPVKCNEEIFK; PVKCNEEIFKV; VKCNEEIFKVI; KCNEEIFKVIK; CNEEIFKVIKK; NEEIFKVIKKV; EEIFKVIKKVL; EIFKVIKKVLT; IFKVIKKVLTE; FKVIKKVLTES; KVIKKVLTESE; VIKKVLTESES; IKKVLTESESN; KKVLTESESNN; KVLTESESNNE; VLTESESNNEL; LTESESNNELK; TESESNNELKN; ESESNNELKNL; SESNNELKNLK; ESNNELKNLKN; SNNELKNLKNY; NNELKNLKNYG; NELKNLKNYGN; ELKNLKNYGNV;
Seq 33	SEQ ID NO 39738-40661/ 8 mers: MKRISILS; KRISILSI; RISILSIL; ISILSILL; SILSILLL; ILSILLLL; LSILLLLL; SILLLLLL; ILLLLLLF; LLLLLLFS; LLLLLFSC; LLLLFSCK; LLLFSCKQ; LLFSCKQY; LFSCKQYG; FSCKQYGD; SCKQYGDV; CKQYGDVK; KQYGDVKS; QYGDVKSL; YGDVKSLT; GDVKSLTE; DVKSLTEV; VKSLTEVA; KSLTEVAT; SLTEVATD; LTEVATDL; TEVATDLE; EVATDLED; VATDLEDD; ATDLEDDN; TDLEDDNS; DLEDDNSF; LEDDNSFA; EDDNSFAS; DDNSFASG; DNSFASGS; NSFASGSV; SFASGSVE; FASGSVES; ASGSVESK; SGSVESKD; GSVESKDQ; SVESKDQI; VESKDQII; ESKDQIIE; SKDQIIEK; KDQIIEKG; DQIIEKGP; QIIEKGPV; IIEKGPVL; IEKGPVLT; EKGPVLTS; KGPVLTSE; GPVLTSEE; PVLTSEEF; VLTSEEFE; LTSEEFER; TSEEFERL; SEEFERLE; EEFERLEA; EFERLEAL; FERLEALK; ERLEALKT; RLEALKTF; LEALKTFL; EALKTFLK; ALKTFLKD; LKTFLKDA; KTFLKDAM; TFLKDAMG; FLKDAMGV; LKDAMGVN; KDAMGVNG; DAMGVNGR; AMGVNGRE; MGVNGREG; GVNGREGD; VNGREGDT; NGREGDTK; GREGDTKA; REGDTKAE; EGDTKAEY; GDTKAEYE; DTKAEYEK; TKAEYEKS; KAEYEKSY; AEYEKSYK; EYEKSYKE; YEKSYKEF; EKSYKEFF; KSYKEFFD; SYKEFFDW; YKEFFDWL; KEFFDWLS; EFFDWLSK; FFDWLSKD; FDWLSKDV; DWLSKDVN; WLSKDVNR; LSKDVNRQ; SKDVNRQK; KDVNRQKE; DVNRQKEF; VNRQKEFV; NRQKEFVS; RQKEFVSF; QKEFVSFF; KEFVSFFN; EFVSFFNN; FVSFFNNI; VSFFNNIC; SFFNNICG; FFNNICGI; FNNICGII; NNICGIIT; NICGIITK; ICGIITKA; CGIITKAV; GIITKAVD; IITKAVDA; ITKAVDAS; TKAVDASK; KAVDASKK; AVDASKKR; VDASKKRY; DASKKRYN; ASKKRYNS; SKKRYNSN; KKRYNSNP; KRYNSNPK; RYNSNPKS; YNSNPKSL; NSNPKSLG; SNPKSLGF; NPKSLGFN; PKSLGFNE; KSLGFNEY; SLGFNEYV; LGFNEYVC; GFNEYVCY; FNEYVCYD; NEYVCYDI; EYVCYDIK; YVCYDIKT; VCYDIKTR; CYDIKTRT; YDIKTRTG; DIKTRTGD; IKTRTGDD; KTRTGDDL; TRTGDDLS; RTGDDLSL; TGDDLSLF; GDDLSLFF; DDLSLFFQ; DLSLFFQK; LSLFFQKV; SLFFQKVA; LFFQKVAD; FFQKVADA; FQKVADAF; QKVADAFG; KVADAFGT; VADAFGTQ; ADAFGTQE; DAFGTQEY; AFGTQEYK; FGTQEYKN; GTQEYKNK; TQEYKNKD; QEYKNKDE; EYKNKDED; YKNKDEDD; KNKDEDDE;

	NKDEDDEN; KDEDDENN; DEDDENNQ; EDDENNQK; DDENNQKP; DENNQKPE; ENNQKPEK; NNQKPEKC; NQKPEKCN; QKPEKCNE; KPEKCNEE; PEKCNEEI; EKCNEEIF; KCNEEIFK; CNEEIFKV; NEEIFKVI; EEIFKVIK; EIFKVIKR; IFKVIKRV; FKVIKRVF; KVIKRVFT; VIKRVFTE; IKRVFTES; KRVFTESE; RVFTESEN; VFTESENN; FTESENNN; TESENNNE; ESENNNEL; SENNNELA; ENNNELAN; NNNELANL; NNELANLK; NELANLKN; ELANLKNL; LANLKNLN; ANLKNLNS; NLKNLNSY; LKNLNSYN; KNLNSYNL; NLNSYNLN; LNSYNLNS; NSYNLNSN; SYNLNSNN; YNLNSNNK; 9 mers: MKRISILSI; KRISILSIL; RISILSILL; ISILSILLL; SILSILLLL; ILSILLLLL; LSILLLLLL; SILLLLLLF; ILLLLLLFS; LLLLLLFSC; LLLLLFSCK; LLLLFSCKQ; LLLFSCKQY; LLFSCKQYG; LFSCKQYGD; FSCKQYGDV; SCKQYGDVK; CKQYGDVKS; KQYGDVKSL; QYGDVKSLT; YGDVKSLTE; GDVKSLTEV; DVKSLTEVA; VKSLTEVAT; KSLTEVATD; SLTEVATDL; LTEVATDLE; TEVATDLED; EVATDLEDD; VATDLEDDN; ATDLEDDNS; TDLEDDNSF; DLEDDNSFA; LEDDNSFAS; EDDNSFASG; DDNSFASGS; DNSFASGSV; NSFASGSVE; SFASGSVES; FASGSVESK; ASGSVESKD; SGSVESKDQ; GSVESKDQI; SVESKDQII; VESKDQIIE; ESKDQIIEK; SKDQIIEKG; KDQIIEKGP; DQIIEKGPV; QIIEKGPVL; IIEKGPVLT; IEKGPVLTS; EKGPVLTSE; KGPVLTSEE; GPVLTSEEF; PVLTSEEFE; VLTSEEFER; LTSEEFERL; TSEEFERLE; SEEFERLEA; EEFERLEAL; EFERLEALK; FERLEALKT; ERLEALKTF; RLEALKTFL; LEALKTFLK; EALKTFLKD; ALKTFLKDA; LKTFLKDAM; KTFLKDAMG; TFLKDAMGV; FLKDAMGVN; LKDAMGVNG; KDAMGVNGR; DAMGVNGRE; AMGVNGREG; MGVNGREGD; GVNGREGDT; VNGREGDTK; NGREGDTKA; GREGDTKAE; REGDTKAEY; EGDTKAEYE; GDTKAEYEK; DTKAEYEKS; TKAEYEKSY; KAEYEKSYK; AEYEKSYKE; EYEKSYKEF; YEKSYKEFF; EKSYKEFFD; KSYKEFFDW; SYKEFFDWL; YKEFFDWLS; KEFFDWLSK; EFFDWLSKD; FFDWLSKDV; FDWLSKDVN; DWLSKDVNR; WLSKDVNRQ; LSKDVNRQK; SKDVNRQKE; KDVNRQKEF; DVNRQKEFV; VNRQKEFVS; NRQKEFVSF; RQKEFVSFF; QKEFVSFFN; KEFVSFFNN; EFVSFFNNI; FVSFFNNIC; VSFFNNICG; SFFNNICGI; FFNNICGII; FNNICGIIT; NNICGIITK; NICGIITKA; ICGIITKAV; CGIITKAVD; GIITKAVDA; IITKAVDAS; ITKAVDASK; TKAVDASKK; KAVDASKKR; AVDASKKRY; VDASKKRYN; DASKKRYNS; ASKKRYNSN; SKKRYNSNP; KKRYNSNPK; KRYNSNPKS; RYNSNPKSL; YNSNPKSLG; NSNPKSLGF; SNPKSLGFN; NPKSLGFNE; PKSLGFNEY; KSLGFNEYV; SLGFNEYVC; LGFNEYVCY; GFNEYVCYD; FNEYVCYDI; NEYVCYDIK; EYVCYDIKT; YVCYDIKTR; VCYDIKTRT; CYDIKTRTG; YDIKTRTGD; DIKTRTGDD; IKTRTGDDL; KTRTGDDLS; TRTGDDLSL; RTGDDLSLF; TGDDLSLFF; GDDLSLFFQ; DDLSLFFQK; DLSLFFQKV; LSLFFQKVA; SLFFQKVAD; LFFQKVADA; FFQKVADAF; FQKVADAFG; QKVADAFGT; KVADAFGTQ; VADAFGTQE; ADAFGTQEY; DAFGTQEYK; AFGTQEYKN; FGTQEYKNK; GTQEYKNKD; TQEYKNKDE; QEYKNKDED; EYKNKDEDD; YKNKDEDDE; KNKDEDDEN; NKDEDDENN; KDEDDENNQ; DEDDENNQK; EDDENNQKP; DDENNQKPE; DENNQKPEK; ENNQKPEKC; NNQKPEKCN; NQKPEKCNE; QKPEKCNEE; KPEKCNEEI; PEKCNEEIF; EKCNEEIFK; KCNEEIFKV; CNEEIFKVI; NEEIFKVIK; EEIFKVIKR; EIFKVIKRV; IFKVIKRVF; FKVIKRVFT; KVIKRVFTE; VIKRVFTES; IKRVFTESE; KRVFTESEN; RVFTESENN;

	VFTESENNN; FTESENNNE; TESENNNEL; ESENNNELA; SENNNELAN; ENNNELANL; NNNELANLK; NNELANLKN; NELANLKNL; ELANLKNLN; LANLKNLNS; ANLKNLNSY; NLKNLNSYN; LKNLNSYNL; KNLNSYNLN; NLNSYNLNS; LNSYNLNSN; NSYNLNSNN; SYNLNSNNK; 10 mers: MKRISILSIL; KRISILSILL; RISILSILLL; ISILSILLLL; SILSILLLLL; ILSILLLLLL; LSILLLLLLF; SILLLLLLFS; ILLLLLLFSC; LLLLLLFSCK; LLLLLFSCKQ; LLLLFSCKQY; LLLFSCKQYG; LLFSCKQYGD; LFSCKQYGDV; FSCKQYGDVK; SCKQYGDVKS; CKQYGDVKSL; KQYGDVKSLT; QYGDVKSLTE; YGDVKSLTEV; GDVKSLTEVA; DVKSLTEVAT; VKSLTEVATD; KSLTEVATDL; SLTEVATDLE; LTEVATDLED; TEVATDLEDD; EVATDLEDDN; VATDLEDDNS; ATDLEDDNSF; TDLEDDNSFA; DLEDDNSFAS; LEDDNSFASG; EDDNSFASGS; DDNSFASGSV; DNSFASGSVE; NSFASGSVES; SFASGSVESK; FASGSVESKD; ASGSVESKDQ; SGSVESKDQI; GSVESKDQII; SVESKDQIIE; VESKDQIIEK; ESKDQIIEKG; SKDQIIEKGP; KDQIIEKGPV; DQIIEKGPVL; QIIEKGPVLT; IIEKGPVLTS; IEKGPVLTSE; EKGPVLTSEE; KGPVLTSEEF; GPVLTSEEFE; PVLTSEEFER; VLTSEEFERL; LTSEEFERLE; TSEEFERLEA; SEEFERLEAL; EEFERLEALK; EFERLEALKT; FERLEALKTF; ERLEALKTFL; RLEALKTFLK; LEALKTFLKD; EALKTFLKDA; ALKTFLKDAM; LKTFLKDAMG; KTFLKDAMGV; TFLKDAMGVN; FLKDAMGVNG; LKDAMGVNGR; KDAMGVNGRE; DAMGVNGREG; AMGVNGREGD; MGVNGREGDT; GVNGREGDTK; VNGREGDTKA; NGREGDTKAE; GREGDTKAEY; REGDTKAEYE; EGDTKAEYEK; GDTKAEYEKS; DTKAEYEKSY; TKAEYEKSYK; KAEYEKSYKE; AEYEKSYKEF; EYEKSYKEFF; YEKSYKEFFD; EKSYKEFFDW; KSYKEFFDWL; SYKEFFDWLS; YKEFFDWLSK; KEFFDWLSKD; EFFDWLSKDV; FFDWLSKDVN; FDWLSKDVNR; DWLSKDVNRQ; WLSKDVNRQK; LSKDVNRQKE; SKDVNRQKEF; KDVNRQKEFV; DVNRQKEFVS; VNRQKEFVSF; NRQKEFVSFF; RQKEFVSFFN; QKEFVSFFNN; KEFVSFFNNI; EFVSFFNNIC; FVSFFNNICG; VSFFNNICGI; SFFNNICGII; FFNNICGIIT; FNNICGIITK; NNICGIITKA; NICGIITKAV; ICGIITKAVD; CGIITKAVDA; GIITKAVDAS; IITKAVDASK; ITKAVDASKK; TKAVDASKKR; KAVDASKKRY; AVDASKKRYN; VDASKKRYNS; DASKKRYNSN; ASKKRYNSNP; SKKRYNSNPK; KKRYNSNPKS; KRYNSNPKSL; RYNSNPKSLG; YNSNPKSLGF; NSNPKSLGFN; SNPKSLGFNE; NPKSLGFNEY; PKSLGFNEYV; KSLGFNEYVC; SLGFNEYVCY; LGFNEYVCYD; GFNEYVCYDI; FNEYVCYDIK; NEYVCYDIKT; EYVCYDIKTR; YVCYDIKTRT; VCYDIKTRTG; CYDIKTRTGD; YDIKTRTGDD; DIKTRTGDDL; IKTRTGDDLS; KTRTGDDLSL; TRTGDDLSLF; RTGDDLSLFF; TGDDLSLFFQ; GDDLSLFFQK; DDLSLFFQKV; DLSLFFQKVA; LSLFFQKVAD; SLFFQKVADA; LFFQKVADAF; FFQKVADAFG; FQKVADAFGT; QKVADAFGTQ; KVADAFGTQE; VADAFGTQEY; ADAFGTQEYK; DAFGTQEYKN; AFGTQEYKNK; FGTQEYKNKD; GTQEYKNKDE; TQEYKNKDED; QEYKNKDEDD; EYKNKDEDDE; YKNKDEDDEN; KNKDEDDENN; NKDEDDENNQ; KDEDDENNQK; DEDDENNQKP; EDDENNQKPE; DDENNQKPEK;

DENNQKPEKC; ENNQKPEKCN; NNQKPEKCNE; NQKPEKCNEE;
QKPEKCNEEI; KPEKCNEEIF; PEKCNEEIFK; EKCNEEIFKV;
KCNEEIFKVI; CNEEIFKVIK; NEEIFKVIKR; EEIFKVIKRV;
EIFKVIKRVF; IFKVIKRVFT; FKVIKRVFTE; KVIKRVFTES;
VIKRVFTESE; IKRVFTESEN; KRVFTESENN; RVFTESENNN;
VFTESENNNE; FTESENNNEL; TESENNNELA; ESENNNELAN;
SENNNELANL; ENNNELANLK; NNNELANLKN; NNELANLKNL;
NELANLKNLN; ELANLKNLNS; LANLKNLNSY; ANLKNLNSYN;
NLKNLNSYNL; LKNLNSYNLN; KNLNSYNLNS; NLNSYNLNSN;
LNSYNLNSNN; NSYNLNSNNK;

11 mers:
MKRISILSILL; KRISILSILLL; RISILSILLLL; ISILSILLLLL;
SILSILLLLLL; ILSILLLLLLF; LSILLLLLLFS; SILLLLLLFSC;
ILLLLLLFSCK; LLLLLLFSCKQ; LLLLLFSCKQY; LLLLFSCKQYG;
LLLFSCKQYGD; LLFSCKQYGDV; LFSCKQYGDVK; FSCKQYGDVKS;
SCKQYGDVKSL; CKQYGDVKSLT; KQYGDVKSLTE; QYGDVKSLTEV;
YGDVKSLTEVA; GDVKSLTEVAT; DVKSLTEVATD; VKSLTEVATDL;
KSLTEVATDLE; SLTEVATDLED; LTEVATDLEDD; TEVATDLEDDN;
EVATDLEDDNS; VATDLEDDNSF; ATDLEDDNSFA; TDLEDDNSFAS;
DLEDDNSFASG; LEDDNSFASGS; EDDNSFASGSV; DDNSFASGSVE;
DNSFASGSVES; NSFASGSVESK; SFASGSVESKD; FASGSVESKDQ;
ASGSVESKDQI; SGSVESKDQII; GSVESKDQIIE; SVESKDQIIEK;
VESKDQIIEKG; ESKDQIIEKGP; SKDQIIEKGPV; KDQIIEKGPVL;
DQIIEKGPVLT; QIIEKGPVLTS; IIEKGPVLTSE; IEKGPVLTSEE;
EKGPVLTSEEF; KGPVLTSEEFE; GPVLTSEEFER; PVLTSEEFERL;
VLTSEEFERLE; LTSEEFERLEA; TSEEFERLEAL; SEEFERLEALK;
EEFERLEALKT; EFERLEALKTF; FERLEALKTFL; ERLEALKTFLK;
RLEALKTFLKD; LEALKTFLKDA; EALKTFLKDAM; ALKTFLKDAMG;
LKTFLKDAMGV; KTFLKDAMGVN; TFLKDAMGVNG; FLKDAMGVNGR;
LKDAMGVNGRE; KDAMGVNGREG; DAMGVNGREGD; AMGVNGREGDT;
MGVNGREGDTK; GVNGREGDTKA; VNGREGDTKAE; NGREGDTKAEY;
GREGDTKAEYE; REGDTKAEYEK; EGDTKAEYEKS; GDTKAEYEKSY;
DTKAEYEKSYK; TKAEYEKSYKE; KAEYEKSYKEF; AEYEKSYKEFF;
EYEKSYKEFFD; YEKSYKEFFDW; EKSYKEFFDWL; KSYKEFFDWLS;
SYKEFFDWLSK; YKEFFDWLSKD; KEFFDWLSKDV; EFFDWLSKDVN;
FFDWLSKDVNR; FDWLSKDVNRQ; DWLSKDVNRQK; WLSKDVNRQKE;
LSKDVNRQKEF; SKDVNRQKEFV; KDVNRQKEFVS; DVNRQKEFVSF;
VNRQKEFVSFF; NRQKEFVSFFN; RQKEFVSFFNN; QKEFVSFFNNI;
KEFVSFFNNIC; EFVSFFNNICG; FVSFFNNICGI; VSFFNNICGII;
SFFNNICGIIT; FFNNICGIITK; FNNICGIITKA; NNICGIITKAV;
NICGIITKAVD; ICGIITKAVDA; CGIITKAVDAS; GIITKAVDASK;
IITKAVDASKK; ITKAVDASKKR; TKAVDASKKRY; KAVDASKKRYN;
AVDASKKRYNS; VDASKKRYNSN; DASKKRYNSNP; ASKKRYNSNPK;
SKKRYNSNPKS; KKRYNSNPKSL; KRYNSNPKSLG; RYNSNPKSLGF;
YNSNPKSLGFN; NSNPKSLGFNE; SNPKSLGFNEY; NPKSLGFNEYV;
PKSLGFNEYVC; KSLGFNEYVCY; SLGFNEYVCYD; LGFNEYVCYDI;
GFNEYVCYDIK; FNEYVCYDIKT; NEYVCYDIKTR; EYVCYDIKTRT;
YVCYDIKTRTG; VCYDIKTRTGD; CYDIKTRTGDD; YDIKTRTGDDL;
DIKTRTGDDLS; IKTRTGDDLSL; KTRTGDDLSLF; TRTGDDLSLFF;
RTGDDLSLFFQ; TGDDLSLFFQK; GDDLSLFFQKV; DDLSLFFQKVA;

	DLSLFFQKVAD; LSLFFQKVADA; SLFFQKVADAF; LFFQKVADAFG; FFQKVADAFGT; FQKVADAFGTQ; QKVADAFGTQE; KVADAFGTQEY; VADAFGTQEYK; ADAFGTQEYKN; DAFGTQEYKNK; AFGTQEYKNKD; FGTQEYKNKDE; GTQEYKNKDED; TQEYKNKDEDD; QEYKNKDEDDE; EYKNKDEDDEN; YKNKDEDDENN; KNKDEDDENNQ; NKDEDDENNQK; KDEDDENNQKP; DEDDENNQKPE; EDDENNQKPEK; DDENNQKPEKC; DENNQKPEKCN; ENNQKPEKCNE; NNQKPEKCNEE; NQKPEKCNEEI; QKPEKCNEEIF; KPEKCNEEIFK; PEKCNEEIFKV; EKCNEEIFKVI; KCNEEIFKVIK; CNEEIFKVIKR; NEEIFKVIKRV; EEIFKVIKRVF; EIFKVIKRVFT; IFKVIKRVFTE; FKVIKRVFTES; KVIKRVFTESE; VIKRVFTESEN; IKRVFTESENN; KRVFTESENNN; RVFTESENNNE; VFTESENNNEL; FTESENNNELA; TESENNNELAN; ESENNNELANL; SENNNELANLK; ENNNELANLKN; NNNELANLKNL; NNELANLKNLN; NELANLKNLNS; ELANLKNLNSY; LANLKNLNSYN; ANLKNLNSYNL; NLKNLNSYNLN; LKNLNSYNLNS; KNLNSYNLNSN; NLNSYNLNSNN; LNSYNLNSNNK;
Seq 34	SEQ ID NO 40612-42220/ 8 mers: MKIKPLIQ; KIKPLIQL; IKPLIQLK; KPLIQLKL; PLIQLKLL; LIQLKLLG; IQLKLLGL; QLKLLGLF; LKLLGLFL; KLLGLFLF; LLGLFLFS; LGLFLFSC; GLFLFSCT; LFLFSCTI; FLFSCTID; LFSCTIDA; FSCTIDAN; SCTIDANL; CTIDANLN; TIDANLNE; IDANLNED; DANLNEDY; ANLNEDYK; NLNEDYKN; LNEDYKNK; NEDYKNKV; EDYKNKVK; DYKNKVKG; YKNKVKGI; KNKVKGIL; NKVKGILN; KVKGILNK; VKGILNKA; KGILNKAA; GILNKAAD; ILNKAADD; LNKAADDQ; NKAADDQE; KAADDQET; AADDQETT; ADDQETTS; DDQETTSA; DQETTSAD; QETTSADT; ETTSADTN; TTSADTNS; TSADTNSN; SADTNSNA; ADTNSNAA; DTNSNAAK; TNSNAAKN; NSNAAKNI; SNAAKNIP; NAAKNIPI; AAKNIPIA; AKNIPIAD; KNIPIADN; NIPIADND; IPIADNDK; PIADNDKV; IADNDKVA; ADNDKVAA; DNDKVAAE; NDKVAAEL; DKVAAELK; KVAAELKK; VAAELKKQ; AAELKKQS; AELKKQSQ; ELKKQSQA; LKKQSQAA; KKQSQAAK; KQSQAAKT; QSQAAKTV; SQAAKTVA; QAAKTVAA; AAKTVAAA; AKTVAAAP; KTVAAAPN; TVAAAPNK; VAAAPNKG; AAAPNKGS; AAPNKGSQ; APNKGSQN; PNKGSQNQ; NKGSQNQP; KGSQNQPQ; GSQNQPQT; SQNQPQTT; QNQPQTTP; NQPQTTPN; QPQTTPNK; PQTTPNKG; QTTPNKGS; TTPNKGSQ; TPNKGSQN; PNKGSQNQ; NKGSQNQQ; KGSQNQQA; GSQNQQAA; SQNQQAAP; QNQQAAPS; NQQAAPSP; QQAAPSPQ; QAAPSPQL; AAPSPQLQ; APSPQLQS; PSPQLQSL; SPQLQSLS; PQLQSLSF; QLQSLSFS; LQSLSFSA; QSLSFSAD; SLSFSADL; LSFSADLS; SFSADLSN; FSADLSNL; SADLSNLP; ADLSNLPK; DLSNLPKT; LSNLPKTT; SNLPKTTA; NLPKTTAA; LPKTTAAR; PKTTAARA; KTTAARAA; TTAARAAS; TAARAASL; AARAASLT; ARAASLTK; RAASLTKQ; AASLTKQR; ASLTKQRI; SLTKQRIP; LTKQRIPI; TKQRIPIQ; KQRIPIQA; QRIPIQAV; RIPIQAVT; IPIQAVTT; PIQAVTTV; IQAVTTVP; QAVTTVPG; AVTTVPGN; VTTVPGNT; TTVPGNTR; TVPGNTRT; VPGNTRTF; PGNTRTFN; GNTRTFNS; NTRTFNSR; TRTFNSRN; RTFNSRNS; TFNSRNSG; FNSRNSGL; NSRNSGLP; SRNSGLPT; RNSGLPTF; NSGLPTFA; SGLPTFAL;

	GLPTFALN; LPTFALNY; PTFALNYS; TFALNYSF; FALNYSFS; ALNYSFSQ; LNYSFSQP; NYSFSQPT; YSFSQPTR; SFSQPTRQ; FSQPTRQQ; SQPTRQQT; QPTRQQTN; PTRQQTNS; TRQQTNSS; RQQTNSSS; QQTNSSSA; QTNSSSAV; TNSSSAVQ; NSSSAVQT; SSSAVQTT; SSAVQTTT; SAVQTTTS; AVQTTTSS; VQTTTSSG; QTTTSSGS; TTTSSGSK; TTSSGSKL; TSSGSKLQ; SSGSKLQT; SGSKLQTL; GSKLQTLK; SKLQTLKN; KLQTLKNE; LQTLKNEL; QTLKNELI; TLKNELIR; LKNELIRA; KNELIRAI; NELIRAIS; ELIRAISE; LIRAISEE; IRAISEEK; RAISEEKN; AISEEKNK; ISEEKNKT; SEEKNKTQ; EEKNKTQN; EKNKTQNN; KNKTQNNF; NKTQNNFG; KTQNNFGF; TQNNFGFR; QNNFGFRE; NNFGFRET; NFGFRETY; FGFRETYD; GFRETYDQ; FRETYDQF; RETYDQFK; ETYDQFKM; TYDQFKMK; YDQFKMKD; DQFKMKDS; QFKMKDSA; FKMKDSAF; KMKDSAFE; MKDSAFEL; KDSAFELL; DSAFELLD; SAFELLDV; AFELLDVI; FELLDVIS; ELLDVISS; LLDVISSA; LDVISSAK; DVISSAKV; VISSAKVY; ISSAKVYD; SSAKVYDR; SAKVYDRS; AKVYDRSY; KVYDRSYA; VYDRSYAP; YDRSYAPQ; DRSYAPQL; RSYAPQLN; SYAPQLNS; YAPQLNSN; APQLNSNT; PQLNSNTP; QLNSNTPE; LNSNTPEA; NSNTPEAE; SNTPEAEN; NTPEAENE; TPEAENER; PEAENERN; EAENERNK; AENERNKF; ENERNKFY; NERNKFYA; ERNKFYAL; RNKFYALM; NKFYALMD; KFYALMDF; FYALMDFD; YALMDFDQ; ALMDFDQY; LMDFDQYK; MDFDQYKI; DFDQYKIE; FDQYKIEQ; DQYKIEQF; QYKIEQFG; YKIEQFGS; KIEQFGSI; IEQFGSIM; EQFGSIME; QFGSIMEA; FGSIMEAL; GSIMEALY; SIMEALYN; IMEALYNE; MEALYNEN; EALYNENQ; ALYNENQN; LYNENQNH; YNENQNHS; NENQNHSL; ENQNHSLI; NQNHSLIR; QNHSLIRE; NHSLIREL; HSLIRELM; SLIRELMI; LIRELMIS; IRELMISG; RELMISGL; ELMISGLG; LMISGLGT; MISGLGTQ; ISGLGTQI; SGLGTQIS; GLGTQISF; LGTQISFE; GTQISFEL; TQISFELA; QISFELAL; ISFELALE; SFELALEE; FELALEEI; ELALEEIN; LALEEINK; ALEEINKK; LEEINKKI; EEINKKIE; EINKKIEI; INKKIEIF; NKKIEIFN; KKIEIFNQ; KIEIFNQD; IEIFNQDY; EIFNQDYL; IFNQDYLN; FNQDYLNA; NQDYLNAK; QDYLNAKI; DYLNAKIN; YLNAKINS; LNAKINSF; NAKINSFD; AKINSFDF; KINSFDFT; INSFDFTM; NSFDFTMK; SFDFTMKL; FDFTMKLK; DFTMKLKE; FTMKLKEL; TMKLKELK; MKLKELKS; KLKELKSK; LKELKSKL; KELKSKLN; ELKSKLNQ; LKSKLNQI; KSKLNQIL; SKLNQILD; KLNQILDK; LNQILDKR; NQILDKRK; QILDKRKE; ILDKRKEW; LDKRKEWS; DKRKEWSR; KRKEWSRQ; RKEWSRQA; KEWSRQAD; EWSRQADG; WSRQADGL; SRQADGLI; RQADGLIA; QADGLIAN; ADGLIANA; DGLIANAS; GLIANASS; LIANASSN; IANASSNS; ANASSNSS; NASSNSSL; ASSNSSLS; SSNSSLSD; SNSSLSDS; NSSLSDSK; SSLSDSKS; SLSDSKSL; LSDSKSLA; SDSKSLAE; DSKSLAEY; SKSLAEYI; KSLAEYIK; SLAEYIKK; LAEYIKKR; AEYIKKRY; EYIKKRYL; YIKKRYLD; IKKRYLDN; KKRYLDNM; KRYLDNMQ; RYLDNMQN; YLDNMQNA; LDNMQNAR; DNMQNARQ; NMQNARQS; MQNARQSV; QNARQSVL; NARQSVLE; ARQSVLEA; RQSVLEAY; QSVLEAYI; SVLEAYIS; VLEAYISI; LEAYISIM; 9 mers:

	MKIKPLIQL; KIKPLIQLK; IKPLIQLKL; KPLIQLKLL; PLIQLKLLG; LIQLKLLGL; IQLKLLGLF; QLKLLGLFL; LKLLGLFLF; KLLGLFLFS; LLGLFLFSC; LGLFLFSCT; GLFLFSCTI; LFLFSCTID; FLFSCTIDA; LFSCTIDAN; FSCTIDANL; SCTIDANLN; CTIDANLNE; TIDANLNED; IDANLNEDY; DANLNEDYK; ANLNEDYKN; NLNEDYKNK; LNEDYKNKV; NEDYKNKVK; EDYKNKVKG; DYKNKVKGI; YKNKVKGIL; KNKVKGILN; NKVKGILNK; KVKGILNKA; VKGILNKAA; KGILNKAAD; GILNKAADD; ILNKAADDQ; LNKAADDQE; NKAADDQET; KAADDQETT; AADDQETTS; ADDQETTSA; DDQETTSAD; DQETTSADT; QETTSADTN; ETTSADTNS; TTSADTNSN; TSADTNSNA; SADTNSNAA; ADTNSNAAK; DTNSNAAKN; TNSNAAKNI; NSNAAKNIP; SNAAKNIPI; NAAKNIPIA; AAKNIPIAD; AKNIPIADN; KNIPIADND; NIPIADNDK; IPIADNDKV; PIADNDKVA; IADNDKVAA; ADNDKVAAE; DNDKVAAEL; NDKVAAELK; DKVAAELKK; KVAAELKKQ; VAAELKKQS; AAELKKQSQ; AELKKQSQA; ELKKQSQAA; LKKQSQAAK; KKQSQAAKT; KQSQAAKTV; QSQAAKTVA; SQAAKTVAA; QAAKTVAAA; AAKTVAAAP; AKTVAAAPN; KTVAAAPNK; TVAAAPNKG; VAAAPNKGS; AAAPNKGSQ; AAPNKGSQN; APNKGSQNQ; PNKGSQNQP; NKGSQNQPQ; KGSQNQPQT; GSQNQPQTT; SQNQPQTTP; QNQPQTTPN; NQPQTTPNK; QPQTTPNKG; PQTTPNKGS; QTTPNKGSQ; TTPNKGSQN; TPNKGSQNQ; PNKGSQNQQ; NKGSQNQQA; KGSQNQQAA; GSQNQQAAP; SQNQQAAPS; QNQQAAPSP; NQQAAPSPQ; QQAAPSPQL; QAAPSPQLQ; AAPSPQLQS; APSPQLQSL; PSPQLQSLS; SPQLQSLSF; PQLQSLSFS; QLQSLSFSA; LQSLSFSAD; QSLSFSADL; SLSFSADLS; LSFSADLSN; SFSADLSNL; FSADLSNLP; SADLSNLPK; ADLSNLPKT; DLSNLPKTT; LSNLPKTTA; SNLPKTTAA; NLPKTTAAR; LPKTTAARA; PKTTAARAA; KTTAARAAS; TTAARAASL; TAARAASLT; AARAASLTK; ARAASLTKQ; RAASLTKQR; AASLTKQRI; ASLTKQRIP; SLTKQRIPI; LTKQRIPIQ; TKQRIPIQA; KQRIPIQAV; QRIPIQAVT; RIPIQAVTT; IPIQAVTTV; PIQAVTTVP; IQAVTTVPG; QAVTTVPGN; AVTTVPGNT; VTTVPGNTR; TTVPGNTRT; TVPGNTRTF; VPGNTRTFN; PGNTRTFNS; GNTRTFNSR; NTRTFNSRN; TRTFNSRNS; RTFNSRNSG; TFNSRNSGL; FNSRNSGLP; NSRNSGLPT; SRNSGLPTF; RNSGLPTFA; NSGLPTFAL; SGLPTFALN; GLPTFALNY; LPTFALNYS; PTFALNYSF; TFALNYSFS; FALNYSFSQ; ALNYSFSQP; LNYSFSQPT; NYSFSQPTR; YSFSQPTRQ; SFSQPTRQQ; FSQPTRQQT; SQPTRQQTN; QPTRQQTNS; PTRQQTNSS; TRQQTNSSS; RQQTNSSSA; QQTNSSSAV; QTNSSSAVQ; TNSSSAVQT; NSSSAVQTT; SSSAVQTTT; SSAVQTTTS; SAVQTTTSS; AVQTTTSSG; VQTTTSSGS; QTTTSSGSK; TTTSSGSKL; TTSSGSKLQ; TSSGSKLQT; SSGSKLQTL; SGSKLQTLK; GSKLQTLKN; SKLQTLKNE; KLQTLKNEL; LQTLKNELI; QTLKNELIR; TLKNELIRA; LKNELIRAI; KNELIRAIS; NELIRAISE; ELIRAISEE; LIRAISEEK; IRAISEEKN; RAISEEKNK; AISEEKNKT; ISEEKNKTQ; SEEKNKTQN; EEKNKTQNN; EKNKTQNNF; KNKTQNNFG; NKTQNNFGF; KTQNNFGFR; TQNNFGFRE; QNNFGFRET; NNFGFRETY; NFGFRETYD; FGFRETYDQ; GFRETYDQF; FRETYDQFK; RETYDQFKM; ETYDQFKMK; TYDQFKMKD; YDQFKMKDS; DQFKMKDSA; QFKMKDSAF; FKMKDSAFE; KMKDSAFEL; MKDSAFELL; KDSAFELLD; DSAFELLDV; SAFELLDVI; AFELLDVIS; FELLDVISS; ELLDVISSA; LLDVISSAK; LDVISSAKV; DVISSAKVY; VISSAKVYD; ISSAKVYDR; SSAKVYDRS; SAKVYDRSY; AKVYDRSYA; KVYDRSYAP; VYDRSYAPQ; YDRSYAPQL; DRSYAPQLN; RSYAPQLNS; SYAPQLNSN; YAPQLNSNT; APQLNSNTP; PQLNSNTPE; QLNSNTPEA; LNSNTPEAE; NSNTPEAEN; SNTPEAENE;

NTPEAENER; TPEAENERN; PEAENERNK; EAENERNKF; AENERNKFY;
ENERNKFYA; NERNKFYAL; ERNKFYALM; RNKFYALMD; NKFYALMDF;
KFYALMDFD; FYALMDFDQ; YALMDFDQY; ALMDFDQYK; LMDFDQYKI;
MDFDQYKIE; DFDQYKIEQ; FDQYKIEQF; DQYKIEQFG; QYKIEQFGS;
YKIEQFGSI; KIEQFGSIM; IEQFGSIME; EQFGSIMEA; QFGSIMEAL;
FGSIMEALY; GSIMEALYN; SIMEALYNE; IMEALYNEN; MEALYNENQ;
EALYNENQN; ALYNENQNH; LYNENQNHS; YNENQNHSL; NENQNHSLI;
ENQNHSLIR; NQNHSLIRE; QNHSLIREL; NHSLIRELM; HSLIRELMI;
SLIRELMIS; LIRELMISG; IRELMISGL; RELMISGLG; ELMISGLGT;
LMISGLGTQ; MISGLGTQI; ISGLGTQIS; SGLGTQISF; GLGTQISFE;
LGTQISFEL; GTQISFELA; TQISFELAL; QISFELALE; ISFELALEE;
SFELALEEI; FELALEEIN; ELALEEINK; LALEEINKK; ALEEINKKI;
LEEINKKIE; EEINKKIEI; EINKKIEIF; INKKIEIFN; NKKIEIFNQ;
KKIEIFNQD; KIEIFNQDY; IEIFNQDYL; EIFNQDYLN; IFNQDYLNA;
FNQDYLNAK; NQDYLNAKI; QDYLNAKIN; DYLNAKINS; YLNAKINSF;
LNAKINSFD; NAKINSFDF; AKINSFDFT; KINSFDFTM; INSFDFTMK;
NSFDFTMKL; SFDFTMKLK; FDFTMKLKE; DFTMKLKEL; FTMKLKELK;
TMKLKELKS; MKLKELKSK; KLKELKSKL; LKELKSKLN; KELKSKLNQ;
ELKSKLNQI; LKSKLNQIL; KSKLNQILD; SKLNQILDK; KLNQILDKR;
LNQILDKRK; NQILDKRKE; QILDKRKEW; ILDKRKEWS; LDKRKEWSR;
DKRKEWSRQ; KRKEWSRQA; RKEWSRQAD; KEWSRQADG; EWSRQADGL;
WSRQADGLI; SRQADGLIA; RQADGLIAN; QADGLIANA; ADGLIANAS;
DGLIANASS; GLIANASSN; LIANASSNS; IANASSNSS; ANASSNSSL;
NASSNSSLS; ASSNSSLSD; SSNSSLSDS; SNSSLSDSK; NSSLSDSKS;
SSLSDSKSL; SLSDSKSLA; LSDSKSLAE; SDSKSLAEY; DSKSLAEYI;
SKSLAEYIK; KSLAEYIKK; SLAEYIKKR; LAEYIKKRY; AEYIKKRYL;
EYIKKRYLD; YIKKRYLDN; IKKRYLDNM; KKRYLDNMQ; KRYLDNMQN;
RYLDNMQNA; YLDNMQNAR; LDNMQNARQ; DNMQNARQS; NMQNARQSV;
MQNARQSVL; QNARQSVLE; NARQSVLEA; ARQSVLEAY; RQSVLEAYI;
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10 mers:
MKIKPLIQLK; KIKPLIQLKL; IKPLIQLKLL; KPLIQLKLLG;
PLIQLKLLGL; LIQLKLLGLF; IQLKLLGLFL; QLKLLGLFLF;
LKLLGLFLFS; KLLGLFLFSC; LLGLFLFSCT; LGLFLFSCTI;
GLFLFSCTID; LFLFSCTIDA; FLFSCTIDAN; LFSCTIDANL;
FSCTIDANLN; SCTIDANLNE; CTIDANLNED; TIDANLNEDY;
IDANLNEDYK; DANLNEDYKN; ANLNEDYKNK; NLNEDYKNKV;
LNEDYKNKVK; NEDYKNKVKG; EDYKNKVKGI; DYKNKVKGIL;
YKNKVKGILN; KNKVKGILNK; NKVKGILNKA; KVKGILNKAA;
VKGILNKAAD; KGILNKAADD; GILNKAADDQ; ILNKAADDQE;
LNKAADDQET; NKAADDQETT; KAADDQETTS; AADDQETTSA;
ADDQETTSAD; DDQETTSADT; DQETTSADTN; QETTSADTNS;
ETTSADTNSN; TTSADTNSNA; TSADTNSNAA; SADTNSNAAK;
ADTNSNAAKN; DTNSNAAKNI; TNSNAAKNIP; NSNAAKNIPI;
SNAAKNIPIA; NAAKNIPIAD; AAKNIPIADN; AKNIPIADND;
KNIPIADNDK; NIPIADNDKV; IPIADNDKVA; PIADNDKVAA;
IADNDKVAAE; ADNDKVAAEL; DNDKVAAELK; NDKVAAELKK;
DKVAAELKKQ; KVAAELKKQS; VAAELKKQSQ; AAELKKQSQA;
AELKKQSQAA; ELKKQSQAAK; LKKQSQAAKT; KKQSQAAKTV;
KQSQAAKTVA; QSQAAKTVAA; SQAAKTVAAA; QAAKTVAAAP;

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FGSIMEALYN; GSIMEALYNE; SIMEALYNEN; IMEALYNENQ;
MEALYNENQN; EALYNENQNH; ALYNENQNHS; LYNENQNHSL;
YNENQNHSLI; NENQNHSLIR; ENQNHSLIRE; NQNHSLIREL;
QNHSLIRELM; NHSLIRELMI; HSLIRELMIS; SLIRELMISG;
LIRELMISGL; IRELMISGLG; RELMISGLGT; ELMISGLGTQ;
LMISGLGTQI; MISGLGTQIS; ISGLGTQISF; SGLGTQISFE;
GLGTQISFEL; LGTQISFELA; GTQISFELAL; TQISFELALE;
QISFELALEE; ISFELALEEI; SFELALEEIN; FELALEEINK;
ELALEEINKK; LALEEINKKI; ALEEINKKIE; LEEINKKIEI;
EEINKKIEIF; EINKKIEIFN; INKKIEIFNQ; NKKIEIFNQD;
KKIEIFNQDY; KIEIFNQDYL; IEIFNQDYLN; EIFNQDYLNA;
IFNQDYLNAK; FNQDYLNAKI; NQDYLNAKIN; QDYLNAKINS;
DYLNAKINSF; YLNAKINSFD; LNAKINSFDF; NAKINSFDFT;
AKINSFDFTM; KINSFDFTMK; INSFDFTMKL; NSFDFTMKLK;
SFDFTMKLKE; FDFTMKLKEL; DFTMKLKELK; FTMKLKELKS;
TMKLKELKSK; MKLKELKSKL; KLKELKSKLN; LKELKSKLNQ;
KELKSKLNQI; ELKSKLNQIL; LKSKLNQILD; KSKLNQILDK;
SKLNQILDKR; KLNQILDKRK; LNQILDKRKE; NQILDKRKEW;
QILDKRKEWS; ILDKRKEWSR; LDKRKEWSRQ; DKRKEWSRQA;
KRKEWSRQAD; RKEWSRQADG; KEWSRQADGL; EWSRQADGLI;
WSRQADGLIA; SRQADGLIAN; RQADGLIANA; QADGLIANAS;
ADGLIANASS; DGLIANASSN; GLIANASSNS; LIANASSNSS;
IANASSNSSL; ANASSNSSLS; NASSNSSLSD; ASSNSSLSDS;
SSNSSLSDSK; SNSSLSDSKS; NSSLSDSKSL; SSLSDSKSLA;
SLSDSKSLAE; LSDSKSLAEY; SDSKSLAEYI; DSKSLAEYIK;
SKSLAEYIKK; KSLAEYIKKR; SLAEYIKKRY; LAEYIKKRYL;
AEYIKKRYLD; EYIKKRYLDN; YIKKRYLDNM; IKKRYLDNMQ;
KKRYLDNMQN; KRYLDNMQNA; RYLDNMQNAR; YLDNMQNARQ;
LDNMQNARQS; DNMQNARQSV; NMQNARQSVL; MQNARQSVLE;
QNARQSVLEA; NARQSVLEAY; ARQSVLEAYI; RQSVLEAYIS;
QSVLEAYISI;

11 mers:
MKIKPLIQLKL; KIKPLIQLKLL; IKPLIQLKLLG; KPLIQLKLLGL;
PLIQLKLLGLF; LIQLKLLGLFL; IQLKLLGLFLF; QLKLLGLFLFS;
LKLLGLFLFSC; KLLGLFLFSCT; LLGLFLFSCTI; LGLFLFSCTID;
GLFLFSCTIDA; LFLFSCTIDAN; FLFSCTIDANL; LFSCTIDANLN;
FSCTIDANLNE; SCTIDANLNED; CTIDANLNEDY; TIDANLNEDYK;
IDANLNEDYKN; DANLNEDYKNK; ANLNEDYKNKV; NLNEDYKNKVK;
LNEDYKNKVKG; NEDYKNKVKGI; EDYKNKVKGIL; DYKNKVKGILN;
YKNKVKGILNK; KNKVKGILNKA; NKVKGILNKAA; KVKGILNKAAD;
VKGILNKAADD; KGILNKAADDQ; GILNKAADDQE; ILNKAADDQET;
LNKAADDQETT; NKAADDQETTS; KAADDQETTSA; AADDQETTSAD;
ADDQETTSADT; DDQETTSADTN; DQETTSADTNS; QETTSADTNSN;
ETTSADTNSNA; TTSADTNSNAA; TSADTNSNAAK; SADTNSNAAKN;
ADTNSNAAKNI; DTNSNAAKNIP; TNSNAAKNIPI; NSNAAKNIPIA;
SNAAKNIPIAD; NAAKNIPIADN; AAKNIPIADND; AKNIPIADNDK;
KNIPIADNDKV; NIPIADNDKVA; IPIADNDKVAA; PIADNDKVAAE;
IADNDKVAAEL; ADNDKVAAELK; DNDKVAAELKK; NDKVAAELKKQ;
DKVAAELKKQS; KVAAELKKQSQ; VAAELKKQSQA; AAELKKQSQAA;
AELKKQSQAAK; ELKKQSQAAKT; LKKQSQAAKTV; KKQSQAAKTVA;

	KQSQAAKTVAA; QSQAAKTVAAA; SQAAKTVAAAP; QAAKTVAAAPN; AAKTVAAAPNK; AKTVAAAPNKG; KTVAAAPNKGS; TVAAAPNKGSQ; VAAAPNKGSQN; AAAPNKGSQNQ; AAPNKGSQNQP; APNKGSQNQPQ; PNKGSQNQPQT; NKGSQNQPQTT; KGSQNQPQTTP; GSQNQPQTTPN; SQNQPQTTPNK; QNQPQTTPNKG; NQPQTTPNKGS; QPQTTPNKGSQ; PQTTPNKGSQN; QTTPNKGSQNQ; TTPNKGSQNQQ; TPNKGSQNQQA; PNKGSQNQQAA; NKGSQNQQAAP; KGSQNQQAAPS; GSQNQQAAPSP; SQNQQAAPSPQ; QNQQAAPSPQL; NQQAAPSPQLQ; QQAAPSPQLQS; QAAPSPQLQSL; AAPSPQLQSLS; APSPQLQSLSF; PSPQLQSLSFS; SPQLQSLSFSA; PQLQSLSFSAD; QLQSLSFSADL; LQSLSFSADLS; QSLSFSADLSN; SLSFSADLSNL; LSFSADLSNLP; SFSADLSNLPK; FSADLSNLPKT; SADLSNLPKTT; ADLSNLPKTTA; DLSNLPKTTAA; LSNLPKTTAAR; SNLPKTTAARA; NLPKTTAARAA; LPKTTAARAAS; PKTTAARAASL; KTTAARAASLT; TTAARAASLTK; TAARAASLTKQ; AARAASLTKQR; ARAASLTKQRI; RAASLTKQRIP; AASLTKQRIPI; ASLTKQRIPIQ; SLTKQRIPIQA; LTKQRIPIQAV; TKQRIPIQAVT; KQRIPIQAVTT; QRIPIQAVTTV; RIPIQAVTTVP; IPIQAVTTVPG; PIQAVTTVPGN; IQAVTTVPGNT; QAVTTVPGNTR; AVTTVPGNTRT; VTTVPGNTRTF; TTVPGNTRTFN; TVPGNTRTFNS; VPGNTRTFNSR; PGNTRTFNSRN; GNTRTFNSRNS; NTRTFNSRNSG; TRTFNSRNSGL; RTFNSRNSGLP; TFNSRNSGLPT; FNSRNSGLPTF; NSRNSGLPTFA; SRNSGLPTFAL; RNSGLPTFALN; NSGLPTFALNY; SGLPTFALNYS; GLPTFALNYSF; LPTFALNYSFS; PTFALNYSFSQ; TFALNYSFSQP; FALNYSFSQPT; ALNYSFSQPTR; LNYSFSQPTRQ; NYSFSQPTRQQ; YSFSQPTRQQT; SFSQPTRQQTN; FSQPTRQQTNS; SQPTRQQTNSS; QPTRQQTNSSS; PTRQQTNSSSA; TRQQTNSSSAV; RQQTNSSSAVQ; QQTNSSSAVQT; QTNSSSAVQTT; TNSSSAVQTTT; NSSSAVQTTTS; SSSAVQTTTSS; SSAVQTTTSSG; SAVQTTTSSGS; AVQTTTSSGSK; VQTTTSSGSKL; QTTTSSGSKLQ; TTTSSGSKLQT; TTSSGSKLQTL; TSSGSKLQTLK; SSGSKLQTLKN; SGSKLQTLKNE; GSKLQTLKNEL; SKLQTLKNELI; KLQTLKNELIR; LQTLKNELIRA; QTLKNELIRAI; TLKNELIRAIS; LKNELIRAISE; KNELIRAISEE; NELIRAISEEK; ELIRAISEEKN; LIRAISEEKNK; IRAISEEKNKT; RAISEEKNKTQ; AISEEKNKTQN; ISEEKNKTQNN; SEEKNKTQNNF; EEKNKTQNNFG; EKNKTQNNFGF; KNKTQNNFGFR; NKTQNNFGFRE; KTQNNFGFRET; TQNNFGFRETY; QNNFGFRETYD; NNFGFRETYDQ; NFGFRETYDQF; FGFRETYDQFK; GFRETYDQFKM; FRETYDQFKMK; RETYDQFKMKD; ETYDQFKMKDS; TYDQFKMKDSA; YDQFKMKDSAF; DQFKMKDSAFE; QFKMKDSAFEL; FKMKDSAFELL; KMKDSAFELLD; MKDSAFELLDV; KDSAFELLDVI; DSAFELLDVIS; SAFELLDVISS; AFELLDVISSA; FELLDVISSAK; ELLDVISSAKV; LLDVISSAKVY; LDVISSAKVYD; DVISSAKVYDR; VISSAKVYDRS; ISSAKVYDRSY; SSAKVYDRSYA; SAKVYDRSYAP; AKVYDRSYAPQ; KVYDRSYAPQL; VYDRSYAPQLN; YDRSYAPQLNS; DRSYAPQLNSN; RSYAPQLNSNT; SYAPQLNSNTP; YAPQLNSNTPE; APQLNSNTPEA; PQLNSNTPEAE; QLNSNTPEAEN; LNSNTPEAENE; NSNTPEAENER; SNTPEAENERN; NTPEAENERNK; TPEAENERNKF; PEAENERNKFY; EAENERNKFYA; AENERNKFYAL; ENERNKFYALM; NERNKFYALMD; ERNKFYALMDF; RNKFYALMDFD; NKFYALMDFDQ; KFYALMDFDQY; FYALMDFDQYK; YALMDFDQYKI; ALMDFDQYKIE; LMDFDQYKIEQ; MDFDQYKIEQF; DFDQYKIEQFG; FDQYKIEQFGS; DQYKIEQFGSI; QYKIEQFGSIM; YKIEQFGSIME;

	KIEQFGSIMEA; IEQFGSIMEAL; EQFGSIMEALY; QFGSIMEALYN; FGSIMEALYNE; GSIMEALYNEN; SIMEALYNENQ; IMEALYNENQN; MEALYNENQNH; EALYNENQNHS; ALYNENQNHSL; LYNENQNHSLI; YNENQNHSLIR; NENQNHSLIRE; ENQNHSLIREL; NQNHSLIRELM; QNHSLIRELMI; NHSLIRELMIS; HSLIRELMISG; SLIRELMISGL; LIRELMISGLG; IRELMISGLGT; RELMISGLGTQ; ELMISGLGTQI; LMISGLGTQIS; MISGLGTQISF; ISGLGTQISFE; SGLGTQISFEL; GLGTQISFELA; LGTQISFELAL; GTQISFELALE; TQISFELALEE; QISFELALEEI; ISFELALEEIN; SFELALEEINK; FELALEEINKK; ELALEEINKKI; LALEEINKKIE; ALEEINKKIEI; LEEINKKIEIF; EEINKKIEIFN; EINKKIEIFNQ; INKKIEIFNQD; NKKIEIFNQDY; KKIEIFNQDYL; KIEIFNQDYLN; IEIFNQDYLNA; EIFNQDYLNAK; IFNQDYLNAKI; FNQDYLNAKIN; NQDYLNAKINS; QDYLNAKINSF; DYLNAKINSFD; YLNAKINSFDF; LNAKINSFDFT; NAKINSFDFTM; AKINSFDFTMK; KINSFDFTMKL; INSFDFTMKLK; NSFDFTMKLKE; SFDFTMKLKEL; FDFTMKLKELK; DFTMKLKELKS; FTMKLKELKSK; TMKLKELKSKL; MKLKELKSKLN; KLKELKSKLNQ; LKELKSKLNQI; KELKSKLNQIL; ELKSKLNQILD; LKSKLNQILDK; KSKLNQILDKR; SKLNQILDKRK; KLNQILDKRKE; LNQILDKRKEW; NQILDKRKEWS; QILDKRKEWSR; ILDKRKEWSRQ; LDKRKEWSRQA; DKRKEWSRQAD; KRKEWSRQADG; RKEWSRQADGL; KEWSRQADGLI; EWSRQADGLIA; WSRQADGLIAN; SRQADGLIANA; RQADGLIANAS; QADGLIANASS; ADGLIANASSN; DGLIANASSNS; GLIANASSNSS; LIANASSNSSL; IANASSNSSLS; ANASSNSSLSD; NASSNSSLSDS; ASSNSSLSDSK; SSNSSLSDSKS; SNSSLSDSKSL; NSSLSDSKSLA; SSLSDSKSLAE; SLSDSKSLAEY; LSDSKSLAEYI; SDSKSLAEYIK; DSKSLAEYIKK; SKSLAEYIKKR; KSLAEYIKKRY; SLAEYIKKRYL; LAEYIKKRYLD; AEYIKKRYLDN; EYIKKRYLDNM; YIKKRYLDNMQ; IKKRYLDNMQN; KKRYLDNMQNA; KRYLDNMQNAR; RYLDNMQNARQ; YLDNMQNARQS; LDNMQNARQSV; DNMQNARQSVL; NMQNARQSVLE; MQNARQSVLEA; QNARQSVLEAY; NARQSVLEAYI; ARQSVLEAYIS; RQSVLEAYISI; QSVLEAYISIM;
Seq 35	SEQ ID NO 42221-43880/ 8 mers: MSSCTIDA; SSCTIDAN; SCTIDANL; CTIDANLN; TIDANLNK; IDANLNKD; DANLNKDY; ANLNKDYK; NLNKDYKN; LNKDYKNK; NKDYKNKV; KDYKNKVE; DYKNKVEE; YKNKVEEL; KNKVEELL; NKVEELLN; KVEELLNS; VEELLNSS; EELLNSST; ELLNSSTD; LLNSSTDD; LNSSTDDQ; NSSTDDQA; SSTDDQAK; STDDQAKI; TDDQAKIS; DDQAKISI; DQAKISIN; QAKISINT; AKISINTG; KISINTGS; ISINTGSN; SINTGSNA; INTGSNAT; NTGSNATK; TGSNATKN; GSNATKNK; SNATKNKT; NATKNKTN; ATKNKTNI; TKNKTNIK; KNKTNIKV; NKTNIKVA; KTNIKVAG; TNIKVAGL; NIKVAGLQ; IKVAGLQK; KVAGLQKN; VAGLQKNT; AGLQKNTQ; GLQKNTQS; LQKNTQSK; QKNTQSKK; KNTQSKKN; NTQSKKNN; TQSKKNNN; QSKKNNNL; SKKNNNLQ; KKNNNLQG; KNNNLQGL; NNNLQGLN; NNLQGLNP; NLQGLNPA; LQGLNPAN; QGLNPANQ; GLNPANQV; LNPANQVN; NPANQVNP; PANQVNPG; ANQVNPGN; NQVNPGNP; QVNPGNPM; VNPGNPMQ; NPGNPMQI; PGNPMQIA; GNPMQIAN; NPMQIANQ; PMQIANQA; MQIANQAN; QIANQANQ;

	IANQANQA; ANQANQAN; NQANQANQ; QANQANQA; ANQANQAN; NQANQANQ; QANQANQA; ANQANQAN; NQANQANQ; QANQANQA; ANQANQAS; NQANQASQ; QANQASQA; ANQASQAS; NQASQASQ; QASQASQA; ASQASQAS; SQASQASQ; QASQASQV; ASQASQVA; SQASQVAS; QASQVASS; ASQVASSA; SQVASSAS; QVASSASQ; VASSASQA; ASSASQAS; SSASQASP; SASQASPV; ASQASPVA; SQASPVAS; QASPVASP; ASPVASPA; SPVASPAT; PVASPATN; VASPATNV; ASPATNVQ; SPATNVQA; PATNVQAT; ATNVQATP; TNVQATPP; NVQATPPK; VQATPPKQ; QATPPKQI; ATPPKQIA; TPPKQIAS; PPKQIASA; PKQIASAQ; KQIASAQA; QIASAQAI; IASAQAIQ; ASAQAIQT; SAQAIQTV; AQAIQTVP; QAIQTVPN; AIQTVPNN; IQTVPNNT; QTVPNNTS; TVPNNTST; VPNNTSTP; PNNTSTPN; NNTSTPNQ; NTSTPNQS; TSTPNQSI; STPNQSII; TPNQSIIK; PNQSIIKP; NQSIIKPQ; QSIIKPQQ; SIIKPQQY; IIKPQQYT; IKPQQYTF; KPQQYTFS; PQQYTFSS; QQYTFSSS; QYTFSSSF; YTFSSSFS; TFSSSFSQ; FSSSFSQP; SSSFSQPT; SSFSQPTS; SFSQPTSQ; FSQPTSQT; SQPTSQTN; QPTSQTNF; PTSQTNFN; TSQTNFNN; SQTNFNNS; QTNFNNSQ; TNFNNSQS; NFNNSQSN; FNNSQSNN; NNSQSNNV; NSQSNNVL; SQSNNVLT; QSNNVLTN; SNNVLTNY; NNVLTNYR; NVLTNYRH; VLTNYRHQ; LTNYRHQT; TNYRHQTQ; NYRHQTQP; YRHQTQPS; RHQTQPSF; HQTQPSFV; QTQPSFVV; TQPSFVVP; QPSFVVPV; PSFVVPVY; SFVVPVYS; FVVPVYSG; VVPVYSGN; VPVYSGNS; PVYSGNSP; VYSGNSPL; YSGNSPLQ; SGNSPLQK; GNSPLQKL; NSPLQKLK; SPLQKLKN; PLQKLKNN; LQKLKNNL; QKLKNNLL; KLKNNLLR; LKNNLLRR; KNNLLRRI; NNLLRRIA; NLLRRIAE; LLRRIAEE; LRRIAEEK; RRIAEEKN; RIAEEKNK; IAEEKNKT; AEEKNKTH; EEKNKTHN; EKNKTHNH; KNKTHNHG; NKTHNHGF; KTHNHGFR; THNHGFRE; HNHGFRET; NHGFRETY; HGFRETYD; GFRETYDQ; FRETYDQF; RETYDQFK; ETYDQFKM; TYDQFKMK; YDQFKMKD; DQFKMKDS; QFKMKDSA; FKMKDSAF; KMKDSAFT; MKDSAFTL; KDSAFTLL; DSAFTLLD; SAFTLLDV; AFTLLDVI; FTLLDVIS; TLLDVISN; LLDVISNI; LDVISNIS; DVISNISV; VISNISVF; ISNISVFD; SNISVFDR; NISVFDRG; ISVFDRGS; SVFDRGSA; VFDRGSAP; FDRGSAPQ; DRGSAPQL; RGSAPQLS; GSAPQLSS; SAPQLSSN; APQLSSNT; PQLSSNTP; QLSSNTPE; LSSNTPEA; SSNTPEAE; SNTPEAES; NTPEAESE; TPEAESER; PEAESERN; EAESERNR; AESERNRL; ESERNRLY; SERNRLYA; ERNRLYAM; RNRLYAMM; NRLYAMMD; RLYAMMDF; LYAMMDFD; YAMMDFDQ; AMMDFDQA; MMDFDQAK; MDFDQAKT; DFDQAKTT; FDQAKTTE; DQAKTTEF; QAKTTEFG; AKTTEFGS; KTTEFGSI; TTEFGSIM; TEFGSIMN; EFGSIMNI; FGSIMNIL; GSIMNILY; SIMNILYQ; IMNILYQE; MNILYQEN; NILYQENQ; ILYQENQN; LYQENQNH; YQENQNHS; QENQNHSL; ENQNHSLI; NQNHSLIR; QNHSLIRS; NHSLIRSL; HSLIRSLI; SLIRSLII; LIRSLIIS; IRSLIISG; RSLIISGL; SLIISGLG; LIISGLGI; IISGLGIQ; ISGLGIQI; SGLGIQIS; GLGIQISL; LGIQISLE; GIQISLES; IQISLEST; QISLESTL; ISLESTLE; SLESTLEE; LESTLEEI; ESTLEEIE; STLEEIEK; TLEEIEKK; LEEIEKKI; EEIEKKIE; EIEKKIES; IEKKIESF; EKKIESFN; KKIESFNT; KIESFNTQ; IESFNTQY; ESFNTQYL; SFNTQYLN;

	FNTQYLNT; NTQYLNTI; TQYLNTII; QYLNTIIN; YLNTIINS; LNTIINSY; NTIINSYT; TIINSYTF; IINSYTFK; INSYTFKD; NSYTFKDK; SYTFKDKL; YTFKDKLK; TFKDKLKE; FKDKLKEL; KDKLKELE; DKLKELES; KLKELESK; LKELESKL; KELESKLN; ELESKLNS; LESKLNSI; ESKLNSIL; SKLNSILA; KLNSILAE; LNSILAEK; NSILAEKK; SILAEKKE; ILAEKKEW; LAEKKEWL; AEKKEWLN; EKKEWLNY; KKEWLNYA; KEWLNYAD; EWLNYADA; WLNYADAI; LNYADAII; NYADAIIT; YADAIITN; ADAIITNT; DAIITNTS; AIITNTSS; IITNTSSN; ITNTSSNS; TNTSSNSK; NTSSNSKR; TSSNSKRN; SSNSKRND; SNSKRNDP; NSKRNDPQ; SKRNDPQS; KRNDPQSL; RNDPQSLG; NDPQSLGQ; DPQSLGQY; PQSLGQYI; QSLGQYIK; SLGQYIKN; LGQYIKNK; GQYIKNKY; QYIKNKYL; YIKNKYLD; IKNKYLDK; KNKYLDKM; NKYLDKMQ; KYLDKMQD; YLDKMQDA; LDKMQDAR; DKMQDARQ; KMQDARQS; MQDARQSA; QDARQSAL; DARQSALD; ARQSALDL; RQSALDLY; QSALDLYL; SALDLYLN; ALDLYLNI; LDLYLNIT; DLYLNITE; LYLNITEI; 9 mers: MSSCTIDAN; SSCTIDANL; SCTIDANLN; CTIDANLNK; TIDANLNKD; IDANLNKDY; DANLNKDYK; ANLNKDYKN; NLNKDYKNK; LNKDYKNKV; NKDYKNKVE; KDYKNKVEE; DYKNKVEEL; YKNKVEELL; KNKVEELLN; NKVEELLNS; KVEELLNSS; VEELLNSST; EELLNSSTD; ELLNSSTDD; LLNSSTDDQ; LNSSTDDQA; NSSTDDQAK; SSTDDQAKI; STDDQAKIS; TDDQAKISI; DDQAKISIN; DQAKISINT; QAKISINTG; AKISINTGS; KISINTGSN; ISINTGSNA; SINTGSNAT; INTGSNATK; NTGSNATKN; TGSNATKNK; GSNATKNKT; SNATKNKTN; NATKNKTNI; ATKNKTNIK; TKNKTNIKV; KNKTNIKVA; NKTNIKVAG; KTNIKVAGL; TNIKVAGLQ; NIKVAGLQK; IKVAGLQKN; KVAGLQKNT; VAGLQKNTQ; AGLQKNTQS; GLQKNTQSK; LQKNTQSKK; QKNTQSKKN; KNTQSKKNN; NTQSKKNNN; TQSKKNNNL; QSKKNNNLQ; SKKNNNLQG; KKNNNLQGL; KNNNLQGLN; NNNLQGLNP; NNLQGLNPA; NLQGLNPAN; LQGLNPANQ; QGLNPANQV; GLNPANQVN; LNPANQVNP; NPANQVNPG; PANQVNPGN; ANQVNPGNP; NQVNPGNPM; QVNPGNPMQ; VNPGNPMQI; NPGNPMQIA; PGNPMQIAN; GNPMQIANQ; NPMQIANQA; PMQIANQAN; MQIANQANQ; QIANQANQA; IANQANQAN; ANQANQANQ; NQANQANQA; QANQANQAN; ANQANQANQ; NQANQANQA; QANQANQAN; ANQANQANQ; NQANQANQA; QANQANQAN; ANQANQANQ; NQANQANQA; QANQANQAS; ANQANQASQ; NQANQASQA; QANQASQAS; ANQASQASQ; NQASQASQA; QASQASQAS; ASQASQASQ; SQASQASQV; QASQASQVA; ASQASQVAS; SQASQVASS; QASQVASSA; ASQVASSAS; SQVASSASQ; QVASSASQA; VASSASQAS; ASSASQASP; SSASQASPV; SASQASPVA; ASQASPVAS; SQASPVASP; QASPVASPA; ASPVASPAT; SPVASPATN; PVASPATNV; VASPATNVQ; ASPATNVQA; SPATNVQAT; PATNVQATP; ATNVQATPP; TNVQATPPK; NVQATPPKQ; VQATPPKQI; QATPPKQIA; ATPPKQIAS; TPPKQIASA; PPKQIASAQ; PKQIASAQA; KQIASAQAI; QIASAQAIQ; IASAQAIQT; ASAQAIQTV; SAQAIQTVP; AQAIQTVPN; QAIQTVPNN; AIQTVPNNT; IQTVPNNTS; QTVPNNTST; TVPNNTSTP; VPNNTSTPN; PNNTSTPNQ; NNTSTPNQS; NTSTPNQSI; TSTPNQSII; STPNQSIIK; TPNQSIIKP; PNQSIIKPQ; NQSIIKPQQ; QSIIKPQQY; SIIKPQQYT; IIKPQQYTF; IKPQQYTFS; KPQQYTFSS; PQQYTFSSS; QQYTFSSSF; QYTFSSSFS; YTFSSSFSQ;

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10 mers:
MSSCTIDANL; SSCTIDANLN; SCTIDANLNK; CTIDANLNKD;
TIDANLNKDY; IDANLNKDYK; DANLNKDYKN; ANLNKDYKNK;
NLNKDYKNKV; LNKDYKNKVE; NKDYKNKVEE; KDYKNKVEEL;
DYKNKVEELL; YKNKVEELLN; KNKVEELLNS; NKVEELLNSS;
KVEELLNSST; VEELLNSSTD; EELLNSSTDD; ELLNSSTDDQ;
LLNSSTDDQA; LNSSTDDQAK; NSSTDDQAKI; SSTDDQAKIS;
STDDQAKISI; TDDQAKISIN; DDQAKISINT; DQAKISINTG;
QAKISINTGS; AKISINTGSN; KISINTGSNA; ISINTGSNAT;
SINTGSNATK; INTGSNATKN; NTGSNATKNK; TGSNATKNKT;
GSNATKNKTN; SNATKNKTNI; NATKNKTNIK; ATKNKTNIKV;
TKNKTNIKVA; KNKTNIKVAG; NKTNIKVAGL; KTNIKVAGLQ;
TNIKVAGLQK; NIKVAGLQKN; IKVAGLQKNT; KVAGLQKNTQ;
VAGLQKNTQS; AGLQKNTQSK; GLQKNTQSKK; LQKNTQSKKN;
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QGLNPANQVN; GLNPANQVNP; LNPANQVNPG; NPANQVNPGN;
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QASQVASSAS; ASQVASSASQ; SQVASSASQA; QVASSASQAS;
VASSASQASP; ASSASQASPV; SSASQASPVA; SASQASPVAS;
ASQASPVASP; SQASPVASPA; QASPVASPAT; ASPVASPATN;
SPVASPATNV; PVASPATNVQ; VASPATNVQA; ASPATNVQAT;
SPATNVQATP; PATNVQATPP; ATNVQATPPK; TNVQATPPKQ;
NVQATPPKQI; VQATPPKQIA; QATPPKQIAS; ATPPKQIASA;
TPPKQIASAQ; PPKQIASAQA; PKQIASAQAI; KQIASAQAIQ;
QIASAQAIQT; IASAQAIQTV; ASAQAIQTVP; SAQAIQTVPN;
AQAIQTVPNN; QAIQTVPNNT; AIQTVPNNTS; IQTVPNNTST;
QTVPNNTSTP; TVPNNTSTPN; VPNNTSTPNQ; PNNTSTPNQS;
NNTSTPNQSI; NTSTPNQSII; TSTPNQSIIK; STPNQSIIKP;
TPNQSIIKPQ; PNQSIIKPQQ; NQSIIKPQQY; QSIIKPQQYT;
SIIKPQQYTF; IIKPQQYTFS; IKPQQYTFSS; KPQQYTFSSS;
PQQYTFSSSF; QQYTFSSSFS; QYTFSSSFSQ; YTFSSSFSQP;
TFSSSFSQPT; FSSSFSQPTS; SSSFSQPTSQ; SSFSQPTSQT;
SFSQPTSQTN; FSQPTSQTNF; SQPTSQTNFN; QPTSQTNFNN;
PTSQTNFNNS; TSQTNFNNSQ; SQTNFNNSQS; QTNFNNSQSN;
TNFNNSQSNN; NFNNSQSNNV; FNNSQSNNVL; NNSQSNNVLT;
NSQSNNVLTN; SQSNNVLTNY; QSNNVLTNYR; SNNVLTNYRH;
NNVLTNYRHQ; NVLTNYRHQT; VLTNYRHQTQ; LTNYRHQTQP;
TNYRHQTQPS; NYRHQTQPSF; YRHQTQPSFV; RHQTQPSFVV;
HQTQPSFVVP; QTQPSFVVPV; TQPSFVVPVY; QPSFVVPVYS;
PSFVVPVYSG; SFVVPVYSGN; FVVPVYSGNS; VVPVYSGNSP;

	VPVYSGNSPL; PVYSGNSPLQ; VYSGNSPLQK; YSGNSPLQKL; SGNSPLQKLK; GNSPLQKLKN; NSPLQKLKNN; SPLQKLKNNL; PLQKLKNNLL; LQKLKNNLLR; QKLKNNLLRR; KLKNNLLRRI; LKNNLLRRIA; KNNLLRRIAE; NNLLRRIAEE; NLLRRIAEEK; LLRRIAEEKN; LRRIAEEKNK; RRIAEEKNKT; RIAEEKNKTH; IAEEKNKTHN; AEEKNKTHNH; EEKNKTHNHG; EKNKTHNHGF; KNKTHNHGFR; NKTHNHGFRE; KTHNHGFRET; THNHGFRETY; HNHGFRETYD; NHGFRETYDQ; HGFRETYDQF; GFRETYDQFK; FRETYDQFKM; RETYDQFKMK; ETYDQFKMKD; TYDQFKMKDS; YDQFKMKDSA; DQFKMKDSAF; QFKMKDSAFT; FKMKDSAFTL; KMKDSAFTLL; MKDSAFTLLD; KDSAFTLLDV; DSAFTLLDVI; SAFTLLDVIS; AFTLLDVISN; FTLLDVISNI; TLLDVISNIS; LLDVISNISV; LDVISNISVF; DVISNISVFD; VISNISVFDR; ISNISVFDRG; SNISVFDRGS; NISVFDRGSA; ISVFDRGSAP; SVFDRGSAPQ; VFDRGSAPQL; FDRGSAPQLS; DRGSAPQLSS; RGSAPQLSSN; GSAPQLSSNT; SAPQLSSNTP; APQLSSNTPE; PQLSSNTPEA; QLSSNTPEAE; LSSNTPEAES; SSNTPEAESE; SNTPEAESER; NTPEAESERN; TPEAESERNR; PEAESERNRL; EAESERNRLY; AESERNRLYA; ESERNRLYAM; SERNRLYAMM; ERNRLYAMMD; RNRLYAMMDF; NRLYAMMDFD; RLYAMMDFDQ; LYAMMDFDQA; YAMMDFDQAK; AMMDFDQAKT; MMDFDQAKTT; MDFDQAKTTE; DFDQAKTTEF; FDQAKTTEFG; DQAKTTEFGS; QAKTTEFGSI; AKTTEFGSIM; KTTEFGSIMN; TTEFGSIMNI; TEFGSIMNIL; EFGSIMNILY; FGSIMNILYQ; GSIMNILYQE; SIMNILYQEN; IMNILYQENQ; MNILYQENQN; NILYQENQNH; ILYQENQNHS; LYQENQNHSL; YQENQNHSLI; QENQNHSLIR; ENQNHSLIRS; NQNHSLIRSL; QNHSLIRSLI; NHSLIRSLII; HSLIRSLIIS; SLIRSLIISG; LIRSLIISGL; IRSLIISGLG; RSLIISGLGI; SLIISGLGIQ; LIISGLGIQI; IISGLGIQIS; ISGLGIQISL; SGLGIQISLE; GLGIQISLES; LGIQISLEST; GIQISLESTL; IQISLESTLE; QISLESTLEE; ISLESTLEEI; SLESTLEEIE; LESTLEEIEK; ESTLEEIEKK; STLEEIEKKI; TLEEIEKKIE; LEEIEKKIES; EEIEKKIESF; EIEKKIESFN; IEKKIESFNT; EKKIESFNTQ; KKIESFNTQY; KIESFNTQYL; IESFNTQYLN; ESFNTQYLNT; SFNTQYLNTI; FNTQYLNTII; NTQYLNTIIN; TQYLNTIINS; QYLNTIINSY; YLNTIINSYT; LNTIINSYTF; NTIINSYTFK; TIINSYTFKD; IINSYTFKDK; INSYTFKDKL; NSYTFKDKLK; SYTFKDKLKE; YTFKDKLKEL; TFKDKLKELE; FKDKLKELES; KDKLKELESK; DKLKELESKL; KLKELESKLN; LKELESKLNS; KELESKLNSI; ELESKLNSIL; LESKLNSILA; ESKLNSILAE; SKLNSILAEK; KLNSILAEKK; LNSILAEKKE; NSILAEKKEW; SILAEKKEWL; ILAEKKEWLN; LAEKKEWLNY; AEKKEWLNYA; EKKEWLNYAD; KKEWLNYADA; KEWLNYADAI; EWLNYADAII; WLNYADAIIT; LNYADAIITN; NYADAIITNT; YADAIITNTS; ADAIITNTSS; DAIITNTSSN; AIITNTSSNS; IITNTSSNSK; ITNTSSNSKR; TNTSSNSKRN; NTSSNSKRND; TSSNSKRNDP; SSNSKRNDPQ; SNSKRNDPQS; NSKRNDPQSL; SKRNDPQSLG; KRNDPQSLGQ; RNDPQSLGQY; NDPQSLGQYI; DPQSLGQYIK; PQSLGQYIKN; QSLGQYIKNK; SLGQYIKNKY; LGQYIKNKYL; GQYIKNKYLD; QYIKNKYLDK; YIKNKYLDKM; IKNKYLDKMQ; KNKYLDKMQD; NKYLDKMQDA;

	KYLDKMQDAR; YLDKMQDARQ; LDKMQDARQS; DKMQDARQSA; KMQDARQSAL; MQDARQSALD; QDARQSALDL; DARQSALDLY; ARQSALDLYL; RQSALDLYLN; QSALDLYLNI; SALDLYLNIT; ALDLYLNITE; LDLYLNITEI; DLYLNITEIR; 11 mers: MSSCTIDANLN; SSCTIDANLNK; SCTIDANLNKD; CTIDANLNKDY; TIDANLNKDYK; IDANLNKDYKN; DANLNKDYKNK; ANLNKDYKNKV; NLNKDYKNKVE; LNKDYKNKVEE; NKDYKNKVEEL; KDYKNKVEELL; DYKNKVEELLN; YKNKVEELLNS; KNKVEELLNSS; NKVEELLNSST; KVEELLNSSTD; VEELLNSSTDD; EELLNSSTDDQ; ELLNSSTDDQA; LLNSSTDDQAK; LNSSTDDQAKI; NSSTDDQAKIS; SSTDDQAKISI; STDDQAKISIN; TDDQAKISINT; DDQAKISINTG; DQAKISINTGS; QAKISINTGSN; AKISINTGSNA; KISINTGSNAT; ISINTGSNATK; SINTGSNATKN; INTGSNATKNK; NTGSNATKNKT; TGSNATKNKTN; GSNATKNKTNI; SNATKNKTNIK; NATKNKTNIKV; ATKNKTNIKVA; TKNKTNIKVAG; KNKTNIKVAGL; NKTNIKVAGLQ; KTNIKVAGLQK; TNIKVAGLQKN; NIKVAGLQKNT; IKVAGLQKNTQ; KVAGLQKNTQS; VAGLQKNTQSK; AGLQKNTQSKK; GLQKNTQSKKN; LQKNTQSKKNN; QKNTQSKKNNN; KNTQSKKNNNL; NTQSKKNNNLQ; TQSKKNNNLQG; QSKKNNNLQGL; SKKNNNLQGLN; KKNNNLQGLNP; KNNNLQGLNPA; NNNLQGLNPAN; NNLQGLNPANQ; NLQGLNPANQV; LQGLNPANQVN; QGLNPANQVNP; GLNPANQVNPG; LNPANQVNPGN; NPANQVNPGNP; PANQVNPGNPM; ANQVNPGNPMQ; NQVNPGNPMQI; QVNPGNPMQIA; VNPGNPMQIAN; NPGNPMQIANQ; PGNPMQIANQA; GNPMQIANQAN; NPMQIANQANQ; PMQIANQANQA; MQIANQANQAN; QIANQANQANQ; IANQANQANQA; ANQANQANQAN; NQANQANQANQ; QANQANQANQA; ANQANQANQAN; NQANQANQANQ; QANQANQANQA; ANQANQANQAS; NQANQANQASQ; QANQANQASQA; ANQANQASQAS; NQANQASQASQ; QANQASQASQA; ANQASQASQAS; NQASQASQASQ; QASQASQASQV; ASQASQASQVA; SQASQASQVAS; QASQASQVASS; ASQASQVASSA; SQASQVASSAS; QASQVASSASQ; ASQVASSASQA; SQVASSASQAS; QVASSASQASP; VASSASQASPV; ASSASQASPVA; SSASQASPVAS; SASQASPVASP; ASQASPVASPA; SQASPVASPAT; QASPVASPATN; ASPVASPATNV; SPVASPATNVQ; PVASPATNVQA; VASPATNVQAT; ASPATNVQATP; SPATNVQATPP; PATNVQATPPK; ATNVQATPPKQ; TNVQATPPKQI; NVQATPPKQIA; VQATPPKQIAS; QATPPKQIASA; ATPPKQIASAQ; TPPKQIASAQA; PPKQIASAQAI; PKQIASAQAIQ; KQIASAQAIQT; QIASAQAIQTV; IASAQAIQTVP; ASAQAIQTVPN; SAQAIQTVPNN; AQAIQTVPNNT; QAIQTVPNNTS; AIQTVPNNTST; IQTVPNNTSTP; QTVPNNTSTPN; TVPNNTSTPNQ; VPNNTSTPNQS; PNNTSTPNQSI; NNTSTPNQSII; NTSTPNQSIIK; TSTPNQSIIKP; STPNQSIIKPQ; TPNQSIIKPQQ; PNQSIIKPQQY; NQSIIKPQQYT; QSIIKPQQYTF; SIIKPQQYTFS; IIKPQQYTFSS; IKPQQYTFSSS; KPQQYTFSSSF; PQQYTFSSSFS; QQYTFSSSFSQ; QYTFSSSFSQP; YTFSSSFSQPT; TFSSSFSQPTS; FSSSFSQPTSQ; SSSFSQPTSQT; SSFSQPTSQTN; SFSQPTSQTNF; FSQPTSQTNFN; SQPTSQTNFNN; QPTSQTNFNNS; PTSQTNFNNSQ; TSQTNFNNSQS; SQTNFNNSQSN; QTNFNNSQSNN; TNFNNSQSNNV; NFNNSQSNNVL; FNNSQSNNVLT; NNSQSNNVLTN; NSQSNNVLTNY; SQSNNVLTNYR; QSNNVLTNYRH; SNNVLTNYRHQ;

	NNVLTNYRHQT; NVLTNYRHQTQ; VLTNYRHQTQP; LTNYRHQTQPS; TNYRHQTQPSF; NYRHQTQPSFV; YRHQTQPSFVV; RHQTQPSFVVP; HQTQPSFVVPV; QTQPSFVVPVY; TQPSFVVPVYS; QPSFVVPVYSG; PSFVVPVYSGN; SFVVPVYSGNS; FVVPVYSGNSP; VVPVYSGNSPL; VPVYSGNSPLQ; PVYSGNSPLQK; VYSGNSPLQKL; YSGNSPLQKLK; SGNSPLQKLKN; GNSPLQKLKNN; NSPLQKLKNNL; SPLQKLKNNLL; PLQKLKNNLLR; LQKLKNNLLRR; QKLKNNLLRRI; KLKNNLLRRIA; LKNNLLRRIAE; KNNLLRRIAEE; NNLLRRIAEEK; NLLRRIAEEKN; LLRRIAEEKNK; LRRIAEEKNKT; RRIAEEKNKTH; RIAEEKNKTHN; IAEEKNKTHNH; AEEKNKTHNHG; EEKNKTHNHGF; EKNKTHNHGFR; KNKTHNHGFRE; NKTHNHGFRET; KTHNHGFRETY; THNHGFRETYD; HNHGFRETYDQ; NHGFRETYDQF; HGFRETYDQFK; GFRETYDQFKM; FRETYDQFKMK; RETYDQFKMKD; ETYDQFKMKDS; TYDQFKMKDSA; YDQFKMKDSAF; DQFKMKDSAFT; QFKMKDSAFTL; FKMKDSAFTLL; KMKDSAFTLLD; MKDSAFTLLDV; KDSAFTLLDVI; DSAFTLLDVIS; SAFTLLDVISN; AFTLLDVISNI; FTLLDVISNIS; TLLDVISNISV; LLDVISNISVF; LDVISNISVFD; DVISNISVFDR; VISNISVFDRG; ISNISVFDRGS; SNISVFDRGSA; NISVFDRGSAP; ISVFDRGSAPQ; SVFDRGSAPQL; VFDRGSAPQLS; FDRGSAPQLSS; DRGSAPQLSSN; RGSAPQLSSNT; GSAPQLSSNTP; SAPQLSSNTPE; APQLSSNTPEA; PQLSSNTPEAE; QLSSNTPEAES; LSSNTPEAESE; SSNTPEAESER; SNTPEAESERN; NTPEAESERNR; TPEAESERNRL; PEAESERNRLY; EAESERNRLYA; AESERNRLYAM; ESERNRLYAMM; SERNRLYAMMD; ERNRLYAMMDF; RNRLYAMMDFD; NRLYAMMDFDQ; RLYAMMDFDQA; LYAMMDFDQAK; YAMMDFDQAKT; AMMDFDQAKTT; MMDFDQAKTTE; MDFDQAKTTEF; DFDQAKTTEFG; FDQAKTTEFGS; DQAKTTEFGSI; QAKTTEFGSIM; AKTTEFGSIMN; KTTEFGSIMNI; TTEFGSIMNIL; TEFGSIMNILY; EFGSIMNILYQ; FGSIMNILYQE; GSIMNILYQEN; SIMNILYQENQ; IMNILYQENQN; MNILYQENQNH; NILYQENQNHS; ILYQENQNHSL; LYQENQNHSLI; YQENQNHSLIR; QENQNHSLIRS; ENQNHSLIRSL; NQNHSLIRSLI; QNHSLIRSLII; NHSLIRSLIIS; HSLIRSLIISG; SLIRSLIISGL; LIRSLIISGLG; IRSLIISGLGI; RSLIISGLGIQ; SLIISGLGIQI; LIISGLGIQIS; IISGLGIQISL; ISGLGIQISLE; SGLGIQISLES; GLGIQISLEST; LGIQISLESTL; GIQISLESTLE; IQISLESTLEE; QISLESTLEEI; ISLESTLEEIE; SLESTLEEIEK; LESTLEEIEKK; ESTLEEIEKKI; STLEEIEKKIE; TLEEIEKKIES; LEEIEKKIESF; EEIEKKIESFN; EIEKKIESFNT; IEKKIESFNTQ; EKKIESFNTQY; KKIESFNTQYL; KIESFNTQYLN; IESFNTQYLNT; ESFNTQYLNTI; SFNTQYLNTII; FNTQYLNTIIN; NTQYLNTIINS; TQYLNTIINSY; QYLNTIINSYT; YLNTIINSYTF; LNTIINSYTFK; NTIINSYTFKD; TIINSYTFKDK; IINSYTFKDKL; INSYTFKDKLK; NSYTFKDKLKE; SYTFKDKLKEL; YTFKDKLKELE; TFKDKLKELES; FKDKLKELESK; KDKLKELESKL; DKLKELESKLN; KLKELESKLNS; LKELESKLNSI; KELESKLNSIL; ELESKLNSILA; LESKLNSILAE; ESKLNSILAEK; SKLNSILAEKK; KLNSILAEKKE; LNSILAEKKEW; NSILAEKKEWL; SILAEKKEWLN; ILAEKKEWLNY; LAEKKEWLNYA; AEKKEWLNYAD; EKKEWLNYADA; KKEWLNYADAI; KEWLNYADAII; EWLNYADAIIT; WLNYADAIITN; LNYADAIITNT; NYADAIITNTS; YADAIITNTSS; ADAIITNTSSN; DAIITNTSSNS; AIITNTSSNSK; IITNTSSNSKR; ITNTSSNSKRN; TNTSSNSKRND; NTSSNSKRNDP; TSSNSKRNDPQ; SSNSKRNDPQS; SNSKRNDPQSL;

	NSKRNDPQSLG; SKRNDPQSLGQ; KRNDPQSLGQY; RNDPQSLGQYI; NDPQSLGQYIK; DPQSLGQYIKN; PQSLGQYIKNK; QSLGQYIKNKY; SLGQYIKNKYL; LGQYIKNKYLD; GQYIKNKYLDK; QYIKNKYLDKM; YIKNKYLDKMQ; IKNKYLDKMQD; KNKYLDKMQDA; NKYLDKMQDAR; KYLDKMQDARQ; YLDKMQDARQS; LDKMQDARQSA; DKMQDARQSAL; KMQDARQSALD; MQDARQSALDL; QDARQSALDLY; DARQSALDLYL; ARQSALDLYLN; RQSALDLYLNI; QSALDLYLNIT; SALDLYLNITE; ALDLYLNITEI; LDLYLNITEIR;
Seq 36	SEQ ID NO 43881-44898/ 8 mers: MKKAKLNI; KKAKLNII; KAKLNIIK; AKLNIIKI; KLNIIKIN; LNIIKINI; NIIKINII; IIKINIIT; IKINIITM; KINIITMI; INIITMIL; NIITMILT; IITMILTL; ITMILTLI; TMILTLIC; MILTLICI; ILTLICIS; LTLICISC; TLICISCA; LICISCAP; ICISCAPF; CISCAPFN; ISCAPFNK; SCAPFNKI; CAPFNKIN; APFNKINP; PFNKINPK; FNKINPKA; NKINPKAN; KINPKANE; INPKANEN; NPKANENT; PKANENTK; KANENTKL; ANENTKLK; NENTKLKK; ENTKLKKN; NTKLKKNT; TKLKKNTR; KLKKNTRL; LKKNTRLK; KKNTRLKK; KNTRLKKP; NTRLKKPA; TRLKKPAN; RLKKPANP; LKKPANPG; KKPANPGE; KPANPGEN; PANPGENI; ANPGENIQ; NPGENIQN; PGENIQNF; GENIQNFK; ENIQNFKD; NIQNFKDK; IQNFKDKS; QNFKDKSG; NFKDKSGD; FKDKSGDL; KDKSGDLG; DKSGDLGA; KSGDLGAS; SGDLGASD; GDLGASDE; DLGASDEK; LGASDEKF; GASDEKFM; ASDEKFMG; SDEKFMGT; DEKFMGTT; EKFMGTTA; KFMGTTAS; FMGTTASE; MGTTASEL; GTTASELK; TTASELKA; TASELKAI; ASELKAIG; SELKAIGK; ELKAIGKE; LKAIGKEL; KAIGKELE; AIGKELED; IGKELEDR; GKELEDRK; KELEDRKN; ELEDRKNQ; LEDRKNQY; EDRKNQYD; DRKNQYDI; RKNQYDIQ; KNQYDIQI; NQYDIQIA; QYDIQIAK; YDIQIAKI; DIQIAKIT; IQIAKITN; QIAKITNE; IAKITNEE; AKITNEES; KITNEESN; ITNEESNL; TNEESNLL; NEESNLLD; EESNLLDT; ESNLLDTY; SNLLDTYI; NLLDTYIR; LLDTYIRA; LDTYIRAY; DTYIRAYE; TYIRAYEL; YIRAYELA; IRAYELAN; RAYELANE; AYELANEN; YELANENE; ELANENEK; LANENEKM; ANENEKML; NENEKMLL; ENEKMLLK; NEKMLLKR; EKMLLKRF; KMLLKRFL; MLLKRFLL; LLKRFLLS; LKRFLLSS; KRFLLSSL; RFLLSSLD; FLLSSLDY; LLSSLDYK; LSSLDYKK; SSLDYKKE; SLDYKKEN; LDYKKENI; DYKKENIE; YKKENIET; KKENIETL; KENIETLK; ENIETLKE; NIETLKEI; IETLKEIL; ETLKEILE; TLKEILEK; LKEILEKL; KEILEKLI; EILEKLIN; ILEKLINN; LEKLINNY; EKLINNYE; KLINNYEN; LINNYEND; INNYENDP; NNYENDPK; NYENDPKI; YENDPKIA; ENDPKIAA; NDPKIAAN; DPKIAANF; PKIAANFL; KIAANFLY; IAANFLYR; AANFLYRI; ANFLYRIA; NFLYRIAL; FLYRIALD; LYRIALDI; YRIALDIQ; RIALDIQL; IALDIQLK; ALDIQLKL; LDIQLKLE; DIQLKLEK; IQLKLEKH; QLKLEKHL; LKLEKHLK; KLEKHLKS; LEKHLKSI; EKHLKSIN; KHLKSINE; HLKSINEK; LKSINEKL; KSINEKLD; SINEKLDT; INEKLDTL; NEKLDTLS; EKLDTLSK; KLDTLSKE; LDTLSKEN; DTLSKENS; TLSKENSK; LSKENSKE; SKENSKED; KENSKEDL; ENSKEDLE; NSKEDLEA; SKEDLEAL; KEDLEALL;

EDLEALLE; DLEALLEQ; LEALLEQV; EALLEQVK; ALLEQVKS; LLEQVKSA; LEQVKSAL; EQVKSALQ; QVKSALQL; VKSALQLQ; KSALQLQE; SALQLQEK; ALQLQEKF; LQLQEKFK; QLQEKFKK; LQEKFKKT; QEKFKKTL; EKFKKTLN; KFKKTLNK; FKKTLNKT; KKTLNKTL; KTLNKTLE; TLNKTLED; LNKTLEDY; NKTLEDYR; KTLEDYRK; TLEDYRKN; LEDYRKNT; EDYRKNTN; DYRKNTNN; YRKNTNNI; RKNTNNIQ; KNTNNIQE; NTNNIQEN; TNNIQENK; NNIQENKV; NIQENKVL; IQENKVLA; QENKVLAE; ENKVLAEH; NKVLAEHF; KVLAEHFN; VLAEHFNK; LAEHFNKY; AEHFNKYY; EHFNKYYK; HFNKYYKD; FNKYYKDS; NKYYKDSD; KYYKDSDS; YYKDSDSL; YKDSDSLQ; KDSDSLQS; DSDSLQSA; SDSLQSAF; DSLQSAFY;

9 mers:
MKKAKLNII; KKAKLNIIK; KAKLNIIKI; AKLNIIKIN; KLNIIKINI; LNIIKINII; NIIKINIIT; IIKINIITM; IKINIITMI; KINIITMIL; INIITMILT; NIITMILTL; IITMILTLI; ITMILTLIC; TMILTLICI; MILTLICIS; ILTLICISC; LTLICISCA; TLICISCAP; LICISCAPF; ICISCAPFN; CISCAPFNK; ISCAPFNKI; SCAPFNKIN; CAPFNKINP; APFNKINPK; PFNKINPKA; FNKINPKAN; NKINPKANE; KINPKANEN; INPKANENT; NPKANENTK; PKANENTKL; KANENTKLK; ANENTKLKK; NENTKLKKN; ENTKLKKNT; NTKLKKNTR; TKLKKNTRL; KLKKNTRLK; LKKNTRLKK; KKNTRLKKP; KNTRLKKPA; NTRLKKPAN; TRLKKPANP; RLKKPANPG; LKKPANPGE; KKPANPGEN; KPANPGENI; PANPGENIQ; ANPGENIQN; NPGENIQNF; PGENIQNFK; GENIQNFKD; ENIQNFKDK; NIQNFKDKS; IQNFKDKSG; QNFKDKSGD; NFKDKSGDL; FKDKSGDLG; KDKSGDLGA; DKSGDLGAS; KSGDLGASD; SGDLGASDE; GDLGASDEK; DLGASDEKF; LGASDEKFM; GASDEKFMG; ASDEKFMGT; SDEKFMGTT; DEKFMGTTA; EKFMGTTAS; KFMGTTASE; FMGTTASEL; MGTTASELK; GTTASELKA; TTASELKAI; TASELKAIG; ASELKAIGK; SELKAIGKE; ELKAIGKEL; LKAIGKELE; KAIGKELED; AIGKELEDR; IGKELEDRK; GKELEDRKN; KELEDRKNQ; ELEDRKNQY; LEDRKNQYD; EDRKNQYDI; DRKNQYDIQ; RKNQYDIQI; KNQYDIQIA; NQYDIQIAK; QYDIQIAKI; YDIQIAKIT; DIQIAKITN; IQIAKITNE; QIAKITNEE; IAKITNEES; AKITNEESN; KITNEESNL; ITNEESNLL; TNEESNLLD; NEESNLLDT; EESNLLDTY; ESNLLDTYI; SNLLDTYIR; NLLDTYIRA; LLDTYIRAY; LDTYIRAYE; DTYIRAYEL; TYIRAYELA; YIRAYELAN; IRAYELANE; RAYELANEN; AYELANENE; YELANENEK; ELANENEKM; LANENEKML; ANENEKMLL; NENEKMLLK; ENEKMLLKR; NEKMLLKRF; EKMLLKRFL; KMLLKRFLL; MLLKRFLLS; LLKRFLLSS; LKRFLLSSL; KRFLLSSLD; RFLLSSLDY; FLLSSLDYK; LLSSLDYKK; LSSLDYKKE; SSLDYKKEN; SLDYKKENI; LDYKKENIE; DYKKENIET; YKKENIETL; KKENIETLK; KENIETLKE; ENIETLKEI; NIETLKEIL; IETLKEILE; ETLKEILEK; TLKEILEKL; LKEILEKLI; KEILEKLIN; EILEKLINN; ILEKLINNY; LEKLINNYE; EKLINNYEN; KLINNYEND; LINNYENDP; INNYENDPK; NNYENDPKI; NYENDPKIA; YENDPKIAA; ENDPKIAAN; NDPKIAANF; DPKIAANFL; PKIAANFLY; KIAANFLYR; IAANFLYRI; AANFLYRIA; ANFLYRIAL; NFLYRIALD; FLYRIALDI; LYRIALDIQ; YRIALDIQL; RIALDIQLK; IALDIQLKL; ALDIQLKLE; LDIQLKLEK; DIQLKLEKH; IQLKLEKHL; QLKLEKHLK; LKLEKHLKS; KLEKHLKSI; LEKHLKSIN; EKHLKSINE; KHLKSINEK; HLKSINEKL; LKSINEKLD; KSINEKLDT;

	SINEKLDTL; INEKLDTLS; NEKLDTLSK; EKLDTLSKE; KLDTLSKEN; LDTLSKENS; DTLSKENSK; TLSKENSKE; LSKENSKED; SKENSKEDL; KENSKEDLE; ENSKEDLEA; NSKEDLEAL; SKEDLEALL; KEDLEALLE; EDLEALLEQ; DLEALLEQV; LEALLEQVK; EALLEQVKS; ALLEQVKSA; LLEQVKSAL; LEQVKSALQ; EQVKSALQL; QVKSALQLQ; VKSALQLQE; KSALQLQEK; SALQLQEKF; ALQLQEKFK; LQLQEKFKK; QLQEKFKKT; LQEKFKKTL; QEKFKKTLN; EKFKKTLNK; KFKKTLNKT; FKKTLNKTL; KKTLNKTLE; KTLNKTLED; TLNKTLEDY; LNKTLEDYR; NKTLEDYRK; KTLEDYRKN; TLEDYRKNT; LEDYRKNTN; EDYRKNTNN; DYRKNTNNI; YRKNTNNIQ; RKNTNNIQE; KNTNNIQEN; NTNNIQENK; TNNIQENKV; NNIQENKVL; NIQENKVLA; IQENKVLAE; QENKVLAEH; ENKVLAEHF; NKVLAEHFN; KVLAEHFNK; VLAEHFNKY; LAEHFNKYY; AEHFNKYYK; EHFNKYYKD; HFNKYYKDS; FNKYYKDSD; NKYYKDSDS; KYYKDSDSL; YYKDSDSLQ; YKDSDSLQS; KDSDSLQSA; DSDSLQSAF; SDSLQSAFY; 10 mers: MKKAKLNIIK; KKAKLNIIKI; KAKLNIIKIN; AKLNIIKINI; KLNIIKINII; LNIIKINIIT; NIIKINIITM; IIKINIITMI; IKINIITMIL; KINIITMILT; INIITMILTL; NIITMILTLI; IITMILTLIC; ITMILTLICI; TMILTLICIS; MILTLICISC; ILTLICISCA; LTLICISCAP; TLICISCAPF; LICISCAPFN; ICISCAPFNK; CISCAPFNKI; ISCAPFNKIN; SCAPFNKINP; CAPFNKINPK; APFNKINPKA; PFNKINPKAN; FNKINPKANE; NKINPKANEN; KINPKANENT; INPKANENTK; NPKANENTKL; PKANENTKLK; KANENTKLKK; ANENTKLKKN; NENTKLKKNT; ENTKLKKNTR; NTKLKKNTRL; TKLKKNTRLK; KLKKNTRLKK; LKKNTRLKKP; KKNTRLKKPA; KNTRLKKPAN; NTRLKKPANP; TRLKKPANPG; RLKKPANPGE; LKKPANPGEN; KKPANPGENI; KPANPGENIQ; PANPGENIQN; ANPGENIQNF; NPGENIQNFK; PGENIQNFKD; GENIQNFKDK; ENIQNFKDKS; NIQNFKDKSG; IQNFKDKSGD; QNFKDKSGDL; NFKDKSGDLG; FKDKSGDLGA; KDKSGDLGAS; DKSGDLGASD; KSGDLGASDE; SGDLGASDEK; GDLGASDEKF; DLGASDEKFM; LGASDEKFMG; GASDEKFMGT; ASDEKFMGTT; SDEKFMGTTA; DEKFMGTTAS; EKFMGTTASE; KFMGTTASEL; FMGTTASELK; MGTTASELKA; GTTASELKAI; TTASELKAIG; TASELKAIGK; ASELKAIGKE; SELKAIGKEL; ELKAIGKELE; LKAIGKELED; KAIGKELEDR; AIGKELEDRK; IGKELEDRKN; GKELEDRKNQ; KELEDRKNQY; ELEDRKNQYD; LEDRKNQYDI; EDRKNQYDIQ; DRKNQYDIQI; RKNQYDIQIA; KNQYDIQIAK; NQYDIQIAKI; QYDIQIAKIT; YDIQIAKITN; DIQIAKITNE; IQIAKITNEE; QIAKITNEES; IAKITNEESN; AKITNEESNL; KITNEESNLL; ITNEESNLLD; TNEESNLLDT; NEESNLLDTY; EESNLLDTYI; ESNLLDTYIR; SNLLDTYIRA; NLLDTYIRAY; LLDTYIRAYE; LDTYIRAYEL; DTYIRAYELA; TYIRAYELAN; YIRAYELANE; IRAYELANEN; RAYELANENE; AYELANENEK; YELANENEKM; ELANENEKML; LANENEKMLL; ANENEKMLLK; NENEKMLLKR; ENEKMLLKRF; NEKMLLKRFL; EKMLLKRFLL; KMLLKRFLLS; MLLKRFLLSS; LLKRFLLSSL; LKRFLLSSLD; KRFLLSSLDY; RFLLSSLDYK; FLLSSLDYKK; LLSSLDYKKE; LSSLDYKKEN; SSLDYKKENI; SLDYKKENIE; LDYKKENIET; DYKKENIETL; YKKENIETLK; KKENIETLKE;

KENIETLKEI; ENIETLKEIL; NIETLKEILE; IETLKEILEK;
ETLKEILEKL; TLKEILEKLI; LKEILEKLIN; KEILEKLINN;
EILEKLINNY; ILEKLINNYE; LEKLINNYEN; EKLINNYEND;
KLINNYENDP; LINNYENDPK; INNYENDPKI; NNYENDPKIA;
NYENDPKIAA; YENDPKIAAN; ENDPKIAANF; NDPKIAANFL;
DPKIAANFLY; PKIAANFLYR; KIAANFLYRI; IAANFLYRIA;
AANFLYRIAL; ANFLYRIALD; NFLYRIALDI; FLYRIALDIQ;
LYRIALDIQL; YRIALDIQLK; RIALDIQLKL; IALDIQLKLE;
ALDIQLKLEK; LDIQLKLEKH; DIQLKLEKHL; IQLKLEKHLK;
QLKLEKHLKS; LKLEKHLKSI; KLEKHLKSIN; LEKHLKSINE;
EKHLKSINEK; KHLKSINEKL; HLKSINEKLD; LKSINEKLDT;
KSINEKLDTL; SINEKLDTLS; INEKLDTLSK; NEKLDTLSKE;
EKLDTLSKEN; KLDTLSKENS; LDTLSKENSK; DTLSKENSKE;
TLSKENSKED; LSKENSKEDL; SKENSKEDLE; KENSKEDLEA;
ENSKEDLEAL; NSKEDLEALL; SKEDLEALLE; KEDLEALLEQ;
EDLEALLEQV; DLEALLEQVK; LEALLEQVKS; EALLEQVKSA;
ALLEQVKSAL; LLEQVKSALQ; LEQVKSALQL; EQVKSALQLQ;
QVKSALQLQE; VKSALQLQEK; KSALQLQEKF; SALQLQEKFK;
ALQLQEKFKK; LQLQEKFKKT; QLQEKFKKTL; LQEKFKKTLN;
QEKFKKTLNK; EKFKKTLNKT; KFKKTLNKTL; FKKTLNKTLE;
KKTLNKTLED; KTLNKTLEDY; TLNKTLEDYR; LNKTLEDYRK;
NKTLEDYRKN; KTLEDYRKNT; TLEDYRKNTN; LEDYRKNTNN;
EDYRKNTNNI; DYRKNTNNIQ; YRKNTNNIQE; RKNTNNIQEN;
KNTNNIQENK; NTNNIQENKV; TNNIQENKVL; NNIQENKVLA;
NIQENKVLAE; IQENKVLAEH; QENKVLAEHF; ENKVLAEHFN;
NKVLAEHFNK; KVLAEHFNKY; VLAEHFNKYY; LAEHFNKYYK;
AEHFNKYYKD; EHFNKYYKDS; HFNKYYKDSD; FNKYYKDSDS;
NKYYKDSDSL; KYYKDSDSLQ; YYKDSDSLQS; YKDSDSLQSA;
KDSDSLQSAF; DSDSLQSAFY;

11 mers:
MKKAKLNIIKI; KKAKLNIIKIN; KAKLNIIKINI; AKLNIIKINII;
KLNIIKINIIT; LNIIKINIITM; NIIKINIITMI; IIKINIITMIL;
IKINIITMILT; KINIITMILTL; INIITMILTLI; NIITMILTLIC;
IITMILTLICI; ITMILTLICIS; TMILTLICISC; MILTLICISCA;
ILTLICISCAP; LTLICISCAPF; TLICISCAPFN; LICISCAPFNK;
ICISCAPFNKI; CISCAPFNKIN; ISCAPFNKINP; SCAPFNKINPK;
CAPFNKINPKA; APFNKINPKAN; PFNKINPKANE; FNKINPKANEN;
NKINPKANENT; KINPKANENTK; INPKANENTKL; NPKANENTKLK;
PKANENTKLKK; KANENTKLKKN; ANENTKLKKNT; NENTKLKKNTR;
ENTKLKKNTRL; NTKLKKNTRLK; TKLKKNTRLKK; KLKKNTRLKKP;
LKKNTRLKKPA; KKNTRLKKPAN; KNTRLKKPANP; NTRLKKPANPG;
TRLKKPANPGE; RLKKPANPGEN; LKKPANPGENI; KKPANPGENIQ;
KPANPGENIQN; PANPGENIQNF; ANPGENIQNFK; NPGENIQNFKD;
PGENIQNFKDK; GENIQNFKDKS; ENIQNFKDKSG; NIQNFKDKSGD;
IQNFKDKSGDL; QNFKDKSGDLG; NFKDKSGDLGA; FKDKSGDLGAS;
KDKSGDLGASD; DKSGDLGASDE; KSGDLGASDEK; SGDLGASDEKF;
GDLGASDEKFM; DLGASDEKFMG; LGASDEKFMGT; GASDEKFMGTT;
ASDEKFMGTTA; SDEKFMGTTAS; DEKFMGTTASE; EKFMGTTASEL;
KFMGTTASELK; FMGTTASELKA; MGTTASELKAI; GTTASELKAIG;
TTASELKAIGK; TASELKAIGKE; ASELKAIGKEL; SELKAIGKELE;

	ELKAIGKELED; LKAIGKELEDR; KAIGKELEDRK; AIGKELEDRKN; IGKELEDRKNQ; GKELEDRKNQY; KELEDRKNQYD; ELEDRKNQYDI; LEDRKNQYDIQ; EDRKNQYDIQI; DRKNQYDIQIA; RKNQYDIQIAK; KNQYDIQIAKI; NQYDIQIAKIT; QYDIQIAKITN; YDIQIAKITNE; DIQIAKITNEE; IQIAKITNEES; QIAKITNEESN; IAKITNEESNL; AKITNEESNLL; KITNEESNLLD; ITNEESNLLDT; TNEESNLLDTY; NEESNLLDTYI; EESNLLDTYIR; ESNLLDTYIRA; SNLLDTYIRAY; NLLDTYIRAYE; LLDTYIRAYEL; LDTYIRAYELA; DTYIRAYELAN; TYIRAYELANE; YIRAYELANEN; IRAYELANENE; RAYELANENEK; AYELANENEKM; YELANENEKML; ELANENEKMLL; LANENEKMLLK; ANENEKMLLKR; NENEKMLLKRF; ENEKMLLKRFL; NEKMLLKRFLL; EKMLLKRFLLS; KMLLKRFLLSS; MLLKRFLLSSL; LLKRFLLSSLD; LKRFLLSSLDY; KRFLLSSLDYK; RFLLSSLDYKK; FLLSSLDYKKE; LLSSLDYKKEN; LSSLDYKKENI; SSLDYKKENIE; SLDYKKENIET; LDYKKENIETL; DYKKENIETLK; YKKENIETLKE; KKENIETLKEI; KENIETLKEIL; ENIETLKEILE; NIETLKEILEK; IETLKEILEKL; ETLKEILEKLI; TLKEILEKLIN; LKEILEKLINN; KEILEKLINNY; EILEKLINNYE; ILEKLINNYEN; LEKLINNYEND; EKLINNYENDP; KLINNYENDPK; LINNYENDPKI; INNYENDPKIA; NNYENDPKIAA; NYENDPKIAAN; YENDPKIAANF; ENDPKIAANFL; NDPKIAANFLY; DPKIAANFLYR; PKIAANFLYRI; KIAANFLYRIA; IAANFLYRIAL; AANFLYRIALD; ANFLYRIALDI; NFLYRIALDIQ; FLYRIALDIQL; LYRIALDIQLK; YRIALDIQLKL; RIALDIQLKLE; IALDIQLKLEK; ALDIQLKLEKH; LDIQLKLEKHL; DIQLKLEKHLK; IQLKLEKHLKS; QLKLEKHLKSI; LKLEKHLKSIN; KLEKHLKSINE; LEKHLKSINEK; EKHLKSINEKL; KHLKSINEKLD; HLKSINEKLDT; LKSINEKLDTL; KSINEKLDTLS; SINEKLDTLSK; INEKLDTLSKE; NEKLDTLSKEN; EKLDTLSKENS; KLDTLSKENSK; LDTLSKENSKE; DTLSKENSKED; TLSKENSKEDL; LSKENSKEDLE; SKENSKEDLEA; KENSKEDLEAL; ENSKEDLEALL; NSKEDLEALLE; SKEDLEALLEQ; KEDLEALLEQV; EDLEALLEQVK; DLEALLEQVKS; LEALLEQVKSA; EALLEQVKSAL; ALLEQVKSALQ; LLEQVKSALQL; LEQVKSALQLQ; EQVKSALQLQE; QVKSALQLQEK; VKSALQLQEKF; KSALQLQEKFK; SALQLQEKFKK; ALQLQEKFKKT; LQLQEKFKKTL; QLQEKFKKTLN; LQEKFKKTLNK; QEKFKKTLNKT; EKFKKTLNKTL; KFKKTLNKTLE; FKKTLNKTLED; KKTLNKTLEDY; KTLNKTLEDYR; TLNKTLEDYRK; LNKTLEDYRKN; NKTLEDYRKNT; KTLEDYRKNTN; TLEDYRKNTNN; LEDYRKNTNNI; EDYRKNTNNIQ; DYRKNTNNIQE; YRKNTNNIQEN; RKNTNNIQENK; KNTNNIQENKV; NTNNIQENKVL; TNNIQENKVLA; NNIQENKVLAE; NIQENKVLAEH; IQENKVLAEHF; QENKVLAEHFN; ENKVLAEHFNK; NKVLAEHFNKY; KVLAEHFNKYY; VLAEHFNKYYK; LAEHFNKYYKD; AEHFNKYYKDS; EHFNKYYKDSD; HFNKYYKDSDS; FNKYYKDSDSL; NKYYKDSDSLQ; KYYKDSDSLQS; YYKDSDSLQSA; YKDSDSLQSAF; KDSDSLQSAFY;
Seq 37	SEQ ID NO 44899-45904/ 8 mers: MKKTKLNI; KKTKLNII; KTKLNIIK; TKLNIIKL; KLNIIKLN; LNIIKLNI; NIIKLNIL; IIKLNILT; IKLNILTT; KLNILTTT; LNILTTTL; NILTTTLT; ILTTTLTL; LTTTLTLI; TTTLTLIC; TTLTLICI; TLTLICIS; LTLICISC; TLICISCA; LICISCAV;

	ICISCAVN; CISCAVNK; ISCAVNKI; SCAVNKID; CAVNKIDP; AVNKIDPE; VNKIDPEP; NKIDPEPK; KIDPEPKS; IDPEPKSK; DPEPKSKT; PEPKSKTN; EPKSKTNK; PKSKTNKK; KSKTNKKE; SKTNKKEN; KTNKKENI; TNKKENIK; NKKENIKN; KKENIKNF; KENIKNFV; ENIKNFVN; NIKNFVNK; IKNFVNKF; KNFVNKFQ; NFVNKFQD; FVNKFQDL; VNKFQDLE; NKFQDLEP; KFQDLEPS; FQDLEPSK; QDLEPSKK; DLEPSKKQ; LEPSKKQN; EPSKKQNK; PSKKQNKD; SKKQNKDL; KKQNKDLE; KQNKDLEP; QNKDLEPL; NKDLEPLR; KDLEPLRE; DLEPLREK; LEPLREKY; EPLREKYP; PLREKYPE; LREKYPEA; REKYPEAT; EKYPEATA; KYPEATAS; YPEATASK; PEATASKL; EATASKLE; ATASKLET; TASKLETT; ASKLETTL; SKLETTLK; KLETTLKI; LETTLKIL; ETTLKILE; TTLKILEA; TLKILEAQ; LKILEAQK; KILEAQKE; ILEAQKEK; LEAQKEKE; EAQKEKEN; AQKEKENI; QKEKENIE; KEKENIEI; EKENIEIA; KENIEIAK; ENIEIAKI; NIEIAKID; IEIAKIDN; EIAKIDNT; IAKIDNTQ; AKIDNTQI; KIDNTQID; IDNTQIDF; DNTQIDFL; NTQIDFLK; TQIDFLKT; QIDFLKTF; IDFLKTFK; DFLKTFKT; FLKTFKTD; LKTFKTDP; KTFKTDPH; TFKTDPHD; FKTDPHDS; KTDPHDSL; TDPHDSLP; DPHDSLPE; PHDSLPED; HDSLPEDE; DSLPEDEK; SLPEDEKM; LPEDEKMQ; PEDEKMQM; EDEKMQMK; DEKMQMKK; EKMQMKKI; KMQMKKII; MQMKKIIY; QMKKIIYS; MKKIIYSS; KKIIYSSL; KIIYSSLN; IIYSSLNY; IYSSLNYE; YSSLNYET; SSLNYETE; SLNYETEK; LNYETEKI; NYETEKIK; YETEKIKI; ETEKIKIL; TEKIKILQ; EKIKILQE; KIKILQEI; IKILQEIL; KILQEILE; ILQEILEK; LQEILEKL; QEILEKLD; EILEKLDK; ILEKLDKN; LEKLDKNL; EKLDKNLQ; KLDKNLQH; LDKNLQHK; DKNLQHKK; KNLQHKKI; NLQHKKIA; LQHKKIAK; QHKKIAKN; HKKIAKNF; KKIAKNFI; KIAKNFIY; IAKNFIYD; AKNFIYDI; KNFIYDIP; NFIYDIPI; FIYDIPII; IYDIPIII; YDIPIIIQ; DIPIIIQS; IPIIIQSR; PIIIQSRL; IIIQSRLD; IIQSRLDI; IQSRLDII; QSRLDIIS; SRLDIISK; RLDIISKV; LDIISKVI; DIISKVIK; IISKVIKN; ISKVIKNP; SKVIKNPI; KVIKNPIK; VIKNPIKD; IKNPIKDE; KNPIKDEL; NPIKDELQ; PIKDELQI; IKDELQIL; KDELQILN; DELQILNQ; ELQILNQK; LQILNQKE; QILNQKEI; ILNQKEIE; LNQKEIEE; NQKEIEEL; QKEIEELL; KEIEELLM; EIEELLMR; IEELLMRI; EELLMRIE; ELLMRIES; LLMRIESE; LMRIESEL; MRIESELK; RIESELKI; IESELKIK; ESELKIKE; SELKIKEN; ELKIKENF; LKIKENFK; KIKENFKK; IKENFKKA; KENFKKAL; ENFKKALN; NFKKALNK; FKKALNKT; KKALNKTI; KALNKTID; ALNKTIDA; LNKTIDAY; NKTIDAYN; KTIDAYNQ; TIDAYNQD; IDAYNQDS; DAYNQDSE; AYNQDSEN; YNQDSENI; NQDSENIK; QDSENIKT; DSENIKTS; SENIKTSA; ENIKTSAE; NIKTSAEQ; IKTSAEQL; KTSAEQLE; TSAEQLEK; SAEQLEKH; AEQLEKHI; EQLEKHIN; QLEKHINE; LEKHINEN; EKHINENY; KHINENYK; HINENYKE; INENYKEF; NENYKEFN; ENYKEFNS; NYKEFNSL; YKEFNSLK; KEFNSLKP; EFNSLKPI; FNSLKPIY; 9 mers: MKKTKLNII; KKTKLNIIK; KTKLNIIKL; TKLNIIKLN; KLNIIKLNI; LNIIKLNIL; NIIKLNILT; IIKLNILTT; IKLNILTTT; KLNILTTTL;

	LNILTTTLT; NILTTTLTL; ILTTTLTLI; LTTTLTLIC; TTTLTLICI; TTLTLICIS; TLTLICISC; LTLICISCA; TLICISCAV; LICISCAVN; ICISCAVNK; CISCAVNKI; ISCAVNKID; SCAVNKIDP; CAVNKIDPE; AVNKIDPEP; VNKIDPEPK; NKIDPEPKS; KIDPEPKSK; IDPEPKSKT; DPEPKSKTN; PEPKSKTNK; EPKSKTNKK; PKSKTNKKE; KSKTNKKEN; SKTNKKENI; KTNKKENIK; TNKKENIKN; NKKENIKNF; KKENIKNFV; KENIKNFVN; ENIKNFVNK; NIKNFVNKF; IKNFVNKFQ; KNFVNKFQD; NFVNKFQDL; FVNKFQDLE; VNKFQDLEP; NKFQDLEPS; KFQDLEPSK; FQDLEPSKK; QDLEPSKKQ; DLEPSKKQN; LEPSKKQNK; EPSKKQNKD; PSKKQNKDL; SKKQNKDLE; KKQNKDLEP; KQNKDLEPL; QNKDLEPLR; NKDLEPLRE; KDLEPLREK; DLEPLREKY; LEPLREKYP; EPLREKYPE; PLREKYPEA; LREKYPEAT; REKYPEATA; EKYPEATAS; KYPEATASK; YPEATASKL; PEATASKLE; EATASKLET; ATASKLETT; TASKLETTL; ASKLETTLK; SKLETTLKI; KLETTLKIL; LETTLKILE; ETTLKILEA; TTLKILEAQ; TLKILEAQK; LKILEAQKE; KILEAQKEK; ILEAQKEKE; LEAQKEKEN; EAQKEKENI; AQKEKENIE; QKEKENIEI; KEKENIEIA; EKENIEIAK; KENIEIAKI; ENIEIAKID; NIEIAKIDN; IEIAKIDNT; EIAKIDNTQ; IAKIDNTQI; AKIDNTQID; KIDNTQIDF; IDNTQIDFL; DNTQIDFLK; NTQIDFLKT; TQIDFLKTF; QIDFLKTFK; IDFLKTFKT; DFLKTFKTD; FLKTFKTDP; LKTFKTDPH; KTFKTDPHD; TFKTDPHDS; FKTDPHDSL; KTDPHDSLP; TDPHDSLPE; DPHDSLPED; PHDSLPEDE; HDSLPEDEK; DSLPEDEKM; SLPEDEKMQ; LPEDEKMQM; PEDEKMQMK; EDEKMQMKK; DEKMQMKKI; EKMQMKKII; KMQMKKIIY; MQMKKIIYS; QMKKIIYSS; MKKIIYSSL; KKIIYSSLN; KIIYSSLNY; IIYSSLNYE; IYSSLNYET; YSSLNYETE; SSLNYETEK; SLNYETEKI; LNYETEKIK; NYETEKIKI; YETEKIKIL; ETEKIKILQ; TEKIKILQE; EKIKILQEI; KIKILQEIL; IKILQEILE; KILQEILEK; ILQEILEKL; LQEILEKLD; QEILEKLDK; EILEKLDKN; ILEKLDKNL; LEKLDKNLQ; EKLDKNLQH; KLDKNLQHK; LDKNLQHKK; DKNLQHKKI; KNLQHKKIA; NLQHKKIAK; LQHKKIAKN; QHKKIAKNF; HKKIAKNFI; KKIAKNFIY; KIAKNFIYD; IAKNFIYDI; AKNFIYDIP; KNFIYDIPI; NFIYDIPII; FIYDIPIII; IYDIPIIIQ; YDIPIIIQS; DIPIIIQSR; IPIIIQSRL; PIIIQSRLD; IIIQSRLDI; IIQSRLDII; IQSRLDIIS; QSRLDIISK; SRLDIISKV; RLDIISKVI; LDIISKVIK; DIISKVIKN; IISKVIKNP; ISKVIKNPI; SKVIKNPIK; KVIKNPIKD; VIKNPIKDE; IKNPIKDEL; KNPIKDELQ; NPIKDELQI; PIKDELQIL; IKDELQILN; KDELQILNQ; DELQILNQK; ELQILNQKE; LQILNQKEI; QILNQKEIE; ILNQKEIEE; LNQKEIEEL; NQKEIEELL; QKEIEELLM; KEIEELLMR; EIEELLMRI; IEELLMRIE; EELLMRIES; ELLMRIESE; LLMRIESEL; LMRIESELK; MRIESELKI; RIESELKIK; IESELKIKE; ESELKIKEN; SELKIKENF; ELKIKENFK; LKIKENFKK; KIKENFKKA; IKENFKKAL; KENFKKALN; ENFKKALNK; NFKKALNKT; FKKALNKTI; KKALNKTID; KALNKTIDA; ALNKTIDAY; LNKTIDAYN; NKTIDAYNQ; KTIDAYNQD; TIDAYNQDS; IDAYNQDSE; DAYNQDSEN; AYNQDSENI; YNQDSENIK; NQDSENIKT; QDSENIKTS; DSENIKTSA; SENIKTSAE; ENIKTSAEQ; NIKTSAEQL; IKTSAEQLE; KTSAEQLEK; TSAEQLEKH; SAEQLEKHI; AEQLEKHIN; EQLEKHINE; QLEKHINEN; LEKHINENY; EKHINENYK; KHINENYKE; HINENYKEF; INENYKEFN; NENYKEFNS; ENYKEFNSL; NYKEFNSLK; YKEFNSLKP; KEFNSLKPI; EFNSLKPIY; 10 mers:

	MKKTKLNIIK; KKTKLNIIKL; KTKLNIIKLN; TKLNIIKLNI; KLNIIKLNIL; LNIIKLNILT; NIIKLNILTT; IIKLNILTTT; IKLNILTTTL; KLNILTTTLT; LNILTTTLTL; NILTTTLTLI; ILTTTLTLIC; LTTTLTLICI; TTTLTLICIS; TTLTLICISC; TLTLICISCA; LTLICISCAV; TLICISCAVN; LICISCAVNK; ICISCAVNKI; CISCAVNKID; ISCAVNKIDP; SCAVNKIDPE; CAVNKIDPEP; AVNKIDPEPK; VNKIDPEPKS; NKIDPEPKSK; KIDPEPKSKT; IDPEPKSKTN; DPEPKSKTNK; PEPKSKTNKK; EPKSKTNKKE; PKSKTNKKEN; KSKTNKKENI; SKTNKKENIK; KTNKKENIKN; TNKKENIKNF; NKKENIKNFV; KKENIKNFVN; KENIKNFVNK; ENIKNFVNKF; NIKNFVNKFQ; IKNFVNKFQD; KNFVNKFQDL; NFVNKFQDLE; FVNKFQDLEP; VNKFQDLEPS; NKFQDLEPSK; KFQDLEPSKK; FQDLEPSKKQ; QDLEPSKKQN; DLEPSKKQNK; LEPSKKQNKD; EPSKKQNKDL; PSKKQNKDLE; SKKQNKDLEP; KKQNKDLEPL; KQNKDLEPLR; QNKDLEPLRE; NKDLEPLREK; KDLEPLREKY; DLEPLREKYP; LEPLREKYPE; EPLREKYPEA; PLREKYPEAT; LREKYPEATA; REKYPEATAS; EKYPEATASK; KYPEATASKL; YPEATASKLE; PEATASKLET; EATASKLETT; ATASKLETTL; TASKLETTLK; ASKLETTLKI; SKLETTLKIL; KLETTLKILE; LETTLKILEA; ETTLKILEAQ; TTLKILEAQK; TLKILEAQKE; LKILEAQKEK; KILEAQKEKE; ILEAQKEKEN; LEAQKEKENI; EAQKEKENIE; AQKEKENIEI; QKEKENIEIA; KEKENIEIAK; EKENIEIAKI; KENIEIAKID; ENIEIAKIDN; NIEIAKIDNT; IEIAKIDNTQ; EIAKIDNTQI; IAKIDNTQID; AKIDNTQIDF; KIDNTQIDFL; IDNTQIDFLK; DNTQIDFLKT; NTQIDFLKTF; TQIDFLKTFK; QIDFLKTFKT; IDFLKTFKTD; DFLKTFKTDP; FLKTFKTDPH; LKTFKTDPHD; KTFKTDPHDS; TFKTDPHDSL; FKTDPHDSLP; KTDPHDSLPE; TDPHDSLPED; DPHDSLPEDE; PHDSLPEDEK; HDSLPEDEKM; DSLPEDEKMQ; SLPEDEKMQM; LPEDEKMQMK; PEDEKMQMKK; EDEKMQMKKI; DEKMQMKKII; EKMQMKKIIY; KMQMKKIIYS; MQMKKIIYSS; QMKKIIYSSL; MKKIIYSSLN; KKIIYSSLNY; KIIYSSLNYE; IIYSSLNYET; IYSSLNYETE; YSSLNYETEK; SSLNYETEKI; SLNYETEKIK; LNYETEKIKI; NYETEKIKIL; YETEKIKILQ; ETEKIKILQE; TEKIKILQEI; EKIKILQEIL; KIKILQEILE; IKILQEILEK; KILQEILEKL; ILQEILEKLD; LQEILEKLDK; QEILEKLDKN; EILEKLDKNL; ILEKLDKNLQ; LEKLDKNLQH; EKLDKNLQHK; KLDKNLQHKK; LDKNLQHKKI; DKNLQHKKIA; KNLQHKKIAK; NLQHKKIAKN; LQHKKIAKNF; QHKKIAKNFI; HKKIAKNFIY; KKIAKNFIYD; KIAKNFIYDI; IAKNFIYDIP; AKNFIYDIPI; KNFIYDIPII; NFIYDIPIII; FIYDIPIIIQ; IYDIPIIIQS; YDIPIIIQSR; DIPIIIQSRL; IPIIIQSRLD; PIIIQSRLDI; IIIQSRLDII; IIQSRLDIIS; IQSRLDIISK; QSRLDIISKV; SRLDIISKVI; RLDIISKVIK; LDIISKVIKN; DIISKVIKNP; IISKVIKNPI; ISKVIKNPIK; SKVIKNPIKD; KVIKNPIKDE; VIKNPIKDEL; IKNPIKDELQ; KNPIKDELQI; NPIKDELQIL; PIKDELQILN; IKDELQILNQ; KDELQILNQK; DELQILNQKE; ELQILNQKEI; LQILNQKEIE; QILNQKEIEE; ILNQKEIEEL; LNQKEIEELL; NQKEIEELLM; QKEIEELLMR; KEIEELLMRI; EIEELLMRIE; IEELLMRIES; EELLMRIESE; ELLMRIESEL; LLMRIESELK; LMRIESELKI;

	MRIESELKIK; RIESELKIKE; IESELKIKEN; ESELKIKENF; SELKIKENFK; ELKIKENFKK; LKIKENFKKA; KIKENFKKAL; IKENFKKALN; KENFKKALNK; ENFKKALNKT; NFKKALNKTI; FKKALNKTID; KKALNKTIDA; KALNKTIDAY; ALNKTIDAYN; LNKTIDAYNQ; NKTIDAYNQD; KTIDAYNQDS; TIDAYNQDSE; IDAYNQDSEN; DAYNQDSENI; AYNQDSENIK; YNQDSENIKT; NQDSENIKTS; QDSENIKTSA; DSENIKTSAE; SENIKTSAEQ; ENIKTSAEQL; NIKTSAEQLE; IKTSAEQLEK; KTSAEQLEKH; TSAEQLEKHI; SAEQLEKHIN; AEQLEKHINE; EQLEKHINEN; QLEKHINENY; LEKHINENYK; EKHINENYKE; KHINENYKEF; HINENYKEFN; INENYKEFNS; NENYKEFNSL; ENYKEFNSLK; NYKEFNSLKP; YKEFNSLKPI; KEFNSLKPIY; 11 mers: MKKTKLNIIKL; KKTKLNIIKLN; KTKLNIIKLNI; TKLNIIKLNIL; KLNIIKLNILT; LNIIKLNILTT; NIIKLNILTTT; IIKLNILTTTL; IKLNILTTTLT; KLNILTTTLTL; LNILTTTLTLI; NILTTTLTLIC; ILTTTLTLICI; LTTTLTLICIS; TTTLTLICISC; TTLTLICISCA; TLTLICISCAV; LTLICISCAVN; TLICISCAVNK; LICISCAVNKI; ICISCAVNKID; CISCAVNKIDP; ISCAVNKIDPE; SCAVNKIDPEP; CAVNKIDPEPK; AVNKIDPEPKS; VNKIDPEPKSK; NKIDPEPKSKT; KIDPEPKSKTN; IDPEPKSKTNK; DPEPKSKTNKK; PEPKSKTNKKE; EPKSKTNKKEN; PKSKTNKKENI; KSKTNKKENIK; SKTNKKENIKN; KTNKKENIKNF; TNKKENIKNFV; NKKENIKNFVN; KKENIKNFVNK; KENIKNFVNKF; ENIKNFVNKFQ; NIKNFVNKFQD; IKNFVNKFQDL; KNFVNKFQDLE; NFVNKFQDLEP; FVNKFQDLEPS; VNKFQDLEPSK; NKFQDLEPSKK; KFQDLEPSKKQ; FQDLEPSKKQN; QDLEPSKKQNK; DLEPSKKQNKD; LEPSKKQNKDL; EPSKKQNKDLE; PSKKQNKDLEP; SKKQNKDLEPL; KKQNKDLEPLR; KQNKDLEPLRE; QNKDLEPLREK; NKDLEPLREKY; KDLEPLREKYP; DLEPLREKYPE; LEPLREKYPEA; EPLREKYPEAT; PLREKYPEATA; LREKYPEATAS; REKYPEATASK; EKYPEATASKL; KYPEATASKLE; YPEATASKLET; PEATASKLETT; EATASKLETTL; ATASKLETTLK; TASKLETTLKI; ASKLETTLKIL; SKLETTLKILE; KLETTLKILEA; LETTLKILEAQ; ETTLKILEAQK; TTLKILEAQKE; TLKILEAQKEK; LKILEAQKEKE; KILEAQKEKEN; ILEAQKEKENI; LEAQKEKENIE; EAQKEKENIEI; AQKEKENIEIA; QKEKENIEIAK; KEKENIEIAKI; EKENIEIAKID; KENIEIAKIDN; ENIEIAKIDNT; NIEIAKIDNTQ; IEIAKIDNTQI; EIAKIDNTQID; IAKIDNTQIDF; AKIDNTQIDFL; KIDNTQIDFLK; IDNTQIDFLKT; DNTQIDFLKTF; NTQIDFLKTFK; TQIDFLKTFKT; QIDFLKTFKTD; IDFLKTFKTDP; DFLKTFKTDPH; FLKTFKTDPHD; LKTFKTDPHDS; KTFKTDPHDSL; TFKTDPHDSLP; FKTDPHDSLPE; KTDPHDSLPED; TDPHDSLPEDE; DPHDSLPEDEK; PHDSLPEDEKM; HDSLPEDEKMQ; DSLPEDEKMQM; SLPEDEKMQMK; LPEDEKMQMKK; PEDEKMQMKKI; EDEKMQMKKII; DEKMQMKKIIY; EKMQMKKIIYS; KMQMKKIIYSS; MQMKKIIYSSL; QMKKIIYSSLN; MKKIIYSSLNY; KKIIYSSLNYE; KIIYSSLNYET; IIYSSLNYETE; IYSSLNYETEK; YSSLNYETEKI; SSLNYETEKIK; SLNYETEKIKI; LNYETEKIKIL; NYETEKIKILQ; YETEKIKILQE; ETEKIKILQEI; TEKIKILQEIL; EKIKILQEILE; KIKILQEILEK; IKILQEILEKL; KILQEILEKLD; ILQEILEKLDK; LQEILEKLDKN; QEILEKLDKNL; EILEKLDKNLQ; ILEKLDKNLQH;

	LEKLDKNLQHK; EKLDKNLQHKK; KLDKNLQHKKI; LDKNLQHKKIA; DKNLQHKKIAK; KNLQHKKIAKN; NLQHKKIAKNF; LQHKKIAKNFI; QHKKIAKNFIY; HKKIAKNFIYD; KKIAKNFIYDI; KIAKNFIYDIP; IAKNFIYDIPI; AKNFIYDIPII; KNFIYDIPIII; NFIYDIPIIIQ; FIYDIPIIIQS; IYDIPIIIQSR; YDIPIIIQSRL; DIPIIIQSRLD; IPIIIQSRLDI; PIIIQSRLDII; IIIQSRLDIIS; IIQSRLDIISK; IQSRLDIISKV; QSRLDIISKVI; SRLDIISKVIK; RLDIISKVIKN; LDIISKVIKNP; DIISKVIKNPI; IISKVIKNPIK; ISKVIKNPIKD; SKVIKNPIKDE; KVIKNPIKDEL; VIKNPIKDELQ; IKNPIKDELQI; KNPIKDELQIL; NPIKDELQILN; PIKDELQILNQ; IKDELQILNQK; KDELQILNQKE; DELQILNQKEI; ELQILNQKEIE; LQILNQKEIEE; QILNQKEIEEL; ILNQKEIEELL; LNQKEIEELLM; NQKEIEELLMR; QKEIEELLMRI; KEIEELLMRIE; EIEELLMRIES; IEELLMRIESE; EELLMRIESEL; ELLMRIESELK; LLMRIESELKI; LMRIESELKIK; MRIESELKIKE; RIESELKIKEN; IESELKIKENF; ESELKIKENFK; SELKIKENFKK; ELKIKENFKKA; LKIKENFKKAL; KIKENFKKALN; IKENFKKALNK; KENFKKALNKT; ENFKKALNKTI; NFKKALNKTID; FKKALNKTIDA; KKALNKTIDAY; KALNKTIDAYN; ALNKTIDAYNQ; LNKTIDAYNQD; NKTIDAYNQDS; KTIDAYNQDSE; TIDAYNQDSEN; IDAYNQDSENI; DAYNQDSENIK; AYNQDSENIKT; YNQDSENIKTS; NQDSENIKTSA; QDSENIKTSAE; DSENIKTSAEQ; SENIKTSAEQL; ENIKTSAEQLE; NIKTSAEQLEK; IKTSAEQLEKH; KTSAEQLEKHI; TSAEQLEKHIN; SAEQLEKHINE; AEQLEKHINEN; EQLEKHINENY; QLEKHINENYK; LEKHINENYKE; EKHINENYKEF; KHINENYKEFN; HINENYKEFNS; INENYKEFNSL; NENYKEFNSLK; ENYKEFNSLKP; NYKEFNSLKPI; YKEFNSLKPIY;
Seq 38	SEQ ID NO 45905-46606/ 8 mers: MRILVGVC; RILVGVCI; ILVGVCII; LVGVCIIA; VGVCIIAL; GVCIIALA; VCIIALAL; CIIALALL; IIALALLG; IALALLGC; ALALLGCY; LALLGCYL; ALLGCYLP; LLGCYLPD; LGCYLPDN; GCYLPDNQ; CYLPDNQE; YLPDNQEQ; LPDNQEQA; PDNQEQAV; DNQEQAVQ; NQEQAVQT; QEQAVQTF; EQAVQTFF; QAVQTFFE; AVQTFFEN; VQTFFENS; QTFFENSE; TFFENSES; FFENSESS; FENSESSD; ENSESSDM; NSESSDMG; SESSDMGS; ESSDMGSD; SSDMGSDE; SDMGSDEI; DMGSDEIV; MGSDEIVT; GSDEIVTE; SDEIVTEG; DEIVTEGI; EIVTEGIF; IVTEGIFS; VTEGIFSS; TEGIFSSL; EGIFSSLK; GIFSSLKL; IFSSLKLY; FSSLKLYA; SSLKLYAS; SLKLYASE; LKLYASEH; KLYASEHR; LYASEHRL; YASEHRLL; ASEHRLLV; SEHRLLVE; EHRLLVEI; HRLLVEIK; RLLVEIKK; LLVEIKKT; LVEIKKTL; VEIKKTLI; EIKKTLIS; IKKTLISL; KKTLISLK; KTLISLKD; TLISLKDP; LISLKDPN; ISLKDPNY; SLKDPNYR; LKDPNYRG; KDPNYRGV; DPNYRGVV; PNYRGVVL; NYRGVVLP; YRGVVLPV; RGVVLPVS; GVVLPVSD; VVLPVSDY; VLPVSDYN; LPVSDYNE; PVSDYNEE; VSDYNEEY; SDYNEEYF; DYNEEYFN; YNEEYFNK; NEEYFNKF; EEYFNKFF; EYFNKFFL; YFNKFFLD; FNKFFLDL; NKFFLDLG; KFFLDLGS; FFLDLGSE; FLDLGSEQ; LDLGSEQS; DLGSEQSK; LGSEQSKD; GSEQSKDL; SEQSKDLI; EQSKDLIK; QSKDLIKL; SKDLIKLF; KDLIKLFI; DLIKLFIM; LIKLFIMV; IKLFIMVK; KLFIMVKN;

LFIMVKNE; FIMVKNEQ; IMVKNEQN; MVKNEQNN; VKNEQNNN;
KNEQNNNK; NEQNNNKF; EQNNNKFM; QNNNKFMR; NNNKFMRI;
NNKFMRIV; NKFMRIVR; KFMRIVRW; FMRIVRWL; MRIVRWLY;
RIVRWLYS; IVRWLYSC; VRWLYSCI; RWLYSCIE; WLYSCIEE;
LYSCIEEL; YSCIEELY; SCIEELYS; CIEELYSP; IEELYSPD;
EELYSPDI; ELYSPDIK; LYSPDIKY; YSPDIKYS; SPDIKYSG;
PDIKYSGE; DIKYSGEE; IKYSGEEG; KYSGEEGS; YSGEEGSP;
SGEEGSPE; GEEGSPEY; EEGSPEYY; EGSPEYYR; GSPEYYRN;
SPEYYRNM; PEYYRNMP; EYYRNMPR; YYRNMPRP; YRNMPRPT;
RNMPRPTA; NMPRPTAY; MPRPTAYQ; PRPTAYQQ; RPTAYQQY;
PTAYQQYL; TAYQQYLK; AYQQYLKV; YQQYLKVK; QQYLKVKR;
QYLKVKRY; YLKVKRYD; LKVKRYDY; KVKRYDYN; VKRYDYNR;
KRYDYNRP; RYDYNRPV; YDYNRPVP; DYNRPVPI; YNRPVPIL;
NRPVPILP; RPVPILPT;

9 mers:
MRILVGVCI; RILVGVCII; ILVGVCIIA; LVGVCIIAL; VGVCIIALA;
GVCIIALAL; VCIIALALL; CIIALALLG; IIALALLGC; IALALLGCY;
ALALLGCYL; LALLGCYLP; ALLGCYLPD; LLGCYLPDN; LGCYLPDNQ;
GCYLPDNQE; CYLPDNQEQ; YLPDNQEQA; LPDNQEQAV; PDNQEQAVQ;
DNQEQAVQT; NQEQAVQTF; QEQAVQTFF; EQAVQTFFE; QAVQTFFEN;
AVQTFFENS; VQTFFENSE; QTFFENSES; TFFENSESS; FFENSESSD;
FENSESSDM; ENSESSDMG; NSESSDMGS; SESSDMGSD; ESSDMGSDE;
SSDMGSDEI; SDMGSDEIV; DMGSDEIVT; MGSDEIVTE; GSDEIVTEG;
SDEIVTEGI; DEIVTEGIF; EIVTEGIFS; IVTEGIFSS; VTEGIFSSL;
TEGIFSSLK; EGIFSSLKL; GIFSSLKLY; IFSSLKLYA; FSSLKLYAS;
SSLKLYASE; SLKLYASEH; LKLYASEHR; KLYASEHRL; LYASEHRLL;
YASEHRLLV; ASEHRLLVE; SEHRLLVEI; EHRLLVEIK; HRLLVEIKK;
RLLVEIKKT; LLVEIKKTL; LVEIKKTLI; VEIKKTLIS; EIKKTLISL;
IKKTLISLK; KKTLISLKD; KTLISLKDP; TLISLKDPN; LISLKDPNY;
ISLKDPNYR; SLKDPNYRG; LKDPNYRGV; KDPNYRGVV; DPNYRGVVL;
PNYRGVVLP; NYRGVVLPV; YRGVVLPVS; RGVVLPVSD; GVVLPVSDY;
VVLPVSDYN; VLPVSDYNE; LPVSDYNEE; PVSDYNEEY; VSDYNEEYF;
SDYNEEYFN; DYNEEYFNK; YNEEYFNKF; NEEYFNKFF; EEYFNKFFL;
EYFNKFFLD; YFNKFFLDL; FNKFFLDLG; NKFFLDLGS; KFFLDLGSE;
FFLDLGSEQ; FLDLGSEQS; LDLGSEQSK; DLGSEQSKD; LGSEQSKDL;
GSEQSKDLI; SEQSKDLIK; EQSKDLIKL; QSKDLIKLF; SKDLIKLFI;
KDLIKLFIM; DLIKLFIMV; LIKLFIMVK; IKLFIMVKN; KLFIMVKNE;
LFIMVKNEQ; FIMVKNEQN; IMVKNEQNN; MVKNEQNNN; VKNEQNNNK;
KNEQNNNKF; NEQNNNKFM; EQNNNKFMR; QNNNKFMRI; NNNKFMRIV;
NNKFMRIVR; NKFMRIVRW; KFMRIVRWL; FMRIVRWLY; MRIVRWLYS;
RIVRWLYSC; IVRWLYSCI; VRWLYSCIE; RWLYSCIEE; WLYSCIEEL;
LYSCIEELY; YSCIEELYS; SCIEELYSP; CIEELYSPD; IEELYSPDI;
EELYSPDIK; ELYSPDIKY; LYSPDIKYS; YSPDIKYSG; SPDIKYSGE;
PDIKYSGEE; DIKYSGEEG; IKYSGEEGS; KYSGEEGSP; YSGEEGSPE;
SGEEGSPEY; GEEGSPEYY; EEGSPEYYR; EGSPEYYRN; GSPEYYRNM;
SPEYYRNMP; PEYYRNMPR; EYYRNMPRP; YYRNMPRPT; YRNMPRPTA;
RNMPRPTAY; NMPRPTAYQ; MPRPTAYQQ; PRPTAYQQY; RPTAYQQYL;
PTAYQQYLK; TAYQQYLKV; AYQQYLKVK; YQQYLKVKR; QQYLKVKRY;
QYLKVKRYD; YLKVKRYDY; LKVKRYDYN; KVKRYDYNR; VKRYDYNRP;
KRYDYNRPV; RYDYNRPVP; YDYNRPVPI; DYNRPVPIL; YNRPVPILP;

	NRPVPILPT; 10 mers: MRILVGVCII; RILVGVCIIA; ILVGVCIIAL; LVGVCIIALA; VGVCIIALAL; GVCIIALALL; VCIIALALLG; CIIALALLGC; IIALALLGCY; IALALLGCYL; ALALLGCYLP; LALLGCYLPD; ALLGCYLPDN; LLGCYLPDNQ; LGCYLPDNQE; GCYLPDNQEQ; CYLPDNQEQA; YLPDNQEQAV; LPDNQEQAVQ; PDNQEQAVQT; DNQEQAVQTF; NQEQAVQTFF; QEQAVQTFFE; EQAVQTFFEN; QAVQTFFENS; AVQTFFENSE; VQTFFENSES; QTFFENSESS; TFFENSESSD; FFENSESSDM; FENSESSDMG; ENSESSDMGS; NSESSDMGSD; SESSDMGSDE; ESSDMGSDEI; SSDMGSDEIV; SDMGSDEIVT; DMGSDEIVTE; MGSDEIVTEG; GSDEIVTEGI; SDEIVTEGIF; DEIVTEGIFS; EIVTEGIFSS; IVTEGIFSSL; VTEGIFSSLK; TEGIFSSLKL; EGIFSSLKLY; GIFSSLKLYA; IFSSLKLYAS; FSSLKLYASE; SSLKLYASEH; SLKLYASEHR; LKLYASEHRL; KLYASEHRLL; LYASEHRLLV; YASEHRLLVE; ASEHRLLVEI; SEHRLLVEIK; EHRLLVEIKK; HRLLVEIKKT; RLLVEIKKTL; LLVEIKKTLI; LVEIKKTLIS; VEIKKTLISL; EIKKTLISLK; IKKTLISLKD; KKTLISLKDP; KTLISLKDPN; TLISLKDPNY; LISLKDPNYR; ISLKDPNYRG; SLKDPNYRGV; LKDPNYRGVV; KDPNYRGVVL; DPNYRGVVLP; PNYRGVVLPV; NYRGVVLPVS; YRGVVLPVSD; RGVVLPVSDY; GVVLPVSDYN; VVLPVSDYNE; VLPVSDYNEE; LPVSDYNEEY; PVSDYNEEYF; VSDYNEEYFN; SDYNEEYFNK; DYNEEYFNKF; YNEEYFNKFF; NEEYFNKFFL; EEYFNKFFLD; EYFNKFFLDL; YFNKFFLDLG; FNKFFLDLGS; NKFFLDLGSE; KFFLDLGSEQ; FFLDLGSEQS; FLDLGSEQSK; LDLGSEQSKD; DLGSEQSKDL; LGSEQSKDLI; GSEQSKDLIK; SEQSKDLIKL; EQSKDLIKLF; QSKDLIKLFI; SKDLIKLFIM; KDLIKLFIMV; DLIKLFIMVK; LIKLFIMVKN; IKLFIMVKNE; KLFIMVKNEQ; LFIMVKNEQN; FIMVKNEQNN; IMVKNEQNNN; MVKNEQNNNK; VKNEQNNNKF; KNEQNNNKFM; NEQNNNKFMR; EQNNNKFMRI; QNNNKFMRIV; NNNKFMRIVR; NNKFMRIVRW; NKFMRIVRWL; KFMRIVRWLY; FMRIVRWLYS; MRIVRWLYSC; RIVRWLYSCI; IVRWLYSCIE; VRWLYSCIEE; RWLYSCIEEL; WLYSCIEELY; LYSCIEELYS; YSCIEELYSP; SCIEELYSPD; CIEELYSPDI; IEELYSPDIK; EELYSPDIKY; ELYSPDIKYS; LYSPDIKYSG; YSPDIKYSGE; SPDIKYSGEE; PDIKYSGEEG; DIKYSGEEGS; IKYSGEEGSP; KYSGEEGSPE; YSGEEGSPEY; SGEEGSPEYY; GEEGSPEYYR; EEGSPEYYRN; EGSPEYYRNM; GSPEYYRNMP; SPEYYRNMPR; PEYYRNMPRP; EYYRNMPRPT; YYRNMPRPTA; YRNMPRPTAY; RNMPRPTAYQ; NMPRPTAYQQ; MPRPTAYQQY; PRPTAYQQYL; RPTAYQQYLK; PTAYQQYLKV; TAYQQYLKVK; AYQQYLKVKR; YQQYLKVKRY; QQYLKVKRYD; QYLKVKRYDY; YLKVKRYDYN; LKVKRYDYNR; KVKRYDYNRP; VKRYDYNRPV; KRYDYNRPVP; RYDYNRPVPI; YDYNRPVPIL; DYNRPVPILP; YNRPVPILPT; 11 mers: MRILVGVCIIA; RILVGVCIIAL; ILVGVCIIALA; LVGVCIIALAL; VGVCIIALALL; GVCIIALALLG; VCIIALALLGC; CIIALALLGCY;

	IIALALLGCYL; IALALLGCYLP; ALALLGCYLPD; LALLGCYLPDN; ALLGCYLPDNQ; LLGCYLPDNQE; LGCYLPDNQEQ; GCYLPDNQEQA; CYLPDNQEQAV; YLPDNQEQAVQ; LPDNQEQAVQT; PDNQEQAVQTF; DNQEQAVQTFF; NQEQAVQTFFE; QEQAVQTFFEN; EQAVQTFFENS; QAVQTFFENSE; AVQTFFENSES; VQTFFENSESS; QTFFENSESSD; TFFENSESSDM; FFENSESSDMG; FENSESSDMGS; ENSESSDMGSD; NSESSDMGSDE; SESSDMGSDEI; ESSDMGSDEIV; SSDMGSDEIVT; SDMGSDEIVTE; DMGSDEIVTEG; MGSDEIVTEGI; GSDEIVTEGIF; SDEIVTEGIFS; DEIVTEGIFSS; EIVTEGIFSSL; IVTEGIFSSLK; VTEGIFSSLKL; TEGIFSSLKLY; EGIFSSLKLYA; GIFSSLKLYAS; IFSSLKLYASE; FSSLKLYASEH; SSLKLYASEHR; SLKLYASEHRL; LKLYASEHRLL; KLYASEHRLLV; LYASEHRLLVE; YASEHRLLVEI; ASEHRLLVEIK; SEHRLLVEIKK; EHRLLVEIKKT; HRLLVEIKKTL; RLLVEIKKTLI; LLVEIKKTLIS; LVEIKKTLISL; VEIKKTLISLK; EIKKTLISLKD; IKKTLISLKDP; KKTLISLKDPN; KTLISLKDPNY; TLISLKDPNYR; LISLKDPNYRG; ISLKDPNYRGV; SLKDPNYRGVV; LKDPNYRGVVL; KDPNYRGVVLP; DPNYRGVVLPV; PNYRGVVLPVS; NYRGVVLPVSD; YRGVVLPVSDY; RGVVLPVSDYN; GVVLPVSDYNE; VVLPVSDYNEE; VLPVSDYNEEY; LPVSDYNEEYF; PVSDYNEEYFN; VSDYNEEYFNK; SDYNEEYFNKF; DYNEEYFNKFF; YNEEYFNKFFL; NEEYFNKFFLD; EEYFNKFFLDL; EYFNKFFLDLG; YFNKFFLDLGS; FNKFFLDLGSE; NKFFLDLGSEQ; KFFLDLGSEQS; FFLDLGSEQSK; FLDLGSEQSKD; LDLGSEQSKDL; DLGSEQSKDLI; LGSEQSKDLIK; GSEQSKDLIKL; SEQSKDLIKLF; EQSKDLIKLFI; QSKDLIKLFIM; SKDLIKLFIMV; KDLIKLFIMVK; DLIKLFIMVKN; LIKLFIMVKNE; IKLFIMVKNEQ; KLFIMVKNEQN; LFIMVKNEQNN; FIMVKNEQNNN; IMVKNEQNNNK; MVKNEQNNNKF; VKNEQNNNKFM; KNEQNNNKFMR; NEQNNNKFMRI; EQNNNKFMRIV; QNNNKFMRIVR; NNNKFMRIVRW; NNKFMRIVRWL; NKFMRIVRWLY; KFMRIVRWLYS; FMRIVRWLYSC; MRIVRWLYSCI; RIVRWLYSCIE; IVRWLYSCIEE; VRWLYSCIEEL; RWLYSCIEELY; WLYSCIEELYS; LYSCIEELYSP; YSCIEELYSPD; SCIEELYSPDI; CIEELYSPDIK; IEELYSPDIKY; EELYSPDIKYS; ELYSPDIKYSG; LYSPDIKYSGE; YSPDIKYSGEE; SPDIKYSGEEG; PDIKYSGEEGS; DIKYSGEEGSP; IKYSGEEGSPE; KYSGEEGSPEY; YSGEEGSPEYY; SGEEGSPEYYR; GEEGSPEYYRN; EEGSPEYYRNM; EGSPEYYRNMP; GSPEYYRNMPR; SPEYYRNMPRP; PEYYRNMPRPT; EYYRNMPRPTA; YYRNMPRPTAY; YRNMPRPTAYQ; RNMPRPTAYQQ; NMPRPTAYQQY; MPRPTAYQQYL; PRPTAYQQYLK; RPTAYQQYLKV; PTAYQQYLKVK; TAYQQYLKVKR; AYQQYLKVKRY; YQQYLKVKRYD; QQYLKVKRYDY; QYLKVKRYDYN; YLKVKRYDYNR; LKVKRYDYNRP; KVKRYDYNRPV; VKRYDYNRPVP; KRYDYNRPVPI; RYDYNRPVPIL; YDYNRPVPILP; DYNRPVPILPT;
Seq 39	SEQ ID NO 46607-47212/ 8 mers: MRNKNIFK; RNKNIFKL; NKNIFKLF; KNIFKLFF; NIFKLFFA; IFKLFFAS; FKLFFASM; KLFFASML; LFFASMLF; FFASMLFV; FASMLFVM; ASMLFVMA; SMLFVMAC; MLFVMACK; LFVMACKA; FVMACKAY; VMACKAYV; MACKAYVE; ACKAYVEE; CKAYVEEK; KAYVEEKK; AYVEEKKE; YVEEKKEI; VEEKKEID; EEKKEIDS; EKKEIDSL; KKEIDSLM; KEIDSLME; EIDSLMED; IDSLMEDV;

DSLMEDVL; SLMEDVLA; LMEDVLAL; MEDVLALV; EDVLALVN;
DVLALVND; VLALVNDS; LALVNDSS; ALVNDSSG; LVNDSSGG;
VNDSSGGK; NDSSGGKF; DSSGGKFK; SSGGKFKD; SGGKFKDY;
GGKFKDYK; GKFKDYKD; KFKDYKDK; FKDYKDKI; KDYKDKIN;
DYKDKINE; YKDKINEL; KDKINELK; DKINELKE; KINELKEN;
INELKENL; NELKENLK; ELKENLKD; LKENLKDI; KENLKDIG;
ENLKDIGN; NLKDIGNA; LKDIGNAE; KDIGNAEL; DIGNAELK;
IGNAELKE; GNAELKEK; NAELKEKL; AELKEKLL; ELKEKLLN;
LKEKLLNL; KEKLLNLQ; EKLLNLQN; KLLNLQNS; LLNLQNSF;
LNLQNSFQ; NLQNSFQD; LQNSFQDK; QNSFQDKL; NSFQDKLA;
SFQDKLAA; FQDKLAAK; QDKLAAKL; DKLAAKLA; KLAAKLAA;
LAAKLAAL; AAKLAALK; AKLAALKA; KLAALKAA; LAALKAAK;
AALKAAKN; ALKAAKNT; LKAAKNTI; KAAKNTIE; AAKNTIEN;
AKNTIENI; KNTIENIT; NTIENITD; TIENITDK; IENITDKD;
ENITDKDQ; NITDKDQD; ITDKDQDI; TDKDQDIS; DKDQDISK;
KDQDISKR; DQDISKRK; QDISKRKI; DISKRKIW; ISKRKIWS;
SKRKIWSE; KRKIWSEA; RKIWSEAK; KIWSEAKL; IWSEAKLV;
WSEAKLVG; SEAKLVGV; EAKLVGVT; AKLVGVTV; KLVGVTVP;
LVGVTVPL; VGVTVPLL; GVTVPLLG; VTVPLLGS; TVPLLGSN;
VPLLGSNT; PLLGSNTS; LLGSNTSG; LGSNTSGN; GSNTSGNG;
SNTSGNGD; NTSGNGDK; TSGNGDKM; SGNGDKMS; GNGDKMSK;
NGDKMSKN; GDKMSKNA; DKMSKNAV; KMSKNAVE; MSKNAVEQ;
SKNAVEQI; KNAVEQID; NAVEQIDK; AVEQIDKV; VEQIDKVI;
EQIDKVIK; QIDKVIKF; IDKVIKFL; DKVIKFLE; KVIKFLEE;
VIKFLEEG; IKFLEEGT; KFLEEGTN;

9 mers:
MRNKNIFKL; RNKNIFKLF; NKNIFKLFF; KNIFKLFFA; NIFKLFFAS;
IFKLFFASM; FKLFFASML; KLFFASMLF; LFFASMLFV; FFASMLFVM;
FASMLFVMA; ASMLFVMAC; SMLFVMACK; MLFVMACKA; LFVMACKAY;
FVMACKAYV; VMACKAYVE; MACKAYVEE; ACKAYVEEK; CKAYVEEKK;
KAYVEEKKE; AYVEEKKEI; YVEEKKEID; VEEKKEIDS; EEKKEIDSL;
EKKEIDSLM; KKEIDSLME; KEIDSLMED; EIDSLMEDV; IDSLMEDVL;
DSLMEDVLA; SLMEDVLAL; LMEDVLALV; MEDVLALVN; EDVLALVND;
DVLALVNDS; VLALVNDSS; LALVNDSSG; ALVNDSSGG; LVNDSSGGK;
VNDSSGGKF; NDSSGGKFK; DSSGGKFKD; SSGGKFKDY; SGGKFKDYK;
GGKFKDYKD; GKFKDYKDK; KFKDYKDKI; FKDYKDKIN; KDYKDKINE;
DYKDKINEL; YKDKINELK; KDKINELKE; DKINELKEN; KINELKENL;
INELKENLK; NELKENLKD; ELKENLKDI; LKENLKDIG; KENLKDIGN;
ENLKDIGNA; NLKDIGNAE; LKDIGNAEL; KDIGNAELK; DIGNAELKE;
IGNAELKEK; GNAELKEKL; NAELKEKLL; AELKEKLLN; ELKEKLLNL;
LKEKLLNLQ; KEKLLNLQN; EKLLNLQNS; KLLNLQNSF; LLNLQNSFQ;
LNLQNSFQD; NLQNSFQDK; LQNSFQDKL; QNSFQDKLA; NSFQDKLAA;
SFQDKLAAK; FQDKLAAKL; QDKLAAKLA; DKLAAKLAA; KLAAKLAAL;
LAAKLAALK; AAKLAALKA; AKLAALKAA; KLAALKAAK; LAALKAAKN;
AALKAAKNT; ALKAAKNTI; LKAAKNTIE; KAAKNTIEN; AAKNTIENI;
AKNTIENIT; KNTIENITD; NTIENITDK; TIENITDKD; IENITDKDQ;
ENITDKDQD; NITDKDQDI; ITDKDQDIS; TDKDQDISK; DKDQDISKR;
KDQDISKRK; DQDISKRKI; QDISKRKIW; DISKRKIWS; ISKRKIWSE;
SKRKIWSEA; KRKIWSEAK; RKIWSEAKL; KIWSEAKLV; IWSEAKLVG;
WSEAKLVGV; SEAKLVGVT; EAKLVGVTV; AKLVGVTVP; KLVGVTVPL;

	LVGVTVPLL; VGVTVPLLG; GVTVPLLGS; VTVPLLGSN; TVPLLGSNT; VPLLGSNTS; PLLGSNTSG; LLGSNTSGN; LGSNTSGNG; GSNTSGNGD; SNTSGNGDK; NTSGNGDKM; TSGNGDKMS; SGNGDKMSK; GNGDKMSKN; NGDKMSKNA; GDKMSKNAV; DKMSKNAVE; KMSKNAVEQ; MSKNAVEQI; SKNAVEQID; KNAVEQIDK; NAVEQIDKV; AVEQIDKVI; VEQIDKVIK; EQIDKVIKF; QIDKVIKFL; IDKVIKFLE; DKVIKFLEE; KVIKFLEEG; VIKFLEEGT; IKFLEEGTN; 10 mers: MRNKNIFKLF; RNKNIFKLFF; NKNIFKLFFA; KNIFKLFFAS; NIFKLFFASM; IFKLFFASML; FKLFFASMLF; KLFFASMLFV; LFFASMLFVM; FFASMLFVMA; FASMLFVMAC; ASMLFVMACK; SMLFVMACKA; MLFVMACKAY; LFVMACKAYV; FVMACKAYVE; VMACKAYVEE; MACKAYVEEK; ACKAYVEEKK; CKAYVEEKKE; KAYVEEKKEI; AYVEEKKEID; YVEEKKEIDS; VEEKKEIDSL; EEKKEIDSLM; EKKEIDSLME; KKEIDSLMED; KEIDSLMEDV; EIDSLMEDVL; IDSLMEDVLA; DSLMEDVLAL; SLMEDVLALV; LMEDVLALVN; MEDVLALVND; EDVLALVNDS; DVLALVNDSS; VLALVNDSSG; LALVNDSSGG; ALVNDSSGGK; LVNDSSGGKF; VNDSSGGKFK; NDSSGGKFKD; DSSGGKFKDY; SSGGKFKDYK; SGGKFKDYKD; GGKFKDYKDK; GKFKDYKDKI; KFKDYKDKIN; FKDYKDKINE; KDYKDKINEL; DYKDKINELK; YKDKINELKE; KDKINELKEN; DKINELKENL; KINELKENLK; INELKENLKD; NELKENLKDI; ELKENLKDIG; LKENLKDIGN; KENLKDIGNA; ENLKDIGNAE; NLKDIGNAEL; LKDIGNAELK; KDIGNAELKE; DIGNAELKEK; IGNAELKEKL; GNAELKEKLL; NAELKEKLLN; AELKEKLLNL; ELKEKLLNLQ; LKEKLLNLQN; KEKLLNLQNS; EKLLNLQNSF; KLLNLQNSFQ; LLNLQNSFQD; LNLQNSFQDK; NLQNSFQDKL; LQNSFQDKLA; QNSFQDKLAA; NSFQDKLAAK; SFQDKLAAKL; FQDKLAAKLA; QDKLAAKLAA; DKLAAKLAAL; KLAAKLAALK; LAAKLAALKA; AAKLAALKAA; AKLAALKAAK; KLAALKAAKN; LAALKAAKNT; AALKAAKNTI; ALKAAKNTIE; LKAAKNTIEN; KAAKNTIENI; AAKNTIENIT; AKNTIENITD; KNTIENITDK; NTIENITDKD; TIENITDKDQ; IENITDKDQD; ENITDKDQDI; NITDKDQDIS; ITDKDQDISK; TDKDQDISKR; DKDQDISKRK; KDQDISKRKI; DQDISKRKIW; QDISKRKIWS; DISKRKIWSE; ISKRKIWSEA; SKRKIWSEAK; KRKIWSEAKL; RKIWSEAKLV; KIWSEAKLVG; IWSEAKLVGV; WSEAKLVGVT; SEAKLVGVTV; EAKLVGVTVP; AKLVGVTVPL; KLVGVTVPLL; LVGVTVPLLG; VGVTVPLLGS; GVTVPLLGSN; VTVPLLGSNT; TVPLLGSNTS; VPLLGSNTSG; PLLGSNTSGN; LLGSNTSGNG; LGSNTSGNGD; GSNTSGNGDK; SNTSGNGDKM; NTSGNGDKMS; TSGNGDKMSK; SGNGDKMSKN; GNGDKMSKNA; NGDKMSKNAV; GDKMSKNAVE; DKMSKNAVEQ; KMSKNAVEQI; MSKNAVEQID; SKNAVEQIDK; KNAVEQIDKV; NAVEQIDKVI; AVEQIDKVIK; VEQIDKVIKF; EQIDKVIKFL; QIDKVIKFLE; IDKVIKFLEE; DKVIKFLEEG; KVIKFLEEGT; VIKFLEEGTN; 11 mers: MRNKNIFKLFF; RNKNIFKLFFA; NKNIFKLFFAS; KNIFKLFFASM; NIFKLFFASML; IFKLFFASMLF; FKLFFASMLFV; KLFFASMLFVM;

	LFFASMLFVMA; FFASMLFVMAC; FASMLFVMACK; ASMLFVMACKA; SMLFVMACKAY; MLFVMACKAYV; LFVMACKAYVE; FVMACKAYVEE; VMACKAYVEEK; MACKAYVEEKK; ACKAYVEEKKE; CKAYVEEKKEI; KAYVEEKKEID; AYVEEKKEIDS; YVEEKKEIDSL; VEEKKEIDSLM; EEKKEIDSLME; EKKEIDSLMED; KKEIDSLMEDV; KEIDSLMEDVL; EIDSLMEDVLA; IDSLMEDVLAL; DSLMEDVLALV; SLMEDVLALVN; LMEDVLALVND; MEDVLALVNDS; EDVLALVNDSS; DVLALVNDSSG; VLALVNDSSGG; LALVNDSSGGK; ALVNDSSGGKF; LVNDSSGGKFK; VNDSSGGKFKD; NDSSGGKFKDY; DSSGGKFKDYK; SSGGKFKDYKD; SGGKFKDYKDK; GGKFKDYKDKI; GKFKDYKDKIN; KFKDYKDKINE; FKDYKDKINEL; KDYKDKINELK; DYKDKINELKE; YKDKINELKEN; KDKINELKENL; DKINELKENLK; KINELKENLKD; INELKENLKDI; NELKENLKDIG; ELKENLKDIGN; LKENLKDIGNA; KENLKDIGNAE; ENLKDIGNAEL; NLKDIGNAELK; LKDIGNAELKE; KDIGNAELKEK; DIGNAELKEKL; IGNAELKEKLL; GNAELKEKLLN; NAELKEKLLNL; AELKEKLLNLQ; ELKEKLLNLQN; LKEKLLNLQNS; KEKLLNLQNSF; EKLLNLQNSFQ; KLLNLQNSFQD; LLNLQNSFQDK; LNLQNSFQDKL; NLQNSFQDKLA; LQNSFQDKLAA; QNSFQDKLAAK; NSFQDKLAAKL; SFQDKLAAKLA; FQDKLAAKLAA; QDKLAAKLAAL; DKLAAKLAALK; KLAAKLAALKA; LAAKLAALKAA; AAKLAALKAAK; AKLAALKAAKN; KLAALKAAKNT; LAALKAAKNTI; AALKAAKNTIE; ALKAAKNTIEN; LKAAKNTIENI; KAAKNTIENIT; AAKNTIENITD; AKNTIENITDK; KNTIENITDKD; NTIENITDKDQ; TIENITDKDQD; IENITDKDQDI; ENITDKDQDIS; NITDKDQDISK; ITDKDQDISKR; TDKDQDISKRK; DKDQDISKRKI; KDQDISKRKIW; DQDISKRKIWS; QDISKRKIWSE; DISKRKIWSEA; ISKRKIWSEAK; SKRKIWSEAKL; KRKIWSEAKLV; RKIWSEAKLVG; KIWSEAKLVGV; IWSEAKLVGVT; WSEAKLVGVTV; SEAKLVGVTVP; EAKLVGVTVPL; AKLVGVTVPLL; KLVGVTVPLLG; LVGVTVPLLGS; VGVTVPLLGSN; GVTVPLLGSNT; VTVPLLGSNTS; TVPLLGSNTSG; VPLLGSNTSGN; PLLGSNTSGNG; LLGSNTSGNGD; LGSNTSGNGDK; GSNTSGNGDKM; SNTSGNGDKMS; NTSGNGDKMSK; TSGNGDKMSKN; SGNGDKMSKNA; GNGDKMSKNAV; NGDKMSKNAVE; GDKMSKNAVEQ; DKMSKNAVEQI; KMSKNAVEQID; MSKNAVEQIDK; SKNAVEQIDKV; KNAVEQIDKVI; NAVEQIDKVIK; AVEQIDKVIKF; VEQIDKVIKFL; EQIDKVIKFLE; QIDKVIKFLEE; IDKVIKFLEEG; DKVIKFLEEGT; KVIKFLEEGTN;
Seq 40	SEQ ID NO 47213-48406 8 mers: MKDNILKN; KDNILKNN; DNILKNNK; NILKNNKL; ILKNNKLI; LKNNKLIA; KNNKLIAI; NNKLIAIF; NKLIAIFL; KLIAIFLL; LIAIFLLH; IAIFLLHV; AIFLLHVL; IFLLHVLT; FLLHVLTV; LLHVLTVL; LHVLTVLI; HVLTVLIL; VLTVLILI; LTVLILIS; TVLILISC; VLILISCS; LILISCSL; ILISCSLE; LISCSLEV; ISCSLEVK; SCSLEVKD; CSLEVKDS; SLEVKDSN; LEVKDSNE; EVKDSNES; VKDSNESK; KDSNESKK; DSNESKKH; SNESKKHK; NESKKHKK; ESKKHKKE; SKKHKKEK; KKHKKEKR; KHKKEKRK; HKKEKRKG; KKEKRKGK; KEKRKGKV; EKRKGKVE; KRKGKVEN; RKGKVENL; KGKVENLL; GKVENLLV; KVENLLVA; VENLLVAI; ENLLVAIN; NLLVAINN; LLVAINNL; LVAINNLK; VAINNLKN; AINNLKNP; INNLKNPT; NNLKNPTK; NLKNPTKP; LKNPTKPA;

	KNPTKPAA; NPTKPAAG; PTKPAAGK; TKPAAGKN; KPAAGKNK; PAAGKNKA; AAGKNKAN; AGKNKANS; GKNKANSK; KNKANSKA; NKANSKAS; KANSKASK; ANSKASKQ; NSKASKQK; SKASKQKN; KASKQKNN; ASKQKNNP; SKQKNNPN; KQKNNPNA; QKNNPNAN; KNNPNANA; NNPNANAN; NPNANANN; PNANANNA; NANANNAP; ANANNAPK; NANNAPKK; ANNAPKKI; NNAPKKIL; NAPKKILD; APKKILDP; PKKILDPE; KKILDPEV; KILDPEVA; ILDPEVAK; LDPEVAKL; DPEVAKLI; PEVAKLIQ; EVAKLIQK; VAKLIQKI; AKLIQKIL; KLIQKILD; LIQKILDR; IQKILDRS; QKILDRSE; KILDRSEN; ILDRSENI; LDRSENII; DRSENIIQ; RSENIIQI; SENIIQIS; ENIIQISE; NIIQISEM; IIQISEMD; IQISEMDS; QISEMDSS; ISEMDSSR; SEMDSSRG; EMDSSRGE; MDSSRGEP; DSSRGEPN; SSRGEPND; SRGEPNDQ; RGEPNDQF; GEPNDQFG; EPNDQFGM; PNDQFGMR; NDQFGMRA; DQFGMRAE; QFGMRAEI; FGMRAEIF; GMRAEIFS; MRAEIFSK; RAEIFSKI; AEIFSKIF; EIFSKIFF; IFSKIFFN; FSKIFFNA; SKIFFNAN; KIFFNANS; IFFNANST; FFNANSTV; FNANSTVH; NANSTVHF; ANSTVHFD; NSTVHFDS; STVHFDSH; TVHFDSHE; VHFDSHEY; HFDSHEYT; FDSHEYTE; DSHEYTEE; SHEYTEER; HEYTEERR; EYTEERRM; YTEERRML; TEERRMLY; EERRMLYT; ERRMLYTS; RRMLYTSL; RMLYTSLN; MLYTSLNF; LYTSLNFN; YTSLNFNE; TSLNFNEG; SLNFNEGK; LNFNEGKI; NFNEGKIF; FNEGKIFN; NEGKIFNL; EGKIFNLG; GKIFNLGQ; KIFNLGQI; IFNLGQIL; FNLGQILS; NLGQILSK; LGQILSKL; GQILSKLS; QILSKLSQ; ILSKLSQD; LSKLSQDS; SKLSQDSN; KLSQDSNY; LSQDSNYR; SQDSNYRG; QDSNYRGL; DSNYRGLV; SNYRGLVK; NYRGLVKE; YRGLVKET; RGLVKETL; GLVKETLI; LVKETLIN; VKETLINR; KETLINRG; ETLINRGF; TLINRGFS; LINRGFSI; INRGFSIQ; NRGFSIQL; RGFSIQLA; GFSIQLAM; FSIQLAME; SIQLAMEE; IQLAMEEI; QLAMEEIS; LAMEEISA; AMEEISAK; MEEISAKI; EEISAKIL; EISAKILN; ISAKILNV; SAKILNVK; AKILNVKD; KILNVKDK; ILNVKDKL; LNVKDKLQ; NVKDKLQQ; VKDKLQQL; KDKLQQLN; DKLQQLNK; KLQQLNKP; LQQLNKPN; QQLNKPNL; QLNKPNLE; LNKPNLET; NKPNLETL; KPNLETLY; PNLETLYN; NLETLYND; LETLYNDF; ETLYNDFE; TLYNDFEK; LYNDFEKL; YNDFEKLT; NDFEKLTS; DFEKLTSL; FEKLTSLK; EKLTSLKE; KLTSLKEK; LTSLKEKW; TSLKEKWL; SLKEKWLK; LKEKWLKD; KEKWLKDT; EKWLKDTD; KWLKDTDD; WLKDTDDL; LKDTDDLI; KDTDDLID; DTDDLIDE; TDDLIDEY; DDLIDEYN; DLIDEYNT; LIDEYNTN; IDEYNTNP; DEYNTNPD; EYNTNPDL; YNTNPDLQ; NTNPDLQT; TNPDLQTD; NPDLQTDV; PDLQTDVS; DLQTDVSK; LQTDVSKL; QTDVSKLN; TDVSKLND; DVSKLNDT; VSKLNDTL; SKLNDTLR; KLNDTLRS; LNDTLRSK; NDTLRSKN; DTLRSKNS; TLRSKNSR; LRSKNSRA; RSKNSRAQ; SKNSRAQF; KNSRAQFA; NSRAQFAN; SRAQFANI; RAQFANIH; AQFANIHD; QFANIHDI; FANIHDII; ANIHDIIL; NIHDIILD; IHDIILDL; HDIILDLV; DIILDLVN; IILDLVNT; ILDLVNTT; LDLVNTTT; DLVNTTTN; LVNTTTNI; VNTTTNIL; NTTTNILA; TTTNILAP; TTNILAPI; TNILAPIQ; 9 mers: MKDNILKNN; KDNILKNNK; DNILKNNKL; NILKNNKLI; ILKNNKLIA;

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	TSLNFNEGKI; SLNFNEGKIF; LNFNEGKIFN; NFNEGKIFNL; FNEGKIFNLG; NEGKIFNLGQ; EGKIFNLGQI; GKIFNLGQIL; KIFNLGQILS; IFNLGQILSK; FNLGQILSKL; NLGQILSKLS; LGQILSKLSQ; GQILSKLSQD; QILSKLSQDS; ILSKLSQDSN; LSKLSQDSNY; SKLSQDSNYR; KLSQDSNYRG; LSQDSNYRGL; SQDSNYRGLV; QDSNYRGLVK; DSNYRGLVKE; SNYRGLVKET; NYRGLVKETL; YRGLVKETLI; RGLVKETLIN; GLVKETLINR; LVKETLINRG; VKETLINRGF; KETLINRGFS; ETLINRGFSI; TLINRGFSIQ; LINRGFSIQL; INRGFSIQLA; NRGFSIQLAM; RGFSIQLAME; GFSIQLAMEE; FSIQLAMEEI; SIQLAMEEIS; IQLAMEEISA; QLAMEEISAK; LAMEEISAKI; AMEEISAKIL; MEEISAKILN; EEISAKILNV; EISAKILNVK; ISAKILNVKD; SAKILNVKDK; AKILNVKDKL; KILNVKDKLQ; ILNVKDKLQQ; LNVKDKLQQL; NVKDKLQQLN; VKDKLQQLNK; KDKLQQLNKP; DKLQQLNKPN; KLQQLNKPNL; LQQLNKPNLE; QQLNKPNLET; QLNKPNLETL; LNKPNLETLY; NKPNLETLYN; KPNLETLYND; PNLETLYNDF; NLETLYNDFE; LETLYNDFEK; ETLYNDFEKL; TLYNDFEKLT; LYNDFEKLTS; YNDFEKLTSL; NDFEKLTSLK; DFEKLTSLKE; FEKLTSLKEK; EKLTSLKEKW; KLTSLKEKWL; LTSLKEKWLK; TSLKEKWLKD; SLKEKWLKDT; LKEKWLKDTD; KEKWLKDTDD; EKWLKDTDDL; KWLKDTDDLI; WLKDTDDLID; LKDTDDLIDE; KDTDDLIDEY; DTDDLIDEYN; TDDLIDEYNT; DDLIDEYNTN; DLIDEYNTNP; LIDEYNTNPD; IDEYNTNPDL; DEYNTNPDLQ; EYNTNPDLQT; YNTNPDLQTD; NTNPDLQTDV; TNPDLQTDVS; NPDLQTDVSK; PDLQTDVSKL; DLQTDVSKLN; LQTDVSKLND; QTDVSKLNDT; TDVSKLNDTL; DVSKLNDTLR; VSKLNDTLRS; SKLNDTLRSK; KLNDTLRSKN; LNDTLRSKNS; NDTLRSKNSR; DTLRSKNSRA; TLRSKNSRAQ; LRSKNSRAQF; RSKNSRAQFA; SKNSRAQFAN; KNSRAQFANI; NSRAQFANIH; SRAQFANIHD; RAQFANIHDI; AQFANIHDII; QFANIHDIIL; FANIHDIILD; ANIHDIILDL; NIHDIILDLV; IHDIILDLVN; HDIILDLVNT; DIILDLVNTT; IILDLVNTTT; ILDLVNTTTN; LDLVNTTTNI; DLVNTTTNIL; LVNTTTNILA; VNTTTNILAP; NTTTNILAPI; TTTNILAPIQ; 11 mers: MKDNILKNNKL; KDNILKNNKLI; DNILKNNKLIA; NILKNNKLIAI; ILKNNKLIAIF; LKNNKLIAIFL; KNNKLIAIFLL; NNKLIAIFLLH; NKLIAIFLLHV; KLIAIFLLHVL; LIAIFLLHVLT; IAIFLLHVLTV; AIFLLHVLTVL; IFLLHVLTVLI; FLLHVLTVLIL; LLHVLTVLILI; LHVLTVLILIS; HVLTVLILISC; VLTVLILISCS; LTVLILISCSL; TVLILISCSLE; VLILISCSLEV; LILISCSLEVK; ILISCSLEVKD; LISCSLEVKDS; ISCSLEVKDSN; SCSLEVKDSNE; CSLEVKDSNES; SLEVKDSNESK; LEVKDSNESKK; EVKDSNESKKH; VKDSNESKKHK; KDSNESKKHKK; DSNESKKHKKE; SNESKKHKKEK; NESKKHKKEKR; ESKKHKKEKRK; SKKHKKEKRKG; KKHKKEKRKGK; KHKKEKRKGKV; HKKEKRKGKVE; KKEKRKGKVEN; KEKRKGKVENL; EKRKGKVENLL; KRKGKVENLLV; RKGKVENLLVA; KGKVENLLVAI; GKVENLLVAIN; KVENLLVAINN; VENLLVAINNL; ENLLVAINNLK; NLLVAINNLKN; LLVAINNLKNP; LVAINNLKNPT; VAINNLKNPTK; AINNLKNPTKP; INNLKNPTKPA; NNLKNPTKPAA; NLKNPTKPAAG; LKNPTKPAAGK;

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	LQTDVSKLNDT; QTDVSKLNDTL; TDVSKLNDTLR; DVSKLNDTLRS; VSKLNDTLRSK; SKLNDTLRSKN; KLNDTLRSKNS; LNDTLRSKNSR; NDTLRSKNSRA; DTLRSKNSRAQ; TLRSKNSRAQF; LRSKNSRAQFA; RSKNSRAQFAN; SKNSRAQFANI; KNSRAQFANIH; NSRAQFANIHD; SRAQFANIHDI; RAQFANIHDII; AQFANIHDIIL; QFANIHDIILD; FANIHDIILDL; ANIHDIILDLV; NIHDIILDLVN; IHDIILDLVNT; HDIILDLVNTT; DIILDLVNTTT; IILDLVNTTTN; ILDLVNTTTNI; LDLVNTTTNIL; DLVNTTTNILA; LVNTTTNILAP; VNTTTNILAPI; NTTTNILAPIQ;
Seq 41	SEQ ID NO 48407-49644/ 8 mers: MKNNKLIA; KNNKLIAI; NNKLIAIF; NKLIAIFL; KLIAIFLL; LIAIFLLH; IAIFLLHI; AIFLLHIL; IFLLHILT; FLLHILTG; LLHILTGL; LHILTGLI; HILTGLIL; ILTGLILL; LTGLILLS; TGLILLSC; GLILLSCS; LILLSCSL; ILLSCSLE; LLSCSLEV; LSCSLEVN; SCSLEVNQ; CSLEVNQD; SLEVNQDD; LEVNQDDN; EVNQDDNQ; VNQDDNQE; NQDDNQEK; QDDNQEKQ; DDNQEKQK; DNQEKQKK; NQEKQKKA; QEKQKKAK; EKQKKAKT; KQKKAKTK; QKKAKTKT; KKAKTKTS; KAKTKTSK; AKTKTSKS; KTKTSKSE; TKTSKSEN; KTSKSENN; TSKSENNS; SKSENNSS; KSENNSSK; SENNSSKM; ENNSSKMK; NNSSKMKK; NSSKMKKL; SSKMKKLS; SKMKKLSK; KMKKLSKN; MKKLSKNA; KKLSKNAK; KLSKNAKN; LSKNAKNK; SKNAKNKK; KNAKNKKP; NAKNKKPT; AKNKKPTV; KNKKPTVD; NKKPTVDN; KKPTVDNL; KPTVDNLL; PTVDNLLV; TVDNLLVA; VDNLLVAI; DNLLVAIN; NLLVAINT; LLVAINTL; LVAINTLK; VAINTLKN; AINTLKNP; INTLKNPP; NTLKNPPK; TLKNPPKT; LKNPPKTA; KNPPKTAG; NPPKTAGK; PPKTAGKN; PKTAGKNK; KTAGKNKS; TAGKNKSN; AGKNKSNS; GKNKSNSA; KNKSNSAA; NKSNSAAA; KSNSAAAL; SNSAAALK; NSAAALKQ; SAAALKQP; AAALKQPN; AALKQPNN; ALKQPNNA; LKQPNNAN; KQPNNANA; QPNNANAL; PNNANALK; NNANALKQ; NANALKQI; ANALKQID; NALKQIDP; ALKQIDPE; LKQIDPEA; KQIDPEAK; QIDPEAKE; IDPEAKEL; DPEAKELI; PEAKELIQ; EAKELIQK; AKELIQKI; KELIQKIL; ELIQKILE; LIQKILER; IQKILERS; QKILERSE; KILERSED; ILERSEDI; LERSEDIV; ERSEDIVQ; RSEDIVQI; SEDIVQIS; EDIVQISE; DIVQISEI; IVQISEID; VQISEIDA; QISEIDAN; ISEIDANK; SEIDANKG; EIDANKGE; IDANKGEP; DANKGEPD; ANKGEPDD; NKGEPDDQ; KGEPDDQF; GEPDDQFE; EPDDQFEM; PDDQFEMK; DDQFEMKA; DQFEMKAE; QFEMKAEI; FEMKAEIF; EMKAEIFS; MKAEIFSK; KAEIFSKI; AEIFSKIF; EIFSKIFF; IFSKIFFN; FSKIFFNA; SKIFFNAG; KIFFNAGS; IFFNAGST; FFNAGSTV; FNAGSTVT; NAGSTVTF; AGSTVTFD; GSTVTFDD; STVTFDDN; TVTFDDNE; VTFDDNEY; TFDDNEYV; FDDNEYVN; DDNEYVNE; DNEYVNER; NEYVNERR; EYVNERRI; YVNERRIL; VNERRILY; NERRILYT; ERRILYTS; RRILYTSL; RILYTSLN; ILYTSLNF; LYTSLNFN; YTSLNFNE; TSLNFNEN; SLNFNENK; LNFNENKI; NFNENKIL; FNENKILN; NENKILNL; ENKILNLG; NKILNLGK; KILNLGKI; ILNLGKIL; LNLGKILS; NLGKILSK; LGKILSKL; GKILSKLS; KILSKLSQ; ILSKLSQD; LSKLSQDS; SKLSQDSN; KLSQDSNY; LSQDSNYR;

	SQDSNYRS; QDSNYRSL; DSNYRSLV; SNYRSLVK; NYRSLVKE; YRSLVKEI; RSLVKEIL; SLVKEILI; LVKEILIN; VKEILINR; KEILINRG; EILINRGF; ILINRGFS; LINRGFSI; INRGFSIQ; NRGFSIQL; RGFSIQLA; GFSIQLAI; FSIQLAIE; SIQLAIEE; IQLAIEEI; QLAIEEIS; LAIEEISL; AIEEISLR; IEEISLRT; EEISLRTL; EISLRTLN; ISLRTLNV; SLRTLNVK; LRTLNVKD; RTLNVKDK; TLNVKDKI; LNVKDKIQ; NVKDKIQH; VKDKIQHL; KDKIQHLN; DKIQHLNK; KIQHLNKP; IQHLNKPN; QHLNKPNL; HLNKPNLK; LNKPNLKT; NKPNLKTL; KPNLKTLY; PNLKTLYH; NLKTLYHD; LKTLYHDF; KTLYHDFN; TLYHDFNK; LYHDFNKL; YHDFNKLI; HDFNKLIP; DFNKLIPL; FNKLIPLK; NKLIPLKE; KLIPLKEK; LIPLKEKW; IPLKEKWL; PLKEKWLK; LKEKWLKD; KEKWLKDV; EKWLKDVD; KWLKDVDD; WLKDVDDI; LKDVDDII; KDVDDIIK; DVDDIIKD; VDDIIKDY; DDIIKDYN; DIIKDYNA; IIKDYNAN; IKDYNANP; KDYNANPE; DYNANPEL; YNANPELR; NANPELRT; ANPELRTD; NPELRTDI; PELRTDIS; ELRTDISK; LRTDISKL; RTDISKLN; TDISKLND; DISKLNDY; ISKLNDYI; SKLNDYII; KLNDYIIS; LNDYIISK; NDYIISKN; DYIISKNS; YIISKNSK; IISKNSKA; ISKNSKAQ; SKNSKAQF; KNSKAQFT; NSKAQFTD; SKAQFTDI; KAQFTDIH; AQFTDIHN; QFTDIHNI; FTDIHNII; TDIHNIIL; DIHNIILN; IHNIILNL; HNIILNLI; NIILNLIN; IILNLINT; ILNLINTT; LNLINTTT; NLINTTTN; LINTTTNI; INTTTNIL; NTTTNILA; TTTNILAP; TTNILAPI; TNILAPIQ; 9 mers: MKNNKLIAI; KNNKLIAIF; NNKLIAIFL; NKLIAIFLL; KLIAIFLLH; LIAIFLLHI; IAIFLLHIL; AIFLLHILT; IFLLHILTG; FLLHILTGL; LLHILTGLI; LHILTGLIL; HILTGLILL; ILTGLILLS; LTGLILLSC; TGLILLSCS; GLILLSCSL; LILLSCSLE; ILLSCSLEV; LLSCSLEVN; LSCSLEVNQ; SCSLEVNQD; CSLEVNQDD; SLEVNQDDN; LEVNQDDNQ; EVNQDDNQE; VNQDDNQEK; NQDDNQEKQ; QDDNQEKQK; DDNQEKQKK; DNQEKQKKA; NQEKQKKAK; QEKQKKAKT; EKQKKAKTK; KQKKAKTKT; QKKAKTKTS; KKAKTKTSK; KAKTKTSKS; AKTKTSKSE; KTKTSKSEN; TKTSKSENN; KTSKSENNS; TSKSENNSS; SKSENNSSK; KSENNSSKM; SENNSSKMK; ENNSSKMKK; NNSSKMKKL; NSSKMKKLS; SSKMKKLSK; SKMKKLSKN; KMKKLSKNA; MKKLSKNAK; KKLSKNAKN; KLSKNAKNK; LSKNAKNKK; SKNAKNKKP; KNAKNKKPT; NAKNKKPTV; AKNKKPTVD; KNKKPTVDN; NKKPTVDNL; KKPTVDNLL; KPTVDNLLV; PTVDNLLVA; TVDNLLVAI; VDNLLVAIN; DNLLVAINT; NLLVAINTL; LLVAINTLK; LVAINTLKN; VAINTLKNP; AINTLKNPP; INTLKNPPK; NTLKNPPKT; TLKNPPKTA; LKNPPKTAG; KNPPKTAGK; NPPKTAGKN; PPKTAGKNK; PKTAGKNKS; KTAGKNKSN; TAGKNKSNS; AGKNKSNSA; GKNKSNSAA; KNKSNSAAA; NKSNSAAAL; KSNSAAALK; SNSAAALKQ; NSAAALKQP; SAAALKQPN; AAALKQPNN; AALKQPNNA; ALKQPNNAN; LKQPNNANA; KQPNNANAL; QPNNANALK; PNNANALKQ; NNANALKQI; NANALKQID; ANALKQIDP; NALKQIDPE; ALKQIDPEA; LKQIDPEAK; KQIDPEAKE; QIDPEAKEL; IDPEAKELI; DPEAKELIQ; PEAKELIQK; EAKELIQKI; AKELIQKIL; KELIQKILE; ELIQKILER; LIQKILERS; IQKILERSE; QKILERSED; KILERSEDI; ILERSEDIV; LERSEDIVQ; ERSEDIVQI; RSEDIVQIS; SEDIVQISE; EDIVQISEI; DIVQISEID; IVQISEIDA;

VQISEIDAN; QISEIDANK; ISEIDANKG; SEIDANKGE; EIDANKGEP; IDANKGEPD; DANKGEPDD; ANKGEPDDQ; NKGEPDDQF; KGEPDDQFE; GEPDDQFEM; EPDDQFEMK; PDDQFEMKA; DDQFEMKAE; DQFEMKAEI; QFEMKAEIF; FEMKAEIFS; EMKAEIFSK; MKAEIFSKI; KAEIFSKIF; AEIFSKIFF; EIFSKIFFN; IFSKIFFNA; FSKIFFNAG; SKIFFNAGS; KIFFNAGST; IFFNAGSTV; FFNAGSTVT; FNAGSTVTF; NAGSTVTFD; AGSTVTFDD; GSTVTFDDN; STVTFDDNE; TVTFDDNEY; VTFDDNEYV; TFDDNEYVN; FDDNEYVNE; DDNEYVNER; DNEYVNERR; NEYVNERRI; EYVNERRIL; YVNERRILY; VNERRILYT; NERRILYTS; ERRILYTSL; RRILYTSLN; RILYTSLNF; ILYTSLNFN; LYTSLNFNE; YTSLNFNEN; TSLNFNENK; SLNFNENKI; LNFNENKIL; NFNENKILN; FNENKILNL; NENKILNLG; ENKILNLGK; NKILNLGKI; KILNLGKIL; ILNLGKILS; LNLGKILSK; NLGKILSKL; LGKILSKLS; GKILSKLSQ; KILSKLSQD; ILSKLSQDS; LSKLSQDSN; SKLSQDSNY; KLSQDSNYR; LSQDSNYRS; SQDSNYRSL; QDSNYRSLV; DSNYRSLVK; SNYRSLVKE; NYRSLVKEI; YRSLVKEIL; RSLVKEILI; SLVKEILIN; LVKEILINR; VKEILINRG; KEILINRGF; EILINRGFS; ILINRGFSI; LINRGFSIQ; INRGFSIQL; NRGFSIQLA; RGFSIQLAI; GFSIQLAIE; FSIQLAIEE; SIQLAIEEI; IQLAIEEIS; QLAIEEISL; LAIEEISLR; AIEEISLRT; IEEISLRTL; EEISLRTLN; EISLRTLNV; ISLRTLNVK; SLRTLNVKD; LRTLNVKDK; RTLNVKDKI; TLNVKDKIQ; LNVKDKIQH; NVKDKIQHL; VKDKIQHLN; KDKIQHLNK; DKIQHLNKP; KIQHLNKPN; IQHLNKPNL; QHLNKPNLK; HLNKPNLKT; LNKPNLKTL; NKPNLKTLY; KPNLKTLYH; PNLKTLYHD; NLKTLYHDF; LKTLYHDFN; KTLYHDFNK; TLYHDFNKL; LYHDFNKLI; YHDFNKLIP; HDFNKLIPL; DFNKLIPLK; FNKLIPLKE; NKLIPLKEK; KLIPLKEKW; LIPLKEKWL; IPLKEKWLK; PLKEKWLKD; LKEKWLKDV; KEKWLKDVD; EKWLKDVDD; KWLKDVDDI; WLKDVDDII; LKDVDDIIK; KDVDDIIKD; DVDDIIKDY; VDDIIKDYN; DDIIKDYNA; DIIKDYNAN; IIKDYNANP; IKDYNANPE; KDYNANPEL; DYNANPELR; YNANPELRT; NANPELRTD; ANPELRTDI; NPELRTDIS; PELRTDISK; ELRTDISKL; LRTDISKLN; RTDISKLND; TDISKLNDY; DISKLNDYI; ISKLNDYII; SKLNDYIIS; KLNDYIISK; LNDYIISKN; NDYIISKNS; DYIISKNSK; YIISKNSKA; IISKNSKAQ; ISKNSKAQF; SKNSKAQFT; KNSKAQFTD; NSKAQFTDI; SKAQFTDIH; KAQFTDIHN; AQFTDIHNI; QFTDIHNII; FTDIHNIIL; TDIHNIILN; DIHNIILNL; IHNIILNLI; HNIILNLIN; NIILNLINT; IILNLINTT; ILNLINTTT; LNLINTTTN; NLINTTTNI; LINTTTNIL; INTTTNILA; NTTTNILAP; TTTNILAPI; TTNILAPIQ;

10 mers:
MKNNKLIAIF; KNNKLIAIFL; NNKLIAIFLL; NKLIAIFLLH; KLIAIFLLHI; LIAIFLLHIL; IAIFLLHILT; AIFLLHILTG; IFLLHILTGL; FLLHILTGLI; LLHILTGLIL; LHILTGLILL; HILTGLILLS; ILTGLILLSC; LTGLILLSCS; TGLILLSCSL; GLILLSCSLE; LILLSCSLEV; ILLSCSLEVN; LLSCSLEVNQ; LSCSLEVNQD; SCSLEVNQDD; CSLEVNQDDN; SLEVNQDDNQ; LEVNQDDNQE; EVNQDDNQEK; VNQDDNQEKQ; NQDDNQEKQK; QDDNQEKQKK; DDNQEKQKKA; DNQEKQKKAK; NQEKQKKAKT; QEKQKKAKTK; EKQKKAKTKT; KQKKAKTKTS; QKKAKTKTSK; KKAKTKTSKS; KAKTKTSKSE; AKTKTSKSEN; KTKTSKSENN; TKTSKSENNS; KTSKSENNSS; TSKSENNSSK; SKSENNSSKM; KSENNSSKMK; SENNSSKMKK; ENNSSKMKKL; NNSSKMKKLS;

	NSSKMKKLSK; SSKMKKLSKN; SKMKKLSKNA; KMKKLSKNAK; MKKLSKNAKN; KKLSKNAKNK; KLSKNAKNKK; LSKNAKNKKP; SKNAKNKKPT; KNAKNKKPTV; NAKNKKPTVD; AKNKKPTVDN; KNKKPTVDNL; NKKPTVDNLL; KKPTVDNLLV; KPTVDNLLVA; PTVDNLLVAI; TVDNLLVAIN; VDNLLVAINT; DNLLVAINTL; NLLVAINTLK; LLVAINTLKN; LVAINTLKNP; VAINTLKNPP; AINTLKNPPK; INTLKNPPKT; NTLKNPPKTA; TLKNPPKTAG; LKNPPKTAGK; KNPPKTAGKN; NPPKTAGKNK; PPKTAGKNKS; PKTAGKNKSN; KTAGKNKSNS; TAGKNKSNSA; AGKNKSNSAA; GKNKSNSAAA; KNKSNSAAAL; NKSNSAAALK; KSNSAAALKQ; SNSAAALKQP; NSAAALKQPN; SAAALKQPNN; AAALKQPNNA; AALKQPNNAN; ALKQPNNANA; LKQPNNANAL; KQPNNANALK; QPNNANALKQ; PNNANALKQI; NNANALKQID; NANALKQIDP; ANALKQIDPE; NALKQIDPEA; ALKQIDPEAK; LKQIDPEAKE; KQIDPEAKEL; QIDPEAKELI; IDPEAKELIQ; DPEAKELIQK; PEAKELIQKI; EAKELIQKIL; AKELIQKILE; KELIQKILER; ELIQKILERS; LIQKILERSE; IQKILERSED; QKILERSEDI; KILERSEDIV; ILERSEDIVQ; LERSEDIVQI; ERSEDIVQIS; RSEDIVQISE; SEDIVQISEI; EDIVQISEID; DIVQISEIDA; IVQISEIDAN; VQISEIDANK; QISEIDANKG; ISEIDANKGE; SEIDANKGEP; EIDANKGEPD; IDANKGEPDD; DANKGEPDDQ; ANKGEPDDQF; NKGEPDDQFE; KGEPDDQFEM; GEPDDQFEMK; EPDDQFEMKA; PDDQFEMKAE; DDQFEMKAEI; DQFEMKAEIF; QFEMKAEIFS; FEMKAEIFSK; EMKAEIFSKI; MKAEIFSKIF; KAEIFSKIFF; AEIFSKIFFN; EIFSKIFFNA; IFSKIFFNAG; FSKIFFNAGS; SKIFFNAGST; KIFFNAGSTV; IFFNAGSTVT; FFNAGSTVTF; FNAGSTVTFD; NAGSTVTFDD; AGSTVTFDDN; GSTVTFDDNE; STVTFDDNEY; TVTFDDNEYV; VTFDDNEYVN; TFDDNEYVNE; FDDNEYVNER; DDNEYVNERR; DNEYVNERRI; NEYVNERRIL; EYVNERRILY; YVNERRILYT; VNERRILYTS; NERRILYTSL; ERRILYTSLN; RRILYTSLNF; RILYTSLNFN; ILYTSLNFNE; LYTSLNFNEN; YTSLNFNENK; TSLNFNENKI; SLNFNENKIL; LNFNENKILN; NFNENKILNL; FNENKILNLG; NENKILNLGK; ENKILNLGKI; NKILNLGKIL; KILNLGKILS; ILNLGKILSK; LNLGKILSKL; NLGKILSKLS; LGKILSKLSQ; GKILSKLSQD; KILSKLSQDS; ILSKLSQDSN; LSKLSQDSNY; SKLSQDSNYR; KLSQDSNYRS; LSQDSNYRSL; SQDSNYRSLV; QDSNYRSLVK; DSNYRSLVKE; SNYRSLVKEI; NYRSLVKEIL; YRSLVKEILI; RSLVKEILIN; SLVKEILINR; LVKEILINRG; VKEILINRGF; KEILINRGFS; EILINRGFSI; ILINRGFSIQ; LINRGFSIQL; INRGFSIQLA; NRGFSIQLAI; RGFSIQLAIE; GFSIQLAIEE; FSIQLAIEEI; SIQLAIEEIS; IQLAIEEISL; QLAIEEISLR; LAIEEISLRT; AIEEISLRTL; IEEISLRTLN; EEISLRTLNV; EISLRTLNVK; ISLRTLNVKD; SLRTLNVKDK; LRTLNVKDKI; RTLNVKDKIQ; TLNVKDKIQH; LNVKDKIQHL; NVKDKIQHLN; VKDKIQHLNK; KDKIQHLNKP; DKIQHLNKPN; KIQHLNKPNL; IQHLNKPNLK; QHLNKPNLKT; HLNKPNLKTL; LNKPNLKTLY; NKPNLKTLYH; KPNLKTLYHD; PNLKTLYHDF; NLKTLYHDFN; LKTLYHDFNK; KTLYHDFNKL; TLYHDFNKLI; LYHDFNKLIP; YHDFNKLIPL; HDFNKLIPLK; DFNKLIPLKE; FNKLIPLKEK; NKLIPLKEKW; KLIPLKEKWL; LIPLKEKWLK;

IPLKEKWLKD; PLKEKWLKDV; LKEKWLKDVD; KEKWLKDVDD;
EKWLKDVDDI; KWLKDVDDII; WLKDVDDIIK; LKDVDDIIKD;
KDVDDIIKDY; DVDDIIKDYN; VDDIIKDYNA; DDIIKDYNAN;
DIIKDYNANP; IIKDYNANPE; IKDYNANPEL; KDYNANPELR;
DYNANPELRT; YNANPELRTD; NANPELRTDI; ANPELRTDIS;
NPELRTDISK; PELRTDISKL; ELRTDISKLN; LRTDISKLND;
RTDISKLNDY; TDISKLNDYI; DISKLNDYII; ISKLNDYIIS;
SKLNDYIISK; KLNDYIISKN; LNDYIISKNS; NDYIISKNSK;
DYIISKNSKA; YIISKNSKAQ; IISKNSKAQF; ISKNSKAQFT;
SKNSKAQFTD; KNSKAQFTDI; NSKAQFTDIH; SKAQFTDIHN;
KAQFTDIHNI; AQFTDIHNII; QFTDIHNIIL; FTDIHNIILN;
TDIHNIILNL; DIHNIILNLI; IHNIILNLIN; HNIILNLINT;
NIILNLINTT; IILNLINTTT; ILNLINTTTN; LNLINTTTNI;
NLINTTTNIL; LINTTTNILA; INTTTNILAP; NTTTNILAPI;
TTTNILAPIQ;

11 mers:
MKNNKLIAIFL; KNNKLIAIFLL; NNKLIAIFLLH; NKLIAIFLLHI;
KLIAIFLLHIL; LIAIFLLHILT; IAIFLLHILTG; AIFLLHILTGL;
IFLLHILTGLI; FLLHILTGLIL; LLHILTGLILL; LHILTGLILLS;
HILTGLILLSC; ILTGLILLSCS; LTGLILLSCSL; TGLILLSCSLE;
GLILLSCSLEV; LILLSCSLEVN; ILLSCSLEVNQ; LLSCSLEVNQD;
LSCSLEVNQDD; SCSLEVNQDDN; CSLEVNQDDNQ; SLEVNQDDNQE;
LEVNQDDNQEK; EVNQDDNQEKQ; VNQDDNQEKQK; NQDDNQEKQKK;
QDDNQEKQKKA; DDNQEKQKKAK; DNQEKQKKAKT; NQEKQKKAKTK;
QEKQKKAKTKT; EKQKKAKTKTS; KQKKAKTKTSK; QKKAKTKTSKS;
KKAKTKTSKSE; KAKTKTSKSEN; AKTKTSKSENN; KTKTSKSENNS;
TKTSKSENNSS; KTSKSENNSSK; TSKSENNSSKM; SKSENNSSKMK;
KSENNSSKMKK; SENNSSKMKKL; ENNSSKMKKLS; NNSSKMKKLSK;
NSSKMKKLSKN; SSKMKKLSKNA; SKMKKLSKNAK; KMKKLSKNAKN;
MKKLSKNAKNK; KKLSKNAKNKK; KLSKNAKNKKP; LSKNAKNKKPT;
SKNAKNKKPTV; KNAKNKKPTVD; NAKNKKPTVDN; AKNKKPTVDNL;
KNKKPTVDNLL; NKKPTVDNLLV; KKPTVDNLLVA; KPTVDNLLVAI;
PTVDNLLVAIN; TVDNLLVAINT; VDNLLVAINTL; DNLLVAINTLK;
NLLVAINTLKN; LLVAINTLKNP; LVAINTLKNPP; VAINTLKNPPK;
AINTLKNPPKT; INTLKNPPKTA; NTLKNPPKTAG; TLKNPPKTAGK;
LKNPPKTAGKN; KNPPKTAGKNK; NPPKTAGKNKS; PPKTAGKNKSN;
PKTAGKNKSNS; KTAGKNKSNSA; TAGKNKSNSAA; AGKNKSNSAAA;
GKNKSNSAAAL; KNKSNSAAALK; NKSNSAAALKQ; KSNSAAALKQP;
SNSAAALKQPN; NSAAALKQPNN; SAAALKQPNNA; AAALKQPNNAN;
AALKQPNNANA; ALKQPNNANAL; LKQPNNANALK; KQPNNANALKQ;
QPNNANALKQI; PNNANALKQID; NNANALKQIDP; NANALKQIDPE;
ANALKQIDPEA; NALKQIDPEAK; ALKQIDPEAKE; LKQIDPEAKEL;
KQIDPEAKELI; QIDPEAKELIQ; IDPEAKELIQK; DPEAKELIQKI;
PEAKELIQKIL; EAKELIQKILE; AKELIQKILER; KELIQKILERS;
ELIQKILERSE; LIQKILERSED; IQKILERSEDI; QKILERSEDIV;
KILERSEDIVQ; ILERSEDIVQI; LERSEDIVQIS; ERSEDIVQISE;
RSEDIVQISEI; SEDIVQISEID; EDIVQISEIDA; DIVQISEIDAN;
IVQISEIDANK; VQISEIDANKG; QISEIDANKGE; ISEIDANKGEP;
SEIDANKGEPD; EIDANKGEPDD; IDANKGEPDDQ; DANKGEPDDQF;
ANKGEPDDQFE; NKGEPDDQFEM; KGEPDDQFEMK; GEPDDQFEMKA;

	EPDDQFEMKAE; PDDQFEMKAEI; DDQFEMKAEIF; DQFEMKAEIFS; QFEMKAEIFSK; FEMKAEIFSKI; EMKAEIFSKIF; MKAEIFSKIFF; KAEIFSKIFFN; AEIFSKIFFNA; EIFSKIFFNAG; IFSKIFFNAGS; FSKIFFNAGST; SKIFFNAGSTV; KIFFNAGSTVT; IFFNAGSTVTF; FFNAGSTVTFD; FNAGSTVTFDD; NAGSTVTFDDN; AGSTVTFDDNE; GSTVTFDDNEY; STVTFDDNEYV; TVTFDDNEYVN; VTFDDNEYVNE; TFDDNEYVNER; FDDNEYVNERR; DDNEYVNERRI; DNEYVNERRIL; NEYVNERRILY; EYVNERRILYT; YVNERRILYTS; VNERRILYTSL; NERRILYTSLN; ERRILYTSLNF; RRILYTSLNFN; RILYTSLNFNE; ILYTSLNFNEN; LYTSLNFNENK; YTSLNFNENKI; TSLNFNENKIL; SLNFNENKILN; LNFNENKILNL; NFNENKILNLG; FNENKILNLGK; NENKILNLGKI; ENKILNLGKIL; NKILNLGKILS; KILNLGKILSK; ILNLGKILSKL; LNLGKILSKLS; NLGKILSKLSQ; LGKILSKLSQD; GKILSKLSQDS; KILSKLSQDSN; ILSKLSQDSNY; LSKLSQDSNYR; SKLSQDSNYRS; KLSQDSNYRSL; LSQDSNYRSLV; SQDSNYRSLVK; QDSNYRSLVKE; DSNYRSLVKEI; SNYRSLVKEIL; NYRSLVKEILI; YRSLVKEILIN; RSLVKEILINR; SLVKEILINRG; LVKEILINRGF; VKEILINRGFS; KEILINRGFSI; EILINRGFSIQ; ILINRGFSIQL; LINRGFSIQLA; INRGFSIQLAI; NRGFSIQLAIE; RGFSIQLAIEE; GFSIQLAIEEI; FSIQLAIEEIS; SIQLAIEEISL; IQLAIEEISLR; QLAIEEISLRT; LAIEEISLRTL; AIEEISLRTLN; IEEISLRTLNV; EEISLRTLNVK; EISLRTLNVKD; ISLRTLNVKDK; SLRTLNVKDKI; LRTLNVKDKIQ; RTLNVKDKIQH; TLNVKDKIQHL; LNVKDKIQHLN; NVKDKIQHLNK; VKDKIQHLNKP; KDKIQHLNKPN; DKIQHLNKPNL; KIQHLNKPNLK; IQHLNKPNLKT; QHLNKPNLKTL; HLNKPNLKTLY; LNKPNLKTLYH; NKPNLKTLYHD; KPNLKTLYHDF; PNLKTLYHDFN; NLKTLYHDFNK; LKTLYHDFNKL; KTLYHDFNKLI; TLYHDFNKLIP; LYHDFNKLIPL; YHDFNKLIPLK; HDFNKLIPLKE; DFNKLIPLKEK; FNKLIPLKEKW; NKLIPLKEKWL; KLIPLKEKWLK; LIPLKEKWLKD; IPLKEKWLKDV; PLKEKWLKDVD; LKEKWLKDVDD; KEKWLKDVDDI; EKWLKDVDDII; KWLKDVDDIIK; WLKDVDDIIKD; LKDVDDIIKDY; KDVDDIIKDYN; DVDDIIKDYNA; VDDIIKDYNAN; DDIIKDYNANP; DIIKDYNANPE; IIKDYNANPEL; IKDYNANPELR; KDYNANPELRT; DYNANPELRTD; YNANPELRTDI; NANPELRTDIS; ANPELRTDISK; NPELRTDISKL; PELRTDISKLN; ELRTDISKLND; LRTDISKLNDY; RTDISKLNDYI; TDISKLNDYII; DISKLNDYIIS; ISKLNDYIISK; SKLNDYIISKN; KLNDYIISKNS; LNDYIISKNSK; NDYIISKNSKA; DYIISKNSKAQ; YIISKNSKAQF; IISKNSKAQFT; ISKNSKAQFTD; SKNSKAQFTDI; KNSKAQFTDIH; NSKAQFTDIHN; SKAQFTDIHNI; KAQFTDIHNII; AQFTDIHNIIL; QFTDIHNIILN; FTDIHNIILNL; TDIHNIILNLI; DIHNIILNLIN; IHNIILNLINT; HNIILNLINTT; NIILNLINTTT; IILNLINTTTN; ILNLINTTTNI; LNLINTTTNIL; NLINTTTNILA; LINTTTNILAP; INTTTNILAPI; NTTTNILAPIQ;
Seq 42	SEQ ID NO 49645-51050/ 8 mers: MKKVKSKY; KKVKSKYL; KVKSKYLA; VKSKYLAL; KSKYLALG; SKYLALGL; KYLALGLL; YLALGLLF; LALGLLFG; ALGLLFGF; LGLLFGFI; GLLFGFIS; LLFGFISC; LFGFISCD; FGFISCDL; GFISCDLF; FISCDLFI; ISCDLFIR; SCDLFIRY; CDLFIRYE; DLFIRYEM; LFIRYEMK; FIRYEMKE; IRYEMKEE; RYEMKEES;

	YEMKEESP; EMKEESPG; MKEESPGL; KEESPGLF; EESPGLFD; ESPGLFDK; SPGLFDKG; PGLFDKGN; GLFDKGNS; LFDKGNSI; FDKGNSIL; DKGNSILE; KGNSILET; GNSILETS; NSILETSE; SILETSEE; ILETSEES; LETSEESI; ETSEESIK; TSEESIKK; SEESIKKP; EESIKKPM; ESIKKPMN; SIKKPMNK; IKKPMNKK; KKPMNKKG; KPMNKKGK; PMNKKGKG; MNKKGKGK; NKKGKGKI; KKGKGKIA; KGKGKIAR; GKGKIARK; KGKIARKK; GKIARKKG; KIARKKGK; IARKKGKS; ARKKGKSK; RKKGKSKV; KKGKSKVS; KGKSKVSR; GKSKVSRK; KSKVSRKE; SKVSRKEP; KVSRKEPY; VSRKEPYI; SRKEPYIH; RKEPYIHS; KEPYIHSL; EPYIHSLK; PYIHSLKR; YIHSLKRD; IHSLKRDS; HSLKRDSA; SLKRDSAN; LKRDSANK; KRDSANKS; RDSANKSN; DSANKSNF; SANKSNFL; ANKSNFLQ; NKSNFLQK; KSNFLQKN; SNFLQKNV; NFLQKNVI; FLQKNVIL; LQKNVILE; QKNVILEE; KNVILEEE; NVILEEES; VILEEESL; ILEEESLK; LEEESLKT; EEESLKTE; EESLKTEL; ESLKTELL; SLKTELLK; LKTELLKE; KTELLKEQ; TELLKEQS; ELLKEQSE; LLKEQSET; LKEQSETR; KEQSETRK; EQSETRKE; QSETRKEK; SETRKEKI; ETRKEKIQ; TRKEKIQK; RKEKIQKQ; KEKIQKQQ; EKIQKQQD; KIQKQQDE; IQKQQDEY; QKQQDEYK; KQQDEYKG; QQDEYKGM; QDEYKGMT; DEYKGMTQ; EYKGMTQG; YKGMTQGS; KGMTQGSL; GMTQGSLN; MTQGSLNS; TQGSLNSL; QGSLNSLS; GSLNSLSG; SLNSLSGE; LNSLSGES; NSLSGESG; SLSGESGE; LSGESGEL; SGESGELK; GESGELKE; ESGELKET; SGELKETI; GELKETIE; ELKETIES; LKETIESN; KETIESNE; ETIESNEI; TIESNEID; IESNEIDI; ESNEIDIT; SNEIDITI; NEIDITID; EIDITIDS; IDITIDSD; DITIDSDL; ITIDSDLR; TIDSDLRP; IDSDLRPK; DSDLRPKS; SDLRPKSS; DLRPKSSL; LRPKSSLQ; RPKSSLQD; PKSSLQDI; KSSLQDIA; SSLQDIAG; SLQDIAGS; LQDIAGSN; QDIAGSNS; DIAGSNSI; IAGSNSIS; AGSNSISY; GSNSISYT; SNSISYTD; NSISYTDE; SISYTDEI; ISYTDEIE; SYTDEIEE; YTDEIEEE; TDEIEEED; DEIEEEDY; EIEEEDYA; IEEEDYAR; EEEDYARY; EEDYARYY; EDYARYYL; DYARYYLD; YARYYLDE; ARYYLDED; RYYLDEDD; YYLDEDDE; YLDEDDED; LDEDDEDD; DEDDEDDE; EDDEDDEY; DDEDDEYY; DEDDEYYE; EDDEYYED; DDEYYEDD; DEYYEDDY; EYYEDDYE; YYEDDYEE; YEDDYEEI; EDDYEEIR; DDYEEIRL; DYEEIRLS; YEEIRLSN; EEIRLSNR; EIRLSNRY; IRLSNRYQ; RLSNRYQS; LSNRYQSY; SNRYQSYL; NRYQSYLE; RYQSYLEG; YQSYLEGV; QSYLEGVK; SYLEGVKY; YLEGVKYN; LEGVKYNV; EGVKYNVD; GVKYNVDS; VKYNVDSA; KYNVDSAI; YNVDSAIN; NVDSAINT; VDSAINTI; DSAINTIN; SAINTINK; AINTINKI; INTINKIY; NTINKIYD; TINKIYDT; INKIYDTY; NKIYDTYT; KIYDTYTL; IYDTYTLF; YDTYTLFS; DTYTLFST; TYTLFSTK; YTLFSTKL; TLFSTKLT; LFSTKLTQ; FSTKLTQM; STKLTQMY; TKLTQMYS; KLTQMYST; LTQMYSTR; TQMYSTRL; QMYSTRLD; MYSTRLDN; YSTRLDNL; STRLDNLA; TRLDNLAK; RLDNLAKA; LDNLAKAK; DNLAKAKA; NLAKAKAK; LAKAKAKE; AKAKAKEE; KAKAKEEA; AKAKEEAA; KAKEEAAK; AKEEAAKF; KEEAAKFT; EEAAKFTK; EAAKFTKE; AAKFTKED; AKFTKEDL; KFTKEDLE; FTKEDLEK; TKEDLEKN; KEDLEKNF; EDLEKNFK; DLEKNFKT; LEKNFKTL; EKNFKTLL; KNFKTLLN; NFKTLLNY; FKTLLNYI; KTLLNYIQ;

	TLLNYIQV; LLNYIQVS; LNYIQVSV; NYIQVSVK; YIQVSVKT; IQVSVKTA; QVSVKTAA; VSVKTAAN; SVKTAANF; VKTAANFV; KTAANFVY; TAANFVYI; AANFVYIN; ANFVYIND; NFVYINDT; FVYINDTH; VYINDTHA; YINDTHAK; INDTHAKR; NDTHAKRK; DTHAKRKL; THAKRKLE; HAKRKLEN; AKRKLENI; KRKLENIE; RKLENIEA; KLENIEAE; LENIEAEI; ENIEAEIK; NIEAEIKT; IEAEIKTL; EAEIKTLI; AEIKTLIA; EIKTLIAK; IKTLIAKI; KTLIAKIK; TLIAKIKE; LIAKIKEQ; IAKIKEQS; AKIKEQSN; KIKEQSNL; IKEQSNLY; KEQSNLYE; EQSNLYEA; QSNLYEAY; SNLYEAYK; NLYEAYKA; LYEAYKAI; YEAYKAIV; EAYKAIVT; AYKAIVTS; YKAIVTSI; KAIVTSIL; AIVTSILL; IVTSILLM; VTSILLMR; TSILLMRD; SILLMRDS; ILLMRDSL; LLMRDSLK; LMRDSLKE; MRDSLKEV; RDSLKEVQ; DSLKEVQG; SLKEVQGI; LKEVQGII; KEVQGIID; EVQGIIDK; VQGIIDKN; QGIIDKNG; GIIDKNGV; IIDKNGVW; IDKNGVWY; 9 mers: MKKVKSKYL; KKVKSKYLA; KVKSKYLAL; VKSKYLALG; KSKYLALGL; SKYLALGLL; KYLALGLLF; YLALGLLFG; LALGLLFGF; ALGLLFGFI; LGLLFGFIS; GLLFGFISC; LLFGFISCD; LFGFISCDL; FGFISCDLF; GFISCDLFI; FISCDLFIR; ISCDLFIRY; SCDLFIRYE; CDLFIRYEM; DLFIRYEMK; LFIRYEMKE; FIRYEMKEE; IRYEMKEES; RYEMKEESP; YEMKEESPG; EMKEESPGL; MKEESPGLF; KEESPGLFD; EESPGLFDK; ESPGLFDKG; SPGLFDKGN; PGLFDKGNS; GLFDKGNSI; LFDKGNSIL; FDKGNSILE; DKGNSILET; KGNSILETS; GNSILETSE; NSILETSEE; SILETSEES; ILETSEESI; LETSEESIK; ETSEESIKK; TSEESIKKP; SEESIKKPM; EESIKKPMN; ESIKKPMNK; SIKKPMNKK; IKKPMNKKG; KKPMNKKGK; KPMNKKGKG; PMNKKGKGK; MNKKGKGKI; NKKGKGKIA; KKGKGKIAR; KGKGKIARK; GKGKIARKK; KGKIARKKG; GKIARKKGK; KIARKKGKS; IARKKGKSK; ARKKGKSKV; RKKGKSKVS; KKGKSKVSR; KGKSKVSRK; GKSKVSRKE; KSKVSRKEP; SKVSRKEPY; KVSRKEPYI; VSRKEPYIH; SRKEPYIHS; RKEPYIHSL; KEPYIHSLK; EPYIHSLKR; PYIHSLKRD; YIHSLKRDS; IHSLKRDSA; HSLKRDSAN; SLKRDSANK; LKRDSANKS; KRDSANKSN; RDSANKSNF; DSANKSNFL; SANKSNFLQ; ANKSNFLQK; NKSNFLQKN; KSNFLQKNV; SNFLQKNVI; NFLQKNVIL; FLQKNVILE; LQKNVILEE; QKNVILEEE; KNVILEEES; NVILEEESL; VILEEESLK; ILEEESLKT; LEEESLKTE; EEESLKTEL; EESLKTELL; ESLKTELLK; SLKTELLKE; LKTELLKEQ; KTELLKEQS; TELLKEQSE; ELLKEQSET; LLKEQSETR; LKEQSETRK; KEQSETRKE; EQSETRKEK; QSETRKEKI; SETRKEKIQ; ETRKEKIQK; TRKEKIQKQ; RKEKIQKQQ; KEKIQKQQD; EKIQKQQDE; KIQKQQDEY; IQKQQDEYK; QKQQDEYKG; KQQDEYKGM; QQDEYKGMT; QDEYKGMTQ; DEYKGMTQG; EYKGMTQGS; YKGMTQGSL; KGMTQGSLN; GMTQGSLNS; MTQGSLNSL; TQGSLNSLS; QGSLNSLSG; GSLNSLSGE; SLNSLSGES; LNSLSGESG; NSLSGESGE; SLSGESGEL; LSGESGELK; SGESGELKE; GESGELKET; ESGELKETI; SGELKETIE; GELKETIES; ELKETIESN; LKETIESNE; KETIESNEI; ETIESNEID; TIESNEIDI; IESNEIDIT; ESNEIDITI; SNEIDITID; NEIDITIDS; EIDITIDSD; IDITIDSDL; DITIDSDLR; ITIDSDLRP; TIDSDLRPK; IDSDLRPKS; DSDLRPKSS; SDLRPKSSL; DLRPKSSLQ; LRPKSSLQD; RPKSSLQDI; PKSSLQDIA; KSSLQDIAG; SSLQDIAGS; SLQDIAGSN; LQDIAGSNS; QDIAGSNSI; DIAGSNSIS; IAGSNSISY;

AGSNSISYT; GSNSISYTD; SNSISYTDE; NSISYTDEI; SISYTDEIE;
ISYTDEIEE; SYTDEIEEE; YTDEIEEED; TDEIEEEDY; DEIEEEDYA;
EIEEEDYAR; IEEEDYARY; EEEDYARYY; EEDYARYYL; EDYARYYLD;
DYARYYLDE; YARYYLDED; ARYYLDEDD; RYYLDEDDE; YYLDEDDED;
YLDEDDEDD; LDEDDEDDE; DEDDEDDEY; EDDEDDEYY; DDEDDEYYE;
DEDDEYYED; EDDEYYEDD; DDEYYEDDY; DEYYEDDYE; EYYEDDYEE;
YYEDDYEEI; YEDDYEEIR; EDDYEEIRL; DDYEEIRLS; DYEEIRLSN;
YEEIRLSNR; EEIRLSNRY; EIRLSNRYQ; IRLSNRYQS; RLSNRYQSY;
LSNRYQSYL; SNRYQSYLE; NRYQSYLEG; RYQSYLEGV; YQSYLEGVK;
QSYLEGVKY; SYLEGVKYN; YLEGVKYNV; LEGVKYNVD; EGVKYNVDS;
GVKYNVDSA; VKYNVDSAI; KYNVDSAIN; YNVDSAINT; NVDSAINTI;
VDSAINTIN; DSAINTINK; SAINTINKI; AINTINKIY; INTINKIYD;
NTINKIYDT; TINKIYDTY; INKIYDTYT; NKIYDTYTL; KIYDTYTLF;
IYDTYTLFS; YDTYTLFST; DTYTLFSTK; TYTLFSTKL; YTLFSTKLT;
TLFSTKLTQ; LFSTKLTQM; FSTKLTQMY; STKLTQMYS; TKLTQMYST;
KLTQMYSTR; LTQMYSTRL; TQMYSTRLD; QMYSTRLDN; MYSTRLDNL;
YSTRLDNLA; STRLDNLAK; TRLDNLAKA; RLDNLAKAK; LDNLAKAKA;
DNLAKAKAK; NLAKAKAKE; LAKAKAKEE; AKAKAKEEA; KAKAKEEAA;
AKAKEEAAK; KAKEEAAKF; AKEEAAKFT; KEEAAKFTK; EEAAKFTKE;
EAAKFTKED; AAKFTKEDL; AKFTKEDLE; KFTKEDLEK; FTKEDLEKN;
TKEDLEKNF; KEDLEKNFK; EDLEKNFKT; DLEKNFKTL; LEKNFKTLL;
EKNFKTLLN; KNFKTLLNY; NFKTLLNYI; FKTLLNYIQ; KTLLNYIQV;
TLLNYIQVS; LLNYIQVSV; LNYIQVSVK; NYIQVSVKT; YIQVSVKTA;
IQVSVKTAA; QVSVKTAAN; VSVKTAANF; SVKTAANFV; VKTAANFVY;
KTAANFVYI; TAANFVYIN; AANFVYIND; ANFVYINDT; NFVYINDTH;
FVYINDTHA; VYINDTHAK; YINDTHAKR; INDTHAKRK; NDTHAKRKL;
DTHAKRKLE; THAKRKLEN; HAKRKLENI; AKRKLENIE; KRKLENIEA;
RKLENIEAE; KLENIEAEI; LENIEAEIK; ENIEAEIKT; NIEAEIKTL;
IEAEIKTLI; EAEIKTLIA; AEIKTLIAK; EIKTLIAKI; IKTLIAKIK;
KTLIAKIKE; TLIAKIKEQ; LIAKIKEQS; IAKIKEQSN; AKIKEQSNL;
KIKEQSNLY; IKEQSNLYE; KEQSNLYEA; EQSNLYEAY; QSNLYEAYK;
SNLYEAYKA; NLYEAYKAI; LYEAYKAIV; YEAYKAIVT; EAYKAIVTS;
AYKAIVTSI; YKAIVTSIL; KAIVTSILL; AIVTSILLM; IVTSILLMR;
VTSILLMRD; TSILLMRDS; SILLMRDSL; ILLMRDSLK; LLMRDSLKE;
LMRDSLKEV; MRDSLKEVQ; RDSLKEVQG; DSLKEVQGI; SLKEVQGII;
LKEVQGIID; KEVQGIIDK; EVQGIIDKN; VQGIIDKNG; QGIIDKNGV;
GIIDKNGVW; IIDKNGVWY;

10 mers:
MKKVKSKYLA; KKVKSKYLAL; KVKSKYLALG; VKSKYLALGL;
KSKYLALGLL; SKYLALGLLF; KYLALGLLFG; YLALGLLFGF;
LALGLLFGFI; ALGLLFGFIS; LGLLFGFISC; GLLFGFISCD;
LLFGFISCDL; LFGFISCDLF; FGFISCDLFI; GFISCDLFIR;
FISCDLFIRY; ISCDLFIRYE; SCDLFIRYEM; CDLFIRYEMK;
DLFIRYEMKE; LFIRYEMKEE; FIRYEMKEES; IRYEMKEESP;
RYEMKEESPG; YEMKEESPGL; EMKEESPGLF; MKEESPGLFD;
KEESPGLFDK; EESPGLFDKG; ESPGLFDKGN; SPGLFDKGNS;
PGLFDKGNSI; GLFDKGNSIL; LFDKGNSILE; FDKGNSILET;
DKGNSILETS; KGNSILETSE; GNSILETSEE; NSILETSEES;
SILETSEESI; ILETSEESIK; LETSEESIKK; ETSEESIKKP;
TSEESIKKPM; SEESIKKPMN; EESIKKPMNK; ESIKKPMNKK;

	SIKKPMNKKG; IKKPMNKKGK; KKPMNKKGKG; KPMNKKGKGK; PMNKKGKGKI; MNKKGKGKIA; NKKGKGKIAR; KKGKGKIARK; KGKGKIARKK; GKGKIARKKG; KGKIARKKGK; GKIARKKGKS; KIARKKGKSK; IARKKGKSKV; ARKKGKSKVS; RKKGKSKVSR; KKGKSKVSRK; KGKSKVSRKE; GKSKVSRKEP; KSKVSRKEPY; SKVSRKEPYI; KVSRKEPYIH; VSRKEPYIHS; SRKEPYIHSL; RKEPYIHSLK; KEPYIHSLKR; EPYIHSLKRD; PYIHSLKRDS; YIHSLKRDSA; IHSLKRDSAN; HSLKRDSANK; SLKRDSANKS; LKRDSANKSN; KRDSANKSNF; RDSANKSNFL; DSANKSNFLQ; SANKSNFLQK; ANKSNFLQKN; NKSNFLQKNV; KSNFLQKNVI; SNFLQKNVIL; NFLQKNVILE; FLQKNVILEE; LQKNVILEEE; QKNVILEEES; KNVILEEESL; NVILEEESLK; VILEEESLKT; ILEEESLKTE; LEEESLKTEL; EEESLKTELL; EESLKTELLK; ESLKTELLKE; SLKTELLKEQ; LKTELLKEQS; KTELLKEQSE; TELLKEQSET; ELLKEQSETR; LLKEQSETRK; LKEQSETRKE; KEQSETRKEK; EQSETRKEKI; QSETRKEKIQ; SETRKEKIQK; ETRKEKIQKQ; TRKEKIQKQQ; RKEKIQKQQD; KEKIQKQQDE; EKIQKQQDEY; KIQKQQDEYK; IQKQQDEYKG; QKQQDEYKGM; KQQDEYKGMT; QQDEYKGMTQ; QDEYKGMTQG; DEYKGMTQGS; EYKGMTQGSL; YKGMTQGSLN; KGMTQGSLNS; GMTQGSLNSL; MTQGSLNSLS; TQGSLNSLSG; QGSLNSLSGE; GSLNSLSGES; SLNSLSGESG; LNSLSGESGE; NSLSGESGEL; SLSGESGELK; LSGESGELKE; SGESGELKET; GESGELKETI; ESGELKETIE; SGELKETIES; GELKETIESN; ELKETIESNE; LKETIESNEI; KETIESNEID; ETIESNEIDI; TIESNEIDIT; IESNEIDITI; ESNEIDITID; SNEIDITIDS; NEIDITIDSD; EIDITIDSDL; IDITIDSDLR; DITIDSDLRP; ITIDSDLRPK; TIDSDLRPKS; IDSDLRPKSS; DSDLRPKSSL; SDLRPKSSLQ; DLRPKSSLQD; LRPKSSLQDI; RPKSSLQDIA; PKSSLQDIAG; KSSLQDIAGS; SSLQDIAGSN; SLQDIAGSNS; LQDIAGSNSI; QDIAGSNSIS; DIAGSNSISY; IAGSNSISYT; AGSNSISYTD; GSNSISYTDE; SNSISYTDEI; NSISYTDEIE; SISYTDEIEE; ISYTDEIEEE; SYTDEIEEED; YTDEIEEEDY; TDEIEEEDYA; DEIEEEDYAR; EIEEEDYARY; IEEEDYARYY; EEEDYARYYL; EEDYARYYLD; EDYARYYLDE; DYARYYLDED; YARYYLDEDD; ARYYLDEDDE; RYYLDEDDED; YYLDEDDEDD; YLDEDDEDDE; LDEDDEDDEY; DEDDEDDEYY; EDDEDDEYYE; DDEDDEYYED; DEDDEYYEDD; EDDEYYEDDY; DDEYYEDDYE; DEYYEDDYEE; EYYEDDYEEI; YYEDDYEEIR; YEDDYEEIRL; EDDYEEIRLS; DDYEEIRLSN; DYEEIRLSNR; YEEIRLSNRY; EEIRLSNRYQ; EIRLSNRYQS; IRLSNRYQSY; RLSNRYQSYL; LSNRYQSYLE; SNRYQSYLEG; NRYQSYLEGV; RYQSYLEGVK; YQSYLEGVKY; QSYLEGVKYN; SYLEGVKYNV; YLEGVKYNVD; LEGVKYNVDS; EGVKYNVDSA; GVKYNVDSAI; VKYNVDSAIN; KYNVDSAINT; YNVDSAINTI; NVDSAINTIN; VDSAINTINK; DSAINTINKI; SAINTINKIY; AINTINKIYD; INTINKIYDT; NTINKIYDTY; TINKIYDTYT; INKIYDTYTL; NKIYDTYTLF; KIYDTYTLFS; IYDTYTLFST; YDTYTLFSTK; DTYTLFSTKL; TYTLFSTKLT; YTLFSTKLTQ; TLFSTKLTQM; LFSTKLTQMY; FSTKLTQMYS; STKLTQMYST; TKLTQMYSTR; KLTQMYSTRL; LTQMYSTRLD; TQMYSTRLDN; QMYSTRLDNL; MYSTRLDNLA; YSTRLDNLAK; STRLDNLAKA;

TRLDNLAKAK; RLDNLAKAKA; LDNLAKAKAK; DNLAKAKAKE;
NLAKAKAKEE; LAKAKAKEEA; AKAKAKEEAA; KAKAKEEAAK;
AKAKEEAAKF; KAKEEAAKFT; AKEEAAKFTK; KEEAAKFTKE;
EEAAKFTKED; EAAKFTKEDL; AAKFTKEDLE; AKFTKEDLEK;
KFTKEDLEKN; FTKEDLEKNF; TKEDLEKNFK; KEDLEKNFKT;
EDLEKNFKTL; DLEKNFKTLL; LEKNFKTLLN; EKNFKTLLNY;
KNFKTLLNYI; NFKTLLNYIQ; FKTLLNYIQV; KTLLNYIQVS;
TLLNYIQVSV; LLNYIQVSVK; LNYIQVSVKT; NYIQVSVKTA;
YIQVSVKTAA; IQVSVKTAAN; QVSVKTAANF; VSVKTAANFV;
SVKTAANFVY; VKTAANFVYI; KTAANFVYIN; TAANFVYIND;
AANFVYINDT; ANFVYINDTH; NFVYINDTHA; FVYINDTHAK;
VYINDTHAKR; YINDTHAKRK; INDTHAKRKL; NDTHAKRKLE;
DTHAKRKLEN; THAKRKLENI; HAKRKLENIE; AKRKLENIEA;
KRKLENIEAE; RKLENIEAEI; KLENIEAEIK; LENIEAEIKT;
ENIEAEIKTL; NIEAEIKTLI; IEAEIKTLIA; EAEIKTLIAK;
AEIKTLIAKI; EIKTLIAKIK; IKTLIAKIKE; KTLIAKIKEQ;
TLIAKIKEQS; LIAKIKEQSN; IAKIKEQSNL; AKIKEQSNLY;
KIKEQSNLYE; IKEQSNLYEA; KEQSNLYEAY; EQSNLYEAYK;
QSNLYEAYKA; SNLYEAYKAI; NLYEAYKAIV; LYEAYKAIVT;
YEAYKAIVTS; EAYKAIVTSI; AYKAIVTSIL; YKAIVTSILL;
KAIVTSILLM; AIVTSILLMR; IVTSILLMRD; VTSILLMRDS;
TSILLMRDSL; SILLMRDSLK; ILLMRDSLKE; LLMRDSLKEV;
LMRDSLKEVQ; MRDSLKEVQG; RDSLKEVQGI; DSLKEVQGII;
SLKEVQGIID; LKEVQGIIDK; KEVQGIIDKN; EVQGIIDKNG;
VQGIIDKNGV; QGIIDKNGVW; GIIDKNGVWY;

11 mers:
MKKVKSKYLAL; KKVKSKYLALG; KVKSKYLALGL; VKSKYLALGLL;
KSKYLALGLLF; SKYLALGLLFG; KYLALGLLFGF; YLALGLLFGFI;
LALGLLFGFIS; ALGLLFGFISC; LGLLFGFISCD; GLLFGFISCDL;
LLFGFISCDLF; LFGFISCDLFI; FGFISCDLFIR; GFISCDLFIRY;
FISCDLFIRYE; ISCDLFIRYEM; SCDLFIRYEMK; CDLFIRYEMKE;
DLFIRYEMKEE; LFIRYEMKEES; FIRYEMKEESP; IRYEMKEESPG;
RYEMKEESPGL; YEMKEESPGLF; EMKEESPGLFD; MKEESPGLFDK;
KEESPGLFDKG; EESPGLFDKGN; ESPGLFDKGNS; SPGLFDKGNSI;
PGLFDKGNSIL; GLFDKGNSILE; LFDKGNSILET; FDKGNSILETS;
DKGNSILETSE; KGNSILETSEE; GNSILETSEES; NSILETSEESI;
SILETSEESIK; ILETSEESIKK; LETSEESIKKP; ETSEESIKKPM;
TSEESIKKPMN; SEESIKKPMNK; EESIKKPMNKK; ESIKKPMNKKG;
SIKKPMNKKGK; IKKPMNKKGKG; KKPMNKKGKGK; KPMNKKGKGKI;
PMNKKGKGKIA; MNKKGKGKIAR; NKKGKGKIARK; KKGKGKIARKK;
KGKGKIARKKG; GKGKIARKKGK; KGKIARKKGKS; GKIARKKGKSK;
KIARKKGKSKV; IARKKGKSKVS; ARKKGKSKVSR; RKKGKSKVSRK;
KKGKSKVSRKE; KGKSKVSRKEP; GKSKVSRKEPY; KSKVSRKEPYI;
SKVSRKEPYIH; KVSRKEPYIHS; VSRKEPYIHSL; SRKEPYIHSLK;
RKEPYIHSLKR; KEPYIHSLKRD; EPYIHSLKRDS; PYIHSLKRDSA;
YIHSLKRDSAN; IHSLKRDSANK; HSLKRDSANKS; SLKRDSANKSN;
LKRDSANKSNF; KRDSANKSNFL; RDSANKSNFLQ; DSANKSNFLQK;
SANKSNFLQKN; ANKSNFLQKNV; NKSNFLQKNVI; KSNFLQKNVIL;
SNFLQKNVILE; NFLQKNVILEE; FLQKNVILEEE; LQKNVILEEES;
QKNVILEEESL; KNVILEEESLK; NVILEEESLKT; VILEEESLKTE;

	ILEEESLKTEL; LEEESLKTELL; EEESLKTELLK; EESLKTELLKE; ESLKTELLKEQ; SLKTELLKEQS; LKTELLKEQSE; KTELLKEQSET; TELLKEQSETR; ELLKEQSETRK; LLKEQSETRKE; LKEQSETRKEK; KEQSETRKEKI; EQSETRKEKIQ; QSETRKEKIQK; SETRKEKIQKQ; ETRKEKIQKQQ; TRKEKIQKQQD; RKEKIQKQQDE; KEKIQKQQDEY; EKIQKQQDEYK; KIQKQQDEYKG; IQKQQDEYKGM; QKQQDEYKGMT; KQQDEYKGMTQ; QQDEYKGMTQG; QDEYKGMTQGS; DEYKGMTQGSL; EYKGMTQGSLN; YKGMTQGSLNS; KGMTQGSLNSL; GMTQGSLNSLS; MTQGSLNSLSG; TQGSLNSLSGE; QGSLNSLSGES; GSLNSLSGESG; SLNSLSGESGE; LNSLSGESGEL; NSLSGESGELK; SLSGESGELKE; LSGESGELKET; SGESGELKETI; GESGELKETIE; ESGELKETIES; SGELKETIESN; GELKETIESNE; ELKETIESNEI; LKETIESNEID; KETIESNEIDI; ETIESNEIDIT; TIESNEIDITI; IESNEIDITID; ESNEIDITIDS; SNEIDITIDSD; NEIDITIDSDL; EIDITIDSDLR; IDITIDSDLRP; DITIDSDLRPK; ITIDSDLRPKS; TIDSDLRPKSS; IDSDLRPKSSL; DSDLRPKSSLQ; SDLRPKSSLQD; DLRPKSSLQDI; LRPKSSLQDIA; RPKSSLQDIAG; PKSSLQDIAGS; KSSLQDIAGSN; SSLQDIAGSNS; SLQDIAGSNSI; LQDIAGSNSIS; QDIAGSNSISY; DIAGSNSISYT; IAGSNSISYTD; AGSNSISYTDE; GSNSISYTDEI; SNSISYTDEIE; NSISYTDEIEE; SISYTDEIEEE; ISYTDEIEEED; SYTDEIEEEDY; YTDEIEEEDYA; TDEIEEEDYAR; DEIEEEDYARY; EIEEEDYARYY; IEEEDYARYYL; EEEDYARYYLD; EEDYARYYLDE; EDYARYYLDED; DYARYYLDEDD; YARYYLDEDDE; ARYYLDEDDED; RYYLDEDDEDD; YYLDEDDEDDE; YLDEDDEDDEY; LDEDDEDDEYY; DEDDEDDEYYE; EDDEDDEYYED; DDEDDEYYEDD; DEDDEYYEDDY; EDDEYYEDDYE; DDEYYEDDYEE; DEYYEDDYEEI; EYYEDDYEEIR; YYEDDYEEIRL; YEDDYEEIRLS; EDDYEEIRLSN; DDYEEIRLSNR; DYEEIRLSNRY; YEEIRLSNRYQ; EEIRLSNRYQS; EIRLSNRYQSY; IRLSNRYQSYL; RLSNRYQSYLE; LSNRYQSYLEG; SNRYQSYLEGV; NRYQSYLEGVK; RYQSYLEGVKY; YQSYLEGVKYN; QSYLEGVKYNV; SYLEGVKYNVD; YLEGVKYNVDS; LEGVKYNVDSA; EGVKYNVDSAI; GVKYNVDSAIN; VKYNVDSAINT; KYNVDSAINTI; YNVDSAINTIN; NVDSAINTINK; VDSAINTINKI; DSAINTINKIY; SAINTINKIYD; AINTINKIYDT; INTINKIYDTY; NTINKIYDTYT; TINKIYDTYTL; INKIYDTYTLF; NKIYDTYTLFS; KIYDTYTLFST; IYDTYTLFSTK; YDTYTLFSTKL; DTYTLFSTKLT; TYTLFSTKLTQ; YTLFSTKLTQM; TLFSTKLTQMY; LFSTKLTQMYS; FSTKLTQMYST; STKLTQMYSTR; TKLTQMYSTRL; KLTQMYSTRLD; LTQMYSTRLDN; TQMYSTRLDNL; QMYSTRLDNLA; MYSTRLDNLAK; YSTRLDNLAKA; STRLDNLAKAK; TRLDNLAKAKA; RLDNLAKAKAK; LDNLAKAKAKE; DNLAKAKAKEE; NLAKAKAKEEA; LAKAKAKEEAA; AKAKAKEEAAK; KAKAKEEAAKF; AKAKEEAAKFT; KAKEEAAKFTK; AKEEAAKFTKE; KEEAAKFTKED; EEAAKFTKEDL; EAAKFTKEDLE; AAKFTKEDLEK; AKFTKEDLEKN; KFTKEDLEKNF; FTKEDLEKNFK; TKEDLEKNFKT; KEDLEKNFKTL; EDLEKNFKTLL; DLEKNFKTLLN; LEKNFKTLLNY; EKNFKTLLNYI; KNFKTLLNYIQ; NFKTLLNYIQV; FKTLLNYIQVS; KTLLNYIQVSV; TLLNYIQVSVK; LLNYIQVSVKT; LNYIQVSVKTA; NYIQVSVKTAA; YIQVSVKTAAN; IQVSVKTAANF; QVSVKTAANFV; VSVKTAANFVY; SVKTAANFVYI; VKTAANFVYIN; KTAANFVYIND; TAANFVYINDT; AANFVYINDTH; ANFVYINDTHA; NFVYINDTHAK; FVYINDTHAKR; VYINDTHAKRK; YINDTHAKRKL; INDTHAKRKLE; NDTHAKRKLEN;

	DTHAKRKLENI; THAKRKLENIE; HAKRKLENIEA; AKRKLENIEAE; KRKLENIEAEI; RKLENIEAEIK; KLENIEAEIKT; LENIEAEIKTL; ENIEAEIKTLI; NIEAEIKTLIA; IEAEIKTLIAK; EAEIKTLIAKI; AEIKTLIAKIK; EIKTLIAKIKE; IKTLIAKIKEQ; KTLIAKIKEQS; TLIAKIKEQSN; LIAKIKEQSNL; IAKIKEQSNLY; AKIKEQSNLYE; KIKEQSNLYEA; IKEQSNLYEAY; KEQSNLYEAYK; EQSNLYEAYKA; QSNLYEAYKAI; SNLYEAYKAIV; NLYEAYKAIVT; LYEAYKAIVTS; YEAYKAIVTSI; EAYKAIVTSIL; AYKAIVTSILL; YKAIVTSILLM; KAIVTSILLMR; AIVTSILLMRD; IVTSILLMRDS; VTSILLMRDSL; TSILLMRDSLK; SILLMRDSLKE; ILLMRDSLKEV; LLMRDSLKEVQ; LMRDSLKEVQG; MRDSLKEVQGI; RDSLKEVQGII; DSLKEVQGIID; SLKEVQGIIDK; LKEVQGIIDKN; KEVQGIIDKNG; EVQGIIDKNGV; VQGIIDKNGVW; QGIIDKNGVWY;
Seq 43	SEQ ID NO 51051-52424/ 8 mers: MKIKSKCL; KIKSKCLA; IKSKCLAL; KSKCLALG; SKCLALGL; KCLALGLL; CLALGLLF; LALGLLFG; ALGLLFGF; LGLLFGFI; GLLFGFIS; LLFGFISC; LFGFISCD; FGFISCDL; GFISCDLF; FISCDLFI; ISCDLFIR; SCDLFIRD; CDLFIRDE; DLFIRDEI; LFIRDEIK; FIRDEIKE; IRDEIKEK; RDEIKEKS; DEIKEKSL; EIKEKSLG; IKEKSLGL; KEKSLGLC; EKSLGLCD; KSLGLCDE; SLGLCDEE; LGLCDEES; GLCDEESS; LCDEESSI; CDEESSIL; DEESSILE; EESSILET; ESSILETG; SSILETGD; SILETGDK; ILETGDKS; LETGDKSV; ETGDKSVK; TGDKSVKK; GDKSVKKS; DKSVKKSL; KSVKKSLN; SVKKSLNK; VKKSLNKK; KKSLNKKG; KSLNKKGK; SLNKKGKD; LNKKGKDK; NKKGKDKV; KKGKDKVA; KGKDKVAR; GKDKVARK; KDKVARKK; DKVARKKV; KVARKKVE; VARKKVEG; ARKKVEGN; RKKVEGNA; KKVEGNAV; KVEGNAVK; VEGNAVKK; EGNAVKKD; GNAVKKDP; NAVKKDPF; AVKKDPFN; VKKDPFNH; KKDPFNHH; KDPFNHHV; DPFNHHVK; PFNHHVKR; FNHHVKRE; NHHVKRES; HHVKRESV; HVKRESVN; VKRESVNN; KRESVNNS; RESVNNSN; ESVNNSNL; SVNNSNLS; VNNSNLSQ; NNSNLSQK; NSNLSQKN; SNLSQKNV; NLSQKNVI; LSQKNVIS; SQKNVISE; QKNVISEE; KNVISEEE; NVISEEEI; VISEEEIL; ISEEEILK; SEEEILKT; EEEILKTK; EEILKTKL; EILKTKLL; ILKTKLLR; LKTKLLRE; KTKLLRER; TKLLRERP; KLLRERPE; LLRERPET; LRERPETR; RERPETRK; ERPETRKE; RPETRKEE; PETRKEEI; ETRKEEIQ; TRKEEIQK; RKEEIQKQ; KEEIQKQQ; EEIQKQQD; EIQKQQDE; IQKQQDEH; QKQQDEHK; KQQDEHKR; QQDEHKRM; QDEHKRML; DEHKRMLQ; EHKRMLQG; HKRMLQGS; KRMLQGSL; RMLQGSLS; MLQGSLSF; LQGSLSFL; QGSLSFLS; GSLSFLSG; SLSFLSGE; LSFLSGES; SFLSGESG; FLSGESGE; LSGESGEL; SGESGELK; GESGELKD; ESGELKDT; SGELKDTI; GELKDTIE; ELKDTIES; LKDTIESN; KDTIESNE; DTIESNEI; TIESNEID; IESNEIDF; ESNEIDFT; SNEIDFTI; NEIDFTID; EIDFTIDS; IDFTIDSD; DFTIDSDL; FTIDSDLR; TIDSDLRL; IDSDLRLK; DSDLRLKS; SDLRLKSD; DLRLKSDL; LRLKSDLQ; RLKSDLQA; LKSDLQAI; KSDLQAIS; SDLQAISG; DLQAISGS; LQAISGSN; QAISGSNS; AISGSNSI; ISGSNSIS; SGSNSISY; GSNSISYT; SNSISYTD; NSISYTDE; SISYTDEI; ISYTDEIE;

	SYTDEIEE; YTDEIEEE; TDEIEEED; DEIEEEDY; EIEEEDYD; IEEEDYDQ; EEEDYDQY; EEDYDQYS; EDYDQYSL; DYDQYSLE; YDQYSLEE; DQYSLEED; QYSLEEDY; YSLEEDYY; SLEEDYYY; LEEDYYYD; EEDYYYDG; EDYYYDGE; DYYYDGET; YYYDGETR; YYDGETRL; YDGETRLS; DGETRLSN; GETRLSNR; ETRLSNRY; TRLSNRYE; RLSNRYES; LSNRYESY; SNRYESYL; NRYESYLE; RYESYLEG; YESYLEGV; ESYLEGVK; SYLEGVKY; YLEGVKYN; LEGVKYNV; EGVKYNVS; GVKYNVSS; VKYNVSSA; KYNVSSAI; YNVSSAIK; NVSSAIKT; VSSAIKTI; SSAIKTIV; SAIKTIVK; AIKTIVKI; IKTIVKIY; KTIVKIYD; TIVKIYDN; IVKIYDNY; VKIYDNYT; KIYDNYTL; IYDNYTLL; YDNYTLLS; DNYTLLST; NYTLLSTK; YTLLSTKQ; TLLSTKQT; LLSTKQTQ; LSTKQTQM; STKQTQMY; TKQTQMYS; KQTQMYST; QTQMYSTR; TQMYSTRL; QMYSTRLD; MYSTRLDN; YSTRLDNL; STRLDNLA; TRLDNLAK; RLDNLAKA; LDNLAKAK; DNLAKAKA; NLAKAKAR; LAKAKARE; AKAKAREE; KAKAREEA; AKAREEAK; KAREEAKK; AREEAKKF; REEAKKFT; EEAKKFTK; EAKKFTKE; AKKFTKEE; KKFTKEEL; KFTKEELE; FTKEELEK; TKEELEKD; KEELEKDL; EELEKDLK; ELEKDLKT; LEKDLKTL; EKDLKTLL; KDLKTLLN; DLKTLLNY; LKTLLNYI; KTLLNYIQ; TLLNYIQV; LLNYIQVS; LNYIQVSA; NYIQVSAR; YIQVSART; IQVSARTA; QVSARTAT; VSARTATN; SARTATNF; ARTATNFV; RTATNFVY; TATNFVYA; ATNFVYAR; TNFVYARE; NFVYAREI; FVYAREIY; VYAREIYS; YAREIYSK; AREIYSKR; REIYSKRK; EIYSKRKL; IYSKRKLD; YSKRKLDA; SKRKLDAI; KRKLDAIE; RKLDAIET; KLDAIETE; LDAIETEI; DAIETEIK; AIETEIKN; IETEIKNL; ETEIKNLI; TEIKNLIL; EIKNLILK; IKNLILKI; KNLILKIK; NLILKIKG; LILKIKGQ; ILKIKGQS; LKIKGQSD; KIKGQSDL; IKGQSDLY; KGQSDLYE; GQSDLYEA; QSDLYEAY; SDLYEAYK; DLYEAYKA; LYEAYKAI; YEAYKAIV; EAYKAIVR; AYKAIVRS; YKAIVRSI; KAIVRSIL; AIVRSILL; IVRSILLM; VRSILLMK; RSILLMKD; SILLMKDS; ILLMKDSL; LLMKDSLK; LMKDSLKI; MKDSLKII; KDSLKIIE; DSLKIIEI; SLKIIEIV; LKIIEIVI; KIIEIVID; IIEIVIDK; IEIVIDKN; EIVIDKNG; IVIDKNGV; VIDKNGVW; IDKNGVWY; 9 mers: MKIKSKCLA; KIKSKCLAL; IKSKCLALG; KSKCLALGL; SKCLALGLL; KCLALGLLF; CLALGLLFG; LALGLLFGF; ALGLLFGFI; LGLLFGFIS; GLLFGFISC; LLFGFISCD; LFGFISCDL; FGFISCDLF; GFISCDLFI; FISCDLFIR; ISCDLFIRD; SCDLFIRDE; CDLFIRDEI; DLFIRDEIK; LFIRDEIKE; FIRDEIKEK; IRDEIKEKS; RDEIKEKSL; DEIKEKSLG; EIKEKSLGL; IKEKSLGLC; KEKSLGLCD; EKSLGLCDE; KSLGLCDEE; SLGLCDEES; LGLCDEESS; GLCDEESSI; LCDEESSIL; CDEESSILE; DEESSILET; EESSILETG; ESSILETGD; SSILETGDK; SILETGDKS; ILETGDKSV; LETGDKSVK; ETGDKSVKK; TGDKSVKKS; GDKSVKKSL; DKSVKKSLN; KSVKKSLNK; SVKKSLNKK; VKKSLNKKG; KKSLNKKGK; KSLNKKGKD; SLNKKGKDK; LNKKGKDKV; NKKGKDKVA; KKGKDKVAR; KGKDKVARK; GKDKVARKK; KDKVARKKV; DKVARKKVE; KVARKKVEG; VARKKVEGN; ARKKVEGNA; RKKVEGNAV; KKVEGNAVK; KVEGNAVKK; VEGNAVKKD; EGNAVKKDP; GNAVKKDPF; NAVKKDPFN; AVKKDPFNH; VKKDPFNHH; KKDPFNHHV; KDPFNHHVK; DPFNHHVKR; PFNHHVKRE;

	FNHHVKRES; NHHVKRESV; HHVKRESVN; HVKRESVNN; VKRESVNNS; KRESVNNSN; RESVNNSNL; ESVNNSNLS; SVNNSNLSQ; VNNSNLSQK; NNSNLSQKN; NSNLSQKNV; SNLSQKNVI; NLSQKNVIS; LSQKNVISE; SQKNVISEE; QKNVISEEE; KNVISEEEI; NVISEEEIL; VISEEEILK; ISEEEILKT; SEEEILKTK; EEEILKTKL; EEILKTKLL; EILKTKLLR; ILKTKLLRE; LKTKLLRER; KTKLLRERP; TKLLRERPE; KLLRERPET; LLRERPETR; LRERPETRK; RERPETRKE; ERPETRKEE; RPETRKEEI; PETRKEEIQ; ETRKEEIQK; TRKEEIQKQ; RKEEIQKQQ; KEEIQKQQD; EEIQKQQDE; EIQKQQDEH; IQKQQDEHK; QKQQDEHKR; KQQDEHKRM; QQDEHKRML; QDEHKRMLQ; DEHKRMLQG; EHKRMLQGS; HKRMLQGSL; KRMLQGSLS; RMLQGSLSF; MLQGSLSFL; LQGSLSFLS; QGSLSFLSG; GSLSFLSGE; SLSFLSGES; LSFLSGESG; SFLSGESGE; FLSGESGEL; LSGESGELK; SGESGELKD; GESGELKDT; ESGELKDTI; SGELKDTIE; GELKDTIES; ELKDTIESN; LKDTIESNE; KDTIESNEI; DTIESNEID; TIESNEIDF; IESNEIDFT; ESNEIDFTI; SNEIDFTID; NEIDFTIDS; EIDFTIDSD; IDFTIDSDL; DFTIDSDLR; FTIDSDLRL; TIDSDLRLK; IDSDLRLKS; DSDLRLKSD; SDLRLKSDL; DLRLKSDLQ; LRLKSDLQA; RLKSDLQAI; LKSDLQAIS; KSDLQAISG; SDLQAISGS; DLQAISGSN; LQAISGSNS; QAISGSNSI; AISGSNSIS; ISGSNSISY; SGSNSISYT; GSNSISYTD; SNSISYTDE; NSISYTDEI; SISYTDEIE; ISYTDEIEE; SYTDEIEEE; YTDEIEEED; TDEIEEEDY; DEIEEEDYD; EIEEEDYDQ; IEEEDYDQY; EEEDYDQYS; EEDYDQYSL; EDYDQYSLE; DYDQYSLEE; YDQYSLEED; DQYSLEEDY; QYSLEEDYY; YSLEEDYYY; SLEEDYYYD; LEEDYYYDG; EEDYYYDGE; EDYYYDGET; DYYYDGETR; YYYDGETRL; YYDGETRLS; YDGETRLSN; DGETRLSNR; GETRLSNRY; ETRLSNRYE; TRLSNRYES; RLSNRYESY; LSNRYESYL; SNRYESYLE; NRYESYLEG; RYESYLEGV; YESYLEGVK; ESYLEGVKY; SYLEGVKYN; YLEGVKYNV; LEGVKYNVS; EGVKYNVSS; GVKYNVSSA; VKYNVSSAI; KYNVSSAIK; YNVSSAIKT; NVSSAIKTI; VSSAIKTIV; SSAIKTIVK; SAIKTIVKI; AIKTIVKIY; IKTIVKIYD; KTIVKIYDN; TIVKIYDNY; IVKIYDNYT; VKIYDNYTL; KIYDNYTLL; IYDNYTLLS; YDNYTLLST; DNYTLLSTK; NYTLLSTKQ; YTLLSTKQT; TLLSTKQTQ; LLSTKQTQM; LSTKQTQMY; STKQTQMYS; TKQTQMYST; KQTQMYSTR; QTQMYSTRL; TQMYSTRLD; QMYSTRLDN; MYSTRLDNL; YSTRLDNLA; STRLDNLAK; TRLDNLAKA; RLDNLAKAK; LDNLAKAKA; DNLAKAKAR; NLAKAKARE; LAKAKAREE; AKAKAREEA; KAKAREEAK; AKAREEAKK; KAREEAKKF; AREEAKKFT; REEAKKFTK; EEAKKFTKE; EAKKFTKEE; AKKFTKEEL; KKFTKEELE; KFTKEELEK; FTKEELEKD; TKEELEKDL; KEELEKDLK; EELEKDLKT; ELEKDLKTL; LEKDLKTLL; EKDLKTLLN; KDLKTLLNY; DLKTLLNYI; LKTLLNYIQ; KTLLNYIQV; TLLNYIQVS; LLNYIQVSA; LNYIQVSAR; NYIQVSART; YIQVSARTA; IQVSARTAT; QVSARTATN; VSARTATNF; SARTATNFV; ARTATNFVY; RTATNFVYA; TATNFVYAR; ATNFVYARE; TNFVYAREI; NFVYAREIY; FVYAREIYS; VYAREIYSK; YAREIYSKR; AREIYSKRK; REIYSKRKL; EIYSKRKLD; IYSKRKLDA; YSKRKLDAI; SKRKLDAIE; KRKLDAIET; RKLDAIETE; KLDAIETEI; LDAIETEIK; DAIETEIKN; AIETEIKNL; IETEIKNLI; ETEIKNLIL; TEIKNLILK; EIKNLILKI; IKNLILKIK; KNLILKIKG; NLILKIKGQ; LILKIKGQS; ILKIKGQSD; LKIKGQSDL; KIKGQSDLY; IKGQSDLYE; KGQSDLYEA; GQSDLYEAY; QSDLYEAYK; SDLYEAYKA; DLYEAYKAI; LYEAYKAIV; YEAYKAIVR; EAYKAIVRS; AYKAIVRSI; YKAIVRSIL; KAIVRSILL; AIVRSILLM; IVRSILLMK; VRSILLMKD; RSILLMKDS; SILLMKDSL;

	ILLMKDSLK; LLMKDSLKI; LMKDSLKII; MKDSLKIIE; KDSLKIIEI; DSLKIIEIV; SLKIIEIVI; LKIIEIVID; KIIEIVIDK; IIEIVIDKN; IEIVIDKNG; EIVIDKNGV; IVIDKNGVW; VIDKNGVWY; 10 mers: MKIKSKCLAL; KIKSKCLALG; IKSKCLALGL; KSKCLALGLL; SKCLALGLLF; KCLALGLLFG; CLALGLLFGF; LALGLLFGFI; ALGLLFGFIS; LGLLFGFISC; GLLFGFISCD; LLFGFISCDL; LFGFISCDLF; FGFISCDLFI; GFISCDLFIR; FISCDLFIRD; ISCDLFIRDE; SCDLFIRDEI; CDLFIRDEIK; DLFIRDEIKE; LFIRDEIKEK; FIRDEIKEKS; IRDEIKEKSL; RDEIKEKSLG; DEIKEKSLGL; EIKEKSLGLC; IKEKSLGLCD; KEKSLGLCDE; EKSLGLCDEE; KSLGLCDEES; SLGLCDEESS; LGLCDEESSI; GLCDEESSIL; LCDEESSILE; CDEESSILET; DEESSILETG; EESSILETGD; ESSILETGDK; SSILETGDKS; SILETGDKSV; ILETGDKSVK; LETGDKSVKK; ETGDKSVKKS; TGDKSVKKSL; GDKSVKKSLN; DKSVKKSLNK; KSVKKSLNKK; SVKKSLNKKG; VKKSLNKKGK; KKSLNKKGKD; KSLNKKGKDK; SLNKKGKDKV; LNKKGKDKVA; NKKGKDKVAR; KKGKDKVARK; KGKDKVARKK; GKDKVARKKV; KDKVARKKVE; DKVARKKVEG; KVARKKVEGN; VARKKVEGNA; ARKKVEGNAV; RKKVEGNAVK; KKVEGNAVKK; KVEGNAVKKD; VEGNAVKKDP; EGNAVKKDPF; GNAVKKDPFN; NAVKKDPFNH; AVKKDPFNHH; VKKDPFNHHV; KKDPFNHHVK; KDPFNHHVKR; DPFNHHVKRE; PFNHHVKRES; FNHHVKRESV; NHHVKRESVN; HHVKRESVNN; HVKRESVNNS; VKRESVNNSN; KRESVNNSNL; RESVNNSNLS; ESVNNSNLSQ; SVNNSNLSQK; VNNSNLSQKN; NNSNLSQKNV; NSNLSQKNVI; SNLSQKNVIS; NLSQKNVISE; LSQKNVISEE; SQKNVISEEE; QKNVISEEEI; KNVISEEEIL; NVISEEEILK; VISEEEILKT; ISEEEILKTK; SEEEILKTKL; EEEILKTKLL; EEILKTKLLR; EILKTKLLRE; ILKTKLLRER; LKTKLLRERP; KTKLLRERPE; TKLLRERPET; KLLRERPETR; LLRERPETRK; LRERPETRKE; RERPETRKEE; ERPETRKEEI; RPETRKEEIQ; PETRKEEIQK; ETRKEEIQKQ; TRKEEIQKQQ; RKEEIQKQQD; KEEIQKQQDE; EEIQKQQDEH; EIQKQQDEHK; IQKQQDEHKR; QKQQDEHKRM; KQQDEHKRML; QQDEHKRMLQ; QDEHKRMLQG; DEHKRMLQGS; EHKRMLQGSL; HKRMLQGSLS; KRMLQGSLSF; RMLQGSLSFL; MLQGSLSFLS; LQGSLSFLSG; QGSLSFLSGE; GSLSFLSGES; SLSFLSGESG; LSFLSGESGE; SFLSGESGEL; FLSGESGELK; LSGESGELKD; SGESGELKDT; GESGELKDTI; ESGELKDTIE; SGELKDTIES; GELKDTIESN; ELKDTIESNE; LKDTIESNEI; KDTIESNEID; DTIESNEIDF; TIESNEIDFT; IESNEIDFTI; ESNEIDFTID; SNEIDFTIDS; NEIDFTIDSD; EIDFTIDSDL; IDFTIDSDLR; DFTIDSDLRL; FTIDSDLRLK; TIDSDLRLKS; IDSDLRLKSD; DSDLRLKSDL; SDLRLKSDLQ; DLRLKSDLQA; LRLKSDLQAI; RLKSDLQAIS; LKSDLQAISG; KSDLQAISGS; SDLQAISGSN; DLQAISGSNS; LQAISGSNSI; QAISGSNSIS; AISGSNSISY; ISGSNSISYT; SGSNSISYTD; GSNSISYTDE; SNSISYTDEI; NSISYTDEIE; SISYTDEIEE; ISYTDEIEEE; SYTDEIEEED; YTDEIEEEDY; TDEIEEEDYD; DEIEEEDYDQ; EIEEEDYDQY; IEEEDYDQYS; EEEDYDQYSL; EEDYDQYSLE; EDYDQYSLEE;

	DYDQYSLEED; YDQYSLEEDY; DQYSLEEDYY; QYSLEEDYYY; YSLEEDYYYD; SLEEDYYYDG; LEEDYYYDGE; EEDYYYDGET; EDYYYDGETR; DYYYDGETRL; YYYDGETRLS; YYDGETRLSN; YDGETRLSNR; DGETRLSNRY; GETRLSNRYE; ETRLSNRYES; TRLSNRYESY; RLSNRYESYL; LSNRYESYLE; SNRYESYLEG; NRYESYLEGV; RYESYLEGVK; YESYLEGVKY; ESYLEGVKYN; SYLEGVKYNV; YLEGVKYNVS; LEGVKYNVSS; EGVKYNVSSA; GVKYNVSSAI; VKYNVSSAIK; KYNVSSAIKT; YNVSSAIKTI; NVSSAIKTIV; VSSAIKTIVK; SSAIKTIVKI; SAIKTIVKIY; AIKTIVKIYD; IKTIVKIYDN; KTIVKIYDNY; TIVKIYDNYT; IVKIYDNYTL; VKIYDNYTLL; KIYDNYTLLS; IYDNYTLLST; YDNYTLLSTK; DNYTLLSTKQ; NYTLLSTKQT; YTLLSTKQTQ; TLLSTKQTQM; LLSTKQTQMY; LSTKQTQMYS; STKQTQMYST; TKQTQMYSTR; KQTQMYSTRL; QTQMYSTRLD; TQMYSTRLDN; QMYSTRLDNL; MYSTRLDNLA; YSTRLDNLAK; STRLDNLAKA; TRLDNLAKAK; RLDNLAKAKA; LDNLAKAKAR; DNLAKAKARE; NLAKAKAREE; LAKAKAREEA; AKAKAREEAK; KAKAREEAKK; AKAREEAKKF; KAREEAKKFT; AREEAKKFTK; REEAKKFTKE; EEAKKFTKEE; EAKKFTKEEL; AKKFTKEELE; KKFTKEELEK; KFTKEELEKD; FTKEELEKDL; TKEELEKDLK; KEELEKDLKT; EELEKDLKTL; ELEKDLKTLL; LEKDLKTLLN; EKDLKTLLNY; KDLKTLLNYI; DLKTLLNYIQ; LKTLLNYIQV; KTLLNYIQVS; TLLNYIQVSA; LLNYIQVSAR; LNYIQVSART; NYIQVSARTA; YIQVSARTAT; IQVSARTATN; QVSARTATNF; VSARTATNFV; SARTATNFVY; ARTATNFVYA; RTATNFVYAR; TATNFVYARE; ATNFVYAREI; TNFVYAREIY; NFVYAREIYS; FVYAREIYSK; VYAREIYSKR; YAREIYSKRK; AREIYSKRKL; REIYSKRKLD; EIYSKRKLDA; IYSKRKLDAI; YSKRKLDAIE; SKRKLDAIET; KRKLDAIETE; RKLDAIETEI; KLDAIETEIK; LDAIETEIKN; DAIETEIKNL; AIETEIKNLI; IETEIKNLIL; ETEIKNLILK; TEIKNLILKI; EIKNLILKIK; IKNLILKIKG; KNLILKIKGQ; NLILKIKGQS; LILKIKGQSD; ILKIKGQSDL; LKIKGQSDLY; KIKGQSDLYE; IKGQSDLYEA; KGQSDLYEAY; GQSDLYEAYK; QSDLYEAYKA; SDLYEAYKAI; DLYEAYKAIV; LYEAYKAIVR; YEAYKAIVRS; EAYKAIVRSI; AYKAIVRSIL; YKAIVRSILL; KAIVRSILLM; AIVRSILLMK; IVRSILLMKD; VRSILLMKDS; RSILLMKDSL; SILLMKDSLK; ILLMKDSLKI; LLMKDSLKII; LMKDSLKIIE; MKDSLKIIEI; KDSLKIIEIV; DSLKIIEIVI; SLKIIEIVID; LKIIEIVIDK; KIIEIVIDKN; IIEIVIDKNG; IEIVIDKNGV; EIVIDKNGVW; IVIDKNGVWY; 11 mers: MKIKSKCLALG; KIKSKCLALGL; IKSKCLALGLL; KSKCLALGLLF; SKCLALGLLFG; KCLALGLLFGF; CLALGLLFGFI; LALGLLFGFIS; ALGLLFGFISC; LGLLFGFISCD; GLLFGFISCDL; LLFGFISCDLF; LFGFISCDLFI; FGFISCDLFIR; GFISCDLFIRD; FISCDLFIRDE; ISCDLFIRDEI; SCDLFIRDEIK; CDLFIRDEIKE; DLFIRDEIKEK; LFIRDEIKEKS; FIRDEIKEKSL; IRDEIKEKSLG; RDEIKEKSLGL; DEIKEKSLGLC; EIKEKSLGLCD; IKEKSLGLCDE; KEKSLGLCDEE; EKSLGLCDEES; KSLGLCDEESS; SLGLCDEESSI; LGLCDEESSIL; GLCDEESSILE; LCDEESSILET; CDEESSILETG; DEESSILETGD;

	EESSILETGDK; ESSILETGDKS; SSILETGDKSV; SILETGDKSVK; ILETGDKSVKK; LETGDKSVKKS; ETGDKSVKKSL; TGDKSVKKSLN; GDKSVKKSLNK; DKSVKKSLNKK; KSVKKSLNKKG; SVKKSLNKKGK; VKKSLNKKGKD; KKSLNKKGKDK; KSLNKKGKDKV; SLNKKGKDKVA; LNKKGKDKVAR; NKKGKDKVARK; KKGKDKVARKK; KGKDKVARKKV; GKDKVARKKVE; KDKVARKKVEG; DKVARKKVEGN; KVARKKVEGNA; VARKKVEGNAV; ARKKVEGNAVK; RKKVEGNAVKK; KKVEGNAVKKD; KVEGNAVKKDP; VEGNAVKKDPF; EGNAVKKDPFN; GNAVKKDPFNH; NAVKKDPFNHH; AVKKDPFNHHV; VKKDPFNHHVK; KKDPFNHHVKR; KDPFNHHVKRE; DPFNHHVKRES; PFNHHVKRESV; FNHHVKRESVN; NHHVKRESVNN; HHVKRESVNNS; HVKRESVNNSN; VKRESVNNSNL; KRESVNNSNLS; RESVNNSNLSQ; ESVNNSNLSQK; SVNNSNLSQKN; VNNSNLSQKNV; NNSNLSQKNVI; NSNLSQKNVIS; SNLSQKNVISE; NLSQKNVISEE; LSQKNVISEEE; SQKNVISEEEI; QKNVISEEEIL; KNVISEEEILK; NVISEEEILKT; VISEEEILKTK; ISEEEILKTKL; SEEEILKTKLL; EEEILKTKLLR; EEILKTKLLRE; EILKTKLLRER; ILKTKLLRERP; LKTKLLRERPE; KTKLLRERPET; TKLLRERPETR; KLLRERPETRK; LLRERPETRKE; LRERPETRKEE; RERPETRKEEI; ERPETRKEEIQ; RPETRKEEIQK; PETRKEEIQKQ; ETRKEEIQKQQ; TRKEEIQKQQD; RKEEIQKQQDE; KEEIQKQQDEH; EEIQKQQDEHK; EIQKQQDEHKR; IQKQQDEHKRM; QKQQDEHKRML; KQQDEHKRMLQ; QQDEHKRMLQG; QDEHKRMLQGS; DEHKRMLQGSL; EHKRMLQGSLS; HKRMLQGSLSF; KRMLQGSLSFL; RMLQGSLSFLS; MLQGSLSFLSG; LQGSLSFLSGE; QGSLSFLSGES; GSLSFLSGESG; SLSFLSGESGE; LSFLSGESGEL; SFLSGESGELK; FLSGESGELKD; LSGESGELKDT; SGESGELKDTI; GESGELKDTIE; ESGELKDTIES; SGELKDTIESN; GELKDTIESNE; ELKDTIESNEI; LKDTIESNEID; KDTIESNEIDF; DTIESNEIDFT; TIESNEIDFTI; IESNEIDFTID; ESNEIDFTIDS; SNEIDFTIDSD; NEIDFTIDSDL; EIDFTIDSDLR; IDFTIDSDLRL; DFTIDSDLRLK; FTIDSDLRLKS; TIDSDLRLKSD; IDSDLRLKSDL; DSDLRLKSDLQ; SDLRLKSDLQA; DLRLKSDLQAI; LRLKSDLQAIS; RLKSDLQAISG; LKSDLQAISGS; KSDLQAISGSN; SDLQAISGSNS; DLQAISGSNSI; LQAISGSNSIS; QAISGSNSISY; AISGSNSISYT; ISGSNSISYTD; SGSNSISYTDE; GSNSISYTDEI; SNSISYTDEIE; NSISYTDEIEE; SISYTDEIEEE; ISYTDEIEEED; SYTDEIEEEDY; YTDEIEEEDYD; TDEIEEEDYDQ; DEIEEEDYDQY; EIEEEDYDQYS; IEEEDYDQYSL; EEEDYDQYSLE; EEDYDQYSLEE; EDYDQYSLEED; DYDQYSLEEDY; YDQYSLEEDYY; DQYSLEEDYYY; QYSLEEDYYYD; YSLEEDYYYDG; SLEEDYYYDGE; LEEDYYYDGET; EEDYYYDGETR; EDYYYDGETRL; DYYYDGETRLS; YYYDGETRLSN; YYDGETRLSNR; YDGETRLSNRY; DGETRLSNRYE; GETRLSNRYES; ETRLSNRYESY; TRLSNRYESYL; RLSNRYESYLE; LSNRYESYLEG; SNRYESYLEGV; NRYESYLEGVK; RYESYLEGVKY; YESYLEGVKYN; ESYLEGVKYNV; SYLEGVKYNVS; YLEGVKYNVSS; LEGVKYNVSSA; EGVKYNVSSAI; GVKYNVSSAIK; VKYNVSSAIKT; KYNVSSAIKTI; YNVSSAIKTIV; NVSSAIKTIVK; VSSAIKTIVKI; SSAIKTIVKIY; SAIKTIVKIYD; AIKTIVKIYDN; IKTIVKIYDNY; KTIVKIYDNYT; TIVKIYDNYTL; IVKIYDNYTLL; VKIYDNYTLLS; KIYDNYTLLST; IYDNYTLLSTK; YDNYTLLSTKQ; DNYTLLSTKQT; NYTLLSTKQTQ; YTLLSTKQTQM; TLLSTKQTQMY; LLSTKQTQMYS; LSTKQTQMYST; STKQTQMYSTR; TKQTQMYSTRL; KQTQMYSTRLD; QTQMYSTRLDN; TQMYSTRLDNL;

	QMYSTRLDNLA; MYSTRLDNLAK; YSTRLDNLAKA; STRLDNLAKAK; TRLDNLAKAKA; RLDNLAKAKAR; LDNLAKAKARE; DNLAKAKAREE; NLAKAKAREEA; LAKAKAREEAK; AKAKAREEAKK; KAKAREEAKKF; AKAREEAKKFT; KAREEAKKFTK; AREEAKKFTKE; REEAKKFTKEE; EEAKKFTKEEL; EAKKFTKEELE; AKKFTKEELEK; KKFTKEELEKD; KFTKEELEKDL; FTKEELEKDLK; TKEELEKDLKT; KEELEKDLKTL; EELEKDLKTLL; ELEKDLKTLLN; LEKDLKTLLNY; EKDLKTLLNYI; KDLKTLLNYIQ; DLKTLLNYIQV; LKTLLNYIQVS; KTLLNYIQVSA; TLLNYIQVSAR; LLNYIQVSART; LNYIQVSARTA; NYIQVSARTAT; YIQVSARTATN; IQVSARTATNF; QVSARTATNFV; VSARTATNFVY; SARTATNFVYA; ARTATNFVYAR; RTATNFVYARE; TATNFVYAREI; ATNFVYAREIY; TNFVYAREIYS; NFVYAREIYSK; FVYAREIYSKR; VYAREIYSKRK; YAREIYSKRKL; AREIYSKRKLD; REIYSKRKLDA; EIYSKRKLDAI; IYSKRKLDAIE; YSKRKLDAIET; SKRKLDAIETE; KRKLDAIETEI; RKLDAIETEIK; KLDAIETEIKN; LDAIETEIKNL; DAIETEIKNLI; AIETEIKNLIL; IETEIKNLILK; ETEIKNLILKI; TEIKNLILKIK; EIKNLILKIKG; IKNLILKIKGQ; KNLILKIKGQS; NLILKIKGQSD; LILKIKGQSDL; ILKIKGQSDLY; LKIKGQSDLYE; KIKGQSDLYEA; IKGQSDLYEAY; KGQSDLYEAYK; GQSDLYEAYKA; QSDLYEAYKAI; SDLYEAYKAIV; DLYEAYKAIVR; LYEAYKAIVRS; YEAYKAIVRSI; EAYKAIVRSIL; AYKAIVRSILL; YKAIVRSILLM; KAIVRSILLMK; AIVRSILLMKD; IVRSILLMKDS; VRSILLMKDSL; RSILLMKDSLK; SILLMKDSLKI; ILLMKDSLKII; LLMKDSLKIIE; LMKDSLKIIEI; MKDSLKIIEIV; KDSLKIIEIVI; DSLKIIEIVID; SLKIIEIVIDK; LKIIEIVIDKN; KIIEIVIDKNG; IIEIVIDKNGV; IEIVIDKNGVW; EIVIDKNGVWY;
Seq 44	SEQ ID NO 52425-54050/ 8 mers: MKKVKSKY; KKVKSKYL; KVKSKYLA; VKSKYLAL; KSKYLALG; SKYLALGL; KYLALGLL; YLALGLLF; LALGLLFG; ALGLLFGF; LGLLFGFI; GLLFGFIS; LLFGFISC; LFGFISCD; FGFISCDL; GFISCDLF; FISCDLFI; ISCDLFIR; SCDLFIRY; CDLFIRYE; DLFIRYEM; LFIRYEMK; FIRYEMKE; IRYEMKEE; RYEMKEES; YEMKEESP; EMKEESPG; MKEESPGL; KEESPGLF; EESPGLFD; ESPGLFDK; SPGLFDKG; PGLFDKGN; GLFDKGNS; LFDKGNSI; FDKGNSIL; DKGNSILE; KGNSILET; GNSILETS; NSILETSE; SILETSEE; ILETSEES; LETSEESI; ETSEESIK; TSEESIKK; SEESIKKP; EESIKKPM; ESIKKPMN; SIKKPMNK; IKKPMNKK; KKPMNKKG; KPMNKKGK; PMNKKGKG; MNKKGKGK; NKKGKGKI; KKGKGKIA; KGKGKIAR; GKGKIARK; KGKIARKN; GKIARKNG; KIARKNGK; IARKNGKS; ARKNGKSK; RKNGKSKV; KNGKSKVS; NGKSKVSG; GKSKVSGK; KSKVSGKE; SKVSGKEP; KVSGKEPF; VSGKEPFI; SGKEPFIH; GKEPFIHS; KEPFIHSF; EPFIHSFK; PFIHSFKR; FIHSFKRD; IHSFKRDA; HSFKRDAA; SFKRDAAN; FKRDAANK; KRDAANKS; RDAANKSN; DAANKSNF; AANKSNFL; ANKSNFLQ; NKSNFLQK; KSNFLQKN; SNFLQKNV; NFLQKNVM; FLQKNVML; LQKNVMLE; QKNVMLEE; KNVMLEEE; NVMLEEES; VMLEEESL; MLEEESLK; LEEESLKT; EEESLKTE; EESLKTEL; ESLKTELL; SLKTELLK; LKTELLKE; KTELLKEQ; TELLKEQS; ELLKEQSE; LLKEQSET; LKEQSETR; KEQSETRK; EQSETRKE;

	QSETRKEK; SETRKEKI; ETRKEKIQ; TRKEKIQK; RKEKIQKQ; KEKIQKQQ; EKIQKQQD; KIQKQQDE; IQKQQDEY; QKQQDEYK; KQQDEYKG; QQDEYKGM; QDEYKGMT; DEYKGMTK; EYKGMTKG; YKGMTKGS; KGMTKGSL; GMTKGSLN; MTKGSLNS; TKGSLNSL; KGSLNSLS; GSLNSLSG; SLNSLSGE; LNSLSGES; NSLSGESG; SLSGESGE; LSGESGEL; SGESGELK; GESGELKE; ESGELKET; SGELKETI; GELKETIE; ELKETIES; LKETIESN; KETIESNE; ETIESNEI; TIESNEID; IESNEIDI; ESNEIDIT; SNEIDITI; NEIDITID; EIDITIDS; IDITIDSD; DITIDSDL; ITIDSDLR; TIDSDLRP; IDSDLRPK; DSDLRPKS; SDLRPKSS; DLRPKSSL; LRPKSSLQ; RPKSSLQD; PKSSLQDI; KSSLQDIA; SSLQDIAG; SLQDIAGS; LQDIAGSN; QDIAGSNS; DIAGSNSI; IAGSNSIS; AGSNSISY; GSNSISYT; SNSISYTD; NSISYTDE; SISYTDEI; ISYTDEIE; SYTDEIEE; YTDEIEEE; TDEIEEED; DEIEEEDY; EIEEEDYA; IEEEDYAR; EEEDYARY; EEDYARYY; EDYARYYL; DYARYYLD; YARYYLDE; ARYYLDED; RYYLDEDD; YYLDEDDE; YLDEDDED; LDEDDEDD; DEDDEDDE; EDDEDDEY; DDEDDEYY; DEDDEYYE; EDDEYYED; DDEYYEDD; DEYYEDDY; EYYEDDYE; YYEDDYEE; YEDDYEEI; EDDYEEIR; DDYEEIRL; DYEEIRLS; YEEIRLSN; EEIRLSNR; EIRLSNRY; IRLSNRYQ; RLSNRYQS; LSNRYQSY; SNRYQSYL; NRYQSYLE; RYQSYLEG; YQSYLEGV; QSYLEGVK; SYLEGVKY; YLEGVKYN; LEGVKYNV; EGVKYNVD; GVKYNVDS; VKYNVDSA; KYNVDSAI; YNVDSAIN; NVDSAINT; VDSAINTI; DSAINTIN; SAINTINK; AINTINKI; INTINKIY; NTINKIYD; TINKIYDT; INKIYDTY; NKIYDTYT; KIYDTYTL; IYDTYTLF; YDTYTLFS; DTYTLFST; TYTLFSTK; YTLFSTKL; TLFSTKLT; LFSTKLTQ; FSTKLTQM; STKLTQMY; TKLTQMYS; KLTQMYST; LTQMYSTR; TQMYSTRL; QMYSTRLD; MYSTRLDN; YSTRLDNL; STRLDNLA; TRLDNLAK; RLDNLAKA; LDNLAKAK; DNLAKAKA; NLAKAKAK; LAKAKAKE; AKAKAKEE; KAKAKEEA; AKAKEEAA; KAKEEAAK; AKEEAAKF; KEEAAKFT; EEAAKFTK; EAAKFTKE; AAKFTKED; AKFTKEDL; KFTKEDLE; FTKEDLEK; TKEDLEKN; KEDLEKNF; EDLEKNFK; DLEKNFKT; LEKNFKTL; EKNFKTLL; KNFKTLLN; NFKTLLNY; FKTLLNYI; KTLLNYIQ; TLLNYIQV; LLNYIQVS; LNYIQVSV; NYIQVSVK; YIQVSVKT; IQVSVKTA; QVSVKTAT; VSVKTATN; SVKTATNF; VKTATNFV; KTATNFVY; TATNFVYI; ATNFVYIN; TNFVYINE; NFVYINEM; FVYINEMH; VYINEMHA; YINEMHAK; INEMHAKR; NEMHAKRK; EMHAKRKL; MHAKRKLE; HAKRKLEN; AKRKLENI; KRKLENIE; RKLENIEA; KLENIEAK; LENIEAKI; ENIEAKIK; NIEAKIKT; IEAKIKTL; EAKIKTLI; AKIKTLIA; KIKTLIAK; IKTLIAKI; KTLIAKIK; TLIAKIKE; LIAKIKEK; IAKIKEKS; AKIKEKSN; KIKEKSNL; IKEKSNLY; KEKSNLYS; EKSNLYSA; KSNLYSAY; SNLYSAYK; NLYSAYKA; LYSAYKAI; YSAYKAIV; SAYKAIVS; AYKAIVSS; YKAIVSSI; KAIVSSIL; AIVSSILL; IVSSILLM; VSSILLMR; SSILLMRD; SILLMRDS; ILLMRDSL; LLMRDSLK; LMRDSLKE; MRDSLKEV; RDSLKEVQ; DSLKEVQY; SLKEVQYA; LKEVQYAI; KEVQYAID; EVQYAIDK; VQYAIDKN; QYAIDKNG; YAIDKNGI; AIDKNGIW; IDKNGIWY; DKNGIWYR; KNGIWYRK; NGIWYRKL; GIWYRKLD; IWYRKLDA; WYRKLDAI; YRKLDAIE; RKLDAIET; KLDAIETE; LDAIETEI; DAIETEIK; AIETEIKN;

IETEIKNL; ETEIKNLI; TEIKNLIL; EIKNLILK; IKNLILKI;
KNLILKIK; NLILKIKG; LILKIKGQ; ILKIKGQS; LKIKGQSD;
KIKGQSDL; IKGQSDLY; KGQSDLYE; GQSDLYEA; QSDLYEAY;
SDLYEAYK; DLYEAYKA; LYEAYKAI; YEAYKAIV; EAYKAIVR;
AYKAIVRS; YKAIVRSI; KAIVRSIL; AIVRSILL; IVRSILLM;
VRSILLMK; RSILLMKD; SILLMKDS; ILLMKDSL; LLMKDSLK;
LMKDSLKI; MKDSLKII; KDSLKIIE; DSLKIIEI; SLKIIEIV;
LKIIEIVI; KIIEIVID; IIEIVIDK; IEIVIDKN; EIVIDKNG;
IVIDKNGV; VIDKNGVW; IDKNGVWY;

9 mers:
MKKVKSKYL; KKVKSKYLA; KVKSKYLAL; VKSKYLALG; KSKYLALGL;
SKYLALGLL; KYLALGLLF; YLALGLLFG; LALGLLFGF; ALGLLFGFI;
LGLLFGFIS; GLLFGFISC; LLFGFISCD; LFGFISCDL; FGFISCDLF;
GFISCDLFI; FISCDLFIR; ISCDLFIRY; SCDLFIRYE; CDLFIRYEM;
DLFIRYEMK; LFIRYEMKE; FIRYEMKEE; IRYEMKEES; RYEMKEESP;
YEMKEESPG; EMKEESPGL; MKEESPGLF; KEESPGLFD; EESPGLFDK;
ESPGLFDKG; SPGLFDKGN; PGLFDKGNS; GLFDKGNSI; LFDKGNSIL;
FDKGNSILE; DKGNSILET; KGNSILETS; GNSILETSE; NSILETSEE;
SILETSEES; ILETSEESI; LETSEESIK; ETSEESIKK; TSEESIKKP;
SEESIKKPM; EESIKKPMN; ESIKKPMNK; SIKKPMNKK; IKKPMNKKG;
KKPMNKKGK; KPMNKKGKG; PMNKKGKGK; MNKKGKGKI; NKKGKGKIA;
KKGKGKIAR; KGKGKIARK; GKGKIARKN; KGKIARKNG; GKIARKNGK;
KIARKNGKS; IARKNGKSK; ARKNGKSKV; RKNGKSKVS; KNGKSKVSG;
NGKSKVSGK; GKSKVSGKE; KSKVSGKEP; SKVSGKEPF; KVSGKEPFI;
VSGKEPFIH; SGKEPFIHS; GKEPFIHSF; KEPFIHSFK; EPFIHSFKR;
PFIHSFKRD; FIHSFKRDA; IHSFKRDAA; HSFKRDAAN; SFKRDAANK;
FKRDAANKS; KRDAANKSN; RDAANKSNF; DAANKSNFL; AANKSNFLQ;
ANKSNFLQK; NKSNFLQKN; KSNFLQKNV; SNFLQKNVM; NFLQKNVML;
FLQKNVMLE; LQKNVMLEE; QKNVMLEEE; KNVMLEEES; NVMLEEESL;
VMLEEESLK; MLEEESLKT; LEEESLKTE; EEESLKTEL; EESLKTELL;
ESLKTELLK; SLKTELLKE; LKTELLKEQ; KTELLKEQS; TELLKEQSE;
ELLKEQSET; LLKEQSETR; LKEQSETRK; KEQSETRKE; EQSETRKEK;
QSETRKEKI; SETRKEKIQ; ETRKEKIQK; TRKEKIQKQ; RKEKIQKQQ;
KEKIQKQQD; EKIQKQQDE; KIQKQQDEY; IQKQQDEYK; QKQQDEYKG;
KQQDEYKGM; QQDEYKGMT; QDEYKGMTK; DEYKGMTKG; EYKGMTKGS;
YKGMTKGSL; KGMTKGSLN; GMTKGSLNS; MTKGSLNSL; TKGSLNSLS;
KGSLNSLSG; GSLNSLSGE; SLNSLSGES; LNSLSGESG; NSLSGESGE;
SLSGESGEL; LSGESGELK; SGESGELKE; GESGELKET; ESGELKETI;
SGELKETIE; GELKETIES; ELKETIESN; LKETIESNE; KETIESNEI;
ETIESNEID; TIESNEIDI; IESNEIDIT; ESNEIDITI; SNEIDITID;
NEIDITIDS; EIDITIDSD; IDITIDSDL; DITIDSDLR; ITIDSDLRP;
TIDSDLRPK; IDSDLRPKS; DSDLRPKSS; SDLRPKSSL; DLRPKSSLQ;
LRPKSSLQD; RPKSSLQDI; PKSSLQDIA; KSSLQDIAG; SSLQDIAGS;
SLQDIAGSN; LQDIAGSNS; QDIAGSNSI; DIAGSNSIS; IAGSNSISY;
AGSNSISYT; GSNSISYTD; SNSISYTDE; NSISYTDEI; SISYTDEIE;
ISYTDEIEE; SYTDEIEEE; YTDEIEEED; TDEIEEEDY; DEIEEEDYA;
EIEEEDYAR; IEEEDYARY; EEEDYARYY; EEDYARYYL; EDYARYYLD;
DYARYYLDE; YARYYLDED; ARYYLDEDD; RYYLDEDDE; YYLDEDDED;
YLDEDDEDD; LDEDDEDDE; DEDDEDDEY; EDDEDDEYY; DDEDDEYYE;
DEDDEYYED; EDDEYYEDD; DDEYYEDDY; DEYYEDDYE; EYYEDDYEE;

	YYEDDYEEI; YEDDYEEIR; EDDYEEIRL; DDYEEIRLS; DYEEIRLSN; YEEIRLSNR; EEIRLSNRY; EIRLSNRYQ; IRLSNRYQS; RLSNRYQSY; LSNRYQSYL; SNRYQSYLE; NRYQSYLEG; RYQSYLEGV; YQSYLEGVK; QSYLEGVKY; SYLEGVKYN; YLEGVKYNV; LEGVKYNVD; EGVKYNVDS; GVKYNVDSA; VKYNVDSAI; KYNVDSAIN; YNVDSAINT; NVDSAINTI; VDSAINTIN; DSAINTINK; SAINTINKI; AINTINKIY; INTINKIYD; NTINKIYDT; TINKIYDTY; INKIYDTYT; NKIYDTYTL; KIYDTYTLF; IYDTYTLFS; YDTYTLFST; DTYTLFSTK; TYTLFSTKL; YTLFSTKLT; TLFSTKLTQ; LFSTKLTQM; FSTKLTQMY; STKLTQMYS; TKLTQMYST; KLTQMYSTR; LTQMYSTRL; TQMYSTRLD; QMYSTRLDN; MYSTRLDNL; YSTRLDNLA; STRLDNLAK; TRLDNLAKA; RLDNLAKAK; LDNLAKAKA; DNLAKAKAK; NLAKAKAKE; LAKAKAKEE; AKAKAKEEA; KAKAKEEAA; AKAKEEAAK; KAKEEAAKF; AKEEAAKFT; KEEAAKFTK; EEAAKFTKE; EAAKFTKED; AAKFTKEDL; AKFTKEDLE; KFTKEDLEK; FTKEDLEKN; TKEDLEKNF; KEDLEKNFK; EDLEKNFKT; DLEKNFKTL; LEKNFKTLL; EKNFKTLLN; KNFKTLLNY; NFKTLLNYI; FKTLLNYIQ; KTLLNYIQV; TLLNYIQVS; LLNYIQVSV; LNYIQVSVK; NYIQVSVKT; YIQVSVKTA; IQVSVKTAT; QVSVKTATN; VSVKTATNF; SVKTATNFV; VKTATNFVY; KTATNFVYI; TATNFVYIN; ATNFVYINE; TNFVYINEM; NFVYINEMH; FVYINEMHA; VYINEMHAK; YINEMHAKR; INEMHAKRK; NEMHAKRKL; EMHAKRKLE; MHAKRKLEN; HAKRKLENI; AKRKLENIE; KRKLENIEA; RKLENIEAK; KLENIEAKI; LENIEAKIK; ENIEAKIKT; NIEAKIKTL; IEAKIKTLI; EAKIKTLIA; AKIKTLIAK; KIKTLIAKI; IKTLIAKIK; KTLIAKIKE; TLIAKIKEK; LIAKIKEKS; IAKIKEKSN; AKIKEKSNL; KIKEKSNLY; IKEKSNLYS; KEKSNLYSA; EKSNLYSAY; KSNLYSAYK; SNLYSAYKA; NLYSAYKAI; LYSAYKAIV; YSAYKAIVS; SAYKAIVSS; AYKAIVSSI; YKAIVSSIL; KAIVSSILL; AIVSSILLM; IVSSILLMR; VSSILLMRD; SSILLMRDS; SILLMRDSL; ILLMRDSLK; LLMRDSLKE; LMRDSLKEV; MRDSLKEVQ; RDSLKEVQY; DSLKEVQYA; SLKEVQYAI; LKEVQYAID; KEVQYAIDK; EVQYAIDKN; VQYAIDKNG; QYAIDKNGI; YAIDKNGIW; AIDKNGIWY; IDKNGIWYR; DKNGIWYRK; KNGIWYRKL; NGIWYRKLD; GIWYRKLDA; IWYRKLDAI; WYRKLDAIE; YRKLDAIET; RKLDAIETE; KLDAIETEI; LDAIETEIK; DAIETEIKN; AIETEIKNL; IETEIKNLI; ETEIKNLIL; TEIKNLILK; EIKNLILKI; IKNLILKIK; KNLILKIKG; NLILKIKGQ; LILKIKGQS; ILKIKGQSD; LKIKGQSDL; KIKGQSDLY; IKGQSDLYE; KGQSDLYEA; GQSDLYEAY; QSDLYEAYK; SDLYEAYKA; DLYEAYKAI; LYEAYKAIV; YEAYKAIVR; EAYKAIVRS; AYKAIVRSI; YKAIVRSIL; KAIVRSILL; AIVRSILLM; IVRSILLMK; VRSILLMKD; RSILLMKDS; SILLMKDSL; ILLMKDSLK; LLMKDSLKI; LMKDSLKII; MKDSLKIIE; KDSLKIIEI; DSLKIIEIV; SLKIIEIVI; LKIIEIVID; KIIEIVIDK; IIEIVIDKN; IEIVIDKNG; EIVIDKNGV; IVIDKNGVW; VIDKNGVWY; 10 mers: MKKVKSKYLA; KKVKSKYLAL; KVKSKYLALG; VKSKYLALGL; KSKYLALGLL; SKYLALGLLF; KYLALGLLFG; YLALGLLFGF; LALGLLFGFI; ALGLLFGFIS; LGLLFGFISC; GLLFGFISCD; LLFGFISCDL; LFGFISCDLF; FGFISCDLFI; GFISCDLFIR; FISCDLFIRY; ISCDLFIRYE; SCDLFIRYEM; CDLFIRYEMK; DLFIRYEMKE; LFIRYEMKEE; FIRYEMKEES; IRYEMKEESP; RYEMKEESPG; YEMKEESPGL; EMKEESPGLF; MKEESPGLFD;

	KEESPGLFDK; EESPGLFDKG; ESPGLFDKGN; SPGLFDKGNS; PGLFDKGNSI; GLFDKGNSIL; LFDKGNSILE; FDKGNSILET; DKGNSILETS; KGNSILETSE; GNSILETSEE; NSILETSEES; SILETSEESI; ILETSEESIK; LETSEESIKK; ETSEESIKKP; TSEESIKKPM; SEESIKKPMN; EESIKKPMNK; ESIKKPMNKK; SIKKPMNKKG; IKKPMNKKGK; KKPMNKKGKG; KPMNKKGKGK; PMNKKGKGKI; MNKKGKGKIA; NKKGKGKIAR; KKGKGKIARK; KGKGKIARKN; GKGKIARKNG; KGKIARKNGK; GKIARKNGKS; KIARKNGKSK; IARKNGKSKV; ARKNGKSKVS; RKNGKSKVSG; KNGKSKVSGK; NGKSKVSGKE; GKSKVSGKEP; KSKVSGKEPF; SKVSGKEPFI; KVSGKEPFIH; VSGKEPFIHS; SGKEPFIHSF; GKEPFIHSFK; KEPFIHSFKR; EPFIHSFKRD; PFIHSFKRDA; FIHSFKRDAA; IHSFKRDAAN; HSFKRDAANK; SFKRDAANKS; FKRDAANKSN; KRDAANKSNF; RDAANKSNFL; DAANKSNFLQ; AANKSNFLQK; ANKSNFLQKN; NKSNFLQKNV; KSNFLQKNVM; SNFLQKNVML; NFLQKNVMLE; FLQKNVMLEE; LQKNVMLEEE; QKNVMLEEES; KNVMLEEESL; NVMLEEESLK; VMLEEESLKT; MLEEESLKTE; LEEESLKTEL; EEESLKTELL; EESLKTELLK; ESLKTELLKE; SLKTELLKEQ; LKTELLKEQS; KTELLKEQSE; TELLKEQSET; ELLKEQSETR; LLKEQSETRK; LKEQSETRKE; KEQSETRKEK; EQSETRKEKI; QSETRKEKIQ; SETRKEKIQK; ETRKEKIQKQ; TRKEKIQKQQ; RKEKIQKQQD; KEKIQKQQDE; EKIQKQQDEY; KIQKQQDEYK; IQKQQDEYKG; QKQQDEYKGM; KQQDEYKGMT; QQDEYKGMTK; QDEYKGMTKG; DEYKGMTKGS; EYKGMTKGSL; YKGMTKGSLN; KGMTKGSLNS; GMTKGSLNSL; MTKGSLNSLS; TKGSLNSLSG; KGSLNSLSGE; GSLNSLSGES; SLNSLSGESG; LNSLSGESGE; NSLSGESGEL; SLSGESGELK; LSGESGELKE; SGESGELKET; GESGELKETI; ESGELKETIE; SGELKETIES; GELKETIESN; ELKETIESNE; LKETIESNEI; KETIESNEID; ETIESNEIDI; TIESNEIDIT; IESNEIDITI; ESNEIDITID; SNEIDITIDS; NEIDITIDSD; EIDITIDSDL; IDITIDSDLR; DITIDSDLRP; ITIDSDLRPK; TIDSDLRPKS; IDSDLRPKSS; DSDLRPKSSL; SDLRPKSSLQ; DLRPKSSLQD; LRPKSSLQDI; RPKSSLQDIA; PKSSLQDIAG; KSSLQDIAGS; SSLQDIAGSN; SLQDIAGSNS; LQDIAGSNSI; QDIAGSNSIS; DIAGSNSISY; IAGSNSISYT; AGSNSISYTD; GSNSISYTDE; SNSISYTDEI; NSISYTDEIE; SISYTDEIEE; ISYTDEIEEE; SYTDEIEEED; YTDEIEEEDY; TDEIEEEDYA; DEIEEEDYAR; EIEEEDYARY; IEEEDYARYY; EEEDYARYYL; EEDYARYYLD; EDYARYYLDE; DYARYYLDED; YARYYLDEDD; ARYYLDEDDE; RYYLDEDDED; YYLDEDDEDD; YLDEDDEDDE; LDEDDEDDEY; DEDDEDDEYY; EDDEDDEYYE; DDEDDEYYED; DEDDEYYEDD; EDDEYYEDDY; DDEYYEDDYE; DEYYEDDYEE; EYYEDDYEEI; YYEDDYEEIR; YEDDYEEIRL; EDDYEEIRLS; DDYEEIRLSN; DYEEIRLSNR; YEEIRLSNRY; EEIRLSNRYQ; EIRLSNRYQS; IRLSNRYQSY; RLSNRYQSYL; LSNRYQSYLE; SNRYQSYLEG; NRYQSYLEGV; RYQSYLEGVK; YQSYLEGVKY; QSYLEGVKYN; SYLEGVKYNV; YLEGVKYNVD; LEGVKYNVDS; EGVKYNVDSA; GVKYNVDSAI; VKYNVDSAIN; KYNVDSAINT; YNVDSAINTI; NVDSAINTIN; VDSAINTINK; DSAINTINKI; SAINTINKIY; AINTINKIYD; INTINKIYDT; NTINKIYDTY; TINKIYDTYT;

	INKIYDTYTL; NKIYDTYTLF; KIYDTYTLFS; IYDTYTLFST; YDTYTLFSTK; DTYTLFSTKL; TYTLFSTKLT; YTLFSTKLTQ; TLFSTKLTQM; LFSTKLTQMY; FSTKLTQMYS; STKLTQMYST; TKLTQMYSTR; KLTQMYSTRL; LTQMYSTRLD; TQMYSTRLDN; QMYSTRLDNL; MYSTRLDNLA; YSTRLDNLAK; STRLDNLAKA; TRLDNLAKAK; RLDNLAKAKA; LDNLAKAKAK; DNLAKAKAKE; NLAKAKAKEE; LAKAKAKEEA; AKAKAKEEAA; KAKAKEEAAK; AKAKEEAAKF; KAKEEAAKFT; AKEEAAKFTK; KEEAAKFTKE; EEAAKFTKED; EAAKFTKEDL; AAKFTKEDLE; AKFTKEDLEK; KFTKEDLEKN; FTKEDLEKNF; TKEDLEKNFK; KEDLEKNFKT; EDLEKNFKTL; DLEKNFKTLL; LEKNFKTLLN; EKNFKTLLNY; KNFKTLLNYI; NFKTLLNYIQ; FKTLLNYIQV; KTLLNYIQVS; TLLNYIQVSV; LLNYIQVSVK; LNYIQVSVKT; NYIQVSVKTA; YIQVSVKTAT; IQVSVKTATN; QVSVKTATNF; VSVKTATNFV; SVKTATNFVY; VKTATNFVYI; KTATNFVYIN; TATNFVYINE; ATNFVYINEM; TNFVYINEMH; NFVYINEMHA; FVYINEMHAK; VYINEMHAKR; YINEMHAKRK; INEMHAKRKL; NEMHAKRKLE; EMHAKRKLEN; MHAKRKLENI; HAKRKLENIE; AKRKLENIEA; KRKLENIEAK; RKLENIEAKI; KLENIEAKIK; LENIEAKIKT; ENIEAKIKTL; NIEAKIKTLI; IEAKIKTLIA; EAKIKTLIAK; AKIKTLIAKI; KIKTLIAKIK; IKTLIAKIKE; KTLIAKIKEK; TLIAKIKEKS; LIAKIKEKSN; IAKIKEKSNL; AKIKEKSNLY; KIKEKSNLYS; IKEKSNLYSA; KEKSNLYSAY; EKSNLYSAYK; KSNLYSAYKA; SNLYSAYKAI; NLYSAYKAIV; LYSAYKAIVS; YSAYKAIVSS; SAYKAIVSSI; AYKAIVSSIL; YKAIVSSILL; KAIVSSILLM; AIVSSILLMR; IVSSILLMRD; VSSILLMRDS; SSILLMRDSL; SILLMRDSLK; ILLMRDSLKE; LLMRDSLKEV; LMRDSLKEVQ; MRDSLKEVQY; RDSLKEVQYA; DSLKEVQYAI; SLKEVQYAID; LKEVQYAIDK; KEVQYAIDKN; EVQYAIDKNG; VQYAIDKNGI; QYAIDKNGIW; YAIDKNGIWY; AIDKNGIWYR; IDKNGIWYRK; DKNGIWYRKL; KNGIWYRKLD; NGIWYRKLDA; GIWYRKLDAI; IWYRKLDAIE; WYRKLDAIET; YRKLDAIETE; RKLDAIETEI; KLDAIETEIK; LDAIETEIKN; DAIETEIKNL; AIETEIKNLI; IETEIKNLIL; ETEIKNLILK; TEIKNLILKI; EIKNLILKIK; IKNLILKIKG; KNLILKIKGQ; NLILKIKGQS; LILKIKGQSD; ILKIKGQSDL; LKIKGQSDLY; KIKGQSDLYE; IKGQSDLYEA; KGQSDLYEAY; GQSDLYEAYK; QSDLYEAYKA; SDLYEAYKAI; DLYEAYKAIV; LYEAYKAIVR; YEAYKAIVRS; EAYKAIVRSI; AYKAIVRSIL; YKAIVRSILL; KAIVRSILLM; AIVRSILLMK; IVRSILLMKD; VRSILLMKDS; RSILLMKDSL; SILLMKDSLK; ILLMKDSLKI; LLMKDSLKII; LMKDSLKIIE; MKDSLKIIEI; KDSLKIIEIV; DSLKIIEIVI; SLKIIEIVID; LKIIEIVIDK; KIIEIVIDKN; IIEIVIDKNG; IEIVIDKNGV; EIVIDKNGVW; IVIDKNGVWY; 11 mers: MKKVKSKYLAL; KKVKSKYLALG; KVKSKYLALGL; VKSKYLALGLL; KSKYLALGLLF; SKYLALGLLFG; KYLALGLLFGF; YLALGLLFGFI; LALGLLFGFIS; ALGLLFGFISC; LGLLFGFISCD; GLLFGFISCDL; LLFGFISCDLF; LFGFISCDLFI; FGFISCDLFIR; GFISCDLFIRY; FISCDLFIRYE; ISCDLFIRYEM; SCDLFIRYEMK; CDLFIRYEMKE;

	DLFIRYEMKEE; LFIRYEMKEES; FIRYEMKEESP; IRYEMKEESPG; RYEMKEESPGL; YEMKEESPGLF; EMKEESPGLFD; MKEESPGLFDK; KEESPGLFDKG; EESPGLFDKGN; ESPGLFDKGNS; SPGLFDKGNSI; PGLFDKGNSIL; GLFDKGNSILE; LFDKGNSILET; FDKGNSILETS; DKGNSILETSE; KGNSILETSEE; GNSILETSEES; NSILETSEESI; SILETSEESIK; ILETSEESIKK; LETSEESIKKP; ETSEESIKKPM; TSEESIKKPMN; SEESIKKPMNK; EESIKKPMNKK; ESIKKPMNKKG; SIKKPMNKKGK; IKKPMNKKGKG; KKPMNKKGKGK; KPMNKKGKGKI; PMNKKGKGKIA; MNKKGKGKIAR; NKKGKGKIARK; KKGKGKIARKN; KGKGKIARKNG; GKGKIARKNGK; KGKIARKNGKS; GKIARKNGKSK; KIARKNGKSKV; IARKNGKSKVS; ARKNGKSKVSG; RKNGKSKVSGK; KNGKSKVSGKE; NGKSKVSGKEP; GKSKVSGKEPF; KSKVSGKEPFI; SKVSGKEPFIH; KVSGKEPFIHS; VSGKEPFIHSF; SGKEPFIHSFK; GKEPFIHSFKR; KEPFIHSFKRD; EPFIHSFKRDA; PFIHSFKRDAA; FIHSFKRDAAN; IHSFKRDAANK; HSFKRDAANKS; SFKRDAANKSN; FKRDAANKSNF; KRDAANKSNFL; RDAANKSNFLQ; DAANKSNFLQK; AANKSNFLQKN; ANKSNFLQKNV; NKSNFLQKNVM; KSNFLQKNVML; SNFLQKNVMLE; NFLQKNVMLEE; FLQKNVMLEEE; LQKNVMLEEES; QKNVMLEEESL; KNVMLEEESLK; NVMLEEESLKT; VMLEEESLKTE; MLEEESLKTEL; LEEESLKTELL; EEESLKTELLK; EESLKTELLKE; ESLKTELLKEQ; SLKTELLKEQS; LKTELLKEQSE; KTELLKEQSET; TELLKEQSETR; ELLKEQSETRK; LLKEQSETRKE; LKEQSETRKEK; KEQSETRKEKI; EQSETRKEKIQ; QSETRKEKIQK; SETRKEKIQKQ; ETRKEKIQKQQ; TRKEKIQKQQD; RKEKIQKQQDE; KEKIQKQQDEY; EKIQKQQDEYK; KIQKQQDEYKG; IQKQQDEYKGM; QKQQDEYKGMT; KQQDEYKGMTK; QQDEYKGMTKG; QDEYKGMTKGS; DEYKGMTKGSL; EYKGMTKGSLN; YKGMTKGSLNS; KGMTKGSLNSL; GMTKGSLNSLS; MTKGSLNSLSG; TKGSLNSLSGE; KGSLNSLSGES; GSLNSLSGESG; SLNSLSGESGE; LNSLSGESGEL; NSLSGESGELK; SLSGESGELKE; LSGESGELKET; SGESGELKETI; GESGELKETIE; ESGELKETIES; SGELKETIESN; GELKETIESNE; ELKETIESNEI; LKETIESNEID; KETIESNEIDI; ETIESNEIDIT; TIESNEIDITI; IESNEIDITID; ESNEIDITIDS; SNEIDITIDSD; NEIDITIDSDL; EIDITIDSDLR; IDITIDSDLRP; DITIDSDLRPK; ITIDSDLRPKS; TIDSDLRPKSS; IDSDLRPKSSL; DSDLRPKSSLQ; SDLRPKSSLQD; DLRPKSSLQDI; LRPKSSLQDIA; RPKSSLQDIAG; PKSSLQDIAGS; KSSLQDIAGSN; SSLQDIAGSNS; SLQDIAGSNSI; LQDIAGSNSIS; QDIAGSNSISY; DIAGSNSISYT; IAGSNSISYTD; AGSNSISYTDE; GSNSISYTDEI; SNSISYTDEIE; NSISYTDEIEE; SISYTDEIEEE; ISYTDEIEEED; SYTDEIEEEDY; YTDEIEEEDYA; TDEIEEEDYAR; DEIEEEDYARY; EIEEEDYARYY; IEEEDYARYYL; EEEDYARYYLD; EEDYARYYLDE; EDYARYYLDED; DYARYYLDEDD; YARYYLDEDDE; ARYYLDEDDED; RYYLDEDDEDD; YYLDEDDEDDE; YLDEDDEDDEY; LDEDDEDDEYY; DEDDEDDEYYE; EDDEDDEYYED; DDEDDEYYEDD; DEDDEYYEDDY; EDDEYYEDDYE; DDEYYEDDYEE; DEYYEDDYEEI; EYYEDDYEEIR; YYEDDYEEIRL; YEDDYEEIRLS; EDDYEEIRLSN; DDYEEIRLSNR; DYEEIRLSNRY; YEEIRLSNRYQ; EEIRLSNRYQS; EIRLSNRYQSY; IRLSNRYQSYL; RLSNRYQSYLE; LSNRYQSYLEG; SNRYQSYLEGV; NRYQSYLEGVK; RYQSYLEGVKY; YQSYLEGVKYN; QSYLEGVKYNV; SYLEGVKYNVD; YLEGVKYNVDS; LEGVKYNVDSA; EGVKYNVDSAI; GVKYNVDSAIN; VKYNVDSAINT; KYNVDSAINTI; YNVDSAINTIN;

	NVDSAINTINK; VDSAINTINKI; DSAINTINKIY; SAINTINKIYD; AINTINKIYDT; INTINKIYDTY; NTINKIYDTYT; TINKIYDTYTL; INKIYDTYTLF; NKIYDTYTLFS; KIYDTYTLFST; IYDTYTLFSTK; YDTYTLFSTKL; DTYTLFSTKLT; TYTLFSTKLTQ; YTLFSTKLTQM; TLFSTKLTQMY; LFSTKLTQMYS; FSTKLTQMYST; STKLTQMYSTR; TKLTQMYSTRL; KLTQMYSTRLD; LTQMYSTRLDN; TQMYSTRLDNL; QMYSTRLDNLA; MYSTRLDNLAK; YSTRLDNLAKA; STRLDNLAKAK; TRLDNLAKAKA; RLDNLAKAKAK; LDNLAKAKAKE; DNLAKAKAKEE; NLAKAKAKEEA; LAKAKAKEEAA; AKAKAKEEAAK; KAKAKEEAAKF; AKAKEEAAKFT; KAKEEAAKFTK; AKEEAAKFTKE; KEEAAKFTKED; EEAAKFTKEDL; EAAKFTKEDLE; AAKFTKEDLEK; AKFTKEDLEKN; KFTKEDLEKNF; FTKEDLEKNFK; TKEDLEKNFKT; KEDLEKNFKTL; EDLEKNFKTLL; DLEKNFKTLLN; LEKNFKTLLNY; EKNFKTLLNYI; KNFKTLLNYIQ; NFKTLLNYIQV; FKTLLNYIQVS; KTLLNYIQVSV; TLLNYIQVSVK; LLNYIQVSVKT; LNYIQVSVKTA; NYIQVSVKTAT; YIQVSVKTATN; IQVSVKTATNF; QVSVKTATNFV; VSVKTATNFVY; SVKTATNFVYI; VKTATNFVYIN; KTATNFVYINE; TATNFVYINEM; ATNFVYINEMH; TNFVYINEMHA; NFVYINEMHAK; FVYINEMHAKR; VYINEMHAKRK; YINEMHAKRKL; INEMHAKRKLE; NEMHAKRKLEN; EMHAKRKLENI; MHAKRKLENIE; HAKRKLENIEA; AKRKLENIEAK; KRKLENIEAKI; RKLENIEAKIK; KLENIEAKIKT; LENIEAKIKTL; ENIEAKIKTLI; NIEAKIKTLIA; IEAKIKTLIAK; EAKIKTLIAKI; AKIKTLIAKIK; KIKTLIAKIKE; IKTLIAKIKEK; KTLIAKIKEKS; TLIAKIKEKSN; LIAKIKEKSNL; IAKIKEKSNLY; AKIKEKSNLYS; KIKEKSNLYSA; IKEKSNLYSAY; KEKSNLYSAYK; EKSNLYSAYKA; KSNLYSAYKAI; SNLYSAYKAIV; NLYSAYKAIVS; LYSAYKAIVSS; YSAYKAIVSSI; SAYKAIVSSIL; AYKAIVSSILL; YKAIVSSILLM; KAIVSSILLMR; AIVSSILLMRD; IVSSILLMRDS; VSSILLMRDSL; SSILLMRDSLK; SILLMRDSLKE; ILLMRDSLKEV; LLMRDSLKEVQ; LMRDSLKEVQY; MRDSLKEVQYA; RDSLKEVQYAI; DSLKEVQYAID; SLKEVQYAIDK; LKEVQYAIDKN; KEVQYAIDKNG; EVQYAIDKNGI; VQYAIDKNGIW; QYAIDKNGIWY; YAIDKNGIWYR; AIDKNGIWYRK; IDKNGIWYRKL; DKNGIWYRKLD; KNGIWYRKLDA; NGIWYRKLDAI; GIWYRKLDAIE; IWYRKLDAIET; WYRKLDAIETE; YRKLDAIETEI; RKLDAIETEIK; KLDAIETEIKN; LDAIETEIKNL; DAIETEIKNLI; AIETEIKNLIL; IETEIKNLILK; ETEIKNLILKI; TEIKNLILKIK; EIKNLILKIKG; IKNLILKIKGQ; KNLILKIKGQS; NLILKIKGQSD; LILKIKGQSDL; ILKIKGQSDLY; LKIKGQSDLYE; KIKGQSDLYEA; IKGQSDLYEAY; KGQSDLYEAYK; GQSDLYEAYKA; QSDLYEAYKAI; SDLYEAYKAIV; DLYEAYKAIVR; LYEAYKAIVRS; YEAYKAIVRSI; EAYKAIVRSIL; AYKAIVRSILL; YKAIVRSILLM; KAIVRSILLMK; AIVRSILLMKD; IVRSILLMKDS; VRSILLMKDSL; RSILLMKDSLK; SILLMKDSLKI; ILLMKDSLKII; LLMKDSLKIIE; LMKDSLKIIEI; MKDSLKIIEIV; KDSLKIIEIVI; DSLKIIEIVID; SLKIIEIVIDK; LKIIEIVIDKN; KIIEIVIDKNG; IIEIVIDKNGV; IEIVIDKNGVW; EIVIDKNGVWY;

Fig. 32.

Antigen designation	HLA-chain; Class 1	Amino acid sequence
NP_212517.1 ; Basic membrane protein A (bmpA) [Borrelia burgdorferi B31; Seq1	HLA-A0101	YSDEIDIIH; IVDAFRYGY; GSDLIWLIGY; YSDEIDIIHH; YSDEIDIIHHA; FTSNHLKTNTF
	HLA-A0201	ILLESIVFL; SLGSEIPKV; LLLILLESI; NLVGMTFRA; YLAPDNVIT; RMYSDEIDI; GVDEDQAYL; KIINKEIIV; FLGGIEGEI; LLILLESIV; ILLLILLES; FLTGYIAAK; LLESIVFLS; GSGHYIIGV; YIAAKLSKT; LIGYRFSDV; FLTGYIAAKL; ILLLILLESI; RMYSDEIDII; FLGGIEGEIV; WLIGYRFSDV; LLLILLESIV; ILLESIVFLS; GLGGIGAIEV; YLAPDNVITS; LILLESIVFL; FLSCSGKGSL; YIGSFADLEA; GLKEGVVGFV; ALNIFTSNHL; LINYGLKEGV; YIIGVDEDQA; ALQNPDMKYA; MISFELEKEI; GVDEDQAYLA; YLAPDNVITST; KLINYGLKEGV; ILLLILLESIV; KMISFELEKEI; KILLLILLESI; LLILLESIVFL; SLGSEIPKVSL; WLIGYRFSDVA; YLSDLEGLKDA; ILLESIVFLSC; VLKESSSNSYL; IIDPIYSNDPI; NLSSKIINKEI; ALQNPDMKYAI; MTFRAQEGAFL; KSFNESALNGV; ELGSGHYIIGV; KLSKTGKIGFL; KISTQYIGSFA; SVATRMYSDEI; FLTGYIAAKLS; GLGGIGAIEVA; YSDEIDIIHHA; YSNDPIPANLV; IVDAFRYGYEA
	HLA-A0301	IVFLSCSGK; KMISFELEK; NLSSKIINK; NIFTSNHLK; FLTGYIAAK; ALNGVKKVK; KTNTFEGGK; VVGFVRNPK; GSLGSEIPK; GIGAIEVAK; YLSDLEGLK; ALQNPDMKY; SIVFLSCSGK; TGYIAAKLSK; GVVGFVRNPK; AFLTGYIAAK; LIIDGTFDDK; SALNGVKKVK; LNIFTSNHLK; IAAKLSKTGK; GVKKVKEEFK; KGSLGSEIPK; SYLSDLEGLK; IGYRFSDVAK; FRYGYEAGAK; RYGYEAGAKY; ALNIFTSNHLK; LTGYIAAKLSK; HLKTNTFEGGK; RMYSDEIDIIH; YIAAKLSKTGK; KVAALQNPDMK; GAFLTGYIAAK; NSYLSDLEGLK; LIGYRFSDVAK; SFNESALNGVK; SLIIDGTFDDK
	HLA-A1101	KMISFELEK; IVFLSCSGK; NIFTSNHLK; KTNTFEGGK; VVGFVRNPK; GSLGSEIPK; GIGAIEVAK; AALQNPDMK; NLSSKIINK; IVDAFRYGY; YLSDLEGLK; GYIAAKLSK; PSNKESYEK; ALNGVKKVK; IIDGTFDDK; AAKLSKTGK; FLTGYIAAK; ESALNGVKK; KESYEKFLK; ALQNPDMKY; KEIIVPSNK; KEIDNLSSK; EAGAKYANK; SIVFLSCSGK; GVVGFVRNPK; LIIDGTFDDK; SALNGVKKVK; GVKKVKEEFK; VAALQNPDMK; SYLSDLEGLK; GSFADLEAGR; IAAKLSKTGK; TGYIAAKLSK; AFLTGYIAAK; IGYRFSDVAK; ITSTTKDVGR; KGSLGSEIPK; LNIFTSNHLK; PANLVGMTFR; GSDLIWLIGY; AALQNPDMKY; ALNIFTSNHLK; KVAALQNPDMK; GAFLTGYIAAK; NSYLSDLEGLK; LTGYIAAKLSK; SLIIDGTFDDK; YIAAKLSKTGK; IVPSNKESYEK; SFNESALNGVK; ESIVFLSCSGK; LIGYRFSDVAK; GSDLIWLIGYR; RAQEGAFLTGY; NTFEGGKLINY; HLKTNTFEGGK; SNKESYEKFLK
	HLA-A2402	KYANKDIKI; SYEKFLKEF; QYIGSFADL; MYSDEIDII; AYLAPDNVI; SYLSDLEGL; GFVRNPKMI; KYAIIDPIY; SYEKFLKEFI; SYLSDLEGLK; IYSNDPIPANL; NYGLKEGVVGF; GFVRNPKMISF; AFLTGYIAAKL; VFLSCSGKGSL
	HLA-A2902	KYAIIDPIY; ALQNPDMKY; YGYEAGAKY; KDIKISTQY; IVPSNKESY; IVDAFRYGY; GEIVDAFRY; LIWLIGYRF; IGVDEDQAY; RYGYEAGAKY; IIGVDEDQAY; VAKELGSGHY; TFEGGKLINY; EIVDAFRYGY; LLILLESIVF; FVRNPKMISF; YIIGVDEDQAY; EIIVPSNKESY; EVAKELGSGHY; VAALQNPDMKY; RAQEGAFLTGY; LVLKESSSNSY; NTFEGGKLINY
	HLA-A6801	NIFTSNHLK; DLIWLIGYR; IVFLSCSGK; EAGRSVATR; ESALNGVKK; FLTGYIAAK; EGEIVDAFR; TSTTKDVGR; KTNTFEGGK; YLSDLEGLK; SFADLEAGR; DVAKVAALQ; VVGFVRNPK; EAGAKYANK; KMISFELEK;

		NLSSKIINK; EFKIELVLK; DNVITSTTK; ESSSNSYLS; SIVFLSCSGK; ITSTTKDVGR; EEFKIELVLK; GSFADLEAGR; LNIFTSNHLK; GVVGFVRNPK; EIVDAFRYGY; LIIDGTFDDK; IAAKLSKTGK; GVKKVKEEFK; VAALQNPDMK; PANLVGMTFR; MTFRAQEGAF; TGYIAAKLSK; IGYRFSDVAK; MKYAIIDPIY; LEAGRSVATR; YEAGAKYANK; IEGEIVDAFR; ESIVFLSCSGK; NSYLSDLEGLK; IPANLVGMTFR; YIAAKLSKTGK; ESALNGVKKVK; LTGYIAAKLSK; IVPSNKESYEK; NPKMISFELEK; DLEAGRSVATR; GIEGEIVDAFR; GAFLTGYIAAK; VITSTTKDVGR; HLKTNTFEGGK; ALNIFTSNHLK; KVAALQNPDMK; MTFRAQEGAFL; NTFEGGKLINY; EVAKELGSGHY; IGSFADLEAGR; EIIVPSNKESY; LIGYRFSDVAK; SLIIDGTFDDK; EGVVGFVRNPK; YIIGVDEDQAY; SFNESALNGVK; GSDLIWLIGYR
	HLA-B0702	APDNVITST; IPANLVGMT; NPKMISFEL; DPIYSNDPI; TTKDVGRAL; NPDMKYAII; IPANLVGMTF; FVRNPKMISF; APDNVITSTT; VPSNKESYEKF; RALNIFTSNHL; HAAGLGGIGAI
	HLA-B0801	NPKMISFEL; FVRNPKMISF;
	HLA-B1501	GLKEGVVGF; YGYEAGAKY; ALQNPDMKY; ISTQYIGSF; IGVDEDQAY; LILLESIVF; TFRAQEGAF; LSKTGKIGF; TTKDVGRAL; VSLIIDGTF; SNHLKTNTF; VLKESSSNSY; FVRNPKMISF; LLILLESIVF; AQEGAFLTGY; VAKELGSGHY; MTFRAQEGAF; KLSKTGKIGF; TQYIGSFADL; KVSLIIDGTF; IIVPSNKESY; KISTQYIGSF; TSNHLKTNTF; YGLKEGVVGF; IIGVDEDQAY; KVAALQNPDM; LQNPDMKYAI; MKYAIIDPIY; FLSCSGKGSL; YIIGVDEDQAY; LVLKESSSNSY; GMTFRAQEGAF; RAQEGAFLTGY; FTSNHLKTNTF; LLLILLESIVF; NTFEGGKLINY; VLKESSSNSYL; DMKYAIIDPIY; GGIEGEIVDAF; RMYSDEIDIIH; EIIVPSNKESY; VAALQNPDMKY; EVAKELGSGHY
	HLA-B2705	FRYGYEAGA; YRFSDVAKV; VRNPKMISF; GRSVATRMY; FRAQEGAFL; FRYGYEAGAK; YRFSDVAKVA; YRFSDVAKVAA; GRALNIFTSNH
	HLA-B3501	IGVDEDQAY; YGYEAGAKY; LIWLIGYRF; NPKMISFEL; LILLESIVF; DPIYSNDPI; PANLVGMTF; VAALQNPDM; DVGRALNIF; IPANLVGMT; TFRAQEGAF; LKESSSNSY; DPIPANLVG; YSDEIDIIH; VSLIIDGTF; IEGEIVDAF; IPANLVGMTF; DPIPANLVGM; MTFRAQEGAF; MKYAIIDPIY; EIVDAFRYGY; IIGVDEDQAY; AALQNPDMKY; EAGRSVATRM; LLILLESIVF; FSDVAKVAAL; TSNHLKTNTF; IIVPSNKESY; KVSLIIDGTF; DLIWLIGYRF; VAKELGSGHY; FVRNPKMISF; YIIGVDEDQAY; EAGRSVATRMY; FTSNHLKTNTF; VAALQNPDMKY; LVLKESSSNSY; VPSNKESYEKF; DPIYSNDPIPA; RAQEGAFLTGY; FRYGYEAGAKY; DMKYAIIDPIY; DPIPANLVGMT; LLLILLESIVF; EVAKELGSGHY; HAAGLGGIGAI; EIIVPSNKESY
	HLA-B4403	EEFKIELVL; GEIVDAFRY; SEIPKVSLI; DEIDIIHHA; SEIPKVSLII; EEFKIELVLK; DEIDIIHHAA; KEIDNLSSKI; GEIVDAFRYGY; EEFKIELVLKE; KEIIVPSNKES; KEIDNLSSKII; KESYEKFLKEF; SEIPKVSLIID
	HLA-B5101	IPKVSLIID; IPANLVGMT; DPIYSNDPI; IPANLVGMTF; IPKVSLIIDG; DPIPANLVGM; IPKVSLIIDGT
	HLA-B5701	
NP_212516.1; Basic membrane protein B (bmpB) [Borrelia burgdorferi B31; Seq2	HLA-A0101	FSCAISGVY; SSENPKISY; IVDAFRYGY; GSDLIWLVGY; ETAKNLGDGY; VSSENPKISY; NKDIEIISEY; ETAKNLGDGYY
	HLA-A0201	MLTDASLLV; NLIAVVFRV; YMLTDASLL; KMYSKGIDV; RIVIFIFGI; YLAPKNFIT; NIGDALYLI; GLRDGVIGL; NLGDGYYVI; KISMLVDGV; FIFGILLTS; QIPENLIAV; KIINKEIIV; VIFIFGILL; FITSVIKNI; FLAGYIAAK; LIWLVGYML; VLDDKSFNS; KGIDVIHFA; GIDVIHFAA; SANEALLRL; ISGVYSSYV; NGSDLIWLV; YANKDIEII; YMLTDASLLV; KMYSKGIDVI; AISGVYSSYV; ALYLITGEYI; KISYGIIDPI; WLVGYMLTDA; LLVSSENPKI; YLAPKNFITS; VQIPENLIAV; GLAGIGVIET; FAAGLAGIGV; QIPENLIAVV;

		MLTDASLLVS; FIFGILLTSC; GVYSSYVSDL; EVFSCAISGV; IVIFIFGILL; LAPKNFITSV; RIVIFIFGIL; VLDDKSFNSS; FIGGMKGNIV; FLAGYIAAKK; YLAPKNFITSV; VLDDKSFNSSA; GLPNANEFEYI; NLGDGYYVIGA; SLLVSSENPKI; GLAGIGVIETA; MLTDASLLVSS; RIVIFIFGILL; LLTSCFSRNGI; YMLTDASLLVS; GIIDPIYGDDV; CAISGVYSSYV; VQIPENLIAVV; GIDVIHFAAGL; FLAGYIAAKKS; QMGLRDGVIGL; VVFRVEQGAFL; MLVDGVLDDKS; VIGADQDQSYL; TIASKMYSKGI
	HLA-A0301	FLAGYIAAK; TIASKMYSK; KIGFIGGMK; VLERKIINK; ILLTSCFSR; EIFIKQILK; ALYLITGEY; LAGYIAAKK; AAKKSFSGK; LLVSSENPK; AISGVYSSY; SSANEALLR; KMYSKGIDV; KNFITSVIK; GIGVIETAK; RTIASKMYSK; FLAGYIAAKK; KVLERKIINK; SLLVSSENPK; AFLAGYIAAK; MLVDGVLDDK; IAAKKSFSGK; YEIFIKQILK; GKIGFIGGMK; GILLTSCFSR; SANEALLRLK; LYLITGEYIK; FRYGYESGAK; CAISGVYSSY; SRNGIESSSK; VDIGRTIASK; RYGYESGAKY; RNGIESSSKK; YESGAKYANK; AGIGVIETAK; PKNFITSVIK; FEYIKVLERK; VFSCAISGVY; ALYLITGEYIK; YIAAKKSFSGK; KMYSKGIDVIH; SSANEALLRLK; FSRNGIESSSK; SSYVSDLDNLK; GAFLAGYIAAK; SANEALLRLKK; AFLAGYIAAKK; ASLLVSSENPK; EVFSCAISGVY; KISYGIIDPIY; RVEQGAFLAGY; SMLVDGVLDDK; LVSSENPKISY
	HLA-A1101	TIASKMYSK; SSANEALLR; YVSDLDNLK; KIGFIGGMK; AAKKSFSGK; EIFIKQILK; NANEFEYIK; IVDAFRYGY; VLERKIINK; AISGVYSSY; ALYLITGEY; ILLTSCFSR; LLVSSENPK; FLAGYIAAK; LVDGVLDDK; GIGVIETAK; YLITGEYIK; LAGYIAAKK; KNFITSVIK; ESGAKYANK; SSENPKISY; RTIASKMYS; RTIASKMYSK; KVLERKIINK; SANEALLRLK; SLLVSSENPK; IAAKKSFSGK; GILLTSCFSR; AFLAGYIAAK; MLVDGVLDDK; NSSANEALLR; FLAGYIAAKK; SYVSDLDNLK; YVSDLDNLKR; ISYGIIDPIY; NQEEYEIFIK; NSFSDVDIGR; GIESSSKKIK; AGIGVIETAK; SSYVSDLDNLK; SSANEALLRLK; SANEALLRLKK; ASLLVSSENPK; ALYLITGEYIK; GAFLAGYIAAK; YIAAKKSFSGK; SMLVDGVLDDK; SVIKNIGDALY; AFLAGYIAAKK; LAGIGVIETAK; RVEQGAFLAGY; ADQDQSYLAPK; EVFSCAISGVY; LVSSENPKISY; KISYGIIDPIY; LPNANEFEYIK
	HLA-A2402	VYSSYVSDL; LYLITGEYI; KYANKDIEI; EYIKNNNVW; SYLAPKNFI; GYMLTDASL; MYSKGIDVI; IFIKQILKL; SYVSDLDNL; GYIAAKKSF; EYEIFIKQI; EYIKVLERK; EYSNSFSDV; EYIKVLERKI; KYANKDIEII; GYMLTDASLL; IFGILLTSCF; NFITSVIKNI; DFPENIEEVF; EYEIFIKQIL; SYVSDLDNLK; LYLITGEYIK; EYIKNNNVWE; MYSKGIDVIHF; EYIKVLERKII; EYSNSFSDVDI; GYMLTDASLLV; SFSDVDIGRTI; EYIKNNNVWEG
	HLA-A2902	SYGIIDPIY; IVPCNQEEY; FSCAISGVY; GNIVDAFRY; ALYLITGEY; YGYESGAKY; LPNANEFEY; IVDAFRYGY; SSENPKISY; VFRVEQGAF; RYGYESGAKY; GLPNANEFEY; VFSCAISGVY; CAISGVYSSY; IIVPCNQEEY; VVFRVEQGAF; VIGADQDQSY; DALYLITGEY; VIKNIGDALY; KGNIVDAFRY; TAKNLGDGYY; ISYGIIDPIY; VSSENPKISY; EVFSCAISGVY; YVIGADQDQSY; EIIVPCNQEEY; SVIKNIGDALY; LVSSENPKISY; IGLPNANEFEY; ETAKNLGDGYY; FIFGILLTSCF; SCAISGVYSSY; RVEQGAFLAGY; KISYGIIDPIY; GNIVDAFRYGY
	HLA-A6801	TIASKMYSK; EIFIKQILK; YVSDLDNLK; NANEFEYIK; SSANEALLR; FLAGYIAAK; EYIKVLERK; ENLIAVVFR; LAGYIAAKK; ILLTSCFSR; YLITGEYIK; SFSDVDIGR; FSCAISGVY; ESGAKYANK; LLVSSENPK; KGNIVDAFR; DIGRTIASK; FEYIKVLER; NGIESSSKK; IVPCNQEEY; LVDGVLDDK; NSFSDVDIGR; NSSANEALLR; YVSDLDNLKR; FLAGYIAAKK; RTIASKMYSK; EFEYIKVLER; IAAKKSFSGK; ETAKNLGDGY; MKGNIVDAFR; MLVDGVLDDK; SANEALLRLK;

		ISYGIIDPIY; CAISGVYSSY; GILLTSCFSR; YEIFIKQILK; SYVSDLDNLK; NIVDAFRYGY; DALYLITGEY; NQEEYEIFIK; EVFSCAISGVY; YIAAKKSFSGK; SSYVSDLDNLK; ETAKNLGDGYY; FGILLTSCFSR; FNSSANEALLR; SSANEALLRLK; EFEYIKVLERK; GAFLAGYIAAK; SANEALLRLKK; SNSFSDVDIGR; GMKGNIVDAFR; NEFEYIKVLER; IPENLIAVVFR; SYVSDLDNLKR; SVIKNIGDALY; EYEIFIKQILK; EIIVPCNQEEY; LPNANEFEYIK; ALYLITGEYIK; FSRNGIESSSK; YVIGADQDQSY; DVDIGRTIASK; EGGKVVQMGLR; NLIAVVFRVEQ; LAGIGVIETAK; FIFGILLTSCF
	HLA-B0702	APKNFITSV; IPENLIAVV; NPKISYGII; FPENIEEVF; VIKNIGDAL; APKNFITSVI; IPENLIAVVF; SVIKNIGDAL; LPNANEFEYI; AVVFRVEQGAF
	HLA-B0801	YIKVLERKI; NLKRNGSDL; YIKVLERKII;
	HLA-B1501	FSCAISGVY; IISEYSNSF; ALYLITGEY; AISGVYSSY; YGYESGAKY; EQGAFLAGY; FGILLTSCF; IGADQDQSY; VFRVEQGAF; KSFSGKIGF; YMLTDASLL; GLRDGVIGL; TAKNLGDGY; VQIPENLIA; KDIEIISEY; SSENPKISY; IGLPNANEF; ISMLVDGVL; GMKGNIVDAF; VVFRVEQGAF; YSKGIDVIHF; ISYGIIDPIY; VSSENPKISY; VQIPENLIAV; VIKNIGDALY; VQMGLRDGVI; TAKNLGDGYY; IIVPCNQEEY; VFSCAISGVY; VIGADQDQSY; IGRTIASKMY; CAISGVYSSY; EIISEYSNSF; VIGLPNANEF; YVIGADQDQSY; FIFGILLTSCF; GVIGLPNANEF; SVIKNIGDALY; LVSSENPKISY; VQIPENLIAVV; AVVFRVEQGAF; EVFSCAISGVY; RVEQGAFLAGY; KISYGIIDPIY; KSFNSSANEAL; ANKDIEIISEY; KMYSKGIDVIH; SCAISGVYSSY; YLAPKNFITSV; IEIISEYSNSF; QIPENLIAVVF; GGMKGNIVDAF; EIIVPCNQEEY
	HLA-B2705	FRYGYESGA; FRVEQGAFL; GRTIASKMY; SRNGIESSS; KRNGSDLIW; FRYGYESGAK; SRNGIESSSK; KRNGSDLIWL; MRIVIFIFGI; SRNGIESSSKK; GRTIASKMYSK; KRNGSDLIWLV; MRIVIFIFGIL
	HLA-B3501	FPENIEEVF; LPNANEFEY; TAKNLGDGY; FSCAISGVY; IISEYSNSF; IGADQDQSY; DPIYGDDVQ; MKGNIVDAF; YGYESGAKY; IPENLIAVV; IKNIGDALY; LIWLVGYML; FNSSANEAL; IGLPNANEF; IVPCNQEEY; FGILLTSCF; FRVEQGAFL; SANEALLRL; YMLTDASLL; IPENLIAVVF; DALYLITGEY; TAKNLGDGYY; CAISGVYSSY; FPENIEEVFS; ISYGIIDPIY; IIVPCNQEEY; VFSCAISGVY; NIVDAFRYGY; EIISEYSNSF; DPIYGDDVQI; VVFRVEQGAF; LPNANEFEYI; DFPENIEEVF; VIKNIGDALY; SFNSSANEAL; VPCNQEEYEI; YSKGIDVIHF; ETAKNLGDGY; FAAGLAGIGV; YVIGADQDQSY; VPCNQEEYEIF; EVFSCAISGVY; NVWEGGKVVQM; NANEFEYIKVL; LVSSENPKISY; FIFGILLTSCF; FPENIEEVFSC; LAGYIAAKKSF; FAAGLAGIGVI; RVEQGAFLAGY; SVIKNIGDALY; KISYGIIDPIY; LVDGVLDDKSF; IGLPNANEFEY; QIPENLIAVVF; FRYGYESGAKY; MKGNIVDAFRY; GVIGLPNANEF; AVVFRVEQGAF; NGSDLIWLVGY; EIIVPCNQEEY; TSVIKNIGDAL; LVGYMLTDASL; ETAKNLGDGYY
	HLA-B4403	NEFEYIKVL; KEIIVPCNQ; EEYEIFIKQ; PENLIAVVF; EEVFSCAIS; EEYEIFIKQI; SENPKISYGI; NEFEYIKVLE; GEYIKNNNVW; KEIIVPCNQE; EEVFSCAISG; EEYEIFIKQIL; SENPKISYGII; IEIISEYSNSF; NEFEYIKVLER; YEIFIKQILKL; EEVFSCAISGV; KEIIVPCNQEE; NEALLRLKKDF
	HLA-B5101	IPENLIAVV; NPKISYGII; LPNANEFEYI; DPIYGDDVQI; LAPKNFITSV; APKNFITSVI; IPENLIAVVF; VPCNQEEYEI; LAPKNFITSVI; FPENIEEVFSC
	HLA-B5701	ISYGIIDPIY; TGEYIKNNNVW
NP_212518.1 ; Basic	HLA-A0101	FSDLSVKLSY; TVDEAMTEDAY
	HLA-A0201	AMTEDAYEV; RLVDEVIDL; FIFITLSLL; KIISGEIIV; GLKEGVIEI;

membrane protein C (bmpC) [Borrelia burgdorferi B31; Seq3		GIFYANPKL; GLNQDQSYI; ITLSLLVFA; RLLTVDEAM; FLAGYIAAK; SIIKDIGKV; SVHDGVVKL; IIVPDSEYA; KSDKVVVGV; KLSYERPDI; YIAPQNVIT; KVGVIFPIA; YANPKLRLV; FMYKEDKVGV; FLAGYIAAKM; FIFITLSLLV; FLTGPMSEHV; VLNNRLVDEV; ALFMYKEDKV; VIYSISSEYI; FITLSLLVFA; WLIGYRFSDL; GLKEGVIEIV; RLVSKKAPSL; KLRDNFGIKL; FGFKAGIFYA; GLNQDQSYIA; YAFDLFKSKL; RLLTVDEAMT; IIDRGLKEGV; ISSEYINNRV; YIAPQNVITSI; FMYKEDKVGVI; KVIYSISSEYI; VIFPIAGITGL; SISSEYINNRV; IIIDRGLKEGV; LIGYRFSDLSV; VLNNRLVDEVI; YINNRVFKGGI; FLAGYIAAKMS; GIFYANPKLRL; KMSRKEKIGFL; SLAIKFRNEEA; SFYDKGYNQSV; KLRDNFGIKLI; LITKSLRPYPI; RFIFITLSLLV; KVGVIFPIAGI; GVIEIVKDPDV; GLGVYDAAKEL; IVPDSEYAFDL; SLFDKEKGKAM
	HLA-A0301	KAMALFMYK; FLAGYIAAK; YIAAKMSRK; SLLVFACFK; KLRDNFGIK; GVLAHGSFY; NLFWLIGYR; VIYSISSEY; ALFMYKEDK; LAHGSFYDK; GIIIDRGLK; SLFDKEKGK; VFACFKSNK; IFYANPKLR; MSEHVKDFK; SEYAFDLFK; YAFDLFKSK; FACFKSNKK; KAMALFMYK; FLAGYIAAK; YIAAKMSRK; SLLVFACFK; KLRDNFGIK; GVLAHGSFY; NLFWLIGYR; VIYSISSEY; ALFMYKEDK; LAHGSFYDK; GIIIDRGLK; SLFDKEKGK; VFACFKSNK; IFYANPKLR; MSEHVKDFK; SEYAFDLFK; YAFDLFKSK; FACFKSNKK; LVFACFKSNKK; KSNKKSIKSDK; TLSLLVFACFK; GVLAHGSFYDK; KSLRPYPIEGK; LLVFACFKSNK; RVFKGGIIIDR; FLTGPMSEHVK; KGKAMALFMYK; KLSYERPDIYY; YIAAKMSRKEK; GLKEGVIEIVK; VSKKAPSLFDK; AMALFMYKEDK; AAFLAGYIAAK; IGYRFSDLSVK; YANPKLRLVSK; VITSIIKDIGK; IQVPKNSLAIK; AMTEDAYEVQK; VVGVLAHGSFY; VVKLRDNFGIK; RFSDLSVKLSY; ITGLGVYDAAK; SSEYINNRVFK; AGYIAAKMSRK; SLRPYPIEGKR; PLNLFWLIGYR; RDNFGIKLITK
	HLA-A1101	KAMALFMYK; SLLVFACFK; SEYAFDLFK; YIAAKMSRK; GIIIDRGLK; MSEHVKDFK; TSIIKDIGK; YAFDLFKSK; GVLAHGSFY; ALFMYKEDK; LAHGSFYDK; VIYSISSEY; SLFDKEKGK; AGIFYANPK; NLFWLIGYR; AAKMSRKEK; FLAGYIAAK; ISSEYINNR; FACFKSNKK; VFACFKSNK; QSVHDGVVK; KLRDNFGIK; LSVKLSYER; GLGVYDAAK; EYINNRVFK; LVFACFKSNK; LSLLVFACFK; HVKDFKFGFK; VLAHGSFYDK; KAGIFYANPK; MTEDAYEVQK; ITSIIKDIGK; KVIYSISSEY; SISSEYINNR; MALFMYKEDK; LTGPMSEHVK; AFLAGYIAAK; SVHDGVVKLR; GYIAAKMSRK; GIFYANPKLR; GKAMALFMYK; IAAKMSRKEK; SEYINNRVFK; KAPSLFDKEK; QVPKNSLAIK; SLRPYPIEGK; DSEYAFDLFK; LSYERPDIYY; KAMALFMYKE; PMSEHVKDFK; VFACFKSNKK; PQNVITSIIK; KLITKSLRPY; NQSVHDGVVK; SKKAPSLFDK; TLSLLVFACFK; GVLAHGSFYDK; LVFACFKSNKK; AAFLAGYIAAK; SSEYINNRVFK; KSLRPYPIEGK; AMALFMYKEDK; AMTEDAYEVQK; KSNKKSIKSDK; ITGLGVYDAAK; KGKAMALFMYK; YIAAKMSRKEK; VSKKAPSLFDK; SEYAFDLFKSK; VVKLRDNFGIK; LVDEVIDLENK; VITSIIKDIGK; YANPKLRLVSK; LLVFACFKSNK; RVFKGGIIIDR; VVGVLAHGSFY; AGYIAAKMSRK; YSISSEYINNR; FLTGPMSEHVK; GPMSEHVKDFK; APQNVITSIIK; IGYRFSDLSVK; IVKDPDVLNNR; IQVPKNSLAIK; GLKEGVIEIVK; AFDYGDIQVPK; KLSYERPDIYY; SIIKDIGKVIY
	HLA-A2402	IYSISSEYI; IYYGIIDAF; IFITLSLLV; SYIAPQNVI; RFIFITLSL; LFWLIGYRF; FYANPKLRL; EYINNRVFK; KFGFKAGIF; IVPDSEYAF; VSKKAPSLF; LSLLVFACF; NPLNLFWLI; IFITLSLLVF; RFIFITLSLL; MYKEDKVGVI; MFKRFIFITL; FYANPKLRLV; EVQKNPLNLF; EYAFDLFKSK; PYPIEGKRLL; YYGIIDAFDY; KNPLNLFWLI; EYAFDLFKSKL; RFIFITLSLLV; SYERPDIYYGI; MYKEDKVGVIF; ITLSLLVFACF; AYEVQKNPLNL; IYYGIIDAFDY; GYRFSDLSVKL;

		QVPKNSLAIKF
	HLA-A2902	SYERPDIYY; YGIIDAFDY; VIYSISSEY; EIIVPDSEY; FGFKAGIFY; LFWLIGYRF; IVPDSEYAF; HVKDFKFGF; IFITLSLLV; YYGIIDAFDY; IFITLSLLVF; KVIYSISSEY; KLITKSLRPY; KFGFKAGIFY; VIGLNQDQSY; IIKDIGKVIY; PLNLFWLIGY; LSYERPDIYY; DAAKELGPKY; IIVPDSEYAF; IAGITGLGVY; YVIGLNQDQSY; RFSDLSVKLSY; IYYGIIDAFDY; VVGVLAHGSFY; KLSYERPDIYY; SIIKDIGKVIY; EIIVPDSEYAF; YDAAKELGPKY; PIAGITGLGVY; FIFITLSLLVF; FKFGFKAGIFY; TVDEAMTEDAY; QVPKNSLAIKF; PMSEHVKDFKF
	HLA-A6801	NLFWLIGYR; EYINNRVFK; MSEHVKDFK; LSVKLSYER; ISSEYINNR; YIAAKMSRK; FLAGYIAAK; SLLVFACFK; YAFDLFKSK; FACFKSNKK; KAMALFMYK; TSIIKDIGK; IFYANPKLR; SEYAFDLFK; LAHGSFYDK; VIYSISSEY; VFACFKSNK; GYIAAKMSR; DAAKELGPK; GIIIDRGLK; EIIVPDSEY; RPYPIEGKR; DYGDIQVPK; ALFMYKEDK; MTEDAYEVQ; QSVHDGVVK; YRFSDLSVK; EAAFLAGYI; MTEDAYEVQK; HVKDFKFGFK; DSEYAFDLFK; LVFACFKSNK; SVHDGVVKLR; SISSEYINNR; GIFYANPKLR; LSLLVFACFK; ITSIIKDIGK; DLSVKLSYER; EYAFDLFKSK; MALFMYKEDK; IAAKMSRKEK; LTGPMSEHVK; GIKLITKSLR; DNFGIKLITK; KVIYSISSEY; SEYINNRVFK; QVPKNSLAIK; LNLFWLIGYR; VFACFKSNKK; LSYERPDIYY; VLAHGSFYDK; FDYGDIQVPK; GYIAAKMSRK; YSISSEYINNR; TLSLLVFACFK; SSEYINNRVFK; LAGYIAAKMSR; YIAAKMSRKEK; LLVFACFKSNK; LVFACFKSNKK; IVKDPDVLNNR; QSVHDGVVKLR; FLTGPMSEHVK; FGIKLITKSLR; RVFKGGIIIDR; AAFLAGYIAAK; YANPKLRLVSK; ITGLGVYDAAK; YVIGLNQDQSY; VITSIIKDIGK; FKAGIFYANPK; LVDEVIDLENK; IGYRFSDLSVK; EHVKDFKFGFK; AMALFMYKEDK; AMTEDAYEVQK; IYYGIIDAFDY; SLRPYPIEGKR; PLNLFWLIGYR; GVLAHGSFYDK; VVKLRDNFGIK; AGIFYANPKLR; VPKNSLAIKFR
	HLA-B0702	APQNVITSI; YPIEGKRLL; FPIAGITGL; RPDIYYGII; GPKYYVIGL; LVSKKAPSL; QVPKNSLAI; RPYPIEGKRL; APQNVITSII; VPKNSLAIKF; YPIEGKRLLT; GPMSEHVKDF; KLRDNFGIKL; RLVSKKAPSL; RPYPIEGKRLL; YPIEGKRLLTV; FPIAGITGLGV; FKRFIFITLSL; NPKLRLVSKKA
	HLA-B0801	FDKEKGKAM; KEKGKAMAL; FKRFIFITL; MFKRFIFITL; FGIKLITKSL; FDKEKGKAMAL; AIKFRNEEAAF; FMYKEDKVGVI; NPKLRLVSKKA; FKRFIFITLSL
	HLA-B1501	VQKNPLNLF; GVLAHGSFY; VIYSISSEY; AAKELGPKY; KFRNEEAAF; KVVVGVLAH; IVPDSEYAF; EIIVPDSEY; HVKDFKFGF; LITKSLRPY; FITLSLLVF; FGFKAGIFY; LSYERPDIY; PMSEHVKDF; YGIIDAFDY; AGITGLGVY; RLLTVDEAM; LSLLVFACF; IGLNQDQSY; KVIYSISSEY; KLITKSLRPY; LSYERPDIYY; KMSRKEKIGF; IIKDIGKVIY; IQVPKNSLAI; AAKELGPKYY; IIVPDSEYAF; IFITLSLLVF; VQKNPLNLFW; VVGVLAHGSF; TLSLLVFACF; IAGITGLGVY; FLAGYIAAKM; KLSYERPDIY; KGKAMALFMY; NLFWLIGYRF; LVSKKAPSLF; WLIGYRFSDL; SSEYINNRVF; YVIGLNQDQSY; ISSEYINNRVF; VVVGVLAHGSF; FIFITLSLLVF; KLSYERPDIYY; AIKFRNEEAAF; RFSDLSVKLSY; SLFDKEKGKAM; VVGVLAHGSFY; LAHGSFYDKGY; EIIVPDSEYAF; FMYKEDKVGVI; RLVSKKAPSLF; VQKNPLNLFWL; SIIKDIGKVIY; PMSEHVKDFKF
	HLA-B2705	YRFSDLSVK; KRFIFITLS; FRNEEAAFL; FKFGFKAGI; KRFIFITLSL; YRFSDLSVKL; KRLLTVDEAM; KRFIFITLSLL; LRLVSKKAPSL; FKFGFKAGIFY; KRLLTVDEAMT
	HLA-B3501	FPIAGITGL; IVPDSEYAF; YPIEGKRLL; LFWLIGYRF; LAGYIAAKM; DPDVLNNRL; IGLNQDQSY; FITLSLLVF; DEAMTEDAY; DSEYAFDLF; EIIVPDSEY; IYYGIIDAF; FGFKAGIFY; NPLNLFWLI; RLLTVDEAM;

		VIYSISSEY; LSLLVFACF; LSYERPDIY; YGIIDAFDY; KFRNEEAAF; AAKELGPKY; YIAPQNVIT; IIVPDSEYAF; IAGITGLGVY; VPKNSLAIKF; DIYYGIIDAF; FLAGYIAAKM; DAAKELGPKY; IFITLSLLVF; DAYEVQKNPL; YPIEGKRLLT; YAFDLFKSKL; KVIYSISSEY; NLFWLIGYRF; FSDLSVKLSY; TLSLLVFACF; FPIAGITGLG; VDEAMTEDAY; VPDSEYAFDL; IKFRNEEAAF; EKIGFLTGPM; EAAFLAGYIA; LSYERPDIYY; EAMTEDAYEV; NEEAAFLAGY; NPLNLFWLIGY; TVDEAMTEDAY; YVIGLNQDQSY; VPDSEYAFDLF; LAHGSFYDKGY; EIIVPDSEYAF; FIFITLSLLVF; YPIEGKRLLTV; FPIAGITGLGV; EAAFLAGYIAA; DAAKELGPKYY; ISSEYINNRVF; FKFGFKAGIFY; VVVGVLAHGSF; YEVQKNPLNLF; VVGVLAHGSFY; RFSDLSVKLSY; ITLSLLVFACF
	HLA-B4403	SEHVKDFKF; KEDKVGVIF; SEYINNRVF; EEAAFLAGY; SEYAFDLFK; GEIIVPDSEY; YEVQKNPLNL; EEAAFLAGYI; NEEAAFLAGY; SEYAFDLFKS; KEKGKAMALF; SEHVKDFKFGF; GEIIVPDSEYA; KEKGKAMALFM; KEDKVGVIFPI; YEVQKNPLNLF; KEKIGFLTGPM; EEAAFLAGYIA
	HLA-B5101	NPLNLFWLI; FPIAGITGL; YPIEGKRLL; APQNVITSI; APQNVITSII; VPKNSLAIKF; IAPQNVITSI; FPIAGITGLG; YPIEGKRLLT; YPIEGKRLLTV; FPIAGITGLGV; IAPQNVITSII
	HLA-B5701	EVQKNPLNLFW
NP_212519.1 B; Basic membrane protein D (bmpD) [Borrelia burgdorferi B31; Seq4	HLA-A0101	ASENVSVNY; VLESFMYGY; NSNIKVVSQY; RSEEVAFLAGY
	HLA-A0201	FMYGYEAGA; YLAPNNVIV; SIMNGIIKV; LIWGIGFRL; KVYYFLIFL; FLIFLFIVA; KVDSLMYSL; YFLIFLFIV; MLKKVYYFL; FAAAGLSGI; FMLKKVYYF; FLAGYFASK; FLGLKEDGL; YYFLIFLFI; EIYFLYFFI; NLLNISFRS; GLKEDGLGL; NISFRSEEV; FLFIVACSS; KVSYFVLQM; SLTKKYLET; FMLKKVYYFL; FLAGYFASKA; RLSDILFQRA; SVNYAIIEGV; VLDGGKTMFL; MLKKVYYFLI; NLIWGIGFRL; ILFQRASENV; AIIEGVYDEI; GLSGIGVIEA; LMYSLTKKYL; YYFLIFLFIV; YVGTFGDFGL; KLKADLNINI; YEIYFLYFFI; YLAPNNVIVS; FLIFLFIVAC; NMYRDGVDII; KIGQSIMNGI; FLFIVACSSS; FQRASENVSV; GIIKVPYDKV; GLKEDGLGLV; GLGLVLNENL; KKVYYFLIFL; FMLKKVYYFLI; YLAPNNVIVSA; KVYYFLIFLFI; FAAAGLSGIGV; SLTKKYLETGV; SLMYSLTKKYL; LLNISFRSEEV; FLGLKEDGLGL; VLESFMYGYEA; KVPYDKVSYFV; GLSGIGVIEAA; FLIFLFIVACS; GVLDGGKTMFL; FIKSKEDIFML; IIFAAAGLSGI; FLAGYFASKAS; TMFLGLKEDGL; STASNMYRDGV; ELGPDHYIIGV; VYYFLIFLFIV; RLSDILFQRAS; KLKADLNINII; KTGKIGFVGGV; VSVNYAIIEGV; YAIIEGVYDEI
	HLA-A0301	FLAGYFASK; FLYFFIKSK; SLMYSLTKK; RSTASNMYR; RLSDILFQR; IYFLYFFIK; LMYSLTKKY; KGFNESSSK; SSKAIRKLK; KIGFVGGVR; GIIKVPYDK; GYFASKASK; ESSSKAIRK; NVIVSAVKK; KVYYFLIFL; ASKASKTGK; NLIWGIGFR; GLVLNENLK; QSIMNGIIK; FMYGYEAGAK; GVYDEIQIPK; AFLAGYFASK; EIYFLYFFIK; AGYFASKASK; IMNGIIKVPY; SLMYSLTKKY; KSKEDIFMLK; YFLYFFIKSK; KSNYSEIYNK; KVLESFMYGY; SSSKAIRKLK; GQSIMNGIIK; LIVDGAFDDK; DSLMYSLTKK; KVYYFLIFLF; VDSLMYSLTK; ADLNINIIEK; YSEIYNKSLK; GTFGDFGLGR; FASKASKTGK; GAKYANSNIK; DIFMLKKVYY; SSDDGKSEAK; GGKTMFLGLK; RASENVSVNY; AVKKVDSLMY; VYYFLIFLFI; KVDSLMYSLTK; KIGFVGGVRGK; VAFLAGYFASK; KSKEDIFMLKK; GLGLVLNENLK; IYFLYFFIKSK; FMYGYEAGAKY; IVACSSSDDGK; KVYYFLIFLFI; SIMNGIIKVPY; LAGYFASKASK; ESSSKAIRKLK; NSNLIWGIGFR; SVNYAIIEGVY; GLGRSTASNMY; YFASKASKTGK
	HLA-A1101	SLMYSLTKK; RSTASNMYR; GIIKVPYDK; SSKAIRKLK; QSIMNGIIK;

		IYFLYFFIK; NVIVSAVKK; RLSDILFQR; SNYSEIYNK; ASKASKTGK; DSLMYSLTK; FLAGYFASK; FLYFFIKSK; ESSSKAIRK; GYFASKASK; IVDGAFDDK; SKEDIFMLK; KVYYFLIFL; GIGVIEAAK; GLVLNENLK; KGFNESSSK; ASENVSVNY; NLIWGIGFR; VLESFMYGY; VYDEIQIPK; KIGFVGGVR; KTMFLGLKE; DLNINIIEK; KEDIFMLKK; AKYANSNIK; SEIYNKSLK; GKTMFLGLK; GVYDEIQIPK; KSNYSEIYNK; EIYFLYFFIK; KSKEDIFMLK; KVLESFMYGY; SSSKAIRKLK; GTFGDFGLGR; AFLAGYFASK; FMYGYEAGAK; SSDDGKSEAK; VACSSSDDGK; GQSIMNGIIK; DSLMYSLTKK; KVYYFLIFLF; LIVDGAFDDK; SLMYSLTKKY; AGYFASKASK; YSEIYNKSLK; YFLYFFIKSK; AVKKVDSLMY; GAKYANSNIK; RASENVSVNY; SGIGVIEAAK; SKEDIFMLKK; GGKTMFLGLK; IMNGIIKVPY; FASKASKTGK; KVDSLMYSLTK; VAFLAGYFASK; KSKEDIFMLKK; SIMNGIIKVPY; SSSDDGKSEAK; IVACSSSDDGK; SLIVDGAFDDK; KADLNINIIEK; KIGFVGGVRGK; SFMYGYEAGAK; IYFLYFFIKSK; GLGLVLNENLK; SVNYAIIEGVY; KVYYFLIFLFI; LAGYFASKASK; NSNLIWGIGFR; ESSSKAIRKLK; LSGIGVIEAAK; APNNVIVSAVK; YEIYFLYFFIK; RSEEVAFLAGY; LVLNENLKSNY
	HLA-A2402	MDNYYEIYF; DNYYEIYFL; VYYFLIFLF; YYFLIFLFI; YYEIYFLYF; NYYEIYFLY; QYVGTFGDF; IYFLYFFIK; PYDKVSYFV; SYLAPNNVI; SYLGDIANL; KYANSNIKV; FMLKKVYYF; MYRDGVDII; YFLIFLFIV; EIYFLYFFI; YEIYFLYFF; VYYFLIFLFI; YYEIYFLYFF; NYYEIYFLYF; PYDKVSYFVL; IFMLKKVYYF; YYFLIFLFIV; MYRDGVDIIF; KVYYFLIFLF; NYSEIYNKSL; KYANSNIKVV; FFIKSKEDIF; IFAAAGLSGI; SYLAPNNVIV; MLKKVYYFLI; YEIYFLYFFI; KVVSQYVGTF; NYYEIYFLYFF; YYEIYFLYFFI; VYYFLIFLFIV; IFMLKKVYYFL; FMLKKVYYFLI; QYVGTFGDFGL; LYFFIKSKEDI; VYDEIQIPKNL; YYFLIFLFIVA; NYSEIYNKSLK; IWGIGFRLSDI; YFFIKSKEDIF; KKVYYFLIFLF; IYFLYFFIKSK
	HLA-A2902	NYYEIYFLY; VYYFLIFLF; LMYSLTKKY; NYAIIEGVY; IFMLKKVYY; KVPYDKVSY; VLESFMYGY; YYEIYFLYF; YGYEAGAKY; DIFMLKKVY; EVAFLAGYF; YYFLIFLFI; FMLKKVYYF; EIYFLYFFI; MNGIIKVPY; SFRSEEVAF; YEIYFLYFF; ASENVSVNY; YFLIFLFIV; MYGYEAGAKY; IMNGIIKVPY; DIFMLKKVYY; NYYEIYFLYF; DNYYEIYFLY; KVYYFLIFLF; SLMYSLTKKY; YYEIYFLYFF; KVLESFMYGY; YYFLIFLFIV; IIGVDQDQSY; AVKKVDSLMY; VLNENLKSNY; VNYAIIEGVY; VYYFLIFLFI; IFMLKKVYYF; RGKVLESFMY; RASENVSVNY; YIIGVDQDQSY; FMYGYEAGAKY; SIMNGIIKVPY; NYYEIYFLYFF; SVNYAIIEGVY; LVLNENLKSNY; MDNYYEIYFLY; IIKVPYDKVSY; VYYFLIFLFIV; YFFIKSKEDIF; QRASENVSVNY; NMYRDGVDIIF; YYEIYFLYFFI; DIFMLKKVYYF; SAVKKVDSLMY; VRGKVLESFMY; EDIFMLKKVYY
	HLA-A6801	NLIWGIGFR; NVIVSAVKK; RSTASNMYR; RLSDILFQR; FLAGYFASK; ESSSKAIRK; NYYEIYFLY; FLYFFIKSK; IYFLYFFIK; SSKAIRKLK; DSLMYSLTK; ETGVLDGGK; SLMYSLTKK; DLNINIIEK; EVAFLAGYF; NNVIVSAVK; EIYFLYFFI; SNYSEIYNK; QSIMNGIIK; SEIYNKSLK; GIIKVPYDK; MYGYEAGAK; GYFASKASK; NESSSKAIR; GLVLNENLK; TFGDFGLGR; IVDGAFDDK; SKEDIFMLK; EIYFLYFFIK; GTFGDFGLGR; FMYGYEAGAK; YSEIYNKSLK; FASKASKTGK; SSSKAIRKLK; DSLMYSLTKK; DNYYEIYFLY; GVYDEIQIPK; LIVDGAFDDK; NNVIVSAVKK; DIFMLKKVYY; KSNYSEIYNK; VACSSSDDGK; EVAFLAGYFA; YFLYFFIKSK; NSNIKVVSQY; SGIGVIEAAK; KSKEDIFMLK; GAKYANSNIK; FNESSSKAIR; FRLSDILFQR; SNLIWGIGFR; KVYYFLIFLF; NSNLIWGIGFR; ESSSKAIRKLK; IVACSSSDDGK; NYSEIYNKSLK; VAFLAGYFASK; YEIYFLYFFIK; LAGYFASKASK; IPKNLLNISFR; IYFLYFFIKSK; YFASKASKTGK;

		MDNYYEIYFLY; EGVYDEIQIPK; SVNYAIIEGVY; NYYEIYFLYFF; SFMYGYEAGAK; FMYGYEAGAKY; EAAKELGPDHY; SLIVDGAFDDK; EVAFLAGYFAS; LGRSTASNMYR; YIIGVDQDQSY; SSSDDGKSEAK; EIYFLYFFIKS; NSYLGDIANLE; MNGIIKVPYDK; SIMNGIIKVPY; LSGIGVIEAAK
	HLA-B0702	APNNVIVSA; VPYDKVSYF; SAVKKVDSL; AIRKLKADL; KASTGNSYL; KVSYFVLQM; APNNVIVSAV; IPKNLLNISF; VPYDKVSYFV; FVGGVRGKVL; GVRGKVLESF; VPYDKVSYFVL; IVSAVKKVDSL
	HLA-B0801	YDKVSYFVL; MLKKVYYFL; FMLKKVYYF; FMLKKVYYFL; MLKKVYYFLI; IPKNLLNISF; FIKSKEDIFM; MLKKVYYFLIF; YDKVSYFVLQM; FIKSKEDIFML; FMLKKVYYFLI
	HLA-B1501	LMYSLTKKY; YGYEAGAKY; FMLKKVYYF; VVSQYVGTF; FQRASENVS; VSLIVDGAF; IGVDQDQSY; GLKEDGLGL; GVLDGGKTM; ASKTGKIGF; SLKIGQSIM; KVPYDKVSY; SFRSEEVAF; GVIEAAKEL; IMNGIIKVPY; SQYVGTFGDF; FQRASENVSV; ISFRSEEVAF; IEKASTGNSY; RASENVSVNY; GVRGKVLESF; AVKKVDSLMY; SLMYSLTKKY; VLNENLKSNY; TVSLIVDGAF; KVLESFMYGY; KVYYFLIFLF; GVLDGGKTMF; VNYAIIEGVY; KVVSQYVGTF; LGRSTASNMY; RGKVLESFMY; AAKELGPDHY; IQIPKNLLNI; NLKSNYSEIY; KASKTGKIGF; IIGVDQDQSY; LMYSLTKKYL; IGFRLSDILF; FMYGYEAGAKY; YIIGVDQDQSY; SIMNGIIKVPY; NMYRDGVDIIF; SVNYAIIEGVY; IIKVPYDKVSY; MLKKVYYFLIF; GLGRSTASNMY; GLKEDGLGLVL; KTVSLIVDGAF; RSEEVAFLAGY; IIEKASTGNSY; LVLNENLKSNY; FQRASENVSVN; VSQYVGTFGDF; YFFIKSKEDIF
	HLA-B2705	YRDGVDIIF; FRSEEVAFL; GRSTASNMY; QRASENVSV; FRLSDILFQR; GRSTASNMYR; KKVDSLMYSL; QRASENVSVNY
	HLA-B3501	YGYEAGAKY; IGVDQDQSY; VPYDKVSYF; VVSQYVGTF; EVAFLAGYF; LKSNYSEIY; VSLIVDGAF; EKASTGNSY; YRDGVDIIF; MDNYYEIYF; YYEIYFLYF; SFRSEEVAF; NYAIIEGVY; YEIYFLYFF; MNGIIKVPY; EEVAFLAGY; LIWGIGFRL; IPKNLLNISF; TVSLIVDGAF; RASENVSVNY; IMNGIIKVPY; KVVSQYVGTF; ISFRSEEVAF; MYRDGVDIIF; MYGYEAGAKY; YVGTFGDFGL; FFIKSKEDIF; KVLESFMYGY; IKVPYDKVSY; YANSNIKVVS; TGVLDGGKTM; IIGVDQDQSY; YYEIYFLYFF; SAVKKVDSLM; APNNVIVSAV; YIIGVDQDQSY; SVNYAIIEGVY; FMYGYEAGAKY; EAAKELGPDHY; SAVKKVDSLMY; SIMNGIIKVPY; VPYDKVSYFVL; NISFRSEEVAF; MDNYYEIYFLY; NMYRDGVDIIF; YFFIKSKEDIF; LVLNENLKSNY; IIEKASTGNSY; KTVSLIVDGAF; IVDGAFDDKGF; YAIIEGVYDEI; FFIKSKEDIFM; TGVLDGGKTMF; DSLMYSLTKKY
	HLA-B4403	EEVAFLAGY; YEIYFLYFF; DEIQIPKNL; KEDGLGLVL; KELGPDHYI; EEVAFLAGYF; SEIYNKSLKI; YEIYFLYFFI; SEEVAFLAGY; SENVSVNYAI; DEIQIPKNLL; SEAKTVSLIV; SEEVAFLAGYF; EEVAFLAGYFA; DEIQIPKNLLN; SENVSVNYAII; KEDIFMLKKVY
	HLA-B5101	VPYDKVSYF; FAAAGLSGI; IPKNLLNIS; VPYDKVSYFV; IPKNLLNISF; VPYDKVSYFVL; LAPNNVIVSAV; FAAAGLSGIGV
	HLA-B5701	ISFRSEEVAF
AAC70056.1; Decorin binding protein A; DbpA [Borrelia afzelii; Seq5	HLA-A0101	ATEEETITF; FTETQTGGKV;
	HLA-A0201	GIYDLILNA; TLLASLLAA; IILTLTLLA; LTLTLLASL; TTADGIIAI; SLLAACSLT; KIILTLTLL; TADGIIAIV; GMQGMKQAV; VMKAKVENI; LLASLLAAC; GMKQAVEEA; FLEATEEET; GIYDLILNAA; TTADGIIAIV; ILTLTLLASL; FLEATEEETI; RVADLTIKFL; KIILTLTLLA; KVMKAKVENI; LTLTLLASLL; KTTADGIIAI; AIVKVMKAKV; LTLLASLLAA; LLASLLAACS; IILTLTLLASL; LLASLLAACSL; LLAACSLTGKA; ILNAAKAVEKI; KTTADGIIAIV; LTLTLLASLLA; TADGIIAIVKV; ILTLTLLASLL; TLTLLASLLAA; GIIAIVKVMKA

	HLA-A0301	IIAIVKVMK; LAACSLTGK; KARLESSVK; AIVKVMKAK; FTETQTGGK; LLAACSLTGK; ILNAAKAVEK; GIIAIVKVMK; KIRVADLTIK; ATEEETITFK; IAIVKVMKAK; TADGIIAIVK; IYDLILNAAK; VMKAKVENIK; ITNEIEKAIK; AFTETQTGGK; GIYDLILNAAK; SLLAACSLTGK; KVGGSQIRAAK; IIAIVKVMKAK; KVMKAKVENIK; TTADGIIAIVK; LILNAAKAVEK; AVEKIGMQGMK; KVENIKEKQTK; SVKDITNEIEK
	HLA-A1101	IIAIVKVMK; AIVKVMKAK; LAACSLTGK; AVEEAAKEK; KQAVEEAAK; FTETQTGGK; KARLESSVK; ATEEETITFK; GIIAIVKVMK; ILNAAKAVEK; TADGIIAIVK; LLAACSLTGK; ITNEIEKAIK; IAIVKVMKAK; VMKAKVENIK; AACSLTGKAR; KIRVADLTIK; KAKVENIKEK; AFTETQTGGK; TTADGIIAIVK; GIYDLILNAAK; SLLAACSLTGK; SVKDITNEIEK; KVMKAKVENIK; KVGGSQIRAAK; AVEKIGMQGMK; IIAIVKVMKAK; LILNAAKAVEK; AVEEAAKEKPK; KVENIKEKQTK; AIKEAEDAGVK; KQAVEEAAKEK; GMKQAVEEAAK; EATEEETITFK; RVADLTIKFLE; DAFTETQTGGK
	HLA-A2402	KYNKIILTL; DFSGIYDLI; KYNKIILTLT; IYDLILNAAK; KYNKIILTLTL; KFLEATEEETI
	HLA-A2902	RVADLTIKF; GAGEEDFSGIY
	HLA-A6801	IIAIVKVMK; FTETQTGGK; LAACSLTGK; EKIGMQGMK; MKAKVENIK; LNAAKAVEK; AIVKVMKAK; ENIKEKQTK; ITNEIEKAIK; TADGIIAIVK; GIIAIVKVMK; QAVEEAAKEK; ILNAAKAVEK; IAIVKVMKAK; LLAACSLTGK; ATEEETITFK; AACSLTGKAR; TTADGIIAIVK; EATEEETITFK; DAFTETQTGGK; SVKDITNEIEK; IIAIVKVMKAK; LAACSLTGKAR; DITNEIEKAIK; GIYDLILNAAK; NIKEKQTKNQK; DGIIAIVKVMK; LILNAAKAVEK; KVMKAKVENIK; MKAKVENIKEK; SLLAACSLTGK; AVEKIGMQGMK; KVENIKEKQTK; KVGGSQIRAAK
	HLA-B0702	RVADLTIKF; KPKTTADGI; MIKYNKIIL; RAAKIRVADL; KPKTTADGII; RVADLTIKFL; LASLLAACSL; KPKTTADGIIA; MIKYNKIILTL
	HLA-B0801	MIKYNKIIL; YNKIILTLTL; RAAKIRVADL; MIKYNKIILTL
	HLA-B1501	RVADLTIKF; GIIAIVKVM; ATEEETITF; RVADLTIKFL; KIRVADLTIKF; SQIRAAKIRVA
	HLA-B2705	KQAVEEAAK; IRVADLTIKF; IRAAKIRVADL
	HLA-B3501	DAGVKTDAF; RVADLTIKF; ATEEETITF; FSGIYDLIL; EATEEETITF; LASLLAACSL; EDAGVKTDAF; NAAKAVEKIGM; LEATEEETITF; GAGEEDFSGIY; KAVEKIGMQGM
	HLA-B4403	GEEDFSGIY; EEDFSGIYD; NEIEKAIKEA; EEDFSGIYDL; KENGAGEEDF; EEDFSGIYDLI; AEDAGVKTDAF
	HLA-B5101	KPKTTADGI; KPKTTADGII; LASLLAACSL;
	HLA-B5701	ATEEETITF; ;
AAC70057.1; Decorin binding protein A; DbpA [Borrelia garinii]; Seq6	HLA-A0101	SSGAFSAMY; FSAMYDLMI; GSSGAFSAMY;
	HLA-A0201	AMYDLMIDV; ILLKLSLIV; LMIDVSKPL; KLSLIVSLL; KISEKPEFI; SLIVSLLVA; AMEEKLNNV; TTADGIIAI; FILKAKIKA; KILLKLSLI; LSLIVSLLV; FSAMYDLMI; GAFSAMYDL; KLSLIVSLLV; SAMYDLMIDV; KILLKLSLIV; FILKAKIKAI; KMTGTVTKEA; KISEKPEFIL; LLKLSLIVSL; GLTGETKIRL; TTADGIIAIA; AMYDLMIDVS; AIAQAMEEKL; ILLKLSLIVSL; KLSLIVSLLVA; FSAMYDLMIDV; MIDVSKPLEEI; LIVSLLVACGL; LKLSLIVSLLV; GAFSAMYDLMI; LLVACGLTGET; ILKAKIKAIQV; LLKLSLIVSLL
	HLA-A0301	FTNTQTGSK; QTGSKISEK; IKYNKILLK; IQVAERFVK; MIKYNKILLK; IQKMTGTVTK; AIQVAERFVK; AFTNTQTGSK; VACGLTGETK; TQTGSKISEK; GSSGAFSAMY; IAIAQAMEEK; ISEKPEFILK; KPLEEIGIQK; KANAKKEGVK; RLESSAQEIK; MYDLMIDVSK; KIKAIQVAER; AMYDLMIDVSK; KISEKPEFILK; GIQKMTGTVTK; QVAERFVKAIK; MTGTVTKEAEK; NVNKKQHDALK; LVACGLTGETK; KAIQVAERFVK; IIAIAQAMEEK; EINKIKANAKK; EAFTNTQTGSK;

		AMEEKLNNVNK; AIKEEAEKLKK
	HLA-A1101	AIAQAMEEK; FTNTQTGSK; IQVAERFVK; QTGSKISEK; SSGAFSAMY; GTVTKEAEK; KAIKEEAEK; IKYNKILLK; SEKPEFILK; MIKYNKILLK; IAIAQAMEEK; AIQVAERFVK; ISEKPEFILK; TQTGSKISEK; VACGLTGETK; KANAKKEGVK; IQKMTGTVTK; VAERFVKAIK; AIKEEAEKLK; GSSGAFSAMY; RLESSAQEIK; AFTNTQTGSK; AQEIKDEINK; KIKAIQVAER; EINKIKANAK; MYDLMIDVSK; AMYDLMIDVSK; KISEKPEFILK; KAIQVAERFVK; SAQEIKDEINK; GIQKMTGTVTK; MTGTVTKEAEK; QVAERFVKAIK; NVNKKQHDALK; AMEEKLNNVNK; NTQTGSKISEK; IIAIAQAMEEK; LVACGLTGETK; KAIKEEAEKLK; AIKEEAEKLKK; EAFTNTQTGSK; FVKAIKEEAEK; EINKIKANAKK
	HLA-A2402	KYNKILLKL; AFSAMYDLMI; KYNKILLKLSL
	HLA-A2902	SSGAFSAMY; ; SGSSGAFSAMY
	HLA-A6801	FTNTQTGSK; QTGSKISEK; AIAQAMEEK; DALKNLEEK; GTVTKEAEK; IKAIQVAER; IQVAERFVK; EFILKAKIK; KAIKEEAEK; SSGAFSAMY; IAIAQAMEEK; EINKIKANAK; MIKYNKILLK; KIKAIQVAER; EIKDEINKIK; TQTGSKISEK; MYDLMIDVSK; VACGLTGETK; ISEKPEFILK; TGTVTKEAEK; VAERFVKAIK; EAFTNTQTGSK; MTGTVTKEAEK; EINKIKANAKK; FVKAIKEEAEK; IIAIAQAMEEK; NVNKKQHDALK; QVAERFVKAIK; NTQTGSKISEK; KAIQVAERFVK; LVACGLTGETK; SAQEIKDEINK; AMYDLMIDVSK; TTADGIIAIAQ
	HLA-B0702	KPEFILKAKI; KPLEEIGIQKM; PPTTADGIIAI
	HLA-B0801	ILKAKIKAI; LLKLSLIVSL; FILKAKIKAI; YNKILLKLSL; KLKKSGSSGAF; LLKLSLIVSLL
	HLA-B1501	LMIDVSKPL; SSGAFSAMY; GIIAIAQAM; KQHDALKNL; IQKMTGTVT; KKSGSSGAF; ILKAKIKAI; KAIQVAERF; GSSGAFSAMY; LLKLSLIVSL; LKKSGSSGAF; GSKISEKPEF; KLKKSGSSGAF; IQVAERFVKAI; KIKAIQVAERF; SGSSGAFSAMY
	HLA-B2705	IRLESSAQEIK
	HLA-B3501	KAIQVAERF; GSSGAFSAM; SSGAFSAMY; KANTAATTT; DGIIAIAQAM; SGSSGAFSAM; GSSGAFSAMY; GAFSAMYDLM; KPLEEIGIQKM; SGSSGAFSAMY; TPPTTADGIIA
	HLA-B4403	EEIGIQKMT; EEIGIQKMTG; SEKPEFILKA; QEIKDEINKI; EEIGIQKMTGT
	HLA-B5101	TPPTTADGI; PPTTADGII; TPPTTADGII; KPEFILKAKI; PPTTADGIIA; PPTTADGIIAI; TPPTTADGIIA
	HLA-B5701	
AAC70021.1; Decorin binding protein B; DbpB [Borrelia burgdorferi]; Seq7	HLA-A0101	
	HLA-A0201	AMFDLMLEV; VLFEAFTGL; LMLEVVESL; FLAMFDLML; LLVACSIGL; IVIALFFKL; ALFFKLLVA; LVACSIGLV; GLVERTNAA; RLLAAKAQI; FLKIIEEEA; GLALREAKV; AQIENQLKV; GIIGLKARV; IALFFKLLV; GQFLAMFDL; AMFDLMLEVV; LAMFDLMLEV; KLLVACSIGL; SLEDVGIIGL; LLVACSIGLV; GLVERTNAAL; SIVIALFFKL; KIIEEEALKL; VIALFFKLLV; FLKIIEEEAL; GVLFEAFTGL; IVIALFFKLL; DLMLEVVESL; ALREAKVQAI; ATGKGVLFEA; FLAMFDLMLEV; KLLVACSIGLV; IVIALFFKLLV; VLFEAFTGLKT; LAMFDLMLEVV; MLEVVESLEDV; ALREAKVQAIV; GQFLAMFDLML; SIVIALFFKLL; AIVETGKFLKI
	HLA-A0301	FTGLKTGSK; KIKKEATGK; SIVIALFFK; IVETGKFLK; KIIEEEALK; VTSGGLALR; LFEAFTGLK; VLFEAFTGLK; KVQAIVETGK; AFTGLKTGSK; AIVETGKFLK; KVTSGGLALR; NTAERLLAAK; ALESSSKDLK; KQNIENGGEK; TNAALESSSK; QIENQLKVVK; DLKNKILKIK; IIEEEALKLK; RTNAALESSSK; GVLFEAFTGLK; GLKARVLEESK; ILKIKKEATGK; SLEDVGIIGLK; KIIEEEALKLK; FLKIIEEEALK; TSGGLALREAK; KQNIENGGEKK; SSKDLKNKILK;

		LVACSIGLVER; EAFTGLKTGSK; AALESSSKDLK
	HLA-A1101	SIVIALFFK; IVETGKFLK; KIIEEEALK; SSSKDLKNK; TAERLLAAK; VTSGGLALR; KAQIENQLK; FTGLKTGSK; NAALESSSK; VQAIVETGK; LFEAFTGLK; KIKKEATGK; IVIALFFKL; NQLKVVKEK; KARVLEESK; VLFEAFTGLK; KVQAIVETGK; AIVETGKFLK; NTAERLLAAK; KVTSGGLALR; KQNIENGGEK; ALESSSKDLK; VACSIGLVER; IIEEEALKLK; TNAALESSSK; AFTGLKTGSK; ESSSKDLKNK; QIENQLKVVK; RTNAALESSSK; GVLFEAFTGLK; AALESSSKDLK; SSKDLKNKILK; TSGGLALREAK; SLEDVGIIGLK; QAIVETGKFLK; KIIEEEALKLK; AQIENQLKVVK; AAKAQIENQLK; GLKARVLEESK; LVACSIGLVER; KQNIENGGEKK; EAFTGLKTGSK; IVIALFFKLLV
	HLA-A2402	QFLAMFDLML; FFKLLVACSI; LFFKLLVACSI; KFLKIIEEEAL
	HLA-A2902	IVIALFFKL;
	HLA-A6801	SIVIALFFK; NAALESSSK; VTSGGLALR; IVETGKFLK; EDVGIIGLK; NNPINTAER; FTGLKTGSK; LFEAFTGLK; TAERLLAAK; KIIEEEALK; NIENGGEKK; NTAERLLAAK; VACSIGLVER; VLFEAFTGLK; KVTSGGLALR; ESSSKDLKNK; TNAALESSSK; DVGIIGLKAR; KVQAIVETGK; AIVETGKFLK; KNNPINTAER; LVACSIGLVER; EAFTGLKTGSK; QAIVETGKFLK; RTNAALESSSK; GVLFEAFTGLK; FLKIIEEEALK; TSGGLALREAK; SSKDLKNKILK; EDVGIIGLKAR; SLEDVGIIGLK; SKNNPINTAER; AALESSSKDLK; SKVTSGGLALR
	HLA-B0702	KVTSGGLAL; NPINTAERL; LVERTNAAL; NPINTAERLL; ALREAKVQAI; SKVTSGGLAL;
	HLA-B0801	ILKIKKEAT; LVERTNAAL; FLKIIEEEAL; FFKLLVACSI;
	HLA-B1501	LMLEVVESL; KVTSGGLAL; QAIVETGKF; AMFDLMLEV; FLAMFDLML; GQFLAMFDL; LLVACSIGL; VLFEAFTGL; AQIENQLKV; VQAIVETGKF; GLVERTNAAL; AQIENQLKVV; GQFLAMFDLM; KLKETGNSGQF; KVQAIVETGKF; GQFLAMFDLML; VQAIVETGKFL; GSKVTSGGLAL
	HLA-B2705	GQFLAMFDL; ; GQFLAMFDLML
	HLA-B3501	NPINTAERL; QFLAMFDLM; LVERTNAAL; EATGKGVLF; QAIVETGKF; FLAMFDLML; NSGQFLAMF; NPINTAERLL; TGNSGQFLAM; ETGNSGQFLAM; LAAKAQIENQL; TGNSGQFLAMF
	HLA-B4403	KETGNSGQF; KEATGKGVLF; EESKNNPINT; AERLLAAKAQI
	HLA-B5101	LAMFDLMLEV; LAMFDLMLEVV
	HLA-B5701	
NP_212694.1 ; Heat shock protein 90 [Borrelia burgdorferi B31]; Seq8	HLA-A0101	DTEVNDLLY; NLEYTNLFY; KSEIKAEEY; YLNKEGLEY; KAEEYNEFY; WSSDGKTGY; ITDSEGSLL; IIDSNDPTY; HTKAEGNLEY; YSNHINYPIY; DSEGSLLPNY; ASDAIDKLKF; SVDGFVSFKEY; QFDTEVNDLLY
	HLA-A0201	LLYLIIHSL; FINIINEFI; IMLSMGQEV; FLRELISNA; FIIFRLCYI; IMDDELDEA; FIVSEKVEV; LLPNYLRFI; KILSELEKL; KLFINRIFI; KLEKISILL; QMQKIMLSM; ELDEAILNL; YLIIHSLYS; LLFEEAMLT; IALFIIFRL; KALESDAYI; NLIPEYEGL; TTFDYENPL; ILLFEEAML; RLCYIIKKV; NILKENPIV; LEYTNLFYV; ILKDHIKEV; IIFRLCYII; ILIFYFKQI; IIDCQDLPL; YSNHINYPI; YQMQKIMLS; TLIKEPSAI; FITDSEGSL; KLYLNKEGL; RMNESQKSI; SAFIVSEKV; ASLIGQFGV; NLFYVPSKA; SMGQEVKEI; GVGFYSAFI; EVNDLLYLI; YLNKEGLEYA; SLLPNYLRFI; IMDDELDEAI; SLYSHKEIFL; YQMQKIMLSM; NLEYTNLFYV; FIIFRLCYII; SLIRFKSSSV; LIMDDELDEA; KIMLSMGQEV; GIIDCQDLPL; ILSKIKSSSV; QIALFIIFRL; FITDSEGSLL; KLNETTALWT; ALWTKNKSEI; ELDEAILNLI; KLFINRIFIT; LLFEEAMLTS; LIFYFKQIAL; KISILLFEEA; YSAFIVSEKV; GQFGVGFYSA; YIIKKVKIKL; MILIFYFKQI; AIDKLKFLSL; GVGFYSAFIV; TLIKEPSAII; DLLYLIIHSL; ILIKDNGIGM; FYFKQIALFI; TTFDYENPLM; YANKWKIQEI; SILLFEEAML; YVPSKAPYDL; KLISLIRFKS; FRLCYIIKKV; ILIFYFKQIA; LIPEYEGLKL; SASLIGQFGV; SLTNEKFKNI; ILLFEEAMLT;

		KQFDTEVNDL; KQIALFIIFRL; IMDDELDEAIL; ALFIIFRLCYI; KILSKIKSSSV; LIMDDELDEAI; ILIFYFKQIAL; GMDEQDLTNHL; KQFDTEVNDLL; IIDCQDLPLNV; ILNLIPEYEGL; ILIMDDELDEA; MLSMGQEVKEI; IINEFIEKDFL; NLIPEYEGLKL; LLYLIIHSLYS; YSNHINYPIYI; TLIKEPSAIII; GNLEYTNLFYV; ILQQNKILSKI; KSASLIGQFGV; FYSAFIVSEKV; SAFIVSEKVEV; MILIFYFKQIA; FYFKQIALFII; ILKDHIKEVNL; RLCYIIKKVKI; GMPSKNPGKFI
	HLA-A0301	KLISLIRFK; IIHSLYSHK; MLTSGMPSK; KIKSSSVKK; SIYYITGGK; HINYPIYIK; KLSKKNPEK; GLKLKAINK; KLKRKSCMK; GVIAKSGTK; SVDGFVSFK; TTALWTKNK; YSAFIVSEK; LQQNKILSK; KVKIKLKRK; MLSMGQEVK; KFLSLTNEK; GMPSKNPGK; QIALFIIFR; ILELNPNNK; LTKVKEILK; IFRLCYIIK; YLNKEGLEY; GVYSDFENR; KIQEIIKKY; NIINEFIEK; LSLTNEKFK; YSHKEIFLR; GLEYANKWK; GSLLPNYLR; KSIYYITGGK; RLCYIIKKVK; KLKRKSCMKK; AMLTSGMPSK; LIIHSLYSHK; ILQQNKILSK; SSVDGFVSFK; ILSELEKLSK; LLYLIIHSLY; IIFRLCYIIK; ITGGKENILK; LTNHLGVIAK; IMLSMGQEVK; TLTKVKEILK; FYSAFIVSEK; YTNLFYVPSK; ALFIIFRLCY; HINYPIYIKY; LLPNYLRFIK; LSKIKSSSVK; YIKYSEPIMK; IIKKVKIKLK; KENPIVAAYK; KFKNIALEPK; FLSLTNEKFK; GTKEFINNLK; IFRLCYIIKK; GTEIKLYLNK; KQIALFIIFR; LYLNKEGLEY; LIGQFGVGFY; EVNLSATLIK; NLIPEYEGLK; IKLKRKSCMK; LFYVPSKAPY; FINNLKQDEK; KTGYEIEKAK; VYSDFENREK; LGVIAKSGTK; CYIIKKVKIK; GNLEYTNLFY; SFDDKSILIK; RMNESQKSIY; KNLEPEKLEK; DAYIWSSDGK; SKIKSSSVKK; SGMPSKNPGK; INIINEFIEK; ISNASDAIDK; YYPNTKPGVK; SMGQEVKEIK; NHINYPIYIK; IIFRLCYIIKK; ILSKIKSSSVK; KLKFLSLTNEK; RMNESQKSIYY; KLNETTALWTK; SLLPNYLRFIK; SLYSHKEIFLR; KILSELEKLSK; HLGVIAKSGTK; YLIIHSLYSHK; ILSELEKLSKK; KIMLSMGQEVK; GFYSAFIVSEK; FIIFRLCYIIK; KLYLNKEGLEY; ISFDDKSILIK; GVYSDFENREK; FINIINEFIEK; KIKLKRKSCMK; LSKIKSSSVKK; IVSEKVEVTSK; SSSVDGFVSFK; KFLSLTNEKFK; SLIGQFGVGFY; ALWTKNKSEIK; SVKKILSELEK; KTGYEIEKAKK; TSGMPSKNPGK; VSEKVEVTSKK; IIKKVKIKLKR; YIIKKVKIKLK; EILQQNKILSK; NVSREILQQNK; KVKEILKDHIK; LISNASDAIDK; FINNLKQDEKK; IIKKYSNHINY; NLFYVPSKAPY; YITGGKENILK; VQNLKNLEPEK; ILKENPIVAAY; IALFIIFRLCY; LYYPNTKPGVK; TSNELKDENFK; DSNDPTYQMQK; LSMGQEVKEIK
	HLA-A1101	SVDGFVSFK; SIYYITGGK; TTALWTKNK; GVIAKSGTK; KLISLIRFK; HINYPIYIK; MLTSGMPSK; YSAFIVSEK; NIINEFIEK; IIHSLYSHK; GVYSDFENR; GSLLPNYLR; KIKSSSVKK; QIALFIIFR; LQQNKILSK; KLSKKNPEK; ASDAIDKLK; AILNLIPEY; LTKVKEILK; KFLSLTNEK; TNLFYVPSK; MLSMGQEVK; LSLTNEKFK; GLKLKAINK; KIEISFDDK; AYIWSSDGK; KVKIKLKRK; LSELEKLSK; TEIKLYLNK; GMPSKNPGK; LIPEYEGLK; YSHKEIFLR; ILELNPNNK; KLKRKSCMK; LPNYLRFIK; GFVSFKEYK; VNLSATLIK; YIIKKVKIK; TNHLGVIAK; NLKNLEPEK; SSVDGFVSFK; AMLTSGMPSK; YTNLFYVPSK; KSIYYITGGK; KQIALFIIFR; IIFRLCYIIK; LTNHLGVIAK; LIIHSLYSHK; GTEIKLYLNK; GTKEFINNLK; ISNASDAIDK; KAEEYNEFYK; ITGGKENILK; ILQQNKILSK; TLTKVKEILK; EVNLSATLIK; IMLSMGQEVK; ETTALWTKNK; ALFIIFRLCY; ILSELEKLSK; KTGYEIEKAK; VSEKVEVTSK; KLKRKSCMKK; RLCYIIKKVK; SFDDKSILIK; YIKYSEPIMK; IIKKVKIKLK; LLPNYLRFIK; VSREILQQNK; SMGQEVKEIK; PILELNPNNK; FINNLKQDEK; LSKIKSSSVK; SGMPSKNPGK; LSELEKLSKK; NLIPEYEGLK; NASDAIDKLK; DAYIWSSDGK; LLYLIIHSLY; QQNKILSKIK; FLSLTNEKFK; FYSAFIVSEK; HINYPIYIKY; KFKNIALEPK; KENPIVAAYK; IIIDSNDPTY;

		INIINEFIEK; SSSVDGFVSFK; IIFRLCYIIKK; SLLPNYLRFIK; TSNELKDENFK; KIMLSMGQEVK; GVYSDFENREK; SVKKILSELEK; KILSELEKLSK; ISFDDKSILIK; KLNETTALWTK; TSGMPSKNPGK; SLYSHKEIFLR; IVSEKVEVTSK; YLIIHSLYSHK; FIIFRLCYIIK; GFYSAFIVSEK; KLKFLSLTNEK; FINIINEFIEK; VQNLKNLEPEK; DSNDPTYQMQK; NVSREILQQNK; EAMLTSGMPSK; KTGYEIEKAKK; LSMGQEVKEIK; APYDLYYPNTK; SLIGQFGVGFY; LISNASDAIDK; IALFIIFRLCY; TTFDYENPLMH; ILSKIKSSSVK; VSEKVEVTSKK; YITGGKENILK; KVKEILKDHIK; ILSELEKLSKK; KFLSLTNEKFK; YIIKKVKIKLK; KIKLKRKSCMK; DTLTKVKEILK; SVDGFVSFKEY; LSKIKSSSVKK; RMNESQKSIYY; SGTEIKLYLNK; IYIKYSEPIMK; EILQQNKILSK; LQQNKILSKIK; ALWTKNKSEIK; LIPEYEGLKLK; KLYLNKEGLEY; KYSEPIMKDGK; SGTKEFINNLK; FINNLKQDEKK; KPILELNPNNK; HLGVIAKSGTK; AIIIDSNDPTY; SNHINYPIYIK
	HLA-A2402	IYIKYSEPI; FYFKQIALF; KFINIINEF; LYLIIHSLY; AYKEKGFEI; YFKQIALFI; TYQMQKIML; LYSHKEIFL; NYLRFIKGI; CYIIKKVKI; DYENPLMHI; KQIALFIIF; SLLPNYLRF; FYKNTTFDY; YYPNTKPGV; SFDDKSILI; LWTKNKSEI; AYIWSSDGK; KFSEFSKEF; NFKKIEEEF; KYSNHINYPI; FYFKQIALFI; IFYFKQIALF; KFLSLTNEKF; KFINIINEFI; IYIKYSEPIM; YFKQIALFII; NYLRFIKGII; YYITGGKENI; QFGVGFYSAF; RFKSSSVDGF; YYPNTKPGVK; EYEGLKLKAI; AYKEKGFEIL; IFITDSEGSL; LFIIFRLCYI; FYSAFIVSEK; LYSHKEIFLR; FYFKQIALFII; EYANKWKIQEI; EYNEFYKNTTF; YFKQIALFIIF; YYPNTKPGVKL; YYITGGKENIL; AYKEKGFEILI; IYIKYSEPIMK; IFITDSEGSLL; IFYFKQIALFI; IYYITGGKENI; FYVPSKAPYDL; TYQMQKIMLSM; VYSDFENREKL; KYSNHINYPIY; LFIIFRLCYII; CYIIKKVKIKL; EYTNLFYVPSK; KFKNIALEPKI; QFGVGFYSAFI; FYSAFIVSEKV; TFDYENPLMHI
	HLA-A2902	FYKNTTFDY; YLNKEGLEY; LFIIFRLCY; FYVPSKAPY; INYPIYIKY; NLEYTNLFY; LYLIIHSLY; SKAPYDLYY; TKAEGNLEY; DTEVNDLLY; FYFKQIALF; KFINIINEF; AILNLIPEY; YSNHINYPI; IIDSNDPTY; KIQEIIKKY; EFYKNTTFDY; HINYPIYIKY; YSNHINYPIY; LYLNKEGLEY; LFYVPSKAPY; IIIDSNDPTY; IWSSDGKTGY; LLYLIIHSLY; ALFIIFRLCY; EAILNLIPEY; HTKAEGNLEY; FDTEVNDLLY; LIGQFGVGFY; KFLSLTNEKF; IFYFKQIALF; RMNESQKSIY; PSKAPYDLYY; YVPSKAPYDLY; YIWSSDGKTGY; IALFIIFRLCY; KLYLNKEGLEY; NLFYVPSKAPY; RMNESQKSIYY; QFDTEVNDLLY; YFKQIALFIIF; DLLYLIIHSLY; EYNEFYKNTTF; KYSNHINYPIY; SLIGQFGVGFY; EGNLEYTNLFY; EFGRCIKEGVY; AIIIDSNDPTY; ILKENPIVAAY; NEFYKNTTFDY; NHINYPIYIKY; EIKAEEYNEFY; IIKKYSNHINY; KWKIQEIIKKY
	HLA-A6801	YSAFIVSEK; QIALFIIFR; YSHKEIFLR; TTALWTKNK; SIYYITGGK; SVDGFVSFK; HINYPIYIK; MLTSGMPSK; GVYSDFENR; NIINEFIEK; ENPIVAAYK; MLSMGQEVK; IIHSLYSHK; ELKDENFKK; LPNYLRFIK; EKVEVTSKK; NLKNLEPEK; VSFKEYKER; TKEFINNLK; GFVSFKEYK; GSLLPNYLR; LTKVKEILK; WTKNKSEIK; SEFSKEFGR; LIPEYEGLK; TNLFYVPSK; EEFKDTLTK; NNKIVQNLK; YIIKKVKIK; EGIEEKEEK; GVIAKSGTK; LSLTNEKFK; AYIWSSDGK; KLISLIRFK; YSDFENREK; NPLMHIHTK; DTEVNDLLY; TGYEIEKAK; MGQEVKEIK; SNASDAIDK; ETTALWTKNK; YTNLFYVPSK; FSEFSKEFGR; EVNLSATLIK; SSVDGFVSFK; FVSFKEYKER; DAYIWSSDGK; FYSAFIVSEK; NASDAIDKLK; GTKEFINNLK; LIIHSLYSHK; EGVYSDFENR; TLTKVKEILK; EAILNLIPEY; EGSLLPNYLR; KSIYYITGGK; FLSLTNEKFK; FINNLKQDEK; NLIPEYEGLK; YIKYSEPIMK; LYSHKEIFLR; EFYKNTTFDY; IIFRLCYIIK; NFKKIEEEFK; FSKEFGRCIK; LTNHLGVIAK; NPEKFSEFSK; TTFDYENPLM; DGFVSFKEYK;

		KAEEYNEFYK; LLYLIIHSLY; NPIVAAYKEK; YSEPIMKDGK; ISNASDAIDK; YSNHINYPIY; ITGGKENILK; HINYPIYIKY; ENPLMHIHTK; TGYEIEKAKK; KQIALFIIFR; INIINEFIEK; LLPNYLRFIK; IIKKVKIKLK; LSKIKSSSVK; NHINYPIYIK; HTKAEGNLEY; EFKDTLTKVK; IIIDSNDPTY; LKFLSLTNEK; SLYSHKEIFLR; EAMLTSGMPSK; TSNELKDENFK; DSNDPTYQMQK; FINIINEFIEK; EYTNLFYVPSK; FIIFRLCYIIK; SSSVDGFVSFK; YITGGKENILK; IIFRLCYIIKK; YLIIHSLYSHK; SVKKILSELEK; ENFKKIEEEFK; NVSREILQQNK; ISFDDKSILIK; GVYSDFENREK; EFINNLKQDEK; LSMGQEVKEIK; FINNLKQDEKK; IIKKVKIKLKR; DTLTKVKEILK; YIIKKVKIKLK; EYKERMNESQK; TTFDYENPLMH; ILSKIKSSSVK; IVSEKVEVTSK; NPNNKIVQNLK; EIKAEEYNEFY; EILQQNKILSK; EFSKEFGRCIK; LISNASDAIDK; GFYSAFIVSEK; IYIKYSEPIMK; EKFKNIALEPK; NLFYVPSKAPY; DLTNHLGVIAK; FKQIALFIIFR; ENPIVAAYKEK; TSGMPSKNPGK; VSEKVEVTSKK; SLIGQFGVGFY; LSKIKSSSVKK; YVPSKAPYDLY; SNASDAIDKLK; LYYPNTKPGVK; SLLPNYLRFIK; SDAYIWSSDGK; GFVSFKEYKER; KFSEFSKEFGR; TKPGVKLFINR; NTTFDYENPLM; IALFIIFRLCY; EEFKDTLTKVK; KIMLSMGQEVK; SGTKEFINNLK; EVNDLLYLIIH; LIPEYEGLKLK; EAILNLIPEYE; EPKIEISFDDK; ILSELEKLSKK; DLLYLIIHSLY; IKAEEYNEFYK; HLGVIAKSGTK; KTGYEIEKAKK
	HLA-B0702	MPSKNPGKF; IPEYEGLKL; VPSKAPYDL; LPLNVSREI; YPIYIKYSE; LIRFKSSSV; SVKKILSEL; YPNTKPGVKL; MPSKNPGKFI; LPLNVSREIL; KVEVTSKKAL; NPNNKIVQNL; YPIYIKYSEPI; YPNTKPGVKLF; LPNYLRFIKGI; KPGVKLFINRI; IPEYEGLKLKA; DPTYQMQKIML; SATLIKEPSAI; AAYKEKGFEIL; EPEKLEKISIL
	HLA-B0801	IDKLKFLSL; NEKFKNIAL; IIKKVKIKL; QMQKIMLSM; IFYFKQIAL; FIIFRLCYI; YLRFIKGII; KIKLKRKSCM; YIIKKVKIKL; HIKEVNLSATL; YFKQIALFIIF; ILIFYFKQIAL
	HLA-B1501	KQIALFIIF; YLNKEGLEY; SSVDGFVSF; WSSDGKTGY; RMNESQKSI; FGVGFYSAF; IAKSGTKEF; QMQKIMLSM; KFINIINEF; FLSLTNEKF; KFSEFSKEF; LLYLIIHSL; KENPIVAAY; KIQEIIKKY; LFIIFRLCY; AILNLIPEY; KSASLIGQF; SLLPNYLRF; TKAEGNLEY; YQMQKIMLS; KLNETTALW; LIGQFGVGF; NTKPGVKLF; IKAEEYNEF; INYPIYIKY; IGQFGVGFY; FYVPSKAPY; YQMQKIMLSM; RMNESQKSIY; HTKAEGNLEY; YSNHINYPIY; LLYLIIHSLY; SLIGQFGVGF; LFYVPSKAPY; IIIDSNDPTY; KQFDTEVNDL; ALFIIFRLCY; SSSVDGFVSF; VIAKSGTKEF; GVKLFINRIF; YLIIHSLYSH; IVAAYKEKGF; HINYPIYIKY; ILIKDNGIGM; IINEFIEKDF; GQFGVGFYSA; PSKAPYDLYY; RFKSSSVDGF; ALEPKIEISF; QFGVGFYSAF; LIGQFGVGFY; KLEKISILLF; EIKAEEYNEF; GQFGVGFYSAF; RMNESQKSIYY; ILKENPIVAAY; GVIAKSGTKEF; SLIGQFGVGFY; KLYLNKEGLEY; KQIALFIIFRL; NLFYVPSKAPY; KQFDTEVNDLL; YFKQIALFIIF; KSSSVDGFVSF; AIIIDSNDPTY; YIWSSDGKTGY; IIKKYSNHINY; TSKKALESDAY; IALEPKIEISF; LIFYFKQIALF; YVPSKAPYDLY; ASLIGQFGVGF; HIKEVNLSATL; ILIFYFKQIAL; IALFIIFRLCY; RIFITDSEGSL; KNKSEIKAEEY
	HLA-B2705	FRLCYIIKK; KQIALFIIF; LQQNKILSK; GRCIKEGVY; KKVKIKLKR; SREILQQNK; YQMQKIMLSM; KRKSCMKKQF; FRLCYIIKKV; KQIALFIIFR; FRLCYIIKKVK; GQFGVGFYSAF; IRFKSSSVDGF; KQIALFIIFRL; ERMNESQKSIY; NREKLISLIRF
	HLA-B3501	MPSKNPGKF; FYVPSKAPY; FGVGFYSAF; WSSDGKTGY; IIDSNDPTY; SSVDGFVSF; KAEEYNEFY; TKAEGNLEY; IPEYEGLKL; TTFDYENPL; YLNKEGLEY; IAKSGTKEF; DTEVNDLLY; NASDAIDKL; YIKYSEPIM; EILIMDDEL; KENPIVAAY; SILLFEEAM; KFINIINEF; LPLNVSREI; KKALESDAY; TFDYENPLM; LISNASDAI; YPIYIKYSE; EKLNETTAL;

		FYFKQIALF; IIDCQDLPL; AILNLIPEY; SKAPYDLYY; IKAEEYNEF; MNESQKSIY; NLEYTNLFY; NPLMHIHTK; EAILNLIPEY; DPTYQMQKIM; YSNHINYPIY; IIIDSNDPTY; VPSKAPYDLY; LPLNVSREIL; YPNTKPGVKL; LFYVPSKAPY; TTFDYENPLM; ISILLFEEAM; LKENPIVAAY; QFGVGFYSAF; SSSVDGFVSF; FDTEVNDLLY; NPNNKIVQNL; YNEFYKNTTF; FKQIALFIIF; EGNLEYTNLF; EFYKNTTFDY; NKSEIKAEEY; HTKAEGNLEY; MDDELDEAIL; IKAEEYNEFY; YQMQKIMLSM; YPNTKPGVKLF; VPSKAPYDLYY; YIWSSDGKTGY; YPIYIKYSEPI; NASDAIDKLKF; IALFIIFRLCY; YFKQIALFIIF; DPTYQMQKIML; IALEPKIEISF; NLFYVPSKAPY; ILKENPIVAAY; LFEEAMLTSGM; AIIIDSNDPTY; TSKKALESDAY; FVSFKEYKERM; YVPSKAPYDLY; QFDTEVNDLLY; EPEKLEKISIL; NPLMHIHTKAE; LIFYFKQIALF; SVDGFVSFKEY; ERMNESQKSIY; EVNDLLYLIIH; DEAILNLIPEY; EYNEFYKNTTF; YKEKGFEILIM
	HLA-B4403	KEIKPILEL; KENPIVAAY; NEFYKNTTF; EEAMLTSGM; KEFINNLKQ; NESQKSIYY; EEFKDTLTK; SEGSLLPNY; REILQQNKI; SEIKAEEYN; TEIKLYLNK; NEFIEKDFL; KEVNLSATL; SEFSKEFGR; TEVNDLLYL; LEKISILLF; KEKGFEILI; QEVKEIKPI; KEILKDHIK; KEIFLRELI; REILQQNKIL; REKLISLIRF; DELDEAILNL; KEIFLRELIS; KEVNLSATLI; SEGSLLPNYL; AEGNLEYTNL; EEFKDTLTKV; EEKLNETTAL; FEILIMDDEL; KEKGFEILIM; KEGLEYANKW; EESGTEIKLY; QEVKEIKPIL; SEIKAEEYNE; KEPSAIIIDS; KEFINNLKQD; TEVNDLLYLI; SEIKAEEYNEF; AEGNLEYTNLF; SEFSKEFGRCI; REILQQNKILS; NEFYKNTTFDY; KEILKDHIKEV; EEKLNETTALW; EEAMLTSGMPS; EESGTEIKLYL; EEFKDTLTKVK; TEVNDLLYLII; DEAILNLIPEY; RELISNASDAI; KEVNLSATLIK; DELDEAILNLI; TEIKLYLNKEG; KEESGTEIKLY; KENILKENPIV; KEFGRCIKEGV
	HLA-B5101	LPLNVSREI; IALEPKIEI; NPGKFINII; MPSKNPGKFI; LPLNVSREIL; EPEKLEKISI; YPNTKPGVKL; YPIYIKYSEPI; LPNYLRFIKGI; KPGVKLFINRI
	HLA-B5701	EGLEYANKW; KLNETTALW; KALESDAYIW; HTKAEGNLEY;
CAA44492.1| Outer surface protein A [Borrelia burgdorferi]; Seq9	HLA-A0101	
	HLA-A0201	YLLGIGLIL; FTLEGTLAA; KTSTLTISV; FTKEDTITV; ALIACKQNV; LLGIGLILA; SLEATVDKL; ILKSGEITV; KVTEGTVVL; STLDEKNSV; TLVSKKVTL; GIGLILALI; YLLGIGLILA; TLDEKNSVSV; ALDDSDTTQA; LLGIGLILAL; NILKSGEITV; TLAADGKTTL; VLKDFTLEGT; YSLEATVDKL; YLLGIGLILAL; LVFTKEDTITV; LLGIGLILALI; ILALIACKQNV; STLDEKNSVSV; ALDDSDTTQAT; VLKDFTLEGTL; SLEATVDKLEL; ILKSGEITVAL; ALIACKQNVST; TTLKVTEGTVV; LAADGKTTLKV; LIACKQNVSTL
	HLA-A0301	VVLSKNILK; KTKNLVFTK; LVSKKVTLK; LILALIACK; LTISVNSQK; KAVEITTLK; AADGKTTLK; ISVNSQKTK; RANGTRLEY; SQTKFEIFK; KSDGSGKAK; TQATKKTGK; MTELVSKEK; TLVSKKVTLK; TLTISVNSQK; TVVLSKNILK; GLILALIACK; TLKELKNALK; LSQTKFEIFK; LAADGKTTLK; VTEGTVVLSK; KLELKGTSDK; TTQATKKTGK; GMTELVSKEK; KYSLEATVDK; KQNVSTLDEK; TIADDLSQTK; TISVNSQKTK; KEDAKTLVSK; GSGKAKEVLK; KTIVRANGTR; GTLEGEKTDK; GKAVEITTLK; GTRLEYTDIK; VSKKVTLKDK; IKSDGSGKAK; TLAADGKTTLK; STLTISVNSQK; KTLVSKKVTLK; KVTEGTVVLSK; TTLKELKNALK; LTISVNSQKTK; GTVVLSKNILK; FTKEDTITVQK; IVRANGTRLEY; TLKDKSSTEEK; LVSKKVTLKDK; KFNEKGETSEK; LTIADDLSQTK; SQKTKNLVFTK; KSSTEEKFNEK; ATKKTGKWDSK
	HLA-A1101	VVLSKNILK, KTKNLVFTK, SQTKFEIFK, LTISVNSQK, ATVDKLELK, LILALIACK, STEEKFNEK, KAVEITTLK, LVSKKVTLK, MTELVSKEK,

		AADGKTTLK, SAGTNLEGK, YSLEATVDK, GSGTLEGEK, TQATKKTGK, RANGTRLEY, IADDLSQTK, ISVNSQKTK, KSDGSGKAK, GGMTELVSK, TEGTVVLSK, EITTLKELK, TIVRANGTR; TVVLSKNILK; TTQATKKTGK; TIADDLSQTK; VTEGTVVLSK; LSQTKFEIFK; SSTEEKFNEK; GLILALIACK; KQNVSTLDEK; TLTISVNSQK; TLVSKKVTLK; TISVNSQKTK; LAADGKTTLK; GMTELVSKEK; TLKELKNALK; KTIVRANGTR; GSGKAKEVLK; GTLEGEKTDK; VSKKVTLKDK; GTRLEYTDIK; KLELKGTSDK; DSAGTNLEGK; STLTISVNSQK; TTLKELKNALK; KVTEGTVVLSK; KTLVSKKVTLK; GTVVLSKNILK; LTIADDLSQTK; TLAADGKTTLK; AVEITTLKELK; LTISVNSQKTK; SQKTKNLVFTK; KSSTEEKFNEK; ATKKTGKWDSK; TLKDKSSTEEK; FTKEDTITVQK; TLEGTLAADGK; LVSKKVTLKDK; MTELVSKEKDK; DLSQTKFEIFK; YTDIKSDGSGK; LVSKEKDKDGK; KFNEKGETSEK; IGLILALIACK
	HLA-A2402	KYLLGIGLI; KWDSKTSTL; KYDSAGTNL; KYLLGIGLIL; KWDSKTSTLTI; KYSLEATVDKL
	HLA-A2902	IVRANGTRLEY; TIADDLSQTKF
	HLA-A6801	LTISVNSQK; ETSEKTIVR; MTELVSKEK; EITTLKELK; TIVRANGTR; KAVEITTLK; DAKTLVSKK; KTKNLVFTK; STEEKFNEK; ATVDKLELK; LVSKKVTLK; SQTKFEIFK; YSLEATVDK; EGTLAADGK; ISVNSQKTK; LILALIACK; DIKSDGSGK; VVLSKNILK; EDAKTLVSK; DSDTTQATK; SAGTNLEGK; TVVLSKNILK; TLTISVNSQK; EATVDKLELK; TIADDLSQTK; DSAGTNLEGK; TTQATKKTGK; LAADGKTTLK; KTIVRANGTR; TISVNSQKTK; TLVSKKVTLK; SSTEEKFNEK; TLKELKNALK; LSQTKFEIFK; VTEGTVVLSK; EDAKTLVSKK; DSDTTQATKK; GLILALIACK;
	HLA-B0702	IVRANGTRL; KVTEGTVVL; LAADGKTTL; LPGGMTELV; TVVLSKNIL; ; KAVEITTLKEL
	HLA-B0801	TLKELKNAL; ; ILKSGEITVAL; YLLGIGLILAL; TLKVTEGTVVL
	HLA-B1501	SQKTKNLVF; RANGTRLEY; YLLGIGLIL; KVTEGTVVL; TLKELKNAL; KAKEVLKDF; IVRANGTRL; LGIGLILAL; TLAADGKTTL; IVRANGTRLEY; YLLGIGLILAL; VQKYDSAGTNL; ILKSGEITVAL; VSKEKDKDGKY; VLKDFTLEGTL; TLKVTEGTVVL; VNSQKTKNLVF
	HLA-B2705	KKYLLGIGL; VRANGTRLEY; GKWDSKTSTL; KKYLLGIGLIL
	HLA-B3501	LAADGKTTL; RANGTRLEY; FTLEGTLAA; TVVLSKNIL; VALDDSDTT; YLLGIGLIL; LPGGMTELV; IADDLSQTKF; LPGGMTELVS; LKVTEGTVVL; YSLEATVDKL; YLLGIGLILAL; NSVSVDLPGGM; IVRANGTRLEY; TIADDLSQTKF; KAVEITTLKEL
	HLA-B4403	KEVLKDFTL; GEITVALDD; KEKDKDGKY; KEDAKTLVS; GEITVALDDS; KEDTITVQKY; GEITVALDDSD; KEVLKDFTLEG
	HLA-B5101	LPGGMTELV;
	HLA-B5701	TTQATKKTGKW;
|BAA22351.1 | Outer surface protein B [Borrelia garinii]; Seq10	HLA-A0101	LTEETEETY; RTNGTTLEY; WSDTSNTLT; ITDDLNTIT; WSDTSNTLTV; ITDDLNTITV; LTDGTITVQNY; ITRTNGTTLEY; WSDTSNTLTVS; YSDMTNDENAT
	HLA-A0201	FLTDGTITV; YLLGFALVL; KLAGTATEI; LLGFALVLA; SLTEETEET; KIKDFVFLT; FLDDTSSGS; SITDDLNTI; GIMLEGNLV; NLVGGKTSV; LVTEDTVKL; VTMSITDDL; YLLGFALVLA; KLFNDTKIFI; LLGFALVLAL; FLDDTSSGST; ITDDLNTITV; FLTDGTITVQ; AVWSDTSNTL; ALIACGQKGA; KLSTKKITRT; KKYLLGFALV; YLLGFALVLAL; FVFLTDGTITV; SITDDLNTITV; LLGFALVLALI; KLFNDTKIFIS; NLVGGKTSVEI; TMSITDDLNTI; MTNDENATKAV; ATVDTVELKGV
	HLA-A0301	KVASKVFKK; KTGKLSTKK; RTNGTTLEY; SSNTKVASK; ATKAVETLK; KLSTKKITR; MTNDENATK; VTLKKEIEK; ETYDSSNTK; TLTVSADSK; KEGTVTLKK; VLALIACGQK; KLAGTATEIK; NTKVASKVFK;

		NTLTVSADSK; TYKTGKLSTK; MLEGNLVGGK; KIFISKEKNK; VQNYDTAGTK; TVTLKKEIEK; TLTVSADSKK; EIKEGTVTLK; DLEALKAALK; DSSNTKVASK; RATVDTVELK; KEIEKAGTVK; YKTGKLSTKK; GSGGKLEGVK; TVELKGVADK; DTKIFISKEK; IKEGTVTLKK; FNDTKIFISK; IMLEGNLVGGK; LVLALIACGQK; ETYKTGKLSTK; KLEGVKSDQSK; FLDDTSSGSTK; LFNDTKIFISK; LVGGKTSVEIK; ITRTNGTTLEY; NTLTVSADSKK; SLTEETEETYK; TVQNYDTAGTK; EIKEGTVTLKK
	HLA-A1101	KVASKVFKK; ATVDTVELK; SSNTKVASK; ATKAVETLK; MTNDENATK; ETYDSSNTK; KTGKLSTKK; VTLKKEIEK; TVKLFNDTK; RTNGTTLEY; TLTVSADSK; LTVSADSKK; VSADSKKIK; LALIACGQK; DTSSGSTKK; TKVASKVFK; EIKDLEALK; KLSTKKITR; TVTLKKEIEK; NTLTVSADSK; TVSADSKKIK; KIFISKEKNK; RATVDTVELK; VQNYDTAGTK; VLALIACGQK; KLAGTATEIK; TVELKGVADK; TLTVSADSKK; NTKVASKVFK; LTEETEETYK; MLEGNLVGGK; GSGGKLEGVK; NATKAVETLK; DSSNTKVASK; DTVKLFNDTK; TKVASKVFKK; EIKEGTVTLK; TVQNYDTAGTK; LVLALIACGQK; ATEIKDLEALK; TVETYDSSNTK; GTVTLKKEIEK; NTLTVSADSKK; IMLEGNLVGGK; SLTEETEETYK; ETYKTGKLSTK; IACGQKGAEPK; NTKVASKVFKK; LFNDTKIFISK; LVGGKTSVEIK; LTVSADSKKIK; SNTKVASKVFK; KLEGVKSDQSK; VADKNDGSGGK; EIKEGTVTLKK
	HLA-A2402	VWSDTSNTL; KYLLGFALV; GFALVLALI; NYDTAGTKL; KYLLGFALVL; DFVFLTDGTI; VWSDTSNTLTV; KYELRATVDTV; KYLLGFALVLA
	HLA-A2902	RTNGTTLEY; DLNTITVETY; SLTEETEETY; ITRTNGTTLEY
	HLA-A6801	ETYDSSNTK; MTNDENATK; DTSSGSTKK; LTVSADSKK; TVKLFNDTK; EIKDLEALK; ATVDTVELK; ATKAVETLK; TLTVSADSK; KVASKVFKK; TKVASKVFK; TKIFISKEK; SSNTKVASK; RTNGTTLEY; EIEKAGTVK; LALIACGQK; QNYDTAGTK; LAGTATEIK; NDTKIFISK; TATEIKDLE; VTLKKEIEK; DTVKLFNDTK; DTKIFISKEK; NATKAVETLK; NTLTVSADSK; NTKVASKVFK; ETEETYKTGK; EIKEGTVTLK; TVTLKKEIEK; TLTVSADSKK; DSSNTKVASK; EVEDSKKDQK; TVSADSKKIK; LTEETEETYK; VLALIACGQK; RATVDTVELK; MLEGNLVGGK; DLEALKAALK; DMTNDENATK; TKVASKVFKK; TVELKGVADK; ETYDSSNTKV; DLNTITVETY; TEIKDLEALK; KIFISKEKNK; KLAGTATEIK; TYKTGKLSTK; ETYKTGKLSTK; NTLTVSADSKK; DTVELKGVADK; TVETYDSSNTK; NTKVASKVFKK; TVQNYDTAGTK; EIKEGTVTLKK; LTVSADSKKIK; ENATKAVETLK; FISKEKNKDGK; LVLALIACGQK; SNTKVASKVFK; SLTEETEETYK; GTVTLKKEIEK; IACGQKGAEPK; DLPLVTEDTVK; LVGGKTSVEIK; ATEIKDLEALK; LFNDTKIFISK; EETEETYKTGK; EKNKDGKYELR; TKIFISKEKNK; TYKTGKLSTKK; NDTKIFISKEK; DSKKDQKDASK; SNTLTVSADSK; EDTVKLFNDTK
	HLA-B0702	ITRTNGTTL; RATVDTVEL; KVFKKQGSL; AVWSDTSNTL; KITRTNGTTL; LPLVTEDTVKL; TAVWSDTSNTL; AVETLKNGIML
	HLA-B0801	MKKYLLGFAL; YLLGFALVLAL
	HLA-B1501	RTNGTTLEY; KLFNDTKIF; YLLGFALVL; NTKVASKVF; LGFALVLAL; LTEETEETY; SLTEETEETY; LVTEDTVKLF; IEKAGTVKLF; ITRTNGTTLEY; YLLGFALVLAL; ISKEKNKDGKY; SSNTKVASKVF; TVKLFNDTKIF; VQNYDTAGTKL; VSADSKKIKDF
	HLA-B2705	KKYLLGFAL; TRTNGTTLEY; LRATVDTVEL; KKYLLGFALVL; LRATVDTVELK
	HLA-B3501	LTEETEETY; FALVLALIA; LPLVTEDTV; RTNGTTLEY; TAVWSDTSN; YLLGFALVL; DASKKDLPL; RATVDTVEL; DLNTITVETY; AVWSDTSNTL; FALVLALIAC; LVTEDTVKLF; TAVWSDTSNT; TRTNGTTLEY; FVFLTDGTIT; SLTEETEETY; LPLVTEDTVK;

		TAVWSDTSNTL; LPLVTEDTVKL; TATEIKDLEAL; YLLGFALVLAL; KAVETLKNGIM; ITRTNGTTLEY; TVKLFNDTKIF; DDLNTITVETY; FVFLTDGTITV
	HLA-B4403	KEIEKAGTV; KEKNKDGKY; EETYKTGKL; AEPKHNDQE; EETEETYKT; AEPKHNDQEV; EETYKTGKLS; VEIKEGTVTL; KEIEKAGTVKL; KEGTVTLKKEI
	HLA-B5101	LPLVTEDTV; FALVLALIA; LPLVTEDTVK; LPLVTEDTVKL
	HLA-B5701	LTEETEETY; GSTKKTAVW; RTNGTTLEY; ; SSGSTKKTAVW; GSLTEETEETY,; ITRTNGTTLEY
AAM22469.1| Outer surface protein C [Borrelia afzelii]; Seq11	HLA-A0101	LSAILMTLF; ITDSNAFVL; ; ITDSNAFVLAV
	HLA-A0201	ILMTLFLFI; SLLAGVHEI; KITDSNAFV; KLFKSVEGL; TLSAILMTL; TLVSSIDEL; ALTNSVKEL; GVHEISTLI; SAILMTLFL; FLFISCNNS; SVKELTSPV; LITEKLSKL; LMTLFLFIS; LVSSIDELA; AQEALTNSV; KLFKSVEGLV; AILMTLFLFI; KITDSNAFVL; NTLSAILMTL; TLVSSIDELA; ILMTLFLFIS; VLAVKEVETL; TLITEKLSKL; LLAGVHEIST; GLVKAAQEAL; AAQEALTNSV; FVLAVKEVET; TLSAILMTLFL; VLAVKEVETLV; LLAGVHEISTL; FVLAVKEVETL; KITDSNAFVLA; SLLAGVHEIST; ITDSNAFVLAV; ILMTLFLFISC; KAAQEALTNSV; SAILMTLFLFI
	HLA-A0301	KLKNSGELK; TLITEKLSK; ELANKAIGK; LANKAIGKK; RVSHADLGK; FISCNNSGK; ITEKLSKLK; AILKTNADK; EISTLITEK; ILMTLFLFI; STLITEKLSK; LITEKLSKLK; KTKGAEELGK; KAILKTNADK; ELANKAIGKK; LFKSVEGLVK; AQEALTNSVK; LFISCNNSGK; DSNAFVLAVK; TSPVVAESPK; GAEELGKLFK; ILKTNADKTK; SKLKNSGELK; VSSIDELANK; HEISTLITEK; ; KLFKSVEGLVK; FLFISCNNSGK; KLRVSHADLGK; TLITEKLSKLK; KLKNSGELKAK; ISTLITEKLSK; LTSPVVAESPK; LVSSIDELANK; LSKLKNSGELK; TLSAILMTLFL; KGAEELGKLFK; AILKTNADKTK
	HLA-A1101	SSIDELANK; TLITEKLSK; RVSHADLGK; AILKTNADK; GVNDDDAKK; ITEKLSKLK; LANKAIGKK; KLKNSGELK; FISCNNSGK; EISTLITEK; PVVAESPKK; SNAFVLAVK; AILMTLFLF; ELANKAIGK; GPNLTEISK; STLITEKLSK; STNPADESAK; VSSIDELANK; TSPVVAESPK; KAILKTNADK; DSNAFVLAVK; AQEALTNSVK; KTKGAEELGK; GAEELGKLFK; LITEKLSKLK; AILMTLFLFI; LFISCNNSGK; LTSPVVAESPK; KLFKSVEGLVK; ASTNPADESAK; LVSSIDELANK; AAQEALTNSVK; TLITEKLSKLK; ISTLITEKLSK; TSPVVAESPKK; AILKTNADKTK; FLFISCNNSGK; LSKLKNSGELK; KGAEELGKLFK; KLKNSGELKAK; KLRVSHADLGK
	HLA-A2402	AILMTLFLF; ILMTLFLFI; SAILMTLFLF; LSAILMTLFLF; NTLSAILMTLF
	HLA-A2902	SAILMTLFLF;
	HLA-A6801	EISTLITEK; FISCNNSGK; ELANKAIGK; SSIDELANK; SNAFVLAVK; LANKAIGKK; ITEKLSKLK; TLITEKLSK; RVSHADLGK; GVNDDDAKK; SPVVAESPK; DSNAFVLAVK; STNPADESAK; CSEEFTNKLR; TSPVVAESPK; ELANKAIGKK; LFISCNNSGK; STLITEKLSK; ELKAKIEDAK; LITEKLSKLK; HEISTLITEK; KTKGAEELGK; SPVVAESPKK; SAILMTLFLF; VSSIDELANK; LTSPVVAESPK; FLFISCNNSGK; LVSSIDELANK; TSPVVAESPKK; ISTLITEKLSK; TLITEKLSKLK; ELKAKIEDAKK; LSKLKNSGELK; QQNGLGAEANR; ASTNPADESAK; TDSNAFVLAVK; MTLFLFISCNN
	HLA-B0702	SVKELTSPV; LVKAAQEAL; SAILMTLFL; AAQEALTNSV; KAAQEALTNSV; GPNLTEISKKI
	HLA-B0801	KLRVSHADL; LVKAAQEAL; ;
	HLA-B1501	LVKAAQEAL; QQNGLGAEA; AQEALTNSV; KKITDSNAF; IQQNGLGAE; SVKELTSPV; KLRVSHADL; LSAILMTLF; TLSAILMTLF; IQQNGLGAEA; SAILMTLFLF; ISKKITDSNAF; LLAGVHEISTL; LSAILMTLFLF

	HLA-B2705	LRVSHADLGK;
	HLA-B3501	KKITDSNAF; SAILMTLFL; LAVKEVETL; LSAILMTLF; DAKKCSEEF; NPADESAKG; SAILMTLFLF; EALTNSVKEL; LAGVHEISTL; NPADESAKGPN; NTLSAILMTLF; FVLAVKEVETL; ISKKITDSNAF
	HLA-B4403	EEFTNKLRV; KELTSPVVA; AEANRNESL; EEFTNKLRVS; AEANRNESLL; AEANRNESLLA; EEFTNKLRVSH; KELTSPVVAES
	HLA-B5101	GPNLTEISKKI; LAGVHEISTLI
	HLA-B5701	ISKKITDSNAF
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]; Seq12	HLA-A0101	GSFKTSLYY; SSDTIKFSEF;
	HLA-A0201	FIICAVFVL; KMKMFIICA; MKMFIICAV; ATFFCIEEA; IICAVFVLI; MFIICAVFV; KMFIICAVFV; FIICAVFVLI; KMKMFIICAV; KMFIICAVFVL; ATFFCIEEAEV; MKMFIICAVFV; KKMKMFIICAV; GLSGQASSDTI; FIICAVFVLIS; TLVIRKEQDGV
	HLA-A0301	AMTNVGSFK; KTSLYYGYK; GSFKTSLYY; NLGTLVIRK; LISSCGNFR; FTVNIKNKK; GQASSDTIK; KAMTNVGSFK; GIKGKEITTK; VGSFKTSLYY; SNLGTLVIRK; VLISSCGNFR; NVGSFKTSLY; KFSEFTVNIK; QLRGHSATFF; FKTSLYYGYK; QSSTNGIKGK; WSNLGTLVIRK; GSFKTSLYYGY; SFKTSLYYGYK; FVLISSCGNFR
	HLA-A1101	KTSLYYGYK; AMTNVGSFK; GSFKTSLYY; SSTNGIKGK; NLGTLVIRK; GQASSDTIK; FTVNIKNKK; LISSCGNFR; FSEFTVNIK; KAMTNVGSFK; VLISSCGNFR; SNLGTLVIRK; QSSTNGIKGK; KFSEFTVNIK; GIKGKEITTK; SEFTVNIKNK; SGQASSDTIK; NVGSFKTSLY; WSNLGTLVIRK; GSFKTSLYYGY; SFKTSLYYGYK; NSEHITFSGDK; FVLISSCGNFR; NVGSFKTSLYY; NVIGTINGQLR; LSGQASSDTIK; SEFTVNIKNKK; FSEFTVNIKNK
	HLA-A2402	KAMTNVGSF; DWSNLGTLV; KFSEFTVNI; MFIICAVFVL; DWSNLGTLVI; MFIICAVFVLI; VFVLISSCGNF; ETINNSEHITF
	HLA-A2902	GSFKTSLYY; FKTSLYYGY; KMFIICAVF; SFKTSLYYGY; NVGSFKTSLY; VGSFKTSLYY; NVGSFKTSLYY; GSFKTSLYYGY
	HLA-A6801	FTVNIKNKK; LISSCGNFR; EAEVNNFVK; KTSLYYGYK; FSEFTVNIK; AMTNVGSFK; EFTVNIKNK; DTIKFSEFT; SSTNGIKGK; EQSSTNGIK; EHITFSGDK; HSATFFCIE; NLGTLVIRK; MTNVGSFKT; NVIGTINGQ; ETINNSEHI; VLISSCGNFR; EEAEVNNFVK; KAMTNVGSFK; EFTVNIKNKK; WSNLGTLVIR; NVGSFKTSLY; VIGTINGQLR; FKTSLYYGYK; HSATFFCIEE; QSSTNGIKGK; ETINNSEHIT; DTIKFSEFTV; NVIGTINGQLR; FVLISSCGNFR; NSEHITFSGDK; FSEFTVNIKNK; WSNLGTLVIRK; ETINNSEHITF; SFKTSLYYGYK; DWSNLGTLVIR; NVGSFKTSLYY; EQSSTNGIKGK; SEFTVNIKNKK; TNVGSFKTSLY
	HLA-B0702	KAMTNVGSF; FVKAMTNVGSF
	HLA-B0801	QLRGHSATF; FVKAMTNVGSF; NGQLRGHSATF
	HLA-B1501	KMFIICAVF; QLRGHSATF; GSFKTSLYY; KAMTNVGSF; VLISSCGNF; GQLRGHSAT; GQLRGHSATF; QLRGHSATFF; GQASSDTIKF; FVLISSCGNF; TINNSEHITF; KMKMFIICAV; VGSFKTSLYY; FVKAMTNVGSF; KMKMFIICAVF; GQLRGHSATFF; KMFIICAVFVL; GSFKTSLYYGY; ASSDTIKFSEF; ETINNSEHITF; FCIEEAEVNNF
	HLA-B2705	GQLRGHSATF; FRSSLSDQGSL
	HLA-B3501	EVNNFVKAM; QASSDTIKF; FIICAVFVL; KAMTNVGSF; QLRGHSATF; MKMFIICAVF; TINNSEHITF; MFIICAVFVL; FVLISSCGNF; NVGSFKTSLY; EAEVNNFVKAM; FVKAMTNVGSF; ETINNSEHITF; FCIEEAEVNNF; NVGSFKTSLYY; MTNVGSFKTSL
	HLA-B4403	SEFTVNIKN; EEAEVNNFV; KEITTKIET; EEQSSTNGI; AEVNNFVKA; AEVNNFVKAM; SEFTVNIKNK; KEITTKIETI; AEVNNFVKAMT; SEFTVNIKNKK; EEAEVNNFVKA
	HLA-B5101	

	HLA-B5701	
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]; Seq13	HLA-A0101	
	HLA-A0201	LIICAVFVL; NLIICAVFV; SLFNPPPVL; KMKNLIICA; FVLIISCKI; ALKNIEEEL; IICAVFVLI; VIDDALKNI; ATGESTEKV; KMKNLIICAV; LIICAVFVLI; NLIICAVFVL; ALKYAKELGV; KVIDDALKNI; IICAVFVLII; SLFNPPPVLPA; LIICAVFVLII; LMQGDDPNNSL; NLIICAVFVLI; KALKYAKELGV; FVLIISCKIDA; KKMKNLIICAV; AVFVLIISCKI
	HLA-A0301	GTNTNDFVK; VFVLIISCK; AVFVLIISCK; SSHDNTPVLK; GTNTNDFVKK; KIDASSEDLK; ESATGESTEK; KVKKQGNIGQK; KLAEPQNIEDK; KQGNIGQKALK; ASSHDNTPVLK; CAVFVLIISCK; FVKKVIDDALK; ATGESTEKVKK; ALKNIEEELEK
	HLA-A1101	GTNTNDFVK; SATGESTEK; GQKALKYAK; VFVLIISCK; PVLKAVQAK; GQQEGKEEK; AVFVLIISCK; SSHDNTPVLK; GTNTNDFVKK; KIDASSEDLK; SSEDLKQNVK; ATGESTEKVK; ESATGESTEK; ASSHDNTPVLK; ATGESTEKVKK; CAVFVLIISCK; ASSEDLKQNVK; KVKKQGNIGQK; KQGNIGQKALK; NIGQKALKYAK; SATGESTEKVK; ALKNIEEELEK; KLAEPQNIEDK; FVKKVIDDALK; NTPVLKAVQAK
	HLA-A2402	
	HLA-A2902	NIGQKALKY; YAKELGVNGSY
	HLA-A6801	GTNTNDFVK; SATGESTEK; ELKDKIDKR; VFVLIISCK; EPQNIEDKK; TNTNDFVKK; DLKQNVKEK; IDASSEDLK; ESATGESTEK; EARKKFQEFK; AVFVLIISCK; SSHDNTPVLK; GTNTNDFVKK; TPVLKAVQAK; DGTNTNDFVK; ELKDKIDKRK; LAEPQNIEDK; SSEDLKQNVK; CAVFVLIISCK; FVKKVIDDALK; NTPVLKAVQAK; EEARKKFQEFK; EIQELKDKIDK; SATGESTEKVK; NIGQKALKYAK; LAEPQNIEDKK; CKIDASSEDLK; QAKDGGQQEGK; DGTNTNDFVKK; ELKDKIDKRKK; ASSHDNTPVLK
	HLA-B0702	TPVLKAVQA; LPASSHDNT; ; LPASSHDNTPV
	HLA-B0801	EARKKFQEF; FVKKVIDDAL;
	HLA-B1501	SLFNPPPVL; KELGVNGSY; NVKEKVEGF; KQGNIGQKAL; MQGDDPNNSL; KMKNLIICAV; YAKELGVNGSY; KMKNLIICAVF; KQNVKEKVEGF; MQGDDPNNSLF; SVNDGTNTNDF; LMQGDDPNNSL; GQKALKYAKEL
	HLA-B2705	GQKALKYAK; ; KRKKELEEARK; KQGNIGQKALK
	HLA-B3501	NPPPVLPAS; EARKKFQEF; LIICAVFVL; MKNLIICAVF; FVKKVIDDAL; TPVLKAVQAK; LPASSHDNTP; YAKELGVNGSY; SVNDGTNTNDF; LPASSHDNTPV; PASSHDNTPVL; NPPPVLPASSH; MQGDDPNNSLF
	HLA-B4403	QEFKEQVES; KELGVNGSY; EEARKKFQEF; EEKEKEIQEL; KELEEARKKF; KEIQELKDKI; EEELEKLAEPQ; QEFKEQVESAT; EELEKLAEPQN
	HLA-B5101	PPPVLPASS; TPVLKAVQA; LPASSHDNT; LPASSHDNTP; NPPPVLPASS; CAVFVLIISC; LPASSHDNTPV
	HLA-B5701	
AAC44770.1| FlaA protein (Borrelia burgdorferi) ; Seq14	HLA-A0101	LTNYVDYVY; KVSVYSLGY; FEDMNGMEY; DSESVFKVY; RLDLTNYVDY; SSKVKNFIFY; LTPSARLQAY; SSTRLDLTNY; HSSKVKNFIFY; WADLIWSNPNY; PSSTRLDLTNY; DIDSESVFKVY; KTMKEIKVSVY
	HLA-A0201	FLLSTVLFA; ILFFLLSTV; KVKNFIFYV; YAGDTILGV; VLFEDMNGM; LIWSNPNYI; AMIMPPFKI; YVYSGASGI; GINNWSVLL; VLLTPSARL; KMRFKAFRV; YVDYVYSGA; LVLDFAELA; YIPNISSRI; TMKEIKVSV; GLIDNIKTM; DLTNYVDYV; RVLYDKLSV; SVYSLGYEI; KAKSILFFL; LLSTVLFAQ; KLREKISIA; LQAYVKNSV; SILFFLLST; LGYEIDLEV; VLYDKLSVS; GLAEGSKRA; VLYDKLSVSI; FIFYVKDLRV; FLGKGLIDNI; SLGYEIDLEV; SILFFLLSTV; FLLSTVLFAQ; RLQAYVKNSV; KTMKEIKVSV; VLFAQETDGL; ILFFLLSTVL; YVYSGASGIV;

		KLSVSIDSDI; FFLLSTVLFA; SKVKNFIFYV; VLFPSYSQSS; LQAYVKNSVV; KAKSILFFLL; YIPNISSRII; YVKNSVVAPA; LLTPSARLQA; RLDLTNYVDYV; SIAEGSFQNFV; SIDSDIDSESV; VLFPSYSQSSA; YSLGYEIDLEV; RLQAYVKNSVV; KVYETSGTESL; YAGDTILGVRV; SLGYEIDLEVL; VVDLGINNWSV; SILFFLLSTVL; KVSVYSLGYEI; FIFYVKDLRVL; LLSTVLFAQET; KSILFFLLSTV; VLLTPSARLQA; SVYSLGYEIDL; YVKNSVVAPAV; LTPSARLQAYV; VLFAQETDGLA; IMPPFKIPFYS; IIKDDVPNYPL; RVLYDKLSVSI; KLKAHETFKRV
	HLA-A0301	KLKAHETFK; RVSKSHSSK; YAYSMGTLK; GSFQNFVEK; LASSKMRFK; KVSVYSLGY; SVVAPAVVK; SAMIMPPFK; RFKAFRVSK; TSGTESLRK; YSMGTLKFK; YSGASGIVK; LIDNIKTMK; GTESLRKLK; GVRVLFPSY; KAFRVSKSH; KVKNFIFYVK; AYSMGTLKFK; SSAMIMPPFK; VYSGASGIVK; GLIDNIKTMK; PLASSKMRFK; EYAYSMGTLK; RKLKAHETFK; VPNYPLASSK; ETSGTESLRK; VSKSHSSKVK; IMPPFKIPFY; SDIDSESVFK; SSKVKNFIFY; NSVVAPAVVK; RLDLTNYVDY; KLKAHETFKR; MRFKAFRVSK; APAVVKSESK; AHETFKRVLK; GESGNQFLGK; SSKMRFKAFR; LVLDFAELAR; FRVSKSHSSK; MIMPPFKIPF; IPNISSRIIK; KISIAEGSFQ; KMRFKAFRVSK; YVYSGASGIVK; RVSKSHSSKVK; MEYAYSMGTLK; MIMPPFKIPFY; KAHETFKRVLK; QSSAMIMPPFK; YAYSMGTLKFK; HSSKVKNFIFY; ILGVRVLFPSY; KTMKEIKVSVY; VLFEDMNGMEY; FLGKGLIDNIK; TSGTESLRKLK; YIPNISSRIIK; ASSKMRFKAFR; LLTPSARLQAY
	HLA-A1101	SAMIMPPFK; SVVAPAVVK; GSFQNFVEK; RVSKSHSSK; YAYSMGTLK; YSMGTLKFK; TSGTESLRK; SVLLTPSAR; KLKAHETFK; GTESLRKLK; LASSKMRFK; KVSVYSLGY; YSGASGIVK; SARLQAYVK; RFKAFRVSK; ESGNQFLGK; VKNFIFYVK; LIDNIKTMK; LTNYVDYVY; DIDSESVFK; AVVKSESKR; RVLFPSYSQ; FVEKIESEK; KSILFFLLS; FIFYVKDLR; GVRVLFPSY; YVKDLRVLY; SVYSLGYEI; STRLDLTNY; SSAMIMPPFK; KVKNFIFYVK; SSKMRFKAFR; ETSGTESLRK; GLIDNIKTMK; AYSMGTLKFK; SSKVKNFIFY; LVLDFAELAR; VSKSHSSKVK; NSVVAPAVVK; PSARLQAYVK; PLASSKMRFK; SSTRLDLTNY; ETFKRVLKLR; SDIDSESVFK; RIIKDDVPNY; KLKAHETFKR; VPNYPLASSK; VYSGASGIVK; ETDGLAEGSK; QSSAMIMPPFK; YVYSGASGIVK; YAYSMGTLKFK; MIMPPFKIPFY; KAHETFKRVLK; ASSKMRFKAFR; RVSKSHSSKVK; TSGTESLRKLK; KMRFKAFRVSK; MEYAYSMGTLK; YVKDLRVLYDK; TPSARLQAYVK; KTMKEIKVSVY; VAPAVVKSESK; YIPNISSRIIK; HSSKVKNFIFY; VLFEDMNGMEY; DVPNYPLASSK; KNSVVAPAVVK; SKVKNFIFYVK; SGESGNQFLGK; AEGSFQNFVEK
	HLA-A2402	SYSQSSAMI; EYAYSMGTL; FFLLSTVLF; LYDKLSVSI; AYSMGTLKF; FYVKDLRVL; SFQNFVEKI; NYPLASSKM; VYSGASGIV; KFKGWADLI; NYIPNISSRI; FYSGESGNQF; LFFLLSTVLF; GYEIDLEVLF; EYAYSMGTLK; DYVYSGASGI; VYETSGTESL; VYSLGYEIDL; RYAGDTILGV; SYSQSSAMIM; FYVKDLRVLY; EYAYSMGTLKF; NYPLASSKMRF; NYIPNISSRII; IWSNPNYIPNI; FYSGESGNQFL; DYVYSGASGIV
	HLA-A2902	YVKDLRVLY; DMNGMEYAY; LTNYVDYVY; KVSVYSLGY; IMPPFKIPF; YEIDLEVLF; GVRVLFPSY; AYSMGTLKF; DLIWSNPNY; FFLLSTVLF; FYVKDLRVLY; IMPPFKIPFY; YAYSMGTLKF; LFEDMNGMEY; DLTNYVDYVY; LFFLLSTVLF; TMKEIKVSVY; SSTRLDLTNY; RIIKDDVPNY; MIMPPFKIPF; SSKVKNFIFY; RLDLTNYVDY; EDMNGMEYAY; IFYVKDLRVLY; VLFEDMNGMEY; MIMPPFKIPFY; AMIMPPFKIPF; EYAYSMGTLKF; HSSKVKNFIFY; ILGVRVLFPSY; ILFFLLSTVLF; FEDMNGMEYAY; DIDSESVFKVY

	HLA-A6801	ETSGTESLR; FIFYVKDLR; YAYSMGTLK; FVEKIESEK; NYIPNISSR; YSMGTLKFK; SAMIMPPFK; LTNYVDYVY; GSFQNFVEK; SVVAPAVVK; SVLLTPSAR; AVVKSESKR; LASSKMRFK; SKMRFKAFR; RVSKSHSSK; NIKTMKEIK; DIDSESVFK; LARDPSSTR; YVKDLRVLY; TFKRVLKLR; ESGNQFLGK; DLIWSNPNY; LIDNIKTMK; SARLQAYVK; MPPFKIPFY; GTESLRKLK; HETFKRVLK; YPLASSKMR; LKAHETFKR; DMNGMEYAY; VKNFIFYVK; RFKAFRVSK; ETFKRVLKLR; ETSGTESLRK; SSAMIMPPFK; NFIFYVKDLR; EYAYSMGTLK; WSVLLTPSAR; LVLDFAELAR; SSKMRFKAFR; ETDGLAEGSK; ELARDPSSTR; EGSFQNFVEK; NSVVAPAVVK; KVKNFIFYVK; YAGDTILGVR; YETSGTESLR; NFVEKIESEK; MRFKAFRVSK; NYPLASSKMR; DLTNYVDYVY; DTILGVRVLF; SDIDSESVFK; GLIDNIKTMK; KLKAHETFKR; DNIKTMKEIK; YAYSMGTLKFK; YVYSGASGIVK; QSSAMIMPPFK; ELVLDFAELAR; ASSKMRFKAFR; ETDGLAEGSKR; NPNYIPNISSR; DVPNYPLASSK; YVKDLRVLYDK; MEYAYSMGTLK; YIPNISSRIIK; MIMPPFKIPFY; HSSKVKNFIFY; TPSARLQAYVK; KNFIFYVKDLR; ESEKPEESSPK; DSDIDSESVFK; HETFKRVLKLR; QNFVEKIESEK; ETFKRVLKLRE; RYAGDTILGVR; TSGTESLRKLK; APAVVKSESKR; RVSKSHSSKVK; YPLASSKMRFK; NWSVLLTPSAR; VAPAVVKSESK; KAHETFKRVLK; VYETSGTESLR; SKVKNFIFYVK
	HLA-B0702	FPSYSQSSA; IPNISSRII; TPSARLQAY; MKRKAKSIL; VPNYPLASS; DPSSTRLDL; APAVVKSES; RVLYDKLSV; IPFYSGESG; KPEDMVVDL; RAEPGELVL; LARDPSSTRL; YPLASSKMRF; RVSKSHSSKV; TPSARLQAYV; KAHETFKRVL; SKRYAGDTIL; APAVVKSESK; YAYSMGTLKF; FPSYSQSSAMI; VPNYPLASSKM; KVYETSGTESL; RVLYDKLSVSI; RVLKLREKISI; LASSKMRFKAF; YVKNSVVAPAV
	HLA-B0801	SSKMRFKAF; EIKVSVYSL; QAYVKNSVV; FPSYSQSSAM; VLKLREKISI; LRKLKAHETF; SLRKLKAHETF; LASSKMRFKAF; FKRVLKLREKI; VLKLREKISIA
	HLA-B1501	YVKDLRVLY; YSGESGNQF; IMPPFKIPF; KVSVYSLGY; GVRVLFPSY; SSAMIMPPF; SSKMRFKAF; LTNYVDYVY; IIKDDVPNY; DMNGMEYAY; VVKSESKRY; GLIDNIKTM; SSKVKNFIF; VLFEDMNGM; LQAYVKNSV; KISIAEGSF; YSQSSAMIM; STRLDLTNY; DLIWSNPNY; YEIDLEVLF; FFLLSTVLF; TMKEIKVSVY; QSSAMIMPPF; MIMPPFKIPF; SIAEGSFQNF; IMPPFKIPFY; YAYSMGTLKF; RIIKDDVPNY; LQAYVKNSVV; SSKVKNFIFY; LFFLLSTVLF; ILFFLLSTVL; ASSKMRFKAF; LTPSARLQAY; LGVRVLFPSY; YVKNSVVAPA; AVVKSESKRY; TMKEIKVSVY; QSSAMIMPPF; MIMPPFKIPF; SIAEGSFQNF; IMPPFKIPFY; YAYSMGTLKF; RIIKDDVPNY; LQAYVKNSVV; SSKVKNFIFY; LFFLLSTVLF; ILFFLLSTVL; ASSKMRFKAF; LTPSARLQAY; LGVRVLFPSY; YVKNSVVAPA; AVVKSESKRY
	HLA-B2705	KRKAKSILF; KRVLKLREK; KRYAGDTIL; RKAKSILFF; RKLKAHETF; ARLQAYVKN; MRFKAFRVSK; FRVSKSHSSK; KRKAKSILFF; KRVLKLREKI; KRAEPGELVL; RKLKAHETFK; KRYAGDTILGV; KRKAKSILFFL; TRLDLTNYVDY; FRVSKSHSSKV; SRIIKDDVPNY; ARLQAYVKNSV; RKLKAHETFKR
	HLA-B3501	TPSARLQAY; MPPFKIPFY; DMNGMEYAY; LTNYVDYVY; EPGELVLDF; FFLLSTVLF; IAEGSFQNF; FPSYSQSSA; NPNYIPNIS; YVKDLRVLY; YSGESGNQF; YSQSSAMIM; SSAMIMPPF; FEDMNGMEY; KVSVYSLGY; DLIWSNPNY; ELVLDFAEL; YEIDLEVLF; LFFLLSTVL; NGMEYAYSM; KPEDMVVDL; FAELARDPS; DSESVFKVY; RAEPGELVL; FKGWADLIW; PSYSQSSAM; IPNISSRII; FPSYSQSSAM; YPLASSKMRF; YAYSMGTLKF; LFEDMNGMEY; EDMNGMEYAY; MIMPPFKIPF; EVLFEDMNGM; QSSAMIMPPF; LFFLLSTVLF; DLTNYVDYVY; MVVDLGINNW; LTPSARLQAY; NPNYIPNISS;

		FYSGESGNQF; LGVRVLFPSY; FYVKDLRVLY; FAQETDGLAE; DSDIDSESVF; SIAEGSFQNF; FPSYSQSSAMI; WADLIWSNPNY; VPNYPLASSKM; FEDMNGMEYAY; LASSKMRFKAF; LFPSYSQSSAM; DMNGMEYAYSM; MIMPPFKIPFY; VLFEDMNGMEY; LLTPSARLQAY; LDLTNYVDYVY; EPGELVLDFAE; DIDSESVFKVY; RAEPGELVLDF; SQSSAMIMPPF; WSVLLTPSARL; IDSDIDSESVF; LGYEIDLEVLF; TVLFAQETDGL
	HLA-B4403	YEIDLEVLF; KEIKVSVYS; AELARDPSS; AEGSFQNFV; GELVLDFAE; KEIKVSVYSL; AEPGELVLDF; GELVLDFAEL; YEIDLEVLFE; REKISIAEGSF; KEIKVSVYSLG; GELVLDFAELA; YEIDLEVLFED
	HLA-B5101	IPNISSRII; FPSYSQSSA; IPFYSGESG; MPPFKIPFY; EPGELVLDF; MPPFKIPFYS; FPSYSQSSAM; YPLASSKMRF; EPGELVLDFA; TPSARLQAYV; FPSYSQSSAMI; MPPFKIPFYSG; KPEDMVVDLGI; VPNYPLASSKM
	HLA-B5701	YSMGTLKFKGW; KTMKEIKVSVY
BAD18055.1 ; FlaB protein [Borrelia garinii]; Seq15	HLA-A0101	NQDEAIAVNIY; ELAVQSGNGTY
	HLA-A0201	SQASWTLRV; QLTDEINRI; AQAAQTAPV; AIAVNIYAA; SLAKIENAI; AVNIYAANV; AQYNQMHML; TTVDANTSL; SQGGVNSPV; QTAPVQEGV; NIYAANVANL; NLNEVEKVLV; VLVRMKELAV; QLTDEINRIA; NLFSGEGAQA; IAVNIYAANV; SLSGSQASWTL; MLSNKSASQNV; AIAVNIYAANV; SQASWTLRVHV; GMQPAKINTPA; KVLVRMKELAV; SLAKIENAIRM; NLFSGEGAQAA
	HLA-A0301	NQMHMLSNK; GSQASWTLR; TVDANTSLAK; YNQMHMLSNK; LSGSQASWTLR; TTVDANTSLAK; LSNKSASQNVR
	HLA-A1101	NQMHMLSNK; GSQASWTLR; AVQSGNGTY; TVDANTSLAK; YNQMHMLSNK; EVEKVLVRMK; TTVDANTSLAK; TTEGNLNEVEK; TAEELGMQPAK; TSLAKIENAIR; QYNQMHMLSNK; LSGSQASWTLR; LSNKSASQNVR
	HLA-A2402	IYAANVANL; YAANVANLF; IYAANVANLF; TYSDADRGSI; IYAANVANLFS
	HLA-A2902	AVQSGNGTY; YAANVANLF; ; ELAVQSGNGTY; EINRIADQAQY
	HLA-A6801	LAKIENAIR; EGNLNEVEK; YAANVANLF; NGTYSDADR; GSQASWTLR; NQMHMLSNK; TSKAINFIQ; NKSASQNVR; EVEKVLVRMK; SLAKIENAIR; TVDANTSLAK; NTSKAINFIQ; SGSQASWTLR; TTVDANTSLA; TTVDANTSLAK; TTEGNLNEVEK; EIEQLTDEINR; LSNKSASQNVR; TSLAKIENAIR; EINRIADQAQY; NLNEVEKVLVR; LSGSQASWTLR; TAEELGMQPAK; QYNQMHMLSNK; NIYAANVANLF; QTAPVQEGVQQ
	HLA-B0702	SPVNVTTTV; QPAKINTPA; QPAPATAPS; LVRMKELAV; TPASLSGSQ; APSQGGVNS; APATAPSQG; APVQEGVQQ; TPASLSGSQA; SPVNVTTTVD; APSQGGVNSP; QPAKINTPAS; APSQGGVNSPV; QPAKINTPASL; APATAPSQGGV; SPVNVTTTVDA; TPASLSGSQAS
	HLA-B0801	KVLVRMKEL; VEKVLVRMKEL
	HLA-B1501	YAANVANLF; AVQSGNGTY; AQAAQTAPV; AQYNQMHML; SQGGVNSPV; SLSGSQASW; SQASWTLRV; IQIEIEQLT; LAVQSGNGTY; SQASWTLRVH; SQNVRTAEEL; VQQEGAQQPA; INRIADQAQY; AQAAQTAPVQ; MQPAKINTPA; ELAVQSGNGTY; NIYAANVANLF; NQDEAIAVNIY; SLSGSQASWTL
	HLA-B2705	NRIADQAQY;
	HLA-B3501	YAANVANLF; QPAPATAPS; SPVNVTTTV; DEAIAVNIY; TTVDANTSL; LAVQSGNGT; QPAKINTPA; AVQSGNGTY; QASWTLRVH; IAVNIYAAN; LAVQSGNGTY; IADQAQYNQM; QPAKINTPAS; LAKIENAIRM; QPAPATAPSQ; YAANVANLFS; TAEELGMQPA; EAIAVNIYAA; QAQYNQMHML; TPASLSGSQA; SPVNVTTTVD; TPASLSGSQAS; ELAVQSGNGTY; NQDEAIAVNIY; QPAKINTPASL; IAVNIYAANVA;

		NIYAANVANLF; SPVNVTTTVDA; EINRIADQAQY; IADQAQYNQMH; APSQGGVNSPV; LAVQSGNGTYS
	HLA-B4403	EELGMQPAKI; NEVEKVLVRM; DEINRIADQA; DEINRIADQAQ
	HLA-B5101	SPVNVTTTV; APATAPSQGGV; APSQGGVNSPV
	HLA-B5701	ASLSGSQASW;
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]; Seq16	HLA-A0101	KTQEKLSSGY; MTDEVVASTT; ASDDAAGMGV; NQDEAIAVNIY; ISDQRANLGAF; RLESIKDSTEY; ELAVQSGNGTY; MIAQANQVPQY
	HLA-A0201	SQASWTLRV; QLTDEINRI; SQAAQTAPV; AMIAQANQV; MIINHNTSA; QVPQYVLSL; AIAVNIYAA; SLAKIENAI; AVNIYAANV; AQYNQMHML; MTDEVVAST; SIKDSTEYA; TTVDANTSL; NLGAFQNRL; SQGGVNSPV; SAMAMIAQA; VVASTTNSI; MISDQRANL; ILTQSAMAM; SILTQSAMA; LTQSAMAMI; TMTDEVVAST; AQANQVPQYV; MIINHNTSAI; ILTQSAMAMI; NIYAANVANL; RMISDQRANL; NLNEVEKVLV; VLVRMKELAV; MAMIAQANQV; QLTDEINRIA; QVPQYVLSLL; NQVPQYVLSL; IAVNIYAANV; SLSGSQASWTL; MLSNKSASQNV; AMAMIAQANQV; AIAVNIYAANV; SQASWTLRVHV; KLSSGYRINRA; SILTQSAMAMI; GMQPAKINTPA; KVLVRMKELAV; MISDQRANLGA; NLFSGEGSQAA; YAIENLKASYA; SLAKIENAIRM; TMTDEVVASTT; ILTQSAMAMIA
	HLA-A0301	SINAANLSK; SQASRNTSK; NQMHMLSNK; GSQASWTLR; FQNRLESIK; LSSGYRINR; NSINAANLSK; TVDANTSLAK; LSQASRNTSK; KLSSGYRINR; NLKASYAQIK; AANLSKTQEK; STEYAIENLK; KTQEKLSSGY; YNQMHMLSNK; AFQNRLESIK; QIRGLSQASR; VPQYVLSLLR; GLSQASRNTSK; MIAQANQVPQY; LSGSQASWTLR; GAFQNRLESIK; KTQEKLSSGYR; TTVDANTSLAK; KINAQIRGLSQ; RLESIKDSTEY; LSNKSASQNVR
	HLA-A1101	SINAANLSK; SQASRNTSK; NQMHMLSNK; GSQASWTLR; AAGMGVSGK; LSSGYRINR; NTSAINASR; TEYAIENLK; AVQSGNGTY; PQYVLSLLR; FQNRLESIK; AQANQVPQY; TVDANTSLAK; STEYAIENLK; LSQASRNTSK; NSINAANLSK; AANLSKTQEK; RANLGAFQNR; KTQEKLSSGY; KLSSGYRINR; AFQNRLESIK; YNQMHMLSNK; IAQANQVPQY; TQEKLSSGYR; NLKASYAQIK; EVEKVLVRMK; TTVDANTSLAK; TTEGNLNEVEK; KTQEKLSSGYR; GAFQNRLESIK; TAEELGMQPAK; GLSQASRNTSK; TSLAKIENAIR; QYNQMHMLSNK; NAANLSKTQEK; QVPQYVLSLLR; AQIRGLSQASR; DSTEYAIENLK; LSGSQASWTLR; GVSGKINAQIR; MIAQANQVPQY; LSNKSASQNVR; SAMAMIAQANQ
	HLA-A2402	IYAANVANL; YAANVANLF; AFQNRLESI; IYAANVANLF; TYSDADRGSI; SYAQIKDATM; IYAANVANLFS
	HLA-A2902	ESIKDSTEY; AVQSGNGTY; YAANVANLF; AIENLKASY; YAIENLKASY; IAQANQVPQY; EYAIENLKASY; ELAVQSGNGTY; EINRIADQAQY; MIAQANQVPQY; RLESIKDSTEY
	HLA-A6801	NTSAINASR; LSSGYRINR; TEYAIENLK; SINAANLSK; ESIKDSTEY; AIRMISDQR; LAKIENAIR; EGNLNEVEK; YAANVANLF; NGTYSDADR; GSQASWTLR; NQMHMLSNK; TSKAINFIQ; MAMIAQANQ; NKSASQNVR; TTNSILTQS; SQASRNTSK; NAIRMISDQR; STEYAIENLK; NSINAANLSK; DAAGMGVSGK; HNTSAINASR; EVEKVLVRMK; SLAKIENAIR; TVDANTSLAK; RANLGAFQNR; QIRGLSQASR; NTSKAINFIQ; LSQASRNTSK; NLKASYAQIK; SGSQASWTLR; TQEKLSSGYR; VPQYVLSLLR; AANLSKTQEK; YAIENLKASY; VSGKINAQIR; TTVDANTSLA; KLSSGYRINR; MIAQANQVPQ; NTSAINASRN; DSTEYAIENLK; TTVDANTSLAK; TTEGNLNEVEK; EIEQLTDEINR; QVPQYVLSLLR; NAANLSKTQEK; ENAIRMISDQR; LSNKSASQNVR; MIAQANQVPQY; TSLAKIENAIR; EINRIADQAQY; NLNEVEKVLVR; LSGSQASWTLR; GAFQNRLESIK;

		TAEELGMQPAK; QYNQMHMLSNK; GVSGKINAQIR; KTQEKLSSGYR; NHNTSAINASR; NIYAANVANLF; EKLSSGYRINR; NNSINAANLSK; QTAPVQEGAQQ; ENLKASYAQIK
	HLA-B0702	SPVNVTTTV; VPQYVLSLL; QPAKINTPA; VVASTTNSI; QPAPATAPS; LVRMKELAV; ASRNTSKAI; IINHNTSAI; TPASLSGSQ; APSQGGVNS; APVQEGAQQ; APATAPSQG; VASTTNSIL; ILTQSAMAM; TPASLSGSQA; VVASTTNSIL; SPVNVTTTVD; APSQGGVNSP; QPAKINTPAS; QASRNTSKAI; MIINHNTSAI; APSQGGVNSPV; QPAKINTPASL; APATAPSQGGV; SPVNVTTTVDA; TPASLSGSQAS; SAINASRNNSI; AANLSKTQEKL; RANLGAFQNRL
	HLA-B0801	YAQIKDATM; KVLVRMKEL; ; VEKVLVRMKEL
	HLA-B1501	AQANQVPQY; DQRANLGAF; YAANVANLF; SQAAQTAPV; AVQSGNGTY; TQEKLSSGY; ILTQSAMAM; AQYNQMHML; SQGGVNSPV; ESIKDSTEY; SLSGSQASW; SQASWTLRV; IQIEIEQLT; AMIAQANQV; YAIENLKASY; LAVQSGNGTY; SQASWTLRVH; KTQEKLSSGY; SQNVRTAEEL; RMISDQRANL; IAQANQVPQY; AQQEGAQQPA; AQIRGLSQAS; NQVPQYVLSL; SQAAQTAPVQ; INRIADQAQY; MQPAKINTPA; SQASRNTSKAI; AQANQVPQYVL; MIAQANQVPQY; ASRNTSKAINF; ELAVQSGNGTY; NIYAANVANLF; NQDEAIAVNIY; RLESIKDSTEY; SLSGSQASWTL
	HLA-B2705	NRIADQAQY; IRGLSQASR; QRANLGAFQ; SRNTSKAINF; QRANLGAFQNR; SRNNSINAANL; IRMISDQRANL
	HLA-B3501	YAANVANLF; YAQIKDATM; QPAPATAPS; RASDDAAGM; ESIKDSTEY; SPVNVTTTV; ILTQSAMAM; DEAIAVNIY; TTVDANTSL; LAVQSGNGT; QPAKINTPA; NSILTQSAM; YAIENLKAS; AVQSGNGTY; QASWTLRVH; VASTTNSIL; IAVNIYAAN; FSGEGSQAA; VPQYVLSLL; LAVQSGNGTY; YAIENLKASY; IADQAQYNQM; SILTQSAMAM; IAQANQVPQY; QPAKINTPAS; LAKIENAIRM; QANQVPQYVL; QPAPATAPSQ; YAANVANLFS; TAEELGMQPA; MIINHNTSAI; EAIAVNIYAA; NRASDDAAGM; QAQYNQMHML; TPASLSGSQA; SPVNVTTTVD; SYAQIKDATM; MAMIAQANQV; MIAQANQVPQY; TPASLSGSQAS; ELAVQSGNGTY; NQDEAIAVNIY; QPAKINTPASL; IAVNIYAANVA; NSILTQSAMAM; NIYAANVANLF; TTNSILTQSAM; EVVASTTNSIL; SPVNVTTTVDA; EINRIADQAQY; IADQAQYNQMH; NASRNNSINAA; ISDQRANLGAF; APSQGGVNSPV; LAVQSGNGTYS; EYAIENLKASY
	HLA-B4403	EELGMQPAKI; NEVEKVLVRM; DEINRIADQA; DEINRIADQAQ
	HLA-B5101	SPVNVTTTV; VPQYVLSLL; APATAPSQGGV; APSQGGVNSPV
	HLA-B5701	ASLSGSQASW;
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen VlsE1 Of Borrelia Burgdorferi; Seq17	HLA-A0101	KSDVKTYFTTV
	HLA-A0201	ILSAIVTAA; KVLGAITGL; LLDKLVKAV; QILSAIVTA; VLGAITGLI; ELLDKLVKA; QLGNGFLDV; KAAGAVSAV; KLVKAVKTA; KTYFTTVAA; FLDVFTSFG; AIGEVVADA; GTAAIGEVV; QILSAIVTAA; KVLGAITGLI; VVADADAAKV; LIGDAVSSGL; KLFGKAGAAA; ELLDKLVKAV; GIAKGIKEIV; AITGLIGDAV; IQLGNGFLDV; AVSGEQILSA; FLDVFTSFGG; FLDVFTSFGGL; GLIGDAVSSGL; ILSAIVTAADA; KSDVKTYFTTV; FTSFGGLVAEA; KTYFTTVAAKL
	HLA-A0301	KLKAVAAAK; KVADKASVK; LVAEAFGFK; AIALRGXAK; KTDLNSLPK; GAAESAVRK; QIAAAIALR; KASVKGIAK; TTVAAKLEK; KGAGKLFGK; KETPPALNK; GTAVEGAIK; TYFTTVAAK; KTYFTTVAAK; GLVAEAFGFK; AAIALRGXAK; FTTVAAKLEK; ALRGXAKDGK; IVEAAGGSEK; KSDISSTTGK; LLDKLVKAVK; SVKGIAKGIK; GLRKVGDSVK; XAKDGKFAVK; TKTDLNSLPK; EAFGFKSDPK; GDAVSSGLRK; KSDPKKSDVK; TVAAKLEKTK; KGAAESAVRK; KVGDSVKAASK; KTKTDLNSLPK; KLFGKAGAAAH; ASKETPPALNK; AVAAAKGENNK; KTDLNSLPKEK; AIKEVSELLDK; ELLDKLVKAVK;

		AAHGDSEAASK; GXAKDGKFAVK
	HLA-A1101	TTVAAKLEK; KTDLNSLPK; LVAEAFGFK; KVADKASVK; AIALRGXAK; GAAESAVRK; VVADADAAK; KASVKGIAK; KLKAVAAAK; GTAVEGAIK; TYFTTVAAK; AAAKGENNK; QIAAAIALR; AAGGSEKLK; AVKDGEKEK; KGAGKLFGK; AFGFKSDPK; DAVSSGLRK; VAAKLEKTK; PIAAAIGDK; AVSAVSGEQ; SDISSTTGK; KTYFTTVAA; KETPPALNK; KTYFTTVAAK; AAIALRGXAK; GLVAEAFGFK; TVAAKLEKTK; KSDISSTTGK; IVEAAGGSEK; SVKGIAKGIK; VAAAKGENNK; FTTVAAKLEK; EAFGFKSDPK; VSELLDKLVK; AADAAEQDGK; XAKDGKFAVK; KSDPKKSDVK; EVVADADAAK; VADKDDPTNK; KGAAESAVRK; TKTDLNSLPK; AFGFKSDPKK; GAEFGQDEXK; AVAAAKGENNK; KTKTDLNSLPK; ASKETPPALNK; TTVAAKLEKTK; KVGDSVKAASK; KTDLNSLPKEK; SVGTAVEGAIK; QVADKDDPTNK; AAAIALRGXAK; TAADAAEQDGK; AIKEVSELLDK; AAHGDSEAASK; ASVKGIAKGIK; EVSELLDKLVK; EAFGFKSDPKK; IALRGXAKDGK; AADAAEQDGKK; AAKVADKASVK; GXAKDGKFAVK; GAEFGQDEXKK; GGLVAEAFGFK; ELLDKLVKAVK; LIGDAVSSGLR
	HLA-A2402	GFLDVFTSF; TYFTTVAAK; YFTTVAAKL; KFYQSVIQL; FYQSVIQLG; TYFTTVAAKL; SFGGLVAEAF; IQLGNGFLDVF
	HLA-A2902	GFLDVFTSF; SVIQLGNGF; ;
	HLA-A6801	TTVAAKLEK; QIAAAIALR; LVAEAFGFK; TYFTTVAAK; VVADADAAK; DAAEQDGKK; DAVSSGLRK; GAAESAVRK; KVADKASVK; FGFKSDPKK; DLNSLPKEK; SDISSTTGK; KLKAVAAAK; GTAVEGAIK; AAAKGENNK; FTTVAAKLEK; EVVADADAAK; EAFGFKSDPK; EAAGGSEKLK; KTYFTTVAAK; DQIAAAIALR; TVAAKLEKTK; SVKGIAKGIK; IVEAAGGSEK; FAVKDGEKEK; NPIAAAIGDK; GLVAEAFGFK; XAKDGKFAVK; VAAAKGENNK; AAIALRGXAK; DADAAKVADK; EAFGFKSDPKK; TTVAAKLEKTK; EIVEAAGGSEK; TAADAAEQDGK; EVSELLDKLVK; YFTTVAAKLEK; LIGDAVSSGLR; AVAAAKGENNK; QVADKDDPTNK; EKSDISSTTGK; ELLDKLVKAVK; AIKGAAESAVR; DDQIAAAIALR; SVGTAVEGAIK; AAHGDSEAASK
	HLA-B0702	AVRKVLGAI; KPEEAKNPI; AASKAAGAV; GASSGTAAI; KAAGAVSAV; KPDSTGSVG; AASKETPPAL; AAESAVRKVL; AVRKVLGAIT; SAVRKVLGAI; KPDSTGSVGT; KPEEAKNPIA; KPEEAKNPIAA; KAASKETPPAL; KPDSTGSVGTA; GAAESAVRKVL; LPKEKSDISST; AVSGEQILSAI; AVSAVSGEQIL; AASKAAGAVSA
	HLA-B0801	; ;
	HLA-B1501	SVIQLGNGF; DQIAAAIAL; GLVAEAFGF; FGKAGAAAH; QLGNGFLDVF; QSVIQLGNGF; YQSVIQLGNGF; IQLGNGFLDVF; TSFGGLVAEAF; KLFGKAGAAAH; ALRGXAKDGKF; GLIGDAVSSGL; AIGDKDGGAEF
	HLA-B2705	RKVLGAITGL;
	HLA-B3501	SVIQLGNGF; SAVSGEQIL; FGGLVAEAF; EAAGGSEKL; KPEEAKNPI; EVVADADAA; LGNGFLDVF; TAAIGEVVA; DPKKSDVKTY; SFGGLVAEAF; AASKETPPAL; QSVIQLGNGF; QLGNGFLDVF; SAIVTAADAA; TSFGGLVAEAF; DPKKSDVKTYF; TAEGASSGTAA; VADKDDPTNKF; KPEEAKNPIAA; YQSVIQLGNGF; KAASKETPPAL; TAVEGAIKEVS
	HLA-B4403	EEAKNPIAA; GEVVADADA; AEFGQDEXK; AEGAIKGAA; KEIVEAAGGS; EEAKNPIAAA; GEVVADADAA; EEAKNPIAAAI; GENNKGAGKLF; AEGASSGTAAI; KEVSELLDKLV; AEGAIKGAAES; SELLDKLVKAV; AEFGQDEXKKD
	HLA-B5101	KPEEAKNPI; LPKEKSDISS; LPKEKSDISST
	HLA-B5701	
CAA57807.1; Associated	HLA-A0101	LSANIEENY; YSEDKANTV; FLDALEAIEY; NSDKIDYAEKY; RLDNYDFKNEY; STDSIFLSEDM

protein A (BapA)[Borrelia burgdorferi]; Seq18	HLA-A0201	FLSEDMIRL; FLFLFVVSL; LLIFLFLFV; FLFVVSLSA; SIFNYLIQL; LIFLFLFVV; YLIKIKIST; KISTDSIFL; ALEAIEYLI; FVVSLSANI; ILKQILADL; LIGSYPDSI; KKISLLIFL; HVFSDAPRI; ISLLIFLFL; FLSEDMIRLI; SLLIFLFLFV; LLIFLFLFVV; RLIGSYPDSI; YLIQLNSDKI; KISLLIFLFL; FLFLFVVSLS; QLNSDKIDYA; QILKQILADL; SVFLDALEAI; FLDALEAIEYL; SLLIFLFLFVV; FLFVVSLSANI; FLFLFVVSLSA; LIFLFLFVVSL; ALEAIEYLIKI; ISLLIFLFLFV; SIFLSEDMIRL; SLSANIEENYT; KKISLLIFLFL
	HLA-A0301	YLIQLNSDK; KANTVKQILK; ALEAIEYLIK; YTETKRAFSK; NYLIQLNSDK; SLLIFLFLFV; APRIRGDLRK; NLINKRLDNY; ILKQILADLPK; FSKEDFNLINK; FNYLIQLNSDK
	HLA-A1101	KQILADLPK; AIEYLIKIK; YLIQLNSDK; TETKRAFSK; GDNARNNFK; KEDFNLINK; KANTVKQILK; YTETKRAFSK; GSYPDSIFNY; SIFLSEDMIR; ALEAIEYLIK; KSHVFSDAPR; HVFSDAPRIR; NSDKIDYAEK; YSEDKANTVK; EAIEYLIKIK; SLSANIEENY; NIEENYTETK; SKEDFNLINK; ILKQILADLPK; FSKEDFNLINK; KYGDNARNNFK
	HLA-A2402	SYPDSIFNY; KISLLIFLF; NYTETKRAF; VFLDALEAI; SLLIFLFLF; SYPDSIFNYL; KYGDNARNNF; ISLLIFLFLF; IFLFLFVVSL; AFSKEDFNLI; KKISLLIFLF; LFVVSLSANI; IFLSEDMIRL; SYPDSIFNYLI; NYLIQLNSDKI; IFLSEDMIRLI; KISLLIFLFLF; KYGDNARNNFK
	HLA-A2902	SYPDSIFNY; DMIRLIGSY; KISLLIFLF; SLLIFLFLF; QLNSDKIDY; FLDALEAIEY; GSYPDSIFNY; SLSANIEENY; NLINKRLDNY; VFLDALEAIEY; KISLLIFLFLF; RLDNYDFKNEY; IGSYPDSIFNY; VSLSANIEENY
	HLA-A6801	YLIQLNSDK; EDFNLINKR; DNARNNFKK; YDFKNEYEK; EENYTETKR; LSANIEENY; SHVFSDAPR; TETKRAFSK; IFLSEDMIR; DNYDFKNEY; HVFSDAPRIR; SIFLSEDMIR; EAIEYLIKIK; YTETKRAFSK; DAPRIRGDLR; YAEKYGDNAR; NIEENYTETK; NSDKIDYAEK; KSHVFSDAPR; YSEDKANTVK; KANTVKQILK; NYDFKNEYEK; GSYPDSIFNY; DSIFLSEDMIR; DNYDFKNEYEK; NIEENYTETKR; NYTETKRAFSK; FNYLIQLNSDK; EKSHVFSDAPR; DYAEKYGDNAR; FSKEDFNLINK; DAPRIRGDLRK; DALEAIEYLIK; DYSEDKANTVK; NNFKKDYSEDK; ILKQILADLPK
	HLA-B0702	YPDSIFNYL; APRIRGDLR; APRIRGDLRK; YPDSIFNYLI; APRIRGDLRKI; RIRGDLRKIGI
	HLA-B0801	
	HLA-B1501	DMIRLIGSY; FLFLFVVSL; LSANIEENY; IGSYPDSIF; KISLLIFLF; NEYEKSHVF; QLNSDKIDY; IQLNSDKIDY; GSYPDSIFNY; SLSANIEENY; KIKISTDSIF; FLDALEAIEY; RLIGSYPDSIF; KQILKQILADL; FKNEYEKSHVF; IGSYPDSIFNY
	HLA-B2705	KRLDNYDFK; KQILADLPK; KRAFSKEDF; ARNNFKKDY; RKIGIKEKSVF; KRAFSKEDFNL; KQILKQILADL
	HLA-B3501	YPDSIFNYL; DALEAIEYL; LDALEAIEY; LSANIEENY; NEYEKSHVF; YPDSIFNYLI; FLDALEAIEY; LDNYDFKNEY; YAEKYGDNAR; VFLDALEAIEY; FKNEYEKSHVF; YPDSIFNYLIQ; RLDNYDFKNEY
	HLA-B4403	NEYEKSHVF; SEDMIRLIGS; EENYTETKRAF; SEDMIRLIGSY; SEDKANTVKQI
	HLA-B5101	EAIEYLIKI; YPDSIFNYL; YPDSIFNYLI; EAIEYLIKIKI
	HLA-B5701	GSYPDSIFNY; VSLSANIEENY
AAL25643.1, P37-47 [Borrelia burgdorferi]; Seq19	HLA-A0101	SSNKDIYNSY; LSSNKDIYNSY
	HLA-A0201	IVYEILEEV; KIPEITEEV; NLSAIEESV; KLKEFLEKL; VIMPIPQTI; YIPEVKEEI; SLNLSTKSV; KINNGLNIV; IYNSYIPEV; FLTQGTSPS; NIDNITENL; FLLLNLVNC; SIAKLLQHL; ITEEVIMPI; KLSQVAQHA; NTWGEGLEI; CAFLLLNLV; FLEKLKKYL; FLTQGTSPSI; YLKDTNNLSA;

		ILEEVIIPET; YIPEVKEEIV; NLVNCKFDSL; IIPETKIPEI; DIYNSYIPEV; IVYEILEEVI; KIPEITEEVI; EIVYEILEEV; MCAFLLLNLV; YLKDTNNLSAI; VIIPETKIPEI; IVYEILEEVII; YIEPRPISSFL; FLTQGTSPSIT; KIPEITEEVIM; TIDFYIEPRPI
	HLA-A0301	ITSTIKSYK; LLLNLVNCK; RSSIRTKIK; NLNSKETPK; KITHPIFDH; EVRSSIRTK; KTSTSEDQK; IIEDLQKLK; SITSTIKSYK; IAKLLQHLSK; TIKSYKELAK; FLLLNLVNCK; KLKEFLEKLK; LQKLKEFLEK; QVAQHAPNSK; KVSDGTEQTK; TSPSITSTIK; IYNSYIPEVK; KSYKELAKEK; FLEKLKKYLK; NLSAIEESVK; KFDSLNLSTK; NLSTKSVDDK; KIEKVKSDGK; INNGLNIVQK; QHAPNSKIEK; KINNGLNIVQK; SIAKLLQHLSK; KLKEFLEKLKK; HLSKSEDQANK; GTSPSITSTIK; AQHAPNSKIEK; STIKSYKELAK; ILEEVIIPETK; PSITSTIKSYK; KSDGKPVPGDK; DIYNSYIPEVK
	HLA-A1101	ITSTIKSYK; KTSTSEDQK; VAQHAPNSK; LLLNLVNCK; RSSIRTKIK; TIDFYIEPR; IIEDLQKLK; NLNSKETPK; NITENLNSK; LSAIEESVK; HAPNSKIEK; ISGKEVEEK; VSDGTEQTK; LSTKSVDDK; SPSITSTIK; SITSTIKSY; AKLLQHLSK; SITSTIKSYK; KSYKELAKEK; QVAQHAPNSK; KVSDGTEQTK; TSPSITSTIK; TIKSYKELAK; QTIDFYIEPR; IAKLLQHLSK; FLLLNLVNCK; SSNKDIYNSY; LQKLKEFLEK; KLKEFLEKLK; KIEKVKSDGK; KFDSLNLSTK; NLSAIEESVK; IYNSYIPEVK; EIIEDLQKLK; LSKSEDQANK; FLEKLKKYLK; SIAKLLQHLSK; STIKSYKELAK; KINNGLNIVQK; SVDDKNNSIAK; GTSPSITSTIK; AQHAPNSKIEK; SQVAQHAPNSK; PSITSTIKSYK; AFLLLNLVNCK; KSDGKPVPGDK; ITENKEQEHEK; KLKEFLEKLKK; DIYNSYIPEVK; HLSKSEDQANK; ILEEVIIPETK; DLQKLKEFLEK
	HLA-A2402	KYLKDTNNL; VYEILEEVI; IYNSYIPEV; VIMPIPQTI; TSPSITSTI; SYIPEVKEEI; VYEILEEVII; SYKELAKEKI; IYNSYIPEVK; KYLKDTNNLS; FYIEPRPISSF; SFLTQGTSPSI; SYIPEVKEEIV
	HLA-A2902	LLNLVNCKF; EFLEKLKKY; SSNKDIYNSY; IMPIPQTIDF; YIPEVKEEIVY; IMPIPQTIDFY; FYIEPRPISSF; FLLLNLVNCKF
	HLA-A6801	ITSTIKSYK; ETPKEISGK; TIDFYIEPR; NITENLNSK; EVRSSIRTK; HAPNSKIEK; FFTNLEEVR; KTSTSEDQK; LSAIEESVK; LSTKSVDDK; DSNFFTNLE; YNSYIPEVK; EEVIIPETK; NLNSKETPK; ENKEQEHEK; IIEDLQKLK; QTIDFYIEPR; SITSTIKSYK; EIIEDLQKLK; EISGKEVEEK; QVAQHAPNSK; TSPSITSTIK; NFFTNLEEVR; NLSAIEESVK; NLEEVRSSIR; TIKSYKELAK; MPIPQTIDFY; IYNSYIPEVK; IAKLLQHLSK; FLEKLKKYLK; KVSDGTEQTK; FLLLNLVNCK; NLSTKSVDDK; KSYKELAKEK; LSKSEDQANK; INNGLNIVQK; DTNNLSAIEE; DSNFFTNLEE; SSNKDIYNSY; DIYNSYIPEVK; STIKSYKELAK; SNFFTNLEEVR; SIAKLLQHLSK; EIDEIIEDLQK; ITENKEQEHEK; EVRSSIRTKIK; HLSKSEDQANK; GTSPSITSTIK; HAPNSKIEKVK; PSITSTIKSYK; CKFDSLNLSTK; DLQKLKEFLEK; KINNGLNIVQK; ILEEVIIPETK; EFLEKLKKYLK
	HLA-B0702	EPRPISSFL; KPVPGDKIL; RPISSFLTQ; MPIPQTIDF; APNSKIEKV; RPISSFLTQG; TPKEISGKEV; SPSITSTIKS; IPEITEEVIM; EVRSSIRTKI; EPRPISSFLT; RPISSFLTQGT; SPSITSTIKSY; KPVPGDKILSS; MPIPQTIDFYI; HPIFDHITGSG
	HLA-B0801	FLEKLKKYL; ; YLKDTNNLSAI
	HLA-B1501	SNKDIYNSY; SITSTIKSY; LLNLVNCKF; AQHAPNSKI; LEIGGDSNF; SSNKDIYNSY; YIEPRPISSF; IMPIPQTIDF; PSITSTIKSY; LLLNLVNCKF; YLKDTNNLSA; LEIGGDSNFF; LSSNKDIYNSY; YLKDTNNLSAI; IMPIPQTIDFY; FYIEPRPISSF; VIMPIPQTIDF; YIPEVKEEIVY; TQNIDNITENL; FLLLNLVNCKF
	HLA-B2705	VRSSIRTKIK;
	HLA-B3501	MPIPQTIDF; KPVPGDKIL; EPRPISSFL; EIGGDSNFF; ILSSNKDIY;

		IPEITEEVI; MPIPQTIDFY; IPEVKEEIVY; IPEITEEVIM; LEIGGDSNFF; SPSITSTIKSY; NPGQDSISNTW; MPIPQTIDFYI; YIPEVKEEIVY; LSSNKDIYNSY; EVEEKITHPIF
	HLA-B4403	EEVIMPIPQ; EEIVYEILE; EEKITHPIF; EEVRSSIRT; YEILEEVII; DEIIEDLQK; SEDQKELEI; PEITEEVIM; PEVKEEIVY; SEDQANKTS; LEIGGDSNF; EEVIMPIPQT; EEIVYEILEE; KEFLEKLKKY; EEVIIPETKI; EEKITHPIFD; VEIDEIIEDL; KEKINNGLNI; DEIIEDLQKL; EEVIMPIPQTI; KEFLEKLKKYL; EEIVYEILEEV; KEVEEKITHPI; EEVRSSIRTKI; PEITEEVIMPI; VEIDEIIEDLQ; YEILEEVIIPE
	HLA-B5101	IPQTIDFYI; MPIPQTIDF; IPETKIPEI; IPEITEEVI; CAFLLLNLV; IPEVKEEIV; KPVPGDKIL; EPRPISSFL; MPIPQTIDFY; TPKEISGKEV; MPIPQTIDFYI
	HLA-B5701	PGQDSISNTW;
NP_212481.1 | fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31]; Seq20	HLA-A0101	YSEFLENYY; HTRDYPGAY; KSGKADLYY; YTEINTLIK; MSDKKIMEL; LSPKENALQY; NSNFKILDAY; MSDKKIMELK; TSYSEFLENY; YTSYSEFLENY; NSNFKILDAYY; KTPKIGLHFTY; TSYSEFLENYY; SLSPKENALQY; WLHTRDYPGAY
	HLA-A0201	FLENYYESL; KLWPSSPNI; LLGAGNLCV; KMSLNYTEI; TLIKEIPFT; FTYCGFEIL; ILQKDMIIL; FTNSLITKI; KLGLVIPKA; KADLYYTQV; ILFIKLWPS; LVLEIYNKI; VLEKRIDSL; LIQSKITML; TMLKVENLI; ILICLNPNT; IQPDYKSLV; LLNYKEEKI; SLSPKENAL; NLCVFYTKL; KTPSLDVLL; KMSDKKIMEL; KLWPSSPNII; VLLGAGNLCV; KLDENLIKKI; FTYCGFEILI; SLVLEIYNKI; NLIQSKITML; NLLNYKEEKI; SLNYTEINTL; IIATNSNFKI; IQSKITMLKV; WLHTRDYPGA; LQKDMIILFI; LLIEKYKKEL; IVLEKRIDSL; IIQPDYKSLV; FTNSLITKII; YTQVKNLRRV; QMKNERIISL; KILICLNPNT; ILFIKLWPSS; KLWPSSPNIIA; ILQKDMIILFI; FQMKNERIISL; ILDAYYRRPKI; LIQSKITMLKV; SLNYTEINTLI; LLIEKYKKELI; KIIQPDYKSLV; SLNDQIKKTNI; GLHFTYCGFEI; CLNPNTTRFHI; NIIATNSNFKI; LLNYKEEKIKI; FLKSKIQNGKI; KIDNKKFKILI; MSLNYTEINTL; LIKEIPFTNSL; FIKLWPSSPNI; SLDVLLGAGNL; QLKDNLDKFNL; NTSYTSYSEFL
	HLA-A0301	KLRFSDFLK; IQSKITMLK; SLNQSLSPK; TTRFHITKK; LQYFKAYKK; IIATNSNFK; HITKKNFKK; KIIKAFQMK; VFYTKLAKK; CVFYTKLAK; LLNINKIQK; IISLEILQK; KLDENLIKK; KNFKKNALK; ALQYFKAYK; KIQNGKIIK; SLVLEIYNK; NLRRVKNKK; GLVIPKAEK; ELILLNINK; KENALQYFK; EIYNKIDNK; KSGKADLYY; NTTRFHITK; QVKNLRRVK; ETTGEIFLK; KTAIKEKEK; KILDAYYRR; AYYRRPKIK; LIQSKITMLK; ILLNINKIQK; ALQYFKAYKK; ISLNQSLSPK; CVFYTKLAKK; RIISLEILQK; ILDAYYRRPK; AYKKGKNSFK; NIIATNSNFK; LCVFYTKLAK; NALQYFKAYK; KSLVLEIYNK; KKNFKKNALK; GAYVFIKNQK; RFHITKKNFK; YTKLAKKSGK; IPFTNSLITK; KLLENIENEK; ITKIIQPDYK; NTTRFHITKK; RIDSLKQQIK; FLKSKIQNGK; KADLYYTQVK; AIKEKEKTPK; MSDKKIMELK; LLNYKEEKIK; AGNLCVFYTK; VLEKRIDSLK; YVFIKNQKNK; SFKTIQNQLK; GELILLNINK; LKLRFSDFLK; TTGEIFLKAK; GKIIKAFQMK; HIKLDENLIK; QYFKAYKKGK; NINKIQKGIK; EIYNKIDNKK; KETTGEIFLK; LGLVIPKAEK; KELLIEKYKK; GLHFTYCGFE; NYTEINTLIK; KNLRRVKNKK; KAYKKGKNSFK; KLRFSDFLKSK; KISLNQSLSPK; KLGLVIPKAEK; NLIQSKITMLK; ALKLRFSDFLK; KMSDKKIMELK; IVLEKRIDSLK; KTNIKELLIEK; NSFKTIQNQLK; KILDAYYRRPK; LQYFKAYKKGK; LILLNINKIQK; GIKEINLLNYK; RFHITKKNFKK; LLGAGNLCVFY; KSKIQNGKIIK; KTPKIGLHFTY; TSYSEFLENYY; HIKLDENLIKK; RDYPGAYVFIK; ILICLNPNTTR; LITKIIQPDYK; NLDKFNLIQSK; KLDENLIKKIK; SLSPKENALQY; QVKNLRRVKNK; SLITKIIQPDY; EIHESNKMSDK; NLCVFYTKLAK; GAGNLCVFYTK; LQKDMIILFIK; IQNQLKDNLDK

	HLA-A1101	SLNQSLSPK; IQSKITMLK; IIATNSNFK; ALQYFKAYK; CVFYTKLAK; SLVLEIYNK; KIIKAFQMK; LQYFKAYKK; NTTRFHITK; IISLEILQK; TTRFHITKK; ETTGEIFLK; KENALQYFK; KIQNGKIIK; KLRFSDFLK; KILDAYYRR; HITKKNFKK; YTEINTLIK; KLDENLIKK; ELILLNINK; KTAIKEKEK; EIYNKIDNK; KAEKNLHIK; NIKELLIEK; LLNINKIQK; GNLCVFYTK; YTQVKNLRR; VFYTKLAKK; KDMIILFIK; KAFQMKNER; RFSDFLKSK; KEINLLNYK; GLVIPKAEK; ESLNDQIKK; KKLGLVIPK; KIMELKEEY; ESNKMSDKK; KNFKKNALK; AYYRRPKIK; NLLNYKEEK; QVKNLRRVK; AYVFIKNQK; YPGAYVFIK; EILIGRNAK; NQLKDNLDK; GAGNLCVFY; KSGKADLYY; TSYSEFLEN; KSLVLEIYNK; RIISLEILQK; ISLNQSLSPK; LIQSKITMLK; NIIATNSNFK; TTGEIFLKAK; ALQYFKAYKK; CVFYTKLAKK; GAYVFIKNQK; TSYSEFLENY; MSDKKIMELK; NTTRFHITKK; YVFIKNQKNK; ITKIIQPDYK; AGNLCVFYTK; NALQYFKAYK; KLLENIENEK; KADLYYTQVK; ILLNINKIQK; KAKEIHESNK; RIDSLKQQIK; ILDAYYRRPK; AIKEKEKTPK; VLEKRIDSLK; EIYNKIDNKK; IPFTNSLITK; TQVKNLRRVK; TNIKELLIEK; YTKLAKKSGK; NINKIQKGIK; HIKLDENLIK; KETTGEIFLK; SFKTIQNQLK; DAYYRRPKIK; LICLNPNTTR; GIKEINLLNY; RFHITKKNFK; KTNIKELLIEK; KISLNQSLSPK; KAYKKGKNSFK; KILDAYYRRPK; KMSDKKIMELK; IVLEKRIDSLK; ALKLRFSDFLK; TSYSEFLENYY; GAGNLCVFYTK; NLIQSKITMLK; NSFKTIQNQLK; GIKEINLLNYK; TAIKEKEKTPK; LILLNINKIQK; KLGLVIPKAEK; NALQYFKAYKK; LITKIIQPDYK; YTQVKNLRRVK; LQYFKAYKKGK; NLCVFYTKLAK; LQKDMIILFIK; IQNQLKDNLDK; KSKIQNGKIIK; KLRFSDFLKSK; SPKENALQYFK; EINLLNYKEEK; KTPKIGLHFTY; ETTGEIFLKAK; QVKNLRRVKNK; HIKLDENLIKK; YTSYSEFLENY; NIKELLIEKYK; EIPFTNSLITK; RDYPGAYVFIK; NLDKFNLIQSK; VLEIYNKIDNK; ILICLNPNTTR; IIKAFQMKNER; KLDENLIKKIK; KGELILLNINK; RFHITKKNFKK; LIPEEEYNQEK; SNFKILDAYYR; SLITKIIQPDY; TYCGFEILIGR; TSYTSYSEFLE; SLSPKENALQY
	HLA-A2402	DYPGAYVFI; DYKSLVLEI; LWPSSPNII; SYTSYSEFL; YYESLNDQI; NYTEINTLI; TYCGFEILI; KYKKELIVL; LYYTQVKNL; TMLKVENLI; HFTYCGFEI; AYKKGKNSF; KTPKIGLHF; IYNKIDNKK; EYNQEKTAI; TSYTSYSEF; EYNNTSYTS; KFNLIQSKI; IYNKIDNKKF; DYPGAYVFIK; NYYESLNDQI; EFLENYYESL; EYNNTSYTSY; ITMLKVENLI; IIATNSNFKI; SYTSYSEFLE; NTSYTSYSEF; HFTYCGFEILI; NFKKNALKLRF; YYTQVKNLRRV; KYKKELIVLEK
	HLA-A2902	YSEFLENYY; YNNTSYTSY; NFKILDAYY; SYSEFLENY; PKIGLHFTY; GAGNLCVFY; KIMELKEEY; KSGKADLYY; KEEYNNTSY; EYNNTSYTSY; SYSEFLENYY; SNFKILDAYY; TSYSEFLENY; DYKSLVLEIY; LSPKENALQY; GIKEINLLNY; IYNKIDNKKF; ENALQYFKAY; NIKELLIEKY; KTPKIGLHFTY; TSYSEFLENYY; SLSPKENALQY; YTSYSEFLENY; ELKEEYNNTSY; SLITKIIQPDY; LLGAGNLCVFY; KVENLIPEEEY; WLHTRDYPGAY; EEYNNTSYTSY; NSNFKILDAYY; TNIKELLIEKY
	HLA-A6801	ETTGEIFLK; NTTRFHITK; YYTQVKNLR; CVFYTKLAK; IIATNSNFK; EIYNKIDNK; ESNKMSDKK; TTRFHITKK; ELILLNINK; HITKKNFKK; KAFQMKNER; YTQVKNLRR; FKILDAYYR; YTEINTLIK; YTSYSEFLE; SLVLEIYNK; IQSKITMLK; EILIGRNAK; ESLNDQIKK; NIKELLIEK; NLLNYKEEK; CGFEILIGR; LQYFKAYKK; IISLEILQK; YPGAYVFIK; LLENIENEK; ALQYFKAYK; NTSYTSYSE; KILDAYYRR; AYVFIKNQK; QVKNLRRVK; IYNKIDNKK; YSEFLENYY; SLNQSLSPK; LLNINKIQK; ELLIEKYKK; ENIENEKEK; KIIKAFQMK; KLRFSDFLK; TSYTSYSEF; DKFNLIQSK; NLRRVKNKK; KTAIKEKEK; ITKIIQPDY; NIIATNSNFK; NTTRFHITKK; CVFYTKLAKK; EIYNKIDNKK; YVFIKNQKNK; NALQYFKAYK; YTKLAKKSGK; NFKILDAYYR; ITKIIQPDYK;

		YYTQVKNLRR; DAYYRRPKIK; NAKENDKLLR; TTGEIFLKAK; LICLNPNTTR; LYYTQVKNLR; MSDKKIMELK; LIQSKITMLK; TSYSEFLENY; NINKIQKGIK; GAYVFIKNQK; NYTEINTLIK; FKILDAYYRR; RIISLEILQK; DYPGAYVFIK; IPFTNSLITK; EYNQEKTAIK; NFKKNALKLR; NTSYTSYSEF; HIKLDENLIK; IKAFQMKNER; FLKSKIQNGK; TSYTSYSEFL; TNIKELLIEK; SFKTIQNQLK; ILLNINKIQK; EYNNTSYTSY; QYFKAYKKGK; NSNFKILDAY; EKTAIKEKEK; ISLNQSLSPK; YYESLNDQIK; ALQYFKAYKK; KAKEIHESNK; DLYYTQVKNLR; ETTGEIFLKAK; EINLLNYKEEK; NSFKTIQNQLK; TYCGFEILIGR; IIKAFQMKNER; NLIQSKITMLK; SNFKILDAYYR; EIPFTNSLITK; ENALQYFKAYK; YTSYSEFLENY; TSYSEFLENYY; ILICLNPNTTR; EIHESNKMSDK; LITKIIQPDYK; NALQYFKAYKK; NFKILDAYYRR; TAIKEKEKTPK; NIKELLIEKYK; NLCVFYTKLAK; TSYTSYSEFLE; IVLEKRIDSLK; NPNTTRFHITK; HIKLDENLIKK; NYYESLNDQIK; YTQVKNLRRVK; LYYTQVKNLRR; NSNFKILDAYY; IYNKIDNKKFK; LILLNINKIQK; KAYKKGKNSFK; SPKENALQYFK; FYTKLAKKSGK; TRFHITKKNFK; NTSYTSYSEFL; GIKEINLLNYK; QVKNLRRVKNK; KTNIKELLIEK; EEYNQEKTAIK; LIPEEEYNQEK; YYESLNDQIKK; KISLNQSLSPK; EEYNNTSYTSY; LQYFKAYKKGK; ERIISLEILQK; LNYTEINTLIK; GAGNLCVFYTK; LLENIENEKEK; NLDKFNLIQSK; NGKIIKAFQMK
	HLA-B0702	QPDYKSLVL; RVKNKKLGL; NPNTTRFHI; WPSSPNIIA; RPKIKETTG; IPFTNSLIT; WPSSPNIIAT; SPKENALQYF; IPKAEKNLHI; KAYKKGKNSF; IVLEKRIDSL; LAKKSGKADL; RPKIKETTGE; NPNTTRFHIT; RPKIKETTGEI; SPNIIATNSNF; RVKNKKLGLVI; IPFTNSLITKI; QPDYKSLVLEI; TPKIGLHFTYC
	HLA-B0801	ALKLRFSDF; LRRVKNKKL; NLRRVKNKKL; QIKKTNIKEL; QMKNERIISL; ITKKNFKKNAL; FLKSKIQNGKI; RPKIKETTGEI; QIKKTNIKELL
	HLA-B1501	LQKDMIILF; YNNTSYTSY; HTRDYPGAY; NQKNKTPSL; TSYTSYSEF; KIMELKEEY; ALKLRFSDF; NIIATNSNF; ITKIIQPDY; YSEFLENYY; GLHFTYCGF; RDYPGAYVF; KSGKADLYY; IQNGKIIKAF; KIKETTGEIF; LLGAGNLCVF; QMKNERIISL; KAYKKGKNSF; GIKEINLLNY; ILQKDMIILF; KMSDKKIMEL; IQKGIKEINL; IQPDYKSLVL; LQKDMIILFI; TSYSEFLENY; NTSYTSYSEF; WLHTRDYPGAY; LLRHCVKGNDY; FQMKNERIISL; ELKEEYNNTSY; LLGAGNLCVFY; VLLGAGNLCVF; HTRDYPGAYVF; KIQNGKIIKAF; SLSPKENALQY; YTSYSEFLENY; IQKGIKEINLL; SLITKIIQPDY; TSYSEFLENYY; LAKKSGKADLY; NQSLSPKENAL; KENALQYFKAY; KVENLIPEEEY; KTPKIGLHFTY; LIKEIPFTNSL; NSNFKILDAYY
	HLA-B2705	KKLGLVIPK; KKNALKLRF; GRNAKENDK; LQYFKAYKK; RRVKNKKLGL; LRFSDFLKSK; TRFHITKKNF; KRIDSLKQQI; KRIDSLKQQIK; RRVKNKKLGLV; TRFHITKKNFK; LRFSDFLKSKI; LRRVKNKKLGL; FQMKNERIISL
	HLA-B3501	NALQYFKAY; SPKENALQY; YSEFLENYY; QPDYKSLVL; IPFTNSLIT; WPSSPNIIA; HTRDYPGAY; FTYCGFEIL; YNNTSYTSY; NFKILDAYY; YKSLVLEIY; TSYTSYSEF; NLIQSKITM; TPKIGLHFTY; WPSSPNIIAT; SPKENALQYF; NSNFKILDAY; NPNTTRFHIT; LKEEYNNTSY; ENALQYFKAY; EYNNTSYTSY; NTSYTSYSEF; TPSLDVLLGA; TSYSEFLENY; FNLIQSKITM; SPNIIATNSNF; WLHTRDYPGAY; MSLNYTEINTL; TSYSEFLENYY; EINTLIKEIPF; YTSYSEFLENY; WPSSPNIIATN; EILQKDMIILF; LAKKSGKADLY; NSNFKILDAYY; TNSNFKILDAY; KVENLIPEEEY; HTRDYPGAYVF; TPSLDVLLGAG; EEYNNTSYTSY; VLLGAGNLCVF; LICLNPNTTRF; ELKEEYNNTSY; IPFTNSLITKI
	HLA-B4403	KEIPFTNSL; SEFLENYYE; AEKNLHIKL; KEIHESNKM; KETTGEIFL;

		EEYNNTSYT; KEEYNNTSY; FEILIGRNA; SEFLENYYES; KEIPFTNSLI; KEIHESNKMS; GEIFLKAKEI; EEYNQEKTAI; TEINTLIKEI; LEILQKDMII; EEYNNTSYTS; AEKNLHIKLD; EEKIKISLNQ; SEFLENYYESL; KEIPFTNSLIT; KENALQYFKAY; EEYNNTSYTSY; KEKTPKIGLHF; KEKEKTPKIGL
	HLA-B5101	IPFTNSLIT; WPSSPNIIA; NPNTTRFHI; IPFTNSLITK; IPKAEKNLHI; WPSSPNIIAT; IPFTNSLITKI; QPDYKSLVLEI
	HLA-B5701	TSYSEFLENY; LSPKENALQY; TSYSEFLENYY; KTPKIGLHFTY
AAC44656.1| P30 Borrelia burgdorferi; Seq21	HLA-A0101	TTNDSSTAY; ETSSDGTAY; DSSTAYKMY; ASKMIDTLY; ELDAILVPY; SSDGTAYPFY; YTTNDSSTAY; VASKMIDTLY; EVELEEITFY; TSSDGTAYPFY; NVASKMIDTLY; VTDKYGQNWTS
	HLA-A0201	SLSLIIFSL; SLIIFSLTV; KLQRSLSLI; AIDSKTLEI; YVNEELDAI; LVHQSFIPV; HQSFIPVPV; MVTSGPFKL; YKMYVNEEL; ELEEITFYT; LTWSDGVAI; LIIFSLTVL; YLRDNLTWS; KMIDTLYRG; SSTAYKMYV; MIDTLYRGI; KMIDTLYRGI; LLVHQSFIPV; TLASPKPYFI; SLIIFSLTVL; KLQRSLSLII; RSLSLIIFSL; NMVTSGPFKL; YVNEELDAIL; SLSLIIFSLT; KMYVNEELDA; LSLIIFSLTV; MIDTLYRGIV; RAIDSKTLEI; SLSLIIFSLTV; YVNEELDAILV; ILNKETGSTYV; KMIDTLYRGIV; SLDPQLAEDNV; KMYVNEELDAI; FIDLLVHQSFI; LVHQSFIPVPV; AIDSKTLEITL; ITLASPKPYFI; LTWSDGVAITA; QLAEDNVASKM; DLLVHQSFIPV; SSDGTAYPFYL
	HLA-A0301	KSYLRILNK; NMVTSGPFK; VTSGPFKLK; GTAYPFYLR; AITAEGIRK; TTNDSSTAY; GSTYVDMVK; GGHKPGLAK; RSLSLIIFS; TTNDSSTAYK; MVTSGPFKLK; KLKERIPSEK; TLEITLASPK; YVDMVKSIIK; RKSYLRILNK; VAITAEGIRK; SLTVLCCDNK; ILNKETGSTY; ENMVTSGPFK; ELGIRAIDSK; QLAEDNVASK; TGGHKPGLAK; SSDGTAYPFY; VLCCDNKERK; TGSTYVDMVK; KTLEITLASPK; NMVTSGPFKLK; GVAITAEGIRK; RIPSEKYVFEK; YTTNDSSTAYK; RILNKETGSTY; KLKERIPSEKY; VTGDPNTGGHK; NTGGHKPGLAK; NVASKMIDTLY; TSSDGTAYPFY; FSLTVLCCDNK; FIPVPVHVTDK
	HLA-A1101	KSYLRILNK; GTAYPFYLR; VTSGPFKLK; AITAEGIRK; GSTYVDMVK; TTNDSSTAY; NMVTSGPFK; LTVLCCDNK; ITLASPKPY; PSEKYVFEK; KISLGAEPR; LAEDNVASK; TNDSSTAYK; ASKMIDTLY; VTDSELGIR; SIIKNGQEY; TTNDSSTAYK; MVTSGPFKLK; TLEITLASPK; VAITAEGIRK; YVDMVKSIIK; SLTVLCCDNK; KLKERIPSEK; ASKMIDTLYR; SSDGTAYPFY; QLAEDNVASK; VLCCDNKERK; TVLCCDNKER; TGSTYVDMVK; RKSYLRILNK; IPSEKYVFEK; TSGPFKLKER; QVTDSELGIR; GVAITAEGIR; KTLEITLASPK; GVAITAEGIRK; TVLCCDNKERK; YTTNDSSTAYK; RIPSEKYVFEK; VTGDPNTGGHK; TSSDGTAYPFY; NTGGHKPGLAK; FSLTVLCCDNK; NMVTSGPFKLK; VASKMIDTLYR; STKISLGAEPR; VTSGPFKLKER; ETGSTYVDMVK; TAEGIRKSYLR; TYVDMVKSIIK; NVASKMIDTLY
	HLA-A2402	FYLRDNLTW; TYVDMVKSI; YYDSNEVEL; SFIPVPVHV; SYLRILNKE; TYVDMVKSII; MYVNEELDAI; AYPFYLRDNL; AYKMYVNEEL; KYYDSNEVEL; YFIDLLVHQSF; MYVNEELDAIL; ITLASPKPYFI; FYTTNDSSTAY
	HLA-A2902	YVFEKDNKY; ETSSDGTAY; SIIKNGQEY; TTNDSSTAY; VFEKDNKYY; ELDAILVPY; FYLRDNLTW; ASKMIDTLY; YFIDLLVHQ; YVFEKDNKYY; YTTNDSSTAY; EVELEEITFY; KYVFEKDNKY; VASKMIDTLY; ILNKETGSTY; KSIIKNGQEY; PVPVHVTDKY; FYTTNDSSTAY; YFIDLLVHQSF; NVASKMIDTLY; KYVFEKDNKYY; GWETSSDGTAY; RILNKETGSTY
	HLA-A6801	GTAYPFYLR; LTVLCCDNK; NMVTSGPFK; GSTYVDMVK; TTNDSSTAY; EGIRKSYLR; VAITAEGIR; ETSSDGTAY; VTSGPFKLK; LAEDNVASK; YVFEKDNKY; TNDSSTAYK; SKMIDTLYR; KISLGAEPR; KSYLRILNK;

		VLCCDNKER; PSEKYVFEK; TTNDSSTAYK; MVTSGPFKLK; TVLCCDNKER; DGTAYPFYLR; QVTDSELGIR; YTTNDSSTAY; ASKMIDTLYR; TSGPFKLKER; ENMVTSGPFK; GVAITAEGIR; YVFEKDNKYY; YVDMVKSIIK; QLAEDNVASK; TGSTYVDMVK; SLTVLCCDNK; IPSEKYVFEK; EVELEEITFY; TLEITLASPK; ITAEGIRKSY; TKISLGAEPR; VAITAEGIRK; ELGIRAIDSK; TAYKMYVNEE; EKYVFEKDNK; STAYKMYVNE; MVKSIIKNGQ; VASKMIDTLY; IPVPVHVTDK; EITLASPKPY; YTTNDSSTAYK; TAEGIRKSYLR; LTVLCCDNKER; ETGSTYVDMVK; STKISLGAEPR; TVLCCDNKERK; VASKMIDTLYR; TSSDGTAYPFY; NVASKMIDTLY; VTSGPFKLKER; DGVAITAEGIR; FSLTVLCCDNK; NMVTSGPFKLK; KTLEITLASPK; TYVDMVKSIIK; NTGGHKPGLAK; GVAITAEGIRK; RIPSEKYVFEK; STAYKMYVNEE; ETSSDGTAYPF; FIPVPVHVTDK; MVTSGPFKLKE; TTNDSSTAYKM
	HLA-B0702	YPFYLRDNL; SPKPYFIDL; KPYFIDLLV; EPRSLDPQL; SPENMVTSG; SPKPYFIDLL; RAIDSKTLEI; GIRKSYLRIL; KPGLAKGWET; SPENMVTSGPF; YPFYLRDNLTW; SPKPYFIDLLV; KISLGAEPRSL
	HLA-B0801	
	HLA-B1501	YVFEKDNKY; TTNDSSTAY; ITLASPKPY; LNKETGSTY; SIIKNGQEY; IIKNGQEYF; ASKMIDTLY; LQRSLSLII; ETSSDGTAY; TLASPKPYF; ENMVTSGPF; SLSLIIFSL; YVFEKDNKYY; LQRSLSLIIF; ITAEGIRKSY; YTTNDSSTAY; ILNKETGSTY; TSSDGTAYPF; KSIIKNGQEY; HQSFIPVPVH; SIIKNGQEYF; GQNWTSPENM; ITLASPKPYF; YVNEELDAIL; SLIIFSLTVL; KMIDTLYRGI; WETSSDGTAY; KLKERIPSEKY; YFIDLLVHQSF; KLQRSLSLIIF; RILNKETGSTY; TSSDGTAYPFY; AITAEGIRKSY; KSIIKNGQEYF; LEITLASPKPY; QLAEDNVASKM; ETSSDGTAYPF
	HLA-B2705	QRSLSLIIF; RKSYLRILNK; QRSLSLIIFSL; RKEGVSTKISL; IRKSYLRILNK
	HLA-B3501	VPVHVTDKY; TTNDSSTAY; ETSSDGTAY; YVFEKDNKY; EVELEEITF; YPFYLRDNL; YVNEELDAI; ELDAILVPY; TAEGIRKSY; LTWSDGVAI; EPRSLDPQL; DSSTAYKMY; VASKMIDTL; SSDGTAYPF; SIIKNGQEY; ENMVTSGPF; YTTNDSSTAY; YVNEELDAIL; VASKMIDTLY; TSSDGTAYPF; YVFEKDNKYY; YPFYLRDNLT; WETSSDGTAY; LAEDNVASKM; EVELEEITFY; EELDAILVPY; KPYFIDLLVH; EITLASPKPY; DPQLAEDNVA; NEVELEEITF; FIDLLVHQSF; ILNKETGSTY; SPKPYFIDLL; LTWSDGVAIT; SPENMVTSGPF; IPVPVHVTDKY; YPFYLRDNLTW; FYTTNDSSTAY; ETSSDGTAYPF; TSSDGTAYPFY; DPNTGGHKPGL; YFIDLLVHQSF; NVASKMIDTLY; DPQLAEDNVAS; TTNDSSTAYKM; MYVNEELDAIL; NEVELEEITFY; NEELDAILVPY; TAYKMYVNEEL; YFDGQVTDSEL; LEITLASPKPY
	HLA-B4403	EELDAILVP; EEITFYTTN; AEDNVASKM; AEGIRKSYL; VELEEITFY; EELDAILVPY; NEVELEEITF; EEITFYTTND; AEPRSLDPQL; AEDNVASKMI; PENMVTSGPF; WETSSDGTAY; EEITFYTTNDS; NEVELEEITFY; LEITLASPKPY; EELDAILVPYP; AEGIRKSYLRI; NEELDAILVPY; AEPRSLDPQLA
	HLA-B5101	KPYFIDLLV; IPVPVHVTD; GPFKLKERI; LASPKPYFI; ; IPVPVHVTDKY; SPKPYFIDLLV
	HLA-B5701	VTDKYGQNW;
NP_045619.1 | immunogenic protein P37, putative [Borrelia	HLA-A0101	FSSVISCKLY; NSNASRHESY; MSSTKSLLEV; MTEIESSKEEY; NSNASRHESYY; ISCKLYKKITY
	HLA-A0201	FMADAKASM; ALLPSLEEA; SLEEAIAKV; NLINKLFIL; FILTILFSS; ILTILFSSV; RINEDLAKV; LLSTAKSYL; SLDKIKSLL; LMADMQPDM; LLPSLEEAI; SMSSTKSLL; ILFSSVISC; YAGYHQFMA; KITYNADQV; FILTILFSSV; KLYKKITYNA; ALLPSLEEAI; SLLSTAKSYL; KLFILTILFS;

burgdorferi B31]; Seq22		LINKLFILTI; NLINKLFILT; FMADAKASMS; ILTILFSSVI; MSSTKSLLEV; KANLALLPSL; LLPSLEEAIA; FILTILFSSVI; SMSSTKSLLEV; NLINKLFILTI; ILFSSVISCKL; KLFILTILFSS; ALLPSLEEAIA; YMDQDTGKKPL; FMADAKASMSS; LINKLFILTIL; NLALLPSLEEA; SLDKIKSLLST; ALEEALSNSNA; YYYAGYHQFMA
	HLA-A0301	SVISCKLYK; SLLEVAKNK; VISCKLYKK; IMTEIESSK; KSYLEQTRR; KLYKKITYN; AIAALKRAK; LFSSVISCK; ALSNSNASR; KLFILTILF; SLLSTAKSY; ILFSSVISCK; KIKSLLSTAK; QTRRGVGSSK; SSVISCKLYK; NIMTEIESSK; SVISCKLYKK; KSLLEVAKNK; LAKVKASLDK; STKSLLEVAK; HCNDAIAALK; KSLLSTAKSY; SNNGSFNTLK; LLEVAKNKQK; GYHQFMADAK; TYMDQDTGKK; KLFILTILFS; SLEEAIAKVK; NTYMDQDTGK; DAKASMSSTK; RINEDLAKVK; SMSSTKSLLE; KSNNGSFNTLK; TILFSSVISCK; ITYNADQVIDK; SLLEVAKNKQK; FSSVISCKLYK; NTYMDQDTGKK; ELNENMTKTNK; KQKELNENMTK; LLPSLEEAIAK; SSTKSLLEVAK; KLFILTILFSS; DLAKVKASLDK; AGYHQFMADAK
	HLA-A1101	SVISCKLYK; VISCKLYKK; AIAALKRAK; SLLEVAKNK; KSYLEQTRR; IMTEIESSK; LFSSVISCK; ALSNSNASR; TYMDQDTGK; PSLEEAIAK; TLKSNDDSK; ASRHESYYY; STAKSYLEQ; FQELNDIYK; YMDQDTGKK; SVISCKLYKK; ILFSSVISCK; SSVISCKLYK; STKSLLEVAK; KSLLEVAKNK; KIKSLLSTAK; NTYMDQDTGK; NIMTEIESSK; RINEDLAKVK; KVKASLDKIK; SNNGSFNTLK; NTLKSNDDSK; TYMDQDTGKK; TYNADQVIDK; QTRRGVGSSK; SLEEAIAKVK; KSLLSTAKSY; LAKVKASLDK; GYHQFMADAK; TILFSSVISCK; KSNNGSFNTLK; SSTKSLLEVAK; ITYNADQVIDK; NTYMDQDTGKK; SSVISCKLYKK; FSSVISCKLYK; SLLEVAKNKQK; STAKSYLEQTR; AGYHQFMADAK; KQKELNENMTK; KSNDDSKRSGR; NSNASRHESYY; ELNENMTKTNK; LLPSLEEAIAK; RNIMTEIESSK; TAKSYLEQTRR; ASMSSTKSLLE; AKNDFEYAQRK; THCNDAIAALK; PSLEEAIAKVK
	HLA-A2402	YYYAGYHQF; YYAGYHQFM; EYNRINEDL; SYYYAGYHQF; YYYAGYHQFM; YYAGYHQFMA; LFSSVISCKL; SYYYAGYHQFM; EYAQRKADRAL; TYNADQVIDKL; YYYAGYHQFMA
	HLA-A2902	YYYAGYHQF; DFQELNDIY; ASRHESYYY; KRAKNDFEY; KLFILTILF; SLLSTAKSY; SYYYAGYHQF; NASRHESYYY; FSSVISCKLY; SNASRHESYYY; ALKRAKNDFEY; LFSSVISCKLY; ISCKLYKKITY
	HLA-A6801	ESSKEEYNR; SVISCKLYK; ESYYYAGYH; IMTEIESSK; EYAQRKADR; LFSSVISCK; KSYLEQTRR; MTKTNKDFQ; TLKSNDDSK; NNGSFNTLK; NDAIAALKR; TYMDQDTGK; NASRHESYY; CNDAIAALK; ALSNSNASR; NDFEYAQRK; EIESSKEEY; VISCKLYKK; NSSSNHTLQ; NTYMDQDTGK; EALSNSNASR; SVISCKLYKK; TAKSYLEQTR; DAKASMSSTK; NIMTEIESSK; ILFSSVISCK; NTLKSNDDSK; STKSLLEVAK; ESYYYAGYHQ; TLKSNDDSKR; SSVISCKLYK; DAIAALKRAK; NADQVIDKLK; TYMDQDTGKK; NASRHESYYY; NSNASRHESY; SNNGSFNTLK; HCNDAIAALK; QTRRGVGSSK; FSSVISCKLY; TYNADQVIDK; DFQELNDIYK; MTKTNKDFQE; CNDAIAALKR; DSKRSGRKPR; FEYAQRKADR; NTYMDQDTGKK; STAKSYLEQTR; EIESSKEEYNR; NTLKSNDDSKR; TAKSYLEQTRR; FSSVISCKLYK; TILFSSVISCK; ITYNADQVIDK; NIQDNEASEAR; ELNENMTKTNK; EEALSNSNASR; NSNASRHESYY; SSVISCKLYKK; MTEIESSKEEY; ESYYYAGYHQF; EYNRINEDLAK; SSTKSLLEVAK; DLAKVKASLDK; RAKNDFEYAQR; KSNNGSFNTLK; THCNDAIAALK; YNADQVIDKLK; HCNDAIAALKR; KSNDDSKRSGR; DFEYAQRKADR; DFQELNDIYKK; DNTYMDQDTGK; IYKKLQDMDSR; EQTRRGVGSSK
	HLA-B0702	AQRKADRAL; KPRSVDNTY; ASMSSTKSL; KPRSVDNTYM; KASMSSTKSL; YAQRKADRAL; KASLDKIKSL; KANLALLPSL; KASMSSTKSLL; KPRSVDNTYMD; LPSLEEAIAKV; GVGSSKANLAL;

		KPLMADMQPDM; KASLDKIKSLL; RKADRALEEAL; SKRSGRKPRSV
	HLA-B0801	YAQRKADRAL;
	HLA-B1501	KLKSNNGSF; FMADAKASM; KQKELNENM; AQRKADRAL; KLFILTILF; SLLSTAKSY; ASRHESYYY; YYYAGYHQF; LMADMQPDM; ALKRAKNDF; SSVISCKLY; SNASRHESY; NMTKTNKDF; MQNDNSSSNH; KSLLSTAKSY; NSNASRHESY; FSSVISCKLY; KQKELNENMT; HQFMADAKASM; ALKRAKNDFEY; NSNASRHESYY; MQNDNSSSNHT; SNSNASRHESY; INKLFILTILF; ISCKLYKKITY; IKSLLSTAKSY
	HLA-B2705	TRRGVGSSK; KRAKNDFEY; NRINEDLAK; KRSGRKPRS; KRSGRKPRSV; SRHESYYYAGY; RRGVGSSKANL; NRINEDLAKVK; HQFMADAKASM; KRAKNDFEYAQ; KQKELNENMTK; GRKPRSVDNTY
	HLA-B3501	EASEARNIM; KPRSVDNTY; FMADAKASM; NASRHESYY; LPSLEEAIA; DFQELNDIY; HCNDAIAAL; EALSNSNAS; LMADMQPDM; YYYAGYHQF; EIESSKEEY; YYAGYHQFM; HESYYYAGY; NASRHESYYY; KPRSVDNTYM; YAQRKADRAL; LPSLEEAIAK; FSSVISCKLY; QFMADAKASM; QPDMQNDNSS; EASEARNIMT; THCNDAIAAL; TEIESSKEEY; KPLMADMQPDM; MTEIESSKEEY; DTHCNDAIAAL; ESYYYAGYHQF; HQFMADAKASM; IAALKRAKNDF; YMDQDTGKKPL; LPSLEEAIAKV; NSNASRHESYY; EALSNSNASRH; NKDFQELNDIY
	HLA-B4403	HESYYYAGY; EEALSNSNA; TEIESSKEEY; EEALSNSNAS; EEYNRINEDL; EEYNRINEDLA
	HLA-B5101	LPSLEEAIA; ; LPSLEEAIAKV; LALLPSLEEAI
	HLA-B5701	ISCKLYKKITY
NP_212281.1 | flagellin [Borrelia burgdorferi B31]; Seq23	HLA-A0101	ESIKNSTEY; KTQEKLSSGY; MTDEVVAATT; ASDDAAGMGV; NQDEAIAVNIY; RLESIKNSTEY; ISDQRANLGAF; ELAVQSGNGTY; MIAQANQVPQY
	HLA-A0201	SQASWTLRV; TMTDEVVAA; QLTDEINRI; AMIAQANQV; MIINHNTSA; QVPQYVLSL; AIAVNIYAA; SLAKIENAI; AVNIYAANV; AQYNQMHML; TTVDANTSL; NLGAFQNRL; SQGGVNSPV; MTDEVVAAT; SAMAMIAQA; AQTAQAAPV; VVAATTNSI; MISDQRANL; ILTQSAMAM; SILTQSAMA; LTQSAMAMI; AQANQVPQYV; MIINHNTSAI; ILTQSAMAMI; NIYAANVANL; TMTDEVVAAT; RMISDQRANL; NLNEVEKVLV; VLVRMKELAV; MAMIAQANQV; AQAAPVQEGV; QLTDEINRIA; ATMTDEVVAA; QVPQYVLSLL; NQVPQYVLSL; IAVNIYAANV; SLSGSQASWTL; MLSNKSASQNV; AMAMIAQANQV; AIAVNIYAANV; SQASWTLRVHV; KLSSGYRINRA; SILTQSAMAMI; GMQPAKINTPA; KVLVRMKELAV; TMTDEVVAATT; MISDQRANLGA; YAIENLKASYA; SLAKIENAIRM; NLFSGEGAQTA; ILTQSAMAMIA
	HLA-A0301	GINAANLSK; SQASRNTSK; NQMHMLSNK; GSQASWTLR; FQNRLESIK; LSSGYRINR; TVDANTSLAK; LSQASRNTSK; KLSSGYRINR; NLKASYAQIK; NGINAANLSK; AANLSKTQEK; STEYAIENLK; KTQEKLSSGY; YNQMHMLSNK; AFQNRLESIK; QIRGLSQASR; VPQYVLSLLR; GLSQASRNTSK; MIAQANQVPQY; LSGSQASWTLR; GAFQNRLESIK; KTQEKLSSGYR; RLESIKNSTEY; TTVDANTSLAK; KINAQIRGLSQ; LSNKSASQNVR
	HLA-A1101	GINAANLSK; SQASRNTSK; NQMHMLSNK; GSQASWTLR; AAGMGVSGK; LSSGYRINR; NTSAINASR; TEYAIENLK; AVQSGNGTY; PQYVLSLLR; FQNRLESIK; AQANQVPQY; TVDANTSLAK; STEYAIENLK; LSQASRNTSK; AANLSKTQEK; RANLGAFQNR; KTQEKLSSGY; KLSSGYRINR; AFQNRLESIK; YNQMHMLSNK; IAQANQVPQY; TQEKLSSGYR; NLKASYAQIK; EVEKVLVRMK; TTVDANTSLAK; TTEGNLNEVEK; KTQEKLSSGYR; GAFQNRLESIK; TAEELGMQPAK; NSTEYAIENLK; GLSQASRNTSK; TSLAKIENAIR; QYNQMHMLSNK; NAANLSKTQEK; QVPQYVLSLLR; AQIRGLSQASR;

		LSGSQASWTLR; GVSGKINAQIR; MIAQANQVPQY; LSNKSASQNVR; SAMAMIAQANQ;
	HLA-A2402	IYAANVANL; YAANVANLF; AFQNRLESI; IYAANVANLF; TYSDADRGSI; SYAQIKDATM; IYAANVANLFS
	HLA-A2902	ESIKNSTEY; AVQSGNGTY; YAANVANLF; AIENLKASY; YAIENLKASY; IAQANQVPQY; EYAIENLKASY; ELAVQSGNGTY; RLESIKNSTEY; EINRIADQAQY; MIAQANQVPQY
	HLA-A6801	NTSAINASR; LSSGYRINR; ESIKNSTEY; TEYAIENLK; AIRMISDQR; LAKIENAIR; EGNLNEVEK; YAANVANLF; NGTYSDADR; GSQASWTLR; NQMHMLSNK; QTAQAAPVQ; TSKAINFIQ; MAMIAQANQ; NKSASQNVR; GINAANLSK; TTNSILTQS; SQASRNTSK; NAIRMISDQR; STEYAIENLK; DAAGMGVSGK; HNTSAINASR; EVEKVLVRMK; SLAKIENAIR; TVDANTSLAK; RANLGAFQNR; QIRGLSQASR; NTSKAINFIQ; LSQASRNTSK; NLKASYAQIK; SGSQASWTLR; TQEKLSSGYR; VPQYVLSLLR; NGINAANLSK; AANLSKTQEK; YAIENLKASY; VSGKINAQIR; TTVDANTSLA; KLSSGYRINR; MIAQANQVPQ; QTAQAAPVQE; NTSAINASRN; NSTEYAIENLK; TTVDANTSLAK; TTEGNLNEVEK; EIEQLTDEINR; QVPQYVLSLLR; NAANLSKTQEK; ENAIRMISDQR; LSNKSASQNVR; MIAQANQVPQY; TSLAKIENAIR; EINRIADQAQY; NLNEVEKVLVR; LSGSQASWTLR; GAFQNRLESIK; TAEELGMQPAK; QYNQMHMLSNK; GVSGKINAQIR; KTQEKLSSGYR; NHNTSAINASR; NIYAANVANLF; EKLSSGYRINR; ENLKASYAQIK
	HLA-B0702	SPVNVTTTV; VPQYVLSLL; QPAKINTPA; VVAATTNSI; QPAPATAPS; LVRMKELAV; ASRNTSKAI; IINHNTSAI; TPASLSGSQ; APSQGGVNS; VAATTNSIL; APATAPSQG; APVQEGVQQ; ILTQSAMAM; TPASLSGSQA; SPVNVTTTVD; VVAATTNSIL; APSQGGVNSP; QPAKINTPAS; QASRNTSKAI; MIINHNTSAI; APSQGGVNSPV; QPAKINTPASL; APATAPSQGGV; SPVNVTTTVDA; TPASLSGSQAS; AANLSKTQEKL; RANLGAFQNRL
	HLA-B0801	YAQIKDATM; KVLVRMKEL; ; VEKVLVRMKEL
	HLA-B1501	AQANQVPQY; DQRANLGAF; YAANVANLF; AVQSGNGTY; TQEKLSSGY; ILTQSAMAM; AQYNQMHML; VVAATTNSI; AQTAQAAPV; SQGGVNSPV; ESIKNSTEY; SLSGSQASW; SQASWTLRV; IQIEIEQLT; AMIAQANQV; YAIENLKASY; LAVQSGNGTY; SQASWTLRVH; KTQEKLSSGY; SQNVRTAEEL; RMISDQRANL; VQQEGAQQPA; IAQANQVPQY; VVAATTNSIL; AQAAPVQEGV; AQIRGLSQAS; NQVPQYVLSL; INRIADQAQY; MQPAKINTPA; SQASRNTSKAI; AQANQVPQYVL; MIAQANQVPQY; ASRNTSKAINF; ELAVQSGNGTY; RLESIKNSTEY; NIYAANVANLF; NQDEAIAVNIY; SLSGSQASWTL
	HLA-B2705	NRIADQAQY; IRGLSQASR; QRANLGAFQ; SRNTSKAINF; QRANLGAFQNR; IRMISDQRANL; SRNNGINAANL
	HLA-B3501	YAANVANLF; YAQIKDATM; QPAPATAPS; RASDDAAGM; SPVNVTTTV; ESIKNSTEY; ILTQSAMAM; DEAIAVNIY; TTVDANTSL; LAVQSGNGT; QPAKINTPA; NSILTQSAM; YAIENLKAS; AVQSGNGTY; QASWTLRVH; VAATTNSIL; IAVNIYAAN; MTDEVVAAT; VPQYVLSLL; LAVQSGNGTY; YAIENLKASY; IADQAQYNQM; SILTQSAMAM; IAQANQVPQY; QPAKINTPAS; LAKIENAIRM; QANQVPQYVL; QPAPATAPSQ; YAANVANLFS; TAEELGMQPA; MIINHNTSAI; EAIAVNIYAA; NRASDDAAGM; QAQYNQMHML; TPASLSGSQA; SPVNVTTTVD; SYAQIKDATM; MAMIAQANQV; MIAQANQVPQY; TPASLSGSQAS; ELAVQSGNGTY; NQDEAIAVNIY; QPAKINTPASL; IAVNIYAANVA; NSILTQSAMAM; NIYAANVANLF; EVVAATTNSIL; TTNSILTQSAM; SPVNVTTTVDA; EINRIADQAQY; NASRNNGINAA; IADQAQYNQMH; ISDQRANLGAF; APSQGGVNSPV; LAVQSGNGTYS; EYAIENLKASY
	HLA-B4403	EELGMQPAKI; NEVEKVLVRM; DEINRIADQA; EEYNRINEDLA

	HLA-B5101	LPSLEEAIA; APATAPSQGGV; APSQGGVNSPV
	HLA-B5701	ASLSGSQASW;
NP_212463.1 | oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) ; [Borrelia burgdorferi B31]; Seq24	HLA-A0101	YSSAVNAIY; TTNDSSTAY; YTQFSSHNY; AIDRETLTY; DSSTAYKMY; FLSIFTQGY; RSDYYSSAV; SSDGTVYTF; YTTNDSSTAY; SSAVNAIYFY; SSHNYSNPEY; YLNTKANGNY; ATPNFSSYSY; ELENEEWTTY; YSSAVNAIYF; EVELEEITFY; YSSAVNAIYFY; FSSHNYSNPEY; TLAIDRETLTY; LTFLSIFTQGY; YADPLTFLSIF
	HLA-A0201	SLFLIIFFL; KLQRSLFLI; IIIEKDFPI; AVNAIYFYA; AIDEKTLEI; LIIFFLTFL; LVHQSFIPV; VLDNGTTPT; SLELFNPEI; YSYAKSLEL; SLGAEPSSL; HQSFIPVPV; WIGDYADPL; MVTSGPFKL; ELEEITFYT; KMIDTMFRG; AIYFYAFNT; KTLEITLES; ITWSDGVAI; FLIIFFLTF; MIDTMFRGI; RSDYYSSAV; YKMYENEEL; YFYAFNTHI; FLIIFFLTFL; MLVHQSFIPV; KMIDTMFRGI; KLQRSLFLII; SLFLIIFFLT; YADPLTFLSI; KMYENEELDA; AIFGSIPPDL; FLSIFTQGYT; NMVTSGPFKL; KLRSDYYSSA; RSLFLIIFFL; SAVNAIYFYA; IIIEKDFPIA; KSLELFNPEI; YAFNTHIKPL; MIDTMFRGIV; TLESPKPYFI; ILERFDLSQL; KVLDNGTTPT; SIPPDLIKNL; RAIDEKTLEI; FLIIFFLTFL; MLVHQSFIPV; KMIDTMFRGI; KLQRSLFLII; SLFLIIFFLT; YADPLTFLSI; KMYENEELDA; AIFGSIPPDL; FLSIFTQGYT; NMVTSGPFKL; KLRSDYYSSA; RSLFLIIFFL; SAVNAIYFYA; IIIEKDFPIA; KSLELFNPEI; YAFNTHIKPL; MIDTMFRGIV; TLESPKPYFI; ILERFDLSQL; KVLDNGTTPT; SIPPDLIKNL; RAIDEKTLEI
	HLA-A0301	KSYLRILNK; ILNKETGSK; NMVTSGPFK; VTSGPFKLK; ELFNPEIAK; LTFLCCNNK; KSVIKNGQK; GSKYVEMVK; AITAEGIRK; TTNDSSTAY; GSIPPDLIK; RATPNFSSY; NSYLFRNDK; GGNKPGLAK; RILNKETGSK; YIYGNSYLFR; TVYTFNLREK; TTNDSSTAYK; MVTSGPFKLK; AIDRETLTYK; FLTFLCCNNK; ATPNFSSYSY; RKSYLRILNK; YFYAFNTHIK; VAITAEGIRK; KLKERIPNEK; YVEMVKSVIK; KPLDNVKIRK; RQAEEIIIEK; TLEITLESPK; SSAVNAIYFY; GNGFPILKLK; TGGNKPGLAK; ENMVTSGPFK; ILNKETGSKY; QLAEDNVASK; RFDLSQLKLK; AIYFYAFNTH; IPVPVHVTEK; YLNTKANGNY; LELFNPEIAK; ASKMIDTMFR; FLCCNNKERK; VLDNGTTPTR; ELGIRAIDEK; KERKEGVSFK; DLSQLKLKNK; RRATPNFSSY; LERFDLSQLK; LKYNTNEANK; KTLEITLESPK; KLKYNTNEANK; MVKSVIKNGQK; KICEFIQNQWK; ILERFDLSQLK; NMVTSGPFKLK; GVAITAEGIRK; RILNKETGSKY; YTTNDSSTAYK; RIPNEKYVFEK; VTGDPNTGGNK; KVLDNGTTPTR; KLKERIPNEKY; TLAIDRETLTY; SLELFNPEIAK; IYFYAFNTHIK; FIPVPVHVTEK; LTFLSIFTQGY; LAIDRETLTYK; GTVYTFNLREK; IFGSIPPDLIK; VLDNGTTPTRR; RATPNFSSYSY; SIPPDLIKNLK; NTGGNKPGLAK; YSSAVNAIYFY
	HLA-A1101	KSYLRILNK; VTSGPFKLK; LTFLCCNNK; AITAEGIRK; NSYLFRNDK; TTNDSSTAY; GSIPPDLIK; GTVYTFNLR; NMVTSGPFK; GSKYVEMVK; SAVNAIYFY; KSVIKNGQK; YTQFSSHNY; ILNKETGSK; LSQLKLKNK; QAEEIIIEK; ELFNPEIAK; AVNAIYFYA; NFSSYSYAK; KALTLAIDR; TVYTFNLRE; NGNGFPILK; LAEDNVASK; TNDSSTAYK; SVIKNGQKY; KYNTNEANK; SKMIDTMFR; AIYFYAFNT; ITLESPKPY; SLFLIIFFL; KTLLAEAGY; LTFLSIFTQ; VTDSELGIR; PVPVHVTEK; RATPNFSSY; AIDRETLTY; GGNKPGLAK; TTNDSSTAYK; TVYTFNLREK; MVTSGPFKLK; SSAVNAIYFY; AIDRETLTYK; YIYGNSYLFR; RILNKETGSK; RQAEEIIIEK; VAITAEGIRK; ATPNFSSYSY; ASKMIDTMFR; TLEITLESPK; KSDLELDPIK; YFYAFNTHIK; YVEMVKSVIK; KLKERIPNEK; AIYFYAFNTH; SSHNYSNPEY; QLAEDNVASK; FLTFLCCNNK; IPNEKYVFEK; KANGNYEIAR; RKSYLRILNK; TGSKYVEMVK; AVNAIYFYAF; KPLDNVKIRK; TSGPFKLKER; YVFEKNNKYY; QVTDSELGIR; KYNTNEANKK; GVAITAEGIR; RFDLSQLKLK; FLCCNNKERK; KTLEITLESPK; KICEFIQNQWK; GVAITAEGIRK; YTTNDSSTAYK; GTVYTFNLREK;

		VTGDPNTGGNK; MVKSVIKNGQK; SLELFNPEIAK; LAIDRETLTYK; TPNFSSYSYAK; SIPPDLIKNLK; RIPNEKYVFEK; KVLDNGTTPTR; VASKMIDTMFR; YSSAVNAIYFY; NTGGNKPGLAK; NMVTSGPFKLK; ILERFDLSQLK; LTFLSIFTQGY; YSNPEYNELIK; VTSGPFKLKER; IYFYAFNTHIK; ETGSKYVEMVK; KLKYNTNEANK; NTHIKPLDNVK; LTFLCCNNKER; TAEGIRKSYLR; AVNAIYFYAFN; RATPNFSSYSY; FIPVPVHVTEK; YPNGNGFPILK; TFLCCNNKERK; KSDLELDPIKR; WTGWNTNILER; IYIYGNSYLFR
	HLA-A2402	SYAKSLELF; YYSSAVNAI; IYIYGNSYL; YYDSNEVEL; FYAFNTHIK; DFPIAPIYI; SYLFRNDKW; DYADPLTFL; IYGNSYLFR; IFTQGYTQF; KLQRSLFLI; YIYGNSYLF; SFIPVPVHV; KYVEMVKSV; IFGSIPPDL; RSLFLIIFF; YFYAFNTHI; KWTGWNTNI; SYLRILNKE; LFLIIFFLT; IYFYAFNTH; IYIYGNSYLF; IYFYAFNTHI; LFLIIFFLTF; DYYSSAVNAI; VYTFNLREKI; KYVEMVKSVI; SYSYAKSLEL; IFGSIPPDLI; GYPNGNGFPI; GWNTNILERF; NYSNPEYNEL; MYENEELDAI; KYYDSNEVEL; NYEIARAGWI; YYSSAVNAIY; KWTGWNTNIL; AYKMYENEEL; KYNTNEANKK; AVNAIYFYAF; YYSSAVNAIYF; SYSYAKSLELF; YFIDMLVHQSF; DYADPLTFLSI; FYAFNTHIKPL; NYSNPEYNELI; KYNTNEANKKI; MYENEELDAIF; IYFYAFNTHIK; LFLIIFFLTFL; IYIYGNSYLFR; GYPNGNGFPIL; ITLESPKPYFI; TTPTRRATPNF; FYTTNDSSTAY
	HLA-A2902	YVFEKNNKY; SVIKNGQKY; GFPILKLKY; DISSDGTVY; YTQFSSHNY; YSSAVNAIY; TTNDSSTAY; FLSIFTQGY; YIYGNSYLF; FLIIFFLTF; YFYAFNTHI; VFEKNNKYY; FPIAPIYIY; PIYIYGNSY; IFTQGYTQF; SAVNAIYFY; AIDRETLTY; YVFEKNNKYY; YYSSAVNAIY; YTTNDSSTAY; TFLSIFTQGY; YLNTKANGNY; IYIYGNSYLF; ELENEEWTTY; EVELEEITFY; GYTQFSSHNY; KYVFEKNNKY; LAIDRETLTY; SSAVNAIYFY; ILNKETGSKY; SIFTQGYTQF; PVPVHVTEKY; DFPIAPIYIY; ATPNFSSYSY; AVNAIYFYAF; NGFPILKLKY; LFLIIFFLTF; YFYAFNTHIK; YSSAVNAIYF; SVIKNGQKYF; RRATPNFSSY; WDISSDGTVY; EITLESPKPY; FYTTNDSSTAY; YFIDMLVHQSF; DYYSSAVNAIY; YSSAVNAIYFY; TYLNTKANGNY; TLAIDRETLTY; KYVFEKNNKYY; YYSSAVNAIYF; SLFLIIFFLTF; FSSHNYSNPEY; RILNKETGSKY; MYENEELDAIF; EIARAGWIGDY; KDFPIAPIYIY; GWDISSDGTVY; RATPNFSSYSY; LTFLSIFTQGY; YADPLTFLSIF; NVASKMIDTMF
	HLA-A6801	GTVYTFNLR; NSYLFRNDK; FYAFNTHIK; LTFLCCNNK; SAVNAIYFY; ELFNPEIAK; NFSSYSYAK; EFIQNQWKK; DLIKNLKLR; YTQFSSHNY; FLCCNNKER; NMVTSGPFK; QAEEIIIEK; TTNDSSTAY; EGIRKSYLR; SKMIDTMFR; YSSAVNAIY; YIYGNSYLF; VAITAEGIR; LTFLSIFTQ; HIKPLDNVK; YVFEKNNKY; TPNFSSYSY; ERFDLSQLK; VTSGPFKLK; NGNGFPILK; GSKYVEMVK; NGFPILKLK; EWTTYLNTK; LAEDNVASK; NAIYFYAFN; TNDSSTAYK; KSYLRILNK; IYGNSYLFR; TVYTFNLRE; SLFLIIFFL; DLELDPIKR; VYTFNLREK; LDNGTTPTR; FPIAPIYIY; KALTLAIDR; SSTAYKMYE; ILNKETGSK; STAYKMYEN; YIYGNSYLFR; TTNDSSTAYK; TVYTFNLREK; MVTSGPFKLK; YFYAFNTHIK; ASKMIDTMFR; QVTDSELGIR; FLTFLCCNNK; DGTVYTFNLR; SSAVNAIYFY; YVEMVKSVIK; YTTNDSSTAY; YVFEKNNKYY; TSGPFKLKER; ENMVTSGPFK; GVAITAEGIR; DPIKRQDILR; FLCCNNKERK; KANGNYEIAR; QLAEDNVASK; TFLCCNNKER; TGSKYVEMVK; IPVPVHVTEK; ELGIRAIDEK; EVELEEITFY; IPNEKYVFEK; TGWNTNILER; SSHNYSNPEY; SSYSYAKSLE; ITAEGIRKSY; TLEITLESPK; EKYVFEKNNK; VAITAEGIRK; ATPNFSSYSY; DLSQLKLKNK; CEFIQNQWKK; STAYKMYENE; NAIYFYAFNT; TAYKMYENEE; YTTNDSSTAYK; LTFLCCNNKER; TAEGIRKSYLR; MVKSVIKNGQK; VASKMIDTMFR; IYIYGNSYLFR;

		YSSAVNAIYFY; WTGWNTNILER; ETGSKYVEMVK; TPNFSSYSYAK; LAIDRETLTYK; GTVYTFNLREK; IYFYAFNTHIK; LTFLSIFTQGY; NTHIKPLDNVK; VTSGPFKLKER; HIKPLDNVKIR; DGVAITAEGIR; NMVTSGPFKLK; YSNPEYNELIK; YPNGNGFPILK; FSSHNYSNPEY; TKANGNYEIAR; NTGGNKPGLAK; DYYSSAVNAIY; FIPVPVHVTEK; KTLEITLESPK; SIPPDLIKNLK; KVLDNGTTPTR; NAIYFYAFNTH; GVAITAEGIRK; RIPNEKYVFEK; SLELFNPEIAK; STAYKMYENEE; NGNGFPILKLK; ERFDLSQLKLK; KICEFIQNQWK; TFLCCNNKERK; ILERFDLSQLK; YGNSYLFRNDK; EIARAGWIGDY; FFLTFLCCNNK; MVTSGPFKLKE; FTQGYTQFSSH; TTNDSSTAYKM
	HLA-B0702	YPNGNGFPI; NPEIAKTLL; SPKPYFIDM; TPTRRATPN; TPNFSSYSY; SPENMVTSG; KPYFIDMLV; DPIKRQDIL; YPNGNGFPIL; KIRKALTLAI; TPTRRATPNF; SPKPYFIDML; APIYIYGNSY; TPNFSSYSYA; KPGLAKGWDI; GIRKSYLRIL; SPENMVTSGPF; APIYIYGNSYL; IPPDLIKNLKL; KPLDNVKIRKA; KISLGAEPSSL; TPTRRATPNFS
	HLA-B0801	FLIIFFLTF; IRKALTLAI; NVKIRKALTL; KIRKALTLAI;
	HLA-B1501	YVFEKNNKY; YSSAVNAIY; TTNDSSTAY; YTQFSSHNY; FLSIFTQGY; FLIIFFLTF; ITLESPKPY; YIYGNSYLF; SVIKNGQKY; VIKNGQKYF; RATPNFSSY; LNKETGSKY; YSYAKSLEL; IQNQWKKNL; SSAVNAIYF; AGYPNGNGF; NLKLRSDYY; ASKMIDTMF; PIYIYGNSY; ENMVTSGPF; KERKEGVSF; RSLFLIIFF; LENEEWTTY; RQAEEIIIE; KTLLAEAGY; YSNPEYNEL; YVFEKNNKYY; ITAEGIRKSY; YTTNDSSTAY; YSSAVNAIYF; IARAGWIGDY; YLNTKANGNY; LQRSLFLIIF; YSYAKSLELF; ISSDGTVYTF; AVNAIYFYAF; SSHNYSNPEY; LAIDRETLTY; ILNKETGSKY; SVIKNGQKYF; HQSFIPVPVH; SSAVNAIYFY; GQNWTSPENM; YAFNTHIKPL; ATPNFSSYSY; SIFTQGYTQF; KSVIKNGQKY; ITLESPKPYF; YENEELDAIF; YYSSAVNAIY; WDISSDGTVY; GQKYFDGQVT; KMIDTMFRGI; YSSAVNAIYFY; LQRSLFLIIFF; LTFLSIFTQGY; KLKERIPNEKY; YFIDMLVHQSF; FSSHNYSNPEY; SLFLIIFFLTF; TLAIDRETLTY; RATPNFSSYSY; LSIFTQGYTQF; KLQRSLFLIIF; AITAEGIRKSY; IAKTLLAEAGY; KSVIKNGQKYF; RILNKETGSKY; LIKNLKLRSDY; LEITLESPKPY; YLFRNDKWTGW; WIGDYADPLTF; QGYTQFSSHNY; IAPIYIYGNSY; QLAEDNVASKM; SAVNAIYFYAF; IQNQWKKNLNI; KMYENEELDAI; IEKDFPIAPIY
	HLA-B2705	ARAGWIGDY; RRATPNFSSY; RQAEEIIIEK; ERFDLSQLKL; QRSLFLIIFF; RKSYLRILNK; KRQDILRQAE; LRILNKETGSK; RRATPNFSSYS; RKEGVSFKISL; QRSLFLIIFFL; LRQAEEIIIEK; ERFDLSQLKLK; IRKSYLRILNK
	HLA-B3501	TPNFSSYSY; FPIAPIYIY; TTNDSSTAY; DPLTFLSIF; SAVNAIYFY; YPNGNGFPI; VPVHVTEKY; YSSAVNAIY; DISSDGTVY; YVFEKNNKY; EPSSLDPQL; VASKMIDTM; EVELEEITF; FLIIFFLTF; YIYGNSYLF; FLSIFTQGY; WTGWNTNIL; YTQFSSHNY; SPKPYFIDM; NPEIAKTLL; RATPNFSSY; WIGDYADPL; LENEEWTTY; ENEELDAIF; TAEGIRKSY; YSNPEYNEL; ITLESPKPY; DSSTAYKMY; VNAIYFYAF; ITWSDGVAI; EANKKICEF; SHNYSNPEY; YYSSAVNAI; ENMVTSGPF; IFTQGYTQF; YPNGNGFPIL; YTTNDSSTAY; LAIDRETLTY; APIYIYGNSY; VASKMIDTMF; YYSSAVNAIY; YENEELDAIF; WDISSDGTVY; LAEDNVASKM; YVFEKNNKYY; YAFNTHIKPL; EVELEEITFY; TPTRRATPNF; ELENEEWTTY; ISSDGTVYTF; AVNAIYFYAF; TFLSIFTQGY; YSSAVNAIYF; LFLIIFFLTF; SSHNYSNPEY; KPYFIDMLVH; NVASKMIDTM; EAGYPNGNGF; DPQLAEDNVA; SPKPYFIDML; NEVELEEITF; EPSSLDPQLA; TPNFSSYSYA; EITLESPKPY; FIDMLVHQSF; SSAVNAIYFY; YLNTKANGNY; YADPLTFLSI; DPLTFLSIFT; IGDYADPLTF; SIFTQGYTQF; YSYAKSLELF; DPNTGGNKPG; DFPIAPIYIY; SPENMVTSGPF;

		SAVNAIYFYAF; IPVPVHVTEKY; YADPLTFLSIF; FYTTNDSSTAY; IAPIYIYGNSY; YSSAVNAIYFY; YFIDMLVHQSF; IAKTLLAEAGY; DPNTGGNKPGL; FSSHNYSNPEY; WIGDYADPLTF; RATPNFSSYSY; NAIYFYAFNTH; TPNFSSYSYAK; NVASKMIDTMF; MYENEELDAIF; YYSSAVNAIYF; DISSDGTVYTF; TLAIDRETLTY; DPQLAEDNVAS; LTFLSIFTQGY; EPSSLDPQLAE; TTNDSSTAYKM; NEVELEEITFY; QAEEIIIEKDF; YPNGNGFPILK; TAYKMYENEEL; TGWNTNILERF; YFDGQVTDSEL; DKWTGWNTNIL; EIARAGWIGDY; DYYSSAVNAIY; LEITLESPKPY; NPEIAKTLLAE; AGWIGDYADPL; APIYIYGNSYL; DAIFGSIPPDL; FYAFNTHIKPL; FPILKLKYNTN
	HLA-B4403	EELDAIFGS; EEIIIEKDF; EEITFYTTN; AEDNVASKM; YEIARAGWI; AEGIRKSYL; KERKEGVSF; AEAGYPNGN; VELEEITFY; NEVELEEITF; EELDAIFGSI; EEITFYTTND; AEPSSLDPQL; YENEELDAIF; AEDNVASKMI; AEEIIIEKDF; NEANKKICEF; PENMVTSGPF; NEELDAIFGS; EEIIIEKDFPI; AEAGYPNGNGF; EEITFYTTNDS; NEVELEEITFY; LEITLESPKPY; IEKDFPIAPIY; AEGIRKSYLRI; NELIKKSDLEL; EELDAIFGSIP
	HLA-B5101	KPYFIDMLV; FPIAPIYIY; YPNGNGFPI; IPVPVHVTE; IPPDLIKNL; GPFKLKERI; DPLTFLSIF; FPIAPIYIYG; FPILKLKYNT; DPLTFLSIFT; IPVPVHVTEK; YPNGNGFPIL; IPPDLIKNLKL; IPVPVHVTEKY; FPILKLKYNTN; SPKPYFIDMLV; FPIAPIYIYGN
	HLA-B5701	RATPNFSSY; DVELENEEW; KICEFIQNQW; NSYLFRNDKW; YTFNLREKITW; LTFLSIFTQGY
AAC44381.1| outer membrane porin protein Oms28 precursor; Seq25	HLA-A0101	MSDVAKGTV; LTKVMAISLY; MSDVAKGTVV; FSNLIINGLLF
	HLA-A0201	FLIEKQIML; KVMAISLYM; ALDETVQEA; GLLFGFVSL; KVLNMVNGL; VAGEATFLI; KAISNVVKV; TLMASERAL; QALDTINKV; FADSNNANI; MVAEGANKV; SVAGEATFL; TINKVTEDV; KVDEVKETL; LLFGFVSLNV; IINGLLFGFV; SVAGEATFLI; LMSDVAKGTV; GMVAEGANKV; SLMSDVAKGT; RALDETVQEA; KVTEDVSSKL; GLNPSNKDQV; VVASQEATIV; GLLFGFVSLNV; SLMSDVAKGTV; KIFSNLIINGL; LMSDVAKGTVV; LIINGLLFGFV; FVGSMSLMSDV; KLDQKDQVNQA; MLNKSPNNKEL; GMVAEGANKVV; KVDEVKETLMA; LMASERALDET; FLIEKQIMLNK; AVQETQKAVSV; MASERALDETV
	HLA-A0301	MLNKSPNNK; VLAKKDVRK; KVTEDVSSK; GMVAEGANK; KVMAISLYM; MSLMSDVAK; VMAISLYMR; NQALDTINK; IMLNKSPNNK; KVMAISLYMR; MVNGLNPSNK; SMSLMSDVAK; LIEKQIMLNK; ASQEATIVAK; QVLAKKDVRK; GANKVVEMSK; ADSNNANILK; SGMVAEGANK; VAQGARDLTK; LTKVMAISLY; ESNDAGVVKK; FLIEKQIMLNK; KVAQGARDLTK; GSMSLMSDVAK; QIMLNKSPNNK; GANKVVEMSKK; MSKKAVQETQK; QVNQALDTINK; NMVNGLNPSNK; CSGMVAEGANK; ALDETVQEAQK; PSNKDQVLAKK
	HLA-A1101	MSLMSDVAK; KVTEDVSSK; SQEATIVAK; MLNKSPNNK; AQGARDLTK; NVLEHSDQK; GMVAEGANK; VMAISLYMR; DSNNANILK; NQALDTINK; KVMAISLYM; VLAKKDVRK; ESNDAGVVK; GEATFLIEK; MVNGLNPSNK; KVMAISLYMR; ASQEATIVAK; SMSLMSDVAK; GANKVVEMSK; IMLNKSPNNK; QVLAKKDVRK; VAQGARDLTK; LIEKQIMLNK; ESNDAGVVKK; AGEATFLIEK; PSNKDQVLAK; SGMVAEGANK; VNQALDTINK; LTKVMAISLY; GSMSLMSDVAK; QVNQALDTINK; QIMLNKSPNNK; KVAQGARDLTK; VAGEATFLIEK; GANKVVEMSKK; QSNVLEHSDQK; VASQEATIVAK; FLIEKQIMLNK; CSGMVAEGANK; NMVNGLNPSNK; MSKKAVQETQK; ALDETVQEAQK; LVESNDAGVVK; FADSNNANILK; SPNNKELELTK; PSNKDQVLAKK; VLEHSDQKDNK
	HLA-A2402	LFGFVSLNVF; VFADSNNANI; TFLIEKQIML; IFSNLIINGLL; VFADSNNANIL

	HLA-A2902	IINGLLFGF; LIINGLLFGF; NLIINGLLFGF
	HLA-A6801	DSNNANILK; MSLMSDVAK; NVLEHSDQK; EFAKVDEVK; VMAISLYMR; ELTKEEFAK; ESNDAGVVK; MLNKSPNNK; VVKVAQGAR; KVTEDVSSK; QVLAKKDVR; EATFLIEKQ; VSSKLEGVR; NQALDTINK; MVNGLNPSNK; NVVKVAQGAR; KVMAISLYMR; DVSSKLEGVR; ESNDAGVVKK; SMSLMSDVAK; GANKVVEMSK; LTKVMAISLY; EEFAKVDEVK; LIEKQIMLNK; QVLAKKDVRK; VAQGARDLTK; EVKETLMASER; MSKKAVQETQK; QVNQALDTINK; TKVMAISLYMR; QIMLNKSPNNK; QSNVLEHSDQK; FADSNNANILK; FLIEKQIMLNK; EGANKVVEMSK; DVRKAISNVVK; ELELTKEEFAK; NMVNGLNPSNK; CSGMVAEGANK; DLTKVMAISLY; GSMSLMSDVAK; LVESNDAGVVK; EDVSSKLEGVR; GANKVVEMSKK; VASQEATIVAK; VAGEATFLIEK; KVAQGARDLTK; MVAEGANKVVE
	HLA-B0702	GVRESSLEL; SPNNKELEL; GARDLTKVM; NPSNKDQVL; KVAQGARDL; VVKKFVGSM; KVMAISLYM; AVQETQKAV; KVVEMSKKAV; KVTEDVSSKL; KAVQETQKAV; GARDLTKVMAI; AVSVAGEATFL; VVKKFVGSMSL; AVQETQKAVSV
	HLA-B0801	ILKPQSNVL; FLIEKQIML; LAKKDVRKAI; FAKVDEVKETL; VLAKKDVRKAI; VVKKFVGSMSL
	HLA-B1501	VSVAGEATF; KVMAISLYM; FGFVSLNVF; TLMASERAL; ILKPQSNVL; GVRESSLEL; NLIINGLLF; FLIEKQIML; IINGLLFGF; VVKKFVGSM; AVSVAGEATF; LTKVMAISLY; LIINGLLFGF; DQKDQVNQAL; MVAEGANKVV; LLFGFVSLNVF; AQGARDLTKVM; FSNLIINGLLF; AQKVLNMVNGL; LMSDVAKGTVV; VVKKFVGSMSL; NLIINGLLFGF; KAVSVAGEATF; ILKPQSNVLEH; GMVAEGANKVV; TQKAVSVAGEA
	HLA-B2705	RKAISNVVK; KKFVGSMSL; VRKAISNVVK;
	HLA-B3501	NPSNKDQVL; FGFVSLNVF; VSVAGEATF; SPNNKELEL; TKVMAISLY; TFLIEKQIM; FSNLIINGL; AVSVAGEATF; LFGFVSLNVF; MASERALDET; VASQEATIVA; NPSNKDQVLA; LIINGLLFGF; MVAEGANKVV; ETLMASERAL; LTKVMAISLY; KAVSVAGEATF; VAEGANKVVEM; EATFLIEKQIM; FSNLIINGLLF; LLFGFVSLNVF; FAKVDEVKETL; NPSNKDQVLAK; ESNDAGVVKKF; VFADSNNANIL; MASERALDETV
	HLA-B4403	DEVKETLMA; EEFAKVDEV; QEAQKVLNM; KELELTKEEF; AEGANKVVEM; DEVKETLMAS; KETLMASERAL; GEATFLIEKQI; AEGANKVVEMS
	HLA-B5101	
	HLA-B5701	
CAA49829.1| p93 [Borrelia burgdorferi]; Seq26	HLA-A0101	DLDYYKGFY; NSNSNSSYY; NMDLEFVNY; STQQGIQRY; FSVRKNFIY; LIAKVITIY; ITDIQGETH; LTNSNSNSSY; NSNSSYYGKY; ESTQQGIQRY; VTDKVIAALL; ESDIDIDSLV; LTNSNSNSSYY; LTGYIIKSFDY; VTDKVIAALLS; TSFSVRKNFIY
	HLA-A0201	MLLIFSFFL; LLIFSFFLI; FLNGFPLNA; QLIDLNTGV; FVNMDLEFV; ILPFTSFSV; YLQDELKNL; LLSENEAGV; VVSESNFEI; KIQEDINEI; YVDSKMILA; NLQKIDPKV; KVITIYNAV; LMLPEDQKL; SLTKENAGL; SLEDLQEQL; LIFLNGFPL; KMDSGKAKL; KLDSAEDNL; FILSENKIL; NTYEQIVGI; KASVDVFSI; SSAELIAKV; KIDTELDNI; KILPFTSFS; ILTGYIIKS; MSIDSSSPV; LVTDKVIAA; VTDKVIAAL; ELIAKVITI; QILNKLENL; FLEVIDPIT; NITETIENL; QIVGIGEFL; SSSPVFLEV; KQLQIKESL; SLYVDSKMI; LQDELKNLV; NLDKAQQKL; STNTYEQIV; KILPFTSFSV; KMLLIFSFFL; MLLIFSFFLI; FLIFLNGFPL; YLQDELKNLV; ALLSENEAGV; LIFSFFLIFL; TMSIDSSSPV; YVDSKMILAA; ILNKLENLKV; SIDSSSPVFL; ILDVNTLKKV; LQLIDLNTGV; KVVSESNFEI; KLKDFVNMDL; SLYVDSKMIL; SLVTDKVIAA; LVTDKVIAAL; ILSGNIESDI; KISKSNNNEV; RLAKFSPKNL; SLNEDLDKDL; GIYEREKDLV; GLSRVYSQWA; VTDKVIAALL;

		NLVILDVNTL; FSVRKNFIYL; RLKESTQQGI; NLGTLQLIDL; GIGEFLARPL; QIVGIGEFLA; KMLLIFSFFLI; YVDSKMILAAV; LLIFSFFLIFL; YLQDELKNLVI; FLEVIDPITNL; FIDDQDKKASV; QLIDLNTGVRL; KLDSAEDNLDV; TTMSIDSSSPV; TLQLIDLNTGV; VILDVNTLKKV; SLVTDKVIAAL; ILSENKILPFT; KMDSGKAKLQI; KLDGKKEFKPV; QILNKLENLKV; SQWAGKTQIFI; KKMLLIFSFFL; GIYEREKDLVV; SLYVDSKMILA; FIYLQDELKNL; KLQILNKLENL; LIAKVITIYNA; LVTDKVIAALL; FFLIFLNGFPL; MSIDSSSPVFL; ILNKLENLKVV; VIDPITNLGTL; SLGDLNNDKNL; LIFLNGFPLNA; SISSKSELDSI; VIAALLSENEA; FEINKNSSLYV; FTSFSVRKNFI; KVDKEKLKDFV
	HLA-A0301	RVYSQWAGK; RILTGYIIK; ILNKLENLK; KTQIFIPLK; ILDVNTLKK; VILDVNTLK; TQIFIPLKK; KAKLQILNK; RSSAELIAK; KLDGKKEFK; MILAAVRDK; KVDKQLQIK; GFYIEPALK; LIAKVITIY; RELSKASSK; FIYLQDELK; KSNNNEVGK; AVYRGDLDY; KLDSKLDGK; KSKDGKVSK; PLNARKVDK; NSNSSYYGK; EINKNSSLY; KVKEEEITK; DLNTGVRLK; ITIYNAVYR; NLRRILTGY; LSKASSKEK; NSNSNSSYY; KMLLIFSFF; VVIKMDSGK; KASSKEKSK; DSNAWRLAK; KTQIFIPLKK; VILDVNTLKK; KMILAAVRDK; SVDVFSISSK; LVILDVNTLK; AWRLAKFSPK; QILNKLENLK; AINLQKIDPK; LPFTSFSVRK; ILPFTSFSVR; SYYGKYFINR; ALDLDRELSK; LVVIKMDSGK; ITDIQGETHK; KVITIYNAVY; KGFYIEPALK; VITIYNAVYR; RRILTGYIIK; AVYRGDLDYY; IDLNTGVRLK; SKLDGKKEFK; AINLDKAQQK; ELSKASSKEK; IEPALKSLTK; LNGFPLNARK; LTNSNSNSSY; NMDLEFVNYK; EINKEKNLPK; SLEDLQEQLK; SNSNSSYYGK; VIKMDSGKAK; KLDSKLDGKK; LLIFSFFLIF; IVGIGEFLAR; FPLNARKVDK; SRVYSQWAGK; ASSKEKSKVK; FLNGFPLNAR; ASLGDLNNDK; SQVDAKKKEK; VYRGDLDYYK; KKLDSKLDGK; EVGKLSPLDK; VDNKAINLQK; KLSPLDKPSY; KNSSLYVDSK; FLNGFPLNARK; ILPFTSFSVRK; KILPFTSFSVR; ILNLRRILTGY; AVYRGDLDYYK; SSYYGKYFINR; LLKSKDGKVSK; ASVDVFSISSK; VVSESNFEINK; LVILDVNTLKK; TSFSVRKNFIY; LSRVYSQWAGK; LTNSNSNSSYY; KVITIYNAVYR; LIDLNTGVRLK; ILDVNTLKKVK; KIQEDINEINK; NSNSNSSYYGK; KAINLDKAQQK; NLVILDVNTLK; NAWRLAKFSPK; KVKEEEITKGK; KEFKPVSEVEK; RVYSQWAGKTQ; LSKASSKEKSK; KASSKEKSKVK; KLPEDKKLDSK; VVIKMDSGKAK; KMLLIFSFFLI; EVDNKAINLQK; ELDKKAINLDK; KAINLQKIDPK
	HLA-A1101	KTQIFIPLK; RVYSQWAGK; TQIFIPLKK; RSSAELIAK; VILDVNTLK; NSNSSYYGK; VVIKMDSGK; RILTGYIIK; KSNNNEVGK; DSNAWRLAK; ITIYNAVYR; KAKLQILNK; TSLNEDLDK; ILNKLENLK; NSSLYVDSK; MILAAVRDK; KSKDGKVSK; KVKEEEITK; FIYLQDELK; KVDKQLQIK; ILDVNTLKK; KATDEEHKK; SLGDLNNDK; AVYRGDLDY; STQQGIQRY; GFYIEPALK; NLMLPEDQK; PSYDDIDSK; KASSKEKSK; KLDGKKEFK; LSKASSKEK; SESNFEINK; KLDSKLDGK; SSKEKSKVK; KPGDVSSPK; QVDAKKKEK; VSEVEKLDK; DVSSPKVDK; NSNSNSSYY; ITETIENLR; KVIAALLSE; MDLEFVNYK; KTQIFIPLKK; SVDVFSISSK; VILDVNTLKK; AINLQKIDPK; LVILDVNTLK; TTSLNEDLDK; AINLDKAQQK; ASLGDLNNDK; VSESNFEINK; AVYRGDLDYY; QILNKLENLK; KMILAAVRDK; SLEDLQEQLK; ALDLDRELSK; GIQRYGIYER; ASSKEKSKVK; NMDLEFVNYK; LVVIKMDSGK; SNSNSSYYGK; SYYGKYFINR; KVITIYNAVY; KGFYIEPALK; ITDIQGETHK; EINKEKNLPK; LPFTSFSVRK; VITIYNAVYR; IVGIGEFLAR; KLDSKLDGKK; VIKMDSGKAK; IQEDINEINK; LTNSNSNSSY; EVGKLSPLDK; SQVDAKKKEK; YIIKSFDYDR; DVQRDTVREK; KNSSLYVDSK; PVSEVEKLDK; LTKENAGLSR; ILPFTSFSVR; FLNGFPLNAR; AVYRGDLDYYK; ASVDVFSISSK; SSYYGKYFINR;

		VVSESNFEINK; LVILDVNTLKK; NSNSNSSYYGK; KIQEDINEINK; KAINLQKIDPK; TIENLRDQLEK; KVITIYNAVYR; TSFSVRKNFIY; VVIKMDSGKAK; ILPFTSFSVRK; KAINLDKAQQK; KILPFTSFSVR; FLNGFPLNARK; QTTSLNEDLDK; LQILNKLENLK; NAWRLAKFSPK; RASLGDLNNDK; VNMDLEFVNYK; LTNSNSNSSYY; EVDNKAINLQK; ISKSNNNEVGK; KASSKEKSKVK; LIDLNTGVRLK; KVKEEEITKGK; KSKVKEEEITK; KSELDSILNLR; NLVILDVNTLK; NLDEFILSENK; YIEPALKSLTK; FVNMDLEFVNY; EALDLDRELSK; LSRVYSQWAGK; LSKASSKEKSK; ESLEDLQEQLK; FINRFIDDQDK; KNFIYLQDELK; SGKAKLQILNK; AGKTQIFIPLK; SLTKENAGLSR; KEFKPVSEVEK; QIVGIGEFLAR; ILDVNTLKKVK; LIFSFFLIFLN; KLPEDKKLDSK
	HLA-A2402	QWAGKTQIF; KMLLIFSFF; DYDRSSAEL; VFLEVIDPI; DFVNMDLEF; FFLIFLNGF; LYVDSKMIL; EFILSENKI; IFSFFLIFL; SFSVRKNFI; LLIFSFFLI; IYEREKDLV; GYIIKSFDY; KKMLLIFSF; YYGKYFINRF; DYDRSSAELI; QWAGKTQIFI; IYLQDELKNL; SFFLIFLNGF; IYNAVYRGDL; KFSPKNLDEF; KMLLIFSFFL; FYIEPALKSL; IYEREKDLVV; KKMLLIFSFF; MLLIFSFFLI; SYYGKYFINRF; YYGKYFINRFI; IYEREKDLVVI; KMLLIFSFFLI; YYKGFYIEPAL; TYEQIVGIGEF; IYLQDELKNLV; PYDSTNTYEQI; VYSQWAGKTQI; KFSPKNLDEFI; FFLIFLNGFPL; SFSVRKNFIYL
	HLA-A2902	GYIIKSFDY; FSVRKNFIY; AVYRGDLDY; LIAKVITIY; EFVNYKGPY; VITIYNAVY; EINKNSSLY; NMDLEFVNY; LIFSFFLIF; DFVNMDLEF; NSNSNSSYY; ENAGLSRVY; VYRGDLDYY; NLRRILTGY; KVITIYNAVY; SFSVRKNFIY; VNMDLEFVNY; ELIAKVITIY; FLIFLNGFPL; AVYRGDLDYY; KLSPLDKPSY; TGYIIKSFDY; FEINKNSSLY; SFFLIFLNGF; LLIFSFFLIF; FVNMDLEFVNY; TSFSVRKNFIY; DLEFVNYKGPY; YNAVYRGDLDY; MLLIFSFFLIF; FILSENKILPF; LTNSNSNSSYY; ILNLRRILTGY; LTGYIIKSFDY; FSFFLIFLNGF; SYYGKYFINRF; NFEINKNSSLY
	HLA-A6801	ITIYNAVYR; ITETIENLR; FIYLQDELK; NSNSSYYGK; ESTQQGIQR; NSSLYVDSK; ELDSILNLR; ETHKADQDK; IIKSFDYDR; DINEINKEK; NEAGVNFAR; DSNAWRLAK; NSNSNSSYY; VVIKMDSGK; LPFTSFSVR; EINKNSSLY; EIESQVDAK; RVYSQWAGK; EAGDENQKR; KTQIFIPLK; DVSSPKVDK; TQIFIPLKK; DVNTLKKVK; EIEKQIEIK; MILAAVRDK; FSFFLIFLN; VILDVNTLK; NLMLPEDQK; ILNKLENLK; MDLEFVNYK; EPALKSLTK; DNKAINLQK; ESQVDAKKK; YYGKYFINR; DSKEEVDNK; NGFPLNARK; NARKVDKEK; LIDLNTGVR; DLNTGVRLK; LSKASSKEK; TTMSIDSSS; DVFSISSKS; DYEALDLDR; FSVRKNFIY; ELLKSKDGK; IQRYGIYER; LIAKVITIY; EKATDEEHK; DIDSLVTDK; SKMILAAVR; TSLNEDLDK; PSYDDIDSK; NITETIENLR; YIIKSFDYDR; LVILDVNTLK; VITIYNAVYR; DSKMILAAVR; TTSLNEDLDK; SYYGKYFINR; QLIDLNTGVR; EIESQVDAKK; NFIYLQDELK; LTKENAGLSR; FLNGFPLNAR; LVVIKMDSGK; SAEDNLDVQR; ELDSILNLRR; ENEAGVNFAR; ELSKASSKEK; ILPFTSFSVR; EIEKQIEIKK; LPFTSFSVRK; EFKPVSEVEK; LTNSNSNSSY; EVEKLDKISK; SVDVFSISSK; DVQRDTVREK; EINKEKNLPK; EVGKLSPLDK; KTQIFIPLKK; IVGIGEFLAR; NSNSSYYGKY; GIQRYGIYER; SNSNSSYYGK; NMDLEFVNYK; ESTQQGIQRY; QILNKLENLK; EDINEINKEK; ELIAKVITIY; ITDIQGETHK; VILDVNTLKK; TNSNSNSSYY; MSIDSSSPVF; DVFSISSKSE; VSESNFEINK; EKATDEEHKK; SLEDLQEQLK; TGYIIKSFDY; NLQKIDPKVK; KGFYIEPALK; NLDVQRDTVR; SSYYGKYFINR; NSNSNSSYYGK; KVITIYNAVYR; DSAEDNLDVQR; DITDIQGETHK; QIVGIGEFLAR; TSFSVRKNFIY; NLVILDVNTLK; QTTSLNEDLDK; LVILDVNTLKK; LTNSNSNSSYY; DLVVIKMDSGK; EVDNKAINLQK; FLNGFPLNARK; AVYRGDLDYYK; ASVDVFSISSK; VVSESNFEINK; ESLEDLQEQLK; TIENLRDQLEK;

		EIEKQIEIKKR; EIKKRDEELLK; SNITETIENLR; EALDLDRELSK; FINRFIDDQDK; KILPFTSFSVR; ILPFTSFSVRK; EIESQVDAKKK; NAVYRGDLDYY; QGIQRYGIYER; ISKSNNNEVGK; DSKLDGKKEFK; ESQVDAKKKEK; VVIKMDSGKAK; NAWRLAKFSPK; FVNMDLEFVNY; SLTKENAGLSR; NARKVDKEKLK; NLDEFILSENK; KSELDSILNLR; GYIIKSFDYDR; VNMDLEFVNYK; ETIENLRDQLE; KAINLDKAQQK; DVFSISSKSEL; FSFFLIFLNGF; SENEAGVNFAR; YIEPALKSLTK; MSIDSSSPVFL; FSVRKNFIYLQ; LQILNKLENLK; QLEKATDEEHK; LSRVYSQWAGK
	HLA-B0702	SVRKNFIYL; KVKDQTTSL; KPVSEVEKL; RPLTNSNSN; KVSKDYEAL; GPYDSTNTY; DPITNLGTL; KPGDVSSPKV; SPKVDKQLQI; LVTDKVIAAL; SPKNLDEFIL; RPLTNSNSNS; ITKGKSRASL; RPLTNSNSNSS; SPVFLEVIDPI; LPEDKKLDSKL; DPKVKDQTTSL; AVRDKDDSNAW; DPITNLGTLQL; SPLDKPSYDDI
	HLA-B0801	EIKKRDEEL; EIKKRDEELL; ITKGKSRASL; FLIFLNGFPL; IAKVITIYNAV; DPKVKDQTTSL; YYKGFYIEPAL; NLRRILTGYII
	HLA-B1501	EQIVGIGEF; AVYRGDLDY; KMLLIFSFF; FSVRKNFIY; STQQGIQRY; LSENKILPF; TNSNSNSSY; LIAKVITIY; QGIQRYGIY; YGKYFINRF; KVKDQTTSL; NLRRILTGY; VITIYNAVY; LTGYIIKSF; LIFSFFLIF; LVILDVNTL; MSIDSSSPV; KQLQIKESL; LIFLNGFPL; NSNSNSSYY; ENAGLSRVY; SQWAGKTQIF; MSIDSSSPVF; KVITIYNAVY; ILSENKILPF; LTNSNSNSSY; KLSPLDKPSY; ILTGYIIKSF; QQGIQRYGIY; LLIFSFFLIF; ELIAKVITIY; AVYRGDLDYY; FLIFLNGFPL; LQIKESLEDL; KENAGLSRVY; YEQIVGIGEF; EQIVGIGEFL; NLKVVSESNF; LQILNKLENL; LEFVNYKGPY; TNSNSNSSYY; FTSFSVRKNF; FEINKNSSLY; KLKDFVNMDL; TMSIDSSSPV; RLKESTQQGI; ITKGKSRASL; LVTDKVIAAL; VNMDLEFVNY; TQQGIQRYGIY; TMSIDSSSPVF; YSQWAGKTQIF; LLSENEAGVNF; ILNLRRILTGY; KSKDGKVSKDY; LTNSNSNSSYY; FSFFLIFLNGF; RILTGYIIKSF; FILSENKILPF; MLLIFSFFLIF; YNAVYRGDLDY; FVNMDLEFVNY; TSFSVRKNFIY; PLTNSNSNSSY; QQKLDSAEDNL; AVRDKDDSNAW; QLIDLNTGVRL; YLQDELKNLVI
	HLA-B2705	WRLAKFSPK; RRILTGYII; YRGDLDYYK; KKMLLIFSF; QRYGIYERE; KQLQIKESL; RRILTGYIIK; QRYGIYEREK; SRVYSQWAGK; KRDEELLKSK; SQWAGKTQIF; KKMLLIFSFF; WRLAKFSPKN; RRILTGYIIKS; YRGDLDYYKGF; WRLAKFSPKNL; LRRILTGYIIK
	HLA-B3501	GPYDSTNTY; DFVNMDLEF; EFVNYKGPY; DPITNLGTL; EALDLDREL; FFLIFLNGF; LIFSFFLIF; LVILDVNTL; VITIYNAVY; FSVRKNFIY; NSNSNSSYY; LPEDQKLPE; LIAKVITIY; LPKPGDVSS; SIDSSSPVF; LSENKILPF; LPFTSFSVR; EINKNSSLY; ENAGLSRVY; LIFLNGFPL; MSIDSSSPVF; NAVYRGDLDY; KVITIYNAVY; LTNSNSNSSY; ESTQQGIQRY; LLIFSFFLIF; SPKNLDEFIL; FLIFLNGFPL; LVTDKVIAAL; ILSENKILPF; AVYRGDLDYY; SQWAGKTQIF; LSENEAGVNF; ELIAKVITIY; NLVILDVNTL; EDLDKDLTTM; NAVYRGDLDYY; FVNMDLEFVNY; YSQWAGKTQIF; YKGPYDSTNTY; TMSIDSSSPVF; SPVFLEVIDPI; FILSENKILPF; MLLIFSFFLIF; DPITNLGTLQL; LTNSNSNSSYY; FSFFLIFLNGF; WAGKTQIFIPL; FFLIFLNGFPL; TKENAGLSRVY; DPKVKDQTTSL; DLEFVNYKGPY; LPEDKKLDSKL; LLSENEAGVNF; MSIDSSSPVFL; NFEINKNSSLY
	HLA-B4403	SENEAGVNF; SELDSILNL; REIEKQIEI; GEFLARPLT; AEDNLDVQR; EEHKKEIES; KEIESQVDA; AELIAKVIT; KESLEDLQE; EEVDNKAIN; SENKILPFT; NEINKEKNL; TELDNIHES; EEVDNKAINL; EELDKKAINL; SENKILPFTS; GEFLARPLTN; AELIAKVITI; SENEAGVNFA; REKDLVVIKM; SEVEKLDKIS; FEINKNSSLY; KEKLKDFVNM; LEFVNYKGPY; EEITKGKSRA; YEQIVGIGEF; SELDSILNLR; AELIAKVITIY; EEITKGKSRAS; EEVDNKAINLQ; SENKILPFTSF;

		SENEAGVNFAR; KESLEDLQEQL; GEFLARPLTNS; EEHKKEIESQV; SELDSILNLRR; FEINKNSSLYV; DEFILSENKIL; SESNFEINKNS; EELLKSKDGKV; AEDNLDVQRDT; KESTQQGIQRY; EELDKKAINLD
	HLA-B5101	LPFTSFSVR; LPKPGDVSS; DPITNLGTL; LPFTSFSVRK; LPKPGDVSSP; SPVFLEVIDPI; LPFTSFSVRKN; LPKPGDVSSPK; SPLDKPSYDDI
	HLA-B5701	STQQGIQRY; ; NAGLSRVYSQW
NP_212375.1 | glycerol kinase (glpK) [Borrelia burgdorferi B31]; Seq27	HLA-A0101	ETTALGAAY; SVSDNGGVY; YLAGLATGY; SSDAEALAS; VSDNGGVYF; SSVSDNGGVY; FAQKEFTQIY; VSDNGGVYFV; ITETTALGAAY; ASSVSDNGGVY; LTQKKEHATDY; SSDAEALASSV
	HLA-A0201	KIMWILDNV; YVLEGSVFI; ALFGAEIPI; LLMQFQADL; VLDSYFSGT; KTLEWDDEL; MVFDKNANI; ILPNEIDAI; WILDNVEGA; GVYFVPAFV; KTDKALFGA; IILEKTGLV; SQLGVITEA; KLLENWNKA; QIYPQPSWV; YILSIDQGT; GMAKNTYGT; EIWGSQLGV; VITEAMANA; LLENWNKAV; LMQFQADLL; GIAGDQFAA; TLEWDDELL; FQSFDILNT; KLLTSIAWG; SIAFQSFDI; QLGVITEAM; FSGTKIMWI; TLLLNIKTL; TIDTWILWNL; ALGAAYLAGL; LLMQFQADLL; ALFGAEIPIA; FIGGAVIQWL; FQADLLECKV; KLLENWNKAV; KTLEWDDELL; LLSILNVPRA; GLATGYWQSA; LVLDSYFSGT; FVPAFVGLGA; KITETTALGA; FQSFDILNTM; FAATFGQACL; IILEKTGLVL; AMVFDKNANI; NLLMQFQADL; RILPNEIDAI; SIPNFEIQEL; SVTYVLEGSV; KIILEKTGLV; VSDNGGVYFV; FSGTKIMWIL; WQSAEEIVSL; SIAFQSFDIL; TQIYPQPSWV; SQLGVITEAM; NVPRAILPEL; VLDSYFSGTKI; FLTVNIGKEPI; IMWILDNVEGA; FTQIYPQPSWV; FQADLLECKVV; ILPNEIDAIGI; SVSDNGGVYFV; NTYGTGCFLTV; TLEWDDELLSI; GTIDTWILWNL; ILPELKESSTI; VITEAMANARI; VIWEKNTGKPI; KTDKALFGAEI; GVYFVPAFVGL; TMKKSIPNFEI; YLAGLATGYWQ; LLSILNVPRAI; GLGAPHWDSYA; ELLSILNVPRA; TALGAAYLAGL; NLLMQFQADLL; LLECKVVRPKI; VLEGSVFIGGA; IISHDKLLTSI; WQVDKIFEPSM; KSVTYVLEGSV; SAEEIVSLWQV; ALGAAYLAGLA; KITETTALGAA; SQLGVITEAMA; GLVLDSYFSGT
	HLA-A0301	KIFEPSMPK; ILWNLTQKK; ATFGQACLK; TSIAWGRKK; IVSLWQVDK; VIWEKNTGK; SSRAMVFDK; LTSIAWGRK; WILWNLTQK; YLAGLATGY; CFLTVNIGK; STIYGKTDK; ATFGQACLKK; LLTSIAWGRK; IIGITRGSTK; VLDSYFSGTK; AATFGQACLK; KLLTSIAWGR; QACLKKGMAK; LTSIAWGRKK; QSFDILNTMK; LLECKVVRPK; WILWNLTQKK; TVIWEKNTGK; MVFDKNANIK; ASRTLLLNIK; SSTIYGKTDK; TSSRAMVFDK; AYLAGLATGY; SFDILNTMKK; NANIKGFAQK; IVWQDRRTAK; GCFLTVNIGK; TWILWNLTQK; RTAKICDQLK; GLGAPHWDSY; DKIFEPSMPK; LLLNIKTLEW; SIDQGTTSSR; ELLSILNVPR; WLRDGLEFFR; EIVSLWQVDK; KLLTSIAWGRK; RTAKICDQLKK; LLTSIAWGRKK; TIIGITRGSTK; QSFDILNTMKK; TTSSRAMVFDK; LVLDSYFSGTK; FAATFGQACLK; GQACLKKGMAK; LLENWNKAVGK; FQSFDILNTMK; KNANIKGFAQK; AIVWQDRRTAK; MQFQADLLECK; AATFGQACLKK; QIYPQPSWVEH; AMVFDKNANIK; WLRDGLEFFRK; AAYLAGLATGY
	HLA-A1101	KIFEPSMPK; ATFGQACLK; SSRAMVFDK; TSIAWGRKK; LTSIAWGRK; STIYGKTDK; IVSLWQVDK; WILWNLTQK; ATDYSNASR; ILWNLTQKK; VIWEKNTGK; TAKICDQLK; ITEAMANAR; FQADLLECK; SVSDNGGVY; KTGLVLDSY; KESSTIYGK; SFDILNTMK; CFLTVNIGK; SMPKNQKEK; ANIKGFAQK; TFGQACLKK; LLSILNVPR; GSTKAHITR; VWQDRRTAK; ATFGQACLKK; TSSRAMVFDK; MVFDKNANIK; TVIWEKNTGK; QSFDILNTMK; RTAKICDQLK; AATFGQACLK; LTSIAWGRKK; VLDSYFSGTK; ASRTLLLNIK; QACLKKGMAK; SSTIYGKTDK; NANIKGFAQK; LLTSIAWGRK; IVWQDRRTAK; WILWNLTQKK; IIGITRGSTK; TWILWNLTQK; TAKICDQLKK; SFDILNTMKK;

		SIDQGTTSSR; KLLTSIAWGR; QFQADLLECK; VITEAMANAR; EIVSLWQVDK; LLECKVVRPK; PSMPKNQKEK; GCFLTVNIGK; TTSSRAMVFDK; QSFDILNTMKK; LVLDSYFSGTK; TIIGITRGSTK; RTAKICDQLKK; KLLTSIAWGRK; MQFQADLLECK; TTVIWEKNTGK; AATFGQACLKK; AIVWQDRRTAK; KICDQLKKEGK; AMVFDKNANIK; GQACLKKGMAK; GVITEAMANAR; TGCFLTVNIGK; NASRTLLLNIK; FAATFGQACLK; NVPRAILPELK; FQSFDILNTMK; AAYLAGLATGY; TWILWNLTQKK; DTWILWNLTQK; SIPNFEIQELR; LLTSIAWGRKK; LSIDQGTTSSR; LLENWNKAVGK; WLRDGLEFFRK; KNANIKGFAQK; ASQNNLLMQFQ
	HLA-A2402	QWLRDGLEF; TYVLEGSVF; DYSNASRTL; IWGSQLGVI; IYGKTDKAL; CFGTIDTWI; IYPQPSWVE; YWQSAEEIV; EWDDELLSI; YFVPAFVGL; TYGTGCFLT; GYWQSAEEI; IYGKTDKALF; QWLRDGLEFF; TYVLEGSVFI; SYARGTIIGI; DYSNASRTLL; TYGTGCFLTV; VWQDRRTAKI; VYFVPAFVGL; SWVEHDPTEI; YFSGTKIMWI; IWEKNTGKPI; SYFSGTKIMW; CFGTIDTWIL; GFAQKEFTQI; IYNAIVWQDR; DYSNASRTLLL; SYFSGTKIMWI; YWQSAEEIVSL; YFSGTKIMWIL; AYLAGLATGYW; VFIGGAVIQWL; VFDKNANIKGF
	HLA-A2902	YLAGLATGY; SVSDNGGVY; ETTALGAAY; ELKESSTIY; QWLRDGLEF; FAQKEFTQIY; AYLAGLATGY; SVSDNGGVYF; SSVSDNGGVY; VTYVLEGSVF; AWGRKKSVTY; GFAQKEFTQIY; ITETTALGAAY; AAYLAGLATGY; IWEKNTGKPIY
	HLA-A6801	DAIGITNQR; ATFGQACLK; LLTSIAWGR; ITEAMANAR; STIYGKTDK; NAIVWQDRR; TAKICDQLK; ETTALGAAY; TSIAWGRKK; LTSIAWGRK; IVSLWQVDK; LLSILNVPR; ATDYSNASR; SSRAMVFDK; WILWNLTQK; EPSMPKNQK; GSTKAHITR; NTYGTGCFL; ESIAFQSFD; DLLECKVVR; TTSSRAMVF; FDILNTMKK; GGAVIQWLR; KIFEPSMPK; YNAIVWQDR; TTALGAAYL; CFLTVNIGK; PNFEIQELR; FQADLLECK; APHWDSYAR; DNVEGARQR; YLAGLATGY; ILDNVEGAR; ENWNKAVGK; MVFDKNANIK; HATDYSNASR; TVIWEKNTGK; QSFDILNTMK; TSSRAMVFDK; ATFGQACLKK; EIVSLWQVDK; RTAKICDQLK; ELLSILNVPR; IPNFEIQELR; VITEAMANAR; AATFGQACLK; NANIKGFAQK; LLTSIAWGRK; WLRDGLEFFR; LTSIAWGRKK; TAKICDQLKK; YNAIVWQDRR; WILDNVEGAR; IYNAIVWQDR; TWILWNLTQK; SIDQGTTSSR; NTYGTGCFLT; SSTIYGKTDK; IVWQDRRTAK; WILWNLTQKK; GAPHWDSYAR; TTALGAAYLA; IDAIGITNQR; IGGAVIQWLR; QACLKKGMAK; ETTALGAAYL; EGKDKIILEK; TTSSRAMVFD; KLLTSIAWGR; DKIFEPSMPK; TTSSRAMVFDK; QSFDILNTMKK; FAATFGQACLK; TTVIWEKNTGK; SIPNFEIQELR; EIDAIGITNQR; TIIGITRGSTK; FIGGAVIQWLR; ESSTIYGKTDK; LSIDQGTTSSR; GVITEAMANAR; DTWILWNLTQK; RTAKICDQLKK; MWILDNVEGAR; IYNAIVWQDRR; MQFQADLLECK; YARGTIIGITR; NVPRAILPELK; LVLDSYFSGTK; ELKESSTIYGK; EHATDYSNASR; NASRTLLLNIK; TGCFLTVNIGK; LLTSIAWGRKK; FQSFDILNTMK; EPSMPKNQKEK; QADLLECKVVR; AATFGQACLKK; TWILWNLTQKK; ETTALGAAYLA; EEIVSLWQVDK; NTMKKSIPNFE; AIVWQDRRTAK; PIYNAIVWQDR; LGAPHWDSYAR; TIYGKTDKALF; ILDNVEGARQR; QWLRDGLEFFR
	HLA-B0702	KAHITRAAL; KPIYNAIVW; VPRAILPEL; MPKNQKEKL; RAALESIAF; RPKITETTA; VPAFVGLGA; AAYLAGLAT; IPNFEIQEL; EPIISHDKL; LPELKESST; IAWGRKKSV; RPKITETTAL; MPKNQKEKLL; LPELKESSTI; DPTEIWGSQL; VPAFVGLGAP; TKAHITRAAL; SVSDNGGVYF; EPIISHDKLL; IPIAGIAGDQF; GARQRAENGEL; VPAFVGLGAPH; APHWDSYARGT; FFRKSSDAEAL; WGRKKSVTYVL; IVWQDRRTAKI; RPKITETTALG; STKAHITRAAL
	HLA-B0801	KAHITRAAL; MPKNQKEKL; RKKSVTYVL; RPKITETTAL;

		FRKSSDAEAL; MPKNQKEKLL; WGRKKSVTYV; WGRKKSVTYVL; FFRKSSDAEAL
	HLA-B1501	AQKEFTQIY; YLAGLATGY; RQRAENGEL; SVSDNGGVY; RAALESIAF; TMKKSIPNF; SQNNLLMQF; WLRDGLEFF; ELKESSTIY; TQIYPQPSW; ETTALGAAY; NQRETTVIW; WGRKKSVTY; ITRGSTKAH; TTSSRAMVF; SLWQVDKIF; QSFDILNTM; SVFIGGAVI; QSAEEIVSL; LGAPHWDSY; WQSAEEIVS; YSNASRTLL; GGVYFVPAF; IQWLRDGLEF; WQSAEEIVSL; TQKKEHATDY; SQLGVITEAM; SVSDNGGVYF; FQSFDILNTM; VTYVLEGSVF; SSVSDNGGVY; GLGAPHWDSY; YLAGLATGYW; FAQKEFTQIY; WEKNTGKPIY; YSNASRTLLL; IAGDQFAATF; RQRAENGELC; ALESIAFQSF; NIKGFAQKEF; ASQNNLLMQF; RQRAENGELCF; ITRAALESIAF; WQVDKIFEPSM; IQWLRDGLEFF; ASSVSDNGGVY; MAKNTYGTGCF; WQSAEEIVSLW; ITETTALGAAY; IVSLWQVDKIF; AAYLAGLATGY; GIAGDQFAATF; IAWGRKKSVTY; AALESIAFQSF; FQADLLECKVV; SVTYVLEGSVF; VIQWLRDGLEF; SSVSDNGGVYF; LTQKKEHATDY; AQKEFTQIYPQ; CLKKGMAKNTY; STKAHITRAAL; GFAQKEFTQIY
	HLA-B2705	RKKSVTYVL; GRKKSVTYVL; QRAENGELCF; RRTAKICDQL; TRAALESIAF; QRETTVIWEK; LRDGLEFFRK; ARGTIIGITR; RRTAKICDQLK; GQACLKKGMAK; RQRAENGELCF
	HLA-B3501	RAALESIAF; IPNFEIQEL; ETTALGAAY; SVSDNGGVY; YPQPSWVEH; LPNEIDAIG; IAFQSFDIL; YLAGLATGY; FAATFGQAC; YFVPAFVGL; IAGDQFAAT; QSFDILNTM; IAGIAGDQF; KPIYNAIVW; HATDYSNAS; MPKNQKEKL; SLWQVDKIF; RAENGELCF; ELKESSTIY; EKNTGKPIY; TYVLEGSVF; APHWDSYAR; QLGVITEAM; LESIAFQSF; YVLEGSVFI; GASQNNLLM; LGAPHWDSY; EAMANARIL; VPRAILPEL; AAYLAGLAT; TTSSRAMVF; TLEWDDELL; EPIISHDKL; VSDNGGVYF; FAQKEFTQIY; IAGDQFAATF; FAATFGQACL; QPSWVEHDPT; LPNEIDAIGI; FQSFDILNTM; SVSDNGGVYF; TETTALGAAY; RPKITETTAL; SSVSDNGGVY; MPKNQKEKLL; EPIISHDKLL; VSLWQVDKIF; TRAALESIAF; NGGVYFVPAF; IQWLRDGLEF; DPTEIWGSQL; SQLGVITEAM; DSYFSGTKIM; QVDKIFEPSM; LPELKESSTI; LPELKESSTIY; IPIAGIAGDQF; IAWGRKKSVTY; VPAFVGLGAPH; LPNEIDAIGIT; AAYLAGLATGY; MAKNTYGTGCF; ITETTALGAAY; AALESIAFQSF; TALGAAYLAGL; IVSLWQVDKIF; QPSWVEHDPTE; ASSVSDNGGVY; WQVDKIFEPSM; ITRAALESIAF; SVTYVLEGSVF; MANARILPNEI; SSVSDNGGVYF; YFSGTKIMWIL; APHWDSYARGT; FFRKSSDAEAL; GASQNNLLMQF
	HLA-B4403	AEIPIAGIA; EEIVSLWQV; NEIDAIGIT; KEFTQIYPQ; AEALASSVS; AEEIVSLWQ; QELRVDGGA; TEIWGSQLG; DELLSILNV; AEIPIAGIAG; TEIWGSQLGV; AEEIVSLWQV; NEIDAIGITN; TETTALGAAY; EEIVSLWQVD; AENGELCFGT; KEFTQIYPQP; QELRVDGGAS; KEFTQIYPQPS; AEIPIAGIAGD; NEIDAIGITNQ; TEIWGSQLGVI; KEPIISHDKLL; AENGELCFGTI; TETTALGAAYL; KEHATDYSNAS; GELCFGTIDTW
	HLA-B5101	VPAFVGLGA; VPRAILPEL; LPNEIDAIG; LPELKESSTI; EPIISHDKLL; LPNEIDAIGIT; IPIAGIAGDQF; IPNFEIQELRV
	HLA-B5701	GTIDTWILW; SAEEIVSLW; KTGLVLDSY; LCFGTIDTW; FTQIYPQPSW; QSAEEIVSLW; TNQRETTVIW; FAQKEFTQIY; ITNQRETTVIW; TGKPIYNAIVW,; DSYFSGTKIMW; KNQKEKLLENW
NP_212342.1 | hypothetical protein BB0208 [Borrelia	HLA-A0101	YIEEKVLKY; NTSLEECYY; YSQEKKDIY; ESSIFKERY; LIEIQNSPY; NTKKLGTTY; ESFIDALEY; LSFYPNIEY; SSKNISFNY; ETYGWIAFY; QTEDFFISF; TLSLNEIFY; FQDTLKCYLY; GSSKNISFNY; FLSFYPNIEY; LIEIQNSPYY; KTLSLNEIFY; KTIKKDSEFY; ATLKKHINKY; YLEEEILALKY; NIETYGWIAFY; KSAFLEIIMHY; NLNTKKLGTTY;

burgdorferi B31]; Seq28		ETYGWIAFYIY; ISFDKTNFNPY
	HLA-A0201	FISDILLYL; MLILTYWPV; YLEEEILAL; FLEIIMHYV; KLLPAMCYL; YLIYCENLV; YLDENKITI; LLPAMCYLI; QTIDILVAV; YLYVIEKTI; KLINIKEKI; SISSQLYKL; YIKSAFLEI; YLLIKSLKT; FFSDFTQYA; TLKCYLYVI; FISFFKTKL; FQDTLKCYL; ILIKXYKYL; SLLEFISFF; IILNFSSNI; KTFEIQNQI; AIKKWILEI; YFLSFYPNI; SLEQTIDIL; QLDYQKSYL; ILALKYNEI; SFIDALEYI; LLYLDENKI; LALKYNEIL; FQTEDFFIS; RMLILTYWPV; KLLPAMCYLI; YLTWFFKDKI; LIYCENLVEL; YLRALKTLSL; SLEQTIDILV; AFLEIIMHYV; CLSKNIFIKI; IQNQIFVYFL; ILNFSSNINI; KXYKYLEEEI; ILTYWPVGCL; QLDYQKSYLL; HINKYIEEKV; ETYGWIAFYI; KFISDILLYL; KLKSSNFLKL; RILKIIIKNI; KLEKPEIIEL; ILALKYNEIL; YFFSDFTQYA; YIKSAFLEII; QLYKLEKPEI; ILLYLDENKI; AIKKWILEIV; KILNILNKNL; KILIKXYKYL; NQLDYQKSYL; KISNNWESFI; YGWIAFYIYA; IIIKNIRFNL; YSISSQLYKL; YLYVIEKTIT; SLLEFISFFK; LLEFISFFKT; FIQISKEANL; VLKYSISSQL; ALKTLSLNEI; RLIKLKRMLI; FSSNINIDSL; YLIYCENLVEL; FQDTLKCYLYV; KTFEIQNQIFV; FVYFLSFYPNI; SLLEFISFFKT; SAFLEIIMHYV; AMCYLIYCENL; IILNFSSNINI; KVLKYSISSQL; NQLDYQKSYLL; YIEEKVLKYSI; QLDYQKSYLLI; LLYLDENKITI; KIIIKNIRFNL; ALKYNEILNYL; KLEKPEIIELI; KXYKYLEEEIL; RLIKLKRMLIL; KLKSSNFLKLI; LILTYWPVGCL; FKFISDILLYL; KRMLILTYWPV; QLYKLEKPEII; ILNYLRALKTL; KQIILNFSSNI; LLPAMCYLIYC; YIYADNKDKKI; CLSKNIFIKIL; YKLEKPEIIEL; KLEDENEKKLL; YQKSYLLIKSL; SQLYKLEKPEI; IIIKNIRFNLI
	HLA-A0301	KLKSSNFLK; ILNYLRALK; ISFFKTKLK; LLEFISFFK; KLKQKINFK; KLGTTYKLK; CLSKNIFIK; LSLNEIFYK; YSISSQLYK; RMKEFFKSK; NIFIKILIK; ATLKKHINK; KIKEIITAK; EIFYKGSSK; HINKYIEEK; SIFKERYIK; KINPNQLDY; KKYLTWFFK; ITIPKKIIK; VIEKTITKK; ETYGWIAFY; LVAVRNRNK; KCYLYVIEK; ILNKNLKYR; YVIEKTITK; VFKSSLTNK; TLSLNEIFY; KFISDILLY; TLKKHINKY; SFYPNIEYK; CQPMKEFFK; FIIMHYVKK; NIRFNLIFK; SSKNISFNY; KILIKXYKY;

		LKYSISSQLYK; EFYDSLATLKK; LLIKSLKTRSR; IFCQRMKEFFK; NFNPYESSIFK; ISFDKTNFNPY; NLNTKKLGTTY; YLDENKITIPK; QISKEANLNTK; ETYGWIAFYIY; SEFYDSLATLK; AFLEIIMHYVK; HFKFISDILLY; KYLEEEILALK; WIAFYIYADNK
	HLA-A1101	SSQLYKLEK; ATLKKHINK; YSISSQLYK; SIFKERYIK; TSLEECYYK; LSLNEIFYK; LLEFISFFK; ISFFKTKLK; KLKSSNFLK; ILNYLRALK; YVIEKTITK; KKYLTWFFK; ITIPKKIIK; NTQNEAIKK; NIFIKILIK; SSKNISFNY; SFYPNIEYK; HINKYIEEK; AFYIYADNK; RMKEFFKSK; LVAVRNRNK; ETYGWIAFY; SYLLIKSLK; EIIMHYVKK; ISNDYEKEK; KLKQKINFK; KIKEIITAK; CLSKNIFIK; CQRMKEFFK; SQEKKDIYK; NPYESSIFK; EIFYKGSSK; KCYLYVIEK; YQKSYLLIK; VIEKTITKK; ILLYLDENK; LVELKNNRK; YIYADNKDK; KLGTTYKLK; NIRFNLIEK; TLSLNEIFY; YLTWFFKDK; LSFYPNIEY; SPYYSQEKK; KILIKXYKY; WILEIVRNK; NSPYYSQEK; AVRNRNKIK; KYIEEKVLK; SSLTNKESR; SDFTQYAPK; VFKSSLTNK; KFISDILLY; KINPNQLDY; TIDILVAVR; ALEYIEKHK; SAFLEIIMH; SLLEFISFFK; KVFKSSLTNK; KSYLLIKSLK; TLSLNEIFYK; SSIFKERYIK; LSFYPNIEYK; KINFKKELMK; IAFYIYADNK; ISSQLYKLEK; KIKILNILNK; YVIEKTITKK; QIFVYFLSFY; LTNKESRLIK; KTLSLNEIFY; NTSLEECYYK; SLKTRSRILK; SAFLEIIMHY; ILNILNKNLK; KYSISSQLYK; FISFFKTKLK; YIYADNKDKK; YSQEKKDIYK; ILVAVRNRNK; KLKQKINFKK; KISNDYEKEK; FSDFTQYAPK; KITIPKKIIK; NTKKLGTTYK; EILNYLRALK; FIDALEYIEK; QTIDILVAVR; ISKEANLNTK; LATLKKHINK; SFFKTKLKQK; KTIKKDSEFY; GSSKNISFNY; KNIRFNLIEK; RSRILKIIIK; KYLTWFFKDK; LIKISNDYEK; TKKYLTWFFK; ATLKKHINKY; KLINIKEKIK; KNIFIKILIK; IYCENLVELK; FLEIIMHYVK; EFYDSLATLK; TYWPVGCLSK; YLEEEILALK; FIKILIKXYK; TEDFFISFDK; KSSLTNKESR; VAVRNRNKIK; KLIEIQNSPY; KYNEILNYLR; DILLYLDENK; NSPYYSQEKK; FVYFLSFYPN; KWILEIVRNK; LEFISFFKTK; KTLSLNEIFYK; LTYWPVGCLSK; SISSQLYKLEK; KSLKTRSRILK; NSLLEFISFFK; ITKKYLTWFFK; KILNILNKNLK; QTEDFFISFDK; KINPNQLDYQK; LIYCENLVELK; ISFFKTKLKQK; SLATLKKHINK; TLKCYLYVIEK; IQNSPYYSQEK; KTKLKQKINFK; SLTNKESRLIK; WIAFYIYADNK; TIPKKIIKIQK; SFIDALEYIEK; AFLEIIMHYVK; KSAFLEIIMHY; IFCQRMKEFFK; ISFDKTNFNPY; YLYVIEKTITK; FLSFYPNIEYK; SEFYDSLATLK; QISKEANLNTK; TYKLKSSNFLK; ISKEANLNTKK; LLEFISFFKTK; LVAVRNRNKIK; ETYGWIAFYIY; IFIKILIKXYK; KYLEEEILALK; YLDENKITIPK; NQIFVYFLSFY; KLIEIQNSPYY; NFNPYESSIFK; ESSIFKERYIK; LKYSISSQLYK; EFYDSLATLKK; AFYIYADNKDK; ELIKISNDYEK; FLEIIMHYVKK; AIKKWILEIVR; FFSDFTQYAPK; LVELKNNRKIK; KKYLTWFFKDK; RILKIIIKNIR; YIEKHKLINIK; KLLPAMCYLIY; VGCLSKNIFIK; CQRMKEFFKSK; SKNIFIKILIK; TIDILVAVRNR; YAPKDFQDTLK
	HLA-A2402	DYQKSYLLI; TYGWIAFYI; IYKQIILNF; TYKLKSSNF; KFQTEDFFI; EYIEKHKLI; YFLSFYPNI; NYLRALKTL; XYKYLEEEI; KYNEILNYL; IYCENLVEL; KYSISSQLY; RYIKSAFLE; SFNYFFSDF; DYEKEKNAF; FFKSKTFEI; SYLLIKSLK; FYKGSSKNI; TFEIQNQIF; KYLTWFFKD; SFIDALEYI; LYKLEKPEI; IQNQIFVYF; CYLIYCENL; FYDSLATLK; TKKYLTWFF; IFCQRMKEF; RYIKSAFLEI; FYPNIEYKHF; VYFLSFYPNI; CYLYVIEKTI; YYKNTQNEAI; TYKLKSSNFL; LYLDENKITI; HYVKKNSQNI; IYADNKDKKI; KYLEEEILAL; TYGWIAFYIY; KYRPENQKVF; NQIFVYFLSF; KFISDILLYL; LYKLEKPEII; XYKYLEEEIL; KYLTWFFKDK; CYLIYCENLV; DYQKSYLLIK; IFCQRMKEFF; ITKKYLTWFF; FFISFDKTNF; IYCENLVELK; EFFKSKTFEI; KYSISSQLYK; NFNPYESSIF; KYIEEKVLKY; KYNEILNYLR; RYIKSAFLEII; KYLTWFFKDKI; KYSISSQLYKL; KFQTEDFFISF;

		EYIEKHKLINI; NYLRALKTLSL; IYADNKDKKIF; CYYKNTQNEAI; FYKGSSKNISF; QYAPKDFQDTL; YWPVGCLSKNI; EYKHFKFISDI; IFKERYIKSAF; SFYPNIEYKHF; FYPNIEYKHFK; TYKLKSSNFLK; TYGWIAFYIYA; KYLEEEILALK; KTITKKYLTWF; TITKKYLTWFF; IIIKNIRFNLI; SSKNISFNYFF; YYKNTQNEAIK; FYIYADNKDKK; ITAKFQTEDFF
	HLA-A2902	YFFSDFTQY; KFISDILLY; EIQNQIFVY; LSFYPNIEY; YIEEKVLKY; NILNKNLKY; SSKNISFNY; ESFIDALEY; AFLEIIMHY; IFVYFLSFY; KINPNQLDY; TLSLNEIFY; ELIKISNDY; KILIKXYKY; KYSISSQLY; ETYGWIAFY; YGWIAFYIY; NTKKLGTTY; NTSLEECYY; KNISFNYFF; FNTSLEECY; FVYFLSFYP; QIFVYFLSF; IEIQNSPYY; FYPNIEYKH; LIEIQNSPY; FIKILIKXY; FISFDKTNF; NYFFSDFTQY; KYIEEKVLKY; KLIEIQNSPY; TYGWIAFYIY; IFIKILIKXY; FEIQNQIFVY; FLSFYPNIEY; QIFVYFLSFY; SAFLEIIMHY; FFISFDKTNF; SFDKTNFNPY; YYSQEKKDIY; FYPNIEYKHF; KTLSLNEIFY; FNTSLEECYY; LLPAMCYLIY; FQDTLKCYLY; QKINPNQLDY; KLKRMLILTY; FKFISDILLY; KTIKKDSEFY; LNILNKNLKY; IKILIKXYKY; VIEKTITKKY; GSSKNISFNY; ALKYNEILNY; AFNTSLEECY; EIQNQIFVYF; LIEIQNSPYY; YFLSFYPNIEY; YLEEEILALKY; YVIEKTITKKY; ILNILNKNLKY; KLIEIQNSPYY; TFEIQNQIFVY; FNYFFSDFTQY; HFKFISDILLY; KSAFLEIIMHY; NLNTKKLGTTY; ISFDKTNFNPY; NQIFVYFLSFY; FIKILIKXYKY; KLLPAMCYLIY; NAFNTSLEECY; NWESFIDALEY; PYYSQEKKDIY; DFQDTLKCYLY; ETYGWIAFYIY; AFNTSLEECYY; KGSSKNISFNY; KFQTEDFFISF; PYESSIFKERY; SFYPNIEYKHF; NIFIKILIKXY; NIETYGWIAFY; IIELIKISNDY
	HLA-A6801	ETYGWIAFY; YSISSQLYK; LLEFISFFK; HINKYIEEK; EIIMHYVKK; EIFYKGSSK; EDFFISFDK; YVIEKTITK; ISFFKTKLK; NSPYYSQEK; ESRLIKLKR; NPYESSIFK; SIFKERYIK; ESFIDALEY; ILNYLRALK; EFISFFKTK; NLVELKNNR; NTQNEAIKK; TSLEECYYK; LSLNEIFYK; SFYPNIEYK; NTSLEECYY; YIYADNKDK; YNEILNYLR; NIRFNLIEK; NPNQLDYQK; ESSIFKERY; SPYYSQEKK; LVAVRNRNK; NIFIKILIK; CLSKNIFIK; ITIPKKIIK; TIDILVAVR; YLTWFFKDK; SSQLYKLEK; SSLTNKESR; SYLLIKSLK; LSFYPNIEY; SSKNISFNY; IFVYFLSFY; DILVAVRNR; EIQNQIFVY; ILNKNLKYR; FVYFLSFYP; ISNDYEKEK; NKNFIQISK; YESSIFKER; LNILNKNLK; ELIKISNDY; NYFFSDFTQ; TLSLNEIFY; FYDSLATLK; YFFSDFTQY; KLKSSNFLK; LVELKNNRK; LLIKSLKTR; TIKKDSEFY; IYADNKDKK; IKILIKXYK; NISFNYFFS; ILLYLDENK; ELKNNRKIK; IKISNDYEK; WILEIVRNK; ENKITIPKK; DENKITIPK; AFYIYADNK; KIKEIITAK; LKIIIKNIR; CQRMKEFFK; LEIIMHYVK; QTIDILVAVR; NTSLEECYYK; EFYDSLATLK; IAFYIYADNK; LSFYPNIEYK; YVIEKTITKK; FISFFKTKLK; SLLEFISFFK; EILNYLRALK; TLSLNEIFYK; YIYADNKDKK; NTKKLGTTYK; ETYGWIAFYI; NSPYYSQEKK; SSIFKERYIK; LIKISNDYEK; QIFVYFLSFY; SAFLEIIMHY; FIKILIKXYK; NYFFSDFTQY; FLEIIMHYVK; NILNKNLKYR; KSYLLIKSLK; DALEYIEKHK; KVFKSSLTNK; YPNIEYKHFK; ISSQLYKLEK; LTNKESRLIK; DILLYLDENK; KYNEILNYLR; ILVAVRNRNK; NLVELKNNRK; TKKYLTWFFK; FYIYADNKDK; ILNILNKNLK; LIKSLKTRSR; LATLKKHINK; FSDFTQYAPK; ILKIIIKNIR; YSQEKKDIYK; FIDALEYIEK; IYCENLVELK; NLKYRPENQK; KSSLTNKESR; YLEEEILALK; FNPYESSIFK; TTYKLKSSNF; EKIKEIITAK; ISKEANLNTK; FLSFYPNIEY; QNSPYYSQEK; TYGWIAFYIY; TYWPVGCLSK; TEDFFISFDK; SFFKTKLKQK; FVYFLSFYPN; NEIFYKGSSK; IDILVAVRNR; FNYFFSDFTQ; LTYWPVGCLS; IPKKIIKIQK; YKLKSSNFLK; KTIKKDSEFY; SLKTRSRILK; DENKITIPKK; LYVIEKTITK; ETYGWIAFYIY; ELIKISNDYEK; WIAFYIYADNK; ESSIFKERYIK; LTYWPVGCLSK;

		QTEDFFISFDK; FLSFYPNIEYK; EFYDSLATLKK; NSLLEFISFFK; NPYESSIFKER; ITKKYLTWFFK; EFISFFKTKLK; LIYCENLVELK; FYPNIEYKHFK; NFNPYESSIFK; YLYVIEKTITK; ISFFKTKLKQK; SISSQLYKLEK; KTLSLNEIFYK; FYIYADNKDKK; TLKCYLYVIEK; NQIFVYFLSFY; IFIKILIKXYK; FNTSLEECYYK; NAFNTSLEECY; TYKLKSSNFLK; IFCQRMKEFFK; EQTIDILVAVR; QISKEANLNTK; YAPKDFQDTLK; LKYNEILNYLR; FFSDFTQYAPK; SFIDALEYIEK; TIPKKIIKIQK; FNYFFSDFTQY; LKYSISSQLYK; TTYKLKSSNFL; TIDILVAVRNR; LLEFISFFKTK; LVAVRNRNKIK; FLEIIMHYVKK; LNILNKNLKYR; SEFYDSLATLK; DNKDKKIFCQR; LLIKSLKTRSR; NEILNYLRALK; YVIEKTITKKY; RILKIIIKNIR; ISFDKTNFNPY; SLATLKKHINK; YYSQEKKDIYK; FKSSLTNKESR; ITAKFQTEDFF; ISKEANLNTKK; LIEKLEDENEK; KTKLKQKINFK; ESFIDALEYIE; KINPNQLDYQK; YYKNTQNEAIK; KSAFLEIIMHY; YIEKHKLINIK; NIETYGWIAFY; INKYIEEKVLK; SYLLIKSLKTR; AIKKWILEIVR; DILVAVRNRNK; SSKNISFNYFF; HFKFISDILLY; KILNILNKNLK; QKSYLLIKSLK; NKIKILNILNK; LYVIEKTITKK; SLTNKESRLIK; ISFNYFFSDFT; QNSPYYSQEKK; FSSNINIDSLE; LSFYPNIEYKH; CENLVELKNNR
	HLA-B0702	APKDFQDTL; KERYIKSAF; YPNIEYKHF; VAVRNRNKI; AVRNRNKIKI; YLRALKTLSL; IVRNKNFIQI; WPVGCLSKNI; LPAMCYLIYC; AVRNRNKIKIL; WPVGCLSKNIF; SPYYSQEKKDI; YPNIEYKHFKF; RPENQKVFKSS; APKDFQDTLKC; IPKKIIKIQKI; KVLKYSISSQL
	HLA-B0801	SLKTRSRIL; FFKSKTFEI; LIKLKRMLI; RLIKLKRML; YLYVIEKTI; ILIKXYKYL; YIKSAFLEI; YLRALKTLSL; LIKLKRMLIL; FFKTKLKQKI; ILALKYNEIL; YIKSAFLEII; YYKNTQNEAI; FKERYIKSAF; IFKERYIKSAF; RMKEFFKSKTF; RLIKLKRMLIL; YIKSAFLEIIM; IPKKIIKIQKI; YQKSYLLIKSL
	HLA-B1501	LSFYPNIEY; IQNQIFVYF; NQLDYQKSY; QIFVYFLSF; SSKNISFNY; SLLEFISFF; FIKILIKXY; YLEEEILAL; ETYGWIAFY; KISNNWESF; TLKKHINKY; KTIKKDSEF; KINPNQLDY; ELIKISNDY; NTKKLGTTY; ESFIDALEY; LIEIQNSPY; IQISKEANL; YSQEKKDIY; YIEEKVLKY; IQKINPNQL; NQKVFKSSL; YFFSDFTQY; IEIQNSPYY; AFLEIIMHY; KFISDILLY; QTEDFFISF; TQNEAIKKW; KIIIKNIRF; KQIILNFSS; IETYGWIAF; TLSLNEIFY; KNSQNIETY; FDKTNFNPY; SQNIETYGW; KLIEIQNSPY; FQTEDFFISF; NQIFVYFLSF; KTFEIQNQIF; KLKRMLILTY; FLSFYPNIEY; YLRALKTLSL; ALKYNEILNY; KIKEIITAKF; SSKNISFNYF; SAFLEIIMHY; ISFNYFFSDF; QIFVYFLSFY; KQKINFKKEL; LLPAMCYLIY; KTIKKDSEFY; IQNQIFVYFL; FEIQNQIFVY; KIFCQRMKEF; IFIKILIKXY; ITAKFQTEDF; GSSKNISFNY; FQDTLKCYLY; WESFIDALEY; VLKYSISSQL; RMKEFFKSKTF; ISFDKTNFNPY; YVIEKTITKKY; KLIEIQNSPYY; IQKINPNQLDY; VLKYSISSQLY; YQKSYLLIKSL; QNIETYGWIAF; KSNEKNSLLEF; NQIFVYFLSFY; YLEEEILALKY; ILNILNKNLKY; IFKERYIKSAF; KSAFLEIIMHY; ALKTLSLNEIF; KLLPAMCYLIY; ILKIIIKNIRF; YFLSFYPNIEY; WILEIVRNKNF; KQIILNFSSNI; YLIYCENLVEL; SSKNISFNYFF; ETYGWIAFYIY; FYKGSSKNISF; FIKILIKXYKY; NLNTKKLGTTY; KQKINFKKELM; TNFNPYESSIF; KFQTEDFFISF; NAFNTSLEECY; TQNEAIKKWIL; GSSKNISFNYF; HFKFISDILLY
	HLA-B2705	SRILKIIIK; LRALKTLSL; KRMLILTYW; IRFNLIEKL; KKLGTTYKL; ERYIKSAFL; YRPENQKVF; SRLIKLKRM; KKWILEIVR; KKYLTWFFK; QRMKEFFKSK; KRMLILTYWP; SRLIKLKRML; YRPENQKVFK; KKLGTTYKLK; NQIFVYFLSF; NRNKIKILNI; KRMLILTYWPV; VRNKNFIQISK; KKWILEIVRNK; SRLIKLKRMLI; SRILKIIIKNI
	HLA-B3501	LPAMCYLIY; YGWIAFYIY; YPNIEYKHF; YFFSDFTQY; LIEIQNSPY; FDKTNFNPY; EIQNQIFVY; ETYGWIAFY; ESFIDALEY; TFEIQNQIF;

		YLEEEILAL; TAKFQTEDF; LSFYPNIEY; IFVYFLSFY; QTEDFFISF; QIFVYFLSF; EFYDSLATL; NSLLEFISF; IQNQIFVYF; FISFDKTNF; YSQEKKDIY; LALKYNEIL; TLSLNEIFY; IEIQNSPYY; APKDFQDTL; IETYGWIAF; NTKKLGTTY; YIEEKVLKY; FLSFYPNIEY; NIETYGWIAF; WESFIDALEY; YADNKDKKIF; FEIQNQIFVY; NFNPYESSIF; TAKFQTEDFF; SAFLEIIMHY; LIEIQNSPYY; FQTEDFFISF; TYGWIAFYIY; FFISFDKTNF; SFDKTNFNPY; FKFISDILLY; YAPKDFQDTL; EIQNQIFVYF; NYFFSDFTQY; KLIEIQNSPY; NPNQLDYQKS; QIFVYFLSFY; WPVGCLSKNI; YYSQEKKDIY; NNWESFIDAL; FKERYIKSAF; LPAMCYLIYC; FSSNINIDSL; YESSIFKERY; WPVGCLSKNIF; NPNQLDYQKSY; YPNIEYKHFKF; NAFNTSLEECY; ETYGWIAFYIY; ISFDKTNFNPY; TFEIQNQIFVY; YFLSFYPNIEY; YVIEKTITKKY; NIETYGWIAFY; LALKYNEILNY; YLEEEILALKY; YIKSAFLEIIM; LATLKKHINKY; FEIQNQIFVYF; FNYFFSDFTQY; NLNTKKLGTTY; LKLIEIQNSPY; YLIYCENLVEL; HFKFISDILLY
	HLA-B4403	EEEILALKY; SEFYDSLAT; IEIQNSPYY; NEILNYLRA; EEILALKYN; FEIQNQIFV; KEFFKSKTF; NEKNSLLEF; LEIVRNKNF; IETYGWIAF; NEIFYKGSS; KEIITAKFQ; FEIQNQIFVY; SEFYDSLATL; NEILNYLRAL; KEIITAKFQT; WESFIDALEY; EEILALKYNE; IEIQNSPYYS; EEILALKYNEI; FEIQNQIFVYF; KEFFKSKTFEI; NEKKLLPAMCY; SEFYDSLATLK; EEKVLKYSISS; DENEKKLLPAM; NEILNYLRALK
	HLA-B5101	LPAMCYLIY; WPVGCLSKNI; LPAMCYLIYC; KPEIIELIKI; IPKKIIKIQKI; WPVGCLSKNIF; SPYYSQEKKDI
	HLA-B5701	KTLSLNEIF; TITKKYLTW; NTKKLGTTY; KTITKKYLTW; NSQNIETYGW; KTFEIQNQI; NTQNEAIKKW; KTLSLNEIFY; ITAKFQTEDFF; KNSQNIETYGW; ISFDKTNFNPY
NP_045482.1 | hypothetical protein BBG22 [Borrelia burgdorferi B31]; Seq29	HLA-A0101	SADTWYTWY; YLEHMILFF; ETKPKNTCY; NTCYISFYRY; RSADTWYTWY; MSPFITGYSY; YSYEEIDPEY;
	HLA-A0201	SLDSLIEYL; SLIEYLEHM; YTWYWAEEI; KLVKRMTMI; FAMEGSILT; KLIQAFTNT; YLLPPFTSQ; YISFYRYDL; FTNTNKFCI; MILFFLEKT; RMTMIYRSA; YQGSLGEPI; FLEKTPVGT; YLEHMILFFL; SLIEYLEHMI; FITGYSYEEI; LLKDKLTFSI; ILFFLEKTPV; YLLPPFTSQS; YTWYWAEEIM; FLEKTPVGTL; VLGISSAPKL; MITQQDYTEI; HMILFFLEKT; IMSPFITGYS; ILTRSKLIQA; SLIEYLEHMIL; MILFFLEKTPV; ILLKDKLTFSI; SLPSNCYAYKV; YSYEEIDPEYL; KVLGISSAPKL; MIYRSADTWYT; YQGSLGEPILL; YAYKVLGISSA; KIDSLGYQGSL; YWAEEIMSPFI; FAMEGSILTRS; SILTRSKLIQA
	HLA-A0301	HMILFFLEK; SLGEPILLK; RIQFRNGNK; KLSGRFLRH; VLGISSAPK; IQAFTNTNK; LVKRMTMIY; IMSPFITGY; LTFSICDGK; LDFSRINFK; INFKGKLVK; AMEGSILTR; KVLGISSAPK; RINFKGKLVK; LIQAFTNTNK; KLTFSICDGK; SLPSNCYAYK; GSLGEPILLK; KLSGRFLRHY; KLVKRMTMIY; KTPVGTLTAK; RSADTWYTWY; LVKRMTMIYR; EHMILFFLEK; MIYRSADTWY; DLDFSRINFK; NTCYISFYRY; MSPFITGYSY; RSLPSNCYAY; EIMSPFITGY; TQQDYTEIKK; ISSAPKLSGR; TSQSGSKETK; QSGSKETKPK; KNTCYISFYR; KLIQAFTNTNK; RSLPSNCYAYK; KLVKRMTMIYR; KTRIQFRNGNK; RINFKGKLVKR; AMEGSILTRSK; SLGHTQEDSYK; IMSPFITGYSY; SLGEPILLKDK; TMIYRSADTWY; ITQQDYTEIKK; FTSQSGSKETK; RSLGHTQEDSY; MITQQDYTEIK
	HLA-A1101	HMILFFLEK; SLGEPILLK; RIQFRNGNK; LTFSICDGK; NTCYISFYR; TQQDYTEIK; IQAFTNTNK; VLGISSAPK; SQSGSKETK; SSAPKLSGR; AMEGSILTR; NTKTRIQFR; KLSGRFLRH; QQDYTEIKK; LVKRMTMIY; LDFSRINFK; SADTWYTWY; TPVGTLTAK; IMSPFITGY; MITQQDYTEI; ITQQDYTEIK; KVLGISSAPK; GSLGEPILLK; LIQAFTNTNK;

		TQQDYTEIKK; TSQSGSKETK; RINFKGKLVK; KTPVGTLTAK; SLPSNCYAYK; NTCYISFYRY; KLTFSICDGK; RSADTWYTWY; LVKRMTMIYR; ISSAPKLSGR; MIYRSADTWY; RSLPSNCYAY; QSGSKETKPK; FAMEGSILTR; MSPFITGYSY; EIMSPFITGY; KLSGRFLRHY; DLDFSRINFK; KLVKRMTMIY; MITQQDYTEIK; RSLPSNCYAYK; KLIQAFTNTNK; ITQQDYTEIKK; AMEGSILTRSK; SQSGSKETKPK; KTRIQFRNGNK; TQQDYTEIKKK; SLGHTQEDSYK; FTSQSGSKETK; KLVKRMTMIYR; SICDGKNIDNR; SLGEPILLKDK; SAPKLSGRFLR; RINFKGKLVKR; NTNKFCIPDGR; LEHMILFFLEK; IMSPFITGYSY; GISSAPKLSGR; TMIYRSADTWY
	HLA-A2402	EYLEHMILF; CYAYKVLGI; SYKNHDHDL; EYLLPPFTS; EYLEHMILFF; YWAEEIMSPF; WYTWYWAEEI; CYISFYRYDL; IQAFTNTNKF; GYQGSLGEPI; AFTNTNKFCI; SYEEIDPEYL; EYLEHMILFFL; YWAEEIMSPFI; WYWAEEIMSPF; TWYTWYWAEEI; IYRSADTWYTW; SYKNHDHDLDF; SYEEIDPEYLL; EYEITKNAPSL; PFITGYSYEEI; WYTWYWAEEIM
	HLA-A2902	SLPSNCYAY; IMSPFITGY; IYRSADTWY; SYEEIDPEY; SADTWYTWY; YLEHMILFF; SPFITGYSY; ETKPKNTCY; TCYISFYRY; LVKRMTMIY; EIMSPFITGY; YSYEEIDPEY; MSPFITGYSY; YWAEEIMSPF; MIYRSADTWY; RSADTWYTWY; NTCYISFYRY; RSLPSNCYAY; EYLEHMILFF; KLVKRMTMIY; SLGHTQEDSY; TMIYRSADTWY; IMSPFITGYSY; GYSYEEIDPEY; YRSADTWYTWY; NAPSLDSLIEY; WYWAEEIMSPF
	HLA-A6801	NTCYISFYR; LTFSICDGK; NTKTRIQFR; HMILFFLEK; SSAPKLSGR; LDFSRINFK; LPSNCYAYK; TPVGTLTAK; NKFCIPDGR; GSTDSDGTR; HDHDLDFSR; IQAFTNTNK; MSPFITGYS; ETKPKNTCY; TQQDYTEIK; NFKGKLVKR; FITGYSYEE; MTMIYRSAD; RIQFRNGNK; LVKRMTMIY; NTCYISFYRY; FAMEGSILTR; LVKRMTMIYR; ENTKTRIQFR; MIYRSADTWY; MSPFITGYSY; KNTCYISFYR; ISSAPKLSGR; LIQAFTNTNK; ITQQDYTEIK; YSYEEIDPEY; TSQSGSKETK; DLDFSRINFK; EHMILFFLEK; EIKKKLENTK; EIMSPFITGY; SLPSNCYAYK; TNKFCIPDGR; DFSRINFKGK; KLTFSICDGK; INFKGKLVKR; KVLGISSAPK; TRIQFRNGNK; TQQDYTEIKK; NTNKFCIPDGR; MITQQDYTEIK; FTSQSGSKETK; SAPKLSGRFLR; SICDGKNIDNR; ITQQDYTEIKK; MSPFITGYSYE; KLVKRMTMIYR; MTMIYRSADTW; GISSAPKLSGR; TMIYRSADTWY; RSLPSNCYAYK; RINFKGKLVKR; MIYRSADTWYT; NTCYISFYRYD; EKTPVGTLTAK; NAPSLDSLIEY; KLIQAFTNTNK
	HLA-B0702	APKLSGRFL; IPDGRSLPS; TPVGTLTAK; TPVGTLTAKF; KPKNTCYISF; LPSNCYAYKV; LPSNCYAYKVL; APSLDSLIEYL; TPVGTLTAKFA; APKLSGRFLRH; IPDGRSLPSNC; EPILLKDKLTF
	HLA-B0801	KGKLVKRMTM; LTRSKLIQAF; ILTRSKLIQAF
	HLA-B1501	IMSPFITGY; LVKRMTMIY; WAEEIMSPF; YLEHMILFF; IQFRNGNKI; YQGSLGEPI; KNIDNRKEY; QAFTNTNKF; SLPSNCYAY; ETKPKNTCY; ILLKDKLTF; IQAFTNTNKF; YSYEEIDPEY; RSLPSNCYAY; RSADTWYTWY; KLSGRFLRHY; LTRSKLIQAF; KLVKRMTMIY; YQGSLGEPIL; MSPFITGYSY; MIYRSADTWY; YWAEEIMSPF; TMIYRSADTW; EIMSPFITGY; SLGHTQEDSY; SSAPKLSGRF; IMSPFITGYSY; TMIYRSADTWY; ILTRSKLIQAF; LIQAFTNTNKF; RSLGHTQEDSY; ISSAPKLSGRF; YQGSLGEPILL
	HLA-B2705	KRMTMIYRS; SRINFKGKL; NRKEYEITK; TRSKLIQAF; GRFLRHYDS; KRMTMIYRSA; FRNGNKIDSL; TRIQFRNGNK; SRINFKGKLVK; YRSADTWYTWY; KRMTMIYRSAD; GRSLPSNCYAY; YKVLGISSAPK
	HLA-B3501	DPEYLLPPF; WAEEIMSPF; SPFITGYSY; QAFTNTNKF; FAMEGSILT; LVKRMTMIY; SADTWYTWY; TPVGTLTAK; SYEEIDPEY; YLEHMILFF;

		IMSPFITGY; YTWYWAEEI; TWYWAEEIM; EPILLKDKL; LGHTQEDSY; TCYISFYRY; IPDGRSLPS; TRSKLIQAF; TPVGTLTAKF; APSLDSLIEY; YTWYWAEEIM; YSYEEIDPEY; MIYRSADTWY; MSPFITGYSY; YWAEEIMSPF; KPKNTCYISF; EIMSPFITGY; RSLPSNCYAY; NTCYISFYRY; WAEEIMSPFI; DPEYLLPPFT; LPSNCYAYKV; EPILLKDKLTF; LPSNCYAYKVL; NAPSLDSLIEY; WYWAEEIMSPF; WYTWYWAEEIM; IMSPFITGYSY; EIDPEYLLPPF; KPKNTCYISFY; TMIYRSADTWY; APSLDSLIEYL; WAEEIMSPFIT; LIEYLEHMILF; TPVGTLTAKFA; FAMEGSILTRS; YRSADTWYTWY; RSLGHTQEDSY; DPEYLLPPFTS; LIQAFTNTNKF; MTMIYRSADTW; PVGTLTAKFAM
	HLA-B4403	EEIDPEYLL; EEIMSPFIT; AEEIMSPFI; YEITKNAPS; EEIDPEYLLP; EEIMSPFITG; AEEIMSPFIT; IEYLEHMILF; YEITKNAPSL; KETKPKNTCY; EEIMSPFITGY; EEIDPEYLLPP; IEYLEHMILFF; KEYEITKNAPS
	HLA-B5101	LPPFTSQSG; LPSNCYAYKV; LPPFTSQSGS; LPSNCYAYKVL; LPPFTSQSGSK; EPILLKDKLTF
	HLA-B5701	RSADTWYTW; ETKPKNTCY; IMSPFITGY; MIYRSADTW; YSYEEIDPEY; MTMIYRSADTW; RSADTWYTWYW
NP_212885.1 | hypothetical protein BB0751 [Borrelia burgdorferi B31]; Seq30	HLA-A0101	KIDDYNLQY; LTKNIFLSY; FLSYKGNSY; YTTSKWTFF; EIDKSKIDDY; YLTKNIFLSY; FSDTTLFQEK; LTSTFLLGIIF; TTSKWTFFDVF; KSGEGDSRLAY
	HLA-A0201	KLFDNNNKL; VVLTSTFLL; SLIKALDEL; FLLGIIFSN; KLENLSFKI; YLTKNIFLS; LTSTFLLGI; KFFDFDFNL; KILIIVVLT; WTFFDVFDL; IIFSNENKV; LISKIETEL; MTKPKIFSI; KIKILIIVV; KLLTEIFVG; FMTKPKIFSI; VLTSTFLLGI; KLFDNNNKLL; NLISKIETEL; LTYNKQNIPV; IISKDGLYFL; TTSKWTFFDV; KMTKERPLNI; TLFQEKNTKL; ILIIVVLTST; FLLGIIFSNE; KIFSINKEKI; KLNKENENNI; IVVLTSTFLL; NLSFKIIRKL; ALDELQKNKL; IIVVLTSTFL; KFFDFDFNLI; IIAEFKADGL; KLENLSFKII; GIIFSNENKV; KIDDYNLQYKI; VVLTSTFLLGI; ILTYNKQNIPV; KLFDNNNKLLT; ALDELQKNKLV; IIVVLTSTFLL; YTTSKWTFFDV; FLSYKGNSYNT; LIIVVLTSTFL; VLTSTFLLGII; YIKGSDENVYL; KILIIVVLTST; KMTKERPLNII; FLLGIIFSNEN; TLTKLGKDWIL; KLLTEIFVGKS
	HLA-A0301	GLYFLNNQK; FLNNQKMTK; KIFSINKEK; NLSFKIIRK; KIEVKWSNK; KLVSRDQKK; LLTEIFVGK; GIGENPSFK; KVARILEEK; LTKNIFLSY; TLFQEKNTK; KNKGVFMTK; GIIFSNENK; PLNIIAEFK; KIDDYNLQY; KQNIPVDNK; ALDELQKNK; KLLTEIFVGK; LTKNIFLSYK; RPLNIIAEFK; KIDDYNLQYK; YFLNNQKMTK; TTLFQEKNTK; YLTKNIFLSY; NTKLENLSFK; SFKIIRKLNK; GSDENVYLTK; INNNYEIISK; TFFDVFDLEK; KDEYYYTTSK; IFLSYKGNSY; LIKALDELQK; NKNKGVFMTK; LEGTLTKLGK; FDFDFNLISK; KLGKDWILTY; FSDTTLFQEK; LLEKEKQINK; KALDELQKNK; LGIGENPSFK; ENLSFKIIRK; LVSRDQKKHK; LSFKIIRKLNK; MTKPKIFSINK; KIFSINKEKIK; YLTKNIFLSYK; SVNNIEVYFNK; KLVSRDQKKHK; LLGIIFSNENK; SLIKALDELQK; NINNNYEIISK; KLENLSFKIIR; FLNNQKMTKER; LYFLNNQKMTK; IIFSNENKVAR; WTFFDVFDLEK; TFFDVFDLEKK; ELGIGENPSFK
	HLA-A1101	GLYFLNNQK; GIIFSNENK; KVARILEEK; KIFSINKEK; GIGENPSFK; KQNIPVDNK; KIEVKWSNK; NLSFKIIRK; TLFQEKNTK; LLTEIFVGK; TKNIFLSYK; FLNNQKMTK; KADGLEIDK; LTKNIFLSY; KLVSRDQKK; KIDDYNLQY; PLNIIAEFK; KNKGVFMTK; ALDELQKNK; TKLENLSFK; NNIEVYFNK; KPKIFSINK; TELEGTLTK; NLQYKIEVK; KDWILTYNK; KGVFMTKPK; LTKNIFLSYK; TTLFQEKNTK; KIDDYNLQYK; TFFDVFDLEK; KLLTEIFVGK; GSDENVYLTK; NTKLENLSFK; KALDELQKNK; KQNIPVDNKK; FSDTTLFQEK; LIKALDELQK;

		VNNIEVYFNK; RPLNIIAEFK; LVSRDQKKHK; ETELEGTLTK; SFKIIRKLNK; STFLLGIIFS; NTFSDTTLFQ; SFKLFDNNNK; INNNYEIISK; SVNNIEVYFNK; MTKPKIFSINK; WTFFDVFDLEK; LSFKIIRKLNK; SLIKALDELQK; KIFSINKEKIK; TFSDTTLFQEK; YLTKNIFLSYK; TFFDVFDLEKK; NINNNYEIISK; PSFKLFDNNNK; LLGIIFSNENK; IIFSNENKVAR; KADGLEIDKSK; KLVSRDQKKHK; STFLLGIIFSN; LYFLNNQKMTK; KGSDENVYLTK; KLENLSFKIIR; SKIDDYNLQYK; KNTKLENLSFK; DTTLFQEKNTK
	HLA-A2402	YYTTSKWTF; VYLTKNIFL; VFMTKPKIF; EYYYTTSKW; VVLTSTFLL; FFDFDFNLI; YYYTTSKWT; LYFLNNQKM; YTTSKWTFF; TYNKQNIPV; YYYTTSKWTF; SYKGNSYNTF; YYTTSKWTFF; KWSNKSVNNI; SYNTFSDTTL; KFFDFDFNLI; VYLTKNIFLS; KWTFFDVFDL; IVVLTSTFLL; TSKWTFFDVF; EYYYTTSKWTF; YYYTTSKWTFF; SYNTFSDTTLF; VFMTKPKIFSI; DWILTYNKQNI; VYLTKNIFLSY; ILIIVVLTSTF; IFSNENKVARI; TTSKWTFFDVF
	HLA-A2902	KIDDYNLQY; SVNNIEVYF; EIISKDGLY; FLSYKGNSY; YYTTSKWTF; KFFDFDFNL; LTKNIFLSY; IISKDGLYF; STFLLGIIF; YLTKNIFLSY; YYYTTSKWTF; IFLSYKGNSY; YYTTSKWTFF; KLGKDWILTY; SKIDDYNLQY; EIISKDGLYF; YIKGSDENVY; ILIKKDKDEY; VYLTKNIFLSY; YYYTTSKWTFF; AYIKGSDENVY; ILIKKDKDEYY; SYNTFSDTTLF; EYYYTTSKWTF; NYEIISKDGLY; LIKKDKDEYYY; KSKIDDYNLQY; NIFLSYKGNSY; ILIIVVLTSTF; ILEEKFFDFDF
	HLA-A6801	FSNENKVAR; NNIEVYFNK; NTFSDTTLF; TLFQEKNTK; GIIFSNENK; KVARILEEK; KIFSINKEK; EVYFNKNEE; ENLSFKIIR; GLYFLNNQK; DEYYYTTSK; LLTEIFVGK; TKNIFLSYK; FLNNQKMTK; NLSFKIIRK; TTSKWTFFD; PLNIIAEFK; FSINKEKIK; NNNYEIISK; NLQYKIEVK; EIISKDGLY; LTKNIFLSY; YTTSKWTFF; EGTLTKLGK; SVNNIEVYF; QNIPVDNKK; NNQKMTKER; FFDVFDLEK; NTKLENLSFK; TFFDVFDLEK; LTKNIFLSYK; TTLFQEKNTK; NTFSDTTLFQ; ETELEGTLTK; ELQKNKLVSR; WTFFDVFDLE; LIKALDELQK; FDFDFNLISK; ENLSFKIIRK; EVYFNKNEEN; LGIGENPSFK; IFSNENKVAR; LVSRDQKKHK; FSDTTLFQEK; LGIIFSNENK; SFKLFDNNNK; RPLNIIAEFK; YLTKNIFLSY; YTTSKWTFFD; NKVARILEEK; NKNKGVFMTK; YKIEVKWSNK; WTFFDVFDLEK; SVNNIEVYFNK; DTTLFQEKNTK; IIFSNENKVAR; MTKPKIFSINK; YLTKNIFLSYK; TFFDVFDLEKK; NTFSDTTLFQE; LSFKIIRKLNK; FLNNQKMTKER; NINNNYEIISK; LYFLNNQKMTK; TFSDTTLFQEK; FVGKSGEGDSR; SLIKALDELQK; ELGIGENPSFK; ELEGTLTKLGK; ENKVARILEEK; KIFSINKEKIK; TTSKWTFFDVF; LLGIIFSNENK; PSFKLFDNNNK; ERPLNIIAEFK; NVYLTKNIFLS; NIFLSYKGNSY; EFKADGLEIDK; DYNLQYKIEVK; STFLLGIIFSN
	HLA-B0702	RPLNIIAEF; KVNSLIKAL; IVVLTSTFL; IVVLTSTFLL; IPVDNKKVNSL; RPLNIIAEFKA
	HLA-B0801	RDQKKHKEL; KIKILIIVVL; NKKVNSLIKAL; YIKGSDENVYL
	HLA-B1501	FLSYKGNSY; LTKNIFLSY; LGKDWILTY; KSVNNIEVY; STFLLGIIF; IIVVLTSTF; LGIGENPSF; IISKDGLYF; NTKLENLSF; SVNNIEVYF; KQINKNKGV; KLFDNNNKL; KVNSLIKAL; KQINKNKGVF; YIKGSDENVY; YLTKNIFLSY; LIIVVLTSTF; KLGKDWILTY; KSVNNIEVYF; ILIKKDKDEY; TSKWTFFDVF; KLFDNNNKLL; KVARILEEKF; IFLSYKGNSY; GVFMTKPKIF; NQKMTKERPL; KQINKNKGVF; YIKGSDENVY; YLTKNIFLSY; LIIVVLTSTF; KLGKDWILTY; KSVNNIEVYF; ILIKKDKDEY; TSKWTFFDVF; KLFDNNNKLL; KVARILEEKF; IFLSYKGNSY; GVFMTKPKIF; NQKMTKERPL
	HLA-B2705	KQINKNKGVF; ARILEEKFFDF; KQINKNKGVFM

	HLA-B3501	RPLNIIAEF; IIVVLTSTF; SKWTFFDVF; FLSYKGNSY; NVYLTKNIF; NTFSDTTLF; SVNNIEVYF; KSVNNIEVY; YKGNSYNTF; LTKNIFLSY; LGKDWILTY; STFLLGIIF; YYTTSKWTF; IKGSDENVY; IVVLTSTFL; NENNINNNY; YIKGSDENVY; TSKWTFFDVF; LIIVVLTSTF; NKSVNNIEVY; YYYTTSKWTF; YLTKNIFLSY; IFLSYKGNSY; YNTFSDTTLF; SGEGDSRLAY; TSTFLLGIIF; IVVLTSTFLL; IPVDNKKVNSL; TTSKWTFFDVF; LTSTFLLGIIF; LSYKGNSYNTF; NIFLSYKGNSY; KSGEGDSRLAY; TKLGKDWILTY; ILIIVVLTSTF; FSNENKVARIL; NSYNTFSDTTL
	HLA-B4403	EENDKDILI; EEKFFDFDF; AEFKADGLE; GEGDSRLAY; GENPSFKLF; NENNINNNY; NENKVARIL; KENENNINN; KERPLNIIA; YEIISKDGL; AEFKADGLEI; YEIISKDGLY; EENDKDILIK; GEGDSRLAYI; YEIISKDGLYF; EEKFFDFDFNL; KENENNINNNY; AEFKADGLEID; KERPLNIIAEF; KELGIGENPSF; NENNINNNYEI; EENDKDILIKK
	HLA-B5101	IPVDNKKVNSL
	HLA-B5701	LTKNIFLSY; KSVNNIEVY; KSKIDDYNLQY; KSGEGDSRLAY; LSYKGNSYNTF
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31]; Seq31	HLA-A0101	TTDNIDIFV; TLEKVAKEY; NTDTDKIGGY; TTDNIDIFVV; TTPMQRIHKY; DTKEDMKILY; GTTPMQRIHKY; TTDNIDIFVVL
	HLA-A0201	ILYSEIAEL; LIIIFTLFL; TTDNIDIFV; KLNLNHLEI; KKLIIIFTL; FLSQACNLS; TLFGTTPMQ; KLIIIFTLFL; FLSQACNLST; KILYSEIAEL; KTTDNIDIFV; TTDNIDIFVV; ALINTDTDKI; TLFLSQACNL; IIFTLFLSQA; KVAKEYAIKL; ILASGIELNRV; FLSQACNLSTM; TLFGTTPMQRI; KTTDNIDIFVV; KLIIIFTLFLS; FTLFLSQACNL; RIHKYDQSFNL; KKLIIIFTLFL; WLNSPSHKEAL; NLTREILASGI; NLNHLEIDDTL; HLEIDDTLEKV; IIIFTLFLSQA
	HLA-A0301	VLFGKRKYK; KVAKEYAIK; STMHKIDTK; ACNLSTMHK; TTPMQRIHK; IIFTLFLSQ; DIFVVLFGK; VVLFGKRKYK; QACNLSTMHK; TLFGTTPMQR; GTTPMQRIHK; IDIFVVLFGK; ILYSEIAELR; LSTMHKIDTK; IFVVLFGKRK; IIIFTLFLSQ; ILASGIELNR; LYSEIAELRK; NAWLNSPSHK; ILYSEIAELRK; HTLFGTTPMQR; SQACNLSTMHK; KILYSEIAELR; VVNAWLNSPSH; FVVLFGKRKYK
	HLA-A1101	STMHKIDTK; TTPMQRIHK; DIFVVLFGK; KVAKEYAIK; VLFGKRKYK; ACNLSTMHK; ALINTDTDK; YSEIAELRK; FVVLFGKRK; KIDTKEDMK; AWLNSPSHK; IIFTLFLSQ; LASGIELNR; QACNLSTMHK; TLFGTTPMQR; GTTPMQRIHK; VVLFGKRKYK; LSTMHKIDTK; ILYSEIAELR; NAWLNSPSHK; TTPMQRIHKY; IDIFVVLFGK; ILASGIELNR; HLEIDDTLEK; IIIFTLFLSQ; LYSEIAELRK; DIFVVLFGKR; YSEIAELRKK; SQACNLSTMHK; ILYSEIAELRK; HTLFGTTPMQR; NIDIFVVLFGK; KILYSEIAELR; FVVLFGKRKYK; DIFVVLFGKRK; VVNAWLNSPSH; NLSTMHKIDTK; EILASGIELNR; VNAWLNSPSHK
	HLA-A2402	KLIIIFTLF; KYDQSFNLT; LFGTTPMQRI; KKLIIIFTLF; GYRLKTTDNI;
	HLA-A2902	VVLFGKRKY; KLIIIFTLF; FVVLFGKRKY; TTPMQRIHKY; IFVVLFGKRKY; GTTPMQRIHKY
	HLA-A6801	DIFVVLFGK; LASGIELNR; TTPMQRIHK; LYSEIAELR; YAIKLGENR; DTDKIGGYR; STMHKIDTK; FVVLFGKRK; YSEIAELRK; TLFGTTPMQ; IFVVLFGKR; YDQSFNLTR; VLFGKRKYK; KVAKEYAIK; TLFGTTPMQR; DIFVVLFGKR; ILYSEIAELR; QACNLSTMHK; ILASGIELNR; NAWLNSPSHK; EYAIKLGENR; EALINTDTDK; GTTPMQRIHK; TTPMQRIHKY; LSTMHKIDTK; IDIFVVLFGK; LYSEIAELRK; DTKEDMKILY; HTLFGTTPMQ; HLEIDDTLEK; TDTDKIGGYR; YSEIAELRKK; VVLFGKRKYK; HTLFGTTPMQR; EILASGIELNR; FVVLFGKRKYK; DIFVVLFGKRK; NTDTDKIGGYR; HKYDQSFNLTR; NIDIFVVLFGK; ILYSEIAELRK; KILYSEIAELR; DTDKIGGYRLK; NLSTMHKIDTK; SQACNLSTMHK; IDIFVVLFGKR; EIDDTLEKVAK;

		LYSEIAELRKK; VNAWLNSPSHK
	HLA-B0702	SPSHKEALI; TPMQRIHKY; ;
	HLA-B0801	RIHKYDQSF; ; ELRKKLNLNHL
	HLA-B1501	RIHKYDQSF; SQACNLSTM; KLIIIFTLF; ILYSEIAEL; FVVLFGKRKY; SQACNLSTMH; LSQACNLSTM; MQRIHKYDQSF; RLKTTDNIDIF; VVNAWLNSPSH; FLSQACNLSTM; WLNSPSHKEAL
	HLA-B2705	YRLKTTDNI; QRIHKYDQSF; YRLKTTDNIDI
	HLA-B3501	TPMQRIHKY; HTLFGTTPM; NAWLNSPSH; QACNLSTMH; FVVLFGKRKY; THTLFGTTPM; FLSQACNLSTM; ITHTLFGTTPM; TTDNIDIFVVL; WLNSPSHKEAL
	HLA-B4403	AELRKKLNL; REILASGIE; KEDMKILYS; REILASGIEL; SEIAELRKKL; GENRTITHTLF; AELRKKLNLNH; REILASGIELN
	HLA-B5101	
	HLA-B5701	ELNRVVNAW; KTTDNIDIF;
NP_045709.1 | lipoprotein BBA36[Borrelia burgdorferi B31]; Seq32	HLA-A0101	VVDAFGADPY;
	HLA-A0201	MMQRISILL; SILLMLLAV; ALSLFFQKV; KLESLKVFL; RISILLMLL; LMLLAVFSC; LLMLLAVFS; KCNEEIFKV; KQFGDVKSL; MMQRISILLM; KVFLKDAMSV; ALSLFFQKVV; SLTPEEAEKL; SSFDNISSIV; LLMLLAVFSC; SLFFQKVVDA; RISILLMLLA; NISSIVSKAV; MLLAVFSCKQ; ISILLMLLAV; MMQRISILLML; FISSFDNISSI; SLTEIDSGNGI; RISILLMLLAV; VLTESESNNEL
	HLA-A0301	MLLAVFSCK; KEFFDWLSK; EALSLFFQK; VSKAVDASK; VCYKIKNSK; LMLLAVFSCK; KLESLKVFLK; YVCYKIKNSK; SLGFKEYVCY; SVNGREEALK; ISLTPEEAEK; IVSKAVDASK; WLSKDVNRQK; PTEQQSLGFK; IPLVVSDVVK; MLLAVFSCKQ; VSKAVDASKK; LKAEYEKSYK; LLMLLAVFSCK; SLGFKEYVCYK; IVSKAVDASKK; ALKAEYEKSYK; SIVSKAVDASK; MSVNGREEALK; VVDAFGADPYK; KGEALSLFFQK; GIPLVVSDVVK
	HLA-A1101	MLLAVFSCK; EALSLFFQK; VSKAVDASK; KEFFDWLSK; KAEYEKSYK; DVVKDLIPK; AFGADPYKK; TEQQSLGFK; SLTPEEAEK; DAFGADPYK; LSKDVNRQK; SNNELKNLK; LESLKVFLK; AVDASKKRR; EALKAEYEK; GFKEYVCYK; SVNGREEALK; LMLLAVFSCK; KLESLKVFLK; IVSKAVDASK; YVCYKIKNSK; ISLTPEEAEK; VSKAVDASKK; GEALSLFFQK; PTEQQSLGFK; FSCKQFGDVK; ESNNELKNLK; DAFGADPYKK; VVDAFGADPY; PVKCNEEIFK; LGFKEYVCYK; LLMLLAVFSCK; SIVSKAVDASK; VVDAFGADPYK; SLGFKEYVCYK; MSVNGREEALK; IVSKAVDASKK; VSDVVKDLIPK; LTESESNNELK; KGEALSLFFQK; ALKAEYEKSYK; SYKEFFDWLSK; KVVDAFGADPY; SFDNISSIVSK; GIPLVVSDVVK; EISLTPEEAEK; VFSCKQFGDVK; RPTEQQSLGFK
	HLA-A2402	FFQKVVDAF; EYEKSYKEF; SYKEFFDWL; EFISSFDNI; MMQRISILL; EYEKSYKEFF; LFFQKVVDAF; ISILLMLLAVF
	HLA-A2902	LGFKEYVCY; SLGFKEYVCY; VVDAFGADPY; EQQSLGFKEY; KVVDAFGADPY
	HLA-A6801	DAFGADPYK; EALSLFFQK; ESESNNELK; EAEKLESLK; EALKAEYEK; MLLAVFSCK; DNISSIVSK; DVVKDLIPK; VSKAVDASK; EEIFKVIKK; LSKDVNRQK; GFKEYVCYK; KAVDASKKR; SLTPEEAEK; KAEYEKSYK; DAFGADPYKK; YVCYKIKNSK; ESNNELKNLK; SVNGREEALK; IVSKAVDASK; FSCKQFGDVK; EEALKAEYEK; LGFKEYVCYK; VSKAVDASKK; LMLLAVFSCK; EEAEKLESLK; KAVDASKKRR; TESESNNELK; WLSKDVNRQK; ISLTPEEAEK; MSVNGREEALK; EISLTPEEAEK; LTESESNNELK; EYVCYKIKNSK; IVSKAVDASKK; FLKDAMSVNGR; SIVSKAVDASK; LLMLLAVFSCK; SLGFKEYVCYK; VSKAVDASKKR; VVDAFGADPYK; SYKEFFDWLSK; FFDWLSKDVNR
	HLA-B0702	KPVKCNEEI; IPLVVSDVV; SVNGREEAL; RPTEQQSLGF;

		KPVKCNEEIF; KIKNSKGEAL; IPKEISLTPE; TPEEAEKLESL; KKRRPTEQQSL
	HLA-B0801	IFKVIKKVL; FFQKVVDAF; MMQRISILL; KIKNSKGEAL; YKIKNSKGEAL; MMQRISILLML
	HLA-B1501	RQKEFISSF; QQSLGFKEY; KQFGDVKSL; MQRISILLM; ILLMLLAVF; MMQRISILL; FFQKVVDAF; LGFKEYVCY; ALKAEYEKSY; MQRISILLML; EQQSLGFKEY; MMQRISILLM; LLAVFSCKQF; VVDAFGADPY; LFFQKVVDAF; NSKGEALSLF; KVVDAFGADPY; ISILLMLLAVF; LSKDVNRQKEF; MQRISILLMLL; MLLAVFSCKQF; SLFFQKVVDAF; AMSVNGREEAL; MMQRISILLML; QSLGFKEYVCY; NSKGEALSLFF; KQFGDVKSLTE; VNRQKEFISSF
	HLA-B2705	QRISILLML; RQKEFISSF; RRPTEQQSL; KQFGDVKSL; QRISILLMLL; NRQKEFISSF; GREEALKAEY; KRRPTEQQSL; RRPTEQQSLGF; QRISILLMLLA
	HLA-B3501	FFQKVVDAF; VDAFGADPY; LAVFSCKQF; LKVFLKDAM; ILLMLLAVF; IPLVVSDVV; QQSLGFKEY; RPTEQQSLGF; KPVKCNEEIF; VVDAFGADPY; LFFQKVVDAF; MSVNGREEAL; SILLMLLAVF; MMQRISILLM; TPEEAEKLES; KVVDAFGADPY; EALKAEYEKSY; TPEEAEKLESL; EAEKLESLKVF; ISILLMLLAVF; ESLKVFLKDAM; SLFFQKVVDAF
	HLA-B4403	TEIDSGNGI; AEKLESLKV; KEISLTPEE; AEKLESLKVF; AEYEKSYKEF; KEFISSFDNI; KEISLTPEEA; EEIFKVIKKV; TEIDSGNGIPL; KEFISSFDNIS; AEYEKSYKEFF; AEKLESLKVFL; EEIFKVIKKVL; KEFFDWLSKDV
	HLA-B5101	IPLVVSDVV; IPKEISLTP; IPLVVSDVVK; DPYKKDNDESV; IPLVVSDVVKD
	HLA-B5701	KSYKEFFDW;
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi]; Seq33	HLA-A0101	VADAFGTQEY; FTESENNNEL; ATDLEDDNSF;
	HLA-A0201	SILSILLLL; KSLGFNEYV; ILSILLLLL; SLTEVATDL; RISILSILL; ILLLLLLFS; LLLLLLFSC; RLEALKTFL; KQYGDVKSL; KCNEEIFKV; LTSEEFERL; SILSILLLLL; ILSILLLLLL; VLTSEEFERL; KTFLKDAMGV; RISILSILLL; SLFFQKVADA; SILSILLLLLL; FVSFFNNICGI; LLFSCKQYGDV; RISILSILLLL
	HLA-A0301	LLLLLFSCK; KEFFDWLSK; ITKAVDASK; LEALKTFLK; RLEALKTFLK; LLLLLLFSCK; LLLLFSCKQY; NSYNLNSNNK; IITKAVDASK; ADAFGTQEYK; SLGFNEYVCY; ITKAVDASKK; GVNGREGDTK; SFASGSVESK; WLSKDVNRQK; TKAEYEKSYK; ILLLLLLFSCK; NSFASGSVESK; IITKAVDASKK; GIITKAVDASK; KVADAFGTQEY; FFNNICGIITK; ASKKRYNSNPK; RISILSILLLL
	HLA-A1101	LLLLLFSCK; ITKAVDASK; KEFFDWLSK; SYNLNSNNK; KAEYEKSYK; FASGSVESK; DAFGTQEYK; ESKDQIIEK; LSKDVNRQK; LEALKTFLK; VLTSEEFER; NSYNLNSNNK; RLEALKTFLK; LLLLLLFSCK; ITKAVDASKK; GVNGREGDTK; IITKAVDASK; SFASGSVESK; FSCKQYGDVK; SILLLLLLFS; ILLLLLLFSCK; NSFASGSVESK; SVESKDQIIEK; GIITKAVDASK; ASKKRYNSNPK; VADAFGTQEYK; TGDDLSLFFQK; KVADAFGTQEY; IITKAVDASKK; SYKEFFDWLSK; KSLGFNEYVCY; SENNNELANLK; RTGDDLSLFFQ; DTKAEYEKSYK; GFNEYVCYDIK
	HLA-A2402	EYEKSYKEF; RYNSNPKSL; FFQKVADAF; SYKEFFDWL; EFVSFFNNI; IFKVIKRVF; SYNLNSNNK; SILLLLLLF; EYEKSYKEFF; LSILLLLLLF; LFFQKVADAF; RYNSNPKSLGF; EFERLEALKTF; ILSILLLLLLF
	HLA-A2902	LGFNEYVCY; SLGFNEYVCY; VADAFGTQEY; LLLLFSCKQY; KVADAFGTQEY; ELANLKNLNSY; KSLGFNEYVCY; ILSILLLLLLF
	HLA-A6801	DAFGTQEYK; YVCYDIKTR; ITKAVDASK; FASGSVESK; ESKDQIIEK; VLTSEEFER; EEIFKVIKR; NNNELANLK; EFERLEALK; LSKDVNRQK;

		SYNLNSNNK; EKCNEEIFK; NNICGIITK; KAVDASKKR; LEALKTFLK; DDLSLFFQK; TKAVDASKK; KAEYEKSYK; NSYNLNSNNK; ITKAVDASKK; EYVCYDIKTR; IITKAVDASK; ENNNELANLK; EEFERLEALK; FSCKQYGDVK; SFASGSVESK; TKAEYEKSYK; PVLTSEEFER; WLSKDVNRQK; TKAVDASKKR; RLEALKTFLK; FNEYVCYDIK; NSFASGSVESK; DTKAEYEKSYK; ITKAVDASKKR; DAFGTQEYKNK; IITKAVDASKK; FLKDAMGVNGR; FFNNICGIITK; SVESKDQIIEK; ELANLKNLNSY; GPVLTSEEFER; GIITKAVDASK; VADAFGTQEYK; LNSYNLNSNNK; SYKEFFDWLSK; MGVNGREGDTK; FFDWLSKDVNR; NEYVCYDIKTR
	HLA-B0702	GPVLTSEEF; KPEKCNEEI; KPEKCNEEIF; KTRTGDDLSL; KKRYNSNPKSL
	HLA-B0801	IFKVIKRVF; FFQKVADAF; ;
	HLA-B1501	RQKEFVSFF; KQYGDVKSL; LLLFSCKQY; LGFNEYVCY; QIIEKGPVL; FFQKVADAF; IFKVIKRVF; NSNPKSLGF; LANLKNLNSY; LLLLFSCKQY; LFFQKVADAF; LSILLLLLLF; YNSNPKSLGF; RTGDDLSLFF; SLGFNEYVCY; VADAFGTQEY; KVADAFGTQEY; LSKDVNRQKEF; KSLGFNEYVCY; SLFFQKVADAF; ELANLKNLNSY; ILSILLLLLLF; LLLLLFSCKQY; KTRTGDDLSLF; KQYGDVKSLTE; VATDLEDDNSF
	HLA-B2705	KRISILSIL; NRQKEFVSF; KRYNSNPKS; KQYGDVKSL; RQKEFVSFF; ERLEALKTF; TRTGDDLSL; KRYNSNPKSL; KRISILSILL; GREGDTKAEY; NRQKEFVSFF; KRISILSILLL; ERLEALKTFLK; TRTGDDLSLFF
	HLA-B3501	GPVLTSEEF; FFQKVADAF; TDLEDDNSF; ADAFGTQEY; NPKSLGFNEY; VADAFGTQEY; LANLKNLNSY; LFFQKVADAF; KPEKCNEEIF; KAVDASKKRY; FTESENNNEL; KVADAFGTQEY; EALKTFLKDAM; VATDLEDDNSF; ELANLKNLNSY; SLFFQKVADAF; DVNRQKEFVSF; EFERLEALKTF; NGREGDTKAEY
	HLA-B4403	EEFERLEAL; SENNNELAN; REGDTKAEY; TEVATDLED; AEYEKSYKEF; SENNNELANL; KEFVSFFNNI; EEFERLEALK; EEIFKVIKRV; EEIFKVIKRVF; EEFERLEALKT; AEYEKSYKEFF; KEFFDWLSKDV; SENNNELANLK
	HLA-B5101	
	HLA-B5701	KSYKEFFDW; KSLGFNEYVCY
NP_045739.1 | BBA66 antigen, P35, putative [Borrelia burgdorferi B31]; Seq34	HLA-A0101	KIEIFNQDY; LSDSKSLAEY; TIDANLNEDY; SSAKVYDRSY; CTIDANLNEDY; LLDVISSAKVY; NSGLPTFALNY; ISSAKVYDRSY; SLSDSKSLAEY; LSDSKSLAEYI
	HLA-A0201	FLFSCTIDA; KMKDSAFEL; LMDFDQYKI; QLQSLSFSA; KLLGLFLFS; SVLEAYISI; QLNSNTPEA; ELLDVISSA; KINSFDFTM; GLFLFSCTI; VLEAYISIM; SLSDSKSLA; NMQNARQSV; FALNYSFSQ; KLQTLKNEL; NSFDFTMKL; TQISFELAL; ALMDFDQYK; SLTKQRIPI; MISGLGTQI; LIQLKLLGL; ALMDFDQYKI; LLDVISSAKV; GLGTQISFEL; KMKDSAFELL; LMISGLGTQI; KLLGLFLFSC; KLQTLKNELI; FKMKDSAFEL; RQADGLIANA; SVLEAYISIM; NLNEDYKNKV; IQLKLLGLFL; ALNYSFSQPT; LLGLFLFSCT; RIPIQAVTTV; LIRELMISGL; FLFSCTIDANL; ALYNENQNHSL; KVYDRSYAPQL; SLIRELMISGL; KINSFDFTMKL; SLAEYIKKRYL; KLLGLFLFSCT; ELLDVISSAKV; SLSFSADLSNL; LLGLFLFSCTI; QLQSLSFSADL; GLFLFSCTIDA; FALNYSFSQPT; LIANASSNSSL; ALEEINKKIEI; GLGTQISFELA; YALMDFDQYKI; FKMKDSAFELL; MQNARQSVLEA; QISFELALEEI; RQSVLEAYISI; KAADDQETTSA; SIMEALYNENQ
	HLA-A0301	KIKPLIQLK; KSLAEYIKK; KTVAAAPNK; LLDVISSAK; QTTTSSGSK; KTQNNFGFR; FTMKLKELK; KLLGLFLFS; ALMDFDQYK; RSYAPQLNS; KLNQILDKR; AARAASLTK; LIRAISEEK; GLPTFALNY; ETYDQFKMK; RAASLTKQR; SLAEYIKKR; ALYNENQNH; ELLDVISSAK;

		KINSFDFTMK; TAARAASLTK; FSADLSNLPK; NSFDFTMKLK; VQTTTSSGSK; SSGSKLQTLK; TMKLKELKSK; KSKLNQILDK; ELIRAISEEK; SSNSSLSDSK; KLNQILDKRK; KVYDRSYAPQ; SKSLAEYIKK; SLAEYIKKRY; SADTNSNAAK; KNKVKGILNK; ELKKQSQAAK; MKIKPLIQLK; AVTTVPGNTR; TTAARAASLTK; TSSGSKLQTLK; ALNYSFSQPTR; AVQTTTSSGSK; SQNQPQTTPNK; FTMKLKELKSK; ASSNSSLSDSK; TSADTNSNAAK; LIRAISEEKNK; AAKTVAAAPNK; SLSDSKSLAEY; SFSADLSNLPK; EIFNQDYLNAK; KLQTLKNELIR; KFYALMDFDQY; KSLAEYIKKRY; LSNLPKTTAAR
	HLA-A1101	KTVAAAPNK; ALMDFDQYK; KSLAEYIKK; KTQNNFGFR; SADLSNLPK; QTTTSSGSK; FTMKLKELK; KIKPLIQLK; AARAASLTK; ETYDQFKMK; ISSAKVYDR; RAISEEKNK; SFDFTMKLK; SGSKLQTLK; LLDVISSAK; LIRAISEEK; LALEEINKK; SNSSLSDSK; NQPQTTPNK; RAASLTKQR; VTTVPGNTR; QTLKNELIR; SIMEALYNE; KLNQILDKR; INSFDFTMK; KVYDRSYAP; GLPTFALNY; SSNSSLSDSK; KINSFDFTMK; NSFDFTMKLK; TAARAASLTK; SSGSKLQTLK; FSADLSNLPK; YALMDFDQYK; SADTNSNAAK; KSKLNQILDK; VQTTTSSGSK; KLNQILDKRK; AVTTVPGNTR; KVYDRSYAPQ; TMKLKELKSK; ELLDVISSAK; KSLAEYIKKR; VISSAKVYDR; IFNQDYLNAK; ELIRAISEEK; MKIKPLIQLK; KTQNNFGFRE; TTAARAASLTK; AVQTTTSSGSK; TSSGSKLQTLK; ASSNSSLSDSK; TSADTNSNAAK; SQNQPQTTPNK; SFSADLSNLPK; TIDANLNEDYK; AAKTVAAAPNK; FTMKLKELKSK; ALNYSFSQPTR; EIFNQDYLNAK; SLSDSKSLAEY; TQNNFGFRETY; KFYALMDFDQY; AKINSFDFTMK; LSNLPKTTAAR; SFELALEEINK; KSLAEYIKKRY; LIRAISEEKNK; KLQTLKNELIR; SIMEALYNENQ; NSGLPTFALNY; INSFDFTMKLK
	HLA-A2402	IQLKLLGLF; DYKNKVKGI; DYLNAKINSF; VYDRSYAPQL; QYKIEQFGSI; EWSRQADGLI; LYNENQNHSL; FYALMDFDQY; DYKNKVKGIL; RYLDNMQNAR; LYNENQNHSLI; IQLKLLGLFLF; EYIKKRYLDNM; NFGFRETYDQF; IFNQDYLNAKI; FYALMDFDQYK; SYAPQLNSNTP
	HLA-A2902	GLPTFALNY; PTFALNYSF; YALMDFDQY; DVISSAKVY; KIEIFNQDY; IDANLNEDY; FYALMDFDQY; QFGSIMEALY; KFYALMDFDQY; CTIDANLNEDY; NSGLPTFALNY; TQNNFGFRETY; YLNAKINSFDF
	HLA-A6801	ETYDQFKMK; FTMKLKELK; NTPEAENER; NYSFSQPTR; DANLNEDYK; QTTTSSGSK; KTVAAAPNK; KTQNNFGFR; RAASLTKQR; ISSAKVYDR; SLAEYIKKR; QTLKNELIR; LIRAISEEK; ELALEEINK; NLPKTTAAR; VTTVPGNTR; YLDNMQNAR; NIPIADNDK; ALMDFDQYK; DVISSAKVY; NNFGFRETY; KLNQILDKR; INSFDFTMK; LLDVISSAK; NSFDFTMKL; ENQNHSLIR; TTSSGSKLQ; QTNSSSAVQ; EIFNQDYLN; LALEEINKK; NSFDFTMKLK; ELIRAISEEK; TAARAASLTK; FSADLSNLPK; ELLDVISSAK; YALMDFDQYK; DSKSLAEYIK; SSNSSLSDSK; LNYSFSQPTR; ELALEEINKK; NKTQNNFGFR; VISSAKVYDR; KINSFDFTMK; AVTTVPGNTR; TTAARAASLT; ELKKQSQAAK; DFTMKLKELK; MKIKPLIQLK; SNTPEAENER; TTTSSGSKLQ; FYALMDFDQY; SSGSKLQTLK; NENQNHSLIR; SADTNSNAAK; ETYDQFKMKD; TTAARAASLTK; DVISSAKVYDR; EIFNQDYLNAK; TSADTNSNAAK; TSSGSKLQTLK; NSNTPEAENER; FYALMDFDQYK; FTMKLKELKSK; LSNLPKTTAAR; QAVTTVPGNTR; NTPEAENERNK; TIDANLNEDYK; EQFGSIMEALY; DSKSLAEYIKK; FGFRETYDQFK; ALNYSFSQPTR; CTIDANLNEDY; DANLNEDYKNK; FDFTMKLKELK; QILDKRKEWSR; INSFDFTMKLK; AAKTVAAAPNK; NSFDFTMKLKE; KSKLNQILDKR; SFSADLSNLPK; AVQTTTSSGSK; LIRAISEEKNK; ASSNSSLSDSK; AARAASLTKQR; TTVPGNTRTFN
	HLA-B0702	SPQLQSLSF; APSPQLQSL; IPIQAVTTV; KPLIQLKLL; APQLNSNTP; KPEKCNEEIF; KTRTGDDLSL; APSPQLQSLSF; APQLNSNTPEA;

		SPQLQSLSFSA; KPLIQLKLLGL; IPIADNDKVAA; IPIQAVTTVPG; AASLTKQRIPI; LPKTTAARAAS; LIANASSNSSL; TPEAENERNKF; KVYDRSYAPQL; APNKGSQNQPQ
	HLA-B0801	QFKMKDSAF; ELKKQSQAA; NERNKFYAL; QLKLLGLFL; KLKELKSKL; YIKKRYLDNM; ELKSKLNQIL; YDQFKMKDSAF
	HLA-B1501	YLNAKINSF; MQNARQSVL; QQAAPSPQL; KQRIPIQAV; KMKDSAFEL; TQISFELAL; IQLKLLGLF; SAKVYDRSY; SQAAKTVAA; QQTNSSSAV; QFKMKDSAF; RQQTNSSSA; RQADGLIAN; TVPGNTRTF; PTFALNYSF; KQSQAAKTV; RQSVLEAYI; SGLGTQISF; DVISSAKVY; TTAARAASL; RQQTNSSSAV; EQFGSIMEAL; QLKLLGLFLF; ISGLGTQISF; SQAAKTVAAA; LQSLSFSADL; TTVPGNTRTF; SSAKVYDRSY; NSRNSGLPTF; KQRIPIQAVT; SLAEYIKKRY; KMKDSAFELL; RQADGLIANA; DQFKMKDSAF; NARQSVLEAY; IANASSNSSL; NQQAAPSPQL; NMQNARQSVL; IQLKLLGLFL; NQNHSLIREL; QNNFGFRETY; RTFNSRNSGL; LMISGLGTQI; YLNAKINSFDF; TQNNFGFRETY; EQFGSIMEALY; MISGLGTQISF; ISSAKVYDRSY; SLSDSKSLAEY; IQLKLLGLFLF; RQADGLIANAS; VTTVPGNTRTF; RQSVLEAYISI; MQNARQSVLEA; ALYNENQNHSL; KQSQAAKTVAA; LLDVISSAKVY; KQRIPIQAVTT; RQQTNSSSAVQ; QNARQSVLEAY; VQTTTSSGSKL; GLPTFALNYSF; KSLAEYIKKRY; FNSRNSGLPTF; KVYDRSYAPQL
	HLA-B2705	SRNSGLPTF; ERNKFYALM; KRKEWSRQA; KRYLDNMQN; ARQSVLEAY; KRYLDNMQNA; ARAASLTKQR; RQQTNSSSAV; KRYLDNMQNAR; QRIPIQAVTTV; ERNKFYALMDF; RQSVLEAYISI; SRNSGLPTFAL; FRETYDQFKMK
	HLA-B3501	YALMDFDQY; SPQLQSLSF; DVISSAKVY; FGSIMEALY; IPIQAVTTV; EAENERNKF; APSPQLQSL; SAKVYDRSY; TVPGNTRTF; LAEYIKKRY; LPTFALNYS; SADTNSNAA; YLNAKINSF; KINSFDFTM; FALNYSFSQ; NAKINSFDF; LPTFALNYSF; NARQSVLEAY; TTVPGNTRTF; FYALMDFDQY; EAENERNKFY; SVLEAYISIM; YKIEQFGSIM; LPKTTAARAA; IANASSNSSL; LSDSKSLAEY; IPIADNDKVA; QFGSIMEALY; LDVISSAKVY; NSRNSGLPTF; IPIQAVTTVP; APSPQLQSLSF; TPEAENERNKF; FALNYSFSQPT; NAKINSFDFTM; IPIADNDKVAA; IPIQAVTTVPG; MISGLGTQISF; LPKTTAARAAS; IADNDKVAAEL; EQFGSIMEALY; LLDVISSAKVY; QSVLEAYISIM; TQNNFGFRETY; QAAPSPQLQSL; SLSDSKSLAEY; QNARQSVLEAY; FNSRNSGLPTF
	HLA-B4403	AENERNKFY; EEINKKIEI; NENQNHSLI; EEINKKIEIF; AENERNKFYA; EEKNKTQNNF; RELMISGLGT; AELKKQSQAA; EEIFKVIKRVF; EEFERLEALKT; AEYEKSYKEFF; KEFFDWLSKDV; SENNNELANLK
	HLA-B5101	IPIQAVTTV; LPKTTAARA; LPTFALNYS; IPIADNDKV; APSPQLQSL; KPLIQLKLL; LPTFALNYSF; LPKTTAARAA; IPIQAVTTVP; LALEEINKKI; IPIQAVTTVPG; LPTFALNYSFS; KPLIQLKLLGL
	HLA-B5701	KTHNHGFRETY; QTQPSFVVPVY
AAT93824.1| BBA66 antigen, P35, putative [Borrelia garinii PBi]; Seq35	HLA-A0101	QSNNVLTNY; YLNTIINSY; KIESFNTQY; LAEKKEWLNY; TIDANLNKDY; EAESERNRLY; NSQSNNVLTNY; CTIDANLNKDY; QTQPSFVVPVY; KTHNHGFRETY
	HLA-A0201	TLLDVISNI; KMKDSAFTL; QLSSNTPEA; TQPSFVVPV; ILAEKKEWL; KMQDARQSA; SLIISGLGI; SLESTLEEI; RQSALDLYL; WLNYADAII; SALDLYLNI; MMDFDQAKT; ALDLYLNIT; YADAIITNT; YAMMDFDQA; YTFSSSFSQ; ASAQAIQTV; YLNTIINSYT; LLDVISNISV; AMMDFDQAKT; KMKDSAFTLL; KMQDARQSAL; FTLLDVISNI; KIESFNTQYL; FKMKDSAFTL; QTQPSFVVPV; LIISGLGIQI; YTFKDKLKEL; LLNSSTDDQA; TLLDVISNIS; LIRSLIISGL; ISLESTLEEI; TLLDVISNISV; ALDLYLNITEI; SLIRSLIISGL; ILYQENQNHSL;

		RLYAMMDFDQA; QIASAQAIQTV; SLGQYIKNKYL; AMMDFDQAKTT; IISGLGIQISL; SLIISGLGIQI; SVFDRGSAPQL; YTFSSSFSQPT; IINSYTFKDKL; FKMKDSAFTLL; NLQGLNPANQV; YLNTIINSYTF; KTTEFGSIMNI; HQTQPSFVVPV; RQSALDLYLNI
	HLA-A0301	KLNSILAEK; TIINSYTFK; ITNTSSNSK; GLQKNTQSK; KLKNNLLRR; SLGQYIKNK; YSGNSPLQK; LLRRIAEEK; STPNQSIIK; QSNNVLTNY; CTIDANLNK; ATKNKTNIK; KIESFNTQY; LQKNTQSKK; YIKNKYLDK; ETYDQFKMK; NLNKDYKNK; YLNTIINSY; ISNISVFDR; NIKVAGLQK; NTIINSYTFK; IITNTSSNSK; IINSYTFKDK; SINTGSNATK; ATNVQATPPK; KLNSILAEKK; VYSGNSPLQK; NLLRRIAEEK; GLQKNTQSKK; SKLNSILAEK; TSTPNQSIIK; NSYTFKDKLK; QSLGQYIKNK; TNIKVAGLQK; QYIKNKYLDK; QYLNTIINSY; SQSNNVLTNY; NTGSNATKNK; SLGQYIKNKY; AGLQKNTQSK; VISNISVFDR; KTNIKVAGLQK; PVYSGNSPLQK; ISINTGSNATK; AIITNTSSNSK; LLNSSTDDQAK; GQYIKNKYLDK; ILAEKKEWLNY; LLRRIAEEKNK; TIINSYTFKDK; KTHNHGFRETY; NTSTPNQSIIK; YSGNSPLQKLK; IITNTSSNSKR; TQYLNTIINSY; HGFRETYDQFK; SSCTIDANLNK
	HLA-A1101	TIINSYTFK; ITNTSSNSK; CTIDANLNK; AMMDFDQAK; KLNSILAEK; STLEEIEKK; STPNQSIIK; YSGNSPLQK; ATKNKTNIK; ETYDQFKMK; ISNISVFDR; SLGQYIKNK; GLQKNTQSK; YTFSSSFSQ; QSNNVLTNY; NIKVAGLQK; SIMNILYQE; KIESFNTQY; KLKNNLLRR; YIKNKYLDK; TNVQATPPK; NSSTDDQAK; ESTLEEIEK; ATNVQATPPK; SINTGSNATK; NTIINSYTFK; IITNTSSNSK; KLNSILAEKK; TSTPNQSIIK; IINSYTFKDK; YAMMDFDQAK; NSYTFKDKLK; ITNTSSNSKR; QSLGQYIKNK; QSNNVLTNYR; GLQKNTQSKK; VISNISVFDR; NTGSNATKNK; VYSGNSPLQK; SQSNNVLTNY; SVFDRGSAPQ; NLLRRIAEEK; SGNSPLQKLK; TNIKVAGLQK; SKLNSILAEK; TQPSFVVPVY; MSSCTIDANLN; SSCTIDANLNK; KTNIKVAGLQK; AIITNTSSNSK; ISINTGSNATK; TIINSYTFKDK; TIDANLNKDYK; PVYSGNSPLQK; NTSTPNQSIIK; SLESTLEEIEK; GQYIKNKYLDK; SQSNNVLTNYR; SSNTPEAESER; YSGNSPLQKLK; TQYLNTIINSY; QTQPSFVVPVY; LLNSSTDDQAK; KTHNHGFRETY; PATNVQATPPK; VAGLQKNTQSK; ESKLNSILAEK; IITNTSSNSKR; SIMNILYQENQ; HGFRETYDQFK
	HLA-A2402	EWLNYADAI; NTIINSYTF; DYKNKVEEL; VYSGNSPLQ; EFGSIMNIL; NYRHQTQPSF; EWLNYADAII; LYQENQNHSL; SFNTQYLNTI; DYKNKVEELL; VYSGNSPLQK; QYLNTIINSY; QYIKNKYLDK; PQQYTFSSSF; LYQENQNHSLI; VYSGNSPLQKL; SFNTQYLNTII; QYIKNKYLDKM; YLNTIINSYTF; NYRHQTQPSFV; SYTFKDKLKEL; LYAMMDFDQAK; SFSQPTSQTNF
	HLA-A2902	YLNTIINSY; KIESFNTQY; QSNNVLTNY; FGSIMNILY; EFGSIMNILY; QYLNTIINSY; SIIKPQQYTF; SQSNNVLTNY; KKIESFNTQY; SLGQYIKNKY; TQPSFVVPVY; YLNTIINSYTF; CTIDANLNKDY; ILAEKKEWLNY; NSQSNNVLTNY; SFSQPTSQTNF; TQYLNTIINSY; KTHNHGFRETY; QTQPSFVVPVY
	HLA-A6801	ETYDQFKMK; TIINSYTFK; NTPEAESER; CTIDANLNK; YTFSSSFSQ; ITNTSSNSK; ISNISVFDR; DANLNKDYK; ESTLEEIEK; TNTSSNSKR; STLEEIEKK; SNNVLTNYR; LYLNITEIR; NKTHNHGFR; STPNQSIIK; NSSTDDQAK; TNVQATPPK; KLNSILAEK; NTIINSYTF; ESFNTQYLN; NIKVAGLQK; LLRRIAEEK; YLDKMQDAR; YSGNSPLQK; DVISNISVF; ENQNHSLIR; QSNNVLTNY; INTGSNATK; SYTFKDKLK; YLNTIINSY; ATKNKTNIK; NTIINSYTFK; ITNTSSNSKR; QSNNVLTNYR; DLYLNITEIR; NSYTFKDKLK; YAMMDFDQAK; ESTLEEIEKK; VISNISVFDR; NTGSNATKNK; TSTPNQSIIK; NATKNKTNIK; IITNTSSNSK; SINTGSNATK; IINSYTFKDK; TNIKVAGLQK;

		ATNVQATPPK; NLLRRIAEEK; SNTPEAESER; YTFSSSFSQP; QYIKNKYLDK; KLNSILAEKK; TPEAESERNR; QSLGQYIKNK; ETYDQFKMKD; EFGSIMNILY; DVISNISVFDR; IITNTSSNSKR; ESKLNSILAEK; NTPEAESERNR; SSNTPEAESER; NTSTPNQSIIK; TIINSYTFKDK; SSCTIDANLNK; ISINTGSNATK; LNTIINSYTFK; TIDANLNKDYK; EKNKTHNHGFR; HGFRETYDQFK; LYAMMDFDQAK; SQSNNVLTNYR; DANLNKDYKNK; AIITNTSSNSK; PVYSGNSPLQK; NKYLDKMQDAR; YTFKDKLKELE; LLNSSTDDQAK; QTQPSFVVPVY; CTIDANLNKDY; TEFGSIMNILY; YSGNSPLQKLK; KTNIKVAGLQK; YTFSSSFSQPT; SLESTLEEIEK; PATNVQATPPK; NSQSNNVLTNY
	HLA-B0702	SPATNVQAT; VPVYSGNSP; KPQQYTFSS; VPNNTSTPN; SERNRLYAM; SPVASPATN; NPMQIANQA; APQLSSNTP; SKRNDPQSL; VPVYSGNSPL; SPVASPATNV; KPQQYTFSSS; APQLSSNTPE; SPLQKLKNNL; KMQDARQSAL; KPQQYTFSSSF; SPLQKLKNNLL; APQLSSNTPEA; SPVASPATNVQ; TPEAESERNRL; PPKQIASAQAI; SPATNVQATPP; VPVYSGNSPLQ; VASSASQASPV; VPNNTSTPNQS
	HLA-B0801	QFKMKDSAF; IIKPQQYTF; YIKNKYLDKM; YDQFKMKDSAF
	HLA-B1501	QQYTFSSSF; YLNTIINSY; KQIASAQAI; NQVNPGNPM; RQSALDLYL; KMKDSAFTL; YQENQNHSL; IQISLESTL; LQKLKNNLL; SQPTSQTNF; MQDARQSAL; SQVASSASQ; QFKMKDSAF; QSNNVLTNY; IIKPQQYTF; GQYIKNKYL; HQTQPSFVV; KNKTHNHGF; QSIIKPQQY; HNHGFRETY; TQSKKNNNL; KMQDARQSA; MQIANQANQ; SQSNNVLTNY; KMQDARQSAL; PQQYTFSSSF; TQPSFVVPVY; FSQPTSQTNF; KMKDSAFTLL; DQFKMKDSAF; KQIASAQAIQ; SIIKPQQYTF; NQNHSLIRSL; SQASPVASPA; NQSIIKPQQY; MQIANQANQA; IQTVPNNTST; SQVASSASQA; TQYLNTIINSY; YLNTIINSYTF; QTQPSFVVPVY; KTHNHGFRETY; ILAEKKEWLNY; RQSALDLYLNI; ILYQENQNHSL; SQVASSASQAS; KQIASAQAIQT; MQIANQANQAN; SQASPVASPAT; HQTQPSFVVPV; QSIIKPQQYTF; SVFDRGSAPQL; LLDVISNISVF; QQYTFSSSFSQ; TNYRHQTQPSF; SLIRSLIISGL; AMMDFDQAKTT
	HLA-B2705	RRIAEEKNK; YRHQTQPSF; NRLYAMMDF; QQYTFSSSF; RQSALDLYL; ERNRLYAMM; IRSLIISGL; KRNDPQSLGQ; ARQSALDLYL; RRIAEEKNKTH; KRNDPQSLGQY; GQYIKNKYLDK; ERNRLYAMMDF; RQSALDLYLNI; YRHQTQPSFVV; FRETYDQFKMK
	HLA-B3501	QPSFVVPVY; YLNTIINSY; NPANQVNPG; SPATNVQAT; QANQASQAS; QASQASQAS; DVISNISVF; QANQANQAS; NTIINSYTF; FGSIMNILY; NPMQIANQA; QASQASQVA; NQVNPGNPM; VPNNTSTPN; SASQASPVA; VASSASQAS; IANQANQAN; WLNYADAII; QANQANQAN; QANQANQAN; QANQANQAN; YAMMDFDQA; YQENQNHSL; VASPATNVQ; FSSSFSQPT; VPVYSGNSPL; DARQSALDLY; NPMQIANQAN; EAESERNRLY; QASPVASPAT; EFGSIMNILY; DFDQAKTTEF; YAMMDFDQAK; QASQASQVAS; TPNQSIIKPQ; SASQASPVAS; YADAIITNTS; FSQPTSQTNF; MSSCTIDANL; QASQVASSAS; ESERNRLYAM; THNHGFRETY; LDVISNISVF; FNNSQSNNVL; NPANQVNPGN; KPQQYTFSSSF; YLNTIINSYTF; PANQVNPGNPM; TPEAESERNRL; VASPATNVQAT; SPVASPATNVQ; QTQPSFVVPVY; MDFDQAKTTEF; TQYLNTIINSY; QAKTTEFGSIM; LLDVISNISVF; YAMMDFDQAKT; VPVYSGNSPLQ; IANQANQANQA; NFNNSQSNNVL; VPNNTSTPNQS; QANQANQANQA; QANQANQANQA; QANQANQANQA; SPLQKLKNNLL
	HLA-B4403	AEKKEWLNY; EEIEKKIES; AESERNRLY; TEFGSIMNI; KELESKLNS; QENQNHSLI; EEINKKIEIF; AENERNKFYA; EEKNKTQNNF; RELMISGLGT; AELKKQSQAA; TEFGSIMNILY; EEKNKTHNHGF; AESERNRLYAM; EEIEKKIESFN; KELESKLNSIL; AEKKEWLNYAD; EELLNSSTDDQ

	HLA-B5101	VPVYSGNSP; DPQSLGQYI; TPPKQIASA; SPVASPATNV; VPVYSGNSPL; PPKQIASAQAI
	HLA-B5701	FSQPTSQTNF; NSILAEKKEW;
NP_045742.1 | hypothetical protein BBA69 [Borrelia burgdorferi B31]; Seq36	HLA-A0101	LLDTYIRAY; LAEHFNKYY; DSDSLQSAF; ILEKLINNY; DSDSLQSAFY; KTLNKTLEDY;
	HLA-A0201	FLYRIALDI; NLLDTYIRA; FMGTTASEL; KMLLKRFLL; NIITMILTL; ALLEQVKSA; TMILTLICI; TLKEILEKL; KLNIIKINI; IITMILTLI; IALDIQLKL; KINIITMIL; FLLSSLDYK; SINEKLDTL; MLLKRFLLS; IAANFLYRI; LTLICISCA; SLDYKKENI; KIAANFLYRI; ALLEQVKSAL; NIITMILTLI; MLLKRFLLSS; ILTLICISCA; ITMILTLICI; KLNIIKINII; NQYDIQIAKI; LLKRFLLSSL; RIALDIQLKL; FLYRIALDIQ; NIIKINIITM; FLYRIALDIQL; MLLKRFLLSSL; LLDTYIRAYEL; MILTLICISCA; FMGTTASELKA; KINIITMILTL; NIIKINIITMI; IITMILTLICI; KLNIIKINIIT; KMLLKRFLLSS
	HLA-A0301	KLKKNTRLK; KVLAEHFNK; RIALDIQLK; KIAANFLYR; FLLSSLDYK; KSALQLQEK; CISCAPFNK; KANENTKLK; MLLKRFLLS; VLAEHFNKY; LLSSLDYKK; NQYDIQIAK; QLKLEKHLK; ALQLQEKFK; RFLLSSLDY; NTNNIQENK; ETLKEILEK; RFLLSSLDYK; KLKKNTRLKK; ALDIQLKLEK; FMGTTASELK; ALQLQEKFKK; LINNYENDPK; IQLKLEKHLK; KTLNKTLEDY; FLLSSLDYKK; VLAEHFNKYY; KANENTKLKK; QEKFKKTLNK; SALQLQEKFK; TASELKAIGK; LAEHFNKYYK; KVLAEHFNKY; CAPFNKINPK; ICISCAPFNK; NLLDTYIRAY; ANENEKMLLK; KRFLLSSLDY; TKLKKNTRLK; KMLLKRFLLS; KNQYDIQIAK; VLAEHFNKYYK; KSALQLQEKFK; KINPKANENTK; KLDTLSKENSK; SINEKLDTLSK; KFMGTTASELK; RAYELANENEK; KVLAEHFNKYY; TTASELKAIGK; TLNKTLEDYRK; KLINNYENDPK; RFLLSSLDYKK; LICISCAPFNK; LANENEKMLLK; IALDIQLKLEK; QVKSALQLQEK; KTLNKTLEDYR; NTKLKKNTRLK
	HLA-A1101	KVLAEHFNK; KIAANFLYR; CISCAPFNK; RIALDIQLK; KSALQLQEK; NTNNIQENK; NQYDIQIAK; ASELKAIGK; KANENTKLK; FLLSSLDYK; LLSSLDYKK; ETLKEILEK; ALQLQEKFK; APFNKINPK; LQLQEKFKK; KLKKNTRLK; AEHFNKYYK; QLKLEKHLK; DTLSKENSK; TASELKAIGK; SALQLQEKFK; KANENTKLKK; KVLAEHFNKY; ALQLQEKFKK; LINNYENDPK; RFLLSSLDYK; LAEHFNKYYK; FLLSSLDYKK; IQLKLEKHLK; ALDIQLKLEK; AIGKELEDRK; KLKKNTRLKK; ICISCAPFNK; FMGTTASELK; CAPFNKINPK; KTLNKTLEDY; TLNKTLEDYR; SINEKLDTLSK; TTASELKAIGK; LICISCAPFNK; RAYELANENEK; SALQLQEKFKK; VLAEHFNKYYK; IALDIQLKLEK; KSALQLQEKFK; TLNKTLEDYRK; KLINNYENDPK; KTLNKTLEDYR; KSGDLGASDEK; KINPKANENTK; KFMGTTASELK; LANENEKMLLK; KAIGKELEDRK; KVLAEHFNKYY; RFLLSSLDYKK; QVKSALQLQEK; KLDTLSKENSK; NTKLKKNTRLK; NIETLKEILEK; LQEKFKKTLNK; DIQLKLEKHLK; KRFLLSSLDYK
	HLA-A2402	DYRKNTNNI; TYIRAYELA; KYYKDSDSL; QYDIQIAKI; NFLYRIALDI; DYKKENIETL; KFMGTTASEL; LYRIALDIQL; ITMILTLICI;
	HLA-A2902	VLAEHFNKY; RFLLSSLDY; PKIAANFLY; LAEHFNKYY; ILEKLINNY; VLAEHFNKYY; KVLAEHFNKY; NLLDTYIRAY; TLICISCAPF; EILEKLINNY; KVLAEHFNKYY
	HLA-A6801	NTNNIQENK; ETLKEILEK; NTKLKKNTR; CISCAPFNK; KIAANFLYR; MGTTASELK; NQYDIQIAK; DTLSKENSK; LLSSLDYKK; FLLSSLDYK; RIALDIQLK; KVLAEHFNK; DTYIRAYEL; EKFKKTLNK; ENEKMLLKR; NPKANENTK; ENIQNFKDK; LNKTLEDYR; QLKLEKHLK; KSALQLQEK; KANENTKLK; ESNLLDTYIR; TLNKTLEDYR; TASELKAIGK; LAEHFNKYYK; LINNYENDPK; CAPFNKINPK; FMGTTASELK; FLLSSLDYKK; SALQLQEKFK; ENTKLKKNTR; NPGENIQNFK; NKVLAEHFNK; KAIGKELEDR; ICISCAPFNK; DTYIRAYELA;

		DLEALLEQVK; TTASELKAIGK; NTKLKKNTRLK; LICISCAPFNK; RAYELANENEK; DPKIAANFLYR; QVKSALQLQEK; KTLNKTLEDYR; TLNKTLEDYRK; LANENEKMLLK; NIETLKEILEK; VLAEHFNKYYK; IALDIQLKLEK; SALQLQEKFKK; DIQLKLEKHLK; EESNLLDTYIR; SINEKLDTLSK; ENKVLAEHFNK; DYKKENIETLK; NPKANENTKLK; KSALQLQEKFK; KFMGTTASELK
	HLA-B0702	KPANPGENI; AANFLYRIAL; NPKANENTKL; IAANFLYRIAL
	HLA-B0801	FKKTLNKTL; ELKAIGKEL; HLKSINEKL; LLKRFLLSSL; QLQEKFKKTL; KFKKTLNKTL; MLLKRFLLSSL; FLYRIALDIQL; IIKINIITMIL
	HLA-B1501	VLAEHFNKY; LICISCAPF; RFLLSSLDY; ILEKLINNY; FMGTTASEL; LLDTYIRAY; TLNKTLEDY; TLICISCAPF; VLAEHFNKYY; KVLAEHFNKY; NLLDTYIRAY; IQIAKITNEE; LLKRFLLSSL; IQENKVLAEH; KTLNKTLEDY; KVLAEHFNKYY; IQENKVLAEHF; LTLICISCAPF; IQNFKDKSGDL; YENDPKIAANF; IQIAKITNEES; FLYRIALDIQL
	HLA-B2705	YRIALDIQL; NQYDIQIAK; KRFLLSSLD; KRFLLSSLDY; YRIALDIQLK; YRIALDIQLKL; KRFLLSSLDYK; RKNQYDIQIAK
	HLA-B3501	NPGENIQNF; LLDTYIRAY; LAEHFNKYY; EESNLLDTY; DPKIAANFL; VLAEHFNKY; LICISCAPF; LANENEKML; SALQLQEKF; DSDSLQSAF; NIITMILTL; SDSLQSAFY; DPKIAANFLY; NLLDTYIRAY; TLICISCAPF; LANENEKMLL; DSDSLQSAFY; AANFLYRIAL; NPKANENTKL; NIIKINIITM; VLAEHFNKYY; IAANFLYRIAL; EALLEQVKSAL; YKDSDSLQSAF; LTLICISCAPF; NKVLAEHFNKY; TNEESNLLDTY; PANPGENIQNF
	HLA-B4403	KEILEKLIN; EESNLLDTY; SELKAIGKEL; EESNLLDTYI; KELEDRKNQY; KEILEKLINN; QENKVLAEHF; KENSKEDLEA; KEDLEALLEQ; KEILEKLINNY; YENDPKIAANF; KENIETLKEIL; NENEKMLLKRF; AEHFNKYYKDS
	HLA-B5101	KPANPGENI; IAANFLYRI;
	HLA-B5701	
AAT93826.1| conserved hypothetical protein BBA69[Borrelia garinii PBi]; Seq37;	HLA-A0101	QLEKHINENY;
	HLA-A0201	FIYDIPIII; ILQEILEKL; TLICISCAV; LLMRIESEL; KLNILTTTL; ILTTTLTLI; SLNYETEKI; NILTTTLTL; KLNIIKLNI; MQMKKIIYS; KQNKDLEPL; LTLICISCA; KILQEILEKL; ILNQKEIEEL; LTLICISCAV; KIAKNFIYDI; KIDNTQIDFL; NILTTTLTLI; FIYDIPIIIQ; KLNILTTTLT; IIYSSLNYET; TLTLICISCA; KLNIIKLNIL; QMKKIIYSSL; MQMKKIIYSS; LTTTLTLICI; LLMRIESELKI; MQMKKIIYSSL; KLNILTTTLTL; ILTTTLTLICI; TLTLICISCAV; FIYDIPIIIQS; ILNQKEIEELL; SLNYETEKIKI; KLETTLKILEA; KIIYSSLNYET; KLNIIKLNILT; QILNQKEIEEL; KLDKNLQHKKI
	HLA-A0301	KIIYSSLNY; KLDKNLQHK; KILQEILEK; KTSAEQLEK; QIDFLKTFK; KTNKKENIK; ASKLETTLK; KMQMKKIIY; TLKILEAQK; KILEAQKEK; SSLNYETEK; NLQHKKIAK; LMRIESELK; QSRLDIISK; KIDPEPKSK; LLMRIESELK; TQIDFLKTFK; RLDIISKVIK; LICISCAVNK; KENFKKALNK; KNLQHKKIAK; TTLKILEAQK; TASKLETTLK; SLNYETEKIK; IQSRLDIISK; KLDKNLQHKK; KKIIYSSLNY; YSSLNYETEK; KENIKNFVNK; ISKVIKNPIK; KFQDLEPSKK; ELKIKENFKK; IKILQEILEK; KALNKTIDAY; IKTSAEQLEK; TLICISCAVNK; ATASKLETTLK; IISKVIKNPIK; IIQSRLDIISK; KIDNTQIDFLK; KIKILQEILEK; ILQEILEKLDK; QLEKHINENYK; ELLMRIESELK; NTQIDFLKTFK; TLKILEAQKEK; NIKTSAEQLEK; LMRIESELKIK
	HLA-A1101	KTSAEQLEK; SSLNYETEK; KILQEILEK; KIIYSSLNY; ASKLETTLK; QIDFLKTFK; KTNKKENIK; KILEAQKEK; KFQDLEPSK; TLKILEAQK; KLDKNLQHK; QSRLDIISK; NLQHKKIAK; KIDPEPKSK; RIESELKIK; KMQMKKIIY; ICISCAVNK; TQIDFLKTFK; TTLKILEAQK; AVNKIDPEPK; TASKLETTLK; LICISCAVNK; LLMRIESELK; IQSRLDIISK; YSSLNYETEK;

		SLNYETEKIK; KLDKNLQHKK; KFQDLEPSKK; ISKVIKNPIK; KQNKDLEPLR; RLDIISKVIK; KENIKNFVNK; KENFKKALNK; AYNQDSENIK; ATASKLETTLK; TLICISCAVNK; IIQSRLDIISK; NTQIDFLKTFK; KIDNTQIDFLK; SSLNYETEKIK; IISKVIKNPIK; KIKILQEILEK; ILQEILEKLDK; ETTLKILEAQK; NIKTSAEQLEK; CAVNKIDPEPK; IYSSLNYETEK; ELLMRIESELK; SLPEDEKMQMK; TLKILEAQKEK; KSKTNKKENIK; QLEKHINENYK
	HLA-A2402	NFIYDIPII; AYNQDSENI; NYETEKIKI; IYSSLNYET; KYPEATASK; KYPEATASKL; NFIYDIPIII; IYSSLNYETE; NYKEFNSLKPI; IYSSLNYETEK
	HLA-A2902	KIIYSSLNY; EFNSLKPIY; KKIAKNFIY; KMQMKKIIY; DLEPLREKY; ; YKEFNSLKPIY
	HLA-A6801	DNTQIDFLK; DIPIIIQSR; NYKEFNSLK; QIDFLKTFK; ENIKNFVNK; SSLNYETEK; TLKILEAQK; ELKIKENFK; ENFKKALNK; KTSAEQLEK; ETEKIKILQ; QNKDLEPLR; EPKSKTNKK; EKHINENYK; EIAKIDNTQ; EKENIEIAK; TTLKILEAQK; TASKLETTLK; YSSLNYETEK; ENYKEFNSLK; TQIDFLKTFK; LLMRIESELK; LICISCAVNK; YDIPIIIQSR; EKYPEATASK; ELKIKENFKK; AVNKIDPEPK; ISKVIKNPIK; ETTLKILEAQ; SLNYETEKIK; IDNTQIDFLK; ETTLKILEAQK; TLICISCAVNK; NTQIDFLKTFK; DAYNQDSENIK; ATASKLETTLK; ESELKIKENFK; NIKTSAEQLEK; IYSSLNYETEK; ELLMRIESELK; IISKVIKNPIK; CAVNKIDPEPK; NENYKEFNSLK; TLKILEAQKEK; NQKEIEELLMR; DPHDSLPEDEK; IIQSRLDIISK; QLEKHINENYK; SSLNYETEKIK
	HLA-B0702	YPEATASKL; IPIIIQSRL; LPEDEKMQM; KIKENFKKAL; EPSKKQNKDL; NPIKDELQIL; IPIIIQSRLDI; YPEATASKLET
	HLA-B0801	MKKIIYSSL; FKKALNKTI; KIKILQEIL; QMKKIIYSSL; KIKENFKKAL; IIKLNILTTTL
	HLA-B1501	TQIDFLKTF; KIIYSSLNY; ALNKTIDAY; KMQMKKIIY; HINENYKEF; KQNKDLEPL; LQILNQKEI; KLNILTTTL; KKIAKNFIY; LQHKKIAKNF; QMKKIIYSSL; KALNKTIDAY; AQKEKENIEI; NQKEIEELLM; QLEKHINENY; MQMKKIIYSSL; EQLEKHINENY; KLNILTTTLTL; IAKIDNTQIDF
	HLA-B2705	SRLDIISKV; MRIESELKI; MRIESELKIK; SRLDIISKVI; SRLDIISKVIK; MQMKKIIYSSL
	HLA-B3501	LPEDEKMQM; YPEATASKL; EFNSLKPIY; TASKLETTL; IPIIIQSRL; KALNKTIDAY; NPIKDELQIL; EKMQMKKIIY; YPEATASKLET; EPLREKYPEAT; YKEFNSLKPIY; EATASKLETTL
	HLA-B4403	EELLMRIES; SELKIKENF; KEIEELLMR; KEFNSLKPI; KEFNSLKPIY; KEIEELLMRI; QEILEKLDKNL; EELLMRIESEL; SENIKTSAEQL; KENIKNFVNKF
	HLA-B5101	IPIIIQSRL; NPIKDELQI; ; IPIIIQSRLDI
	HLA-B5701	
NP_045573.1 | hypothetical protein BBI42 [Borrelia burgdorferi B31]; Seq38	HLA-A0101	PVSDYNEEY; FMRIVRWLY; VSDYNEEYF; YSGEEGSPEY; SSDMGSDEIV; YSGEEGSPEYY; GSDEIVTEGIF
	HLA-A0201	WLYSCIEEL; KLYASEHRL; YLPDNQEQA; ILVGVCIIA; ALALLGCYL; YASEHRLLV; LVGVCIIAL; LLVEIKKTL; DLIKLFIMV; TAYQQYLKV; YLPDNQEQAV; ILVGVCIIAL; KLYASEHRLL; LLVEIKKTLI; GIFSSLKLYA; IVTEGIFSSL; RIVRWLYSCI; SLKDPNYRGV; RLLVEIKKTL; LVGVCIIALA; RILVGVCIIA; KLYASEHRLLV; ILVGVCIIALA; RILVGVCIIAL; WLYSCIEELYS; YASEHRLLVEI; RLLVEIKKTLI; IIALALLGCYL
	HLA-A0301	LIKLFIMVK; GIFSSLKLY; PTAYQQYLK; ELYSPDIKY; VTEGIFSSLK; KFMRIVRWLY; RPTAYQQYLK; DLIKLFIMVK; TAYQQYLKVK; SLKLYASEHR; FLDLGSEQSK; IIALALLGCY; EIKKTLISLK;

		WLYSCIEELY; MVKNEQNNNK; SDYNEEYFNK; IVTEGIFSSLK; KLYASEHRLLV; IMVKNEQNNNK; CIIALALLGCY; TAYQQYLKVKR
	HLA-A1101	LIKLFIMVK; PTAYQQYLK; GIFSSLKLY; IALALLGCY; KVKRYDYNR; ISLKDPNYR; TEGIFSSLK; AYQQYLKVK; VTEGIFSSLK; TAYQQYLKVK; MVKNEQNNNK; DLIKLFIMVK; SDYNEEYFNK; RPTAYQQYLK; GSEQSKDLIK; IIALALLGCY; EIKKTLISLK; TLISLKDPNY; LISLKDPNYR; KFMRIVRWLY; IVTEGIFSSLK; ASEHRLLVEIK; VSDYNEEYFNK; TAYQQYLKVKR; TLISLKDPNYR; SSLKLYASEHR; CIIALALLGCY; KTLISLKDPNY; IMVKNEQNNNK; PTAYQQYLKVK; GSPEYYRNMPR; CIEELYSPDIK; KDLIKLFIMVK
	HLA-A2402	LYASEHRLL; KFMRIVRWL; DYNRPVPIL; DYNEEYFNK; NYRGVVLPV; DYNEEYFNKF; RYDYNRPVPI; EYFNKFFLDL; LYASEHRLLV; RWLYSCIEEL; KFMRIVRWLY; DYNEEYFNKFF; RYDYNRPVPIL; RWLYSCIEELY; CYLPDNQEQAV; YYRNMPRPTAY
	HLA-A2902	ELYSPDIKY; FMRIVRWLY; LYSCIEELY; PVSDYNEEY; YLKVKRYDY; IALALLGCY; KFMRIVRWLY; QYLKVKRYDY; TLISLKDPNY; YSGEEGSPEY; WLYSCIEELY; YRNMPRPTAY; IIALALLGCY; YQQYLKVKRY; DYNEEYFNKF; YYRNMPRPTAY; CIIALALLGCY; NMPRPTAYQQY; VLPVSDYNEEY; KYSGEEGSPEY; YSGEEGSPEYY; RWLYSCIEELY; DYNEEYFNKFF
	HLA-A6801	EQNNNKFMR; PTAYQQYLK; KVKRYDYNR; NNKFMRIVR; LIKLFIMVK; DYNEEYFNK; ISLKDPNYR; YQQYLKVKR; EEGSPEYYR; LYSCIEELY; ELYSPDIKY; QTFFENSES; TEGIFSSLK; FMRIVRWLY; MVKNEQNNNK; EIKKTLISLK; VTEGIFSSLK; TAYQQYLKVK; SLKLYASEHR; DLIKLFIMVK; LISLKDPNYR; NNNKFMRIVR; SPEYYRNMPR; RPTAYQQYLK; WLYSCIEELY; SDYNEEYFNK; NEQNNNKFMR; EGIFSSLKLY; TAYQQYLKVKR; IVTEGIFSSLK; TLISLKDPNYR; SSLKLYASEHR; YLKVKRYDYNR; IMVKNEQNNNK; PTAYQQYLKVK; CIEELYSPDIK; QNNNKFMRIVR; CIIALALLGCY; GSPEYYRNMPR; NKFMRIVRWLY
	HLA-B0702	DPNYRGVVL; RPTAYQQYL; YASEHRLLV; MPRPTAYQQ; SPEYYRNMP; IVTEGIFSSL; SPEYYRNMPR; MPRPTAYQQY; MPRPTAYQQYL; RPTAYQQYLKV; DPNYRGVVLPV; LPVSDYNEEYF; RILVGVCIIAL; YASEHRLLVEI
	HLA-B0801	YLKVKRYDY; EIKKTLISL; ; MPRPTAYQQYL; FMRIVRWLYSC
	HLA-B1501	QQYLKVKRY; FMRIVRWLY; YLKVKRYDY; RNMPRPTAY; QSKDLIKLF; NQEQAVQTF; GVVLPVSDY; IALALLGCY; ELYSPDIKY; KLYASEHRL; SGEEGSPEY; YQQYLKVKRY; YSGEEGSPEY; WLYSCIEELY; IIALALLGCY; ILVGVCIIAL; EQSKDLIKLF; NQEQAVQTFF; IVTEGIFSSL; TLISLKDPNY; KLYASEHRLL; RGVVLPVSDY; QQYLKVKRYDY; YSGEEGSPEYY; MVKNEQNNNKF; NMPRPTAYQQY; YYRNMPRPTAY; VLPVSDYNEEY; CIIALALLGCY
	HLA-B2705	HRLLVEIKK; KRYDYNRPV; MRILVGVCI; YQQYLKVKR; QQYLKVKRY; YRNMPRPTAY; KRYDYNRPVP; KRYDYNRPVPI; HRLLVEIKKTL; YRGVVLPVSDY; VRWLYSCIEEL; QQYLKVKRYDY; MRIVRWLYSCI
	HLA-B3501	DPNYRGVVL; LPDNQEQAV; NQEQAVQTF; IALALLGCY; LPVSDYNEE; PVSDYNEEY; SGEEGSPEY; YNEEYFNKF; LVGVCIIAL; LPVSDYNEEY; MPRPTAYQQY; YSGEEGSPEY; LPDNQEQAVQ; WLYSCIEELY; YRNMPRPTAY; FFENSESSDM; IIALALLGCY; LPVSDYNEEYF; MPRPTAYQQYL; LPDNQEQAVQT; YSGEEGSPEYY; MVKNEQNNNKF; YYRNMPRPTAY; YASEHRLLVEI; LVGVCIIALAL; DPNYRGVVLPV; TFFENSESSDM
	HLA-B4403	NEEYFNKFF; EEYFNKFFL; VEIKKTLIS; DEIVTEGIF; SEHRLLVEI; GEEGSPEYY; EELYSPDIKY; DEIVTEGIFS; VEIKKTLISL; SEQSKDLIKLF; EELYSPDIKYS; EEYFNKFFLDL; EEGSPEYYRNM;

		TEGIFSSLKLY
	HLA-B5101	LPDNQEQAV; LPVSDYNEEY; LPVSDYNEEYF; MPRPTAYQQYL
	HLA-B5701	
NP_051318.1 | revA protein[Borrelia burgdorferi B31]; Seq39	HLA-A0101	
	HLA-A0201	SLMEDVLAL; FVMACKAYV; KLVGVTVPL; LMEDVLALV; KLAAKLAAL; KIWSEAKLV; LFFASMLFV; MLFVMACKA; FQDKLAAKL; LVGVTVPLL; FASMLFVMA; FFASMLFVM; SLMEDVLALV; KLFFASMLFV; KLVGVTVPLL; KMSKNAVEQI; SMLFVMACKA; NIFKLFFASM; NLKDIGNAEL; NLQNSFQDKL; FFASMLFVMA; MLFVMACKAYV; KIWSEAKLVGV; KLFFASMLFVM; KLAAKLAALKA; FKLFFASMLFV; NIFKLFFASML; FQDKLAAKLAA
	HLA-A0301	SMLFVMACK; KLAALKAAK; LAAKLAALK; LVNDSSGGK; KLFFASMLF; NLQNSFQDK; KLAAKLAALK; ASMLFVMACK; ALVNDSSGGK; SSGGKFKDYK; KLFFASMLFV; KLLNLQNSFQ; AKLAALKAAK; TSGNGDKMSK; MLFVMACKAY; KINELKENLK; GSNTSGNGDK; NSFQDKLAAK; LLNLQNSFQDK; LVNDSSGGKFK; VMACKAYVEEK; FASMLFVMACK; KLFFASMLFVM; ISKRKIWSEAK; KLAAKLAALKA; SMLFVMACKAY; MSKNAVEQIDK; NTSGNGDKMSK
	HLA-A1101	SMLFVMACK; LVNDSSGGK; KLAALKAAK; LAAKLAALK; NTIENITDK; SFQDKLAAK; SGNGDKMSK; NLQNSFQDK; ASMLFVMACK; KLAAKLAALK; KINELKENLK; MACKAYVEEK; SSGGKFKDYK; NSFQDKLAAK; TSGNGDKMSK; GSNTSGNGDK; ALVNDSSGGK; ITDKDQDISK; AVEQIDKVIK; LVNDSSGGKFK; FASMLFVMACK; VMACKAYVEEK; NTSGNGDKMSK; MACKAYVEEKK; AAKLAALKAAK; MSKNAVEQIDK; LLNLQNSFQDK; ISKRKIWSEAK; LALVNDSSGGK; SMLFVMACKAY; NITDKDQDISK; DSSGGKFKDYK
	HLA-A2402	FFASMLFVM; DYKDKINEL; KLFFASMLF; IFKLFFASML; IFKLFFASMLF
	HLA-A2902	FFASMLFVM; KLLNLQNSF; MLFVMACKAY; SMLFVMACKAY
	HLA-A6801	NTIENITDK; LAAKLAALK; LVNDSSGGK; SMLFVMACK; CKAYVEEKK; KLAALKAAK; NLQNSFQDK; MACKAYVEEK; NSFQDKLAAK; ASMLFVMACK; MLFVMACKAY; DYKDKINELK; TSGNGDKMSK; SSGGKFKDYK; KLAAKLAALK; KINELKENLK; DIGNAELKEK; ITDKDQDISK; MACKAYVEEKK; NTSGNGDKMSK; FASMLFVMACK; DSSGGKFKDYK; LVNDSSGGKFK; MSKNAVEQIDK; NLKDIGNAELK; NAVEQIDKVIK; ITDKDQDISKR; VMACKAYVEEK; NITDKDQDISK; LALVNDSSGGK; LLNLQNSFQDK; ISKRKIWSEAK
	HLA-B0702	KLAAKLAAL; VPLLGSNTSG;
	HLA-B0801	IFKLFFASM; KLAAKLAAL; IFKLFFASML; EAKLVGVTVPL; QDKLAAKLAAL
	HLA-B1501	KLLNLQNSF; KLFFASMLF; SLMEDVLAL; EQIDKVIKF; KLVGVTVPL; KLAAKLAAL; LFVMACKAY; MLFVMACKAY; LVNDSSGGKF; NLKDIGNAEL; KLVGVTVPLL; EQIDKVIKFL; SMLFVMACKAY; ALVNDSSGGKF; KLFFASMLFVM; IFKLFFASMLF; KEKLLNLQNSF
	HLA-B2705	KRKIWSEAK; RKIWSEAKL; MRNKNIFKL; KRKIWSEAKL; MRNKNIFKLF; MRNKNIFKLFF
	HLA-B3501	FFASMLFVM; LFVMACKAY; VPLLGSNTS; FASMLFVMA; MLFVMACKAY; FASMLFVMAC; LVNDSSGGKF; LFFASMLFVM; FKLFFASMLF; NAVEQIDKVI; NIFKLFFASM; DSLMEDVLAL; EAKLVGVTVPL; SMLFVMACKAY
	HLA-B4403	AELKEKLLN; KEKLLNLQN; KENLKDIGN; KEIDSLMED; EEKKEIDSL; AELKEKLLNL; EEKKEIDSLM; KENLKDIGNA; SEAKLVGVTV; KEIDSLMEDVL; KEKLLNLQNSF; AELKEKLLNLQ
	HLA-B5101	VPLLGSNTS; LAALKAAKNTI
	HLA-B5701	
NP_045737.1	HLA-A0101	YTEERRMLY; DTDDLIDEY; STVHFDSHEY; NSTVHFDSHEY;

| BBA64 antigen, P35 [Borrelia burgdorferi B31]; Seq40		QTDVSKLNDTL; LKDTDDLIDEY; QLNKPNLETLY
	HLA-A0201	ILISCSLEV; FLLHVLTVL; ILDPEVAKL; TLINRGFSI; TLYNDFEKL; LIAIFLLHV; KILDRSENI; VLILISCSL; LLHVLTVLI; HVLTVLILI; AMEEISAKI; NLLVAINNL; NIHDIILDL; NLGQILSKL; KIFNLGQIL; IILDLVNTT; QLAMEEISA; TTTNILAPI; AQFANIHDI; KLIAIFLLHV; FLLHVLTVLI; LILISCSLEV; NIHDIILDLV; AIFLLHVLTV; KIFFNANSTV; KILDPEVAKL; ILDPEVAKLI; LLHVLTVLIL; LAMEEISAKI; KILDRSENII; GMRAEIFSKI; KLQQLNKPNL; LIAIFLLHVL; QLNKPNLETL; IILDLVNTTT; TVLILISCSL; EIFSKIFFNA; KLTSLKEKWL; FSIQLAMEEI; FLLHVLTVLIL; KLIAIFLLHVL; VLILISCSLEV; TLINRGFSIQL; LLHVLTVLILI; ILDLVNTTTNI; LIDEYNTNPDL; ILDRSENIIQI; QLAMEEISAKI; KLSQDSNYRGL; IAIFLLHVLTV; KILDPEVAKLI; AQFANIHDIIL; AIFLLHVLTVL; LTVLILISCSL; ILNVKDKLQQL; NILKNNKLIAI; FANIHDIILDL
	HLA-A0301	KLIAIFLLH; GMRAEIFSK; KLNDTLRSK; LLVAINNLK; ISAKILNVK; KILDPEVAK; KLIQKILDR; LISCSLEVK; KLSQDSNYR; TSLKEKWLK; TVHFDSHEY; KLIAIFLLH; GMRAEIFSK; KLNDTLRSK; LLVAINNLK; ISAKILNVK; KILDPEVAK; KLIQKILDR; LISCSLEVK; KLSQDSNYR; TSLKEKWLK; TVHFDSHEY; KIFNLGQILSK; KLTSLKEKWLK; QLNKPNLETLY; KIFFNANSTVH; LILISCSLEVK; ISAKILNVKDK; ILSKLSQDSNY; IQLAMEEISAK; NVKDKLQQLNK
	HLA-A1101	TSLNFNEGK; TSLKEKWLK; KILDPEVAK; GMRAEIFSK; NANANNAPK; ISAKILNVK; KLNDTLRSK; LAMEEISAK; ETLYNDFEK; LLVAINNLK; LISCSLEVK; KLIAIFLLH; TVHFDSHEY; DSNYRGLVK; YTEERRMLY; KLSQDSNYR; LVKETLINR; KLIQKILDR; EVKDSNESK; AINNLKNPTK; YTSLNFNEGK; ILISCSLEVK; LTSLKEKWLK; KANSKASKQK; NANANNAPKK; STVHFDSHEY; NLLVAINNLK; QLAMEEISAK; EISAKILNVK; IFNLGQILSK; AAGKNKANSK; SAKILNVKDK; FGMRAEIFSK; IQISEMDSSR; EVKDSNESKK; KIFNLGQILSK; VAINNLKNPTK; KLTSLKEKWLK; IQLAMEEISAK; LILISCSLEVK; SQDSNYRGLVK; NVKDKLQQLNK; ISAKILNVKDK; VSKLNDTLRSK; SLEVKDSNESK; IIQISEMDSSR; QFGMRAEIFSK; NLETLYNDFEK; KIFFNANSTVH
	HLA-A2402	RMLYTSLNF; QFANIHDII; IFLLHVLTV; EYNTNPDLQ; KWLKDTDDL; QFGMRAEIF; KWLKDTDDLI; IFLLHVLTVL; FFNANSTVHF; QFANIHDIIL; NYRGLVKETL; IFLLHVLTVLI; IFFNANSTVHF; NYRGLVKETLI; LYNDFEKLTSL
	HLA-A2902	TVHFDSHEY; NKPNLETLY; YTEERRMLY; RMLYTSLNF; STVHFDSHEY; FFNANSTVHF; EYTEERRMLY; QLNKPNLETLY; IFFNANSTVHF; ILSKLSQDSNY
	HLA-A6801	ETLYNDFEK; DSHEYTEER; EVKDSNESK; QISEMDSSR; LLVAINNLK; TSLNFNEGK; DTLRSKNSR; NANANNAPK; TVHFDSHEY; ISAKILNVK; EPNDQFGMR; LAMEEISAK; TSLKEKWLK; YTEERRMLY; VSKLNDTLR; DFEKLTSLK; LISCSLEVK; LVKETLINR; EIFSKIFFN; DSNESKKHK; DSNYRGLVK; ESKKHKKEK; TTNILAPIQ; KLSQDSNYR; NPTKPAAGK; STVHFDSHE; FSIQLAMEE; DTDDLIDEY; YTSLNFNEGK; DVSKLNDTLR; DSHEYTEERR; EVKDSNESKK; NANANNAPKK; EISAKILNVK; STVHFDSHEY; LTSLKEKWLK; ESKKHKKEKR; NLLVAINNLK; DSNESKKHKK; TTTNILAPIQ; ILISCSLEVK; QLAMEEISAK; IQISEMDSSR; FGMRAEIFSK; NDFEKLTSLK; LETLYNDFEK; FDSHEYTEER; EYTEERRMLY; MLYTSLNFNE; IFNLGQILSK; AINNLKNPTK; SAKILNVKDK; LSKLSQDSNYR; IIQISEMDSSR; LYTSLNFNEGK; ENLLVAINNLK; NLETLYNDFEK; ISAKILNVKDK; NVKDKLQQLNK; NPNANANNAPK; HFDSHEYTEER; VAINNLKNPTK; NSTVHFDSHEY; EEISAKILNVK; TDVSKLNDTLR; KIFNLGQILSK; LILISCSLEVK; NTTTNILAPIQ; VAKLIQKILDR;

		KLTSLKEKWLK; ESKKHKKEKRK; ETLINRGFSIQ
	HLA-B0702	KPAAGKNKA; LVNTTTNIL; KPAAGKNKAN; APKKILDPEV; KPNLETLYNDF; APKKILDPEVA; NPDLQTDVSKL; KPAAGKNKANS
	HLA-B0801	VAKLIQKIL; ILKNNKLIAI; LLHVLTVLIL;
	HLA-B1501	RMLYTSLNF; TVHFDSHEY; RSKNSRAQF; AQFANIHDI; YTEERRMLY; FNANSTVHF; LNFNEGKIF; VLILISCSL; KLIAIFLLH; KIFNLGQIL; TLINRGFSI; STVHFDSHEY; FFNANSTVHF; DQFGMRAEIF; LSKLSQDSNY; SLNFNEGKIF; AQFANIHDII; SSRGEPNDQF; GMRAEIFSKIF; AQFANIHDIIL; LVKETLINRGF; QLNKPNLETLY; ILKNNKLIAIF; ILSKLSQDSNY; KLIAIFLLHVL; IFFNANSTVHF; TLRSKNSRAQF; IQKILDRSENI; TLINRGFSIQL; QQLNKPNLETL; INRGFSIQLAM; TSLNFNEGKIF
	HLA-B2705	KRKGKVENL; RRMLYTSLN; YRGLVKETL; ERRMLYTSL; MRAEIFSKI; RMLYTSLNF; RRMLYTSLNF; MRAEIFSKIF; LRSKNSRAQF; KRKGKVENLL; MRAEIFSKIFF; KRKGKVENLLV; ERRMLYTSLNF; RRMLYTSLNFN
	HLA-B3501	TVHFDSHEY; FANIHDIIL; IAIFLLHVL; NPDLQTDVS; LVNTTTNIL; DTDDLIDEY; FFNANSTVH; RAEIFSKIF; EPNDQFGMR; FNANSTVHF; NPNANANNA; FFNANSTVHF; STVHFDSHEY; EPNDQFGMRA; MRAEIFSKIF; NPNANANNAP; RAEIFSKIFF; DLVNTTTNIL; KPNLETLYNDF; FANIHDIILDL; NSTVHFDSHEY; EPNDQFGMRAE; NPDLQTDVSKL; LAMEEISAKIL; IFFNANSTVHF; LKDTDDLIDEY; NPNANANNAPK; NANSTVHFDSH; MRAEIFSKIFF; TSLNFNEGKIF
	HLA-B4403	AEIFSKIFF; EEISAKILN; KETLINRGF; SEMDSSRGE; GEPNDQFGM; EEISAKILNV; SENIIQISEM; AEIFSKIFFN; AEIFSKIFFNA; SEMDSSRGEPN; EEISAKILNVK; KETLINRGFSI; HEYTEERRMLY; SENIIQISEMD
	HLA-B5101	IAIFLLHVL; LAMEEISAKI; LHVLTVLILI; IAIFLLHVLTV
	HLA-B5701	KLTSLKEKW; STVHFDSHEY; NSTVHFDSHEY
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi]; Seq41	HLA-A0101	FTDIHNIIL; YVNERRILY; DVDDIIKDY; RTDISKLNDY; STVTFDDNEY; FTDIHNIILN; FTDIHNIILNL; HLNKPNLKTLY; GSTVTFDDNEY; RTDISKLNDYI
	HLA-A0201	FLLHILTGL; ILLSCSLEV; VTFDDNEYV; ILINRGFSI; NLINTTTNI; HILTGLILL; NLLVAINTL; TLYHDFNKL; KLNDYIISK; AQFTDIHNI; LIAIFLLHI; GLILLSCSL; QLAIEEISL; FTDIHNIIL; YIISKNSKA; NLGKILSKL; KILERSEDI; SIQLAIEEI; TTTNILAPI; LLHILTGLI; TVDNLLVAI; ALKQIDPEA; ILTGLILLS; ILNLINTTT; KLIAIFLLHI; FLLHILTGLI; LILLSCSLEV; TLYHDFNKLI; KIFFNAGSTV; KILERSEDIV; NLINTTTNIL; LIAIFLLHIL; YVNERRILYT; KLIPLKEKWL; IQLAIEEISL; KTLYHDFNKL; TVTFDDNEYV; FSIQLAIEEI; LLHILTGLIL; SQDSNYRSLV; LINTTTNILA; EIFSKIFFNA; AQFTDIHNII; FLLHILTGLIL; KLIAIFLLHIL; GLILLSCSLEV; ILINRGFSIQL; ILNLINTTTNI; FTDIHNIILNL; STVTFDDNEYV; NLINTTTNILA; AIFLLHILTGL; LLHILTGLILL; KLSQDSNYRSL; AQFTDIHNIIL; IIKDYNANPEL; KLNDYIISKNS; ILNLGKILSKL; KTLYHDFNKLI; SIQLAIEEISL; ILERSEDIVQI
	HLA-A0301	KLNDYIISK; KSNSAAALK; KLIAIFLLH; LLVAINTLK; KTLYHDFNK; KLSKNAKNK; ISLRTLNVK; YVNERRILY; SSKMKKLSK; EMKAEIFSK; KLSQDSNYR; TSLNFNENK; DSNYRSLVK; LNLGKILSK; ILNLGKILSK; NLLVAINTLK; AINTLKNPPK; LIPLKEKWLK; KQPNNANALK; KMKKLSKNAK; QDSNYRSLVK; KLSKNAKNKK; NSSKMKKLSK; SLRTLNVKDK; KSENNSSKMK; SENNSSKMKK; EISLRTLNVK; SKLNDYIISK; IQHLNKPNLK; YTSLNFNENK; NKSNSAAALK; LKNPPKTAGK; TSKSENNSSK; QKKAKTKTSK; HDFNKLIPLK; SLVKEILINR; ALKQIDPEAK; FEMKAEIFSK; KILNLGKILSK;

		HLNKPNLKTLY; KLIPLKEKWLK; KIQHLNKPNLK; KTSKSENNSSK; TLKNPPKTAGK; KSENNSSKMKK; KQKKAKTKTSK; NLKTLYHDFNK; ILSKLSQDSNY; ISKLNDYIISK; RSLVKEILINR; ISLRTLNVKDK; IVQISEIDANK; NVKDKIQHLNK
	HLA-A1101	KTLYHDFNK; KSNSAAALK; KLNDYIISK; TSLNFNENK; SSKMKKLSK; ISLRTLNVK; LLVAINTLK; KLIAIFLLH; QISEIDANK; DSNYRSLVK; YVNERRILY; EMKAEIFSK; KLSKNAKNK; LVKEILINR; KLSQDSNYR; LAIEEISLR; AINTLKNPPK; YTSLNFNENK; ILNLGKILSK; TSKSENNSSK; VQISEIDANK; NSSKMKKLSK; KSENNSSKMK; IQHLNKPNLK; NLLVAINTLK; KQPNNANALK; EISLRTLNVK; KLSKNAKNKK; KMKKLSKNAK; SLVKEILINR; ALKQIDPEAK; STVTFDDNEY; SENNSSKMKK; SKLNDYIISK; EVNQDDNQEK; LIPLKEKWLK; SLRTLNVKDK; HDFNKLIPLK; KTSKSENNSSK; KIQHLNKPNLK; KILNLGKILSK; VAINTLKNPPK; IVQISEIDANK; KSENNSSKMKK; KLIPLKEKWLK; SQDSNYRSLVK; ISKLNDYIISK; RSLVKEILINR; NVKDKIQHLNK; ISLRTLNVKDK; TLKNPPKTAGK; NLKTLYHDFNK; IQLAIEEISLR; KQKKAKTKTSK; NALKQIDPEAK; LYTSLNFNENK
	HLA-A2402	LYHDFNKLI; KWLKDVDDI; NYRSLVKEI; QFTDIHNII; RILYTSLNF; EYVNERRIL; KWLKDVDDII; FFNAGSTVTF; IFLLHILTGL; NYRSLVKEIL; IFLLHILTGLI; IFFNAGSTVTF; NYRSLVKEILI; LYHDFNKLIPL
	HLA-A2902	YVNERRILY; TVTFDDNEY; EYVNERRILY; FFNAGSTVTF; STVTFDDNEY; HLNKPNLKTLY; ILSKLSQDSNY; YIISKNSKAQF; IFFNAGSTVTF
	HLA-A6801	LAIEEISLR; ELIQKILER; TSLNFNENK; LLVAINTLK; QISEIDANK; EMKAEIFSK; LVKEILINR; DYNANPELR; TVTFDDNEY; DSNYRSLVK; KSNSAAALK; DFNKLIPLK; ENNSSKMKK; KTLYHDFNK; QPNNANALK; EIFSKIFFN; DNEYVNERR; DYIISKNSK; YVNERRILY; DDNEYVNER; LSKNAKNKK; TTNILAPIQ; KLSQDSNYR; KLNDYIISK; ENKILNLGK; YTSLNFNENK; EVNQDDNQEK; EISLRTLNVK; QLAIEEISLR; TSKSENNSSK; STVTFDDNEY; SLVKEILINR; NLLVAINTLK; NSSKMKKLSK; TTTNILAPIQ; DDNEYVNERR; HDFNKLIPLK; NKSNSAAALK; FEMKAEIFSK; LIPLKEKWLK; ILNLGKILSK; NDYIISKNSK; LKTLYHDFNK; LSKLSQDSNYR; LYTSLNFNENK; IVQISEIDANK; KTSKSENNSSK; NVKDKIQHLNK; NLKTLYHDFNK; TFDDNEYVNER; ISKLNDYIISK; DNLLVAINTLK; IQLAIEEISLR; EEISLRTLNVK; VAINTLKNPPK; NALKQIDPEAK; DFNKLIPLKEK; NTTTNILAPIQ; TLKNPPKTAGK
	HLA-B0702	KPTVDNLLV; KPNLKTLYH; KPTVDNLLVA; KPTVDNLLVAI; NPELRTDISKL; KPNLKTLYHDF; QPNNANALKQI
	HLA-B0801	
	HLA-B1501	YVNERRILY; FNAGSTVTF; KQPNNANAL; RILYTSLNF; ISKNSKAQF; ILINRGFSI; TVTFDDNEY; NLKTLYHDF; AQFTDIHNI; KLIAIFLLH; GLILLSCSL; IQHLNKPNL; FFNAGSTVTF; KQIDPEAKEL; IQLAIEEISL; LSKLSQDSNY; DQFEMKAEIF; AQFTDIHNII; STVTFDDNEY; IISKNSKAQF; EMKAEIFSKIF; IFFNAGSTVTF; LVKEILINRGF; AQFTDIHNIIL; ALKQPNNANAL; ILSKLSQDSNY; HLNKPNLKTLY; YIISKNSKAQF; ILINRGFSIQL; KLIAIFLLHIL; KLSQDSNYRSL; KQIDPEAKELI
	HLA-B2705	RRILYTSLN; KKAKTKTSK; ERRILYTSL; YRSLVKEIL; RRILYTSLNF; KQKKAKTKTSK; ERRILYTSLNF; RRILYTSLNFN
	HLA-B3501	TVTFDDNEY; YVNERRILY; FNAGSTVTF; IAIFLLHIL; FFNAGSTVT; LINTTTNIL; NKSNSAAAL; NLLVAINTL; EPDDQFEMK; KAEIFSKIF; FFNAGSTVTF; STVTFDDNEY; MKAEIFSKIF; MKNNKLIAIF; EPDDQFEMKA; DQFEMKAEIF; IFFNAGSTVTF; KPNLKTLYHDF;

		DANKGEPDDQF; LAIEEISLRTL; EPDDQFEMKAE; MKAEIFSKIFF; NPELRTDISKL; YIISKNSKAQF
	HLA-B4403	KEILINRGF; AEIFSKIFF; SEIDANKGE; FEMKAEIFS; GEPDDQFEM; EEISLRTLN; EEISLRTLNV; KEILINRGFS; AEIFSKIFFN; SEIDANKGEP; SEDIVQISEI; KEILINRGFSI; AEIFSKIFFNA; SEIDANKGEPD; NEYVNERRILY
	HLA-B5101	IAIFLLHIL; ; IPLKEKWLKDV; KPTVDNLLVAI
	HLA-B5701	KLIPLKEKW; STVTFDDNEY; GSTVTFDDNEY
AAL84596.1| BBK32 [Borrelia burgdorferi]; Seq42	HLA-A0101	FSTKLTQMY; ISCDLFIRY; IIDKNGVWY; YTDEIEEEDY; NTINKIYDTY; FISCDLFIRY; YLDEDDEDDEY; DSAINTINKIY
	HLA-A0201	LLNYIQVSV; GLFDKGNSI; YLEGVKYNV; KTAANFVYI; KLENIEAEI; NLYEAYKAI; AIVTSILLM; KTLLNYIQV; LMRDSLKEV; YLALGLLFG; TLLNYIQVS; ILETSEESI; ALGLLFGFI; SLSGESGEL; MTQGSLNSL; TLLNYIQVSV; LLMRDSLKEV; LLFGFISCDL; GLFDKGNSIL; RLSNRYQSYL; NLYEAYKAIV; KLTQMYSTRL; QMYSTRLDNL; KIYDTYTLFS; GMTQGSLNSL; SILETSEESI; YLALGLLFGF; TLFSTKLTQM; LALGLLFGFI; YLALGLLFGFI; KIYDTYTLFST; SLQDIAGSNSI; KTLLNYIQVSV; ILLMRDSLKEV; GLLFGFISCDL; YTDEIEEEDYA; ILEEESLKTEL; TINKIYDTYTL; QMYSTRLDNLA; LLNYIQVSVKT; TQMYSTRLDNL; NLYEAYKAIVT; YINDTHAKRKL
	HLA-A0301	ILLMRDSLK; RLSNRYQSY; SIKKPMNKK; SLKRDSANK; RLDNLAKAK; DTYTLFSTK; QSNLYEAYK; IVTSILLMR; KLTQMYSTR; KIKEQSNLY; VILEEESLK; ESIKKPMNK; STRLDNLAK; ISCDLFIRY; ESLKTELLK; KGKSKVSRK; IARKKGKSK; KNFKTLLNY; QSYLEGVKY; LNYIQVSVK; LLNYIQVSVK; SLSGESGELK; SILLMRDSLK; KIARKKGKSK; KPMNKKGKGK; AIVTSILLMR; RYQSYLEGVK; GIIDKNGVWY; FVYINDTHAK; SANKSNFLQK; ITIDSDLRPK; RKEPYIHSLK; LLKEQSETRK; CDLFIRYEMK; YDTYTLFSTK; EQSNLYEAYK; YINDTHAKRK; KLENIEAEIK; HSLKRDSANK; SVKTAANFVY; KIQKQQDEYK; NVILEEESLK; KIYDTYTLFS; YSTRLDNLAK; FISCDLFIRY; ILETSEESIK; YTLFSTKLTQ; TLLNYIQVSVK; TLFSTKLTQMY; RLDNLAKAKAK; TSILLMRDSLK; SLKEVQGIIDK; ILETSEESIKK; ELLKEQSETRK; SIKKPMNKKGK; SILETSEESIK; FVYINDTHAKR; KAKEEAAKFTK; STRLDNLAKAK; DSANKSNFLQK; NVDSAINTINK
	HLA-A1101	DTYTLFSTK; QSNLYEAYK; STRLDNLAK; ILLMRDSLK; SIKKPMNKK; ISCDLFIRY; VILEEESLK; IVTSILLMR; TIDSDLRPK; ESIKKPMNK; ESLKTELLK; SLKRDSANK; ETSEESIKK; DSAINTINK; LSGESGELK; VYINDTHAK; ANKSNFLQK; RLDNLAKAK; YQSYLEGVK; AEIKTLIAK; FISCDLFIR; YINDTHAKR; KLTQMYSTR; SANKSNFLQ; SANKSNFLQK; SILLMRDSLK; ITIDSDLRPK; SLSGESGELK; FVYINDTHAK; KIQKQQDEYK; AIVTSILLMR; NVILEEESLK; HSLKRDSANK; YINDTHAKRK; YSTRLDNLAK; LLNYIQVSVK; KIARKKGKSK; SVKTAANFVY; ESIKKPMNKK; KAKAKEEAAK; EQSNLYEAYK; RYQSYLEGVK; KIYDTYTLFS; KLENIEAEIK; FISCDLFIRY; TSILLMRDSLK; SILETSEESIK; TLLNYIQVSVK; NVDSAINTINK; KAIVTSILLMR; STRLDNLAKAK; STKLTQMYSTR; NSLSGESGELK; KAKEEAAKFTK; AAKFTKEDLEK; TLFSTKLTQMY; SIKKPMNKKGK; DSANKSNFLQK; SLKEVQGIIDK; MYSTRLDNLAK; FTKEDLEKNFK; KEQSNLYEAYK; ILETSEESIKK; QSETRKEKIQK; IYDTYTLFSTK; RLDNLAKAKAK; FVYINDTHAKR; VYINDTHAKRK; VSVKTAANFVY
	HLA-A2402	KYLALGLLF; AYKAIVTSI; YYEDDYEEI; TYTLFSTKL; MYSTRLDNL; VYINDTHAK; GFISCDLFI; NFKTLLNYI; RYQSYLEGV; KIYDTYTLF; LFGFISCDLF; EYYEDDYEEI; AYKAIVTSIL; EYKGMTQGSL; IYDTYTLFST; SYLEGVKYNV; RYQSYLEGVK; VYINDTHAKR;

		KYLALGLLFGF; KYNVDSAINTI; AYKAIVTSILL; YYEDDYEEIRL; IYDTYTLFSTK; LFGFISCDLFI; VYINDTHAKRK; RYQSYLEGVKY; MYSTRLDNLAK
	HLA-A2902	QSYLEGVKY; FSTKLTQMY; IAGSNSISY; KYLALGLLF; ISCDLFIRY; IIDKNGVWY; EQSNLYEAY; AINTINKIY; VKTAANFVY; KIYDTYTLF; TINKIYDTY; RLSNRYQSY; KNFKTLLNY; YQSYLEGVKY; FISCDLFIRY; SVKTAANFVY; GIIDKNGVWY; LFSTKLTQMY; YLALGLLFGF; SAINTINKIY; EIEEEDYARY; YTDEIEEEDY; DIAGSNSISY; NTINKIYDTY; TLFSTKLTQMY; GFISCDLFIRY; RYQSYLEGVKY; VSVKTAANFVY; YLDEDDEDDEY; EIEEEDYARYY; KYLALGLLFGF; SYTDEIEEEDY; DYEEIRLSNRY
	HLA-A6801	DTYTLFSTK; IVTSILLMR; YINDTHAKR; ETSEESIKK; DITIDSDLR; QSNLYEAYK; FISCDLFIR; DSAINTINK; EPYIHSLKR; ESIKKPMNK; EIEEEDYAR; DLFIRYEMK; ETRKEKIQK; ESLKTELLK; KLTQMYSTR; FSTKLTQMY; TINKIYDTY; STRLDNLAK; ILLMRDSLK; LLKEQSETR; VYINDTHAK; LNYIQVSVK; SIKKPMNKK; SANKSNFLQ; EQSETRKEK; TAANFVYIN; EESPGLFDK; VILEEESLK; YQSYLEGVK; FVYINDTHAK; NVILEEESLK; ESIKKPMNKK; NTINKIYDTY; SANKSNFLQK; ITIDSDLRPK; EQSNLYEAYK; YSTRLDNLAK; LLNYIQVSVK; EIKTLIAKIK; AIVTSILLMR; SILLMRDSLK; YINDTHAKRK; ELLKEQSETR; DYEEIRLSNR; VYINDTHAKR; EAEIKTLIAK; HSLKRDSANK; DIAGSNSISY; IDITIDSDLR; GFISCDLFIR; YYEDDYEEIR; SVKTAANFVY; SLSGESGELK; YDTYTLFSTK; DSANKSNFLQ; FISCDLFIRY; SAINTINKIY; EESLKTELLK; DEIEEEDYAR; CDLFIRYEMK; FVYINDTHAKR; STKLTQMYSTR; EYYEDDYEEIR; TSILLMRDSLK; FTKEDLEKNFK; DSANKSNFLQK; NFVYINDTHAK; EIDITIDSDLR; FGFISCDLFIR; NVDSAINTINK; KAIVTSILLMR; NSLSGESGELK; TLLNYIQVSVK; MYSTRLDNLAK; TLFSTKLTQMY; DITIDSDLRPK; STRLDNLAKAK; ELLKEQSETRK; SILETSEESIK; DSAINTINKIY; DDYEEIRLSNR; EKIQKQQDEYK; MNKKGKGKIAR; EAAKFTKEDLE; QSETRKEKIQK; DTYTLFSTKLT
	HLA-B0702	KVKSKYLAL; RPKSSLQDI; KPMNKKGKG; IARKKGKSKV; RPKSSLQDIA; KPMNKKGKGKI; SPGLFDKGNSI; RPKSSLQDIAG; KVKSKYLALGL
	HLA-B0801	KVKSKYLAL; MKKVKSKYL; HAKRKLENI; YIQVSVKTAA; MKKVKSKYLAL
	HLA-B1501	RLSNRYQSY; EQSNLYEAY; KIKEQSNLY; KQQDEYKGM; KIYDTYTLF; QSYLEGVKY; FSTKLTQMY; KAKEEAAKF; IAGSNSISY; AINTINKIY; KVKSKYLAL; VSVKTAANF; LMRDSLKEV; GLFDKGNSI; EMKEESPGL; LQKNVILEE; ISCDLFIRY; KNFKTLLNY; YQSYLEGVKY; YLALGLLFGF; SVKTAANFVY; KSKVSRKEPY; EMKEESPGLF; QVSVKTAANF; SAINTINKIY; GMTQGSLNSL; GIIDKNGVWY; FTKEDLEKNF; GLFDKGNSIL; RLSNRYQSYL; DIAGSNSISY; LLFGFISCDL; IQVSVKTAANF; LLFGFISCDLF; TLFSTKLTQMY; KSKYLALGLLF; IQKQQDEYKGM; VSVKTAANFVY; EIRLSNRYQSY; QDIAGSNSISY; IAKIKEQSNLY; KAKAKEEAAKF; TQMYSTRLDNL; YLDEDDEDDEY
	HLA-B2705	IRLSNRYQSY; TRLDNLAKAK; KRDSANKSNF; RKKGKSKVSR; NRYQSYLEGV; NRYQSYLEGVK; IRLSNRYQSYL; RKKGKSKVSRK; ARKKGKSKVSR; SRKEPYIHSLK; KRKLENIEAEI
	HLA-B3501	IAGSNSISY; EQSNLYEAY; LALGLLFGF; FSTKLTQMY; TINKIYDTY; DEDDEDDEY; ISCDLFIRY; EDDEDDEYY; NFVYINDTH; SAINTINKIY; FISCDLFIRY; EIEEEDYARY; SVKTAANFVY; DIAGSNSISY; LFSTKLTQMY; YQSYLEGVKY; YLALGLLFGF; YTDEIEEEDY; LDEDDEDDEY; NTINKIYDTY; KAIVTSILLM; QVSVKTAANF; DEDDEDDEYY; YLDEDDEDDEY; EIEEEDYARYY; ETSEESIKKPM;

		IAKIKEQSNLY; EAYKAIVTSIL; VSVKTAANFVY; IKEQSNLYEAY; TLFSTKLTQMY; DSAINTINKIY; YTLFSTKLTQM; ISCDLFIRYEM; LDEDDEDDEYY; YKAIVTSILLM; QDIAGSNSISY
	HLA-B4403	EEEDYARYY; EEIRLSNRY; NEIDITIDS; GELKETIES; EEDYARYYL; DEDDEDDEY; EESLKTELL; AEIKTLIAK; DEIEEEDYA; SEESIKKPM; EEIRLSNRYQ; EEEDYARYYL; AEIKTLIAKI; DEDDEDDEYY; YEMKEESPGL; NEIDITIDSD; EEESLKTELL; EEIRLSNRYQS; NEIDITIDSDL; YEMKEESPGLF; DEIEEEDYARY; EEEDYARYYLD; AEIKTLIAKIK; KEKIQKQQDEY; DEDDEYYEDDY
	HLA-B5101	LALGLLFGFI; SPGLFDKGNSI
	HLA-B5701	ISCDLFIRY; ; VSVKTAANFVY
AAL84590.1| BBK32 [Borrelia afzelii]; Seq43	HLA-A0101	LSTKQTQMY; YSLEEDYYY; VIDKNGVWY; ISGSNSISY; YTDEIEEEDY; LLSTKQTQMY; SSAIKTIVKIY; ATNFVYAREIY; VSARTATNFVY
	HLA-A0201	LLMKDSLKI; KIYDNYTLL; MLQGSLSFL; KLDAIETEI; FTIDSDLRL; LLNYIQVSA; YLEGVKYNV; FLSGESGEL; KTLLNYIQV; GLCDEESSI; RTATNFVYA; TLLNYIQVS; RLKSDLQAI; LLSTKQTQM; AIVRSILLM; ALGLLFGFI; RMLQGSLSFL; TLLNYIQVSA; LLFGFISCDL; LLMKDSLKII; RLSNRYESYL; QMYSTRLDNL; ILLMKDSLKI; SILETGDKSV; KIYDNYTLLS; MLQGSLSFLS; GLCDEESSIL; LALGLLFGFI; KIYDNYTLLST; LMKDSLKIIEI; GLLFGFISCDL; QVSARTATNFV; ILLMKDSLKII; RMLQGSLSFLS; QMYSTRLDNLA; LLNYIQVSART; TQMYSTRLDNL; TIVKIYDNYTL; CLALGLLFGFI; SLGLCDEESSI; KTLLNYIQVSA
	HLA-A0301	KSVKKSLNK; IVRSILLMK; ILLMKDSLK; SSAIKTIVK; KIIEIVIDK; RLDNLAKAK; KVEGNAVKK; RLSNRYESY; SVKKSLNKK; SLNKKGKDK; ISGSNSISY; TIDSDLRLK; STRLDNLAK; KYNVSSAIK; VISEEEILK; KIKGQSDLY; AIVRSILLMK; FVYAREIYSK; SILLMKDSLK; FLSGESGELK; VSSAIKTIVK; KSLNKKGKDK; VKYNVSSAIK; AISGSNSISY; SVNNSNLSQK; GQSDLYEAYK; LLRERPETRK; IVIDKNGVWY; KLDAIETEIK; LLNYIQVSAR; KSVKKSLNKK; LLSTKQTQMY; YDNYTLLSTK; RTATNFVYAR; FTIDSDLRLK; ILETGDKSVK; NVISEEEILK; KTIVKIYDNY; EIKNLILKIK; YSTRLDNLAK; ILKTKLLRER; KKFTKEELEK; RYESYLEGVK; ETEIKNLILK; KLLRERPETRK; RSILLMKDSLK; FVYAREIYSKR; KAIVRSILLMK; TLLNYIQVSAR; GVKYNVSSAIK; SLKIIEIVIDK; ILETGDKSVKK; VSARTATNFVY; TLLSTKQTQMY; NVSSAIKTIVK; SILETGDKSVK; RMLQGSLSFLS; KAREEAKKFTK; STRLDNLAKAK; SVKKSLNKKGK
	HLA-A1101	SSAIKTIVK; KSVKKSLNK; SSILETGDK; KIIEIVIDK; SVKKSLNKK; IVRSILLMK; STRLDNLAK; VISEEEILK; TATNFVYAR; TIDSDLRLK; KVEGNAVKK; ILLMKDSLK; QSDLYEAYK; KAKAREEAK; LSGESGELK; TEIKNLILK; VYAREIYSK; ETGDKSVKK; KYNVSSAIK; SVNNSNLSQ; RLDNLAKAK; FISCDLFIR; SLNKKGKDK; ISGSNSISY; VNNSNLSQK; SVNNSNLSQK; FVYAREIYSK; AIVRSILLMK; SILLMKDSLK; VSSAIKTIVK; RTATNFVYAR; FTIDSDLRLK; KSVKKSLNKK; GQSDLYEAYK; NVISEEEILK; YSTRLDNLAK; AISGSNSISY; KTIVKIYDNY; ETEIKNLILK; KSLNKKGKDK; KLDAIETEIK; KAKAREEAKK; ISEEEILKTK; IVIDKNGVWY; FLSGESGELK; KAIVRSILLMK; RSILLMKDSLK; SILETGDKSVK; NVSSAIKTIVK; KLLRERPETRK; GVKYNVSSAIK; STRLDNLAKAK; SVKKSLNKKGK; FVYAREIYSKR; ATNFVYAREIY; STKQTQMYSTR; VISEEEILKTK; SFLSGESGELK; SLKIIEIVIDK; MYSTRLDNLAK; VSARTATNFVY; KGQSDLYEAYK; TLLNYIQVSAR; ESVNNSNLSQK; KAREEAKKFTK; FTKEELEKDLK; IYDNYTLLSTK; QAISGSNSISY; SSAIKTIVKIY; ILETGDKSVKK; LAKAKAREEAK
	HLA-A2402	AYKAIVRSI; MYSTRLDNL; VYAREIYSK; GFISCDLFI; KYNVSSAIK;

		YYYDGETRL; IYSKRKLDAI; LFGFISCDLF; AYKAIVRSIL; VYAREIYSKR; DYYYDGETRL; SYLEGVKYNV; KYNVSSAIKTI; AYKAIVRSILL; LFGFISCDLFI; IYDNYTLLSTK; VYAREIYSKRK; MYSTRLDNLAK
	HLA-A2902	YSLEEDYYY; ESYLEGVKY; QYSLEEDYY; VIDKNGVWY; ISGSNSISY; YYYDGETRL; DQYSLEEDY; RMLQGSLSF; TIVKIYDNY; IVIDKNGVWY; QYSLEEDYYY; YESYLEGVKY; SARTATNFVY; LLSTKQTQMY; YTDEIEEEDY; DQYSLEEDYY; EIEEEDYDQY; KTIVKIYDNY; SAIKTIVKIY; VSARTATNFVY; DQYSLEEDYYY; QAISGSNSISY; RYESYLEGVKY; SYTDEIEEEDY; TLLSTKQTQMY; EIVIDKNGVWY; DYDQYSLEEDY
	HLA-A6801	TATNFVYAR; FISCDLFIR; DPFNHHVKR; YAREIYSKR; EILKTKLLR; DYYYDGETR; ETRKEEIQK; ETGDKSVKK; DFTIDSDLR; DLFIRDEIK; QSDLYEAYK; SVKKSLNKK; SSILETGDK; IVRSILLMK; LNYIQVSAR; SSAIKTIVK; TIVKIYDNY; DNYTLLSTK; ESYLEGVKY; STRLDNLAK; KIIEIVIDK; YEAYKAIVR; VISEEEILK; KVEGNAVKK; TIDSDLRLK; TEIKNLILK; ILLMKDSLK; NFVYAREIY; VYAREIYSK; FVYAREIYSK; RTATNFVYAR; FTIDSDLRLK; NVISEEEILK; SVNNSNLSQK; LLNYIQVSAR; ETEIKNLILK; ESSILETGDK; EDYYYDGETR; YSTRLDNLAK; EIQKQQDEHK; FLSGESGELK; EIKNLILKIK; IDFTIDSDLR; SILLMKDSLK; EEILKTKLLR; YAREIYSKRK; VYAREIYSKR; VSSAIKTIVK; GFISCDLFIR; LYEAYKAIVR; AIVRSILLMK; TATNFVYARE; ESVNNSNLSQ; TKQTQMYSTR; FVYAREIYSKR; ESVNNSNLSQK; STKQTQMYSTR; EIDFTIDSDLR; DLYEAYKAIVR; NVSSAIKTIVK; EIQKQQDEHKR; FTKEELEKDLK; TLLNYIQVSAR; FGFISCDLFIR; EILKTKLLRER; NFVYAREIYSK; DLFIRDEIKEK; MYSTRLDNLAK; RSILLMKDSLK; GVKYNVSSAIK; ATNFVYAREIY; ETRLSNRYESY; DFTIDSDLRLK; STRLDNLAKAK; SVKKSLNKKGK; KAIVRSILLMK; LAKAKAREEAK; QAISGSNSISY; SLKIIEIVIDK; EESSILETGDK; EIVIDKNGVWY; DQYSLEEDYYY; YYDGETRLSNR; SILETGDKSVK; DTIESNEIDFT
	HLA-B0702	RPETRKEEI; SARTATNFV; KAIVRSILL; KIKSKCLAL; GVKYNVSSAI; YAREIYSKRKL; VARKKVEGNAV; SARTATNFVYA
	HLA-B0801	YSKRKLDAI; KIKSKCLAL; EIKEKSLGL; RLKSDLQAI; EAKKFTKEEL; ILKIKGQSDL; YIQVSARTAT; YAREIYSKRKL; VARKKVEGNAV
	HLA-B1501	RMLQGSLSF; GQSDLYEAY; RLSNRYESY; YSLEEDYYY; VSARTATNF; ISGSNSISY; KQQDEHKRM; AIKTIVKIY; FLSGESGEL; KIKGQSDLY; KAREEAKKF; IVIDKNGVW; LSTKQTQMY; AISGSNSISY; QVSARTATNF; IVIDKNGVWY; LQAISGSNSI; SARTATNFVY; LLSTKQTQMY; RMLQGSLSFL; KQQDEHKRML; SAIKTIVKIY; KTIVKIYDNY; KQTQMYSTRL; LLFGFISCDL; IQVSARTATNF; QAISGSNSISY; VSARTATNFVY; LLFGFISCDLF; ILKIKGQSDLY; KSKCLALGLLF; SSAIKTIVKIY; IQKQQDEHKRM; ETRLSNRYESY; KAKAREEAKKF; TLLSTKQTQMY; TQMYSTRLDNL; DQYSLEEDYYY; LMKDSLKIIEI; ATNFVYAREIY; SQKNVISEEEI
	HLA-B2705	RMLQGSLSF; ARTATNFVY; KRMLQGSLS; KQTQMYSTR; KRMLQGSLSF; TRLSNRYESY; TRLDNLAKAK; AREEAKKFTK; KRESVNNSNL; NRYESYLEGV; KKVEGNAVKK; KRMLQGSLSFL; NRYESYLEGVK; TRLSNRYESYL; ARTATNFVYAR; ARKKVEGNAVK
	HLA-B3501	YSLEEDYYY; NFVYAREIY; LALGLLFGF; LSTKQTQMY; FTIDSDLRL; ESYLEGVKY; RMLQGSLSF; ISGSNSISY; SARTATNFVY; EIEEEDYDQY; YTDEIEEEDY; SAIKTIVKIY; YESYLEGVKY; LLSTKQTQMY; IVIDKNGVWY; QAISGSNSISY; TLLSTKQTQMY; EIVIDKNGVWY; IKGQSDLYEAY; VSARTATNFVY; YTLLSTKQTQM; YDQYSLEEDYY; EAYKAIVRSIL
	HLA-B4403	EEILKTKLL; NEIDFTIDS; EEEDYDQYS; EELEKDLKT; GELKDTIES;

		GETRLSNRY; REIYSKRKL; KEKSLGLCD; EEILKTKLLR; EEEDYDQYSL; TEIKNLILKI; DEIKEKSLGL; EEIQKQQDEH; EEDYYYDGET; EELEKDLKTL; EEEILKTKLL; NEIDFTIDSD; NEIDFTIDSDL; DEIEEEDYDQY; EELEKDLKTLL; IEIVIDKNGVW; EEILKTKLLRE; REIYSKRKLDA; EEEDYDQYSLE; SEEEILKTKLL
	HLA-B5101	LALGLLFGFI;
	HLA-B5701	VSARTATNF; ; VSARTATNFVY
AAL84595.1| BBK32 [Borrelia garinii]; Seq44	HLA-A0101	FSTKLTQMY; AIDKNGIWY; ISCDLFIRY; YTDEIEEEDY; NTINKIYDTY; FISCDLFIRY; YLDEDDEDDEY; DSAINTINKIY; VSVKTATNFVY
	HLA-A0201	LLNYIQVSV; GLFDKGNSI; YLEGVKYNV; KTATNFVYI; SLKEVQYAI; AIVSSILLM; KTLLNYIQV; LMRDSLKEV; NLYSAYKAI; KLENIEAKI; YLALGLLFG; KVSGKEPFI; TLLNYIQVS; ILETSEESI; ALGLLFGFI; SLSGESGEL; KAIVSSILL; MLEEESLKT; TLLNYIQVSV; LLMRDSLKEV; LLFGFISCDL; GLFDKGNSIL; RLSNRYQSYL; NLYSAYKAIV; KLTQMYSTRL; QMYSTRLDNL; KIYDTYTLFS; GMTKGSLNSL; SILETSEESI; VMLEEESLKT; YLALGLLFGF; TLFSTKLTQM; SAYKAIVSSI; LALGLLFGFI; YLALGLLFGFI; KIYDTYTLFST; SLQDIAGSNSI; KTLLNYIQVSV; ILLMRDSLKEV; MLEEESLKTEL; GLLFGFISCDL; YTDEIEEEDYA; TINKIYDTYTL; QMYSTRLDNLA; LLNYIQVSVKT; TQMYSTRLDNL; QVSVKTATNFV; YINEMHAKRKL
	HLA-A0301	KSNLYSAYK; ILLMRDSLK; RLSNRYQSY; SIKKPMNKK; TLIAKIKEK; RLDNLAKAK; DTYTLFSTK; VMLEEESLK; IVSSILLMR; KLTQMYSTR; KIKEKSNLY; ESIKKPMNK; STRLDNLAK; KEPFIHSFK; ISCDLFIRY; ESLKTELLK; KNFKTLLNY; QSYLEGVKY; LNYIQVSVK; AIDKNGIWY; LLNYIQVSVK; SLSGESGELK; SILLMRDSLK; KTLIAKIKEK; FVYINEMHAK; KIARKNGKSK; KPMNKKGKGK; KIKTLIAKIK; QQDEYKGMTK; AIVSSILLMR; AANKSNFLQK; RYQSYLEGVK; NVMLEEESLK; ITIDSDLRPK; GKEPFIHSFK; LLKEQSETRK; CDLFIRYEMK; YDTYTLFSTK; EKSNLYSAYK; KLENIEAKIK; SVKTATNFVY; KIQKQQDEYK; EAKIKTLIAK; KIYDTYTLFS; YINEMHAKRK; YSTRLDNLAK; FISCDLFIRY; ILETSEESIK; HSFKRDAANK; YTLFSTKLTQ; TLLNYIQVSVK; TLFSTKLTQMY; RLDNLAKAKAK; SLKEVQYAIDK; SSILLMRDSLK; ILETSEESIKK; FVYINEMHAKR; ELLKEQSETRK; SIKKPMNKKGK; SILETSEESIK; KQQDEYKGMTK; KAKEEAAKFTK; STRLDNLAKAK; NVDSAINTINK
	HLA-A1101	KSNLYSAYK; DTYTLFSTK; IVSSILLMR; STRLDNLAK; ILLMRDSLK; SIKKPMNKK; TLIAKIKEK; ISCDLFIRY; TIDSDLRPK; ESIKKPMNK; VMLEEESLK; ESLKTELLK; ETSEESIKK; VYINEMHAK; DSAINTINK; LSGESGELK; ANKSNFLQK; RLDNLAKAK; YQSYLEGVK; FISCDLFIR; YINEMHAKR; AKIKTLIAK; KEPFIHSFK; KLTQMYSTR; SFKRDAANK; ATNFVYINE; AANKSNFLQK; SILLMRDSLK; ITIDSDLRPK; FVYINEMHAK; KTLIAKIKEK; HSFKRDAANK; SLSGESGELK; NVMLEEESLK; AIVSSILLMR; KIQKQQDEYK; YINEMHAKRK; KIARKNGKSK; YSTRLDNLAK; LLNYIQVSVK; SVKTATNFVY; ESIKKPMNKK; KIKTLIAKIK; KAKAKEEAAK; RYQSYLEGVK; QQDEYKGMTK; KIYDTYTLFS; FISCDLFIRY; SSILLMRDSLK; SILETSEESIK; TLLNYIQVSVK; KAIVSSILLMR; NVDSAINTINK; KQQDEYKGMTK; SLKEVQYAIDK; STRLDNLAKAK; STKLTQMYSTR; NSLSGESGELK; KAKEEAAKFTK; AAKFTKEDLEK; TLFSTKLTQMY; SIKKPMNKKGK; MYSTRLDNLAK; SGKEPFIHSFK; FTKEDLEKNFK; FVYINEMHAKR; DAANKSNFLQK; ILETSEESIKK; QSETRKEKIQK; ATNFVYINEMH; VYINEMHAKRK; IYDTYTLFSTK; RLDNLAKAKAK; VSVKTATNFVY
	HLA-A2402	KYLALGLLF; AYKAIVSSI; YYEDDYEEI; TYTLFSTKL; MYSTRLDNL; GFISCDLFI; VYINEMHAK; NFKTLLNYI; KTATNFVYI; RYQSYLEGV;

		QYAIDKNGI; KIYDTYTLF; LFGFISCDLF; AYKAIVSSIL; EYYEDDYEEI; IYDTYTLFST; SYLEGVKYNV; RYQSYLEGVK; KYLALGLLFGF; KYNVDSAINTI; AYKAIVSSILL; YYEDDYEEIRL; IYDTYTLFSTK; LFGFISCDLFI; RYQSYLEGVKY; VYINEMHAKRK; MYSTRLDNLAK
	HLA-A2902	QSYLEGVKY; FSTKLTQMY; IAGSNSISY; VKTATNFVY; KYLALGLLF; ISCDLFIRY; AINTINKIY; KIYDTYTLF; TINKIYDTY; RLSNRYQSY; KNFKTLLNY; VYINEMHAK; EKSNLYSAY; YAIDKNGIWY; YQSYLEGVKY; SVKTATNFVY; FISCDLFIRY; LFSTKLTQMY; YLALGLLFGF; SAINTINKIY; EIEEEDYARY; YTDEIEEEDY; DIAGSNSISY; NTINKIYDTY; TLFSTKLTQMY; GFISCDLFIRY; VSVKTATNFVY; QYAIDKNGIWY; RYQSYLEGVKY; YLDEDDEDDEY; EIEEEDYARYY; KYLALGLLFGF; SYTDEIEEEDY; DYEEIRLSNRY; LMRDSLKEVQY
	HLA-A6801	DTYTLFSTK; EPFIHSFKR; YINEMHAKR; IVSSILLMR; ETSEESIKK; DITIDSDLR; FISCDLFIR; DSAINTINK; ESIKKPMNK; EIEEEDYAR; DLFIRYEMK; ETRKEKIQK; ESLKTELLK; KSNLYSAYK; TLIAKIKEK; KLTQMYSTR; FSTKLTQMY; TINKIYDTY; STRLDNLAK; ILLMRDSLK; LLKEQSETR; LNYIQVSVK; VYINEMHAK; SIKKPMNKK; EQSETRKEK; EESPGLFDK; YQSYLEGVK; FVYINEMHAK; HSFKRDAANK; NVMLEEESLK; ESIKKPMNKK; NTINKIYDTY; ITIDSDLRPK; AIVSSILLMR; YINEMHAKRK; YSTRLDNLAK; LLNYIQVSVK; SILLMRDSLK; EKSNLYSAYK; ELLKEQSETR; DYEEIRLSNR; VYINEMHAKR; EAKIKTLIAK; DIAGSNSISY; AANKSNFLQK; IDITIDSDLR; GFISCDLFIR; YYEDDYEEIR; SVKTATNFVY; SLSGESGELK; DAANKSNFLQ; YDTYTLFSTK; FISCDLFIRY; SAINTINKIY; EESLKTELLK; TATNFVYINE; DEIEEEDYAR; CDLFIRYEMK; FVYINEMHAKR; STKLTQMYSTR; EYYEDDYEEIR; FTKEDLEKNFK; DAANKSNFLQK; NFVYINEMHAK; SSILLMRDSLK; EIDITIDSDLR; FGFISCDLFIR; KAIVSSILLMR; NVDSAINTINK; NSLSGESGELK; TLLNYIQVSVK; MYSTRLDNLAK; TLFSTKLTQMY; DITIDSDLRPK; STRLDNLAKAK; ELLKEQSETRK; SILETSEESIK; DSAINTINKIY; SLKEVQYAIDK; DDYEEIRLSNR; EKIQKQQDEYK; MNKKGKGKIAR; EAAKFTKEDLE; QSETRKEKIQK; SGKEPFIHSFK; DTYTLFSTKLT
	HLA-B0702	KVKSKYLAL; RPKSSLQDI; KPMNKKGKG; IARKNGKSKV; RPKSSLQDIA; SAYKAIVSSI; KPMNKKGKGKI; SPGLFDKGNSI; SAYKAIVSSIL; RPKSSLQDIAG; KVKSKYLALGL
	HLA-B0801	KVKSKYLAL; MKKVKSKYL; HAKRKLENI; ; MKKVKSKYLAL
	HLA-B1501	RLSNRYQSY; KIKEKSNLY; KQQDEYKGM; KIYDTYTLF; QSYLEGVKY; FSTKLTQMY; KAKEEAAKF; IAGSNSISY; AINTINKIY; KVKSKYLAL; LMRDSLKEV; MTKGSLNSL; VSVKTATNF; GLFDKGNSI; EMKEESPGL; ISCDLFIRY; KNFKTLLNY; YQSYLEGVKY; YLALGLLFGF; SVKTATNFVY; KSKVSGKEPF; YAIDKNGIWY; EMKEESPGLF; SAINTINKIY; SGKEPFIHSF; QVSVKTATNF; FTKEDLEKNF; GMTKGSLNSL; GLFDKGNSIL; VQYAIDKNGI; RLSNRYQSYL; DIAGSNSISY; KEKSNLYSAY; LLFGFISCDL; LMRDSLKEVQY; IQVSVKTATNF; LLFGFISCDLF; TLFSTKLTQMY; KSKYLALGLLF; IQKQQDEYKGM; VSVKTATNFVY; VQYAIDKNGIW; EIRLSNRYQSY; QDIAGSNSISY; IAKIKEKSNLY; KAKAKEEAAKF; TQMYSTRLDNL; YLDEDDEDDEY; VSGKEPFIHSF
	HLA-B2705	RKLENIEAK; IRLSNRYQSY; KRKLENIEAK; KRDAANKSNF; TRLDNLAKAK; NRYQSYLEGV; NRYQSYLEGVK; RKNGKSKVSGK; IRLSNRYQSYL; KRKLENIEAKI; KQQDEYKGMTK
	HLA-B3501	IAGSNSISY; LALGLLFGF; EKSNLYSAY; FSTKLTQMY; TINKIYDTY; DEDDEDDEY; ISCDLFIRY; EDDEDDEYY; YAIDKNGIW; DAANKSNFL;

		TNFVYINEM; YAIDKNGIWY; SAINTINKIY; FISCDLFIRY; EIEEEDYARY; SVKTATNFVY; DIAGSNSISY; LFSTKLTQMY; YQSYLEGVKY; YLALGLLFGF; YTDEIEEEDY; LDEDDEDDEY; NTINKIYDTY; KAIVSSILLM; DEDDEDDEYY; QVSVKTATNF; TATNFVYINEM; YLDEDDEDDEY; EIEEEDYARYY; ETSEESIKKPM; TLFSTKLTQMY; DSAINTINKIY; VSVKTATNFVY; YTLFSTKLTQM; ISCDLFIRYEM; LDEDDEDDEYY; IAKIKEKSNLY; QDIAGSNSISY; NKSNFLQKNVM; YKAIVSSILLM
	HLA-B4403	EEEDYARYY; EEIRLSNRY; NEIDITIDS; GELKETIES; EEDYARYYL; DEDDEDDEY; EESLKTELL; KEVQYAIDK; DEIEEEDYA; SEESIKKPM; EEIRLSNRYQ; EEEDYARYYL; DEDDEDDEYY; YEMKEESPGL; NEIDITIDSD; EEESLKTELL; EEIRLSNRYQS; NEIDITIDSDL; YEMKEESPGLF; DEIEEEDYARY; EEEDYARYYLD; KEKIQKQQDEY; KEVQYAIDKNG; DEDDEYYEDDY
	HLA-B5101	LALGLLFGFI; SPGLFDKGNSI
	HLA-B5701	VSVKTATNF; ISCDLFIRY; VSGKEPFIHSF; VSVKTATNFVY

Fig. 33.

Antigen designation	Class 2 Antigen peptide sequences
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31	13 mers: MNKILLLILLESI; NKILLLILLESIV; KILLLILLESIVF; ILLLILLESIVFL; LLLILLESIVFLS; LLILLESIVFLSC; LILLESIVFLSCS; ILLESIVFLSCSG; LLESIVFLSCSGK; LESIVFLSCSGKG; ESIVFLSCSGKGS; SIVFLSCSGKGSL; IVFLSCSGKGSLG; VFLSCSGKGSLGS; FLSCSGKGSLGSE; LSCSGKGSLGSEI; SCSGKGSLGSEIP; CSGKGSLGSEIPK; SGKGSLGSEIPKV; GKGSLGSEIPKVS; KGSLGSEIPKVSL; GSLGSEIPKVSLI; SLGSEIPKVSLII; LGSEIPKVSLIID; GSEIPKVSLIIDG; SEIPKVSLIIDGT; EIPKVSLIIDGTF; IPKVSLIIDGTFD; PKVSLIIDGTFDD; KVSLIIDGTFDDK; VSLIIDGTFDDKS; SLIIDGTFDDKSF; LIIDGTFDDKSFN; IIDGTFDDKSFNE; IDGTFDDKSFNES; DGTFDDKSFNESA; GTFDDKSFNESAL; TFDDKSFNESALN; FDDKSFNESALNG; DDKSFNESALNGV; DKSFNESALNGVK; KSFNESALNGVKK; SFNESALNGVKKV; FNESALNGVKKVK; NESALNGVKKVKE; ESALNGVKKVKEE; SALNGVKKVKEEF; ALNGVKKVKEEFK; LNGVKKVKEEFKI; NGVKKVKEEFKIE; GVKKVKEEFKIEL; VKKVKEEFKIELV; KKVKEEFKIELVL; KVKEEFKIELVLK; VKEEFKIELVLKE; KEEFKIELVLKES; EEFKIELVLKESS; EFKIELVLKESSS; FKIELVLKESSSN; KIELVLKESSSNS; IELVLKESSSNSY; ELVLKESSSNSYL; LVLKESSSNSYLS; VLKESSSNSYLSD; LKESSSNSYLSDL; KESSSNSYLSDLE; ESSSNSYLSDLEG; SSSNSYLSDLEGL; SSNSYLSDLEGLK; SNSYLSDLEGLKD; NSYLSDLEGLKDA; SYLSDLEGLKDAG; YLSDLEGLKDAGS; LSDLEGLKDAGSD; SDLEGLKDAGSDL; DLEGLKDAGSDLI; LEGLKDAGSDLIW; EGLKDAGSDLIWL; GLKDAGSDLIWLI; LKDAGSDLIWLIG; KDAGSDLIWLIGY; DAGSDLIWLIGYR; AGSDLIWLIGYRF; GSDLIWLIGYRFS; SDLIWLIGYRFSD; DLIWLIGYRFSDV; LIWLIGYRFSDVA; IWLIGYRFSDVAK; WLIGYRFSDVAKV; LIGYRFSDVAKVA; IGYRFSDVAKVAA; GYRFSDVAKVAAL; YRFSDVAKVAALQ; RFSDVAKVAALQN; FSDVAKVAALQNP; SDVAKVAALQNPD; DVAKVAALQNPDM; VAKVAALQNPDMK; AKVAALQNPDMKY; KVAALQNPDMKYA; VAALQNPDMKYAI; AALQNPDMKYAII; ALQNPDMKYAIID; LQNPDMKYAIIDP; QNPDMKYAIIDPI; NPDMKYAIIDPIY; PDMKYAIIDPIYS; DMKYAIIDPIYSN; MKYAIIDPIYSND; KYAIIDPIYSNDP; YAIIDPIYSNDPI; AIIDPIYSNDPIP; IIDPIYSNDPIPA; IDPIYSNDPIPAN; DPIYSNDPIPANL; PIYSNDPIPANLV; IYSNDPIPANLVG; YSNDPIPANLVGM; SNDPIPANLVGMT; NDPIPANLVGMTF; DPIPANLVGMTFR; PIPANLVGMTFRA; IPANLVGMTFRAQ; PANLVGMTFRAQE; ANLVGMTFRAQEG; NLVGMTFRAQEGA; LVGMTFRAQEGAF; VGMTFRAQEGAFL; GMTFRAQEGAFLT; MTFRAQEGAFLTG; TFRAQEGAFLTGY; FRAQEGAFLTGYI; RAQEGAFLTGYIA; AQEGAFLTGYIAA; QEGAFLTGYIAAK; EGAFLTGYIAAKL; GAFLTGYIAAKLS; AFLTGYIAAKLSK; FLTGYIAAKLSKT; LTGYIAAKLSKTG; TGYIAAKLSKTGK; GYIAAKLSKTGKI; YIAAKLSKTGKIG; IAAKLSKTGKIGF; AAKLSKTGKIGFL; AKLSKTGKIGFLG; KLSKTGKIGFLGG; LSKTGKIGFLGGI; SKTGKIGFLGGIE; KTGKIGFLGGIEG; TGKIGFLGGIEGE; GKIGFLGGIEGEI; KIGFLGGIEGEIV; IGFLGGIEGEIVD; GFLGGIEGEIVDA; FLGGIEGEIVDAF; LGGIEGEIVDAFR; GGIEGEIVDAFRY; GIEGEIVDAFRYG; IEGEIVDAFRYGY; EGEIVDAFRYGYE; GEIVDAFRYGYEA; EIVDAFRYGYEAG; IVDAFRYGYEAGA; VDAFRYGYEAGAK; DAFRYGYEAGAKY; AFRYGYEAGAKYA; FRYGYEAGAKYAN; RYGYEAGAKYANK; YGYEAGAKYANKD; GYEAGAKYANKDI; YEAGAKYANKDIK; EAGAKYANKDIKI; AGAKYANKDIKIS; GAKYANKDIKIST; AKYANKDIKISTQ; KYANKDIKISTQY; YANKDIKISTQYI; ANKDIKISTQYIG; NKDIKISTQYIGS; KDIKISTQYIGSF; DIKISTQYIGSFA; IKISTQYIGSFAD; KISTQYIGSFADL; ISTQYIGSFADLE; STQYIGSFADLEA; TQYIGSFADLEAG; QYIGSFADLEAGR; YIGSFADLEAGRS; IGSFADLEAGRSV; GSFADLEAGRSVA; SFADLEAGRSVAT; FADLEAGRSVATR; ADLEAGRSVATRM; DLEAGRSVATRMY; LEAGRSVATRMYS; EAGRSVATRMYSD; AGRSVATRMYSDE; GRSVATRMYSDEI; RSVATRMYSDEID; SVATRMYSDEIDI; VATRMYSDEIDII; ATRMYSDEIDIIH; TRMYSDEIDIIHH;

RMYSDEIDIIHHA; MYSDEIDIIHHAA; YSDEIDIIHHAAG; SDEIDIIHHAAGL;
DEIDIIHHAAGLG; EIDIIHHAAGLGG; IDIIHHAAGLGGI; DIIHHAAGLGGIG;
IIHHAAGLGGIGA; IHHAAGLGGIGAI; HHAAGLGGIGAIE; HAAGLGGIGAIEV;
AAGLGGIGAIEVA; AGLGGIGAIEVAK; GLGGIGAIEVAKE; LGGIGAIEVAKEL;
GGIGAIEVAKELG; GIGAIEVAKELGS; IGAIEVAKELGSG; GAIEVAKELGSGH;
AIEVAKELGSGHY; IEVAKELGSGHYI; EVAKELGSGHYII; VAKELGSGHYIIG;
AKELGSGHYIIGV; KELGSGHYIIGVD; ELGSGHYIIGVDE; LGSGHYIIGVDED;
GSGHYIIGVDEDQ; SGHYIIGVDEDQA; GHYIIGVDEDQAY; HYIIGVDEDQAYL;
YIIGVDEDQAYLA; IIGVDEDQAYLAP; IGVDEDQAYLAPD; GVDEDQAYLAPDN;
VDEDQAYLAPDNV; DEDQAYLAPDNVI; EDQAYLAPDNVIT; DQAYLAPDNVITS;
QAYLAPDNVITST; AYLAPDNVITSTT; YLAPDNVITSTTK; LAPDNVITSTTKD;
APDNVITSTTKDV; PDNVITSTTKDVG; DNVITSTTKDVGR; NVITSTTKDVGRA;
VITSTTKDVGRAL; ITSTTKDVGRALN; TSTTKDVGRALNI; STTKDVGRALNIF;
TTKDVGRALNIFT; TKDVGRALNIFTS; KDVGRALNIFTSN; DVGRALNIFTSNH;
VGRALNIFTSNHL; GRALNIFTSNHLK; RALNIFTSNHLKT; ALNIFTSNHLKTN;
LNIFTSNHLKTNT; NIFTSNHLKTNTF; IFTSNHLKTNTFE; FTSNHLKTNTFEG;
TSNHLKTNTFEGG; SNHLKTNTFEGGK; NHLKTNTFEGGKL; HLKTNTFEGGKLI;
LKTNTFEGGKLIN; KTNTFEGGKLINY; TNTFEGGKLINYG; NTFEGGKLINYGL;
TFEGGKLINYGLK; FEGGKLINYGLKE; EGGKLINYGLKEG; GGKLINYGLKEGV;
GKLINYGLKEGVV; KLINYGLKEGVVG; LINYGLKEGVVGF; INYGLKEGVVGFV;
NYGLKEGVVGFVR; YGLKEGVVGFVRN; GLKEGVVGFVRNP; LKEGVVGFVRNPK;
KEGVVGFVRNPKM; EGVVGFVRNPKMI; GVVGFVRNPKMIS; VVGFVRNPKMISF;
VGFVRNPKMISFE; GFVRNPKMISFEL; FVRNPKMISFELE; VRNPKMISFELEK;
RNPKMISFELEKE; NPKMISFELEKEI; PKMISFELEKEID; KMISFELEKEIDN;
MISFELEKEIDNL; ISFELEKEIDNLS; SFELEKEIDNLSS; FELEKEIDNLSSK;
ELEKEIDNLSSKI; LEKEIDNLSSKII; EKEIDNLSSKIIN; KEIDNLSSKIINK;
EIDNLSSKIINKE; IDNLSSKIINKEI; DNLSSKIINKEII; NLSSKIINKEIIV;
LSSKIINKEIIVP; SSKIINKEIIVPS; SKIINKEIIVPSN; KIINKEIIVPSNK;
IINKEIIVPSNKE; INKEIIVPSNKES; NKEIIVPSNKESY; KEIIVPSNKESYE;
EIIVPSNKESYEK; IIVPSNKESYEKF; IVPSNKESYEKFL; VPSNKESYEKFLK;
PSNKESYEKFLKE; SNKESYEKFLKEF; NKESYEKFLKEFI;

14 mers:
MNKILLLILLESIV; NKILLLILLESIVF; KILLLILLESIVFL;
ILLLILLESIVFLS; LLLILLESIVFLSC; LLILLESIVFLSCS;
LILLESIVFLSCSG; ILLESIVFLSCSGK; LLESIVFLSCSGKG;
LESIVFLSCSGKGS; ESIVFLSCSGKGSL; SIVFLSCSGKGSLG;
IVFLSCSGKGSLGS; VFLSCSGKGSLGSE; FLSCSGKGSLGSEI;
LSCSGKGSLGSEIP; SCSGKGSLGSEIPK; CSGKGSLGSEIPKV;
SGKGSLGSEIPKVS; GKGSLGSEIPKVSL; KGSLGSEIPKVSLI;
GSLGSEIPKVSLII; SLGSEIPKVSLIID; LGSEIPKVSLIIDG;
GSEIPKVSLIIDGT; SEIPKVSLIIDGTF; EIPKVSLIIDGTFD;
IPKVSLIIDGTFDD; PKVSLIIDGTFDDK; KVSLIIDGTFDDKS;
VSLIIDGTFDDKSF; SLIIDGTFDDKSFN; LIIDGTFDDKSFNE;
IIDGTFDDKSFNES; IDGTFDDKSFNESA; DGTFDDKSFNESAL;
GTFDDKSFNESALN; TFDDKSFNESALNG; FDDKSFNESALNGV;
DDKSFNESALNGVK; DKSFNESALNGVKK; KSFNESALNGVKKV;
SFNESALNGVKKVK; FNESALNGVKKVKE; NESALNGVKKVKEE;
ESALNGVKKVKEEF; SALNGVKKVKEEFK; ALNGVKKVKEEFKI;
LNGVKKVKEEFKIE; NGVKKVKEEFKIEL; GVKKVKEEFKIELV;
VKKVKEEFKIELVL; KKVKEEFKIELVLK; KVKEEFKIELVLKE;
VKEEFKIELVLKES; KEEFKIELVLKESS; EEFKIELVLKESSS;
EFKIELVLKESSSN; FKIELVLKESSSNS; KIELVLKESSSNSY;
IELVLKESSSNSYL; ELVLKESSSNSYLS; LVLKESSSNSYLSD;
VLKESSSNSYLSDL; LKESSSNSYLSDLE; KESSSNSYLSDLEG;
ESSSNSYLSDLEGL; SSSNSYLSDLEGLK; SSNSYLSDLEGLKD;
SNSYLSDLEGLKDA; NSYLSDLEGLKDAG; SYLSDLEGLKDAGS;

	YLSDLEGLKDAGSD; LSDLEGLKDAGSDL; SDLEGLKDAGSDLI; DLEGLKDAGSDLIW; LEGLKDAGSDLIWL; EGLKDAGSDLIWLI; GLKDAGSDLIWLIG; LKDAGSDLIWLIGY; KDAGSDLIWLIGYR; DAGSDLIWLIGYRF; AGSDLIWLIGYRFS; GSDLIWLIGYRFSD; SDLIWLIGYRFSDV; DLIWLIGYRFSDVA; LIWLIGYRFSDVAK; IWLIGYRFSDVAKV; WLIGYRFSDVAKVA; LIGYRFSDVAKVAA; IGYRFSDVAKVAAL; GYRFSDVAKVAALQ; YRFSDVAKVAALQN; RFSDVAKVAALQNP; FSDVAKVAALQNPD; SDVAKVAALQNPDM; DVAKVAALQNPDMK; VAKVAALQNPDMKY; AKVAALQNPDMKYA; KVAALQNPDMKYAI; VAALQNPDMKYAII; AALQNPDMKYAIID; ALQNPDMKYAIIDP; LQNPDMKYAIIDPI; QNPDMKYAIIDPIY; NPDMKYAIIDPIYS; PDMKYAIIDPIYSN; DMKYAIIDPIYSND; MKYAIIDPIYSNDP; KYAIIDPIYSNDPI; YAIIDPIYSNDPIP; AIIDPIYSNDPIPA; IIDPIYSNDPIPAN; IDPIYSNDPIPANL; DPIYSNDPIPANLV; PIYSNDPIPANLVG; IYSNDPIPANLVGM; YSNDPIPANLVGMT; SNDPIPANLVGMTF; NDPIPANLVGMTFR; DPIPANLVGMTFRA; PIPANLVGMTFRAQ; IPANLVGMTFRAQE; PANLVGMTFRAQEG; ANLVGMTFRAQEGA; NLVGMTFRAQEGAF; LVGMTFRAQEGAFL; VGMTFRAQEGAFLT; GMTFRAQEGAFLTG; MTFRAQEGAFLTGY; TFRAQEGAFLTGYI; FRAQEGAFLTGYIA; RAQEGAFLTGYIAA; AQEGAFLTGYIAAK; QEGAFLTGYIAAKL; EGAFLTGYIAAKLS; GAFLTGYIAAKLSK; AFLTGYIAAKLSKT; FLTGYIAAKLSKTG; LTGYIAAKLSKTGK; TGYIAAKLSKTGKI; GYIAAKLSKTGKIG; YIAAKLSKTGKIGF; IAAKLSKTGKIGFL; AAKLSKTGKIGFLG; AKLSKTGKIGFLGG; KLSKTGKIGFLGGI; LSKTGKIGFLGGIE; SKTGKIGFLGGIEG; KTGKIGFLGGIEGE; TGKIGFLGGIEGEI; GKIGFLGGIEGEIV; KIGFLGGIEGEIVD; IGFLGGIEGEIVDA; GFLGGIEGEIVDAF; FLGGIEGEIVDAFR; LGGIEGEIVDAFRY; GGIEGEIVDAFRYG; GIEGEIVDAFRYGY; IEGEIVDAFRYGYE; EGEIVDAFRYGYEA; GEIVDAFRYGYEAG; EIVDAFRYGYEAGA; IVDAFRYGYEAGAK; VDAFRYGYEAGAKY; DAFRYGYEAGAKYA; AFRYGYEAGAKYAN; FRYGYEAGAKYANK; RYGYEAGAKYANKD; YGYEAGAKYANKDI; GYEAGAKYANKDIK; YEAGAKYANKDIKI; EAGAKYANKDIKIS; AGAKYANKDIKIST; GAKYANKDIKISTQ; AKYANKDIKISTQY; KYANKDIKISTQYI; YANKDIKISTQYIG; ANKDIKISTQYIGS; NKDIKISTQYIGSF; KDIKISTQYIGSFA; DIKISTQYIGSFAD; IKISTQYIGSFADL; KISTQYIGSFADLE; ISTQYIGSFADLEA; STQYIGSFADLEAG; TQYIGSFADLEAGR; QYIGSFADLEAGRS; YIGSFADLEAGRSV; IGSFADLEAGRSVA; GSFADLEAGRSVAT; SFADLEAGRSVATR; FADLEAGRSVATRM; ADLEAGRSVATRMY; DLEAGRSVATRMYS; LEAGRSVATRMYSD; EAGRSVATRMYSDE; AGRSVATRMYSDEI; GRSVATRMYSDEID; RSVATRMYSDEIDI; SVATRMYSDEIDII; VATRMYSDEIDIIH; ATRMYSDEIDIIHH; TRMYSDEIDIIHHA; RMYSDEIDIIHHAA; MYSDEIDIIHHAAG; YSDEIDIIHHAAGL; SDEIDIIHHAAGLG; DEIDIIHHAAGLGG; EIDIIHHAAGLGGI; IDIIHHAAGLGGIG; DIIHHAAGLGGIGA; IIHHAAGLGGIGAI; IHHAAGLGGIGAIE; HHAAGLGGIGAIEV; HAAGLGGIGAIEVA; AAGLGGIGAIEVAK; AGLGGIGAIEVAKE; GLGGIGAIEVAKEL; LGGIGAIEVAKELG; GGIGAIEVAKELGS; GIGAIEVAKELGSG; IGAIEVAKELGSGH; GAIEVAKELGSGHY; AIEVAKELGSGHYI; IEVAKELGSGHYII; EVAKELGSGHYIIG; VAKELGSGHYIIGV; AKELGSGHYIIGVD; KELGSGHYIIGVDE; ELGSGHYIIGVDED; LGSGHYIIGVDEDQ; GSGHYIIGVDEDQA; SGHYIIGVDEDQAY; GHYIIGVDEDQAYL; HYIIGVDEDQAYLA; YIIGVDEDQAYLAP; IIGVDEDQAYLAPD; IGVDEDQAYLAPDN; GVDEDQAYLAPDNV; VDEDQAYLAPDNVI; DEDQAYLAPDNVIT; EDQAYLAPDNVITS;

DQAYLAPDNVITST; QAYLAPDNVITSTT; AYLAPDNVITSTTK;
YLAPDNVITSTTKD; LAPDNVITSTTKDV; APDNVITSTTKDVG;
PDNVITSTTKDVGR; DNVITSTTKDVGRA; NVITSTTKDVGRAL;
VITSTTKDVGRALN; ITSTTKDVGRALNI; TSTTKDVGRALNIF;
STTKDVGRALNIFT; TTKDVGRALNIFTS; TKDVGRALNIFTSN;
KDVGRALNIFTSNH; DVGRALNIFTSNHL; VGRALNIFTSNHLK;
GRALNIFTSNHLKT; RALNIFTSNHLKTN; ALNIFTSNHLKTNT;
LNIFTSNHLKTNTF; NIFTSNHLKTNTFE; IFTSNHLKTNTFEG;
FTSNHLKTNTFEGG; TSNHLKTNTFEGGK; SNHLKTNTFEGGKL;
NHLKTNTFEGGKLI; HLKTNTFEGGKLIN; LKTNTFEGGKLINY;
KTNTFEGGKLINYG; TNTFEGGKLINYGL; NTFEGGKLINYGLK;
TFEGGKLINYGLKE; FEGGKLINYGLKEG; EGGKLINYGLKEGV;
GGKLINYGLKEGVV; GKLINYGLKEGVVG; KLINYGLKEGVVGF;
LINYGLKEGVVGFV; INYGLKEGVVGFVR; NYGLKEGVVGFVRN;
YGLKEGVVGFVRNP; GLKEGVVGFVRNPK; LKEGVVGFVRNPKM;
KEGVVGFVRNPKMI; EGVVGFVRNPKMIS; GVVGFVRNPKMISF;
VVGFVRNPKMISFE; VGFVRNPKMISFEL; GFVRNPKMISFELE;
FVRNPKMISFELEK; VRNPKMISFELEKE; RNPKMISFELEKEI;
NPKMISFELEKEID; PKMISFELEKEIDN; KMISFELEKEIDNL;
MISFELEKEIDNLS; ISFELEKEIDNLSS; SFELEKEIDNLSSK;
FELEKEIDNLSSKI; ELEKEIDNLSSKII; LEKEIDNLSSKIIN;
EKEIDNLSSKIINK; KEIDNLSSKIINKE; EIDNLSSKIINKEI;
IDNLSSKIINKEII; DNLSSKIINKEIIV; NLSSKIINKEIIVP;
LSSKIINKEIIVPS; SSKIINKEIIVPSN; SKIINKEIIVPSNK;
KIINKEIIVPSNKE; IINKEIIVPSNKES; INKEIIVPSNKESY;
NKEIIVPSNKESYE; KEIIVPSNKESYEK; EIIVPSNKESYEKF;
IIVPSNKESYEKFL; IVPSNKESYEKFLK; VPSNKESYEKFLKE;
PSNKESYEKFLKEF; SNKESYEKFLKEFI;

15 mers:
MNKILLLILLESIVF; NKILLLILLESIVFL; KILLLILLESIVFLS;
ILLLILLESIVFLSC; LLLILLESIVFLSCS; LLILLESIVFLSCSG;
LILLESIVFLSCSGK; ILLESIVFLSCSGKG; LLESIVFLSCSGKGS;
LESIVFLSCSGKGSL; ESIVFLSCSGKGSLG; SIVFLSCSGKGSLGS;
IVFLSCSGKGSLGSE; VFLSCSGKGSLGSEI; FLSCSGKGSLGSEIP;
LSCSGKGSLGSEIPK; SCSGKGSLGSEIPKV; CSGKGSLGSEIPKVS;
SGKGSLGSEIPKVSL; GKGSLGSEIPKVSLI; KGSLGSEIPKVSLII;
GSLGSEIPKVSLIID; SLGSEIPKVSLIIDG; LGSEIPKVSLIIDGT;
GSEIPKVSLIIDGTF; SEIPKVSLIIDGTFD; EIPKVSLIIDGTFDD;
IPKVSLIIDGTFDDK; PKVSLIIDGTFDDKS; KVSLIIDGTFDDKSF;
VSLIIDGTFDDKSFN; SLIIDGTFDDKSFNE; LIIDGTFDDKSFNES;
IIDGTFDDKSFNESA; IDGTFDDKSFNESAL; DGTFDDKSFNESALN;
GTFDDKSFNESALNG; TFDDKSFNESALNGV; FDDKSFNESALNGVK;
DDKSFNESALNGVKK; DKSFNESALNGVKKV; KSFNESALNGVKKVK;
SFNESALNGVKKVKE; FNESALNGVKKVKEE; NESALNGVKKVKEEF;
ESALNGVKKVKEEFK; SALNGVKKVKEEFKI; ALNGVKKVKEEFKIE;
LNGVKKVKEEFKIEL; NGVKKVKEEFKIELV; GVKKVKEEFKIELVL;
VKKVKEEFKIELVLK; KKVKEEFKIELVLKE; KVKEEFKIELVLKES;
VKEEFKIELVLKESS; KEEFKIELVLKESSS; EEFKIELVLKESSSN;
EFKIELVLKESSSNS; FKIELVLKESSSNSY; KIELVLKESSSNSYL;
IELVLKESSSNSYLS; ELVLKESSSNSYLSD; LVLKESSSNSYLSDL;
VLKESSSNSYLSDLE; LKESSSNSYLSDLEG; KESSSNSYLSDLEGL;
ESSSNSYLSDLEGLK; SSSNSYLSDLEGLKD; SSNSYLSDLEGLKDA;
SNSYLSDLEGLKDAG; NSYLSDLEGLKDAGS; SYLSDLEGLKDAGSD;
YLSDLEGLKDAGSDL; LSDLEGLKDAGSDLI; SDLEGLKDAGSDLIW;
DLEGLKDAGSDLIWL; LEGLKDAGSDLIWLI; EGLKDAGSDLIWLIG;
GLKDAGSDLIWLIGY; LKDAGSDLIWLIGYR; KDAGSDLIWLIGYRF;

	DAGSDLIWLIGYRFS; AGSDLIWLIGYRFSD; GSDLIWLIGYRFSDV; SDLIWLIGYRFSDVA; DLIWLIGYRFSDVAK; LIWLIGYRFSDVAKV; IWLIGYRFSDVAKVA; WLIGYRFSDVAKVAA; LIGYRFSDVAKVAAL; IGYRFSDVAKVAALQ; GYRFSDVAKVAALQN; YRFSDVAKVAALQNP; RFSDVAKVAALQNPD; FSDVAKVAALQNPDM; SDVAKVAALQNPDMK; DVAKVAALQNPDMKY; VAKVAALQNPDMKYA; AKVAALQNPDMKYAI; KVAALQNPDMKYAII; VAALQNPDMKYAIID; AALQNPDMKYAIIDP; ALQNPDMKYAIIDPI; LQNPDMKYAIIDPIY; QNPDMKYAIIDPIYS; NPDMKYAIIDPIYSN; PDMKYAIIDPIYSND; DMKYAIIDPIYSNDP; MKYAIIDPIYSNDPI; KYAIIDPIYSNDPIP; YAIIDPIYSNDPIPA; AIIDPIYSNDPIPAN; IIDPIYSNDPIPANL; IDPIYSNDPIPANLV; DPIYSNDPIPANLVG; PIYSNDPIPANLVGM; IYSNDPIPANLVGMT; YSNDPIPANLVGMTF; SNDPIPANLVGMTFR; NDPIPANLVGMTFRA; DPIPANLVGMTFRAQ; PIPANLVGMTFRAQE; IPANLVGMTFRAQEG; PANLVGMTFRAQEGA; ANLVGMTFRAQEGAF; NLVGMTFRAQEGAFL; LVGMTFRAQEGAFLT; VGMTFRAQEGAFLTG; GMTFRAQEGAFLTGY; MTFRAQEGAFLTGYI; TFRAQEGAFLTGYIA; FRAQEGAFLTGYIAA; RAQEGAFLTGYIAAK; AQEGAFLTGYIAAKL; QEGAFLTGYIAAKLS; EGAFLTGYIAAKLSK; GAFLTGYIAAKLSKT; AFLTGYIAAKLSKTG; FLTGYIAAKLSKTGK; LTGYIAAKLSKTGKI; TGYIAAKLSKTGKIG; GYIAAKLSKTGKIGF; YIAAKLSKTGKIGFL; IAAKLSKTGKIGFLG; AAKLSKTGKIGFLGG; AKLSKTGKIGFLGGI; KLSKTGKIGFLGGIE; LSKTGKIGFLGGIEG; SKTGKIGFLGGIEGE; KTGKIGFLGGIEGEI; TGKIGFLGGIEGEIV; GKIGFLGGIEGEIVD; KIGFLGGIEGEIVDA; IGFLGGIEGEIVDAF; GFLGGIEGEIVDAFR; FLGGIEGEIVDAFRY; LGGIEGEIVDAFRYG; GGIEGEIVDAFRYGY; GIEGEIVDAFRYGYE; IEGEIVDAFRYGYEA; EGEIVDAFRYGYEAG; GEIVDAFRYGYEAGA; EIVDAFRYGYEAGAK; IVDAFRYGYEAGAKY; VDAFRYGYEAGAKYA; DAFRYGYEAGAKYAN; AFRYGYEAGAKYANK; FRYGYEAGAKYANKD; RYGYEAGAKYANKDI; YGYEAGAKYANKDIK; GYEAGAKYANKDIKI; YEAGAKYANKDIKIS; EAGAKYANKDIKIST; AGAKYANKDIKISTQ; GAKYANKDIKISTQY; AKYANKDIKISTQYI; KYANKDIKISTQYIG; YANKDIKISTQYIGS; ANKDIKISTQYIGSF; NKDIKISTQYIGSFA; KDIKISTQYIGSFAD; DIKISTQYIGSFADL; IKISTQYIGSFADLE; KISTQYIGSFADLEA; ISTQYIGSFADLEAG; STQYIGSFADLEAGR; TQYIGSFADLEAGRS; QYIGSFADLEAGRSV; YIGSFADLEAGRSVA; IGSFADLEAGRSVAT; GSFADLEAGRSVATR; SFADLEAGRSVATRM; FADLEAGRSVATRMY; ADLEAGRSVATRMYS; DLEAGRSVATRMYSD; LEAGRSVATRMYSDE; EAGRSVATRMYSDEI; AGRSVATRMYSDEID; GRSVATRMYSDEIDI; RSVATRMYSDEIDII; SVATRMYSDEIDIIH; VATRMYSDEIDIIHH; ATRMYSDEIDIIHHA; TRMYSDEIDIIHHAA; RMYSDEIDIIHHAAG; MYSDEIDIIHHAAGL; YSDEIDIIHHAAGLG; SDEIDIIHHAAGLGG; DEIDIIHHAAGLGGI; EIDIIHHAAGLGGIG; IDIIHHAAGLGGIGA; DIIHHAAGLGGIGAI; IIHHAAGLGGIGAIE; IHHAAGLGGIGAIEV; HHAAGLGGIGAIEVA; HAAGLGGIGAIEVAK; AAGLGGIGAIEVAKE; AGLGGIGAIEVAKEL; GLGGIGAIEVAKELG; LGGIGAIEVAKELGS; GGIGAIEVAKELGSG; GIGAIEVAKELGSGH; IGAIEVAKELGSGHY; GAIEVAKELGSGHYI; AIEVAKELGSGHYII; IEVAKELGSGHYIIG; EVAKELGSGHYIIGV; VAKELGSGHYIIGVD; AKELGSGHYIIGVDE; KELGSGHYIIGVDED; ELGSGHYIIGVDEDQ; LGSGHYIIGVDEDQA; GSGHYIIGVDEDQAY; SGHYIIGVDEDQAYL; GHYIIGVDEDQAYLA; HYIIGVDEDQAYLAP; YIIGVDEDQAYLAPD; IIGVDEDQAYLAPDN; IGVDEDQAYLAPDNV; GVDEDQAYLAPDNVI; VDEDQAYLAPDNVIT; DEDQAYLAPDNVITS; EDQAYLAPDNVITST; DQAYLAPDNVITSTT; QAYLAPDNVITSTTK; AYLAPDNVITSTTKD; YLAPDNVITSTTKDV; LAPDNVITSTTKDVG; APDNVITSTTKDVGR; PDNVITSTTKDVGRA; DNVITSTTKDVGRAL; NVITSTTKDVGRALN;

VITSTTKDVGRALNI; ITSTTKDVGRALNIF; TSTTKDVGRALNIFT;
STTKDVGRALNIFTS; TTKDVGRALNIFTSN; TKDVGRALNIFTSNH;
KDVGRALNIFTSNHL; DVGRALNIFTSNHLK; VGRALNIFTSNHLKT;
GRALNIFTSNHLKTN; RALNIFTSNHLKTNT; ALNIFTSNHLKTNTF;
LNIFTSNHLKTNTFE; NIFTSNHLKTNTFEG; IFTSNHLKTNTFEGG;
FTSNHLKTNTFEGGK; TSNHLKTNTFEGGKL; SNHLKTNTFEGGKLI;
NHLKTNTFEGGKLIN; HLKTNTFEGGKLINY; LKTNTFEGGKLINYG;
KTNTFEGGKLINYGL; TNTFEGGKLINYGLK; NTFEGGKLINYGLKE;
TFEGGKLINYGLKEG; FEGGKLINYGLKEGV; EGGKLINYGLKEGVV;
GGKLINYGLKEGVVG; GKLINYGLKEGVVGF; KLINYGLKEGVVGFV;
LINYGLKEGVVGFVR; INYGLKEGVVGFVRN; NYGLKEGVVGFVRNP;
YGLKEGVVGFVRNPK; GLKEGVVGFVRNPKM; LKEGVVGFVRNPKMI;
KEGVVGFVRNPKMIS; EGVVGFVRNPKMISF; GVVGFVRNPKMISFE;
VVGFVRNPKMISFEL; VGFVRNPKMISFELE; GFVRNPKMISFELEK;
FVRNPKMISFELEKE; VRNPKMISFELEKEI; RNPKMISFELEKEID;
NPKMISFELEKEIDN; PKMISFELEKEIDNL; KMISFELEKEIDNLS;
MISFELEKEIDNLSS; ISFELEKEIDNLSSK; SFELEKEIDNLSSKI;
FELEKEIDNLSSKII; ELEKEIDNLSSKIIN; LEKEIDNLSSKIINK;
EKEIDNLSSKIINKE; KEIDNLSSKIINKEI; EIDNLSSKIINKEII;
IDNLSSKIINKEIIV; DNLSSKIINKEIIVP; NLSSKIINKEIIVPS;
LSSKIINKEIIVPSN; SSKIINKEIIVPSNK; SKIINKEIIVPSNKE;
KIINKEIIVPSNKES; IINKEIIVPSNKESY; INKEIIVPSNKESYE;
NKEIIVPSNKESYEK; KEIIVPSNKESYEKF; EIIVPSNKESYEKFL;
IIVPSNKESYEKFLK; IVPSNKESYEKFLKE; VPSNKESYEKFLKEF;
PSNKESYEKFLKEFI;

16 mers:
MNKILLLILLESIVFL; NKILLLILLESIVFLS; KILLLILLESIVFLSC;
ILLLILLESIVFLSCS; LLLILLESIVFLSCSG; LLILLESIVFLSCSGK;
LILLESIVFLSCSGKG; ILLESIVFLSCSGKGS; LLESIVFLSCSGKGSL;
LESIVFLSCSGKGSLG; ESIVFLSCSGKGSLGS; SIVFLSCSGKGSLGSE;
IVFLSCSGKGSLGSEI; VFLSCSGKGSLGSEIP; FLSCSGKGSLGSEIPK;
LSCSGKGSLGSEIPKV; SCSGKGSLGSEIPKVS; CSGKGSLGSEIPKVSL;
SGKGSLGSEIPKVSLI; GKGSLGSEIPKVSLII; KGSLGSEIPKVSLIID;
GSLGSEIPKVSLIIDG; SLGSEIPKVSLIIDGT; LGSEIPKVSLIIDGTF;
GSEIPKVSLIIDGTFD; SEIPKVSLIIDGTFDD; EIPKVSLIIDGTFDDK;
IPKVSLIIDGTFDDKS; PKVSLIIDGTFDDKSF; KVSLIIDGTFDDKSFN;
VSLIIDGTFDDKSFNE; SLIIDGTFDDKSFNES; LIIDGTFDDKSFNESA;
IIDGTFDDKSFNESAL; IDGTFDDKSFNESALN; DGTFDDKSFNESALNG;
GTFDDKSFNESALNGV; TFDDKSFNESALNGVK; FDDKSFNESALNGVKK;
DDKSFNESALNGVKKV; DKSFNESALNGVKKVK; KSFNESALNGVKKVKE;
SFNESALNGVKKVKEE; FNESALNGVKKVKEEF; NESALNGVKKVKEEFK;
ESALNGVKKVKEEFKI; SALNGVKKVKEEFKIE; ALNGVKKVKEEFKIEL;
LNGVKKVKEEFKIELV; NGVKKVKEEFKIELVL; GVKKVKEEFKIELVLK;
VKKVKEEFKIELVLKE; KKVKEEFKIELVLKES; KVKEEFKIELVLKESS;
VKEEFKIELVLKESSS; KEEFKIELVLKESSSN; EEFKIELVLKESSSNS;
EFKIELVLKESSSNSY; FKIELVLKESSSNSYL; KIELVLKESSSNSYLS;
IELVLKESSSNSYLSD; ELVLKESSSNSYLSDL; LVLKESSSNSYLSDLE;
VLKESSSNSYLSDLEG; LKESSSNSYLSDLEGL; KESSSNSYLSDLEGLK;
ESSSNSYLSDLEGLKD; SSSNSYLSDLEGLKDA; SSNSYLSDLEGLKDAG;
SNSYLSDLEGLKDAGS; NSYLSDLEGLKDAGSD; SYLSDLEGLKDAGSDL;
YLSDLEGLKDAGSDLI; LSDLEGLKDAGSDLIW; SDLEGLKDAGSDLIWL;
DLEGLKDAGSDLIWLI; LEGLKDAGSDLIWLIG; EGLKDAGSDLIWLIGY;
GLKDAGSDLIWLIGYR; LKDAGSDLIWLIGYRF; KDAGSDLIWLIGYRFS;
DAGSDLIWLIGYRFSD; AGSDLIWLIGYRFSDV; GSDLIWLIGYRFSDVA;
SDLIWLIGYRFSDVAK; DLIWLIGYRFSDVAKV; LIWLIGYRFSDVAKVA;
IWLIGYRFSDVAKVAA; WLIGYRFSDVAKVAAL; LIGYRFSDVAKVAALQ;

	IGYRFSDVAKVAALQN; GYRFSDVAKVAALQNP; YRFSDVAKVAALQNPD; RFSDVAKVAALQNPDM; FSDVAKVAALQNPDMK; SDVAKVAALQNPDMKY; DVAKVAALQNPDMKYA; VAKVAALQNPDMKYAI; AKVAALQNPDMKYAII; KVAALQNPDMKYAIID; VAALQNPDMKYAIIDP; AALQNPDMKYAIIDPI; ALQNPDMKYAIIDPIY; LQNPDMKYAIIDPIYS; QNPDMKYAIIDPIYSN; NPDMKYAIIDPIYSND; PDMKYAIIDPIYSNDP; DMKYAIIDPIYSNDPI; MKYAIIDPIYSNDPIP; KYAIIDPIYSNDPIPA; YAIIDPIYSNDPIPAN; AIIDPIYSNDPIPANL; IIDPIYSNDPIPANLV; IDPIYSNDPIPANLVG; DPIYSNDPIPANLVGM; PIYSNDPIPANLVGMT; IYSNDPIPANLVGMTF; YSNDPIPANLVGMTFR; SNDPIPANLVGMTFRA; NDPIPANLVGMTFRAQ; DPIPANLVGMTFRAQE; PIPANLVGMTFRAQEG; IPANLVGMTFRAQEGA; PANLVGMTFRAQEGAF; ANLVGMTFRAQEGAFL; NLVGMTFRAQEGAFLT; LVGMTFRAQEGAFLTG; VGMTFRAQEGAFLTGY; GMTFRAQEGAFLTGYI; MTFRAQEGAFLTGYIA; TFRAQEGAFLTGYIAA; FRAQEGAFLTGYIAAK; RAQEGAFLTGYIAAKL; AQEGAFLTGYIAAKLS; QEGAFLTGYIAAKLSK; EGAFLTGYIAAKLSKT; GAFLTGYIAAKLSKTG; AFLTGYIAAKLSKTGK; FLTGYIAAKLSKTGKI; LTGYIAAKLSKTGKIG; TGYIAAKLSKTGKIGF; GYIAAKLSKTGKIGFL; YIAAKLSKTGKIGFLG; IAAKLSKTGKIGFLGG; AAKLSKTGKIGFLGGI; AKLSKTGKIGFLGGIE; KLSKTGKIGFLGGIEG; LSKTGKIGFLGGIEGE; SKTGKIGFLGGIEGEI; KTGKIGFLGGIEGEIV; TGKIGFLGGIEGEIVD; GKIGFLGGIEGEIVDA; KIGFLGGIEGEIVDAF; IGFLGGIEGEIVDAFR; GFLGGIEGEIVDAFRY; FLGGIEGEIVDAFRYG; LGGIEGEIVDAFRYGY; GGIEGEIVDAFRYGYE; GIEGEIVDAFRYGYEA; IEGEIVDAFRYGYEAG; EGEIVDAFRYGYEAGA; GEIVDAFRYGYEAGAK; EIVDAFRYGYEAGAKY; IVDAFRYGYEAGAKYA; VDAFRYGYEAGAKYAN; DAFRYGYEAGAKYANK; AFRYGYEAGAKYANKD; FRYGYEAGAKYANKDI; RYGYEAGAKYANKDIK; YGYEAGAKYANKDIKI; GYEAGAKYANKDIKIS; YEAGAKYANKDIKIST; EAGAKYANKDIKISTQ; AGAKYANKDIKISTQY; GAKYANKDIKISTQYI; AKYANKDIKISTQYIG; KYANKDIKISTQYIGS; YANKDIKISTQYIGSF; ANKDIKISTQYIGSFA; NKDIKISTQYIGSFAD; KDIKISTQYIGSFADL; DIKISTQYIGSFADLE; IKISTQYIGSFADLEA; KISTQYIGSFADLEAG; ISTQYIGSFADLEAGR; STQYIGSFADLEAGRS; TQYIGSFADLEAGRSV; QYIGSFADLEAGRSVA; YIGSFADLEAGRSVAT; IGSFADLEAGRSVATR; GSFADLEAGRSVATRM; SFADLEAGRSVATRMY; FADLEAGRSVATRMYS; ADLEAGRSVATRMYSD; DLEAGRSVATRMYSDE; LEAGRSVATRMYSDEI; EAGRSVATRMYSDEID; AGRSVATRMYSDEIDI; GRSVATRMYSDEIDII; RSVATRMYSDEIDIIH; SVATRMYSDEIDIIHH; VATRMYSDEIDIIHHA; ATRMYSDEIDIIHHAA; TRMYSDEIDIIHHAAG; RMYSDEIDIIHHAAGL; MYSDEIDIIHHAAGLG; YSDEIDIIHHAAGLGG; SDEIDIIHHAAGLGGI; DEIDIIHHAAGLGGIG; EIDIIHHAAGLGGIGA; IDIIHHAAGLGGIGAI; DIIHHAAGLGGIGAIE; IIHHAAGLGGIGAIEV; IHHAAGLGGIGAIEVA; HHAAGLGGIGAIEVAK; HAAGLGGIGAIEVAKE; AAGLGGIGAIEVAKEL; AGLGGIGAIEVAKELG; GLGGIGAIEVAKELGS; LGGIGAIEVAKELGSG; GGIGAIEVAKELGSGH; GIGAIEVAKELGSGHY; IGAIEVAKELGSGHYI; GAIEVAKELGSGHYII; AIEVAKELGSGHYIIG; IEVAKELGSGHYIIGV; EVAKELGSGHYIIGVD; VAKELGSGHYIIGVDE; AKELGSGHYIIGVDED; KELGSGHYIIGVDEDQ; ELGSGHYIIGVDEDQA; LGSGHYIIGVDEDQAY; GSGHYIIGVDEDQAYL; SGHYIIGVDEDQAYLA; GHYIIGVDEDQAYLAP; HYIIGVDEDQAYLAPD; YIIGVDEDQAYLAPDN; IIGVDEDQAYLAPDNV; IGVDEDQAYLAPDNVI; GVDEDQAYLAPDNVIT; VDEDQAYLAPDNVITS; DEDQAYLAPDNVITST; EDQAYLAPDNVITSTT; DQAYLAPDNVITSTTK; QAYLAPDNVITSTTKD; AYLAPDNVITSTTKDV; YLAPDNVITSTTKDVG; LAPDNVITSTTKDVGR; APDNVITSTTKDVGRA; PDNVITSTTKDVGRAL; DNVITSTTKDVGRALN; NVITSTTKDVGRALNI; VITSTTKDVGRALNIF; ITSTTKDVGRALNIFT; TSTTKDVGRALNIFTS; STTKDVGRALNIFTSN; TTKDVGRALNIFTSNH; TKDVGRALNIFTSNHL; KDVGRALNIFTSNHLK; DVGRALNIFTSNHLKT; VGRALNIFTSNHLKTN;

	GRALNIFTSNHLKTNT; RALNIFTSNHLKTNTF; ALNIFTSNHLKTNTFE; LNIFTSNHLKTNTFEG; NIFTSNHLKTNTFEGG; IFTSNHLKTNTFEGGK; FTSNHLKTNTFEGGKL; TSNHLKTNTFEGGKLI; SNHLKTNTFEGGKLIN; NHLKTNTFEGGKLINY; HLKTNTFEGGKLINYG; LKTNTFEGGKLINYGL; KTNTFEGGKLINYGLK; TNTFEGGKLINYGLKE; NTFEGGKLINYGLKEG; TFEGGKLINYGLKEGV; FEGGKLINYGLKEGVV; EGGKLINYGLKEGVVG; GGKLINYGLKEGVVGF; GKLINYGLKEGVVGFV; KLINYGLKEGVVGFVR; LINYGLKEGVVGFVRN; INYGLKEGVVGFVRNP; NYGLKEGVVGFVRNPK; YGLKEGVVGFVRNPKM; GLKEGVVGFVRNPKMI; LKEGVVGFVRNPKMIS; KEGVVGFVRNPKMISF; EGVVGFVRNPKMISFE; GVVGFVRNPKMISFEL; VVGFVRNPKMISFELE; VGFVRNPKMISFELEK; GFVRNPKMISFELEKE; FVRNPKMISFELEKEI; VRNPKMISFELEKEID; RNPKMISFELEKEIDN; NPKMISFELEKEIDNL; PKMISFELEKEIDNLS; KMISFELEKEIDNLSS; MISFELEKEIDNLSSK; ISFELEKEIDNLSSKI; SFELEKEIDNLSSKII; FELEKEIDNLSSKIIN; ELEKEIDNLSSKIINK; LEKEIDNLSSKIINKE; EKEIDNLSSKIINKEI; KEIDNLSSKIINKEII; EIDNLSSKIINKEIIV; IDNLSSKIINKEIIVP; DNLSSKIINKEIIVPS; NLSSKIINKEIIVPSN; LSSKIINKEIIVPSNK; SSKIINKEIIVPSNKE; SKIINKEIIVPSNKES; KIINKEIIVPSNKESY; IINKEIIVPSNKESYE; INKEIIVPSNKESYEK; NKEIIVPSNKESYEKF; KEIIVPSNKESYEKFL; EIIVPSNKESYEKFLK; IIVPSNKESYEKFLKE; IVPSNKESYEKFLKEF; VPSNKESYEKFLKEFI;
NP_212516.1 Basic membrane protein B (bmpB) [Borrelia burgdorferi B31	13 mers: MRIVIFIFGILLT; RIVIFIFGILLTS; IVIFIFGILLTSC; VIFIFGILLTSCF; IFIFGILLTSCFS; FIFGILLTSCFSR; IFGILLTSCFSRN; FGILLTSCFSRNG; GILLTSCFSRNGI; ILLTSCFSRNGIE; LLTSCFSRNGIES; LTSCFSRNGIESS; TSCFSRNGIESSS; SCFSRNGIESSSK; CFSRNGIESSSKK; FSRNGIESSSKKI; SRNGIESSSKKIK; RNGIESSSKKIKI; NGIESSSKKIKIS; GIESSSKKIKISM; IESSSKKIKISML; ESSSKKIKISMLV; SSSKKIKISMLVD; SSKKIKISMLVDG; SKKIKISMLVDGV; KKIKISMLVDGVL; KIKISMLVDGVLD; IKISMLVDGVLDD; KISMLVDGVLDDK; ISMLVDGVLDDKS; SMLVDGVLDDKSF; MLVDGVLDDKSFN; LVDGVLDDKSFNS; VDGVLDDKSFNSS; DGVLDDKSFNSSA; GVLDDKSFNSSAN; VLDDKSFNSSANE; LDDKSFNSSANEA; DDKSFNSSANEAL; DKSFNSSANEALL; KSFNSSANEALLR; SFNSSANEALLRL; FNSSANEALLRLK; NSSANEALLRLKK; SSANEALLRLKKD; SANEALLRLKKDF; ANEALLRLKKDFP; NEALLRLKKDFPE; EALLRLKKDFPEN; ALLRLKKDFPENI; LLRLKKDFPENIE; LRLKKDFPENIEE; RLKKDFPENIEEV; LKKDFPENIEEVF; KKDFPENIEEVFS; KDFPENIEEVFSC; DFPENIEEVFSCA; FPENIEEVFSCAI; PENIEEVFSCAIS; ENIEEVFSCAISG; NIEEVFSCAISGV; IEEVFSCAISGVY; EEVFSCAISGVYS; EVFSCAISGVYSS; VFSCAISGVYSSY; FSCAISGVYSSYV; SCAISGVYSSYVS; CAISGVYSSYVSD; AISGVYSSYVSDL; ISGVYSSYVSDLD; SGVYSSYVSDLDN; GVYSSYVSDLDNL; VYSSYVSDLDNLK; YSSYVSDLDNLKR; SSYVSDLDNLKRN; SYVSDLDNLKRNG; YVSDLDNLKRNGS; VSDLDNLKRNGSD; SDLDNLKRNGSDL; DLDNLKRNGSDLI; LDNLKRNGSDLIW; DNLKRNGSDLIWL; NLKRNGSDLIWLV; LKRNGSDLIWLVG; KRNGSDLIWLVGY; RNGSDLIWLVGYM; NGSDLIWLVGYML; GSDLIWLVGYMLT; SDLIWLVGYMLTD; DLIWLVGYMLTDA; LIWLVGYMLTDAS; IWLVGYMLTDASL; WLVGYMLTDASLL; LVGYMLTDASLLV; VGYMLTDASLLVS; GYMLTDASLLVSS; YMLTDASLLVSSE; MLTDASLLVSSEN; LTDASLLVSSENP; TDASLLVSSENPK; DASLLVSSENPKI; ASLLVSSENPKIS; SLLVSSENPKISY; LLVSSENPKISYG; LVSSENPKISYGI; VSSENPKISYGII; SSENPKISYGIID; SENPKISYGIIDP; ENPKISYGIIDPI; NPKISYGIIDPIY; PKISYGIIDPIYG; KISYGIIDPIYGD; ISYGIIDPIYGDD; SYGIIDPIYGDDV; YGIIDPIYGDDVQ; GIIDPIYGDDVQI; IIDPIYGDDVQIP; IDPIYGDDVQIPE; DPIYGDDVQIPEN; PIYGDDVQIPENL; IYGDDVQIPENLI; YGDDVQIPENLIA; GDDVQIPENLIAV; DDVQIPENLIAVV; DVQIPENLIAVVF; VQIPENLIAVVFR; QIPENLIAVVFRV; IPENLIAVVFRVE; PENLIAVVFRVEQ; ENLIAVVFRVEQG; NLIAVVFRVEQGA; LIAVVFRVEQGAF;

IAVVFRVEQGAFL; AVVFRVEQGAFLA; VVFRVEQGAFLAG; VFRVEQGAFLAGY;
FRVEQGAFLAGYI; RVEQGAFLAGYIA; VEQGAFLAGYIAA; EQGAFLAGYIAAK;
QGAFLAGYIAAKK; GAFLAGYIAAKKS; AFLAGYIAAKKSF; FLAGYIAAKKSFS;
LAGYIAAKKSFSG; AGYIAAKKSFSGK; GYIAAKKSFSGKI; YIAAKKSFSGKIG;
IAAKKSFSGKIGF; AAKKSFSGKIGFI; AKKSFSGKIGFIG; KKSFSGKIGFIGG;
KSFSGKIGFIGGM; SFSGKIGFIGGMK; FSGKIGFIGGMKG; SGKIGFIGGMKGN;
GKIGFIGGMKGNI; KIGFIGGMKGNIV; IGFIGGMKGNIVD; GFIGGMKGNIVDA;
FIGGMKGNIVDAF; IGGMKGNIVDAFR; GGMKGNIVDAFRY; GMKGNIVDAFRYG;
MKGNIVDAFRYGY; KGNIVDAFRYGYE; GNIVDAFRYGYES; NIVDAFRYGYESG;
IVDAFRYGYESGA; VDAFRYGYESGAK; DAFRYGYESGAKY; AFRYGYESGAKYA;
FRYGYESGAKYAN; RYGYESGAKYANK; YGYESGAKYANKD; GYESGAKYANKDI;
YESGAKYANKDIE; ESGAKYANKDIEI; SGAKYANKDIEII; GAKYANKDIEIIS;
AKYANKDIEIISE; KYANKDIEIISEY; YANKDIEIISEYS; ANKDIEIISEYSN;
NKDIEIISEYSNS; KDIEIISEYSNSF; DIEIISEYSNSFS; IEIISEYSNSFSD;
EIISEYSNSFSDV; IISEYSNSFSDVD; ISEYSNSFSDVDI; SEYSNSFSDVDIG;
EYSNSFSDVDIGR; YSNSFSDVDIGRT; SNSFSDVDIGRTI; NSFSDVDIGRTIA;
SFSDVDIGRTIAS; FSDVDIGRTIASK; SDVDIGRTIASKM; DVDIGRTIASKMY;
VDIGRTIASKMYS; DIGRTIASKMYSK; IGRTIASKMYSKG; GRTIASKMYSKGI;
RTIASKMYSKGID; TIASKMYSKGIDV; IASKMYSKGIDVI; ASKMYSKGIDVIH;
SKMYSKGIDVIHF; KMYSKGIDVIHFA; MYSKGIDVIHFAA; YSKGIDVIHFAAG;
SKGIDVIHFAAGL; KGIDVIHFAAGLA; GIDVIHFAAGLAG; IDVIHFAAGLAGI;
DVIHFAAGLAGIG; VIHFAAGLAGIGV; IHFAAGLAGIGVI; HFAAGLAGIGVIE;
FAAGLAGIGVIET; AAGLAGIGVIETA; AGLAGIGVIETAK; GLAGIGVIETAKN;
LAGIGVIETAKNL; AGIGVIETAKNLG; GIGVIETAKNLGD; IGVIETAKNLGDG;
GVIETAKNLGDGY; VIETAKNLGDGYY; IETAKNLGDGYYV; ETAKNLGDGYYVI;
TAKNLGDGYYVIG; AKNLGDGYYVIGA; KNLGDGYYVIGAD; NLGDGYYVIGADQ;
LGDGYYVIGADQD; GDGYYVIGADQDQ; DGYYVIGADQDQS; GYYVIGADQDQSY;
YYVIGADQDQSYL; YVIGADQDQSYLA; VIGADQDQSYLAP; IGADQDQSYLAPK;
GADQDQSYLAPKN; ADQDQSYLAPKNF; DQDQSYLAPKNFI; QDQSYLAPKNFIT;
DQSYLAPKNFITS; QSYLAPKNFITSV; SYLAPKNFITSVI; YLAPKNFITSVIK;
LAPKNFITSVIKN; APKNFITSVIKNI; PKNFITSVIKNIG; KNFITSVIKNIGD;
NFITSVIKNIGDA; FITSVIKNIGDAL; ITSVIKNIGDALY; TSVIKNIGDALYL;
SVIKNIGDALYLI; VIKNIGDALYLIT; IKNIGDALYLITG; KNIGDALYLITGE;
NIGDALYLITGEY; IGDALYLITGEYI; GDALYLITGEYIK; DALYLITGEYIKN;
ALYLITGEYIKNN; LYLITGEYIKNNN; YLITGEYIKNNNV; LITGEYIKNNNVW;
ITGEYIKNNNVWE; TGEYIKNNNVWEG; GEYIKNNNVWEGG; EYIKNNNVWEGGK;
YIKNNNVWEGGKV; IKNNNVWEGGKVV; KNNNVWEGGKVVQ; NNNVWEGGKVVQM;
NNVWEGGKVVQMG; NVWEGGKVVQMGL; VWEGGKVVQMGLR; WEGGKVVQMGLRD;
EGGKVVQMGLRDG; GGKVVQMGLRDGV; GKVVQMGLRDGVI; KVVQMGLRDGVIG;
VVQMGLRDGVIGL; VQMGLRDGVIGLP; QMGLRDGVIGLPN; MGLRDGVIGLPNA;
GLRDGVIGLPNAN; LRDGVIGLPNANE; RDGVIGLPNANEF; DGVIGLPNANEFE;
GVIGLPNANEFEY; VIGLPNANEFEYI; IGLPNANEFEYIK; GLPNANEFEYIKV;
LPNANEFEYIKVL; PNANEFEYIKVLE; NANEFEYIKVLER; ANEFEYIKVLERK;
NEFEYIKVLERKI; EFEYIKVLERKII; FEYIKVLERKIIN; EYIKVLERKIINK;
YIKVLERKIINKE; IKVLERKIINKEI; KVLERKIINKEII; VLERKIINKEIIV;
LERKIINKEIIVP; ERKIINKEIIVPC; RKIINKEIIVPCN; KIINKEIIVPCNQ;
IINKEIIVPCNQE; INKEIIVPCNQEE; NKEIIVPCNQEEY; KEIIVPCNQEEYE;
EIIVPCNQEEYEI; IIVPCNQEEYEIF; IVPCNQEEYEIFI; VPCNQEEYEIFIK;
PCNQEEYEIFIKQ; CNQEEYEIFIKQI; NQEEYEIFIKQIL; QEEYEIFIKQILK;
EEYEIFIKQILKL;

14 mers:
MRIVIFIFGILLTS; RIVIFIFGILLTSC; IVIFIFGILLTSCF;
VIFIFGILLTSCFS; IFIFGILLTSCFSR; FIFGILLTSCFSRN;
IFGILLTSCFSRNG; FGILLTSCFSRNGI; GILLTSCFSRNGIE;
ILLTSCFSRNGIES; LLTSCFSRNGIESS; LTSCFSRNGIESSS;
TSCFSRNGIESSSK; SCFSRNGIESSSKK; CFSRNGIESSSKKI;

	FSRNGIESSSKKIK; SRNGIESSSKKIKI; RNGIESSSKKIKIS; NGIESSSKKIKISM; GIESSSKKIKISML; IESSSKKIKISMLV; ESSSKKIKISMLVD; SSSKKIKISMLVDG; SSKKIKISMLVDGV; SKKIKISMLVDGVL; KKIKISMLVDGVLD; KIKISMLVDGVLDD; IKISMLVDGVLDDK; KISMLVDGVLDDKS; ISMLVDGVLDDKSF; SMLVDGVLDDKSFN; MLVDGVLDDKSFNS; LVDGVLDDKSFNSS; VDGVLDDKSFNSSA; DGVLDDKSFNSSAN; GVLDDKSFNSSANE; VLDDKSFNSSANEA; LDDKSFNSSANEAL; DDKSFNSSANEALL; DKSFNSSANEALLR; KSFNSSANEALLRL; SFNSSANEALLRLK; FNSSANEALLRLKK; NSSANEALLRLKKD; SSANEALLRLKKDF; SANEALLRLKKDFP; ANEALLRLKKDFPE; NEALLRLKKDFPEN; EALLRLKKDFPENI; ALLRLKKDFPENIE; LLRLKKDFPENIEE; LRLKKDFPENIEEV; RLKKDFPENIEEVF; LKKDFPENIEEVFS; KKDFPENIEEVFSC; KDFPENIEEVFSCA; DFPENIEEVFSCAI; FPENIEEVFSCAIS; PENIEEVFSCAISG; ENIEEVFSCAISGV; NIEEVFSCAISGVY; IEEVFSCAISGVYS; EEVFSCAISGVYSS; EVFSCAISGVYSSY; VFSCAISGVYSSYV; FSCAISGVYSSYVS; SCAISGVYSSYVSD; CAISGVYSSYVSDL; AISGVYSSYVSDLD; ISGVYSSYVSDLDN; SGVYSSYVSDLDNL; GVYSSYVSDLDNLK; VYSSYVSDLDNLKR; YSSYVSDLDNLKRN; SSYVSDLDNLKRNG; SYVSDLDNLKRNGS; YVSDLDNLKRNGSD; VSDLDNLKRNGSDL; SDLDNLKRNGSDLI; DLDNLKRNGSDLIW; LDNLKRNGSDLIWL; DNLKRNGSDLIWLV; NLKRNGSDLIWLVG; LKRNGSDLIWLVGY; KRNGSDLIWLVGYM; RNGSDLIWLVGYML; NGSDLIWLVGYMLT; GSDLIWLVGYMLTD; SDLIWLVGYMLTDA; DLIWLVGYMLTDAS; LIWLVGYMLTDASL; IWLVGYMLTDASLL; WLVGYMLTDASLLV; LVGYMLTDASLLVS; VGYMLTDASLLVSS; GYMLTDASLLVSSE; YMLTDASLLVSSEN; MLTDASLLVSSENP; LTDASLLVSSENPK; TDASLLVSSENPKI; DASLLVSSENPKIS; ASLLVSSENPKISY; SLLVSSENPKISYG; LLVSSENPKISYGI; LVSSENPKISYGII; VSSENPKISYGIID; SSENPKISYGIIDP; SENPKISYGIIDPI; ENPKISYGIIDPIY; NPKISYGIIDPIYG; PKISYGIIDPIYGD; KISYGIIDPIYGDD; ISYGIIDPIYGDDV; SYGIIDPIYGDDVQ; YGIIDPIYGDDVQI; GIIDPIYGDDVQIP; IIDPIYGDDVQIPE; IDPIYGDDVQIPEN; DPIYGDDVQIPENL; PIYGDDVQIPENLI; IYGDDVQIPENLIA; YGDDVQIPENLIAV; GDDVQIPENLIAVV; DDVQIPENLIAVVF; DVQIPENLIAVVFR; VQIPENLIAVVFRV; QIPENLIAVVFRVE; IPENLIAVVFRVEQ; PENLIAVVFRVEQG; ENLIAVVFRVEQGA; NLIAVVFRVEQGAF; LIAVVFRVEQGAFL; IAVVFRVEQGAFLA; AVVFRVEQGAFLAG; VVFRVEQGAFLAGY; VFRVEQGAFLAGYI; FRVEQGAFLAGYIA; RVEQGAFLAGYIAA; VEQGAFLAGYIAAK; EQGAFLAGYIAAKK; QGAFLAGYIAAKKS; GAFLAGYIAAKKSF; AFLAGYIAAKKSFS; FLAGYIAAKKSFSG; LAGYIAAKKSFSGK; AGYIAAKKSFSGKI; GYIAAKKSFSGKIG; YIAAKKSFSGKIGF; IAAKKSFSGKIGFI; AAKKSFSGKIGFIG; AKKSFSGKIGFIGG; KKSFSGKIGFIGGM; KSFSGKIGFIGGMK; SFSGKIGFIGGMKG; FSGKIGFIGGMKGN; SGKIGFIGGMKGNI; GKIGFIGGMKGNIV; KIGFIGGMKGNIVD; IGFIGGMKGNIVDA; GFIGGMKGNIVDAF; FIGGMKGNIVDAFR; IGGMKGNIVDAFRY; GGMKGNIVDAFRYG; GMKGNIVDAFRYGY; MKGNIVDAFRYGYE; KGNIVDAFRYGYES; GNIVDAFRYGYESG; NIVDAFRYGYESGA; IVDAFRYGYESGAK; VDAFRYGYESGAKY; DAFRYGYESGAKYA; AFRYGYESGAKYAN; FRYGYESGAKYANK; RYGYESGAKYANKD; YGYESGAKYANKDI; GYESGAKYANKDIE; YESGAKYANKDIEI; ESGAKYANKDIEII; SGAKYANKDIEIIS; GAKYANKDIEIISE; AKYANKDIEIISEY; KYANKDIEIISEYS; YANKDIEIISEYSN; ANKDIEIISEYSNS; NKDIEIISEYSNSF; KDIEIISEYSNSFS;

DIEIISEYSNSFSD; IEIISEYSNSFSDV; EIISEYSNSFSDVD;
IISEYSNSFSDVDI; ISEYSNSFSDVDIG; SEYSNSFSDVDIGR;
EYSNSFSDVDIGRT; YSNSFSDVDIGRTI; SNSFSDVDIGRTIA;
NSFSDVDIGRTIAS; SFSDVDIGRTIASK; FSDVDIGRTIASKM;
SDVDIGRTIASKMY; DVDIGRTIASKMYS; VDIGRTIASKMYSK;
DIGRTIASKMYSKG; IGRTIASKMYSKGI; GRTIASKMYSKGID;
RTIASKMYSKGIDV; TIASKMYSKGIDVI; IASKMYSKGIDVIH;
ASKMYSKGIDVIHF; SKMYSKGIDVIHFA; KMYSKGIDVIHFAA;
MYSKGIDVIHFAAG; YSKGIDVIHFAAGL; SKGIDVIHFAAGLA;
KGIDVIHFAAGLAG; GIDVIHFAAGLAGI; IDVIHFAAGLAGIG;
DVIHFAAGLAGIGV; VIHFAAGLAGIGVI; IHFAAGLAGIGVIE;
HFAAGLAGIGVIET; FAAGLAGIGVIETA; AAGLAGIGVIETAK;
AGLAGIGVIETAKN; GLAGIGVIETAKNL; LAGIGVIETAKNLG;
AGIGVIETAKNLGD; GIGVIETAKNLGDG; IGVIETAKNLGDGY;
GVIETAKNLGDGYY; VIETAKNLGDGYYV; IETAKNLGDGYYVI;
ETAKNLGDGYYVIG; TAKNLGDGYYVIGA; AKNLGDGYYVIGAD;
KNLGDGYYVIGADQ; NLGDGYYVIGADQD; LGDGYYVIGADQDQ;
GDGYYVIGADQDQS; DGYYVIGADQDQSY; GYYVIGADQDQSYL;
YYVIGADQDQSYLA; YVIGADQDQSYLAP; VIGADQDQSYLAPK;
IGADQDQSYLAPKN; GADQDQSYLAPKNF; ADQDQSYLAPKNFI;
DQDQSYLAPKNFIT; QDQSYLAPKNFITS; DQSYLAPKNFITSV;
QSYLAPKNFITSVI; SYLAPKNFITSVIK; YLAPKNFITSVIKN;
LAPKNFITSVIKNI; APKNFITSVIKNIG; PKNFITSVIKNIGD;
KNFITSVIKNIGDA; NFITSVIKNIGDAL; FITSVIKNIGDALY;
ITSVIKNIGDALYL; TSVIKNIGDALYLI; SVIKNIGDALYLIT;
VIKNIGDALYLITG; IKNIGDALYLITGE; KNIGDALYLITGEY;
NIGDALYLITGEYI; IGDALYLITGEYIK; GDALYLITGEYIKN;
DALYLITGEYIKNN; ALYLITGEYIKNNN; LYLITGEYIKNNNV;
YLITGEYIKNNNVW; LITGEYIKNNNVWE; ITGEYIKNNNVWEG;
TGEYIKNNNVWEGG; GEYIKNNNVWEGGK; EYIKNNNVWEGGKV;
YIKNNNVWEGGKVV; IKNNNVWEGGKVVQ; KNNNVWEGGKVVQM;
NNNVWEGGKVVQMG; NNVWEGGKVVQMGL; NVWEGGKVVQMGLR;
VWEGGKVVQMGLRD; WEGGKVVQMGLRDG; EGGKVVQMGLRDGV;
GGKVVQMGLRDGVI; GKVVQMGLRDGVIG; KVVQMGLRDGVIGL;
VVQMGLRDGVIGLP; VQMGLRDGVIGLPN; QMGLRDGVIGLPNA;
MGLRDGVIGLPNAN; GLRDGVIGLPNANE; LRDGVIGLPNANEF;
RDGVIGLPNANEFE; DGVIGLPNANEFEY; GVIGLPNANEFEYI;
VIGLPNANEFEYIK; IGLPNANEFEYIKV; GLPNANEFEYIKVL;
LPNANEFEYIKVLE; PNANEFEYIKVLER; NANEFEYIKVLERK;
ANEFEYIKVLERKI; NEFEYIKVLERKII; EFEYIKVLERKIIN;
FEYIKVLERKIINK; EYIKVLERKIINKE; YIKVLERKIINKEI;
IKVLERKIINKEII; KVLERKIINKEIIV; VLERKIINKEIIVP;
LERKIINKEIIVPC; ERKIINKEIIVPCN; RKIINKEIIVPCNQ;
KIINKEIIVPCNQE; IINKEIIVPCNQEE; INKEIIVPCNQEEY;
NKEIIVPCNQEEYE; KEIIVPCNQEEYEI; EIIVPCNQEEYEIF;
IIVPCNQEEYEIFI; IVPCNQEEYEIFIK; VPCNQEEYEIFIKQ;
PCNQEEYEIFIKQI; CNQEEYEIFIKQIL; NQEEYEIFIKQILK;
QEEYEIFIKQILKL;

15 mers:
MRIVIFIFGILLTSC; RIVIFIFGILLTSCF; IVIFIFGILLTSCFS;
VIFIFGILLTSCFSR; IFIFGILLTSCFSRN; FIFGILLTSCFSRNG;
IFGILLTSCFSRNGI; FGILLTSCFSRNGIE; GILLTSCFSRNGIES;
ILLTSCFSRNGIESS; LLTSCFSRNGIESSS; LTSCFSRNGIESSSK;
TSCFSRNGIESSSKK; SCFSRNGIESSSKKI; CFSRNGIESSSKKIK;
FSRNGIESSSKKIKI; SRNGIESSSKKIKIS; RNGIESSSKKIKISM;
NGIESSSKKIKISML; GIESSSKKIKISMLV; IESSSKKIKISMLVD;

	ESSSKKIKISMLVDG; SSSKKIKISMLVDGV; SSKKIKISMLVDGVL; SKKIKISMLVDGVLD; KKIKISMLVDGVLDD; KIKISMLVDGVLDDK; IKISMLVDGVLDDKS; KISMLVDGVLDDKSF; ISMLVDGVLDDKSFN; SMLVDGVLDDKSFNS; MLVDGVLDDKSFNSS; LVDGVLDDKSFNSSA; VDGVLDDKSFNSSAN; DGVLDDKSFNSSANE; GVLDDKSFNSSANEA; VLDDKSFNSSANEAL; LDDKSFNSSANEALL; DDKSFNSSANEALLR; DKSFNSSANEALLRL; KSFNSSANEALLRLK; SFNSSANEALLRLKK; FNSSANEALLRLKKD; NSSANEALLRLKKDF; SSANEALLRLKKDFP; SANEALLRLKKDFPE; ANEALLRLKKDFPEN; NEALLRLKKDFPENI; EALLRLKKDFPENIE; ALLRLKKDFPENIEE; LLRLKKDFPENIEEV; LRLKKDFPENIEEVF; RLKKDFPENIEEVFS; LKKDFPENIEEVFSC; KKDFPENIEEVFSCA; KDFPENIEEVFSCAI; DFPENIEEVFSCAIS; FPENIEEVFSCAISG; PENIEEVFSCAISGV; ENIEEVFSCAISGVY; NIEEVFSCAISGVYS; IEEVFSCAISGVYSS; EEVFSCAISGVYSSY; EVFSCAISGVYSSYV; VFSCAISGVYSSYVS; FSCAISGVYSSYVSD; SCAISGVYSSYVSDL; CAISGVYSSYVSDLD; AISGVYSSYVSDLDN; ISGVYSSYVSDLDNL; SGVYSSYVSDLDNLK; GVYSSYVSDLDNLKR; VYSSYVSDLDNLKRN; YSSYVSDLDNLKRNG; SSYVSDLDNLKRNGS; SYVSDLDNLKRNGSD; YVSDLDNLKRNGSDL; VSDLDNLKRNGSDLI; SDLDNLKRNGSDLIW; DLDNLKRNGSDLIWL; LDNLKRNGSDLIWLV; DNLKRNGSDLIWLVG; NLKRNGSDLIWLVGY; LKRNGSDLIWLVGYM; KRNGSDLIWLVGYML; RNGSDLIWLVGYMLT; NGSDLIWLVGYMLTD; GSDLIWLVGYMLTDA; SDLIWLVGYMLTDAS; DLIWLVGYMLTDASL; LIWLVGYMLTDASLL; IWLVGYMLTDASLLV; WLVGYMLTDASLLVS; LVGYMLTDASLLVSS; VGYMLTDASLLVSSE; GYMLTDASLLVSSEN; YMLTDASLLVSSENP; MLTDASLLVSSENPK; LTDASLLVSSENPKI; TDASLLVSSENPKIS; DASLLVSSENPKISY; ASLLVSSENPKISYG; SLLVSSENPKISYGI; LLVSSENPKISYGII; LVSSENPKISYGIID; VSSENPKISYGIIDP; SSENPKISYGIIDPI; SENPKISYGIIDPIY; ENPKISYGIIDPIYG; NPKISYGIIDPIYGD; PKISYGIIDPIYGDD; KISYGIIDPIYGDDV; ISYGIIDPIYGDDVQ; SYGIIDPIYGDDVQI; YGIIDPIYGDDVQIP; GIIDPIYGDDVQIPE; IIDPIYGDDVQIPEN; IDPIYGDDVQIPENL; DPIYGDDVQIPENLI; PIYGDDVQIPENLIA; IYGDDVQIPENLIAV; YGDDVQIPENLIAVV; GDDVQIPENLIAVVF; DDVQIPENLIAVVFR; DVQIPENLIAVVFRV; VQIPENLIAVVFRVE; QIPENLIAVVFRVEQ; IPENLIAVVFRVEQG; PENLIAVVFRVEQGA; ENLIAVVFRVEQGAF; NLIAVVFRVEQGAFL; LIAVVFRVEQGAFLA; IAVVFRVEQGAFLAG; AVVFRVEQGAFLAGY; VVFRVEQGAFLAGYI; VFRVEQGAFLAGYIA; FRVEQGAFLAGYIAA; RVEQGAFLAGYIAAK; VEQGAFLAGYIAAKK; EQGAFLAGYIAAKKS; QGAFLAGYIAAKKSF; GAFLAGYIAAKKSFS; AFLAGYIAAKKSFSG; FLAGYIAAKKSFSGK; LAGYIAAKKSFSGKI; AGYIAAKKSFSGKIG; GYIAAKKSFSGKIGF; YIAAKKSFSGKIGFI; IAAKKSFSGKIGFIG; AAKKSFSGKIGFIGG; AKKSFSGKIGFIGGM; KKSFSGKIGFIGGMK; KSFSGKIGFIGGMKG; SFSGKIGFIGGMKGN; FSGKIGFIGGMKGNI; SGKIGFIGGMKGNIV; GKIGFIGGMKGNIVD; KIGFIGGMKGNIVDA; IGFIGGMKGNIVDAF; GFIGGMKGNIVDAFR; FIGGMKGNIVDAFRY; IGGMKGNIVDAFRYG; GGMKGNIVDAFRYGY; GMKGNIVDAFRYGYE; MKGNIVDAFRYGYES; KGNIVDAFRYGYESG; GNIVDAFRYGYESGA; NIVDAFRYGYESGAK; IVDAFRYGYESGAKY; VDAFRYGYESGAKYA; DAFRYGYESGAKYAN; AFRYGYESGAKYANK; FRYGYESGAKYANKD; RYGYESGAKYANKDI; YGYESGAKYANKDIE; GYESGAKYANKDIEI; YESGAKYANKDIEII; ESGAKYANKDIEIIS; SGAKYANKDIEIISE; GAKYANKDIEIISEY; AKYANKDIEIISEYS; KYANKDIEIISEYSN; YANKDIEIISEYSNS; ANKDIEIISEYSNSF; NKDIEIISEYSNSFS; KDIEIISEYSNSFSD; DIEIISEYSNSFSDV; IEIISEYSNSFSDVD; EIISEYSNSFSDVDI; IISEYSNSFSDVDIG; ISEYSNSFSDVDIGR; SEYSNSFSDVDIGRT;

EYSNSFSDVDIGRTI; YSNSFSDVDIGRTIA; SNSFSDVDIGRTIAS;
NSFSDVDIGRTIASK; SFSDVDIGRTIASKM; FSDVDIGRTIASKMY;
SDVDIGRTIASKMYS; DVDIGRTIASKMYSK; VDIGRTIASKMYSKG;
DIGRTIASKMYSKGI; IGRTIASKMYSKGID; GRTIASKMYSKGIDV;
RTIASKMYSKGIDVI; TIASKMYSKGIDVIH; IASKMYSKGIDVIHF;
ASKMYSKGIDVIHFA; SKMYSKGIDVIHFAA; KMYSKGIDVIHFAAG;
MYSKGIDVIHFAAGL; YSKGIDVIHFAAGLA; SKGIDVIHFAAGLAG;
KGIDVIHFAAGLAGI; GIDVIHFAAGLAGIG; IDVIHFAAGLAGIGV;
DVIHFAAGLAGIGVI; VIHFAAGLAGIGVIE; IHFAAGLAGIGVIET;
HFAAGLAGIGVIETA; FAAGLAGIGVIETAK; AAGLAGIGVIETAKN;
AGLAGIGVIETAKNL; GLAGIGVIETAKNLG; LAGIGVIETAKNLGD;
AGIGVIETAKNLGDG; GIGVIETAKNLGDGY; IGVIETAKNLGDGYY;
GVIETAKNLGDGYYV; VIETAKNLGDGYYVI; IETAKNLGDGYYVIG;
ETAKNLGDGYYVIGA; TAKNLGDGYYVIGAD; AKNLGDGYYVIGADQ;
KNLGDGYYVIGADQD; NLGDGYYVIGADQDQ; LGDGYYVIGADQDQS;
GDGYYVIGADQDQSY; DGYYVIGADQDQSYL; GYYVIGADQDQSYLA;
YYVIGADQDQSYLAP; YVIGADQDQSYLAPK; VIGADQDQSYLAPKN;
IGADQDQSYLAPKNF; GADQDQSYLAPKNFI; ADQDQSYLAPKNFIT;
DQDQSYLAPKNFITS; QDQSYLAPKNFITSV; DQSYLAPKNFITSVI;
QSYLAPKNFITSVIK; SYLAPKNFITSVIKN; YLAPKNFITSVIKNI;
LAPKNFITSVIKNIG; APKNFITSVIKNIGD; PKNFITSVIKNIGDA;
KNFITSVIKNIGDAL; NFITSVIKNIGDALY; FITSVIKNIGDALYL;
ITSVIKNIGDALYLI; TSVIKNIGDALYLIT; SVIKNIGDALYLITG;
VIKNIGDALYLITGE; IKNIGDALYLITGEY; KNIGDALYLITGEYI;
NIGDALYLITGEYIK; IGDALYLITGEYIKN; GDALYLITGEYIKNN;
DALYLITGEYIKNNN; ALYLITGEYIKNNNV; LYLITGEYIKNNNVW;
YLITGEYIKNNNVWE; LITGEYIKNNNVWEG; ITGEYIKNNNVWEGG;
TGEYIKNNNVWEGGK; GEYIKNNNVWEGGKV; EYIKNNNVWEGGKVV;
YIKNNNVWEGGKVVQ; IKNNNVWEGGKVVQM; KNNNVWEGGKVVQMG;
NNNVWEGGKVVQMGL; NNVWEGGKVVQMGLR; NVWEGGKVVQMGLRD;
VWEGGKVVQMGLRDG; WEGGKVVQMGLRDGV; EGGKVVQMGLRDGVI;
GGKVVQMGLRDGVIG; GKVVQMGLRDGVIGL; KVVQMGLRDGVIGLP;
VVQMGLRDGVIGLPN; VQMGLRDGVIGLPNA; QMGLRDGVIGLPNAN;
MGLRDGVIGLPNANE; GLRDGVIGLPNANEF; LRDGVIGLPNANEFE;
RDGVIGLPNANEFEY; DGVIGLPNANEFEYI; GVIGLPNANEFEYIK;
VIGLPNANEFEYIKV; IGLPNANEFEYIKVL; GLPNANEFEYIKVLE;
LPNANEFEYIKVLER; PNANEFEYIKVLERK; NANEFEYIKVLERKI;
ANEFEYIKVLERKII; NEFEYIKVLERKIIN; EFEYIKVLERKIINK;
FEYIKVLERKIINKE; EYIKVLERKIINKEI; YIKVLERKIINKEII;
IKVLERKIINKEIIV; KVLERKIINKEIIVP; VLERKIINKEIIVPC;
LERKIINKEIIVPCN; ERKIINKEIIVPCNQ; RKIINKEIIVPCNQE;
KIINKEIIVPCNQEE; IINKEIIVPCNQEEY; INKEIIVPCNQEEYE;
NKEIIVPCNQEEYEI; KEIIVPCNQEEYEIF; EIIVPCNQEEYEIFI;
IIVPCNQEEYEIFIK; IVPCNQEEYEIFIKQ; VPCNQEEYEIFIKQI;
PCNQEEYEIFIKQIL; CNQEEYEIFIKQILK; NQEEYEIFIKQILKL;

16 mers:
MRIVIFIFGILLTSCF; RIVIFIFGILLTSCFS; IVIFIFGILLTSCFSR;
VIFIFGILLTSCFSRN; IFIFGILLTSCFSRNG; FIFGILLTSCFSRNGI;
IFGILLTSCFSRNGIE; FGILLTSCFSRNGIES; GILLTSCFSRNGIESS;
ILLTSCFSRNGIESSS; LLTSCFSRNGIESSSK; LTSCFSRNGIESSSKK;
TSCFSRNGIESSSKKI; SCFSRNGIESSSKKIK; CFSRNGIESSSKKIKI;
FSRNGIESSSKKIKIS; SRNGIESSSKKIKISM; RNGIESSSKKIKISML;
NGIESSSKKIKISMLV; GIESSSKKIKISMLVD; IESSSKKIKISMLVDG;
ESSSKKIKISMLVDGV; SSSKKIKISMLVDGVL; SSKKIKISMLVDGVLD;
SKKIKISMLVDGVLDD; KKIKISMLVDGVLDDK; KIKISMLVDGVLDDKS;
IKISMLVDGVLDDKSF; KISMLVDGVLDDKSFN; ISMLVDGVLDDKSFNS;

	SMLVDGVLDDKSFNSS; MLVDGVLDDKSFNSSA; LVDGVLDDKSFNSSAN; VDGVLDDKSFNSSANE; DGVLDDKSFNSSANEA; GVLDDKSFNSSANEAL; VLDDKSFNSSANEALL; LDDKSFNSSANEALLR; DDKSFNSSANEALLRL; DKSFNSSANEALLRLK; KSFNSSANEALLRLKK; SFNSSANEALLRLKKD; FNSSANEALLRLKKDF; NSSANEALLRLKKDFP; SSANEALLRLKKDFPE; SANEALLRLKKDFPEN; ANEALLRLKKDFPENI; NEALLRLKKDFPENIE; EALLRLKKDFPENIEE; ALLRLKKDFPENIEEV; LLRLKKDFPENIEEVF; LRLKKDFPENIEEVFS; RLKKDFPENIEEVFSC; LKKDFPENIEEVFSCA; KKDFPENIEEVFSCAI; KDFPENIEEVFSCAIS; DFPENIEEVFSCAISG; FPENIEEVFSCAISGV; PENIEEVFSCAISGVY; ENIEEVFSCAISGVYS; NIEEVFSCAISGVYSS; IEEVFSCAISGVYSSY; EEVFSCAISGVYSSYV; EVFSCAISGVYSSYVS; VFSCAISGVYSSYVSD; FSCAISGVYSSYVSDL; SCAISGVYSSYVSDLD; CAISGVYSSYVSDLDN; AISGVYSSYVSDLDNL; ISGVYSSYVSDLDNLK; SGVYSSYVSDLDNLKR; GVYSSYVSDLDNLKRN; VYSSYVSDLDNLKRNG; YSSYVSDLDNLKRNGS; SSYVSDLDNLKRNGSD; SYVSDLDNLKRNGSDL; YVSDLDNLKRNGSDLI; VSDLDNLKRNGSDLIW; SDLDNLKRNGSDLIWL; DLDNLKRNGSDLIWLV; LDNLKRNGSDLIWLVG; DNLKRNGSDLIWLVGY; NLKRNGSDLIWLVGYM; LKRNGSDLIWLVGYML; KRNGSDLIWLVGYMLT; RNGSDLIWLVGYMLTD; NGSDLIWLVGYMLTDA; GSDLIWLVGYMLTDAS; SDLIWLVGYMLTDASL; DLIWLVGYMLTDASLL; LIWLVGYMLTDASLLV; IWLVGYMLTDASLLVS; WLVGYMLTDASLLVSS; LVGYMLTDASLLVSSE; VGYMLTDASLLVSSEN; GYMLTDASLLVSSENP; YMLTDASLLVSSENPK; MLTDASLLVSSENPKI; LTDASLLVSSENPKIS; TDASLLVSSENPKISY; DASLLVSSENPKISYG; ASLLVSSENPKISYGI; SLLVSSENPKISYGII; LLVSSENPKISYGIID; LVSSENPKISYGIIDP; VSSENPKISYGIIDPI; SSENPKISYGIIDPIY; SENPKISYGIIDPIYG; ENPKISYGIIDPIYGD; NPKISYGIIDPIYGDD; PKISYGIIDPIYGDDV; KISYGIIDPIYGDDVQ; ISYGIIDPIYGDDVQI; SYGIIDPIYGDDVQIP; YGIIDPIYGDDVQIPE; GIIDPIYGDDVQIPEN; IIDPIYGDDVQIPENL; IDPIYGDDVQIPENLI; DPIYGDDVQIPENLIA; PIYGDDVQIPENLIAV; IYGDDVQIPENLIAVV; YGDDVQIPENLIAVVF; GDDVQIPENLIAVVFR; DDVQIPENLIAVVFRV; DVQIPENLIAVVFRVE; VQIPENLIAVVFRVEQ; QIPENLIAVVFRVEQG; IPENLIAVVFRVEQGA; PENLIAVVFRVEQGAF; ENLIAVVFRVEQGAFL; NLIAVVFRVEQGAFLA; LIAVVFRVEQGAFLAG; IAVVFRVEQGAFLAGY; AVVFRVEQGAFLAGYI; VVFRVEQGAFLAGYIA; VFRVEQGAFLAGYIAA; FRVEQGAFLAGYIAAK; RVEQGAFLAGYIAAKK; VEQGAFLAGYIAAKKS; EQGAFLAGYIAAKKSF; QGAFLAGYIAAKKSFS; GAFLAGYIAAKKSFSG; AFLAGYIAAKKSFSGK; FLAGYIAAKKSFSGKI; LAGYIAAKKSFSGKIG; AGYIAAKKSFSGKIGF; GYIAAKKSFSGKIGFI; YIAAKKSFSGKIGFIG; IAAKKSFSGKIGFIGG; AAKKSFSGKIGFIGGM; AKKSFSGKIGFIGGMK; KKSFSGKIGFIGGMKG; KSFSGKIGFIGGMKGN; SFSGKIGFIGGMKGNI; FSGKIGFIGGMKGNIV; SGKIGFIGGMKGNIVD; GKIGFIGGMKGNIVDA; KIGFIGGMKGNIVDAF; IGFIGGMKGNIVDAFR; GFIGGMKGNIVDAFRY; FIGGMKGNIVDAFRYG; IGGMKGNIVDAFRYGY; GGMKGNIVDAFRYGYE; GMKGNIVDAFRYGYES; MKGNIVDAFRYGYESG; KGNIVDAFRYGYESGA; GNIVDAFRYGYESGAK; NIVDAFRYGYESGAKY; IVDAFRYGYESGAKYA; VDAFRYGYESGAKYAN; DAFRYGYESGAKYANK; AFRYGYESGAKYANKD; FRYGYESGAKYANKDI; RYGYESGAKYANKDIE; YGYESGAKYANKDIEI; GYESGAKYANKDIEII; YESGAKYANKDIEIIS; ESGAKYANKDIEIISE; SGAKYANKDIEIISEY; GAKYANKDIEIISEYS; AKYANKDIEIISEYSN; KYANKDIEIISEYSNS; YANKDIEIISEYSNSF; ANKDIEIISEYSNSFS; NKDIEIISEYSNSFSD; KDIEIISEYSNSFSDV; DIEIISEYSNSFSDVD; IEIISEYSNSFSDVDI; EIISEYSNSFSDVDIG; IISEYSNSFSDVDIGR; ISEYSNSFSDVDIGRT; SEYSNSFSDVDIGRTI; EYSNSFSDVDIGRTIA; YSNSFSDVDIGRTIAS; SNSFSDVDIGRTIASK; NSFSDVDIGRTIASKM; SFSDVDIGRTIASKMY; FSDVDIGRTIASKMYS; SDVDIGRTIASKMYSK; DVDIGRTIASKMYSKG; VDIGRTIASKMYSKGI;

	DIGRTIASKMYSKGID; IGRTIASKMYSKGIDV; GRTIASKMYSKGIDVI; RTIASKMYSKGIDVIH; TIASKMYSKGIDVIHF; IASKMYSKGIDVIHFA; ASKMYSKGIDVIHFAA; SKMYSKGIDVIHFAAG; KMYSKGIDVIHFAAGL; MYSKGIDVIHFAAGLA; YSKGIDVIHFAAGLAG; SKGIDVIHFAAGLAGI; KGIDVIHFAAGLAGIG; GIDVIHFAAGLAGIGV; IDVIHFAAGLAGIGVI; DVIHFAAGLAGIGVIE; VIHFAAGLAGIGVIET; IHFAAGLAGIGVIETA; HFAAGLAGIGVIETAK; FAAGLAGIGVIETAKN; AAGLAGIGVIETAKNL; AGLAGIGVIETAKNLG; GLAGIGVIETAKNLGD; LAGIGVIETAKNLGDG; AGIGVIETAKNLGDGY; GIGVIETAKNLGDGYY; IGVIETAKNLGDGYYV; GVIETAKNLGDGYYVI; VIETAKNLGDGYYVIG; IETAKNLGDGYYVIGA; ETAKNLGDGYYVIGAD; TAKNLGDGYYVIGADQ; AKNLGDGYYVIGADQD; KNLGDGYYVIGADQDQ; NLGDGYYVIGADQDQS; LGDGYYVIGADQDQSY; GDGYYVIGADQDQSYL; DGYYVIGADQDQSYLA; GYYVIGADQDQSYLAP; YYVIGADQDQSYLAPK; YVIGADQDQSYLAPKN; VIGADQDQSYLAPKNF; IGADQDQSYLAPKNFI; GADQDQSYLAPKNFIT; ADQDQSYLAPKNFITS; DQDQSYLAPKNFITSV; QDQSYLAPKNFITSVI; DQSYLAPKNFITSVIK; QSYLAPKNFITSVIKN; SYLAPKNFITSVIKNI; YLAPKNFITSVIKNIG; LAPKNFITSVIKNIGD; APKNFITSVIKNIGDA; PKNFITSVIKNIGDAL; KNFITSVIKNIGDALY; NFITSVIKNIGDALYL; FITSVIKNIGDALYLI; ITSVIKNIGDALYLIT; TSVIKNIGDALYLITG; SVIKNIGDALYLITGE; VIKNIGDALYLITGEY; IKNIGDALYLITGEYI; KNIGDALYLITGEYIK; NIGDALYLITGEYIKN; IGDALYLITGEYIKNN; GDALYLITGEYIKNNN; DALYLITGEYIKNNNV; ALYLITGEYIKNNNVW; LYLITGEYIKNNNVWE; YLITGEYIKNNNVWEG; LITGEYIKNNNVWEGG; ITGEYIKNNNVWEGGK; TGEYIKNNNVWEGGKV; GEYIKNNNVWEGGKVV; EYIKNNNVWEGGKVVQ; YIKNNNVWEGGKVVQM; IKNNNVWEGGKVVQMG; KNNNVWEGGKVVQMGL; NNNVWEGGKVVQMGLR; NNVWEGGKVVQMGLRD; NVWEGGKVVQMGLRDG; VWEGGKVVQMGLRDGV; WEGGKVVQMGLRDGVI; EGGKVVQMGLRDGVIG; GGKVVQMGLRDGVIGL; GKVVQMGLRDGVIGLP; KVVQMGLRDGVIGLPN; VVQMGLRDGVIGLPNA; VQMGLRDGVIGLPNAN; QMGLRDGVIGLPNANE; MGLRDGVIGLPNANEF; GLRDGVIGLPNANEFE; LRDGVIGLPNANEFEY; RDGVIGLPNANEFEYI; DGVIGLPNANEFEYIK; GVIGLPNANEFEYIKV; VIGLPNANEFEYIKVL; IGLPNANEFEYIKVLE; GLPNANEFEYIKVLER; LPNANEFEYIKVLERK; PNANEFEYIKVLERKI; NANEFEYIKVLERKII; ANEFEYIKVLERKIIN; NEFEYIKVLERKIINK; EFEYIKVLERKIINKE; FEYIKVLERKIINKEI; EYIKVLERKIINKEII; YIKVLERKIINKEIIV; IKVLERKIINKEIIVP; KVLERKIINKEIIVPC; VLERKIINKEIIVPCN; LERKIINKEIIVPCNQ; ERKIINKEIIVPCNQE; RKIINKEIIVPCNQEE; KIINKEIIVPCNQEEY; IINKEIIVPCNQEEYE; INKEIIVPCNQEEYEI; NKEIIVPCNQEEYEIF; KEIIVPCNQEEYEIFI; EIIVPCNQEEYEIFIK; IIVPCNQEEYEIFIKQ; IVPCNQEEYEIFIKQI; VPCNQEEYEIFIKQIL; PCNQEEYEIFIKQILK; CNQEEYEIFIKQILKL;
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31	13 mers: MFKRFIFITLSLL; FKRFIFITLSLLV; KRFIFITLSLLVF; RFIFITLSLLVFA; FIFITLSLLVFAC; IFITLSLLVFACF; FITLSLLVFACFK; ITLSLLVFACFKS; TLSLLVFACFKSN; LSLLVFACFKSNK; SLLVFACFKSNKK; LLVFACFKSNKKS; LVFACFKSNKKSI; VFACFKSNKKSIK; FACFKSNKKSIKS; ACFKSNKKSIKSD; CFKSNKKSIKSDK; FKSNKKSIKSDKV; KSNKKSIKSDKVV; SNKKSIKSDKVVV; NKKSIKSDKVVVG; KKSIKSDKVVVGV; KSIKSDKVVVGVL; SIKSDKVVVGVLA; IKSDKVVVGVLAH; KSDKVVVGVLAHG; SDKVVVGVLAHGS; DKVVVGVLAHGSF; KVVVGVLAHGSFY; VVVGVLAHGSFYD; VVGVLAHGSFYDK; VGVLAHGSFYDKG; GVLAHGSFYDKGY; VLAHGSFYDKGYN; LAHGSFYDKGYNQ; AHGSFYDKGYNQS; HGSFYDKGYNQSV; GSFYDKGYNQSVH; SFYDKGYNQSVHD; FYDKGYNQSVHDG; YDKGYNQSVHDGV; DKGYNQSVHDGVV; KGYNQSVHDGVVK; GYNQSVHDGVVKL; YNQSVHDGVVKLR; NQSVHDGVVKLRD; QSVHDGVVKLRDN; SVHDGVVKLRDNF;

	VHDGVVKLRDNFG; HDGVVKLRDNFGI; DGVVKLRDNFGIK; GVVKLRDNFGIKL; VVKLRDNFGIKLI; VKLRDNFGIKLIT; KLRDNFGIKLITK; LRDNFGIKLITKS; RDNFGIKLITKSL; DNFGIKLITKSLR; NFGIKLITKSLRP; FGIKLITKSLRPY; GIKLITKSLRPYP; IKLITKSLRPYPI; KLITKSLRPYPIE; LITKSLRPYPIEG; ITKSLRPYPIEGK; TKSLRPYPIEGKR; KSLRPYPIEGKRL; SLRPYPIEGKRLL; LRPYPIEGKRLLT; RPYPIEGKRLLTV; PYPIEGKRLLTVD; YPIEGKRLLTVDE; PIEGKRLLTVDEA; IEGKRLLTVDEAM; EGKRLLTVDEAMT; GKRLLTVDEAMTE; KRLLTVDEAMTED; RLLTVDEAMTEDA; LLTVDEAMTEDAY; LTVDEAMTEDAYE; TVDEAMTEDAYEV; VDEAMTEDAYEVQ; DEAMTEDAYEVQK; EAMTEDAYEVQKN; AMTEDAYEVQKNP; MTEDAYEVQKNPL; TEDAYEVQKNPLN; EDAYEVQKNPLNL; DAYEVQKNPLNLF; AYEVQKNPLNLFW; YEVQKNPLNLFWL; EVQKNPLNLFWLI; VQKNPLNLFWLIG; QKNPLNLFWLIGY; KNPLNLFWLIGYR; NPLNLFWLIGYRF; PLNLFWLIGYRFS; LNLFWLIGYRFSD; NLFWLIGYRFSDL; LFWLIGYRFSDLS; FWLIGYRFSDLSV; WLIGYRFSDLSVK; LIGYRFSDLSVKL; IGYRFSDLSVKLS; GYRFSDLSVKLSY; YRFSDLSVKLSYE; RFSDLSVKLSYER; FSDLSVKLSYERP; SDLSVKLSYERPD; DLSVKLSYERPDI; LSVKLSYERPDIY; SVKLSYERPDIYY; VKLSYERPDIYYG; KLSYERPDIYYGI; LSYERPDIYYGII; SYERPDIYYGIID; YERPDIYYGIIDA; ERPDIYYGIIDAF; RPDIYYGIIDAFD; PDIYYGIIDAFDY; DIYYGIIDAFDYG; IYYGIIDAFDYGD; YYGIIDAFDYGDI; YGIIDAFDYGDIQ; GIIDAFDYGDIQV; IIDAFDYGDIQVP; IDAFDYGDIQVPK; DAFDYGDIQVPKN; AFDYGDIQVPKNS; FDYGDIQVPKNSL; DYGDIQVPKNSLA; YGDIQVPKNSLAI; GDIQVPKNSLAIK; DIQVPKNSLAIKF; IQVPKNSLAIKFR; QVPKNSLAIKFRN; VPKNSLAIKFRNE; PKNSLAIKFRNEE; KNSLAIKFRNEEA; NSLAIKFRNEEAA; SLAIKFRNEEAAF; LAIKFRNEEAAFL; AIKFRNEEAAFLA; IKFRNEEAAFLAG; KFRNEEAAFLAGY; FRNEEAAFLAGYI; RNEEAAFLAGYIA; NEEAAFLAGYIAA; EEAAFLAGYIAAK; EAAFLAGYIAAKM; AAFLAGYIAAKMS; AFLAGYIAAKMSR; FLAGYIAAKMSRK; LAGYIAAKMSRKE; AGYIAAKMSRKEK; GYIAAKMSRKEKI; YIAAKMSRKEKIG; IAAKMSRKEKIGF; AAKMSRKEKIGFL; AKMSRKEKIGFLT; KMSRKEKIGFLTG; MSRKEKIGFLTGP; SRKEKIGFLTGPM; RKEKIGFLTGPMS; KEKIGFLTGPMSE; EKIGFLTGPMSEH; KIGFLTGPMSEHV; IGFLTGPMSEHVK; GFLTGPMSEHVKD; FLTGPMSEHVKDF; LTGPMSEHVKDFK; TGPMSEHVKDFKF; GPMSEHVKDFKFG; PMSEHVKDFKFGF; MSEHVKDFKFGFK; SEHVKDFKFGFKA; EHVKDFKFGFKAG; HVKDFKFGFKAGI; VKDFKFGFKAGIF; KDFKFGFKAGIFY; DFKFGFKAGIFYA; FKFGFKAGIFYAN; KFGFKAGIFYANP; FGFKAGIFYANPK; GFKAGIFYANPKL; FKAGIFYANPKLR; KAGIFYANPKLRL; AGIFYANPKLRLV; GIFYANPKLRLVS; IFYANPKLRLVSK; FYANPKLRLVSKK; YANPKLRLVSKKA; ANPKLRLVSKKAP; NPKLRLVSKKAPS; PKLRLVSKKAPSL; KLRLVSKKAPSLF; LRLVSKKAPSLFD; RLVSKKAPSLFDK; LVSKKAPSLFDKE; VSKKAPSLFDKEK; SKKAPSLFDKEKG; KKAPSLFDKEKGK; KAPSLFDKEKGKA; APSLFDKEKGKAM; PSLFDKEKGKAMA; SLFDKEKGKAMAL; LFDKEKGKAMALF; FDKEKGKAMALFM; DKEKGKAMALFMY; KEKGKAMALFMYK; EKGKAMALFMYKE; KGKAMALFMYKED; GKAMALFMYKEDK; KAMALFMYKEDKV; AMALFMYKEDKVG; MALFMYKEDKVGV; ALFMYKEDKVGVI; LFMYKEDKVGVIF; FMYKEDKVGVIFP; MYKEDKVGVIFPI; YKEDKVGVIFPIA; KEDKVGVIFPIAG; EDKVGVIFPIAGI; DKVGVIFPIAGIT; KVGVIFPIAGITG; VGVIFPIAGITGL; GVIFPIAGITGLG; VIFPIAGITGLGV; IFPIAGITGLGVY; FPIAGITGLGVYD; PIAGITGLGVYDA; IAGITGLGVYDAA; AGITGLGVYDAAK; GITGLGVYDAAKE; ITGLGVYDAAKEL; TGLGVYDAAKELG; GLGVYDAAKELGP; LGVYDAAKELGPK; GVYDAAKELGPKY; VYDAAKELGPKYY; YDAAKELGPKYYV; DAAKELGPKYYVI; AAKELGPKYYVIG; AKELGPKYYVIGL; KELGPKYYVIGLN; ELGPKYYVIGLNQ; LGPKYYVIGLNQD; GPKYYVIGLNQDQ; PKYYVIGLNQDQS; KYYVIGLNQDQSY; YYVIGLNQDQSYI; YVIGLNQDQSYIA; VIGLNQDQSYIAP; IGLNQDQSYIAPQ; GLNQDQSYIAPQN; LNQDQSYIAPQNV; NQDQSYIAPQNVI; QDQSYIAPQNVIT; DQSYIAPQNVITS; QSYIAPQNVITSI; SYIAPQNVITSII; YIAPQNVITSIIK; IAPQNVITSIIKD; APQNVITSIIKDI; PQNVITSIIKDIG; QNVITSIIKDIGK; NVITSIIKDIGKV; VITSIIKDIGKVI; ITSIIKDIGKVIY; TSIIKDIGKVIYS; SIIKDIGKVIYSI; IIKDIGKVIYSIS; IKDIGKVIYSISS; KDIGKVIYSISSE; DIGKVIYSISSEY; IGKVIYSISSEYI;

GKVIYSISSEYIN; KVIYSISSEYINN; VIYSISSEYINNR; IYSISSEYINNRV; YSISSEYINNRVF; SISSEYINNRVFK; ISSEYINNRVFKG; SSEYINNRVFKGG; SEYINNRVFKGGI; EYINNRVFKGGII; YINNRVFKGGIII; INNRVFKGGIIID; NNRVFKGGIIIDR; NRVFKGGIIIDRG; RVFKGGIIIDRGL; VFKGGIIIDRGLK; FKGGIIIDRGLKE; KGGIIIDRGLKEG; GGIIIDRGLKEGV; GIIIDRGLKEGVI; IIIDRGLKEGVIE; IIDRGLKEGVIEI; IDRGLKEGVIEIV; DRGLKEGVIEIVK; RGLKEGVIEIVKD; GLKEGVIEIVKDP; LKEGVIEIVKDPD; KEGVIEIVKDPDV; EGVIEIVKDPDVL; GVIEIVKDPDVLN; VIEIVKDPDVLNN; IEIVKDPDVLNNR; EIVKDPDVLNNRL; IVKDPDVLNNRLV; VKDPDVLNNRLVD; KDPDVLNNRLVDE; DPDVLNNRLVDEV; PDVLNNRLVDEVI; DVLNNRLVDEVID; VLNNRLVDEVIDL; LNNRLVDEVIDLE; NNRLVDEVIDLEN; NRLVDEVIDLENK; RLVDEVIDLENKI; LVDEVIDLENKII; VDEVIDLENKIIS; DEVIDLENKIISG; EVIDLENKIISGE; VIDLENKIISGEI; IDLENKIISGEII; DLENKIISGEIIV; LENKIISGEIIVP; ENKIISGEIIVPD; NKIISGEIIVPDS; KIISGEIIVPDSE; IISGEIIVPDSEY; ISGEIIVPDSEYA; SGEIIVPDSEYAF; GEIIVPDSEYAFD; EIIVPDSEYAFDL; IIVPDSEYAFDLF; IVPDSEYAFDLFK; VPDSEYAFDLFKS; PDSEYAFDLFKSK; DSEYAFDLFKSKL;

14 mers:
MFKRFIFITLSLLV; FKRFIFITLSLLVF; KRFIFITLSLLVFA; RFIFITLSLLVFAC; FIFITLSLLVFACF; IFITLSLLVFACFK; FITLSLLVFACFKS; ITLSLLVFACFKSN; TLSLLVFACFKSNK; LSLLVFACFKSNKK; SLLVFACFKSNKKS; LLVFACFKSNKKSI; LVFACFKSNKKSIK; VFACFKSNKKSIKS; FACFKSNKKSIKSD; ACFKSNKKSIKSDK; CFKSNKKSIKSDKV; FKSNKKSIKSDKVV; KSNKKSIKSDKVVV; SNKKSIKSDKVVVG; NKKSIKSDKVVVGV; KKSIKSDKVVVGVL; KSIKSDKVVVGVLA; SIKSDKVVVGVLAH; IKSDKVVVGVLAHG; KSDKVVVGVLAHGS; SDKVVVGVLAHGSF; DKVVVGVLAHGSFY; KVVVGVLAHGSFYD; VVVGVLAHGSFYDK; VVGVLAHGSFYDKG; VGVLAHGSFYDKGY; GVLAHGSFYDKGYN; VLAHGSFYDKGYNQ; LAHGSFYDKGYNQS; AHGSFYDKGYNQSV; HGSFYDKGYNQSVH; GSFYDKGYNQSVHD; SFYDKGYNQSVHDG; FYDKGYNQSVHDGV; YDKGYNQSVHDGVV; DKGYNQSVHDGVVK; KGYNQSVHDGVVKL; GYNQSVHDGVVKLR; YNQSVHDGVVKLRD; NQSVHDGVVKLRDN; QSVHDGVVKLRDNF; SVHDGVVKLRDNFG; VHDGVVKLRDNFGI; HDGVVKLRDNFGIK; DGVVKLRDNFGIKL; GVVKLRDNFGIKLI; VVKLRDNFGIKLIT; VKLRDNFGIKLITK; KLRDNFGIKLITKS; LRDNFGIKLITKSL; RDNFGIKLITKSLR; DNFGIKLITKSLRP; NFGIKLITKSLRPY; FGIKLITKSLRPYP; GIKLITKSLRPYPI; IKLITKSLRPYPIE; KLITKSLRPYPIEG; LITKSLRPYPIEGK; ITKSLRPYPIEGKR; TKSLRPYPIEGKRL; KSLRPYPIEGKRLL; SLRPYPIEGKRLLT; LRPYPIEGKRLLTV; RPYPIEGKRLLTVD; PYPIEGKRLLTVDE; YPIEGKRLLTVDEA; PIEGKRLLTVDEAM; IEGKRLLTVDEAMT; EGKRLLTVDEAMTE; GKRLLTVDEAMTED; KRLLTVDEAMTEDA; RLLTVDEAMTEDAY; LLTVDEAMTEDAYE; LTVDEAMTEDAYEV; TVDEAMTEDAYEVQ; VDEAMTEDAYEVQK; DEAMTEDAYEVQKN; EAMTEDAYEVQKNP; AMTEDAYEVQKNPL; MTEDAYEVQKNPLN; TEDAYEVQKNPLNL; EDAYEVQKNPLNLF; DAYEVQKNPLNLFW; AYEVQKNPLNLFWL; YEVQKNPLNLFWLI; EVQKNPLNLFWLIG; VQKNPLNLFWLIGY; QKNPLNLFWLIGYR; KNPLNLFWLIGYRF; NPLNLFWLIGYRFS; PLNLFWLIGYRFSD; LNLFWLIGYRFSDL; NLFWLIGYRFSDLS; LFWLIGYRFSDLSV; FWLIGYRFSDLSVK; WLIGYRFSDLSVKL; LIGYRFSDLSVKLS; IGYRFSDLSVKLSY; GYRFSDLSVKLSYE; YRFSDLSVKLSYER; RFSDLSVKLSYERP; FSDLSVKLSYERPD; SDLSVKLSYERPDI; DLSVKLSYERPDIY; LSVKLSYERPDIYY; SVKLSYERPDIYYG; VKLSYERPDIYYGI; KLSYERPDIYYGII;

	LSYERPDIYYGIID; SYERPDIYYGIIDA; YERPDIYYGIIDAF; ERPDIYYGIIDAFD; RPDIYYGIIDAFDY; PDIYYGIIDAFDYG; DIYYGIIDAFDYGD; IYYGIIDAFDYGDI; YYGIIDAFDYGDIQ; YGIIDAFDYGDIQV; GIIDAFDYGDIQVP; IIDAFDYGDIQVPK; IDAFDYGDIQVPKN; DAFDYGDIQVPKNS; AFDYGDIQVPKNSL; FDYGDIQVPKNSLA; DYGDIQVPKNSLAI; YGDIQVPKNSLAIK; GDIQVPKNSLAIKF; DIQVPKNSLAIKFR; IQVPKNSLAIKFRN; QVPKNSLAIKFRNE; VPKNSLAIKFRNEE; PKNSLAIKFRNEEA; KNSLAIKFRNEEAA; NSLAIKFRNEEAAF; SLAIKFRNEEAAFL; LAIKFRNEEAAFLA; AIKFRNEEAAFLAG; IKFRNEEAAFLAGY; KFRNEEAAFLAGYI; FRNEEAAFLAGYIA; RNEEAAFLAGYIAA; NEEAAFLAGYIAAK; EEAAFLAGYIAAKM; EAAFLAGYIAAKMS; AAFLAGYIAAKMSR; AFLAGYIAAKMSRK; FLAGYIAAKMSRKE; LAGYIAAKMSRKEK; AGYIAAKMSRKEKI; GYIAAKMSRKEKIG; YIAAKMSRKEKIGF; IAAKMSRKEKIGFL; AAKMSRKEKIGFLT; AKMSRKEKIGFLTG; KMSRKEKIGFLTGP; MSRKEKIGFLTGPM; SRKEKIGFLTGPMS; RKEKIGFLTGPMSE; KEKIGFLTGPMSEH; EKIGFLTGPMSEHV; KIGFLTGPMSEHVK; IGFLTGPMSEHVKD; GFLTGPMSEHVKDF; FLTGPMSEHVKDFK; LTGPMSEHVKDFKF; TGPMSEHVKDFKFG; GPMSEHVKDFKFGF; PMSEHVKDFKFGFK; MSEHVKDFKFGFKA; SEHVKDFKFGFKAG; EHVKDFKFGFKAGI; HVKDFKFGFKAGIF; VKDFKFGFKAGIFY; KDFKFGFKAGIFYA; DFKFGFKAGIFYAN; FKFGFKAGIFYANP; KFGFKAGIFYANPK; FGFKAGIFYANPKL; GFKAGIFYANPKLR; FKAGIFYANPKLRL; KAGIFYANPKLRLV; AGIFYANPKLRLVS; GIFYANPKLRLVSK; IFYANPKLRLVSKK; FYANPKLRLVSKKA; YANPKLRLVSKKAP; ANPKLRLVSKKAPS; NPKLRLVSKKAPSL; PKLRLVSKKAPSLF; KLRLVSKKAPSLFD; LRLVSKKAPSLFDK; RLVSKKAPSLFDKE; LVSKKAPSLFDKEK; VSKKAPSLFDKEKG; SKKAPSLFDKEKGK; KKAPSLFDKEKGKA; KAPSLFDKEKGKAM; APSLFDKEKGKAMA; PSLFDKEKGKAMAL; SLFDKEKGKAMALF; LFDKEKGKAMALFM; FDKEKGKAMALFMY; DKEKGKAMALFMYK; KEKGKAMALFMYKE; EKGKAMALFMYKED; KGKAMALFMYKEDK; GKAMALFMYKEDKV; KAMALFMYKEDKVG; AMALFMYKEDKVGV; MALFMYKEDKVGVI; ALFMYKEDKVGVIF; LFMYKEDKVGVIFP; FMYKEDKVGVIFPI; MYKEDKVGVIFPIA; YKEDKVGVIFPIAG; KEDKVGVIFPIAGI; EDKVGVIFPIAGIT; DKVGVIFPIAGITG; KVGVIFPIAGITGL; VGVIFPIAGITGLG; GVIFPIAGITGLGV; VIFPIAGITGLGVY; IFPIAGITGLGVYD; FPIAGITGLGVYDA; PIAGITGLGVYDAA; IAGITGLGVYDAAK; AGITGLGVYDAAKE; GITGLGVYDAAKEL; ITGLGVYDAAKELG; TGLGVYDAAKELGP; GLGVYDAAKELGPK; LGVYDAAKELGPKY; GVYDAAKELGPKYY; VYDAAKELGPKYYV; YDAAKELGPKYYVI; DAAKELGPKYYVIG; AAKELGPKYYVIGL; AKELGPKYYVIGLN; KELGPKYYVIGLNQ; ELGPKYYVIGLNQD; LGPKYYVIGLNQDQ; GPKYYVIGLNQDQS; PKYYVIGLNQDQSY; KYYVIGLNQDQSYI; YYVIGLNQDQSYIA; YVIGLNQDQSYIAP; VIGLNQDQSYIAPQ; IGLNQDQSYIAPQN; GLNQDQSYIAPQNV; LNQDQSYIAPQNVI; NQDQSYIAPQNVIT; QDQSYIAPQNVITS; DQSYIAPQNVITSI; QSYIAPQNVITSII; SYIAPQNVITSIIK; YIAPQNVITSIIKD; IAPQNVITSIIKDI; APQNVITSIIKDIG; PQNVITSIIKDIGK; QNVITSIIKDIGKV; NVITSIIKDIGKVI; VITSIIKDIGKVIY; ITSIIKDIGKVIYS; TSIIKDIGKVIYSI; SIIKDIGKVIYSIS; IIKDIGKVIYSISS; IKDIGKVIYSISSE; KDIGKVIYSISSEY; DIGKVIYSISSEYI; IGKVIYSISSEYIN; GKVIYSISSEYINN; KVIYSISSEYINNR; VIYSISSEYINNRV; IYSISSEYINNRVF; YSISSEYINNRVFK; SISSEYINNRVFKG; ISSEYINNRVFKGG; SSEYINNRVFKGGI; SEYINNRVFKGGII;

EYINNRVFKGGIII; YINNRVFKGGIIID; INNRVFKGGIIIDR;
NNRVFKGGIIIDRG; NRVFKGGIIIDRGL; RVFKGGIIIDRGLK;
VFKGGIIIDRGLKE; FKGGIIIDRGLKEG; KGGIIIDRGLKEGV;
GGIIIDRGLKEGVI; GIIIDRGLKEGVIE; IIIDRGLKEGVIEI;
IIDRGLKEGVIEIV; IDRGLKEGVIEIVK; DRGLKEGVIEIVKD;
RGLKEGVIEIVKDP; GLKEGVIEIVKDPD; LKEGVIEIVKDPDV;
KEGVIEIVKDPDVL; EGVIEIVKDPDVLN; GVIEIVKDPDVLNN;
VIEIVKDPDVLNNR; IEIVKDPDVLNNRL; EIVKDPDVLNNRLV;
IVKDPDVLNNRLVD; VKDPDVLNNRLVDE; KDPDVLNNRLVDEV;
DPDVLNNRLVDEVI; PDVLNNRLVDEVID; DVLNNRLVDEVIDL;
VLNNRLVDEVIDLE; LNNRLVDEVIDLEN; NNRLVDEVIDLENK;
NRLVDEVIDLENKI; RLVDEVIDLENKII; LVDEVIDLENKIIS;
VDEVIDLENKIISG; DEVIDLENKIISGE; EVIDLENKIISGEI;
VIDLENKIISGEII; IDLENKIISGEIIV; DLENKIISGEIIVP;
LENKIISGEIIVPD; ENKIISGEIIVPDS; NKIISGEIIVPDSE;
KIISGEIIVPDSEY; IISGEIIVPDSEYA; ISGEIIVPDSEYAF;
SGEIIVPDSEYAFD; GEIIVPDSEYAFDL; EIIVPDSEYAFDLF;
IIVPDSEYAFDLFK; IVPDSEYAFDLFKS; VPDSEYAFDLFKSK;
PDSEYAFDLFKSKL;

15 mers:
MFKRFIFITLSLLVF; FKRFIFITLSLLVFA; KRFIFITLSLLVFAC;
RFIFITLSLLVFACF; FIFITLSLLVFACFK; IFITLSLLVFACFKS;
FITLSLLVFACFKSN; ITLSLLVFACFKSNK; TLSLLVFACFKSNKK;
LSLLVFACFKSNKKS; SLLVFACFKSNKKSI; LLVFACFKSNKKSIK;
LVFACFKSNKKSIKS; VFACFKSNKKSIKSD; FACFKSNKKSIKSDK;
ACFKSNKKSIKSDKV; CFKSNKKSIKSDKVV; FKSNKKSIKSDKVVV;
KSNKKSIKSDKVVVG; SNKKSIKSDKVVVGV; NKKSIKSDKVVVGVL;
KKSIKSDKVVVGVLA; KSIKSDKVVVGVLAH; SIKSDKVVVGVLAHG;
IKSDKVVVGVLAHGS; KSDKVVVGVLAHGSF; SDKVVVGVLAHGSFY;
DKVVVGVLAHGSFYD; KVVVGVLAHGSFYDK; VVVGVLAHGSFYDKG;
VVGVLAHGSFYDKGY; VGVLAHGSFYDKGYN; GVLAHGSFYDKGYNQ;
VLAHGSFYDKGYNQS; LAHGSFYDKGYNQSV; AHGSFYDKGYNQSVH;
HGSFYDKGYNQSVHD; GSFYDKGYNQSVHDG; SFYDKGYNQSVHDGV;
FYDKGYNQSVHDGVV; YDKGYNQSVHDGVVK; DKGYNQSVHDGVVKL;
KGYNQSVHDGVVKLR; GYNQSVHDGVVKLRD; YNQSVHDGVVKLRDN;
NQSVHDGVVKLRDNF; QSVHDGVVKLRDNFG; SVHDGVVKLRDNFGI;
VHDGVVKLRDNFGIK; HDGVVKLRDNFGIKL; DGVVKLRDNFGIKLI;
GVVKLRDNFGIKLIT; VVKLRDNFGIKLITK; VKLRDNFGIKLITKS;
KLRDNFGIKLITKSL; LRDNFGIKLITKSLR; RDNFGIKLITKSLRP;
DNFGIKLITKSLRPY; NFGIKLITKSLRPYP; FGIKLITKSLRPYPI;
GIKLITKSLRPYPIE; IKLITKSLRPYPIEG; KLITKSLRPYPIEGK;
LITKSLRPYPIEGKR; ITKSLRPYPIEGKRL; TKSLRPYPIEGKRLL;
KSLRPYPIEGKRLLT; SLRPYPIEGKRLLTV; LRPYPIEGKRLLTVD;
RPYPIEGKRLLTVDE; PYPIEGKRLLTVDEA; YPIEGKRLLTVDEAM;
PIEGKRLLTVDEAMT; IEGKRLLTVDEAMTE; EGKRLLTVDEAMTED;
GKRLLTVDEAMTEDA; KRLLTVDEAMTEDAY; RLLTVDEAMTEDAYE;
LLTVDEAMTEDAYEV; LTVDEAMTEDAYEVQ; TVDEAMTEDAYEVQK;
VDEAMTEDAYEVQKN; DEAMTEDAYEVQKNP; EAMTEDAYEVQKNPL;
AMTEDAYEVQKNPLN; MTEDAYEVQKNPLNL; TEDAYEVQKNPLNLF;
EDAYEVQKNPLNLFW; DAYEVQKNPLNLFWL; AYEVQKNPLNLFWLI;
YEVQKNPLNLFWLIG; EVQKNPLNLFWLIGY; VQKNPLNLFWLIGYR;
QKNPLNLFWLIGYRF; KNPLNLFWLIGYRFS; NPLNLFWLIGYRFSD;
PLNLFWLIGYRFSDL; LNLFWLIGYRFSDLS; NLFWLIGYRFSDLSV;
LFWLIGYRFSDLSVK; FWLIGYRFSDLSVKL; WLIGYRFSDLSVKLS;
LIGYRFSDLSVKLSY; IGYRFSDLSVKLSYE; GYRFSDLSVKLSYER;
YRFSDLSVKLSYERP; RFSDLSVKLSYERPD; FSDLSVKLSYERPDI;

	SDLSVKLSYERPDIY; DLSVKLSYERPDIYY; LSVKLSYERPDIYYG; SVKLSYERPDIYYGI; VKLSYERPDIYYGII; KLSYERPDIYYGIID; LSYERPDIYYGIIDA; SYERPDIYYGIIDAF; YERPDIYYGIIDAFD; ERPDIYYGIIDAFDY; RPDIYYGIIDAFDYG; PDIYYGIIDAFDYGD; DIYYGIIDAFDYGDI; IYYGIIDAFDYGDIQ; YYGIIDAFDYGDIQV; YGIIDAFDYGDIQVP; GIIDAFDYGDIQVPK; IIDAFDYGDIQVPKN; IDAFDYGDIQVPKNS; DAFDYGDIQVPKNSL; AFDYGDIQVPKNSLA; FDYGDIQVPKNSLAI; DYGDIQVPKNSLAIK; YGDIQVPKNSLAIKF; GDIQVPKNSLAIKFR; DIQVPKNSLAIKFRN; IQVPKNSLAIKFRNE; QVPKNSLAIKFRNEE; VPKNSLAIKFRNEEA; PKNSLAIKFRNEEAA; KNSLAIKFRNEEAAF; NSLAIKFRNEEAAFL; SLAIKFRNEEAAFLA; LAIKFRNEEAAFLAG; AIKFRNEEAAFLAGY; IKFRNEEAAFLAGYI; KFRNEEAAFLAGYIA; FRNEEAAFLAGYIAA; RNEEAAFLAGYIAAK; NEEAAFLAGYIAAKM; EEAAFLAGYIAAKMS; EAAFLAGYIAAKMSR; AAFLAGYIAAKMSRK; AFLAGYIAAKMSRKE; FLAGYIAAKMSRKEK; LAGYIAAKMSRKEKI; AGYIAAKMSRKEKIG; GYIAAKMSRKEKIGF; YIAAKMSRKEKIGFL; IAAKMSRKEKIGFLT; AAKMSRKEKIGFLTG; AKMSRKEKIGFLTGP; KMSRKEKIGFLTGPM; MSRKEKIGFLTGPMS; SRKEKIGFLTGPMSE; RKEKIGFLTGPMSEH; KEKIGFLTGPMSEHV; EKIGFLTGPMSEHVK; KIGFLTGPMSEHVKD; IGFLTGPMSEHVKDF; GFLTGPMSEHVKDFK; FLTGPMSEHVKDFKF; LTGPMSEHVKDFKFG; TGPMSEHVKDFKFGF; GPMSEHVKDFKFGFK; PMSEHVKDFKFGFKA; MSEHVKDFKFGFKAG; SEHVKDFKFGFKAGI; EHVKDFKFGFKAGIF; HVKDFKFGFKAGIFY; VKDFKFGFKAGIFYA; KDFKFGFKAGIFYAN; DFKFGFKAGIFYANP; FKFGFKAGIFYANPK; KFGFKAGIFYANPKL; FGFKAGIFYANPKLR; GFKAGIFYANPKLRL; FKAGIFYANPKLRLV; KAGIFYANPKLRLVS; AGIFYANPKLRLVSK; GIFYANPKLRLVSKK; IFYANPKLRLVSKKA; FYANPKLRLVSKKAP; YANPKLRLVSKKAPS; ANPKLRLVSKKAPSL; NPKLRLVSKKAPSLF; PKLRLVSKKAPSLFD; KLRLVSKKAPSLFDK; LRLVSKKAPSLFDKE; RLVSKKAPSLFDKEK; LVSKKAPSLFDKEKG; VSKKAPSLFDKEKGK; SKKAPSLFDKEKGKA; KKAPSLFDKEKGKAM; KAPSLFDKEKGKAMA; APSLFDKEKGKAMAL; PSLFDKEKGKAMALF; SLFDKEKGKAMALFM; LFDKEKGKAMALFMY; FDKEKGKAMALFMYK; DKEKGKAMALFMYKE; KEKGKAMALFMYKED; EKGKAMALFMYKEDK; KGKAMALFMYKEDKV; GKAMALFMYKEDKVG; KAMALFMYKEDKVGV; AMALFMYKEDKVGVI; MALFMYKEDKVGVIF; ALFMYKEDKVGVIFP; LFMYKEDKVGVIFPI; FMYKEDKVGVIFPIA; MYKEDKVGVIFPIAG; YKEDKVGVIFPIAGI; KEDKVGVIFPIAGIT; EDKVGVIFPIAGITG; DKVGVIFPIAGITGL; KVGVIFPIAGITGLG; VGVIFPIAGITGLGV; GVIFPIAGITGLGVY; VIFPIAGITGLGVYD; IFPIAGITGLGVYDA; FPIAGITGLGVYDAA; PIAGITGLGVYDAAK; IAGITGLGVYDAAKE; AGITGLGVYDAAKEL; GITGLGVYDAAKELG; ITGLGVYDAAKELGP; TGLGVYDAAKELGPK; GLGVYDAAKELGPKY; LGVYDAAKELGPKYY; GVYDAAKELGPKYYV; VYDAAKELGPKYYVI; YDAAKELGPKYYVIG; DAAKELGPKYYVIGL; AAKELGPKYYVIGLN; AKELGPKYYVIGLNQ; KELGPKYYVIGLNQD; ELGPKYYVIGLNQDQ; LGPKYYVIGLNQDQS; GPKYYVIGLNQDQSY; PKYYVIGLNQDQSYI; KYYVIGLNQDQSYIA; YYVIGLNQDQSYIAP; YVIGLNQDQSYIAPQ; VIGLNQDQSYIAPQN; IGLNQDQSYIAPQNV; GLNQDQSYIAPQNVI; LNQDQSYIAPQNVIT; NQDQSYIAPQNVITS; QDQSYIAPQNVITSI; DQSYIAPQNVITSII; QSYIAPQNVITSIIK; SYIAPQNVITSIIKD; YIAPQNVITSIIKDI; IAPQNVITSIIKDIG; APQNVITSIIKDIGK; PQNVITSIIKDIGKV; QNVITSIIKDIGKVI; NVITSIIKDIGKVIY; VITSIIKDIGKVIYS; ITSIIKDIGKVIYSI; TSIIKDIGKVIYSIS; SIIKDIGKVIYSISS; IIKDIGKVIYSISSE; IKDIGKVIYSISSEY; KDIGKVIYSISSEYI; DIGKVIYSISSEYIN; IGKVIYSISSEYINN; GKVIYSISSEYINNR; KVIYSISSEYINNRV; VIYSISSEYINNRVF;

IYSISSEYINNRVFK; YSISSEYINNRVFKG; SISSEYINNRVFKGG;
ISSEYINNRVFKGGI; SSEYINNRVFKGGII; SEYINNRVFKGGIII;
EYINNRVFKGGIIID; YINNRVFKGGIIIDR; INNRVFKGGIIIDRG;
NNRVFKGGIIIDRGL; NRVFKGGIIIDRGLK; RVFKGGIIIDRGLKE;
VFKGGIIIDRGLKEG; FKGGIIIDRGLKEGV; KGGIIIDRGLKEGVI;
GGIIIDRGLKEGVIE; GIIIDRGLKEGVIEI; IIIDRGLKEGVIEIV;
IIDRGLKEGVIEIVK; IDRGLKEGVIEIVKD; DRGLKEGVIEIVKDP;
RGLKEGVIEIVKDPD; GLKEGVIEIVKDPDV; LKEGVIEIVKDPDVL;
KEGVIEIVKDPDVLN; EGVIEIVKDPDVLNN; GVIEIVKDPDVLNNR;
VIEIVKDPDVLNNRL; IEIVKDPDVLNNRLV; EIVKDPDVLNNRLVD;
IVKDPDVLNNRLVDE; VKDPDVLNNRLVDEV; KDPDVLNNRLVDEVI;
DPDVLNNRLVDEVID; PDVLNNRLVDEVIDL; DVLNNRLVDEVIDLE;
VLNNRLVDEVIDLEN; LNNRLVDEVIDLENK; NNRLVDEVIDLENKI;
NRLVDEVIDLENKII; RLVDEVIDLENKIIS; LVDEVIDLENKIISG;
VDEVIDLENKIISGE; DEVIDLENKIISGEI; EVIDLENKIISGEII;
VIDLENKIISGEIIV; IDLENKIISGEIIVP; DLENKIISGEIIVPD;
LENKIISGEIIVPDS; ENKIISGEIIVPDSE; NKIISGEIIVPDSEY;
KIISGEIIVPDSEYA; IISGEIIVPDSEYAF; ISGEIIVPDSEYAFD;
SGEIIVPDSEYAFDL; GEIIVPDSEYAFDLF; EIIVPDSEYAFDLFK;
IIVPDSEYAFDLFKS; IVPDSEYAFDLFKSK; VPDSEYAFDLFKSKL;

16 mers:
MFKRFIFITLSLLVFA; FKRFIFITLSLLVFAC; KRFIFITLSLLVFACF;
RFIFITLSLLVFACFK; FIFITLSLLVFACFKS; IFITLSLLVFACFKSN;
FITLSLLVFACFKSNK; ITLSLLVFACFKSNKK; TLSLLVFACFKSNKKS;
LSLLVFACFKSNKKSI; SLLVFACFKSNKKSIK; LLVFACFKSNKKSIKS;
LVFACFKSNKKSIKSD; VFACFKSNKKSIKSDK; FACFKSNKKSIKSDKV;
ACFKSNKKSIKSDKVV; CFKSNKKSIKSDKVVV; FKSNKKSIKSDKVVVG;
KSNKKSIKSDKVVVGV; SNKKSIKSDKVVVGVL; NKKSIKSDKVVVGVLA;
KKSIKSDKVVVGVLAH; KSIKSDKVVVGVLAHG; SIKSDKVVVGVLAHGS;
IKSDKVVVGVLAHGSF; KSDKVVVGVLAHGSFY; SDKVVVGVLAHGSFYD;
DKVVVGVLAHGSFYDK; KVVVGVLAHGSFYDKG; VVVGVLAHGSFYDKGY;
VVGVLAHGSFYDKGYN; VGVLAHGSFYDKGYNQ; GVLAHGSFYDKGYNQS;
VLAHGSFYDKGYNQSV; LAHGSFYDKGYNQSVH; AHGSFYDKGYNQSVHD;
HGSFYDKGYNQSVHDG; GSFYDKGYNQSVHDGV; SFYDKGYNQSVHDGVV;
FYDKGYNQSVHDGVVK; YDKGYNQSVHDGVVKL; DKGYNQSVHDGVVKLR;
KGYNQSVHDGVVKLRD; GYNQSVHDGVVKLRDN; YNQSVHDGVVKLRDNF;
NQSVHDGVVKLRDNFG; QSVHDGVVKLRDNFGI; SVHDGVVKLRDNFGIK;
VHDGVVKLRDNFGIKL; HDGVVKLRDNFGIKLI; DGVVKLRDNFGIKLIT;
GVVKLRDNFGIKLITK; VVKLRDNFGIKLITKS; VKLRDNFGIKLITKSL;
KLRDNFGIKLITKSLR; LRDNFGIKLITKSLRP; RDNFGIKLITKSLRPY;
DNFGIKLITKSLRPYP; NFGIKLITKSLRPYPI; FGIKLITKSLRPYPIE;
GIKLITKSLRPYPIEG; IKLITKSLRPYPIEGK; KLITKSLRPYPIEGKR;
LITKSLRPYPIEGKRL; ITKSLRPYPIEGKRLL; TKSLRPYPIEGKRLLT;
KSLRPYPIEGKRLLTV; SLRPYPIEGKRLLTVD; LRPYPIEGKRLLTVDE;
RPYPIEGKRLLTVDEA; PYPIEGKRLLTVDEAM; YPIEGKRLLTVDEAMT;
PIEGKRLLTVDEAMTE; IEGKRLLTVDEAMTED; EGKRLLTVDEAMTEDA;
GKRLLTVDEAMTEDAY; KRLLTVDEAMTEDAYE; RLLTVDEAMTEDAYEV;
LLTVDEAMTEDAYEVQ; LTVDEAMTEDAYEVQK; TVDEAMTEDAYEVQKN;
VDEAMTEDAYEVQKNP; DEAMTEDAYEVQKNPL; EAMTEDAYEVQKNPLN;
AMTEDAYEVQKNPLNL; MTEDAYEVQKNPLNLF; TEDAYEVQKNPLNLFW;
EDAYEVQKNPLNLFWL; DAYEVQKNPLNLFWLI; AYEVQKNPLNLFWLIG;
YEVQKNPLNLFWLIGY; EVQKNPLNLFWLIGYR; VQKNPLNLFWLIGYRF;
QKNPLNLFWLIGYRFS; KNPLNLFWLIGYRFSD; NPLNLFWLIGYRFSDL;
PLNLFWLIGYRFSDLS; LNLFWLIGYRFSDLSV; NLFWLIGYRFSDLSVK;
LFWLIGYRFSDLSVKL; FWLIGYRFSDLSVKLS; WLIGYRFSDLSVKLSY;
LIGYRFSDLSVKLSYE; IGYRFSDLSVKLSYER; GYRFSDLSVKLSYERP;

	YRFSDLSVKLSYERPD; RFSDLSVKLSYERPDI; FSDLSVKLSYERPDIY; SDLSVKLSYERPDIYY; DLSVKLSYERPDIYYG; LSVKLSYERPDIYYGI; SVKLSYERPDIYYGII; VKLSYERPDIYYGIID; KLSYERPDIYYGIIDA; LSYERPDIYYGIIDAF; SYERPDIYYGIIDAFD; YERPDIYYGIIDAFDY; ERPDIYYGIIDAFDYG; RPDIYYGIIDAFDYGD; PDIYYGIIDAFDYGDI; DIYYGIIDAFDYGDIQ; IYYGIIDAFDYGDIQV; YYGIIDAFDYGDIQVP; YGIIDAFDYGDIQVPK; GIIDAFDYGDIQVPKN; IIDAFDYGDIQVPKNS; IDAFDYGDIQVPKNSL; DAFDYGDIQVPKNSLA; AFDYGDIQVPKNSLAI; FDYGDIQVPKNSLAIK; DYGDIQVPKNSLAIKF; YGDIQVPKNSLAIKFR; GDIQVPKNSLAIKFRN; DIQVPKNSLAIKFRNE; IQVPKNSLAIKFRNEE; QVPKNSLAIKFRNEEA; VPKNSLAIKFRNEEAA; PKNSLAIKFRNEEAAF; KNSLAIKFRNEEAAFL; NSLAIKFRNEEAAFLA; SLAIKFRNEEAAFLAG; LAIKFRNEEAAFLAGY; AIKFRNEEAAFLAGYI; IKFRNEEAAFLAGYIA; KFRNEEAAFLAGYIAA; FRNEEAAFLAGYIAAK; RNEEAAFLAGYIAAKM; NEEAAFLAGYIAAKMS; EEAAFLAGYIAAKMSR; EAAFLAGYIAAKMSRK; AAFLAGYIAAKMSRKE; AFLAGYIAAKMSRKEK; FLAGYIAAKMSRKEKI; LAGYIAAKMSRKEKIG; AGYIAAKMSRKEKIGF; GYIAAKMSRKEKIGFL; YIAAKMSRKEKIGFLT; IAAKMSRKEKIGFLTG; AAKMSRKEKIGFLTGP; AKMSRKEKIGFLTGPM; KMSRKEKIGFLTGPMS; MSRKEKIGFLTGPMSE; SRKEKIGFLTGPMSEH; RKEKIGFLTGPMSEHV; KEKIGFLTGPMSEHVK; EKIGFLTGPMSEHVKD; KIGFLTGPMSEHVKDF; IGFLTGPMSEHVKDFK; GFLTGPMSEHVKDFKF; FLTGPMSEHVKDFKFG; LTGPMSEHVKDFKFGF; TGPMSEHVKDFKFGFK; GPMSEHVKDFKFGFKA; PMSEHVKDFKFGFKAG; MSEHVKDFKFGFKAGI; SEHVKDFKFGFKAGIF; EHVKDFKFGFKAGIFY; HVKDFKFGFKAGIFYA; VKDFKFGFKAGIFYAN; KDFKFGFKAGIFYANP; DFKFGFKAGIFYANPK; FKFGFKAGIFYANPKL; KFGFKAGIFYANPKLR; FGFKAGIFYANPKLRL; GFKAGIFYANPKLRLV; FKAGIFYANPKLRLVS; KAGIFYANPKLRLVSK; AGIFYANPKLRLVSKK; GIFYANPKLRLVSKKA; IFYANPKLRLVSKKAP; FYANPKLRLVSKKAPS; YANPKLRLVSKKAPSL; ANPKLRLVSKKAPSLF; NPKLRLVSKKAPSLFD; PKLRLVSKKAPSLFDK; KLRLVSKKAPSLFDKE; LRLVSKKAPSLFDKEK; RLVSKKAPSLFDKEKG; LVSKKAPSLFDKEKGK; VSKKAPSLFDKEKGKA; SKKAPSLFDKEKGKAM; KKAPSLFDKEKGKAMA; KAPSLFDKEKGKAMAL; APSLFDKEKGKAMALF; PSLFDKEKGKAMALFM; SLFDKEKGKAMALFMY; LFDKEKGKAMALFMYK; FDKEKGKAMALFMYKE; DKEKGKAMALFMYKED; KEKGKAMALFMYKEDK; EKGKAMALFMYKEDKV; KGKAMALFMYKEDKVG; GKAMALFMYKEDKVGV; KAMALFMYKEDKVGVI; AMALFMYKEDKVGVIF; MALFMYKEDKVGVIFP; ALFMYKEDKVGVIFPI; LFMYKEDKVGVIFPIA; FMYKEDKVGVIFPIAG; MYKEDKVGVIFPIAGI; YKEDKVGVIFPIAGIT; KEDKVGVIFPIAGITG; EDKVGVIFPIAGITGL; DKVGVIFPIAGITGLG; KVGVIFPIAGITGLGV; VGVIFPIAGITGLGVY; GVIFPIAGITGLGVYD; VIFPIAGITGLGVYDA; IFPIAGITGLGVYDAA; FPIAGITGLGVYDAAK; PIAGITGLGVYDAAKE; IAGITGLGVYDAAKEL; AGITGLGVYDAAKELG; GITGLGVYDAAKELGP; ITGLGVYDAAKELGPK; TGLGVYDAAKELGPKY; GLGVYDAAKELGPKYY; LGVYDAAKELGPKYYV; GVYDAAKELGPKYYVI; VYDAAKELGPKYYVIG; YDAAKELGPKYYVIGL; DAAKELGPKYYVIGLN; AAKELGPKYYVIGLNQ; AKELGPKYYVIGLNQD; KELGPKYYVIGLNQDQ; ELGPKYYVIGLNQDQS; LGPKYYVIGLNQDQSY; GPKYYVIGLNQDQSYI; PKYYVIGLNQDQSYIA; KYYVIGLNQDQSYIAP; YYVIGLNQDQSYIAPQ; YVIGLNQDQSYIAPQN; VIGLNQDQSYIAPQNV; IGLNQDQSYIAPQNVI; GLNQDQSYIAPQNVIT; LNQDQSYIAPQNVITS; NQDQSYIAPQNVITSI; QDQSYIAPQNVITSII; DQSYIAPQNVITSIIK; QSYIAPQNVITSIIKD; SYIAPQNVITSIIKDI; YIAPQNVITSIIKDIG; IAPQNVITSIIKDIGK; APQNVITSIIKDIGKV; PQNVITSIIKDIGKVI; QNVITSIIKDIGKVIY; NVITSIIKDIGKVIYS; VITSIIKDIGKVIYSI; ITSIIKDIGKVIYSIS; TSIIKDIGKVIYSISS; SIIKDIGKVIYSISSE; IIKDIGKVIYSISSEY; IKDIGKVIYSISSEYI; KDIGKVIYSISSEYIN; DIGKVIYSISSEYINN; IGKVIYSISSEYINNR;

	GKVIYSISSEYINNRV; KVIYSISSEYINNRVF; VIYSISSEYINNRVFK; IYSISSEYINNRVFKG; YSISSEYINNRVFKGG; SISSEYINNRVFKGGI; ISSEYINNRVFKGGII; SSEYINNRVFKGGIII; SEYINNRVFKGGIIID; EYINNRVFKGGIIIDR; YINNRVFKGGIIIDRG; INNRVFKGGIIIDRGL; NNRVFKGGIIIDRGLK; NRVFKGGIIIDRGLKE; RVFKGGIIIDRGLKEG; VFKGGIIIDRGLKEGV; FKGGIIIDRGLKEGVI; KGGIIIDRGLKEGVIE; GGIIIDRGLKEGVIEI; GIIIDRGLKEGVIEIV; IIIDRGLKEGVIEIVK; IIDRGLKEGVIEIVKD; IDRGLKEGVIEIVKDP; DRGLKEGVIEIVKDPD; RGLKEGVIEIVKDPDV; GLKEGVIEIVKDPDVL; LKEGVIEIVKDPDVLN; KEGVIEIVKDPDVLNN; EGVIEIVKDPDVLNNR; GVIEIVKDPDVLNNRL; VIEIVKDPDVLNNRLV; IEIVKDPDVLNNRLVD; EIVKDPDVLNNRLVDE; IVKDPDVLNNRLVDEV; VKDPDVLNNRLVDEVI; KDPDVLNNRLVDEVID; DPDVLNNRLVDEVIDL; PDVLNNRLVDEVIDLE; DVLNNRLVDEVIDLEN; VLNNRLVDEVIDLENK; LNNRLVDEVIDLENKI; NNRLVDEVIDLENKII; NRLVDEVIDLENKIIS; RLVDEVIDLENKIISG; LVDEVIDLENKIISGE; VDEVIDLENKIISGEI; DEVIDLENKIISGEII; EVIDLENKIISGEIIV; VIDLENKIISGEIIVP; IDLENKIISGEIIVPD; DLENKIISGEIIVPDS; LENKIISGEIIVPDSE; ENKIISGEIIVPDSEY; NKIISGEIIVPDSEYA; KIISGEIIVPDSEYAF; IISGEIIVPDSEYAFD; ISGEIIVPDSEYAFDL; SGEIIVPDSEYAFDLF; GEIIVPDSEYAFDLFK; EIIVPDSEYAFDLFKS; IIVPDSEYAFDLFKSK; IVPDSEYAFDLFKSKL;
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31	13 mers: MDNYYEIYFLYFF; DNYYEIYFLYFFI; NYYEIYFLYFFIK; YYEIYFLYFFIKS; YEIYFLYFFIKSK; EIYFLYFFIKSKE; IYFLYFFIKSKED; YFLYFFIKSKEDI; FLYFFIKSKEDIF; LYFFIKSKEDIFM; YFFIKSKEDIFML; FFIKSKEDIFMLK; FIKSKEDIFMLKK; IKSKEDIFMLKKV; KSKEDIFMLKKVY; SKEDIFMLKKVYY; KEDIFMLKKVYYF; EDIFMLKKVYYFL; DIFMLKKVYYFLI; IFMLKKVYYFLIF; FMLKKVYYFLIFL; MLKKVYYFLIFLF; LKKVYYFLIFLFI; KKVYYFLIFLFIV; KVYYFLIFLFIVA; VYYFLIFLFIVAC; YYFLIFLFIVACS; YFLIFLFIVACSS; FLIFLFIVACSSS; LIFLFIVACSSSD; IFLFIVACSSSDD; FLFIVACSSSDDG; LFIVACSSSDDGK; FIVACSSSDDGKS; IVACSSSDDGKSE; VACSSSDDGKSEA; ACSSSDDGKSEAK; CSSSDDGKSEAKT; SSSDDGKSEAKTV; SSDDGKSEAKTVS; SDDGKSEAKTVSL; DDGKSEAKTVSLI; DGKSEAKTVSLIV; GKSEAKTVSLIVD; KSEAKTVSLIVDG; SEAKTVSLIVDGA; EAKTVSLIVDGAF; AKTVSLIVDGAFD; KTVSLIVDGAFDD; TVSLIVDGAFDDK; VSLIVDGAFDDKG; SLIVDGAFDDKGF; LIVDGAFDDKGFN; IVDGAFDDKGFNE; VDGAFDDKGFNES; DGAFDDKGFNESS; GAFDDKGFNESSS; AFDDKGFNESSSK; FDDKGFNESSSKA; DDKGFNESSSKAI; DKGFNESSSKAIR; KGFNESSSKAIRK; GFNESSSKAIRKL; FNESSSKAIRKLK; NESSSKAIRKLKA; ESSSKAIRKLKAD; SSSKAIRKLKADL; SSKAIRKLKADLN; SKAIRKLKADLNI; KAIRKLKADLNIN; AIRKLKADLNINI; IRKLKADLNINII; RKLKADLNINIIE; KLKADLNINIIEK; LKADLNINIIEKA; KADLNINIIEKAS; ADLNINIIEKAST; DLNINIIEKASTG; LNINIIEKASTGN; NINIIEKASTGNS; INIIEKASTGNSY; NIIEKASTGNSYL; IIEKASTGNSYLG; IEKASTGNSYLGD; EKASTGNSYLGDI; KASTGNSYLGDIA; ASTGNSYLGDIAN; STGNSYLGDIANL; TGNSYLGDIANLE; GNSYLGDIANLED; NSYLGDIANLEDG; SYLGDIANLEDGN; YLGDIANLEDGNS; LGDIANLEDGNSN; GDIANLEDGNSNL; DIANLEDGNSNLI; IANLEDGNSNLIW; ANLEDGNSNLIWG; NLEDGNSNLIWGI; LEDGNSNLIWGIG; EDGNSNLIWGIGF; DGNSNLIWGIGFR; GNSNLIWGIGFRL; NSNLIWGIGFRLS; SNLIWGIGFRLSD; NLIWGIGFRLSDI; LIWGIGFRLSDIL; IWGIGFRLSDILF; WGIGFRLSDILFQ; GIGFRLSDILFQR; IGFRLSDILFQRA; GFRLSDILFQRAS; FRLSDILFQRASE; RLSDILFQRASEN; LSDILFQRASENV; SDILFQRASENVS; DILFQRASENVSV; ILFQRASENVSVN; LFQRASENVSVNY; FQRASENVSVNYA; QRASENVSVNYAI; RASENVSVNYAII; ASENVSVNYAIIE; SENVSVNYAIIEG; ENVSVNYAIIEGV; NVSVNYAIIEGVY; VSVNYAIIEGVYD; SVNYAIIEGVYDE; VNYAIIEGVYDEI; NYAIIEGVYDEIQ; YAIIEGVYDEIQI; AIIEGVYDEIQIP;

	IIEGVYDEIQIPK; IEGVYDEIQIPKN; EGVYDEIQIPKNL; GVYDEIQIPKNLL; VYDEIQIPKNLLN; YDEIQIPKNLLNI; DEIQIPKNLLNIS; EIQIPKNLLNISF; IQIPKNLLNISFR; QIPKNLLNISFRS; IPKNLLNISFRSE; PKNLLNISFRSEE; KNLLNISFRSEEV; NLLNISFRSEEVA; LLNISFRSEEVAF; LNISFRSEEVAFL; NISFRSEEVAFLA; ISFRSEEVAFLAG; SFRSEEVAFLAGY; FRSEEVAFLAGYF; RSEEVAFLAGYFA; SEEVAFLAGYFAS; EEVAFLAGYFASK; EVAFLAGYFASKA; VAFLAGYFASKAS; AFLAGYFASKASK; FLAGYFASKASKT; LAGYFASKASKTG; AGYFASKASKTGK; GYFASKASKTGKI; YFASKASKTGKIG; FASKASKTGKIGF; ASKASKTGKIGFV; SKASKTGKIGFVG; KASKTGKIGFVGG; ASKTGKIGFVGGV; SKTGKIGFVGGVR; KTGKIGFVGGVRG; TGKIGFVGGVRGK; GKIGFVGGVRGKV; KIGFVGGVRGKVL; IGFVGGVRGKVLE; GFVGGVRGKVLES; FVGGVRGKVLESF; VGGVRGKVLESFM; GGVRGKVLESFMY; GVRGKVLESFMYG; VRGKVLESFMYGY; RGKVLESFMYGYE; GKVLESFMYGYEA; KVLESFMYGYEAG; VLESFMYGYEAGA; LESFMYGYEAGAK; ESFMYGYEAGAKY; SFMYGYEAGAKYA; FMYGYEAGAKYAN; MYGYEAGAKYANS; YGYEAGAKYANSN; GYEAGAKYANSNI; YEAGAKYANSNIK; EAGAKYANSNIKV; AGAKYANSNIKVV; GAKYANSNIKVVS; AKYANSNIKVVSQ; KYANSNIKVVSQY; YANSNIKVVSQYV; ANSNIKVVSQYVG; NSNIKVVSQYVGT; SNIKVVSQYVGTF; NIKVVSQYVGTFG; IKVVSQYVGTFGD; KVVSQYVGTFGDF; VVSQYVGTFGDFG; VSQYVGTFGDFGL; SQYVGTFGDFGLG; QYVGTFGDFGLGR; YVGTFGDFGLGRS; VGTFGDFGLGRST; GTFGDFGLGRSTA; TFGDFGLGRSTAS; FGDFGLGRSTASN; GDFGLGRSTASNM; DFGLGRSTASNMY; FGLGRSTASNMYR; GLGRSTASNMYRD; LGRSTASNMYRDG; GRSTASNMYRDGV; RSTASNMYRDGVD; STASNMYRDGVDI; TASNMYRDGVDII; ASNMYRDGVDIIF; SNMYRDGVDIIFA; NMYRDGVDIIFAA; MYRDGVDIIFAAA; YRDGVDIIFAAAG; RDGVDIIFAAAGL; DGVDIIFAAAGLS; GVDIIFAAAGLSG; VDIIFAAAGLSGI; DIIFAAAGLSGIG; IIFAAAGLSGIGV; IFAAAGLSGIGVI; FAAAGLSGIGVIE; AAAGLSGIGVIEA; AAGLSGIGVIEAA; AGLSGIGVIEAAK; GLSGIGVIEAAKE; LSGIGVIEAAKEL; SGIGVIEAAKELG; GIGVIEAAKELGP; IGVIEAAKELGPD; GVIEAAKELGPDH; VIEAAKELGPDHY; IEAAKELGPDHYI; EAAKELGPDHYII; AAKELGPDHYIIG; AKELGPDHYIIGV; KELGPDHYIIGVD; ELGPDHYIIGVDQ; LGPDHYIIGVDQD; GPDHYIIGVDQDQ; PDHYIIGVDQDQS; DHYIIGVDQDQSY; HYIIGVDQDQSYL; YIIGVDQDQSYLA; IIGVDQDQSYLAP; IGVDQDQSYLAPN; GVDQDQSYLAPNN; VDQDQSYLAPNNV; DQDQSYLAPNNVI; QDQSYLAPNNVIV; DQSYLAPNNVIVS; QSYLAPNNVIVSA; SYLAPNNVIVSAV; YLAPNNVIVSAVK; LAPNNVIVSAVKK; APNNVIVSAVKKV; PNNVIVSAVKKVD; NNVIVSAVKKVDS; NVIVSAVKKVDSL; VIVSAVKKVDSLM; IVSAVKKVDSLMY; VSAVKKVDSLMYS; SAVKKVDSLMYSL; AVKKVDSLMYSLT; VKKVDSLMYSLTK; KKVDSLMYSLTKK; KVDSLMYSLTKKY; VDSLMYSLTKKYL; DSLMYSLTKKYLE; SLMYSLTKKYLET; LMYSLTKKYLETG; MYSLTKKYLETGV; YSLTKKYLETGVL; SLTKKYLETGVLD; LTKKYLETGVLDG; TKKYLETGVLDGG; KKYLETGVLDGGK; KYLETGVLDGGKT; YLETGVLDGGKTM; LETGVLDGGKTMF; ETGVLDGGKTMFL; TGVLDGGKTMFLG; GVLDGGKTMFLGL; VLDGGKTMFLGLK; LDGGKTMFLGLKE; DGGKTMFLGLKED; GGKTMFLGLKEDG; GKTMFLGLKEDGL; KTMFLGLKEDGLG; TMFLGLKEDGLGL; MFLGLKEDGLGLV; FLGLKEDGLGLVL; LGLKEDGLGLVLN; GLKEDGLGLVLNE; LKEDGLGLVLNEN; KEDGLGLVLNENL; EDGLGLVLNENLK; DGLGLVLNENLKS; GLGLVLNENLKSN; LGLVLNENLKSNY; GLVLNENLKSNYS; LVLNENLKSNYSE; VLNENLKSNYSEI; LNENLKSNYSEIY; NENLKSNYSEIYN; ENLKSNYSEIYNK; NLKSNYSEIYNKS; LKSNYSEIYNKSL; KSNYSEIYNKSLK; SNYSEIYNKSLKI; NYSEIYNKSLKIG; YSEIYNKSLKIGQ; SEIYNKSLKIGQS; EIYNKSLKIGQSI; IYNKSLKIGQSIM; YNKSLKIGQSIMN; NKSLKIGQSIMNG; KSLKIGQSIMNGI; SLKIGQSIMNGII; LKIGQSIMNGIIK; KIGQSIMNGIIKV; IGQSIMNGIIKVP; GQSIMNGIIKVPY; QSIMNGIIKVPYD; SIMNGIIKVPYDK; IMNGIIKVPYDKV; MNGIIKVPYDKVS; NGIIKVPYDKVSY; GIIKVPYDKVSYF; IIKVPYDKVSYFV; IKVPYDKVSYFVL; KVPYDKVSYFVLQ; VPYDKVSYFVLQM; PYDKVSYFVLQME; YDKVSYFVLQMEN; 14 mers: MDNYYEIYFLYFFI; DNYYEIYFLYFFIK; NYYEIYFLYFFIKS;

	YYEIYFLYFFIKSK; YEIYFLYFFIKSKE; EIYFLYFFIKSKED; IYFLYFFIKSKEDI; YFLYFFIKSKEDIF; FLYFFIKSKEDIFM; LYFFIKSKEDIFML; YFFIKSKEDIFMLK; FFIKSKEDIFMLKK; FIKSKEDIFMLKKV; IKSKEDIFMLKKVY; KSKEDIFMLKKVYY; SKEDIFMLKKVYYF; KEDIFMLKKVYYFL; EDIFMLKKVYYFLI; DIFMLKKVYYFLIF; IFMLKKVYYFLIFL; FMLKKVYYFLIFLF; MLKKVYYFLIFLFI; LKKVYYFLIFLFIV; KKVYYFLIFLFIVA; KVYYFLIFLFIVAC; VYYFLIFLFIVACS; YYFLIFLFIVACSS; YFLIFLFIVACSSS; FLIFLFIVACSSSD; LIFLFIVACSSSDD; IFLFIVACSSSDDG; FLFIVACSSSDDGK; LFIVACSSSDDGKS; FIVACSSSDDGKSE; IVACSSSDDGKSEA; VACSSSDDGKSEAK; ACSSSDDGKSEAKT; CSSSDDGKSEAKTV; SSSDDGKSEAKTVS; SSDDGKSEAKTVSL; SDDGKSEAKTVSLI; DDGKSEAKTVSLIV; DGKSEAKTVSLIVD; GKSEAKTVSLIVDG; KSEAKTVSLIVDGA; SEAKTVSLIVDGAF; EAKTVSLIVDGAFD; AKTVSLIVDGAFDD; KTVSLIVDGAFDDK; TVSLIVDGAFDDKG; VSLIVDGAFDDKGF; SLIVDGAFDDKGFN; LIVDGAFDDKGFNE; IVDGAFDDKGFNES; VDGAFDDKGFNESS; DGAFDDKGFNESSS; GAFDDKGFNESSSK; AFDDKGFNESSSKA; FDDKGFNESSSKAI; DDKGFNESSSKAIR; DKGFNESSSKAIRK; KGFNESSSKAIRKL; GFNESSSKAIRKLK; FNESSSKAIRKLKA; NESSSKAIRKLKAD; ESSSKAIRKLKADL; SSSKAIRKLKADLN; SSKAIRKLKADLNI; SKAIRKLKADLNIN; KAIRKLKADLNINI; AIRKLKADLNINII; IRKLKADLNINIIE; RKLKADLNINIIEK; KLKADLNINIIEKA; LKADLNINIIEKAS; KADLNINIIEKAST; ADLNINIIEKASTG; DLNINIIEKASTGN; LNINIIEKASTGNS; NINIIEKASTGNSY; INIIEKASTGNSYL; NIIEKASTGNSYLG; IIEKASTGNSYLGD; IEKASTGNSYLGDI; EKASTGNSYLGDIA; KASTGNSYLGDIAN; ASTGNSYLGDIANL; STGNSYLGDIANLE; TGNSYLGDIANLED; GNSYLGDIANLEDG; NSYLGDIANLEDGN; SYLGDIANLEDGNS; YLGDIANLEDGNSN; LGDIANLEDGNSNL; GDIANLEDGNSNLI; DIANLEDGNSNLIW; IANLEDGNSNLIWG; ANLEDGNSNLIWGI; NLEDGNSNLIWGIG; LEDGNSNLIWGIGF; EDGNSNLIWGIGFR; DGNSNLIWGIGFRL; GNSNLIWGIGFRLS; NSNLIWGIGFRLSD; SNLIWGIGFRLSDI; NLIWGIGFRLSDIL; LIWGIGFRLSDILF; IWGIGFRLSDILFQ; WGIGFRLSDILFQR; GIGFRLSDILFQRA; IGFRLSDILFQRAS; GFRLSDILFQRASE; FRLSDILFQRASEN; RLSDILFQRASENV; LSDILFQRASENVS; SDILFQRASENVSV; DILFQRASENVSVN; ILFQRASENVSVNY; LFQRASENVSVNYA; FQRASENVSVNYAI; QRASENVSVNYAII; RASENVSVNYAIIE; ASENVSVNYAIIEG; SENVSVNYAIIEGV; ENVSVNYAIIEGVY; NVSVNYAIIEGVYD; VSVNYAIIEGVYDE; SVNYAIIEGVYDEI; VNYAIIEGVYDEIQ; NYAIIEGVYDEIQI; YAIIEGVYDEIQIP; AIIEGVYDEIQIPK; IIEGVYDEIQIPKN; IEGVYDEIQIPKNL; EGVYDEIQIPKNLL; GVYDEIQIPKNLLN; VYDEIQIPKNLLNI; YDEIQIPKNLLNIS; DEIQIPKNLLNISF; EIQIPKNLLNISFR; IQIPKNLLNISFRS; QIPKNLLNISFRSE; IPKNLLNISFRSEE; PKNLLNISFRSEEV; KNLLNISFRSEEVA; NLLNISFRSEEVAF; LLNISFRSEEVAFL; LNISFRSEEVAFLA; NISFRSEEVAFLAG; ISFRSEEVAFLAGY; SFRSEEVAFLAGYF; FRSEEVAFLAGYFA; RSEEVAFLAGYFAS; SEEVAFLAGYFASK; EEVAFLAGYFASKA; EVAFLAGYFASKAS; VAFLAGYFASKASK; AFLAGYFASKASKT; FLAGYFASKASKTG; LAGYFASKASKTGK; AGYFASKASKTGKI; GYFASKASKTGKIG; YFASKASKTGKIGF; FASKASKTGKIGFV; ASKASKTGKIGFVG; SKASKTGKIGFVGG; KASKTGKIGFVGGV; ASKTGKIGFVGGVR; SKTGKIGFVGGVRG; KTGKIGFVGGVRGK; TGKIGFVGGVRGKV; GKIGFVGGVRGKVL; KIGFVGGVRGKVLE; IGFVGGVRGKVLES;

	GFVGGVRGKVLESF; FVGGVRGKVLESFM; VGGVRGKVLESFMY; GGVRGKVLESFMYG; GVRGKVLESFMYGY; VRGKVLESFMYGYE; RGKVLESFMYGYEA; GKVLESFMYGYEAG; KVLESFMYGYEAGA; VLESFMYGYEAGAK; LESFMYGYEAGAKY; ESFMYGYEAGAKYA; SFMYGYEAGAKYAN; FMYGYEAGAKYANS; MYGYEAGAKYANSN; YGYEAGAKYANSNI; GYEAGAKYANSNIK; YEAGAKYANSNIKV; EAGAKYANSNIKVV; AGAKYANSNIKVVS; GAKYANSNIKVVSQ; AKYANSNIKVVSQY; KYANSNIKVVSQYV; YANSNIKVVSQYVG; ANSNIKVVSQYVGT; NSNIKVVSQYVGTF; SNIKVVSQYVGTFG; NIKVVSQYVGTFGD; IKVVSQYVGTFGDF; KVVSQYVGTFGDFG; VVSQYVGTFGDFGL; VSQYVGTFGDFGLG; SQYVGTFGDFGLGR; QYVGTFGDFGLGRS; YVGTFGDFGLGRST; VGTFGDFGLGRSTA; GTFGDFGLGRSTAS; TFGDFGLGRSTASN; FGDFGLGRSTASNM; GDFGLGRSTASNMY; DFGLGRSTASNMYR; FGLGRSTASNMYRD; GLGRSTASNMYRDG; LGRSTASNMYRDGV; GRSTASNMYRDGVD; RSTASNMYRDGVDI; STASNMYRDGVDII; TASNMYRDGVDIIF; ASNMYRDGVDIIFA; SNMYRDGVDIIFAA; NMYRDGVDIIFAAA; MYRDGVDIIFAAAG; YRDGVDIIFAAAGL; RDGVDIIFAAAGLS; DGVDIIFAAAGLSG; GVDIIFAAAGLSGI; VDIIFAAAGLSGIG; DIIFAAAGLSGIGV; IIFAAAGLSGIGVI; IFAAAGLSGIGVIE; FAAAGLSGIGVIEA; AAAGLSGIGVIEAA; AAGLSGIGVIEAAK; AGLSGIGVIEAAKE; GLSGIGVIEAAKEL; LSGIGVIEAAKELG; SGIGVIEAAKELGP; GIGVIEAAKELGPD; IGVIEAAKELGPDH; GVIEAAKELGPDHY; VIEAAKELGPDHYI; IEAAKELGPDHYII; EAAKELGPDHYIIG; AAKELGPDHYIIGV; AKELGPDHYIIGVD; KELGPDHYIIGVDQ; ELGPDHYIIGVDQD; LGPDHYIIGVDQDQ; GPDHYIIGVDQDQS; PDHYIIGVDQDQSY; DHYIIGVDQDQSYL; HYIIGVDQDQSYLA; YIIGVDQDQSYLAP; IIGVDQDQSYLAPN; IGVDQDQSYLAPNN; GVDQDQSYLAPNNV; VDQDQSYLAPNNVI; DQDQSYLAPNNVIV; QDQSYLAPNNVIVS; DQSYLAPNNVIVSA; QSYLAPNNVIVSAV; SYLAPNNVIVSAVK; YLAPNNVIVSAVKK; LAPNNVIVSAVKKV; APNNVIVSAVKKVD; PNNVIVSAVKKVDS; NNVIVSAVKKVDSL; NVIVSAVKKVDSLM; VIVSAVKKVDSLMY; IVSAVKKVDSLMYS; VSAVKKVDSLMYSL; SAVKKVDSLMYSLT; AVKKVDSLMYSLTK; VKKVDSLMYSLTKK; KKVDSLMYSLTKKY; KVDSLMYSLTKKYL; VDSLMYSLTKKYLE; DSLMYSLTKKYLET; SLMYSLTKKYLETG; LMYSLTKKYLETGV; MYSLTKKYLETGVL; YSLTKKYLETGVLD; SLTKKYLETGVLDG; LTKKYLETGVLDGG; TKKYLETGVLDGGK; KKYLETGVLDGGKT; KYLETGVLDGGKTM; YLETGVLDGGKTMF; LETGVLDGGKTMFL; ETGVLDGGKTMFLG; TGVLDGGKTMFLGL; GVLDGGKTMFLGLK; VLDGGKTMFLGLKE; LDGGKTMFLGLKED; DGGKTMFLGLKEDG; GGKTMFLGLKEDGL; GKTMFLGLKEDGLG; KTMFLGLKEDGLGL; TMFLGLKEDGLGLV; MFLGLKEDGLGLVL; FLGLKEDGLGLVLN; LGLKEDGLGLVLNE; GLKEDGLGLVLNEN; LKEDGLGLVLNENL; KEDGLGLVLNENLK; EDGLGLVLNENLKS; DGLGLVLNENLKSN; GLGLVLNENLKSNY; LGLVLNENLKSNYS; GLVLNENLKSNYSE; LVLNENLKSNYSEI; VLNENLKSNYSEIY; LNENLKSNYSEIYN; NENLKSNYSEIYNK; ENLKSNYSEIYNKS; NLKSNYSEIYNKSL; LKSNYSEIYNKSLK; KSNYSEIYNKSLKI; SNYSEIYNKSLKIG; NYSEIYNKSLKIGQ; YSEIYNKSLKIGQS; SEIYNKSLKIGQSI; EIYNKSLKIGQSIM; IYNKSLKIGQSIMN; YNKSLKIGQSIMNG; NKSLKIGQSIMNGI; KSLKIGQSIMNGII; SLKIGQSIMNGIIK; LKIGQSIMNGIIKV; KIGQSIMNGIIKVP; IGQSIMNGIIKVPY; GQSIMNGIIKVPYD; QSIMNGIIKVPYDK; SIMNGIIKVPYDKV; IMNGIIKVPYDKVS; MNGIIKVPYDKVSY; NGIIKVPYDKVSYF; GIIKVPYDKVSYFV; IIKVPYDKVSYFVL; IKVPYDKVSYFVLQ; KVPYDKVSYFVLQM;

VPYDKVSYFVLQME; PYDKVSYFVLQMEN;

15 mers:
MDNYYEIYFLYFFIK; DNYYEIYFLYFFIKS; NYYEIYFLYFFIKSK;
YYEIYFLYFFIKSKE; YEIYFLYFFIKSKED; EIYFLYFFIKSKEDI;
IYFLYFFIKSKEDIF; YFLYFFIKSKEDIFM; FLYFFIKSKEDIFML;
LYFFIKSKEDIFMLK; YFFIKSKEDIFMLKK; FFIKSKEDIFMLKKV;
FIKSKEDIFMLKKVY; IKSKEDIFMLKKVYY; KSKEDIFMLKKVYYF;
SKEDIFMLKKVYYFL; KEDIFMLKKVYYFLI; EDIFMLKKVYYFLIF;
DIFMLKKVYYFLIFL; IFMLKKVYYFLIFLF; FMLKKVYYFLIFLFI;
MLKKVYYFLIFLFIV; LKKVYYFLIFLFIVA; KKVYYFLIFLFIVAC;
KVYYFLIFLFIVACS; VYYFLIFLFIVACSS; YYFLIFLFIVACSSS;
YFLIFLFIVACSSSD; FLIFLFIVACSSSDD; LIFLFIVACSSSDDG;
IFLFIVACSSSDDGK; FLFIVACSSSDDGKS; LFIVACSSSDDGKSE;
FIVACSSSDDGKSEA; IVACSSSDDGKSEAK; VACSSSDDGKSEAKT;
ACSSSDDGKSEAKTV; CSSSDDGKSEAKTVS; SSSDDGKSEAKTVSL;
SSDDGKSEAKTVSLI; SDDGKSEAKTVSLIV; DDGKSEAKTVSLIVD;
DGKSEAKTVSLIVDG; GKSEAKTVSLIVDGA; KSEAKTVSLIVDGAF;
SEAKTVSLIVDGAFD; EAKTVSLIVDGAFDD; AKTVSLIVDGAFDDK;
KTVSLIVDGAFDDKG; TVSLIVDGAFDDKGF; VSLIVDGAFDDKGFN;
SLIVDGAFDDKGFNE; LIVDGAFDDKGFNES; IVDGAFDDKGFNESS;
VDGAFDDKGFNESSS; DGAFDDKGFNESSSK; GAFDDKGFNESSSKA;
AFDDKGFNESSSKAI; FDDKGFNESSSKAIR; DDKGFNESSSKAIRK;
DKGFNESSSKAIRKL; KGFNESSSKAIRKLK; GFNESSSKAIRKLKA;
FNESSSKAIRKLKAD; NESSSKAIRKLKADL; ESSSKAIRKLKADLN;
SSSKAIRKLKADLNI; SSKAIRKLKADLNIN; SKAIRKLKADLNINI;
KAIRKLKADLNINII; AIRKLKADLNINIIE; IRKLKADLNINIIEK;
RKLKADLNINIIEKA; KLKADLNINIIEKAS; LKADLNINIIEKAST;
KADLNINIIEKASTG; ADLNINIIEKASTGN; DLNINIIEKASTGNS;
LNINIIEKASTGNSY; NINIIEKASTGNSYL; INIIEKASTGNSYLG;
NIIEKASTGNSYLGD; IIEKASTGNSYLGDI; IEKASTGNSYLGDIA;
EKASTGNSYLGDIAN; KASTGNSYLGDIANL; ASTGNSYLGDIANLE;
STGNSYLGDIANLED; TGNSYLGDIANLEDG; GNSYLGDIANLEDGN;
NSYLGDIANLEDGNS; SYLGDIANLEDGNSN; YLGDIANLEDGNSNL;
LGDIANLEDGNSNLI; GDIANLEDGNSNLIW; DIANLEDGNSNLIWG;
IANLEDGNSNLIWGI; ANLEDGNSNLIWGIG; NLEDGNSNLIWGIGF;
LEDGNSNLIWGIGFR; EDGNSNLIWGIGFRL; DGNSNLIWGIGFRLS;
GNSNLIWGIGFRLSD; NSNLIWGIGFRLSDI; SNLIWGIGFRLSDIL;
NLIWGIGFRLSDILF; LIWGIGFRLSDILFQ; IWGIGFRLSDILFQR;
WGIGFRLSDILFQRA; GIGFRLSDILFQRAS; IGFRLSDILFQRASE;
GFRLSDILFQRASEN; FRLSDILFQRASENV; RLSDILFQRASENVS;
LSDILFQRASENVSV; SDILFQRASENVSVN; DILFQRASENVSVNY;
ILFQRASENVSVNYA; LFQRASENVSVNYAI; FQRASENVSVNYAII;
QRASENVSVNYAIIE; RASENVSVNYAIIEG; ASENVSVNYAIIEGV;
SENVSVNYAIIEGVY; ENVSVNYAIIEGVYD; NVSVNYAIIEGVYDE;
VSVNYAIIEGVYDEI; SVNYAIIEGVYDEIQ; VNYAIIEGVYDEIQI;
NYAIIEGVYDEIQIP; YAIIEGVYDEIQIPK; AIIEGVYDEIQIPKN;
IIEGVYDEIQIPKNL; IEGVYDEIQIPKNLL; EGVYDEIQIPKNLLN;
GVYDEIQIPKNLLNI; VYDEIQIPKNLLNIS; YDEIQIPKNLLNISF;
DEIQIPKNLLNISFR; EIQIPKNLLNISFRS; IQIPKNLLNISFRSE;
QIPKNLLNISFRSEE; IPKNLLNISFRSEEV; PKNLLNISFRSEEVA;
KNLLNISFRSEEVAF; NLLNISFRSEEVAFL; LLNISFRSEEVAFLA;
LNISFRSEEVAFLAG; NISFRSEEVAFLAGY; ISFRSEEVAFLAGYF;
SFRSEEVAFLAGYFA; FRSEEVAFLAGYFAS; RSEEVAFLAGYFASK;
SEEVAFLAGYFASKA; EEVAFLAGYFASKAS; EVAFLAGYFASKASK;
VAFLAGYFASKASKT; AFLAGYFASKASKTG; FLAGYFASKASKTGK;
LAGYFASKASKTGKI; AGYFASKASKTGKIG; GYFASKASKTGKIGF;

	YFASKASKTGKIGFV; FASKASKTGKIGFVG; ASKASKTGKIGFVGG; SKASKTGKIGFVGGV; KASKTGKIGFVGGVR; ASKTGKIGFVGGVRG; SKTGKIGFVGGVRGK; KTGKIGFVGGVRGKV; TGKIGFVGGVRGKVL; GKIGFVGGVRGKVLE; KIGFVGGVRGKVLES; IGFVGGVRGKVLESF; GFVGGVRGKVLESFM; FVGGVRGKVLESFMY; VGGVRGKVLESFMYG; GGVRGKVLESFMYGY; GVRGKVLESFMYGYE; VRGKVLESFMYGYEA; RGKVLESFMYGYEAG; GKVLESFMYGYEAGA; KVLESFMYGYEAGAK; VLESFMYGYEAGAKY; LESFMYGYEAGAKYA; ESFMYGYEAGAKYAN; SFMYGYEAGAKYANS; FMYGYEAGAKYANSN; MYGYEAGAKYANSNI; YGYEAGAKYANSNIK; GYEAGAKYANSNIKV; YEAGAKYANSNIKVV; EAGAKYANSNIKVVS; AGAKYANSNIKVVSQ; GAKYANSNIKVVSQY; AKYANSNIKVVSQYV; KYANSNIKVVSQYVG; YANSNIKVVSQYVGT; ANSNIKVVSQYVGTF; NSNIKVVSQYVGTFG; SNIKVVSQYVGTFGD; NIKVVSQYVGTFGDF; IKVVSQYVGTFGDFG; KVVSQYVGTFGDFGL; VVSQYVGTFGDFGLG; VSQYVGTFGDFGLGR; SQYVGTFGDFGLGRS; QYVGTFGDFGLGRST; YVGTFGDFGLGRSTA; VGTFGDFGLGRSTAS; GTFGDFGLGRSTASN; TFGDFGLGRSTASNM; FGDFGLGRSTASNMY; GDFGLGRSTASNMYR; DFGLGRSTASNMYRD; FGLGRSTASNMYRDG; GLGRSTASNMYRDGV; LGRSTASNMYRDGVD; GRSTASNMYRDGVDI; RSTASNMYRDGVDII; STASNMYRDGVDIIF; TASNMYRDGVDIIFA; ASNMYRDGVDIIFAA; SNMYRDGVDIIFAAA; NMYRDGVDIIFAAAG; MYRDGVDIIFAAAGL; YRDGVDIIFAAAGLS; RDGVDIIFAAAGLSG; DGVDIIFAAAGLSGI; GVDIIFAAAGLSGIG; VDIIFAAAGLSGIGV; DIIFAAAGLSGIGVI; IIFAAAGLSGIGVIE; IFAAAGLSGIGVIEA; FAAAGLSGIGVIEAA; AAAGLSGIGVIEAAK; AAGLSGIGVIEAAKE; AGLSGIGVIEAAKEL; GLSGIGVIEAAKELG; LSGIGVIEAAKELGP; SGIGVIEAAKELGPD; GIGVIEAAKELGPDH; IGVIEAAKELGPDHY; GVIEAAKELGPDHYI; VIEAAKELGPDHYII; IEAAKELGPDHYIIG; EAAKELGPDHYIIGV; AAKELGPDHYIIGVD; AKELGPDHYIIGVDQ; KELGPDHYIIGVDQD; ELGPDHYIIGVDQDQ; LGPDHYIIGVDQDQS; GPDHYIIGVDQDQSY; PDHYIIGVDQDQSYL; DHYIIGVDQDQSYLA; HYIIGVDQDQSYLAP; YIIGVDQDQSYLAPN; IIGVDQDQSYLAPNN; IGVDQDQSYLAPNNV; GVDQDQSYLAPNNVI; VDQDQSYLAPNNVIV; DQDQSYLAPNNVIVS; QDQSYLAPNNVIVSA; DQSYLAPNNVIVSAV; QSYLAPNNVIVSAVK; SYLAPNNVIVSAVKK; YLAPNNVIVSAVKKV; LAPNNVIVSAVKKVD; APNNVIVSAVKKVDS; PNNVIVSAVKKVDSL; NNVIVSAVKKVDSLM; NVIVSAVKKVDSLMY; VIVSAVKKVDSLMYS; IVSAVKKVDSLMYSL; VSAVKKVDSLMYSLT; SAVKKVDSLMYSLTK; AVKKVDSLMYSLTKK; VKKVDSLMYSLTKKY; KKVDSLMYSLTKKYL; KVDSLMYSLTKKYLE; VDSLMYSLTKKYLET; DSLMYSLTKKYLETG; SLMYSLTKKYLETGV; LMYSLTKKYLETGVL; MYSLTKKYLETGVLD; YSLTKKYLETGVLDG; SLTKKYLETGVLDGG; LTKKYLETGVLDGGK; TKKYLETGVLDGGKT; KKYLETGVLDGGKTM; KYLETGVLDGGKTMF; YLETGVLDGGKTMFL; LETGVLDGGKTMFLG; ETGVLDGGKTMFLGL; TGVLDGGKTMFLGLK; GVLDGGKTMFLGLKE; VLDGGKTMFLGLKED; LDGGKTMFLGLKEDG; DGGKTMFLGLKEDGL; GGKTMFLGLKEDGLG; GKTMFLGLKEDGLGL; KTMFLGLKEDGLGLV; TMFLGLKEDGLGLVL; MFLGLKEDGLGLVLN; FLGLKEDGLGLVLNE; LGLKEDGLGLVLNEN; GLKEDGLGLVLNENL; LKEDGLGLVLNENLK; KEDGLGLVLNENLKS; EDGLGLVLNENLKSN; DGLGLVLNENLKSNY; GLGLVLNENLKSNYS; LGLVLNENLKSNYSE; GLVLNENLKSNYSEI; LVLNENLKSNYSEIY; VLNENLKSNYSEIYN; LNENLKSNYSEIYNK; NENLKSNYSEIYNKS; ENLKSNYSEIYNKSL; NLKSNYSEIYNKSLK; LKSNYSEIYNKSLKI; KSNYSEIYNKSLKIG; SNYSEIYNKSLKIGQ; NYSEIYNKSLKIGQS; YSEIYNKSLKIGQSI; SEIYNKSLKIGQSIM; EIYNKSLKIGQSIMN; IYNKSLKIGQSIMNG; YNKSLKIGQSIMNGI; NKSLKIGQSIMNGII; KSLKIGQSIMNGIIK; SLKIGQSIMNGIIKV; LKIGQSIMNGIIKVP;

KIGQSIMNGIIKVPY; IGQSIMNGIIKVPYD; GQSIMNGIIKVPYDK;
QSIMNGIIKVPYDKV; SIMNGIIKVPYDKVS; IMNGIIKVPYDKVSY;
MNGIIKVPYDKVSYF; NGIIKVPYDKVSYFV; GIIKVPYDKVSYFVL;
IIKVPYDKVSYFVLQ; IKVPYDKVSYFVLQM; KVPYDKVSYFVLQME;
VPYDKVSYFVLQMEN;

16 mers:
MDNYYEIYFLYFFIKS; DNYYEIYFLYFFIKSK; NYYEIYFLYFFIKSKE;
YYEIYFLYFFIKSKED; YEIYFLYFFIKSKEDI; EIYFLYFFIKSKEDIF;
IYFLYFFIKSKEDIFM; YFLYFFIKSKEDIFML; FLYFFIKSKEDIFMLK;
LYFFIKSKEDIFMLKK; YFFIKSKEDIFMLKKV; FFIKSKEDIFMLKKVY;
FIKSKEDIFMLKKVYY; IKSKEDIFMLKKVYYF; KSKEDIFMLKKVYYFL;
SKEDIFMLKKVYYFLI; KEDIFMLKKVYYFLIF; EDIFMLKKVYYFLIFL;
DIFMLKKVYYFLIFLF; IFMLKKVYYFLIFLFI; FMLKKVYYFLIFLFIV;
MLKKVYYFLIFLFIVA; LKKVYYFLIFLFIVAC; KKVYYFLIFLFIVACS;
KVYYFLIFLFIVACSS; VYYFLIFLFIVACSSS; YYFLIFLFIVACSSSD;
YFLIFLFIVACSSSDD; FLIFLFIVACSSSDDG; LIFLFIVACSSSDDGK;
IFLFIVACSSSDDGKS; FLFIVACSSSDDGKSE; LFIVACSSSDDGKSEA;
FIVACSSSDDGKSEAK; IVACSSSDDGKSEAKT; VACSSSDDGKSEAKTV;
ACSSSDDGKSEAKTVS; CSSSDDGKSEAKTVSL; SSSDDGKSEAKTVSLI;
SSDDGKSEAKTVSLIV; SDDGKSEAKTVSLIVD; DDGKSEAKTVSLIVDG;
DGKSEAKTVSLIVDGA; GKSEAKTVSLIVDGAF; KSEAKTVSLIVDGAFD;
SEAKTVSLIVDGAFDD; EAKTVSLIVDGAFDDK; AKTVSLIVDGAFDDKG;
KTVSLIVDGAFDDKGF; TVSLIVDGAFDDKGFN; VSLIVDGAFDDKGFNE;
SLIVDGAFDDKGFNES; LIVDGAFDDKGFNESS; IVDGAFDDKGFNESSS;
VDGAFDDKGFNESSSK; DGAFDDKGFNESSSKA; GAFDDKGFNESSSKAI;
AFDDKGFNESSSKAIR; FDDKGFNESSSKAIRK; DDKGFNESSSKAIRKL;
DKGFNESSSKAIRKLK; KGFNESSSKAIRKLKA; GFNESSSKAIRKLKAD;
FNESSSKAIRKLKADL; NESSSKAIRKLKADLN; ESSSKAIRKLKADLNI;
SSSKAIRKLKADLNIN; SSKAIRKLKADLNINI; SKAIRKLKADLNINII;
KAIRKLKADLNINIIE; AIRKLKADLNINIIEK; IRKLKADLNINIIEKA;
RKLKADLNINIIEKAS; KLKADLNINIIEKAST; LKADLNINIIEKASTG;
KADLNINIIEKASTGN; ADLNINIIEKASTGNS; DLNINIIEKASTGNSY;
LNINIIEKASTGNSYL; NINIIEKASTGNSYLG; INIIEKASTGNSYLGD;
NIIEKASTGNSYLGDI; IIEKASTGNSYLGDIA; IEKASTGNSYLGDIAN;
EKASTGNSYLGDIANL; KASTGNSYLGDIANLE; ASTGNSYLGDIANLED;
STGNSYLGDIANLEDG; TGNSYLGDIANLEDGN; GNSYLGDIANLEDGNS;
NSYLGDIANLEDGNSN; SYLGDIANLEDGNSNL; YLGDIANLEDGNSNLI;
LGDIANLEDGNSNLIW; GDIANLEDGNSNLIWG; DIANLEDGNSNLIWGI;
IANLEDGNSNLIWGIG; ANLEDGNSNLIWGIGF; NLEDGNSNLIWGIGFR;
LEDGNSNLIWGIGFRL; EDGNSNLIWGIGFRLS; DGNSNLIWGIGFRLSD;
GNSNLIWGIGFRLSDI; NSNLIWGIGFRLSDIL; SNLIWGIGFRLSDILF;
NLIWGIGFRLSDILFQ; LIWGIGFRLSDILFQR; IWGIGFRLSDILFQRA;
WGIGFRLSDILFQRAS; GIGFRLSDILFQRASE; IGFRLSDILFQRASEN;
GFRLSDILFQRASENV; FRLSDILFQRASENVS; RLSDILFQRASENVSV;
LSDILFQRASENVSVN; SDILFQRASENVSVNY; DILFQRASENVSVNYA;
ILFQRASENVSVNYAI; LFQRASENVSVNYAII; FQRASENVSVNYAIIE;
QRASENVSVNYAIIEG; RASENVSVNYAIIEGV; ASENVSVNYAIIEGVY;
SENVSVNYAIIEGVYD; ENVSVNYAIIEGVYDE; NVSVNYAIIEGVYDEI;
VSVNYAIIEGVYDEIQ; SVNYAIIEGVYDEIQI; VNYAIIEGVYDEIQIP;
NYAIIEGVYDEIQIPK; YAIIEGVYDEIQIPKN; AIIEGVYDEIQIPKNL;
IIEGVYDEIQIPKNLL; IEGVYDEIQIPKNLLN; EGVYDEIQIPKNLLNI;
GVYDEIQIPKNLLNIS; VYDEIQIPKNLLNISF; YDEIQIPKNLLNISFR;
DEIQIPKNLLNISFRS; EIQIPKNLLNISFRSE; IQIPKNLLNISFRSEE;
QIPKNLLNISFRSEEV; IPKNLLNISFRSEEVA; PKNLLNISFRSEEVAF;
KNLLNISFRSEEVAFL; NLLNISFRSEEVAFLA; LLNISFRSEEVAFLAG;
LNISFRSEEVAFLAGY; NISFRSEEVAFLAGYF; ISFRSEEVAFLAGYFA;

	SFRSEEVAFLAGYFAS; FRSEEVAFLAGYFASK; RSEEVAFLAGYFASKA; SEEVAFLAGYFASKAS; EEVAFLAGYFASKASK; EVAFLAGYFASKASKT; VAFLAGYFASKASKTG; AFLAGYFASKASKTGK; FLAGYFASKASKTGKI; LAGYFASKASKTGKIG; AGYFASKASKTGKIGF; GYFASKASKTGKIGFV; YFASKASKTGKIGFVG; FASKASKTGKIGFVGG; ASKASKTGKIGFVGGV; SKASKTGKIGFVGGVR; KASKTGKIGFVGGVRG; ASKTGKIGFVGGVRGK; SKTGKIGFVGGVRGKV; KTGKIGFVGGVRGKVL; TGKIGFVGGVRGKVLE; GKIGFVGGVRGKVLES; KIGFVGGVRGKVLESF; IGFVGGVRGKVLESFM; GFVGGVRGKVLESFMY; FVGGVRGKVLESFMYG; VGGVRGKVLESFMYGY; GGVRGKVLESFMYGYE; GVRGKVLESFMYGYEA; VRGKVLESFMYGYEAG; RGKVLESFMYGYEAGA; GKVLESFMYGYEAGAK; KVLESFMYGYEAGAKY; VLESFMYGYEAGAKYA; LESFMYGYEAGAKYAN; ESFMYGYEAGAKYANS; SFMYGYEAGAKYANSN; FMYGYEAGAKYANSNI; MYGYEAGAKYANSNIK; YGYEAGAKYANSNIKV; GYEAGAKYANSNIKVV; YEAGAKYANSNIKVVS; EAGAKYANSNIKVVSQ; AGAKYANSNIKVVSQY; GAKYANSNIKVVSQYV; AKYANSNIKVVSQYVG; KYANSNIKVVSQYVGT; YANSNIKVVSQYVGTF; ANSNIKVVSQYVGTFG; NSNIKVVSQYVGTFGD; SNIKVVSQYVGTFGDF; NIKVVSQYVGTFGDFG; IKVVSQYVGTFGDFGL; KVVSQYVGTFGDFGLG; VVSQYVGTFGDFGLGR; VSQYVGTFGDFGLGRS; SQYVGTFGDFGLGRST; QYVGTFGDFGLGRSTA; YVGTFGDFGLGRSTAS; VGTFGDFGLGRSTASN; GTFGDFGLGRSTASNM; TFGDFGLGRSTASNMY; FGDFGLGRSTASNMYR; GDFGLGRSTASNMYRD; DFGLGRSTASNMYRDG; FGLGRSTASNMYRDGV; GLGRSTASNMYRDGVD; LGRSTASNMYRDGVDI; GRSTASNMYRDGVDII; RSTASNMYRDGVDIIF; STASNMYRDGVDIIFA; TASNMYRDGVDIIFAA; ASNMYRDGVDIIFAAA; SNMYRDGVDIIFAAAG; NMYRDGVDIIFAAAGL; MYRDGVDIIFAAAGLS; YRDGVDIIFAAAGLSG; RDGVDIIFAAAGLSGI; DGVDIIFAAAGLSGIG; GVDIIFAAAGLSGIGV; VDIIFAAAGLSGIGVI; DIIFAAAGLSGIGVIE; IIFAAAGLSGIGVIEA; IFAAAGLSGIGVIEAA; FAAAGLSGIGVIEAAK; AAAGLSGIGVIEAAKE; AAGLSGIGVIEAAKEL; AGLSGIGVIEAAKELG; GLSGIGVIEAAKELGP; LSGIGVIEAAKELGPD; SGIGVIEAAKELGPDH; GIGVIEAAKELGPDHY; IGVIEAAKELGPDHYI; GVIEAAKELGPDHYII; VIEAAKELGPDHYIIG; IEAAKELGPDHYIIGV; EAAKELGPDHYIIGVD; AAKELGPDHYIIGVDQ; AKELGPDHYIIGVDQD; KELGPDHYIIGVDQDQ; ELGPDHYIIGVDQDQS; LGPDHYIIGVDQDQSY; GPDHYIIGVDQDQSYL; PDHYIIGVDQDQSYLA; DHYIIGVDQDQSYLAP; HYIIGVDQDQSYLAPN; YIIGVDQDQSYLAPNN; IIGVDQDQSYLAPNNV; IGVDQDQSYLAPNNVI; GVDQDQSYLAPNNVIV; VDQDQSYLAPNNVIVS; DQDQSYLAPNNVIVSA; QDQSYLAPNNVIVSAV; DQSYLAPNNVIVSAVK; QSYLAPNNVIVSAVKK; SYLAPNNVIVSAVKKV; YLAPNNVIVSAVKKVD; LAPNNVIVSAVKKVDS; APNNVIVSAVKKVDSL; PNNVIVSAVKKVDSLM; NNVIVSAVKKVDSLMY; NVIVSAVKKVDSLMYS; VIVSAVKKVDSLMYSL; IVSAVKKVDSLMYSLT; VSAVKKVDSLMYSLTK; SAVKKVDSLMYSLTKK; AVKKVDSLMYSLTKKY; VKKVDSLMYSLTKKYL; KKVDSLMYSLTKKYLE; KVDSLMYSLTKKYLET; VDSLMYSLTKKYLETG; DSLMYSLTKKYLETGV; SLMYSLTKKYLETGVL; LMYSLTKKYLETGVLD; MYSLTKKYLETGVLDG; YSLTKKYLETGVLDGG; SLTKKYLETGVLDGGK; LTKKYLETGVLDGGKT; TKKYLETGVLDGGKTM; KKYLETGVLDGGKTMF; KYLETGVLDGGKTMFL; YLETGVLDGGKTMFLG; LETGVLDGGKTMFLGL; ETGVLDGGKTMFLGLK; TGVLDGGKTMFLGLKE; GVLDGGKTMFLGLKED; VLDGGKTMFLGLKEDG; LDGGKTMFLGLKEDGL; DGGKTMFLGLKEDGLG; GGKTMFLGLKEDGLGL; GKTMFLGLKEDGLGLV; KTMFLGLKEDGLGLVL; TMFLGLKEDGLGLVLN; MFLGLKEDGLGLVLNE; FLGLKEDGLGLVLNEN; LGLKEDGLGLVLNENL; GLKEDGLGLVLNENLK; LKEDGLGLVLNENLKS; KEDGLGLVLNENLKSN; EDGLGLVLNENLKSNY; DGLGLVLNENLKSNYS; GLGLVLNENLKSNYSE; LGLVLNENLKSNYSEI; GLVLNENLKSNYSEIY; LVLNENLKSNYSEIYN; VLNENLKSNYSEIYNK; LNENLKSNYSEIYNKS; NENLKSNYSEIYNKSL; ENLKSNYSEIYNKSLK; NLKSNYSEIYNKSLKI; LKSNYSEIYNKSLKIG;

	KSNYSEIYNKSLKIGQ; SNYSEIYNKSLKIGQS; NYSEIYNKSLKIGQSI; YSEIYNKSLKIGQSIM; SEIYNKSLKIGQSIMN; EIYNKSLKIGQSIMNG; IYNKSLKIGQSIMNGI; YNKSLKIGQSIMNGII; NKSLKIGQSIMNGIIK; KSLKIGQSIMNGIIKV; SLKIGQSIMNGIIKVP; LKIGQSIMNGIIKVPY; KIGQSIMNGIIKVPYD; IGQSIMNGIIKVPYDK; GQSIMNGIIKVPYDKV; QSIMNGIIKVPYDKVS; SIMNGIIKVPYDKVSY; IMNGIIKVPYDKVSYF; MNGIIKVPYDKVSYFV; NGIIKVPYDKVSYFVL; GIIKVPYDKVSYFVLQ; IIKVPYDKVSYFVLQM; IKVPYDKVSYFVLQME; KVPYDKVSYFVLQMEN;
AAC70056.1 Decorin binding protein A; DbpA [Borrelia afzelii	13 mers: MIKYNKIILTLTL; IKYNKIILTLTLL; KYNKIILTLTLLA; YNKIILTLTLLAS; NKIILTLTLLASL; KIILTLTLLASLL; IILTLTLLASLLA; ILTLTLLASLLAA; LTLTLLASLLAAC; TLTLLASLLAACS; LTLLASLLAACSL; TLLASLLAACSLT; LLASLLAACSLTG; LASLLAACSLTGK; ASLLAACSLTGKA; SLLAACSLTGKAR; LLAACSLTGKARL; LAACSLTGKARLE; AACSLTGKARLES; ACSLTGKARLESS; CSLTGKARLESSV; SLTGKARLESSVK; LTGKARLESSVKD; TGKARLESSVKDI; GKARLESSVKDIT; KARLESSVKDITN; ARLESSVKDITNE; RLESSVKDITNEI; LESSVKDITNEIE; ESSVKDITNEIEK; SSVKDITNEIEKA; SVKDITNEIEKAI; VKDITNEIEKAIK; KDITNEIEKAIKE; DITNEIEKAIKEA; ITNEIEKAIKEAE; TNEIEKAIKEAED; NEIEKAIKEAEDA; EIEKAIKEAEDAG; IEKAIKEAEDAGV; EKAIKEAEDAGVK; KAIKEAEDAGVKT; AIKEAEDAGVKTD; IKEAEDAGVKTDA; KEAEDAGVKTDAF; EAEDAGVKTDAFT; AEDAGVKTDAFTE; EDAGVKTDAFTET; DAGVKTDAFTETQ; AGVKTDAFTETQT; GVKTDAFTETQTG; VKTDAFTETQTGG; KTDAFTETQTGGK; TDAFTETQTGGKV; DAFTETQTGGKVG; AFTETQTGGKVGG; FTETQTGGKVGGS; TETQTGGKVGGSQ; ETQTGGKVGGSQI; TQTGGKVGGSQIR; QTGGKVGGSQIRA; TGGKVGGSQIRAA; GGKVGGSQIRAAK; GKVGGSQIRAAKI; KVGGSQIRAAKIR; VGGSQIRAAKIRV; GGSQIRAAKIRVA; GSQIRAAKIRVAD; SQIRAAKIRVADL; QIRAAKIRVADLT; IRAAKIRVADLTI; RAAKIRVADLTIK; AAKIRVADLTIKF; AKIRVADLTIKFL; KIRVADLTIKFLE; IRVADLTIKFLEA; RVADLTIKFLEAT; VADLTIKFLEATE; ADLTIKFLEATEE; DLTIKFLEATEEE; LTIKFLEATEEET; TIKFLEATEEETI; IKFLEATEEETIT; KFLEATEEETITF; FLEATEEETITFK; LEATEEETITFKE; EATEEETITFKEN; ATEEETITFKENG; TEEETITFKENGA; EEETITFKENGAG; EETITFKENGAGE; ETITFKENGAGEE; TITFKENGAGEED; ITFKENGAGEEDF; TFKENGAGEEDFS; FKENGAGEEDFSG; KENGAGEEDFSGI; ENGAGEEDFSGIY; NGAGEEDFSGIYD; GAGEEDFSGIYDL; AGEEDFSGIYDLI; GEEDFSGIYDLIL; EEDFSGIYDLILN; EDFSGIYDLILNA; DFSGIYDLILNAA; FSGIYDLILNAAK; SGIYDLILNAAKA; GIYDLILNAAKAV; IYDLILNAAKAVE; YDLILNAAKAVEK; DLILNAAKAVEKI; LILNAAKAVEKIG; ILNAAKAVEKIGM; LNAAKAVEKIGMQ; NAAKAVEKIGMQG; AAKAVEKIGMQGM; AKAVEKIGMQGMK; KAVEKIGMQGMKQ; AVEKIGMQGMKQA; VEKIGMQGMKQAV; EKIGMQGMKQAVE; KIGMQGMKQAVEE; IGMQGMKQAVEEA; GMQGMKQAVEEAA; MQGMKQAVEEAAK; QGMKQAVEEAAKE; GMKQAVEEAAKEK; MKQAVEEAAKEKP; KQAVEEAAKEKPK; QAVEEAAKEKPKT; AVEEAAKEKPKTT; VEEAAKEKPKTTA; EEAAKEKPKTTAD; EAAKEKPKTTADG; AAKEKPKTTADGI; AKEKPKTTADGII; KEKPKTTADGIIA; EKPKTTADGIIAI; KPKTTADGIIAIV; PKTTADGIIAIVK; KTTADGIIAIVKV; TTADGIIAIVKVM; TADGIIAIVKVMK; ADGIIAIVKVMKA; DGIIAIVKVMKAK; GIIAIVKVMKAKV; IIAIVKVMKAKVE; IAIVKVMKAKVEN; AIVKVMKAKVENI; IVKVMKAKVENIK; VKVMKAKVENIKE; KVMKAKVENIKEK; VMKAKVENIKEKQ; MKAKVENIKEKQT; KAKVENIKEKQTK; AKVENIKEKQTKN; KVENIKEKQTKNQ; VENIKEKQTKNQK; 14 mers: MIKYNKIILTLTLL; IKYNKIILTLTLLA; KYNKIILTLTLLAS; YNKIILTLTLLASL; NKIILTLTLLASLL; KIILTLTLLASLLA; IILTLTLLASLLAA; ILTLTLLASLLAAC; LTLTLLASLLAACS; TLTLLASLLAACSL; LTLLASLLAACSLT; TLLASLLAACSLTG;

LLASLLAACSLTGK; LASLLAACSLTGKA; ASLLAACSLTGKAR;
SLLAACSLTGKARL; LLAACSLTGKARLE; LAACSLTGKARLES;
AACSLTGKARLESS; ACSLTGKARLESSV; CSLTGKARLESSVK;
SLTGKARLESSVKD; LTGKARLESSVKDI; TGKARLESSVKDIT;
GKARLESSVKDITN; KARLESSVKDITNE; ARLESSVKDITNEI;
RLESSVKDITNEIE; LESSVKDITNEIEK; ESSVKDITNEIEKA;
SSVKDITNEIEKAI; SVKDITNEIEKAIK; VKDITNEIEKAIKE;
KDITNEIEKAIKEA; DITNEIEKAIKEAE; ITNEIEKAIKEAED;
TNEIEKAIKEAEDA; NEIEKAIKEAEDAG; EIEKAIKEAEDAGV;
IEKAIKEAEDAGVK; EKAIKEAEDAGVKT; KAIKEAEDAGVKTD;
AIKEAEDAGVKTDA; IKEAEDAGVKTDAF; KEAEDAGVKTDAFT;
EAEDAGVKTDAFTE; AEDAGVKTDAFTET; EDAGVKTDAFTETQ;
DAGVKTDAFTETQT; AGVKTDAFTETQTG; GVKTDAFTETQTGG;
VKTDAFTETQTGGK; KTDAFTETQTGGKV; TDAFTETQTGGKVG;
DAFTETQTGGKVGG; AFTETQTGGKVGGS; FTETQTGGKVGGSQ;
TETQTGGKVGGSQI; ETQTGGKVGGSQIR; TQTGGKVGGSQIRA;
QTGGKVGGSQIRAA; TGGKVGGSQIRAAK; GGKVGGSQIRAAKI;
GKVGGSQIRAAKIR; KVGGSQIRAAKIRV; VGGSQIRAAKIRVA;
GGSQIRAAKIRVAD; GSQIRAAKIRVADL; SQIRAAKIRVADLT;
QIRAAKIRVADLTI; IRAAKIRVADLTIK; RAAKIRVADLTIKF;
AAKIRVADLTIKFL; AKIRVADLTIKFLE; KIRVADLTIKFLEA;
IRVADLTIKFLEAT; RVADLTIKFLEATE; VADLTIKFLEATEE;
ADLTIKFLEATEEE; DLTIKFLEATEEET; LTIKFLEATEEETI;
TIKFLEATEEETIT; IKFLEATEEETITF; KFLEATEEETITFK;
FLEATEEETITFKE; LEATEEETITFKEN; EATEEETITFKENG;
ATEEETITFKENGA; TEEETITFKENGAG; EEETITFKENGAGE;
EETITFKENGAGEE; ETITFKENGAGEED; TITFKENGAGEEDF;
ITFKENGAGEEDFS; TFKENGAGEEDFSG; FKENGAGEEDFSGI;
KENGAGEEDFSGIY; ENGAGEEDFSGIYD; NGAGEEDFSGIYDL;
GAGEEDFSGIYDLI; AGEEDFSGIYDLIL; GEEDFSGIYDLILN;
EEDFSGIYDLILNA; EDFSGIYDLILNAA; DFSGIYDLILNAAK;
FSGIYDLILNAAKA; SGIYDLILNAAKAV; GIYDLILNAAKAVE;
IYDLILNAAKAVEK; YDLILNAAKAVEKI; DLILNAAKAVEKIG;
LILNAAKAVEKIGM; ILNAAKAVEKIGMQ; LNAAKAVEKIGMQG;
NAAKAVEKIGMQGM; AAKAVEKIGMQGMK; AKAVEKIGMQGMKQ;
KAVEKIGMQGMKQA; AVEKIGMQGMKQAV; VEKIGMQGMKQAVE;
EKIGMQGMKQAVEE; KIGMQGMKQAVEEA; IGMQGMKQAVEEAA;
GMQGMKQAVEEAAK; MQGMKQAVEEAAKE; QGMKQAVEEAAKEK;
GMKQAVEEAAKEKP; MKQAVEEAAKEKPK; KQAVEEAAKEKPKT;
QAVEEAAKEKPKTT; AVEEAAKEKPKTTA; VEEAAKEKPKTTAD;
EEAAKEKPKTTADG; EAAKEKPKTTADGI; AAKEKPKTTADGII;
AKEKPKTTADGIIA; KEKPKTTADGIIAI; EKPKTTADGIIAIV;
KPKTTADGIIAIVK; PKTTADGIIAIVKV; KTTADGIIAIVKVM;
TTADGIIAIVKVMK; TADGIIAIVKVMKA; ADGIIAIVKVMKAK;
DGIIAIVKVMKAKV; GIIAIVKVMKAKVE; IIAIVKVMKAKVEN;
IAIVKVMKAKVENI; AIVKVMKAKVENIK; IVKVMKAKVENIKE;
VKVMKAKVENIKEK; KVMKAKVENIKEKQ; VMKAKVENIKEKQT;
MKAKVENIKEKQTK; KAKVENIKEKQTKN; AKVENIKEKQTKNQ;
KVENIKEKQTKNQK;

15 mers:
MIKYNKIILTLTLLA; IKYNKIILTLTLLAS; KYNKIILTLTLLASL;
YNKIILTLTLLASLL; NKIILTLTLLASLLA; KIILTLTLLASLLAA;
IILTLTLLASLLAAC; ILTLTLLASLLAACS; LTLTLLASLLAACSL;
TLTLLASLLAACSLT; LTLLASLLAACSLTG; TLLASLLAACSLTGK;
LLASLLAACSLTGKA; LASLLAACSLTGKAR; ASLLAACSLTGKARL;
SLLAACSLTGKARLE; LLAACSLTGKARLES; LAACSLTGKARLESS;

AACSLTGKARLESSV; ACSLTGKARLESSVK; CSLTGKARLESSVKD;
SLTGKARLESSVKDI; LTGKARLESSVKDIT; TGKARLESSVKDITN;
GKARLESSVKDITNE; KARLESSVKDITNEI; ARLESSVKDITNEIE;
RLESSVKDITNEIEK; LESSVKDITNEIEKA; ESSVKDITNEIEKAI;
SSVKDITNEIEKAIK; SVKDITNEIEKAIKE; VKDITNEIEKAIKEA;
KDITNEIEKAIKEAE; DITNEIEKAIKEAED; ITNEIEKAIKEAEDA;
TNEIEKAIKEAEDAG; NEIEKAIKEAEDAGV; EIEKAIKEAEDAGVK;
IEKAIKEAEDAGVKT; EKAIKEAEDAGVKTD; KAIKEAEDAGVKTDA;
AIKEAEDAGVKTDAF; IKEAEDAGVKTDAFT; KEAEDAGVKTDAFTE;
EAEDAGVKTDAFTET; AEDAGVKTDAFTETQ; EDAGVKTDAFTETQT;
DAGVKTDAFTETQTG; AGVKTDAFTETQTGG; GVKTDAFTETQTGGK;
VKTDAFTETQTGGKV; KTDAFTETQTGGKVG; TDAFTETQTGGKVGG;
DAFTETQTGGKVGGS; AFTETQTGGKVGGSQ; FTETQTGGKVGGSQI;
TETQTGGKVGGSQIR; ETQTGGKVGGSQIRA; TQTGGKVGGSQIRAA;
QTGGKVGGSQIRAAK; TGGKVGGSQIRAAKI; GGKVGGSQIRAAKIR;
GKVGGSQIRAAKIRV; KVGGSQIRAAKIRVA; VGGSQIRAAKIRVAD;
GGSQIRAAKIRVADL; GSQIRAAKIRVADLT; SQIRAAKIRVADLTI;
QIRAAKIRVADLTIK; IRAAKIRVADLTIKF; RAAKIRVADLTIKFL;
AAKIRVADLTIKFLE; AKIRVADLTIKFLEA; KIRVADLTIKFLEAT;
IRVADLTIKFLEATE; RVADLTIKFLEATEE; VADLTIKFLEATEEE;
ADLTIKFLEATEEET; DLTIKFLEATEEETI; LTIKFLEATEEETIT;
TIKFLEATEEETITF; IKFLEATEEETITFK; KFLEATEEETITFKE;
FLEATEEETITFKEN; LEATEEETITFKENG; EATEEETITFKENGA;
ATEEETITFKENGAG; TEEETITFKENGAGE; EEETITFKENGAGEE;
EETITFKENGAGEED; ETITFKENGAGEEDF; TITFKENGAGEEDFS;
ITFKENGAGEEDFSG; TFKENGAGEEDFSGI; FKENGAGEEDFSGIY;
KENGAGEEDFSGIYD; ENGAGEEDFSGIYDL; NGAGEEDFSGIYDLI;
GAGEEDFSGIYDLIL; AGEEDFSGIYDLILN; GEEDFSGIYDLILNA;
EEDFSGIYDLILNAA; EDFSGIYDLILNAAK; DFSGIYDLILNAAKA;
FSGIYDLILNAAKAV; SGIYDLILNAAKAVE; GIYDLILNAAKAVEK;
IYDLILNAAKAVEKI; YDLILNAAKAVEKIG; DLILNAAKAVEKIGM;
LILNAAKAVEKIGMQ; ILNAAKAVEKIGMQG; LNAAKAVEKIGMQGM;
NAAKAVEKIGMQGMK; AAKAVEKIGMQGMKQ; AKAVEKIGMQGMKQA;
KAVEKIGMQGMKQAV; AVEKIGMQGMKQAVE; VEKIGMQGMKQAVEE;
EKIGMQGMKQAVEEA; KIGMQGMKQAVEEAA; IGMQGMKQAVEEAAK;
GMQGMKQAVEEAAKE; MQGMKQAVEEAAKEK; QGMKQAVEEAAKEKP;
GMKQAVEEAAKEKPK; MKQAVEEAAKEKPKT; KQAVEEAAKEKPKTT;
QAVEEAAKEKPKTTA; AVEEAAKEKPKTTAD; VEEAAKEKPKTTADG;
EEAAKEKPKTTADGI; EAAKEKPKTTADGII; AAKEKPKTTADGIIA;
AKEKPKTTADGIIAI; KEKPKTTADGIIAIV; EKPKTTADGIIAIVK;
KPKTTADGIIAIVKV; PKTTADGIIAIVKVM; KTTADGIIAIVKVMK;
TTADGIIAIVKVMKA; TADGIIAIVKVMKAK; ADGIIAIVKVMKAKV;
DGIIAIVKVMKAKVE; GIIAIVKVMKAKVEN; IIAIVKVMKAKVENI;
IAIVKVMKAKVENIK; AIVKVMKAKVENIKE; IVKVMKAKVENIKEK;
VKVMKAKVENIKEKQ; KVMKAKVENIKEKQT; VMKAKVENIKEKQTK;
MKAKVENIKEKQTKN; KAKVENIKEKQTKNQ; AKVENIKEKQTKNQK;

16 mers:
MIKYNKIILTLTLLAS; IKYNKIILTLTLLASL; KYNKIILTLTLLASLL;
YNKIILTLTLLASLLA; NKIILTLTLLASLLAA; KIILTLTLLASLLAAC;
IILTLTLLASLLAACS; ILTLTLLASLLAACSL; LTLTLLASLLAACSLT;
TLTLLASLLAACSLTG; LTLLASLLAACSLTGK; TLLASLLAACSLTGKA;
LLASLLAACSLTGKAR; LASLLAACSLTGKARL; ASLLAACSLTGKARLE;
SLLAACSLTGKARLES; LLAACSLTGKARLESS; LAACSLTGKARLESSV;
AACSLTGKARLESSVK; ACSLTGKARLESSVKD; CSLTGKARLESSVKDI;
SLTGKARLESSVKDIT; LTGKARLESSVKDITN; TGKARLESSVKDITNE;
GKARLESSVKDITNEI; KARLESSVKDITNEIE; ARLESSVKDITNEIEK;

	RLESSVKDITNEIEKA; LESSVKDITNEIEKAI; ESSVKDITNEIEKAIK; SSVKDITNEIEKAIKE; SVKDITNEIEKAIKEA; VKDITNEIEKAIKEAE; KDITNEIEKAIKEAED; DITNEIEKAIKEAEDA; ITNEIEKAIKEAEDAG; TNEIEKAIKEAEDAGV; NEIEKAIKEAEDAGVK; EIEKAIKEAEDAGVKT; IEKAIKEAEDAGVKTD; EKAIKEAEDAGVKTDA; KAIKEAEDAGVKTDAF; AIKEAEDAGVKTDAFT; IKEAEDAGVKTDAFTE; KEAEDAGVKTDAFTET; EAEDAGVKTDAFTETQ; AEDAGVKTDAFTETQT; EDAGVKTDAFTETQTG; DAGVKTDAFTETQTGG; AGVKTDAFTETQTGGK; GVKTDAFTETQTGGKV; VKTDAFTETQTGGKVG; KTDAFTETQTGGKVGG; TDAFTETQTGGKVGGS; DAFTETQTGGKVGGSQ; AFTETQTGGKVGGSQI; FTETQTGGKVGGSQIR; TETQTGGKVGGSQIRA; ETQTGGKVGGSQIRAA; TQTGGKVGGSQIRAAK; QTGGKVGGSQIRAAKI; TGGKVGGSQIRAAKIR; GGKVGGSQIRAAKIRV; GKVGGSQIRAAKIRVA; KVGGSQIRAAKIRVAD; VGGSQIRAAKIRVADL; GGSQIRAAKIRVADLT; GSQIRAAKIRVADLTI; SQIRAAKIRVADLTIK; QIRAAKIRVADLTIKF; IRAAKIRVADLTIKFL; RAAKIRVADLTIKFLE; AAKIRVADLTIKFLEA; AKIRVADLTIKFLEAT; KIRVADLTIKFLEATE; IRVADLTIKFLEATEE; RVADLTIKFLEATEEE; VADLTIKFLEATEEET; ADLTIKFLEATEEETI; DLTIKFLEATEEETIT; LTIKFLEATEEETITF; TIKFLEATEEETITFK; IKFLEATEEETITFKE; KFLEATEEETITFKEN; FLEATEEETITFKENG; LEATEEETITFKENGA; EATEEETITFKENGAG; ATEEETITFKENGAGE; TEEETITFKENGAGEE; EEETITFKENGAGEED; EETITFKENGAGEEDF; ETITFKENGAGEEDFS; TITFKENGAGEEDFSG; ITFKENGAGEEDFSGI; TFKENGAGEEDFSGIY; FKENGAGEEDFSGIYD; KENGAGEEDFSGIYDL; ENGAGEEDFSGIYDLI; NGAGEEDFSGIYDLIL; GAGEEDFSGIYDLILN; AGEEDFSGIYDLILNA; GEEDFSGIYDLILNAA; EEDFSGIYDLILNAAK; EDFSGIYDLILNAAKA; DFSGIYDLILNAAKAV; FSGIYDLILNAAKAVE; SGIYDLILNAAKAVEK; GIYDLILNAAKAVEKI; IYDLILNAAKAVEKIG; YDLILNAAKAVEKIGM; DLILNAAKAVEKIGMQ; LILNAAKAVEKIGMQG; ILNAAKAVEKIGMQGM; LNAAKAVEKIGMQGMK; NAAKAVEKIGMQGMKQ; AAKAVEKIGMQGMKQA; AKAVEKIGMQGMKQAV; KAVEKIGMQGMKQAVE; AVEKIGMQGMKQAVEE; VEKIGMQGMKQAVEEA; EKIGMQGMKQAVEEAA; KIGMQGMKQAVEEAAK; IGMQGMKQAVEEAAKE; GMQGMKQAVEEAAKEK; MQGMKQAVEEAAKEKP; QGMKQAVEEAAKEKPK; GMKQAVEEAAKEKPKT; MKQAVEEAAKEKPKTT; KQAVEEAAKEKPKTTA; QAVEEAAKEKPKTTAD; AVEEAAKEKPKTTADG; VEEAAKEKPKTTADGI; EEAAKEKPKTTADGII; EAAKEKPKTTADGIIA; AAKEKPKTTADGIIAI; AKEKPKTTADGIIAIV; KEKPKTTADGIIAIVK; EKPKTTADGIIAIVKV; KPKTTADGIIAIVKVM; PKTTADGIIAIVKVMK; KTTADGIIAIVKVMKA; TTADGIIAIVKVMKAK; TADGIIAIVKVMKAKV; ADGIIAIVKVMKAKVE; DGIIAIVKVMKAKVEN; GIIAIVKVMKAKVENI; IIAIVKVMKAKVENIK; IAIVKVMKAKVENIKE; AIVKVMKAKVENIKEK; IVKVMKAKVENIKEKQ; VKVMKAKVENIKEKQT; KVMKAKVENIKEKQTK; VMKAKVENIKEKQTKN; MKAKVENIKEKQTKNQ; KAKVENIKEKQTKNQK;
AAC70057.1 Decorin binding protein A; DbpA [Borrelia garinii]	13 mers: MIKYNKILLKLSL; IKYNKILLKLSLI; KYNKILLKLSLIV; YNKILLKLSLIVS; NKILLKLSLIVSL; KILLKLSLIVSLL; ILLKLSLIVSLLV; LLKLSLIVSLLVA; LKLSLIVSLLVAC; KLSLIVSLLVACG; LSLIVSLLVACGL; SLIVSLLVACGLT; LIVSLLVACGLTG; IVSLLVACGLTGE; VSLLVACGLTGET; SLLVACGLTGETK; LLVACGLTGETKI; LVACGLTGETKIR; VACGLTGETKIRL; ACGLTGETKIRLE; CGLTGETKIRLES; GLTGETKIRLESS; LTGETKIRLESSA; TGETKIRLESSAQ; GETKIRLESSAQE; ETKIRLESSAQEI; TKIRLESSAQEIK; KIRLESSAQEIKD; IRLESSAQEIKDE; RLESSAQEIKDEI; LESSAQEIKDEIN; ESSAQEIKDEINK; SSAQEIKDEINKI; SAQEIKDEINKIK; AQEIKDEINKIKA; QEIKDEINKIKAN; EIKDEINKIKANA; IKDEINKIKANAK; KDEINKIKANAKK; DEINKIKANAKKE; EINKIKANAKKEG; INKIKANAKKEGV; NKIKANAKKEGVK; KIKANAKKEGVKF;

IKANAKKEGVKFE; KANAKKEGVKFEA; ANAKKEGVKFEAF; NAKKEGVKFEAFT; AKKEGVKFEAFTN; KKEGVKFEAFTNT; KEGVKFEAFTNTQ; EGVKFEAFTNTQT; GVKFEAFTNTQTG; VKFEAFTNTQTGS; KFEAFTNTQTGSK; FEAFTNTQTGSKI; EAFTNTQTGSKIS; AFTNTQTGSKISE; FTNTQTGSKISEK; TNTQTGSKISEKP; NTQTGSKISEKPE; TQTGSKISEKPEF; QTGSKISEKPEFI; TGSKISEKPEFIL; GSKISEKPEFILK; SKISEKPEFILKA; KISEKPEFILKAK; ISEKPEFILKAKI; SEKPEFILKAKIK; EKPEFILKAKIKA; KPEFILKAKIKAI; PEFILKAKIKAIQ; EFILKAKIKAIQV; FILKAKIKAIQVA; ILKAKIKAIQVAE; LKAKIKAIQVAER; KAKIKAIQVAERF; AKIKAIQVAERFV; KIKAIQVAERFVK; IKAIQVAERFVKA; KAIQVAERFVKAI; AIQVAERFVKAIK; IQVAERFVKAIKE; QVAERFVKAIKEE; VAERFVKAIKEEA; AERFVKAIKEEAE; ERFVKAIKEEAEK; RFVKAIKEEAEKL; FVKAIKEEAEKLK; VKAIKEEAEKLKK; KAIKEEAEKLKKS; AIKEEAEKLKKSG; IKEEAEKLKKSGS; KEEAEKLKKSGSS; EEAEKLKKSGSSG; EAEKLKKSGSSGA; AEKLKKSGSSGAF; EKLKKSGSSGAFS; KLKKSGSSGAFSA; LKKSGSSGAFSAM; KKSGSSGAFSAMY; KSGSSGAFSAMYD; SGSSGAFSAMYDL; GSSGAFSAMYDLM; SSGAFSAMYDLMI; SGAFSAMYDLMID; GAFSAMYDLMIDV; AFSAMYDLMIDVS; FSAMYDLMIDVSK; SAMYDLMIDVSKP; AMYDLMIDVSKPL; MYDLMIDVSKPLE; YDLMIDVSKPLEE; DLMIDVSKPLEEI; LMIDVSKPLEEIG; MIDVSKPLEEIGI; IDVSKPLEEIGIQ; DVSKPLEEIGIQK; VSKPLEEIGIQKM; SKPLEEIGIQKMT; KPLEEIGIQKMTG; PLEEIGIQKMTGT; LEEIGIQKMTGTV; EEIGIQKMTGTVT; EIGIQKMTGTVTK; IGIQKMTGTVTKE; GIQKMTGTVTKEA; IQKMTGTVTKEAE; QKMTGTVTKEAEK; KMTGTVTKEAEKT; MTGTVTKEAEKTP; TGTVTKEAEKTPP; GTVTKEAEKTPPT; TVTKEAEKTPPTT; VTKEAEKTPPTTA; TKEAEKTPPTTAD; KEAEKTPPTTADG; EAEKTPPTTADGI; AEKTPPTTADGII; EKTPPTTADGIIA; KTPPTTADGIIAI; TPPTTADGIIAIA; PPTTADGIIAIAQ; PTTADGIIAIAQA; TTADGIIAIAQAM; TADGIIAIAQAME; ADGIIAIAQAMEE; DGIIAIAQAMEEK; GIIAIAQAMEEKL; IIAIAQAMEEKLN; IAIAQAMEEKLNN; AIAQAMEEKLNNV; IAQAMEEKLNNVN; AQAMEEKLNNVNK; QAMEEKLNNVNKK; AMEEKLNNVNKKQ; MEEKLNNVNKKQH; EEKLNNVNKKQHD; EKLNNVNKKQHDA; KLNNVNKKQHDAL; LNNVNKKQHDALK; NNVNKKQHDALKN; NVNKKQHDALKNL; VNKKQHDALKNLE; NKKQHDALKNLEE; KKQHDALKNLEEK; KQHDALKNLEEKA; QHDALKNLEEKAN; HDALKNLEEKANT; DALKNLEEKANTA; ALKNLEEKANTAA; LKNLEEKANTAAT; KNLEEKANTAATT; NLEEKANTAATTT;

14 mers:
MIKYNKILLKLSLI; IKYNKILLKLSLIV; KYNKILLKLSLIVS; YNKILLKLSLIVSL; NKILLKLSLIVSLL; KILLKLSLIVSLLV; ILLKLSLIVSLLVA; LLKLSLIVSLLVAC; LKLSLIVSLLVACG; KLSLIVSLLVACGL; LSLIVSLLVACGLT; SLIVSLLVACGLTG; LIVSLLVACGLTGE; IVSLLVACGLTGET; VSLLVACGLTGETK; SLLVACGLTGETKI; LLVACGLTGETKIR; LVACGLTGETKIRL; VACGLTGETKIRLE; ACGLTGETKIRLES; CGLTGETKIRLESS; GLTGETKIRLESSA; LTGETKIRLESSAQ; TGETKIRLESSAQE; GETKIRLESSAQEI; ETKIRLESSAQEIK; TKIRLESSAQEIKD; KIRLESSAQEIKDE; IRLESSAQEIKDEI; RLESSAQEIKDEIN; LESSAQEIKDEINK; ESSAQEIKDEINKI; SSAQEIKDEINKIK; SAQEIKDEINKIKA; AQEIKDEINKIKAN; QEIKDEINKIKANA; EIKDEINKIKANAK; IKDEINKIKANAKK; KDEINKIKANAKKE; DEINKIKANAKKEG; EINKIKANAKKEGV; INKIKANAKKEGVK; NKIKANAKKEGVKF; KIKANAKKEGVKFE; IKANAKKEGVKFEA; KANAKKEGVKFEAF; ANAKKEGVKFEAFT; NAKKEGVKFEAFTN; AKKEGVKFEAFTNT; KKEGVKFEAFTNTQ; KEGVKFEAFTNTQT; EGVKFEAFTNTQTG; GVKFEAFTNTQTGS; VKFEAFTNTQTGSK; KFEAFTNTQTGSKI; FEAFTNTQTGSKIS; EAFTNTQTGSKISE; AFTNTQTGSKISEK; FTNTQTGSKISEKP; TNTQTGSKISEKPE; NTQTGSKISEKPEF; TQTGSKISEKPEFI; QTGSKISEKPEFIL; TGSKISEKPEFILK; GSKISEKPEFILKA; SKISEKPEFILKAK;

KISEKPEFILKAKI; ISEKPEFILKAKIK; SEKPEFILKAKIKA;
EKPEFILKAKIKAI; KPEFILKAKIKAIQ; PEFILKAKIKAIQV;
EFILKAKIKAIQVA; FILKAKIKAIQVAE; ILKAKIKAIQVAER;
LKAKIKAIQVAERF; KAKIKAIQVAERFV; AKIKAIQVAERFVK;
KIKAIQVAERFVKA; IKAIQVAERFVKAI; KAIQVAERFVKAIK;
AIQVAERFVKAIKE; IQVAERFVKAIKEE; QVAERFVKAIKEEA;
VAERFVKAIKEEAE; AERFVKAIKEEAEK; ERFVKAIKEEAEKL;
RFVKAIKEEAEKLK; FVKAIKEEAEKLKK; VKAIKEEAEKLKKS;
KAIKEEAEKLKKSG; AIKEEAEKLKKSGS; IKEEAEKLKKSGSS;
KEEAEKLKKSGSSG; EEAEKLKKSGSSGA; EAEKLKKSGSSGAF;
AEKLKKSGSSGAFS; EKLKKSGSSGAFSA; KLKKSGSSGAFSAM;
LKKSGSSGAFSAMY; KKSGSSGAFSAMYD; KSGSSGAFSAMYDL;
SGSSGAFSAMYDLM; GSSGAFSAMYDLMI; SSGAFSAMYDLMID;
SGAFSAMYDLMIDV; GAFSAMYDLMIDVS; AFSAMYDLMIDVSK;
FSAMYDLMIDVSKP; SAMYDLMIDVSKPL; AMYDLMIDVSKPLE;
MYDLMIDVSKPLEE; YDLMIDVSKPLEEI; DLMIDVSKPLEEIG;
LMIDVSKPLEEIGI; MIDVSKPLEEIGIQ; IDVSKPLEEIGIQK;
DVSKPLEEIGIQKM; VSKPLEEIGIQKMT; SKPLEEIGIQKMTG;
KPLEEIGIQKMTGT; PLEEIGIQKMTGTV; LEEIGIQKMTGTVT;
EEIGIQKMTGTVTK; EIGIQKMTGTVTKE; IGIQKMTGTVTKEA;
GIQKMTGTVTKEAE; IQKMTGTVTKEAEK; QKMTGTVTKEAEKT;
KMTGTVTKEAEKTP; MTGTVTKEAEKTPP; TGTVTKEAEKTPPT;
GTVTKEAEKTPPTT; TVTKEAEKTPPTTA; VTKEAEKTPPTTAD;
TKEAEKTPPTTADG; KEAEKTPPTTADGI; EAEKTPPTTADGII;
AEKTPPTTADGIIA; EKTPPTTADGIIAI; KTPPTTADGIIAIA;
TPPTTADGIIAIAQ; PPTTADGIIAIAQA; PTTADGIIAIAQAM;
TTADGIIAIAQAME; TADGIIAIAQAMEE; ADGIIAIAQAMEEK;
DGIIAIAQAMEEKL; GIIAIAQAMEEKLN; IIAIAQAMEEKLNN;
IAIAQAMEEKLNNV; AIAQAMEEKLNNVN; IAQAMEEKLNNVNK;
AQAMEEKLNNVNKK; QAMEEKLNNVNKKQ; AMEEKLNNVNKKQH;
MEEKLNNVNKKQHD; EEKLNNVNKKQHDA; EKLNNVNKKQHDAL;
KLNNVNKKQHDALK; LNNVNKKQHDALKN; NNVNKKQHDALKNL;
NVNKKQHDALKNLE; VNKKQHDALKNLEE; NKKQHDALKNLEEK;
KKQHDALKNLEEKA; KQHDALKNLEEKAN; QHDALKNLEEKANT;
HDALKNLEEKANTA; DALKNLEEKANTAA; ALKNLEEKANTAAT;
LKNLEEKANTAATT; KNLEEKANTAATTT;

15 mers:
MIKYNKILLKLSLIV; IKYNKILLKLSLIVS; KYNKILLKLSLIVSL;
YNKILLKLSLIVSLL; NKILLKLSLIVSLLV; KILLKLSLIVSLLVA;
ILLKLSLIVSLLVAC; LLKLSLIVSLLVACG; LKLSLIVSLLVACGL;
KLSLIVSLLVACGLT; LSLIVSLLVACGLTG; SLIVSLLVACGLTGE;
LIVSLLVACGLTGET; IVSLLVACGLTGETK; VSLLVACGLTGETKI;
SLLVACGLTGETKIR; LLVACGLTGETKIRL; LVACGLTGETKIRLE;
VACGLTGETKIRLES; ACGLTGETKIRLESS; CGLTGETKIRLESSA;
GLTGETKIRLESSAQ; LTGETKIRLESSAQE; TGETKIRLESSAQEI;
GETKIRLESSAQEIK; ETKIRLESSAQEIKD; TKIRLESSAQEIKDE;
KIRLESSAQEIKDEI; IRLESSAQEIKDEIN; RLESSAQEIKDEINK;
LESSAQEIKDEINKI; ESSAQEIKDEINKIK; SSAQEIKDEINKIKA;
SAQEIKDEINKIKAN; AQEIKDEINKIKANA; QEIKDEINKIKANAK;
EIKDEINKIKANAKK; IKDEINKIKANAKKE; KDEINKIKANAKKEG;
DEINKIKANAKKEGV; EINKIKANAKKEGVK; INKIKANAKKEGVKF;
NKIKANAKKEGVKFE; KIKANAKKEGVKFEA; IKANAKKEGVKFEAF;
KANAKKEGVKFEAFT; ANAKKEGVKFEAFTN; NAKKEGVKFEAFTNT;
AKKEGVKFEAFTNTQ; KKEGVKFEAFTNTQT; KEGVKFEAFTNTQTG;
EGVKFEAFTNTQTGS; GVKFEAFTNTQTGSK; VKFEAFTNTQTGSKI;
KFEAFTNTQTGSKIS; FEAFTNTQTGSKISE; EAFTNTQTGSKISEK;

AFTNTQTGSKISEKP; FTNTQTGSKISEKPE; TNTQTGSKISEKPEF;
NTQTGSKISEKPEFI; TQTGSKISEKPEFIL; QTGSKISEKPEFILK;
TGSKISEKPEFILKA; GSKISEKPEFILKAK; SKISEKPEFILKAKI;
KISEKPEFILKAKIK; ISEKPEFILKAKIKA; SEKPEFILKAKIKAI;
EKPEFILKAKIKAIQ; KPEFILKAKIKAIQV; PEFILKAKIKAIQVA;
EFILKAKIKAIQVAE; FILKAKIKAIQVAER; ILKAKIKAIQVAERF;
LKAKIKAIQVAERFV; KAKIKAIQVAERFVK; AKIKAIQVAERFVKA;
KIKAIQVAERFVKAI; IKAIQVAERFVKAIK; KAIQVAERFVKAIKE;
AIQVAERFVKAIKEE; IQVAERFVKAIKEEA; QVAERFVKAIKEEAE;
VAERFVKAIKEEAEK; AERFVKAIKEEAEKL; ERFVKAIKEEAEKLK;
RFVKAIKEEAEKLKK; FVKAIKEEAEKLKKS; VKAIKEEAEKLKKSG;
KAIKEEAEKLKKSGS; AIKEEAEKLKKSGSS; IKEEAEKLKKSGSSG;
KEEAEKLKKSGSSGA; EEAEKLKKSGSSGAF; EAEKLKKSGSSGAFS;
AEKLKKSGSSGAFSA; EKLKKSGSSGAFSAM; KLKKSGSSGAFSAMY;
LKKSGSSGAFSAMYD; KKSGSSGAFSAMYDL; KSGSSGAFSAMYDLM;
SGSSGAFSAMYDLMI; GSSGAFSAMYDLMID; SSGAFSAMYDLMIDV;
SGAFSAMYDLMIDVS; GAFSAMYDLMIDVSK; AFSAMYDLMIDVSKP;
FSAMYDLMIDVSKPL; SAMYDLMIDVSKPLE; AMYDLMIDVSKPLEE;
MYDLMIDVSKPLEEI; YDLMIDVSKPLEEIG; DLMIDVSKPLEEIGI;
LMIDVSKPLEEIGIQ; MIDVSKPLEEIGIQK; IDVSKPLEEIGIQKM;
DVSKPLEEIGIQKMT; VSKPLEEIGIQKMTG; SKPLEEIGIQKMTGT;
KPLEEIGIQKMTGTV; PLEEIGIQKMTGTVT; LEEIGIQKMTGTVTK;
EEIGIQKMTGTVTKE; EIGIQKMTGTVTKEA; IGIQKMTGTVTKEAE;
GIQKMTGTVTKEAEK; IQKMTGTVTKEAEKT; QKMTGTVTKEAEKTP;
KMTGTVTKEAEKTPP; MTGTVTKEAEKTPPT; TGTVTKEAEKTPPTT;
GTVTKEAEKTPPTTA; TVTKEAEKTPPTTAD; VTKEAEKTPPTTADG;
TKEAEKTPPTTADGI; KEAEKTPPTTADGII; EAEKTPPTTADGIIA;
AEKTPPTTADGIIAI; EKTPPTTADGIIAIA; KTPPTTADGIIAIAQ;
TPPTTADGIIAIAQA; PPTTADGIIAIAQAM; PTTADGIIAIAQAME;
TTADGIIAIAQAMEE; TADGIIAIAQAMEEK; ADGIIAIAQAMEEKL;
DGIIAIAQAMEEKLN; GIIAIAQAMEEKLNN; IIAIAQAMEEKLNNV;
IAIAQAMEEKLNNVN; AIAQAMEEKLNNVNK; IAQAMEEKLNNVNKK;
AQAMEEKLNNVNKKQ; QAMEEKLNNVNKKQH; AMEEKLNNVNKKQHD;
MEEKLNNVNKKQHDA; EEKLNNVNKKQHDAL; EKLNNVNKKQHDALK;
KLNNVNKKQHDALKN; LNNVNKKQHDALKNL; NNVNKKQHDALKNLE;
NVNKKQHDALKNLEE; VNKKQHDALKNLEEK; NKKQHDALKNLEEKA;
KKQHDALKNLEEKAN; KQHDALKNLEEKANT; QHDALKNLEEKANTA;
HDALKNLEEKANTAA; DALKNLEEKANTAAT; ALKNLEEKANTAATT;
LKNLEEKANTAATTT;

16 mers:
MIKYNKILLKLSLIVS; IKYNKILLKLSLIVSL; KYNKILLKLSLIVSLL;
YNKILLKLSLIVSLLV; NKILLKLSLIVSLLVA; KILLKLSLIVSLLVAC;
ILLKLSLIVSLLVACG; LLKLSLIVSLLVACGL; LKLSLIVSLLVACGLT;
KLSLIVSLLVACGLTG; LSLIVSLLVACGLTGE; SLIVSLLVACGLTGET;
LIVSLLVACGLTGETK; IVSLLVACGLTGETKI; VSLLVACGLTGETKIR;
SLLVACGLTGETKIRL; LLVACGLTGETKIRLE; LVACGLTGETKIRLES;
VACGLTGETKIRLESS; ACGLTGETKIRLESSA; CGLTGETKIRLESSAQ;
GLTGETKIRLESSAQE; LTGETKIRLESSAQEI; TGETKIRLESSAQEIK;
GETKIRLESSAQEIKD; ETKIRLESSAQEIKDE; TKIRLESSAQEIKDEI;
KIRLESSAQEIKDEIN; IRLESSAQEIKDEINK; RLESSAQEIKDEINKI;
LESSAQEIKDEINKIK; ESSAQEIKDEINKIKA; SSAQEIKDEINKIKAN;
SAQEIKDEINKIKANA; AQEIKDEINKIKANAK; QEIKDEINKIKANAKK;
EIKDEINKIKANAKKE; IKDEINKIKANAKKEG; KDEINKIKANAKKEGV;
DEINKIKANAKKEGVK; EINKIKANAKKEGVKF; INKIKANAKKEGVKFE;
NKIKANAKKEGVKFEA; KIKANAKKEGVKFEAF; IKANAKKEGVKFEAFT;
KANAKKEGVKFEAFTN; ANAKKEGVKFEAFTNT; NAKKEGVKFEAFTNTQ;

	AKKEGVKFEAFTNTQT; KKEGVKFEAFTNTQTG; KEGVKFEAFTNTQTGS; EGVKFEAFTNTQTGSK; GVKFEAFTNTQTGSKI; VKFEAFTNTQTGSKIS; KFEAFTNTQTGSKISE; FEAFTNTQTGSKISEK; EAFTNTQTGSKISEKP; AFTNTQTGSKISEKPE; FTNTQTGSKISEKPEF; TNTQTGSKISEKPEFI; NTQTGSKISEKPEFIL; TQTGSKISEKPEFILK; QTGSKISEKPEFILKA; TGSKISEKPEFILKAK; GSKISEKPEFILKAKI; SKISEKPEFILKAKIK; KISEKPEFILKAKIKA; ISEKPEFILKAKIKAI; SEKPEFILKAKIKAIQ; EKPEFILKAKIKAIQV; KPEFILKAKIKAIQVA; PEFILKAKIKAIQVAE; EFILKAKIKAIQVAER; FILKAKIKAIQVAERF; ILKAKIKAIQVAERFV; LKAKIKAIQVAERFVK; KAKIKAIQVAERFVKA; AKIKAIQVAERFVKAI; KIKAIQVAERFVKAIK; IKAIQVAERFVKAIKE; KAIQVAERFVKAIKEE; AIQVAERFVKAIKEEA; IQVAERFVKAIKEEAE; QVAERFVKAIKEEAEK; VAERFVKAIKEEAEKL; AERFVKAIKEEAEKLK; ERFVKAIKEEAEKLKK; RFVKAIKEEAEKLKKS; FVKAIKEEAEKLKKSG; VKAIKEEAEKLKKSGS; KAIKEEAEKLKKSGSS; AIKEEAEKLKKSGSSG; IKEEAEKLKKSGSSGA; KEEAEKLKKSGSSGAF; EEAEKLKKSGSSGAFS; EAEKLKKSGSSGAFSA; AEKLKKSGSSGAFSAM; EKLKKSGSSGAFSAMY; KLKKSGSSGAFSAMYD; LKKSGSSGAFSAMYDL; KKSGSSGAFSAMYDLM; KSGSSGAFSAMYDLMI; SGSSGAFSAMYDLMID; GSSGAFSAMYDLMIDV; SSGAFSAMYDLMIDVS; SGAFSAMYDLMIDVSK; GAFSAMYDLMIDVSKP; AFSAMYDLMIDVSKPL; FSAMYDLMIDVSKPLE; SAMYDLMIDVSKPLEE; AMYDLMIDVSKPLEEI; MYDLMIDVSKPLEEIG; YDLMIDVSKPLEEIGI; DLMIDVSKPLEEIGIQ; LMIDVSKPLEEIGIQK; MIDVSKPLEEIGIQKM; IDVSKPLEEIGIQKMT; DVSKPLEEIGIQKMTG; VSKPLEEIGIQKMTGT; SKPLEEIGIQKMTGTV; KPLEEIGIQKMTGTVT; PLEEIGIQKMTGTVTK; LEEIGIQKMTGTVTKE; EEIGIQKMTGTVTKEA; EIGIQKMTGTVTKEAE; IGIQKMTGTVTKEAEK; GIQKMTGTVTKEAEKT; IQKMTGTVTKEAEKTP; QKMTGTVTKEAEKTPP; KMTGTVTKEAEKTPPT; MTGTVTKEAEKTPPTT; TGTVTKEAEKTPPTTA; GTVTKEAEKTPPTTAD; TVTKEAEKTPPTTADG; VTKEAEKTPPTTADGI; TKEAEKTPPTTADGII; KEAEKTPPTTADGIIA; EAEKTPPTTADGIIAI; AEKTPPTTADGIIAIA; EKTPPTTADGIIAIAQ; KTPPTTADGIIAIAQA; TPPTTADGIIAIAQAM; PPTTADGIIAIAQAME; PTTADGIIAIAQAMEE; TTADGIIAIAQAMEEK; TADGIIAIAQAMEEKL; ADGIIAIAQAMEEKLN; DGIIAIAQAMEEKLNN; GIIAIAQAMEEKLNNV; IIAIAQAMEEKLNNVN; IAIAQAMEEKLNNVNK; AIAQAMEEKLNNVNKK; IAQAMEEKLNNVNKKQ; AQAMEEKLNNVNKKQH; QAMEEKLNNVNKKQHD; AMEEKLNNVNKKQHDA; MEEKLNNVNKKQHDAL; EEKLNNVNKKQHDALK; EKLNNVNKKQHDALKN; KLNNVNKKQHDALKNL; LNNVNKKQHDALKNLE; NNVNKKQHDALKNLEE; NVNKKQHDALKNLEEK; VNKKQHDALKNLEEKA; NKKQHDALKNLEEKAN; KKQHDALKNLEEKANT; KQHDALKNLEEKANTA; QHDALKNLEEKANTAA; HDALKNLEEKANTAAT; DALKNLEEKANTAATT; ALKNLEEKANTAATTT;
AAC70021.1 Decorin binding protein B; DbpB [Borrelia burgdorferi]	13 mers: SIVIALFFKLLVA; IVIALFFKLLVAC; VIALFFKLLVACS; IALFFKLLVACSI; ALFFKLLVACSIG; LFFKLLVACSIGL; FFKLLVACSIGLV; FKLLVACSIGLVE; KLLVACSIGLVER; LLVACSIGLVERT; LVACSIGLVERTN; VACSIGLVERTNA; ACSIGLVERTNAA; CSIGLVERTNAAL; SIGLVERTNAALE; IGLVERTNAALES; GLVERTNAALESS; LVERTNAALESSS; VERTNAALESSSK; ERTNAALESSSKD; RTNAALESSSKDL; TNAALESSSKDLK; NAALESSSKDLKN; AALESSSKDLKNK; ALESSSKDLKNKI; LESSSKDLKNKIL; ESSSKDLKNKILK; SSSKDLKNKILKI; SSKDLKNKILKIK; SKDLKNKILKIKK; KDLKNKILKIKKE; DLKNKILKIKKEA; LKNKILKIKKEAT; KNKILKIKKEATG; NKILKIKKEATGK; KILKIKKEATGKG; ILKIKKEATGKGV; LKIKKEATGKGVL; KIKKEATGKGVLF; IKKEATGKGVLFE; KKEATGKGVLFEA; KEATGKGVLFEAF; EATGKGVLFEAFT; ATGKGVLFEAFTG; TGKGVLFEAFTGL; GKGVLFEAFTGLK; KGVLFEAFTGLKT; GVLFEAFTGLKTG; VLFEAFTGLKTGS; LFEAFTGLKTGSK; FEAFTGLKTGSKV; EAFTGLKTGSKVT;

AFTGLKTGSKVTS; FTGLKTGSKVTSG; TGLKTGSKVTSGG; GLKTGSKVTSGGL;
LKTGSKVTSGGLA; KTGSKVTSGGLAL; TGSKVTSGGLALR; GSKVTSGGLALRE;
SKVTSGGLALREA; KVTSGGLALREAK; VTSGGLALREAKV; TSGGLALREAKVQ;
SGGLALREAKVQA; GGLALREAKVQAI; GLALREAKVQAIV; LALREAKVQAIVE;
ALREAKVQAIVET; LREAKVQAIVETG; REAKVQAIVETGK; EAKVQAIVETGKF;
AKVQAIVETGKFL; KVQAIVETGKFLK; VQAIVETGKFLKI; QAIVETGKFLKII;
AIVETGKFLKIIE; IVETGKFLKIIEE; VETGKFLKIIEEE; ETGKFLKIIEEEA;
TGKFLKIIEEEAL; GKFLKIIEEEALK; KFLKIIEEEALKL; FLKIIEEEALKLK;
LKIIEEEALKLKE; KIIEEEALKLKET; IIEEEALKLKETG; IEEEALKLKETGN;
EEEALKLKETGNS; EEALKLKETGNSG; EALKLKETGNSGQ; ALKLKETGNSGQF;
LKLKETGNSGQFL; KLKETGNSGQFLA; LKETGNSGQFLAM; KETGNSGQFLAMF;
ETGNSGQFLAMFD; TGNSGQFLAMFDL; GNSGQFLAMFDLM; NSGQFLAMFDLML;
SGQFLAMFDLMLE; GQFLAMFDLMLEV; QFLAMFDLMLEVV; FLAMFDLMLEVVE;
LAMFDLMLEVVES; AMFDLMLEVVESL; MFDLMLEVVESLE; FDLMLEVVESLED;
DLMLEVVESLEDV; LMLEVVESLEDVG; MLEVVESLEDVGI; LEVVESLEDVGII;
EVVESLEDVGIIG; VVESLEDVGIIGL; VESLEDVGIIGLK; ESLEDVGIIGLKA;
SLEDVGIIGLKAR; LEDVGIIGLKARV; EDVGIIGLKARVL; DVGIIGLKARVLE;
VGIIGLKARVLEE; GIIGLKARVLEES; IIGLKARVLEESK; IGLKARVLEESKN;
GLKARVLEESKNN; LKARVLEESKNNP; KARVLEESKNNPI; ARVLEESKNNPIN;
RVLEESKNNPINT; VLEESKNNPINTA; LEESKNNPINTAE; EESKNNPINTAER;
ESKNNPINTAERL; SKNNPINTAERLL; KNNPINTAERLLA; NNPINTAERLLAA;
NPINTAERLLAAK; PINTAERLLAAKA; INTAERLLAAKAQ; NTAERLLAAKAQI;
TAERLLAAKAQIE; AERLLAAKAQIEN; ERLLAAKAQIENQ; RLLAAKAQIENQL;
LLAAKAQIENQLK; LAAKAQIENQLKV; AAKAQIENQLKVV; AKAQIENQLKVVK;
KAQIENQLKVVKE; AQIENQLKVVKEK; QIENQLKVVKEKQ; IENQLKVVKEKQN;
ENQLKVVKEKQNI; NQLKVVKEKQNIE; QLKVVKEKQNIEN; LKVVKEKQNIENG;
KVVKEKQNIENGG; VVKEKQNIENGGE; VKEKQNIENGGEK; KEKQNIENGGEKK;
EKQNIENGGEKKN; KQNIENGGEKKNN; QNIENGGEKKNNK; NIENGGEKKNNKS;
IENGGEKKNNKSK; ENGGEKKNNKSKK; NGGEKKNNKSKKK; GGEKKNNKSKKKK;

14 mers:
SIVIALFFKLLVAC; IVIALFFKLLVACS; VIALFFKLLVACSI;
IALFFKLLVACSIG; ALFFKLLVACSIGL; LFFKLLVACSIGLV;
FFKLLVACSIGLVE; FKLLVACSIGLVER; KLLVACSIGLVERT;
LLVACSIGLVERTN; LVACSIGLVERTNA; VACSIGLVERTNAA;
ACSIGLVERTNAAL; CSIGLVERTNAALE; SIGLVERTNAALES;
IGLVERTNAALESS; GLVERTNAALESSS; LVERTNAALESSSK;
VERTNAALESSSKD; ERTNAALESSSKDL; RTNAALESSSKDLK;
TNAALESSSKDLKN; NAALESSSKDLKNK; AALESSSKDLKNKI;
ALESSSKDLKNKIL; LESSSKDLKNKILK; ESSSKDLKNKILKI;
SSSKDLKNKILKIK; SSKDLKNKILKIKK; SKDLKNKILKIKKE;
KDLKNKILKIKKEA; DLKNKILKIKKEAT; LKNKILKIKKEATG;
KNKILKIKKEATGK; NKILKIKKEATGKG; KILKIKKEATGKGV;
ILKIKKEATGKGVL; LKIKKEATGKGVLF; KIKKEATGKGVLFE;
IKKEATGKGVLFEA; KKEATGKGVLFEAF; KEATGKGVLFEAFT;
EATGKGVLFEAFTG; ATGKGVLFEAFTGL; TGKGVLFEAFTGLK;
GKGVLFEAFTGLKT; KGVLFEAFTGLKTG; GVLFEAFTGLKTGS;
VLFEAFTGLKTGSK; LFEAFTGLKTGSKV; FEAFTGLKTGSKVT;
EAFTGLKTGSKVTS; AFTGLKTGSKVTSG; FTGLKTGSKVTSGG;
TGLKTGSKVTSGGL; GLKTGSKVTSGGLA; LKTGSKVTSGGLAL;
KTGSKVTSGGLALR; TGSKVTSGGLALRE; GSKVTSGGLALREA;
SKVTSGGLALREAK; KVTSGGLALREAKV; VTSGGLALREAKVQ;
TSGGLALREAKVQA; SGGLALREAKVQAI; GGLALREAKVQAIV;
GLALREAKVQAIVE; LALREAKVQAIVET; ALREAKVQAIVETG;
LREAKVQAIVETGK; REAKVQAIVETGKF; EAKVQAIVETGKFL;
AKVQAIVETGKFLK; KVQAIVETGKFLKI; VQAIVETGKFLKII;
QAIVETGKFLKIIE; AIVETGKFLKIIEE; IVETGKFLKIIEEE;

VETGKFLKIIEEEA; ETGKFLKIIEEEAL; TGKFLKIIEEEALK;
GKFLKIIEEEALKL; KFLKIIEEEALKLK; FLKIIEEEALKLKE;
LKIIEEEALKLKET; KIIEEEALKLKETG; IIEEEALKLKETGN;
IEEEALKLKETGNS; EEEALKLKETGNSG; EEALKLKETGNSGQ;
EALKLKETGNSGQF; ALKLKETGNSGQFL; LKLKETGNSGQFLA;
KLKETGNSGQFLAM; LKETGNSGQFLAMF; KETGNSGQFLAMFD;
ETGNSGQFLAMFDL; TGNSGQFLAMFDLM; GNSGQFLAMFDLML;
NSGQFLAMFDLMLE; SGQFLAMFDLMLEV; GQFLAMFDLMLEVV;
QFLAMFDLMLEVVE; FLAMFDLMLEVVES; LAMFDLMLEVVESL;
AMFDLMLEVVESLE; MFDLMLEVVESLED; FDLMLEVVESLEDV;
DLMLEVVESLEDVG; LMLEVVESLEDVGI; MLEVVESLEDVGII;
LEVVESLEDVGIIG; EVVESLEDVGIIGL; VVESLEDVGIIGLK;
VESLEDVGIIGLKA; ESLEDVGIIGLKAR; SLEDVGIIGLKARV;
LEDVGIIGLKARVL; EDVGIIGLKARVLE; DVGIIGLKARVLEE;
VGIIGLKARVLEES; GIIGLKARVLEESK; IIGLKARVLEESKN;
IGLKARVLEESKNN; GLKARVLEESKNNP; LKARVLEESKNNPI;
KARVLEESKNNPIN; ARVLEESKNNPINT; RVLEESKNNPINTA;
VLEESKNNPINTAE; LEESKNNPINTAER; EESKNNPINTAERL;
ESKNNPINTAERLL; SKNNPINTAERLLA; KNNPINTAERLLAA;
NNPINTAERLLAAK; NPINTAERLLAAKA; PINTAERLLAAKAQ;
INTAERLLAAKAQI; NTAERLLAAKAQIE; TAERLLAAKAQIEN;
AERLLAAKAQIENQ; ERLLAAKAQIENQL; RLLAAKAQIENQLK;
LLAAKAQIENQLKV; LAAKAQIENQLKVV; AAKAQIENQLKVVK;
AKAQIENQLKVVKE; KAQIENQLKVVKEK; AQIENQLKVVKEKQ;
QIENQLKVVKEKQN; IENQLKVVKEKQNI; ENQLKVVKEKQNIE;
NQLKVVKEKQNIEN; QLKVVKEKQNIENG; LKVVKEKQNIENGG;
KVVKEKQNIENGGE; VVKEKQNIENGGEK; VKEKQNIENGGEKK;
KEKQNIENGGEKKN; EKQNIENGGEKKNN; KQNIENGGEKKNNK;
QNIENGGEKKNNKS; NIENGGEKKNNKSK; IENGGEKKNNKSKK;
ENGGEKKNNKSKKK; NGGEKKNNKSKKKK;

15 mers:
SIVIALFFKLLVACS; IVIALFFKLLVACSI; VIALFFKLLVACSIG;
IALFFKLLVACSIGL; ALFFKLLVACSIGLV; LFFKLLVACSIGLVE;
FFKLLVACSIGLVER; FKLLVACSIGLVERT; KLLVACSIGLVERTN;
LLVACSIGLVERTNA; LVACSIGLVERTNAA; VACSIGLVERTNAAL;
ACSIGLVERTNAALE; CSIGLVERTNAALES; SIGLVERTNAALESS;
IGLVERTNAALESSS; GLVERTNAALESSSK; LVERTNAALESSSKD;
VERTNAALESSSKDL; ERTNAALESSSKDLK; RTNAALESSSKDLKN;
TNAALESSSKDLKNK; NAALESSSKDLKNKI; AALESSSKDLKNKIL;
ALESSSKDLKNKILK; LESSSKDLKNKILKI; ESSSKDLKNKILKIK;
SSSKDLKNKILKIKK; SSKDLKNKILKIKKE; SKDLKNKILKIKKEA;
KDLKNKILKIKKEAT; DLKNKILKIKKEATG; LKNKILKIKKEATGK;
KNKILKIKKEATGKG; NKILKIKKEATGKGV; KILKIKKEATGKGVL;
ILKIKKEATGKGVLF; LKIKKEATGKGVLFE; KIKKEATGKGVLFEA;
IKKEATGKGVLFEAF; KKEATGKGVLFEAFT; KEATGKGVLFEAFTG;
EATGKGVLFEAFTGL; ATGKGVLFEAFTGLK; TGKGVLFEAFTGLKT;
GKGVLFEAFTGLKTG; KGVLFEAFTGLKTGS; GVLFEAFTGLKTGSK;
VLFEAFTGLKTGSKV; LFEAFTGLKTGSKVT; FEAFTGLKTGSKVTS;
EAFTGLKTGSKVTSG; AFTGLKTGSKVTSGG; FTGLKTGSKVTSGGL;
TGLKTGSKVTSGGLA; GLKTGSKVTSGGLAL; LKTGSKVTSGGLALR;
KTGSKVTSGGLALRE; TGSKVTSGGLALREA; GSKVTSGGLALREAK;
SKVTSGGLALREAKV; KVTSGGLALREAKVQ; VTSGGLALREAKVQA;
TSGGLALREAKVQAI; SGGLALREAKVQAIV; GGLALREAKVQAIVE;
GLALREAKVQAIVET; LALREAKVQAIVETG; ALREAKVQAIVETGK;
LREAKVQAIVETGKF; REAKVQAIVETGKFL; EAKVQAIVETGKFLK;
AKVQAIVETGKFLKI; KVQAIVETGKFLKII; VQAIVETGKFLKIIE;

QAIVETGKFLKIIEE; AIVETGKFLKIIEEE; IVETGKFLKIIEEEA;
VETGKFLKIIEEEAL; ETGKFLKIIEEEALK; TGKFLKIIEEEALKL;
GKFLKIIEEEALKLK; KFLKIIEEEALKLKE; FLKIIEEEALKLKET;
LKIIEEEALKLKETG; KIIEEEALKLKETGN; IIEEEALKLKETGNS;
IEEEALKLKETGNSG; EEEALKLKETGNSGQ; EEALKLKETGNSGQF;
EALKLKETGNSGQFL; ALKLKETGNSGQFLA; LKLKETGNSGQFLAM;
KLKETGNSGQFLAMF; LKETGNSGQFLAMFD; KETGNSGQFLAMFDL;
ETGNSGQFLAMFDLM; TGNSGQFLAMFDLML; GNSGQFLAMFDLMLE;
NSGQFLAMFDLMLEV; SGQFLAMFDLMLEVV; GQFLAMFDLMLEVVE;
QFLAMFDLMLEVVES; FLAMFDLMLEVVESL; LAMFDLMLEVVESLE;
AMFDLMLEVVESLED; MFDLMLEVVESLEDV; FDLMLEVVESLEDVG;
DLMLEVVESLEDVGI; LMLEVVESLEDVGII; MLEVVESLEDVGIIG;
LEVVESLEDVGIIGL; EVVESLEDVGIIGLK; VVESLEDVGIIGLKA;
VESLEDVGIIGLKAR; ESLEDVGIIGLKARV; SLEDVGIIGLKARVL;
LEDVGIIGLKARVLE; EDVGIIGLKARVLEE; DVGIIGLKARVLEES;
VGIIGLKARVLEESK; GIIGLKARVLEESKN; IIGLKARVLEESKNN;
IGLKARVLEESKNNP; GLKARVLEESKNNPI; LKARVLEESKNNPIN;
KARVLEESKNNPINT; ARVLEESKNNPINTA; RVLEESKNNPINTAE;
VLEESKNNPINTAER; LEESKNNPINTAERL; EESKNNPINTAERLL;
ESKNNPINTAERLLA; SKNNPINTAERLLAA; KNNPINTAERLLAAK;
NNPINTAERLLAAKA; NPINTAERLLAAKAQ; PINTAERLLAAKAQI;
INTAERLLAAKAQIE; NTAERLLAAKAQIEN; TAERLLAAKAQIENQ;
AERLLAAKAQIENQL; ERLLAAKAQIENQLK; RLLAAKAQIENQLKV;
LLAAKAQIENQLKVV; LAAKAQIENQLKVVK; AAKAQIENQLKVVKE;
AKAQIENQLKVVKEK; KAQIENQLKVVKEKQ; AQIENQLKVVKEKQN;
QIENQLKVVKEKQNI; IENQLKVVKEKQNIE; ENQLKVVKEKQNIEN;
NQLKVVKEKQNIENG; QLKVVKEKQNIENGG; LKVVKEKQNIENGGE;
KVVKEKQNIENGGEK; VVKEKQNIENGGEKK; VKEKQNIENGGEKKN;
KEKQNIENGGEKKNN; EKQNIENGGEKKNNK; KQNIENGGEKKNNKS;
QNIENGGEKKNNKSK; NIENGGEKKNNKSKK; IENGGEKKNNKSKKK;
ENGGEKKNNKSKKKK;

16 mers:
SIVIALFFKLLVACSI; IVIALFFKLLVACSIG; VIALFFKLLVACSIGL;
IALFFKLLVACSIGLV; ALFFKLLVACSIGLVE; LFFKLLVACSIGLVER;
FFKLLVACSIGLVERT; FKLLVACSIGLVERTN; KLLVACSIGLVERTNA;
LLVACSIGLVERTNAA; LVACSIGLVERTNAAL; VACSIGLVERTNAALE;
ACSIGLVERTNAALES; CSIGLVERTNAALESS; SIGLVERTNAALESSS;
IGLVERTNAALESSSK; GLVERTNAALESSSKD; LVERTNAALESSSKDL;
VERTNAALESSSKDLK; ERTNAALESSSKDLKN; RTNAALESSSKDLKNK;
TNAALESSSKDLKNKI; NAALESSSKDLKNKIL; AALESSSKDLKNKILK;
ALESSSKDLKNKILKI; LESSSKDLKNKILKIK; ESSSKDLKNKILKIKK;
SSSKDLKNKILKIKKE; SSKDLKNKILKIKKEA; SKDLKNKILKIKKEAT;
KDLKNKILKIKKEATG; DLKNKILKIKKEATGK; LKNKILKIKKEATGKG;
KNKILKIKKEATGKGV; NKILKIKKEATGKGVL; KILKIKKEATGKGVLF;
ILKIKKEATGKGVLFE; LKIKKEATGKGVLFEA; KIKKEATGKGVLFEAF;
IKKEATGKGVLFEAFT; KKEATGKGVLFEAFTG; KEATGKGVLFEAFTGL;
EATGKGVLFEAFTGLK; ATGKGVLFEAFTGLKT; TGKGVLFEAFTGLKTG;
GKGVLFEAFTGLKTGS; KGVLFEAFTGLKTGSK; GVLFEAFTGLKTGSKV;
VLFEAFTGLKTGSKVT; LFEAFTGLKTGSKVTS; FEAFTGLKTGSKVTSG;
EAFTGLKTGSKVTSGG; AFTGLKTGSKVTSGGL; FTGLKTGSKVTSGGLA;
TGLKTGSKVTSGGLAL; GLKTGSKVTSGGLALR; LKTGSKVTSGGLALRE;
KTGSKVTSGGLALREA; TGSKVTSGGLALREAK; GSKVTSGGLALREAKV;
SKVTSGGLALREAKVQ; KVTSGGLALREAKVQA; VTSGGLALREAKVQAI;
TSGGLALREAKVQAIV; SGGLALREAKVQAIVE; GGLALREAKVQAIVET;
GLALREAKVQAIVETG; LALREAKVQAIVETGK; ALREAKVQAIVETGKF;
LREAKVQAIVETGKFL; REAKVQAIVETGKFLK; EAKVQAIVETGKFLKI;

	AKVQAIVETGKFLKII; KVQAIVETGKFLKIIE; VQAIVETGKFLKIIEE; QAIVETGKFLKIIEEE; AIVETGKFLKIIEEEA; IVETGKFLKIIEEEAL; VETGKFLKIIEEEALK; ETGKFLKIIEEEALKL; TGKFLKIIEEEALKLK; GKFLKIIEEEALKLKE; KFLKIIEEEALKLKET; FLKIIEEEALKLKETG; LKIIEEEALKLKETGN; KIIEEEALKLKETGNS; IIEEEALKLKETGNSG; IEEEALKLKETGNSGQ; EEEALKLKETGNSGQF; EEALKLKETGNSGQFL; EALKLKETGNSGQFLA; ALKLKETGNSGQFLAM; LKLKETGNSGQFLAMF; KLKETGNSGQFLAMFD; LKETGNSGQFLAMFDL; KETGNSGQFLAMFDLM; ETGNSGQFLAMFDLML; TGNSGQFLAMFDLMLE; GNSGQFLAMFDLMLEV; NSGQFLAMFDLMLEVV; SGQFLAMFDLMLEVVE; GQFLAMFDLMLEVVES; QFLAMFDLMLEVVESL; FLAMFDLMLEVVESLE; LAMFDLMLEVVESLED; AMFDLMLEVVESLEDV; MFDLMLEVVESLEDVG; FDLMLEVVESLEDVGI; DLMLEVVESLEDVGII; LMLEVVESLEDVGIIG; MLEVVESLEDVGIIGL; LEVVESLEDVGIIGLK; EVVESLEDVGIIGLKA; VVESLEDVGIIGLKAR; VESLEDVGIIGLKARV; ESLEDVGIIGLKARVL; SLEDVGIIGLKARVLE; LEDVGIIGLKARVLEE; EDVGIIGLKARVLEES; DVGIIGLKARVLEESK; VGIIGLKARVLEESKN; GIIGLKARVLEESKNN; IIGLKARVLEESKNNP; IGLKARVLEESKNNPI; GLKARVLEESKNNPIN; LKARVLEESKNNPINT; KARVLEESKNNPINTA; ARVLEESKNNPINTAE; RVLEESKNNPINTAER; VLEESKNNPINTAERL; LEESKNNPINTAERLL; EESKNNPINTAERLLA; ESKNNPINTAERLLAA; SKNNPINTAERLLAAK; KNNPINTAERLLAAKA; NNPINTAERLLAAKAQ; NPINTAERLLAAKAQI; PINTAERLLAAKAQIE; INTAERLLAAKAQIEN; NTAERLLAAKAQIENQ; TAERLLAAKAQIENQL; AERLLAAKAQIENQLK; ERLLAAKAQIENQLKV; RLLAAKAQIENQLKVV; LLAAKAQIENQLKVVK; LAAKAQIENQLKVVKE; AAKAQIENQLKVVKEK; AKAQIENQLKVVKEKQ; KAQIENQLKVVKEKQN; AQIENQLKVVKEKQNI; QIENQLKVVKEKQNIE; IENQLKVVKEKQNIEN; ENQLKVVKEKQNIENG; NQLKVVKEKQNIENGG; QLKVVKEKQNIENGGE; LKVVKEKQNIENGGEK; KVVKEKQNIENGGEKK; VVKEKQNIENGGEKKN; VKEKQNIENGGEKKNN; KEKQNIENGGEKKNNK; EKQNIENGGEKKNNKS; KQNIENGGEKKNNKSK; QNIENGGEKKNNKSKK; NIENGGEKKNNKSKKK; IENGGEKKNNKSKKKK;
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31]	13 mers: MILIFYFKQIALF; ILIFYFKQIALFI; LIFYFKQIALFII; IFYFKQIALFIIF; FYFKQIALFIIFR; YFKQIALFIIFRL; FKQIALFIIFRLC; KQIALFIIFRLCY; QIALFIIFRLCYI; IALFIIFRLCYII; ALFIIFRLCYIIK; LFIIFRLCYIIKK; FIIFRLCYIIKKV; IIFRLCYIIKKVK; IFRLCYIIKKVKI; FRLCYIIKKVKIK; RLCYIIKKVKIKL; LCYIIKKVKIKLK; CYIIKKVKIKLKR; YIIKKVKIKLKRK; IIKKVKIKLKRKS; IKKVKIKLKRKSC; KKVKIKLKRKSCM; KVKIKLKRKSCMK; VKIKLKRKSCMKK; KIKLKRKSCMKKQ; IKLKRKSCMKKQF; KLKRKSCMKKQFD; LKRKSCMKKQFDT; KRKSCMKKQFDTE; RKSCMKKQFDTEV; KSCMKKQFDTEVN; SCMKKQFDTEVND; CMKKQFDTEVNDL; MKKQFDTEVNDLL; KKQFDTEVNDLLY; KQFDTEVNDLLYL; QFDTEVNDLLYLI; FDTEVNDLLYLII; DTEVNDLLYLIIH; TEVNDLLYLIIHS; EVNDLLYLIIHSL; VNDLLYLIIHSLY; NDLLYLIIHSLYS; DLLYLIIHSLYSH; LLYLIIHSLYSHK; LYLIIHSLYSHKE; YLIIHSLYSHKEI; LIIHSLYSHKEIF; IIHSLYSHKEIFL; IHSLYSHKEIFLR; HSLYSHKEIFLRE; SLYSHKEIFLREL; LYSHKEIFLRELI; YSHKEIFLRELIS; SHKEIFLRELISN; HKEIFLRELISNA; KEIFLRELISNAS; EIFLRELISNASD; IFLRELISNASDA; FLRELISNASDAI; LRELISNASDAID; RELISNASDAIDK; ELISNASDAIDKL; LISNASDAIDKLK; ISNASDAIDKLKF; SNASDAIDKLKFL; NASDAIDKLKFLS; ASDAIDKLKFLSL; SDAIDKLKFLSLT; DAIDKLKFLSLTN; AIDKLKFLSLTNE; IDKLKFLSLTNEK; DKLKFLSLTNEKF; KLKFLSLTNEKFK; LKFLSLTNEKFKN; KFLSLTNEKFKNI; FLSLTNEKFKNIA; LSLTNEKFKNIAL; SLTNEKFKNIALE; LTNEKFKNIALEP; TNEKFKNIALEPK; NEKFKNIALEPKI; EKFKNIALEPKIE; KFKNIALEPKIEI; FKNIALEPKIEIS; KNIALEPKIEISF; NIALEPKIEISFD; IALEPKIEISFDD; ALEPKIEISFDDK; LEPKIEISFDDKS; EPKIEISFDDKSI;

	PKIEISFDDKSIL; KIEISFDDKSILI; IEISFDDKSILIK; EISFDDKSILIKD; ISFDDKSILIKDN; SFDDKSILIKDNG; FDDKSILIKDNGI; DDKSILIKDNGIG; DKSILIKDNGIGM; KSILIKDNGIGMD; SILIKDNGIGMDE; ILIKDNGIGMDEQ; LIKDNGIGMDEQD; IKDNGIGMDEQDL; KDNGIGMDEQDLT; DNGIGMDEQDLTN; NGIGMDEQDLTNH; GIGMDEQDLTNHL; IGMDEQDLTNHLG; GMDEQDLTNHLGV; MDEQDLTNHLGVI; DEQDLTNHLGVIA; EQDLTNHLGVIAK; QDLTNHLGVIAKS; DLTNHLGVIAKSG; LTNHLGVIAKSGT; TNHLGVIAKSGTK; NHLGVIAKSGTKE; HLGVIAKSGTKEF; LGVIAKSGTKEFI; GVIAKSGTKEFIN; VIAKSGTKEFINN; IAKSGTKEFINNL; AKSGTKEFINNLK; KSGTKEFINNLKQ; SGTKEFINNLKQD; GTKEFINNLKQDE; TKEFINNLKQDEK; KEFINNLKQDEKK; EFINNLKQDEKKS; FINNLKQDEKKSA; INNLKQDEKKSAS; NNLKQDEKKSASL; NLKQDEKKSASLI; LKQDEKKSASLIG; KQDEKKSASLIGQ; QDEKKSASLIGQF; DEKKSASLIGQFG; EKKSASLIGQFGV; KKSASLIGQFGVG; KSASLIGQFGVGF; SASLIGQFGVGFY; ASLIGQFGVGFYS; SLIGQFGVGFYSA; LIGQFGVGFYSAF; IGQFGVGFYSAFI; GQFGVGFYSAFIV; QFGVGFYSAFIVS; FGVGFYSAFIVSE; GVGFYSAFIVSEK; VGFYSAFIVSEKV; GFYSAFIVSEKVE; FYSAFIVSEKVEV; YSAFIVSEKVEVT; SAFIVSEKVEVTS; AFIVSEKVEVTSK; FIVSEKVEVTSKK; IVSEKVEVTSKKA; VSEKVEVTSKKAL; SEKVEVTSKKALE; EKVEVTSKKALES; KVEVTSKKALESD; VEVTSKKALESDA; EVTSKKALESDAY; VTSKKALESDAYI; TSKKALESDAYIW; SKKALESDAYIWS; KKALESDAYIWSS; KALESDAYIWSSD; ALESDAYIWSSDG; LESDAYIWSSDGK; ESDAYIWSSDGKT; SDAYIWSSDGKTG; DAYIWSSDGKTGY; AYIWSSDGKTGYE; YIWSSDGKTGYEI; IWSSDGKTGYEIE; WSSDGKTGYEIEK; SSDGKTGYEIEKA; SDGKTGYEIEKAK; DGKTGYEIEKAKK; GKTGYEIEKAKKE; KTGYEIEKAKKEE; TGYEIEKAKKEES; GYEIEKAKKEESG; YEIEKAKKEESGT; EIEKAKKEESGTE; IEKAKKEESGTEI; EKAKKEESGTEIK; KAKKEESGTEIKL; AKKEESGTEIKLY; KKEESGTEIKLYL; KEESGTEIKLYLN; EESGTEIKLYLNK; ESGTEIKLYLNKE; SGTEIKLYLNKEG; GTEIKLYLNKEGL; TEIKLYLNKEGLE; EIKLYLNKEGLEY; IKLYLNKEGLEYA; KLYLNKEGLEYAN; LYLNKEGLEYANK; YLNKEGLEYANKW; LNKEGLEYANKWK; NKEGLEYANKWKI; KEGLEYANKWKIQ; EGLEYANKWKIQE; GLEYANKWKIQEI; LEYANKWKIQEII; EYANKWKIQEIIK; YANKWKIQEIIKK; ANKWKIQEIIKKY; NKWKIQEIIKKYS; KWKIQEIIKKYSN; WKIQEIIKKYSNH; KIQEIIKKYSNHI; IQEIIKKYSNHIN; QEIIKKYSNHINY; EIIKKYSNHINYP; IIKKYSNHINYPI; IKKYSNHINYPIY; KKYSNHINYPIYI; KYSNHINYPIYIK; YSNHINYPIYIKY; SNHINYPIYIKYS; NHINYPIYIKYSE; HINYPIYIKYSEP; INYPIYIKYSEPI; NYPIYIKYSEPIM; YPIYIKYSEPIMK; PIYIKYSEPIMKD; IYIKYSEPIMKDG; YIKYSEPIMKDGK; IKYSEPIMKDGKQ; KYSEPIMKDGKQE; YSEPIMKDGKQEG; SEPIMKDGKQEGI; EPIMKDGKQEGIE; PIMKDGKQEGIEE; IMKDGKQEGIEEK; MKDGKQEGIEEKE; KDGKQEGIEEKEE; DGKQEGIEEKEEK; GKQEGIEEKEEKL; KQEGIEEKEEKLN; QEGIEEKEEKLNE; EGIEEKEEKLNET; GIEEKEEKLNETT; IEEKEEKLNETTA; EEKEEKLNETTAL; EKEEKLNETTALW; KEEKLNETTALWT; EEKLNETTALWTK; EKLNETTALWTKN; KLNETTALWTKNK; LNETTALWTKNKS; NETTALWTKNKSE; ETTALWTKNKSEI; TTALWTKNKSEIK; TALWTKNKSEIKA; ALWTKNKSEIKAE; LWTKNKSEIKAEE; WTKNKSEIKAEEY; TKNKSEIKAEEYN; KNKSEIKAEEYNE; NKSEIKAEEYNEF; KSEIKAEEYNEFY; SEIKAEEYNEFYK; EIKAEEYNEFYKN; IKAEEYNEFYKNT; KAEEYNEFYKNTT; AEEYNEFYKNTTF; EEYNEFYKNTTFD; EYNEFYKNTTFDY; YNEFYKNTTFDYE; NEFYKNTTFDYEN; EFYKNTTFDYENP; FYKNTTFDYENPL; YKNTTFDYENPLM; KNTTFDYENPLMH; NTTFDYENPLMHI; TTFDYENPLMHIH; TFDYENPLMHIHT; FDYENPLMHIHTK; DYENPLMHIHTKA; YENPLMHIHTKAE; ENPLMHIHTKAEG; NPLMHIHTKAEGN; PLMHIHTKAEGNL; LMHIHTKAEGNLE; MHIHTKAEGNLEY; HIHTKAEGNLEYT; IHTKAEGNLEYTN; HTKAEGNLEYTNL; TKAEGNLEYTNLF; KAEGNLEYTNLFY; AEGNLEYTNLFYV; EGNLEYTNLFYVP; GNLEYTNLFYVPS; NLEYTNLFYVPSK; LEYTNLFYVPSKA; EYTNLFYVPSKAP; YTNLFYVPSKAPY; TNLFYVPSKAPYD; NLFYVPSKAPYDL; LFYVPSKAPYDLY; FYVPSKAPYDLYY; YVPSKAPYDLYYP; VPSKAPYDLYYPN; PSKAPYDLYYPNT; SKAPYDLYYPNTK; KAPYDLYYPNTKP; APYDLYYPNTKPG; PYDLYYPNTKPGV; YDLYYPNTKPGVK; DLYYPNTKPGVKL; LYYPNTKPGVKLF; YYPNTKPGVKLFI;

	YPNTKPGVKLFIN; PNTKPGVKLFINR; NTKPGVKLFINRI; TKPGVKLFINRIF; KPGVKLFINRIFI; PGVKLFINRIFIT; GVKLFINRIFITD; VKLFINRIFITDS; KLFINRIFITDSE; LFINRIFITDSEG; FINRIFITDSEGS; INRIFITDSEGSL; NRIFITDSEGSLL; RIFITDSEGSLLP; IFITDSEGSLLPN; FITDSEGSLLPNY; ITDSEGSLLPNYL; TDSEGSLLPNYLR; DSEGSLLPNYLRF; SEGSLLPNYLRFI; EGSLLPNYLRFIK; GSLLPNYLRFIKG; SLLPNYLRFIKGI; LLPNYLRFIKGII; LPNYLRFIKGIID; PNYLRFIKGIIDC; NYLRFIKGIIDCQ; YLRFIKGIIDCQD; LRFIKGIIDCQDL; RFIKGIIDCQDLP; FIKGIIDCQDLPL; IKGIIDCQDLPLN; KGIIDCQDLPLNV; GIIDCQDLPLNVS; IIDCQDLPLNVSR; IDCQDLPLNVSRE; DCQDLPLNVSREI; CQDLPLNVSREIL; QDLPLNVSREILQ; DLPLNVSREILQQ; LPLNVSREILQQN; PLNVSREILQQNK; LNVSREILQQNKI; NVSREILQQNKIL; VSREILQQNKILS; SREILQQNKILSK; REILQQNKILSKI; EILQQNKILSKIK; ILQQNKILSKIKS; LQQNKILSKIKSS; QQNKILSKIKSSS; QNKILSKIKSSSV; NKILSKIKSSSVK; KILSKIKSSSVKK; ILSKIKSSSVKKI; LSKIKSSSVKKIL; SKIKSSSVKKILS; KIKSSSVKKILSE; IKSSSVKKILSEL; KSSSVKKILSELE; SSSVKKILSELEK; SSVKKILSELEKL; SVKKILSELEKLS; VKKILSELEKLSK; KKILSELEKLSKK; KILSELEKLSKKN; ILSELEKLSKKNP; LSELEKLSKKNPE; SELEKLSKKNPEK; ELEKLSKKNPEKF; LEKLSKKNPEKFS; EKLSKKNPEKFSE; KLSKKNPEKFSEF; LSKKNPEKFSEFS; SKKNPEKFSEFSK; KKNPEKFSEFSKE; KNPEKFSEFSKEF; NPEKFSEFSKEFG; PEKFSEFSKEFGR; EKFSEFSKEFGRC; KFSEFSKEFGRCI; FSEFSKEFGRCIK; SEFSKEFGRCIKE; EFSKEFGRCIKEG; FSKEFGRCIKEGV; SKEFGRCIKEGVY; KEFGRCIKEGVYS; EFGRCIKEGVYSD; FGRCIKEGVYSDF; GRCIKEGVYSDFE; RCIKEGVYSDFEN; CIKEGVYSDFENR; IKEGVYSDFENRE; KEGVYSDFENREK; EGVYSDFENREKL; GVYSDFENREKLI; VYSDFENREKLIS; YSDFENREKLISL; SDFENREKLISLI; DFENREKLISLIR; FENREKLISLIRF; ENREKLISLIRFK; NREKLISLIRFKS; REKLISLIRFKSS; EKLISLIRFKSSS; KLISLIRFKSSSV; LISLIRFKSSSVD; ISLIRFKSSSVDG; SLIRFKSSSVDGF; LIRFKSSSVDGFV; IRFKSSSVDGFVS; RFKSSSVDGFVSF; FKSSSVDGFVSFK; KSSSVDGFVSFKE; SSSVDGFVSFKEY; SSVDGFVSFKEYK; SVDGFVSFKEYKE; VDGFVSFKEYKER; DGFVSFKEYKERM; GFVSFKEYKERMN; FVSFKEYKERMNE; VSFKEYKERMNES; SFKEYKERMNESQ; FKEYKERMNESQK; KEYKERMNESQKS; EYKERMNESQKSI; YKERMNESQKSIY; KERMNESQKSIYY; ERMNESQKSIYYI; RMNESQKSIYYIT; MNESQKSIYYITG; NESQKSIYYITGG; ESQKSIYYITGGK; SQKSIYYITGGKE; QKSIYYITGGKEN; KSIYYITGGKENI; SIYYITGGKENIL; IYYITGGKENILK; YYITGGKENILKE; YITGGKENILKEN; ITGGKENILKENP; TGGKENILKENPI; GGKENILKENPIV; GKENILKENPIVA; KENILKENPIVAA; ENILKENPIVAAY; NILKENPIVAAYK; ILKENPIVAAYKE; LKENPIVAAYKEK; KENPIVAAYKEKG; ENPIVAAYKEKGF; NPIVAAYKEKGFE; PIVAAYKEKGFEI; IVAAYKEKGFEIL; VAAYKEKGFEILI; AAYKEKGFEILIM; AYKEKGFEILIMD; YKEKGFEILIMDD; KEKGFEILIMDDE; EKGFEILIMDDEL; KGFEILIMDDELD; GFEILIMDDELDE; FEILIMDDELDEA; EILIMDDELDEAI; ILIMDDELDEAIL; LIMDDELDEAILN; IMDDELDEAILNL; MDDELDEAILNLI; DDELDEAILNLIP; DELDEAILNLIPE; ELDEAILNLIPEY; LDEAILNLIPEYE; DEAILNLIPEYEG; EAILNLIPEYEGL; AILNLIPEYEGLK; ILNLIPEYEGLKL; LNLIPEYEGLKLK; NLIPEYEGLKLKA; LIPEYEGLKLKAI; IPEYEGLKLKAIN; PEYEGLKLKAINK; EYEGLKLKAINKN; YEGLKLKAINKNE; EGLKLKAINKNET; GLKLKAINKNETS; LKLKAINKNETSN; KLKAINKNETSNE; LKAINKNETSNEL; KAINKNETSNELK; AINKNETSNELKD; INKNETSNELKDE; NKNETSNELKDEN; KNETSNELKDENF; NETSNELKDENFK; ETSNELKDENFKK; TSNELKDENFKKI; SNELKDENFKKIE; NELKDENFKKIEE; ELKDENFKKIEEE; LKDENFKKIEEEF; KDENFKKIEEEFK; DENFKKIEEEFKD; ENFKKIEEEFKDT; NFKKIEEEFKDTL; FKKIEEEFKDTLT; KKIEEEFKDTLTK; KIEEEFKDTLTKV; IEEEFKDTLTKVK; EEEFKDTLTKVKE; EEFKDTLTKVKEI; EFKDTLTKVKEIL; FKDTLTKVKEILK; KDTLTKVKEILKD; DTLTKVKEILKDH; TLTKVKEILKDHI; LTKVKEILKDHIK; TKVKEILKDHIKE; KVKEILKDHIKEV; VKEILKDHIKEVN; KEILKDHIKEVNL; EILKDHIKEVNLS; ILKDHIKEVNLSA; LKDHIKEVNLSAT; KDHIKEVNLSATL; DHIKEVNLSATLI; HIKEVNLSATLIK; IKEVNLSATLIKE; KEVNLSATLIKEP;

EVNLSATLIKEPS; VNLSATLIKEPSA; NLSATLIKEPSAI; LSATLIKEPSAII; SATLIKEPSAIII; ATLIKEPSAIIID; TLIKEPSAIIIDS; LIKEPSAIIIDSN; IKEPSAIIIDSND; KEPSAIIIDSNDP; EPSAIIIDSNDPT; PSAIIIDSNDPTY; SAIIIDSNDPTYQ; AIIIDSNDPTYQM; IIIDSNDPTYQMQ; IIDSNDPTYQMQK; IDSNDPTYQMQKI; DSNDPTYQMQKIM; SNDPTYQMQKIML; NDPTYQMQKIMLS; DPTYQMQKIMLSM; PTYQMQKIMLSMG; TYQMQKIMLSMGQ; YQMQKIMLSMGQE; QMQKIMLSMGQEV; MQKIMLSMGQEVK; QKIMLSMGQEVKE; KIMLSMGQEVKEI; IMLSMGQEVKEIK; MLSMGQEVKEIKP; LSMGQEVKEIKPI; SMGQEVKEIKPIL; MGQEVKEIKPILE; GQEVKEIKPILEL; QEVKEIKPILELN; EVKEIKPILELNP; VKEIKPILELNPN; KEIKPILELNPNN; EIKPILELNPNNK; IKPILELNPNNKI; KPILELNPNNKIV; PILELNPNNKIVQ; ILELNPNNKIVQN; LELNPNNKIVQNL; ELNPNNKIVQNLK; LNPNNKIVQNLKN; NPNNKIVQNLKNL; PNNKIVQNLKNLE; NNKIVQNLKNLEP; NKIVQNLKNLEPE; KIVQNLKNLEPEK; IVQNLKNLEPEKL; VQNLKNLEPEKLE; QNLKNLEPEKLEK; NLKNLEPEKLEKI; LKNLEPEKLEKIS; KNLEPEKLEKISI; NLEPEKLEKISIL; LEPEKLEKISILL; EPEKLEKISILLF; PEKLEKISILLFE; EKLEKISILLFEE; KLEKISILLFEEA; LEKISILLFEEAM; EKISILLFEEAML; KISILLFEEAMLT; ISILLFEEAMLTS; SILLFEEAMLTSG; ILLFEEAMLTSGM; LLFEEAMLTSGMP; LFEEAMLTSGMPS; FEEAMLTSGMPSK; EEAMLTSGMPSKN; EAMLTSGMPSKNP; AMLTSGMPSKNPG; MLTSGMPSKNPGK; LTSGMPSKNPGKF; TSGMPSKNPGKFI; SGMPSKNPGKFIN; GMPSKNPGKFINI; MPSKNPGKFINII; PSKNPGKFINIIN; SKNPGKFINIINE; KNPGKFINIINEF; NPGKFINIINEFI; PGKFINIINEFIE; GKFINIINEFIEK; KFINIINEFIEKD; FINIINEFIEKDF; INIINEFIEKDFL;

14 mers:
MILIFYFKQIALFI; ILIFYFKQIALFII; LIFYFKQIALFIIF; IFYFKQIALFIIFR; FYFKQIALFIIFRL; YFKQIALFIIFRLC; FKQIALFIIFRLCY; KQIALFIIFRLCYI; QIALFIIFRLCYII; IALFIIFRLCYIIK; ALFIIFRLCYIIKK; LFIIFRLCYIIKKV; FIIFRLCYIIKKVK; IIFRLCYIIKKVKI; IFRLCYIIKKVKIK; FRLCYIIKKVKIKL; RLCYIIKKVKIKLK; LCYIIKKVKIKLKR; CYIIKKVKIKLKRK; YIIKKVKIKLKRKS; IIKKVKIKLKRKSC; IKKVKIKLKRKSCM; KKVKIKLKRKSCMK; KVKIKLKRKSCMKK; VKIKLKRKSCMKKQ; KIKLKRKSCMKKQF; IKLKRKSCMKKQFD; KLKRKSCMKKQFDT; LKRKSCMKKQFDTE; KRKSCMKKQFDTEV; RKSCMKKQFDTEVN; KSCMKKQFDTEVND; SCMKKQFDTEVNDL; CMKKQFDTEVNDLL; MKKQFDTEVNDLLY; KKQFDTEVNDLLYL; KQFDTEVNDLLYLI; QFDTEVNDLLYLII; FDTEVNDLLYLIIH; DTEVNDLLYLIIHS; TEVNDLLYLIIHSL; EVNDLLYLIIHSLY; VNDLLYLIIHSLYS; NDLLYLIIHSLYSH; DLLYLIIHSLYSHK; LLYLIIHSLYSHKE; LYLIIHSLYSHKEI; YLIIHSLYSHKEIF; LIIHSLYSHKEIFL; IIHSLYSHKEIFLR; IHSLYSHKEIFLRE; HSLYSHKEIFLREL; SLYSHKEIFLRELI; LYSHKEIFLRELIS; YSHKEIFLRELISN; SHKEIFLRELISNA; HKEIFLRELISNAS; KEIFLRELISNASD; EIFLRELISNASDA; IFLRELISNASDAI; FLRELISNASDAID; LRELISNASDAIDK; RELISNASDAIDKL; ELISNASDAIDKLK; LISNASDAIDKLKF; ISNASDAIDKLKFL; SNASDAIDKLKFLS; NASDAIDKLKFLSL; ASDAIDKLKFLSLT; SDAIDKLKFLSLTN; DAIDKLKFLSLTNE; AIDKLKFLSLTNEK; IDKLKFLSLTNEKF; DKLKFLSLTNEKFK; KLKFLSLTNEKFKN; LKFLSLTNEKFKNI; KFLSLTNEKFKNIA; FLSLTNEKFKNIAL; LSLTNEKFKNIALE; SLTNEKFKNIALEP; LTNEKFKNIALEPK; TNEKFKNIALEPKI; NEKFKNIALEPKIE; EKFKNIALEPKIEI; KFKNIALEPKIEIS; FKNIALEPKIEISF; KNIALEPKIEISFD; NIALEPKIEISFDD; IALEPKIEISFDDK; ALEPKIEISFDDKS; LEPKIEISFDDKSI; EPKIEISFDDKSIL; PKIEISFDDKSILI; KIEISFDDKSILIK; IEISFDDKSILIKD; EISFDDKSILIKDN;

	ISFDDKSILIKDNG; SFDDKSILIKDNGI; FDDKSILIKDNGIG; DDKSILIKDNGIGM; DKSILIKDNGIGMD; KSILIKDNGIGMDE; SILIKDNGIGMDEQ; ILIKDNGIGMDEQD; LIKDNGIGMDEQDL; IKDNGIGMDEQDLT; KDNGIGMDEQDLTN; DNGIGMDEQDLTNH; NGIGMDEQDLTNHL; GIGMDEQDLTNHLG; IGMDEQDLTNHLGV; GMDEQDLTNHLGVI; MDEQDLTNHLGVIA; DEQDLTNHLGVIAK; EQDLTNHLGVIAKS; QDLTNHLGVIAKSG; DLTNHLGVIAKSGT; LTNHLGVIAKSGTK; TNHLGVIAKSGTKE; NHLGVIAKSGTKEF; HLGVIAKSGTKEFI; LGVIAKSGTKEFIN; GVIAKSGTKEFINN; VIAKSGTKEFINNL; IAKSGTKEFINNLK; AKSGTKEFINNLKQ; KSGTKEFINNLKQD; SGTKEFINNLKQDE; GTKEFINNLKQDEK; TKEFINNLKQDEKK; KEFINNLKQDEKKS; EFINNLKQDEKKSA; FINNLKQDEKKSAS; INNLKQDEKKSASL; NNLKQDEKKSASLI; NLKQDEKKSASLIG; LKQDEKKSASLIGQ; KQDEKKSASLIGQF; QDEKKSASLIGQFG; DEKKSASLIGQFGV; EKKSASLIGQFGVG; KKSASLIGQFGVGF; KSASLIGQFGVGFY; SASLIGQFGVGFYS; ASLIGQFGVGFYSA; SLIGQFGVGFYSAF; LIGQFGVGFYSAFI; IGQFGVGFYSAFIV; GQFGVGFYSAFIVS; QFGVGFYSAFIVSE; FGVGFYSAFIVSEK; GVGFYSAFIVSEKV; VGFYSAFIVSEKVE; GFYSAFIVSEKVEV; FYSAFIVSEKVEVT; YSAFIVSEKVEVTS; SAFIVSEKVEVTSK; AFIVSEKVEVTSKK; FIVSEKVEVTSKKA; IVSEKVEVTSKKAL; VSEKVEVTSKKALE; SEKVEVTSKKALES; EKVEVTSKKALESD; KVEVTSKKALESDA; VEVTSKKALESDAY; EVTSKKALESDAYI; VTSKKALESDAYIW; TSKKALESDAYIWS; SKKALESDAYIWSS; KKALESDAYIWSSD; KALESDAYIWSSDG; ALESDAYIWSSDGK; LESDAYIWSSDGKT; ESDAYIWSSDGKTG; SDAYIWSSDGKTGY; DAYIWSSDGKTGYE; AYIWSSDGKTGYEI; YIWSSDGKTGYEIE; IWSSDGKTGYEIEK; WSSDGKTGYEIEKA; SSDGKTGYEIEKAK; SDGKTGYEIEKAKK; DGKTGYEIEKAKKE; GKTGYEIEKAKKEE; KTGYEIEKAKKEES; TGYEIEKAKKEESG; GYEIEKAKKEESGT; YEIEKAKKEESGTE; EIEKAKKEESGTEI; IEKAKKEESGTEIK; EKAKKEESGTEIKL; KAKKEESGTEIKLY; AKKEESGTEIKLYL; KKEESGTEIKLYLN; KEESGTEIKLYLNK; EESGTEIKLYLNKE; ESGTEIKLYLNKEG; SGTEIKLYLNKEGL; GTEIKLYLNKEGLE; TEIKLYLNKEGLEY; EIKLYLNKEGLEYA; IKLYLNKEGLEYAN; KLYLNKEGLEYANK; LYLNKEGLEYANKW; YLNKEGLEYANKWK; LNKEGLEYANKWKI; NKEGLEYANKWKIQ; KEGLEYANKWKIQE; EGLEYANKWKIQEI; GLEYANKWKIQEII; LEYANKWKIQEIIK; EYANKWKIQEIIKK; YANKWKIQEIIKKY; ANKWKIQEIIKKYS; NKWKIQEIIKKYSN; KWKIQEIIKKYSNH; WKIQEIIKKYSNHI; KIQEIIKKYSNHIN; IQEIIKKYSNHINY; QEIIKKYSNHINYP; EIIKKYSNHINYPI; IIKKYSNHINYPIY; IKKYSNHINYPIYI; KKYSNHINYPIYIK; KYSNHINYPIYIKY; YSNHINYPIYIKYS; SNHINYPIYIKYSE; NHINYPIYIKYSEP; HINYPIYIKYSEPI; INYPIYIKYSEPIM; NYPIYIKYSEPIMK; YPIYIKYSEPIMKD; PIYIKYSEPIMKDG; IYIKYSEPIMKDGK; YIKYSEPIMKDGKQ; IKYSEPIMKDGKQE; KYSEPIMKDGKQEG; YSEPIMKDGKQEGI; SEPIMKDGKQEGIE; EPIMKDGKQEGIEE; PIMKDGKQEGIEEK; IMKDGKQEGIEEKE; MKDGKQEGIEEKEE; KDGKQEGIEEKEEK; DGKQEGIEEKEEKL; GKQEGIEEKEEKLN; KQEGIEEKEEKLNE; QEGIEEKEEKLNET; EGIEEKEEKLNETT; GIEEKEEKLNETTA; IEEKEEKLNETTAL; EEKEEKLNETTALW; EKEEKLNETTALWT; KEEKLNETTALWTK; EEKLNETTALWTKN; EKLNETTALWTKNK; KLNETTALWTKNKS; LNETTALWTKNKSE; NETTALWTKNKSEI; ETTALWTKNKSEIK; TTALWTKNKSEIKA; TALWTKNKSEIKAE; ALWTKNKSEIKAEE; LWTKNKSEIKAEEY; WTKNKSEIKAEEYN; TKNKSEIKAEEYNE; KNKSEIKAEEYNEF;

	NKSEIKAEEYNEFY; KSEIKAEEYNEFYK; SEIKAEEYNEFYKN; EIKAEEYNEFYKNT; IKAEEYNEFYKNTT; KAEEYNEFYKNTTF; AEEYNEFYKNTTFD; EEYNEFYKNTTFDY; EYNEFYKNTTFDYE; YNEFYKNTTFDYEN; NEFYKNTTFDYENP; EFYKNTTFDYENPL; FYKNTTFDYENPLM; YKNTTFDYENPLMH; KNTTFDYENPLMHI; NTTFDYENPLMHIH; TTFDYENPLMHIHT; TFDYENPLMHIHTK; FDYENPLMHIHTKA; DYENPLMHIHTKAE; YENPLMHIHTKAEG; ENPLMHIHTKAEGN; NPLMHIHTKAEGNL; PLMHIHTKAEGNLE; LMHIHTKAEGNLEY; MHIHTKAEGNLEYT; HIHTKAEGNLEYTN; IHTKAEGNLEYTNL; HTKAEGNLEYTNLF; TKAEGNLEYTNLFY; KAEGNLEYTNLFYV; AEGNLEYTNLFYVP; EGNLEYTNLFYVPS; GNLEYTNLFYVPSK; NLEYTNLFYVPSKA; LEYTNLFYVPSKAP; EYTNLFYVPSKAPY; YTNLFYVPSKAPYD; TNLFYVPSKAPYDL; NLFYVPSKAPYDLY; LFYVPSKAPYDLYY; FYVPSKAPYDLYYP; YVPSKAPYDLYYPN; VPSKAPYDLYYPNT; PSKAPYDLYYPNTK; SKAPYDLYYPNTKP; KAPYDLYYPNTKPG; APYDLYYPNTKPGV; PYDLYYPNTKPGVK; YDLYYPNTKPGVKL; DLYYPNTKPGVKLF; LYYPNTKPGVKLFI; YYPNTKPGVKLFIN; YPNTKPGVKLFINR; PNTKPGVKLFINRI; NTKPGVKLFINRIF; TKPGVKLFINRIFI; KPGVKLFINRIFIT; PGVKLFINRIFITD; GVKLFINRIFITDS; VKLFINRIFITDSE; KLFINRIFITDSEG; LFINRIFITDSEGS; FINRIFITDSEGSL; INRIFITDSEGSLL; NRIFITDSEGSLLP; RIFITDSEGSLLPN; IFITDSEGSLLPNY; FITDSEGSLLPNYL; ITDSEGSLLPNYLR; TDSEGSLLPNYLRF; DSEGSLLPNYLRFI; SEGSLLPNYLRFIK; EGSLLPNYLRFIKG; GSLLPNYLRFIKGI; SLLPNYLRFIKGII; LLPNYLRFIKGIID; LPNYLRFIKGIIDC; PNYLRFIKGIIDCQ; NYLRFIKGIIDCQD; YLRFIKGIIDCQDL; LRFIKGIIDCQDLP; RFIKGIIDCQDLPL; FIKGIIDCQDLPLN; IKGIIDCQDLPLNV; KGIIDCQDLPLNVS; GIIDCQDLPLNVSR; IIDCQDLPLNVSRE; IDCQDLPLNVSREI; DCQDLPLNVSREIL; CQDLPLNVSREILQ; QDLPLNVSREILQQ; DLPLNVSREILQQN; LPLNVSREILQQNK; PLNVSREILQQNKI; LNVSREILQQNKIL; NVSREILQQNKILS; VSREILQQNKILSK; SREILQQNKILSKI; REILQQNKILSKIK; EILQQNKILSKIKS; ILQQNKILSKIKSS; LQQNKILSKIKSSS; QQNKILSKIKSSSV; QNKILSKIKSSSVK; NKILSKIKSSSVKK; KILSKIKSSSVKKI; ILSKIKSSSVKKIL; LSKIKSSSVKKILS; SKIKSSSVKKILSE; KIKSSSVKKILSEL; IKSSSVKKILSELE; KSSSVKKILSELEK; SSSVKKILSELEKL; SSVKKILSELEKLS; SVKKILSELEKLSK; VKKILSELEKLSKK; KKILSELEKLSKKN; KILSELEKLSKKNP; ILSELEKLSKKNPE; LSELEKLSKKNPEK; SELEKLSKKNPEKF; ELEKLSKKNPEKFS; LEKLSKKNPEKFSE; EKLSKKNPEKFSEF; KLSKKNPEKFSEFS; LSKKNPEKFSEFSK; SKKNPEKFSEFSKE; KKNPEKFSEFSKEF; KNPEKFSEFSKEFG; NPEKFSEFSKEFGR; PEKFSEFSKEFGRC; EKFSEFSKEFGRCI; KFSEFSKEFGRCIK; FSEFSKEFGRCIKE; SEFSKEFGRCIKEG; EFSKEFGRCIKEGV; FSKEFGRCIKEGVY; SKEFGRCIKEGVYS; KEFGRCIKEGVYSD; EFGRCIKEGVYSDF; FGRCIKEGVYSDFE; GRCIKEGVYSDFEN; RCIKEGVYSDFENR; CIKEGVYSDFENRE; IKEGVYSDFENREK; KEGVYSDFENREKL; EGVYSDFENREKLI; GVYSDFENREKLIS; VYSDFENREKLISL; YSDFENREKLISLI; SDFENREKLISLIR; DFENREKLISLIRF; FENREKLISLIRFK; ENREKLISLIRFKS; NREKLISLIRFKSS; REKLISLIRFKSSS; EKLISLIRFKSSSV; KLISLIRFKSSSVD; LISLIRFKSSSVDG; ISLIRFKSSSVDGF; SLIRFKSSSVDGFV; LIRFKSSSVDGFVS; IRFKSSSVDGFVSF; RFKSSSVDGFVSFK; FKSSSVDGFVSFKE; KSSSVDGFVSFKEY; SSSVDGFVSFKEYK; SSVDGFVSFKEYKE; SVDGFVSFKEYKER; VDGFVSFKEYKERM;

	DGFVSFKEYKERMN; GFVSFKEYKERMNE; FVSFKEYKERMNES; VSFKEYKERMNESQ; SFKEYKERMNESQK; FKEYKERMNESQKS; KEYKERMNESQKSI; EYKERMNESQKSIY; YKERMNESQKSIYY; KERMNESQKSIYYI; ERMNESQKSIYYIT; RMNESQKSIYYITG; MNESQKSIYYITGG; NESQKSIYYITGGK; ESQKSIYYITGGKE; SQKSIYYITGGKEN; QKSIYYITGGKENI; KSIYYITGGKENIL; SIYYITGGKENILK; IYYITGGKENILKE; YYITGGKENILKEN; YITGGKENILKENP; ITGGKENILKENPI; TGGKENILKENPIV; GGKENILKENPIVA; GKENILKENPIVAA; KENILKENPIVAAY; ENILKENPIVAAYK; NILKENPIVAAYKE; ILKENPIVAAYKEK; LKENPIVAAYKEKG; KENPIVAAYKEKGF; ENPIVAAYKEKGFE; NPIVAAYKEKGFEI; PIVAAYKEKGFEIL; IVAAYKEKGFEILI; VAAYKEKGFEILIM; AAYKEKGFEILIMD; AYKEKGFEILIMDD; YKEKGFEILIMDDE; KEKGFEILIMDDEL; EKGFEILIMDDELD; KGFEILIMDDELDE; GFEILIMDDELDEA; FEILIMDDELDEAI; EILIMDDELDEAIL; ILIMDDELDEAILN; LIMDDELDEAILNL; IMDDELDEAILNLI; MDDELDEAILNLIP; DDELDEAILNLIPE; DELDEAILNLIPEY; ELDEAILNLIPEYE; LDEAILNLIPEYEG; DEAILNLIPEYEGL; EAILNLIPEYEGLK; AILNLIPEYEGLKL; ILNLIPEYEGLKLK; LNLIPEYEGLKLKA; NLIPEYEGLKLKAI; LIPEYEGLKLKAIN; IPEYEGLKLKAINK; PEYEGLKLKAINKN; EYEGLKLKAINKNE; YEGLKLKAINKNET; EGLKLKAINKNETS; GLKLKAINKNETSN; LKLKAINKNETSNE; KLKAINKNETSNEL; LKAINKNETSNELK; KAINKNETSNELKD; AINKNETSNELKDE; INKNETSNELKDEN; NKNETSNELKDENF; KNETSNELKDENFK; NETSNELKDENFKK; ETSNELKDENFKKI; TSNELKDENFKKIE; SNELKDENFKKIEE; NELKDENFKKIEEE; ELKDENFKKIEEEF; LKDENFKKIEEEFK; KDENFKKIEEEFKD; DENFKKIEEEFKDT; ENFKKIEEEFKDTL; NFKKIEEEFKDTLT; FKKIEEEFKDTLTK; KKIEEEFKDTLTKV; KIEEEFKDTLTKVK; IEEEFKDTLTKVKE; EEEFKDTLTKVKEI; EEFKDTLTKVKEIL; EFKDTLTKVKEILK; FKDTLTKVKEILKD; KDTLTKVKEILKDH; DTLTKVKEILKDHI; TLTKVKEILKDHIK; LTKVKEILKDHIKE; TKVKEILKDHIKEV; KVKEILKDHIKEVN; VKEILKDHIKEVNL; KEILKDHIKEVNLS; EILKDHIKEVNLSA; ILKDHIKEVNLSAT; LKDHIKEVNLSATL; KDHIKEVNLSATLI; DHIKEVNLSATLIK; HIKEVNLSATLIKE; IKEVNLSATLIKEP; KEVNLSATLIKEPS; EVNLSATLIKEPSA; VNLSATLIKEPSAI; NLSATLIKEPSAII; LSATLIKEPSAIII; SATLIKEPSAIIID; ATLIKEPSAIIIDS; TLIKEPSAIIIDSN; LIKEPSAIIIDSND; IKEPSAIIIDSNDP; KEPSAIIIDSNDPT; EPSAIIIDSNDPTY; PSAIIIDSNDPTYQ; SAIIIDSNDPTYQM; AIIIDSNDPTYQMQ; IIIDSNDPTYQMQK; IIDSNDPTYQMQKI; IDSNDPTYQMQKIM; DSNDPTYQMQKIML; SNDPTYQMQKIMLS; NDPTYQMQKIMLSM; DPTYQMQKIMLSMG; PTYQMQKIMLSMGQ; TYQMQKIMLSMGQE; YQMQKIMLSMGQEV; QMQKIMLSMGQEVK; MQKIMLSMGQEVKE; QKIMLSMGQEVKEI; KIMLSMGQEVKEIK; IMLSMGQEVKEIKP; MLSMGQEVKEIKPI; LSMGQEVKEIKPIL; SMGQEVKEIKPILE; MGQEVKEIKPILEL; GQEVKEIKPILELN; QEVKEIKPILELNP; EVKEIKPILELNPN; VKEIKPILELNPNN; KEIKPILELNPNNK; EIKPILELNPNNKI; IKPILELNPNNKIV; KPILELNPNNKIVQ; PILELNPNNKIVQN; ILELNPNNKIVQNL; LELNPNNKIVQNLK; ELNPNNKIVQNLKN; LNPNNKIVQNLKNL; NPNNKIVQNLKNLE; PNNKIVQNLKNLEP; NNKIVQNLKNLEPE; NKIVQNLKNLEPEK; KIVQNLKNLEPEKL; IVQNLKNLEPEKLE; VQNLKNLEPEKLEK; QNLKNLEPEKLEKI; NLKNLEPEKLEKIS; LKNLEPEKLEKISI; KNLEPEKLEKISIL; NLEPEKLEKISILL; LEPEKLEKISILLF; EPEKLEKISILLFE; PEKLEKISILLFEE;

EKLEKISILLFEEA; KLEKISILLFEEAM; LEKISILLFEEAML;
EKISILLFEEAMLT; KISILLFEEAMLTS; ISILLFEEAMLTSG;
SILLFEEAMLTSGM; ILLFEEAMLTSGMP; LLFEEAMLTSGMPS;
LFEEAMLTSGMPSK; FEEAMLTSGMPSKN; EEAMLTSGMPSKNP;
EAMLTSGMPSKNPG; AMLTSGMPSKNPGK; MLTSGMPSKNPGKF;
LTSGMPSKNPGKFI; TSGMPSKNPGKFIN; SGMPSKNPGKFINI;
GMPSKNPGKFINII; MPSKNPGKFINIIN; PSKNPGKFINIINE;
SKNPGKFINIINEF; KNPGKFINIINEFI; NPGKFINIINEFIE;
PGKFINIINEFIEK; GKFINIINEFIEKD; KFINIINEFIEKDF;
FINIINEFIEKDFL;

15 mers:
MILIFYFKQIALFII; ILIFYFKQIALFIIF; LIFYFKQIALFIIFR;
IFYFKQIALFIIFRL; FYFKQIALFIIFRLC; YFKQIALFIIFRLCY;
FKQIALFIIFRLCYI; KQIALFIIFRLCYII; QIALFIIFRLCYIIK;
IALFIIFRLCYIIKK; ALFIIFRLCYIIKKV; LFIIFRLCYIIKKVK;
FIIFRLCYIIKKVKI; IIFRLCYIIKKVKIK; IFRLCYIIKKVKIKL;
FRLCYIIKKVKIKLK; RLCYIIKKVKIKLKR; LCYIIKKVKIKLKRK;
CYIIKKVKIKLKRKS; YIIKKVKIKLKRKSC; IIKKVKIKLKRKSCM;
IKKVKIKLKRKSCMK; KKVKIKLKRKSCMKK; KVKIKLKRKSCMKKQ;
VKIKLKRKSCMKKQF; KIKLKRKSCMKKQFD; IKLKRKSCMKKQFDT;
KLKRKSCMKKQFDTE; LKRKSCMKKQFDTEV; KRKSCMKKQFDTEVN;
RKSCMKKQFDTEVND; KSCMKKQFDTEVNDL; SCMKKQFDTEVNDLL;
CMKKQFDTEVNDLLY; MKKQFDTEVNDLLYL; KKQFDTEVNDLLYLI;
KQFDTEVNDLLYLII; QFDTEVNDLLYLIIH; FDTEVNDLLYLIIHS;
DTEVNDLLYLIIHSL; TEVNDLLYLIIHSLY; EVNDLLYLIIHSLYS;
VNDLLYLIIHSLYSH; NDLLYLIIHSLYSHK; DLLYLIIHSLYSHKE;
LLYLIIHSLYSHKEI; LYLIIHSLYSHKEIF; YLIIHSLYSHKEIFL;
LIIHSLYSHKEIFLR; IIHSLYSHKEIFLRE; IHSLYSHKEIFLREL;
HSLYSHKEIFLRELI; SLYSHKEIFLRELIS; LYSHKEIFLRELISN;
YSHKEIFLRELISNA; SHKEIFLRELISNAS; HKEIFLRELISNASD;
KEIFLRELISNASDA; EIFLRELISNASDAI; IFLRELISNASDAID;
FLRELISNASDAIDK; LRELISNASDAIDKL; RELISNASDAIDKLK;
ELISNASDAIDKLKF; LISNASDAIDKLKFL; ISNASDAIDKLKFLS;
SNASDAIDKLKFLSL; NASDAIDKLKFLSLT; ASDAIDKLKFLSLTN;
SDAIDKLKFLSLTNE; DAIDKLKFLSLTNEK; AIDKLKFLSLTNEKF;
IDKLKFLSLTNEKFK; DKLKFLSLTNEKFKN; KLKFLSLTNEKFKNI;
LKFLSLTNEKFKNIA; KFLSLTNEKFKNIAL; FLSLTNEKFKNIALE;
LSLTNEKFKNIALEP; SLTNEKFKNIALEPK; LTNEKFKNIALEPKI;
TNEKFKNIALEPKIE; NEKFKNIALEPKIEI; EKFKNIALEPKIEIS;
KFKNIALEPKIEISF; FKNIALEPKIEISFD; KNIALEPKIEISFDD;
NIALEPKIEISFDDK; IALEPKIEISFDDKS; ALEPKIEISFDDKSI;
LEPKIEISFDDKSIL; EPKIEISFDDKSILI; PKIEISFDDKSILIK;
KIEISFDDKSILIKD; IEISFDDKSILIKDN; EISFDDKSILIKDNG;
ISFDDKSILIKDNGI; SFDDKSILIKDNGIG; FDDKSILIKDNGIGM;
DDKSILIKDNGIGMD; DKSILIKDNGIGMDE; KSILIKDNGIGMDEQ;
SILIKDNGIGMDEQD; ILIKDNGIGMDEQDL; LIKDNGIGMDEQDLT;
IKDNGIGMDEQDLTN; KDNGIGMDEQDLTNH; DNGIGMDEQDLTNHL;
NGIGMDEQDLTNHLG; GIGMDEQDLTNHLGV; IGMDEQDLTNHLGVI;
GMDEQDLTNHLGVIA; MDEQDLTNHLGVIAK; DEQDLTNHLGVIAKS;
EQDLTNHLGVIAKSG; QDLTNHLGVIAKSGT; DLTNHLGVIAKSGTK;
LTNHLGVIAKSGTKE; TNHLGVIAKSGTKEF; NHLGVIAKSGTKEFI;
HLGVIAKSGTKEFIN; LGVIAKSGTKEFINN; GVIAKSGTKEFINNL;
VIAKSGTKEFINNLK; IAKSGTKEFINNLKQ; AKSGTKEFINNLKQD;
KSGTKEFINNLKQDE; SGTKEFINNLKQDEK; GTKEFINNLKQDEKK;
TKEFINNLKQDEKKS; KEFINNLKQDEKKSA; EFINNLKQDEKKSAS;
FINNLKQDEKKSASL; INNLKQDEKKSASLI; NNLKQDEKKSASLIG;

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CAA44492.1| Outer surface protein A [Borrelia burgdorferi]	13 mers: MKKYLLGIGLILA; KKYLLGIGLILAL; KYLLGIGLILALI; YLLGIGLILALIA; LLGIGLILALIAC; LGIGLILALIACK; GIGLILALIACKQ; IGLILALIACKQN; GLILALIACKQNV; LILALIACKQNVS; ILALIACKQNVST; LALIACKQNVSTL; ALIACKQNVSTLD; LIACKQNVSTLDE; IACKQNVSTLDEK; ACKQNVSTLDEKN; CKQNVSTLDEKNS; KQNVSTLDEKNSV; QNVSTLDEKNSVS; NVSTLDEKNSVSV; VSTLDEKNSVSVD; STLDEKNSVSVDL; TLDEKNSVSVDLP; LDEKNSVSVDLPG; DEKNSVSVDLPGG; EKNSVSVDLPGGM; KNSVSVDLPGGMT; NSVSVDLPGGMTE; SVSVDLPGGMTEL; VSVDLPGGMTELV; SVDLPGGMTELVS; VDLPGGMTELVSK; DLPGGMTELVSKE; LPGGMTELVSKEK; PGGMTELVSKEKD; GGMTELVSKEKDK; GMTELVSKEKDKD; MTELVSKEKDKDG; TELVSKEKDKDGK; ELVSKEKDKDGKY; LVSKEKDKDGKYS; VSKEKDKDGKYSL; SKEKDKDGKYSLE; KEKDKDGKYSLEA; EKDKDGKYSLEAT; KDKDGKYSLEATV; DKDGKYSLEATVD; KDGKYSLEATVDK; DGKYSLEATVDKL; GKYSLEATVDKLE; KYSLEATVDKLEL; YSLEATVDKLELK; SLEATVDKLELKG; LEATVDKLELKGT; EATVDKLELKGTS; ATVDKLELKGTSD; TVDKLELKGTSDK; VDKLELKGTSDKN; DKLELKGTSDKNN; KLELKGTSDKNNG;

	LELKGTSDKNNGS; ELKGTSDKNNGSG; LKGTSDKNNGSGT; KGTSDKNNGSGTL; GTSDKNNGSGTLE; TSDKNNGSGTLEG; SDKNNGSGTLEGE; DKNNGSGTLEGEK; KNNGSGTLEGEKT; NNGSGTLEGEKTD; NGSGTLEGEKTDK; GSGTLEGEKTDKS; SGTLEGEKTDKSK; GTLEGEKTDKSKV; TLEGEKTDKSKVK; LEGEKTDKSKVKL; EGEKTDKSKVKLT; GEKTDKSKVKLTI; EKTDKSKVKLTIA; KTDKSKVKLTIAD; TDKSKVKLTIADD; DKSKVKLTIADDL; KSKVKLTIADDLS; SKVKLTIADDLSQ; KVKLTIADDLSQT; VKLTIADDLSQTK; KLTIADDLSQTKF; LTIADDLSQTKFE; TIADDLSQTKFEI; IADDLSQTKFEIF; ADDLSQTKFEIFK; DDLSQTKFEIFKE; DLSQTKFEIFKED; LSQTKFEIFKEDA; SQTKFEIFKEDAK; QTKFEIFKEDAKT; TKFEIFKEDAKTL; KFEIFKEDAKTLV; FEIFKEDAKTLVS; EIFKEDAKTLVSK; IFKEDAKTLVSKK; FKEDAKTLVSKKV; KEDAKTLVSKKVT; EDAKTLVSKKVTL; DAKTLVSKKVTLK; AKTLVSKKVTLKD; KTLVSKKVTLKDK; TLVSKKVTLKDKS; LVSKKVTLKDKSS; VSKKVTLKDKSST; SKKVTLKDKSSTE; KKVTLKDKSSTEE; KVTLKDKSSTEEK; VTLKDKSSTEEKF; TLKDKSSTEEKFN; LKDKSSTEEKFNE; KDKSSTEEKFNEK; DKSSTEEKFNEKG; KSSTEEKFNEKGE; SSTEEKFNEKGET; STEEKFNEKGETS; TEEKFNEKGETSE; EEKFNEKGETSEK; EKFNEKGETSEKT; KFNEKGETSEKTI; FNEKGETSEKTIV; NEKGETSEKTIVR; EKGETSEKTIVRA; KGETSEKTIVRAN; GETSEKTIVRANG; ETSEKTIVRANGT; TSEKTIVRANGTR; SEKTIVRANGTRL; EKTIVRANGTRLE; KTIVRANGTRLEY; TIVRANGTRLEYT; IVRANGTRLEYTD; VRANGTRLEYTDI; RANGTRLEYTDIK; ANGTRLEYTDIKS; NGTRLEYTDIKSD; GTRLEYTDIKSDG; TRLEYTDIKSDGS; RLEYTDIKSDGSG; LEYTDIKSDGSGK; EYTDIKSDGSGKA; YTDIKSDGSGKAK; TDIKSDGSGKAKE; DIKSDGSGKAKEV; IKSDGSGKAKEVL; KSDGSGKAKEVLK; SDGSGKAKEVLKD; DGSGKAKEVLKDF; GSGKAKEVLKDFT; SGKAKEVLKDFTL; GKAKEVLKDFTLE; KAKEVLKDFTLEG; AKEVLKDFTLEGT; KEVLKDFTLEGTL; EVLKDFTLEGTLA; VLKDFTLEGTLAA; LKDFTLEGTLAAD; KDFTLEGTLAADG; DFTLEGTLAADGK; FTLEGTLAADGKT; TLEGTLAADGKTT; LEGTLAADGKTTL; EGTLAADGKTTLK; GTLAADGKTTLKV; TLAADGKTTLKVT; LAADGKTTLKVTE; AADGKTTLKVTEG; ADGKTTLKVTEGT; DGKTTLKVTEGTV; GKTTLKVTEGTVV; KTTLKVTEGTVVL; TTLKVTEGTVVLS; TLKVTEGTVVLSK; LKVTEGTVVLSKN; KVTEGTVVLSKNI; VTEGTVVLSKNIL; TEGTVVLSKNILK; EGTVVLSKNILKS; GTVVLSKNILKSG; TVVLSKNILKSGE; VVLSKNILKSGEI; VLSKNILKSGEIT; LSKNILKSGEITV; SKNILKSGEITVA; KNILKSGEITVAL; NILKSGEITVALD; ILKSGEITVALDD; LKSGEITVALDDS; KSGEITVALDDSD; SGEITVALDDSDT; GEITVALDDSDTT; EITVALDDSDTTQ; ITVALDDSDTTQA; TVALDDSDTTQAT; VALDDSDTTQATK; ALDDSDTTQATKK; LDDSDTTQATKKT; DDSDTTQATKKTG; DSDTTQATKKTGK; SDTTQATKKTGKW; DTTQATKKTGKWD; TTQATKKTGKWDS; TQATKKTGKWDSK; QATKKTGKWDSKT; ATKKTGKWDSKTS; TKKTGKWDSKTST; KKTGKWDSKTSTL; KTGKWDSKTSTLT; TGKWDSKTSTLTI; GKWDSKTSTLTIS; KWDSKTSTLTISV; WDSKTSTLTISVN; DSKTSTLTISVNS; SKTSTLTISVNSQ; KTSTLTISVNSQK; TSTLTISVNSQKT; STLTISVNSQKTK; TLTISVNSQKTKN; LTISVNSQKTKNL; TISVNSQKTKNLV; ISVNSQKTKNLVF; SVNSQKTKNLVFT; VNSQKTKNLVFTK; NSQKTKNLVFTKE; SQKTKNLVFTKED; QKTKNLVFTKEDT; KTKNLVFTKEDTI; TKNLVFTKEDTIT; KNLVFTKEDTITV; NLVFTKEDTITVQ; LVFTKEDTITVQK; VFTKEDTITVQKY; FTKEDTITVQKYD; TKEDTITVQKYDS; KEDTITVQKYDSA; EDTITVQKYDSAG; DTITVQKYDSAGT; TITVQKYDSAGTN; ITVQKYDSAGTNL; TVQKYDSAGTNLE; VQKYDSAGTNLEG; QKYDSAGTNLEGK; KYDSAGTNLEGKA; YDSAGTNLEGKAV; DSAGTNLEGKAVE; SAGTNLEGKAVEI; AGTNLEGKAVEIT; GTNLEGKAVEITT; TNLEGKAVEITTL; NLEGKAVEITTLK; LEGKAVEITTLKE; EGKAVEITTLKEL; GKAVEITTLKELK; KAVEITTLKELKN; AVEITTLKELKNA; VEITTLKELKNAL; EITTLKELKNALK; 14 mers: MKKYLLGIGLILAL; KKYLLGIGLILALI; KYLLGIGLILALIA; YLLGIGLILALIAC; LLGIGLILALIACK; LGIGLILALIACKQ; GIGLILALIACKQN; IGLILALIACKQNV; GLILALIACKQNVS; LILALIACKQNVST; ILALIACKQNVSTL; LALIACKQNVSTLD;

	ALIACKQNVSTLDE; LIACKQNVSTLDEK; IACKQNVSTLDEKN; ACKQNVSTLDEKNS; CKQNVSTLDEKNSV; KQNVSTLDEKNSVS; QNVSTLDEKNSVSV; NVSTLDEKNSVSVD; VSTLDEKNSVSVDL; STLDEKNSVSVDLP; TLDEKNSVSVDLPG; LDEKNSVSVDLPGG; DEKNSVSVDLPGGM; EKNSVSVDLPGGMT; KNSVSVDLPGGMTE; NSVSVDLPGGMTEL; SVSVDLPGGMTELV; VSVDLPGGMTELVS; SVDLPGGMTELVSK; VDLPGGMTELVSKE; DLPGGMTELVSKEK; LPGGMTELVSKEKD; PGGMTELVSKEKDK; GGMTELVSKEKDKD; GMTELVSKEKDKDG; MTELVSKEKDKDGK; TELVSKEKDKDGKY; ELVSKEKDKDGKYS; LVSKEKDKDGKYSL; VSKEKDKDGKYSLE; SKEKDKDGKYSLEA; KEKDKDGKYSLEAT; EKDKDGKYSLEATV; KDKDGKYSLEATVD; DKDGKYSLEATVDK; KDGKYSLEATVDKL; DGKYSLEATVDKLE; GKYSLEATVDKLEL; KYSLEATVDKLELK; YSLEATVDKLELKG; SLEATVDKLELKGT; LEATVDKLELKGTS; EATVDKLELKGTSD; ATVDKLELKGTSDK; TVDKLELKGTSDKN; VDKLELKGTSDKNN; DKLELKGTSDKNNG; KLELKGTSDKNNGS; LELKGTSDKNNGSG; ELKGTSDKNNGSGT; LKGTSDKNNGSGTL; KGTSDKNNGSGTLE; GTSDKNNGSGTLEG; TSDKNNGSGTLEGE; SDKNNGSGTLEGEK; DKNNGSGTLEGEKT; KNNGSGTLEGEKTD; NNGSGTLEGEKTDK; NGSGTLEGEKTDKS; GSGTLEGEKTDKSK; SGTLEGEKTDKSKV; GTLEGEKTDKSKVK; TLEGEKTDKSKVKL; LEGEKTDKSKVKLT; EGEKTDKSKVKLTI; GEKTDKSKVKLTIA; EKTDKSKVKLTIAD; KTDKSKVKLTIADD; TDKSKVKLTIADDL; DKSKVKLTIADDLS; KSKVKLTIADDLSQ; SKVKLTIADDLSQT; KVKLTIADDLSQTK; VKLTIADDLSQTKF; KLTIADDLSQTKFE; LTIADDLSQTKFEI; TIADDLSQTKFEIF; IADDLSQTKFEIFK; ADDLSQTKFEIFKE; DDLSQTKFEIFKED; DLSQTKFEIFKEDA; LSQTKFEIFKEDAK; SQTKFEIFKEDAKT; QTKFEIFKEDAKTL; TKFEIFKEDAKTLV; KFEIFKEDAKTLVS; FEIFKEDAKTLVSK; EIFKEDAKTLVSKK; IFKEDAKTLVSKKV; FKEDAKTLVSKKVT; KEDAKTLVSKKVTL; EDAKTLVSKKVTLK; DAKTLVSKKVTLKD; AKTLVSKKVTLKDK; KTLVSKKVTLKDKS; TLVSKKVTLKDKSS; LVSKKVTLKDKSST; VSKKVTLKDKSSTE; SKKVTLKDKSSTEE; KKVTLKDKSSTEEK; KVTLKDKSSTEEKF; VTLKDKSSTEEKFN; TLKDKSSTEEKFNE; LKDKSSTEEKFNEK; KDKSSTEEKFNEKG; DKSSTEEKFNEKGE; KSSTEEKFNEKGET; SSTEEKFNEKGETS; STEEKFNEKGETSE; TEEKFNEKGETSEK; EEKFNEKGETSEKT; EKFNEKGETSEKTI; KFNEKGETSEKTIV; FNEKGETSEKTIVR; NEKGETSEKTIVRA; EKGETSEKTIVRAN; KGETSEKTIVRANG; GETSEKTIVRANGT; ETSEKTIVRANGTR; TSEKTIVRANGTRL; SEKTIVRANGTRLE; EKTIVRANGTRLEY; KTIVRANGTRLEYT; TIVRANGTRLEYTD; IVRANGTRLEYTDI; VRANGTRLEYTDIK; RANGTRLEYTDIKS; ANGTRLEYTDIKSD; NGTRLEYTDIKSDG; GTRLEYTDIKSDGS; TRLEYTDIKSDGSG; RLEYTDIKSDGSGK; LEYTDIKSDGSGKA; EYTDIKSDGSGKAK; YTDIKSDGSGKAKE; TDIKSDGSGKAKEV; DIKSDGSGKAKEVL; IKSDGSGKAKEVLK; KSDGSGKAKEVLKD; SDGSGKAKEVLKDF; DGSGKAKEVLKDFT; GSGKAKEVLKDFTL; SGKAKEVLKDFTLE; GKAKEVLKDFTLEG; KAKEVLKDFTLEGT; AKEVLKDFTLEGTL; KEVLKDFTLEGTLA; EVLKDFTLEGTLAA; VLKDFTLEGTLAAD; LKDFTLEGTLAADG; KDFTLEGTLAADGK; DFTLEGTLAADGKT; FTLEGTLAADGKTT; TLEGTLAADGKTTL; LEGTLAADGKTTLK; EGTLAADGKTTLKV; GTLAADGKTTLKVT; TLAADGKTTLKVTE; LAADGKTTLKVTEG; AADGKTTLKVTEGT; ADGKTTLKVTEGTV; DGKTTLKVTEGTVV; GKTTLKVTEGTVVL; KTTLKVTEGTVVLS; TTLKVTEGTVVLSK; TLKVTEGTVVLSKN; LKVTEGTVVLSKNI; KVTEGTVVLSKNIL; VTEGTVVLSKNILK; TEGTVVLSKNILKS; EGTVVLSKNILKSG;

GTVVLSKNILKSGE; TVVLSKNILKSGEI; VVLSKNILKSGEIT;
VLSKNILKSGEITV; LSKNILKSGEITVA; SKNILKSGEITVAL;
KNILKSGEITVALD; NILKSGEITVALDD; ILKSGEITVALDDS;
LKSGEITVALDDSD; KSGEITVALDDSDT; SGEITVALDDSDTT;
GEITVALDDSDTTQ; EITVALDDSDTTQA; ITVALDDSDTTQAT;
TVALDDSDTTQATK; VALDDSDTTQATKK; ALDDSDTTQATKKT;
LDDSDTTQATKKTG; DDSDTTQATKKTGK; DSDTTQATKKTGKW;
SDTTQATKKTGKWD; DTTQATKKTGKWDS; TTQATKKTGKWDSK;
TQATKKTGKWDSKT; QATKKTGKWDSKTS; ATKKTGKWDSKTST;
TKKTGKWDSKTSTL; KKTGKWDSKTSTLT; KTGKWDSKTSTLTI;
TGKWDSKTSTLTIS; GKWDSKTSTLTISV; KWDSKTSTLTISVN;
WDSKTSTLTISVNS; DSKTSTLTISVNSQ; SKTSTLTISVNSQK;
KTSTLTISVNSQKT; TSTLTISVNSQKTK; STLTISVNSQKTKN;
TLTISVNSQKTKNL; LTISVNSQKTKNLV; TISVNSQKTKNLVF;
ISVNSQKTKNLVFT; SVNSQKTKNLVFTK; VNSQKTKNLVFTKE;
NSQKTKNLVFTKED; SQKTKNLVFTKEDT; QKTKNLVFTKEDTI;
KTKNLVFTKEDTIT; TKNLVFTKEDTITV; KNLVFTKEDTITVQ;
NLVFTKEDTITVQK; LVFTKEDTITVQKY; VFTKEDTITVQKYD;
FTKEDTITVQKYDS; TKEDTITVQKYDSA; KEDTITVQKYDSAG;
EDTITVQKYDSAGT; DTITVQKYDSAGTN; TITVQKYDSAGTNL;
ITVQKYDSAGTNLE; TVQKYDSAGTNLEG; VQKYDSAGTNLEGK;
QKYDSAGTNLEGKA; KYDSAGTNLEGKAV; YDSAGTNLEGKAVE;
DSAGTNLEGKAVEI; SAGTNLEGKAVEIT; AGTNLEGKAVEITT;
GTNLEGKAVEITTL; TNLEGKAVEITTLK; NLEGKAVEITTLKE;
LEGKAVEITTLKEL; EGKAVEITTLKELK; GKAVEITTLKELKN;
KAVEITTLKELKNA; AVEITTLKELKNAL; VEITTLKELKNALK;

15 mers:
MKKYLLGIGLILALI; KKYLLGIGLILALIA; KYLLGIGLILALIAC;
YLLGIGLILALIACK; LLGIGLILALIACKQ; LGIGLILALIACKQN;
GIGLILALIACKQNV; IGLILALIACKQNVS; GLILALIACKQNVST;
LILALIACKQNVSTL; ILALIACKQNVSTLD; LALIACKQNVSTLDE;
ALIACKQNVSTLDEK; LIACKQNVSTLDEKN; IACKQNVSTLDEKNS;
ACKQNVSTLDEKNSV; CKQNVSTLDEKNSVS; KQNVSTLDEKNSVSV;
QNVSTLDEKNSVSVD; NVSTLDEKNSVSVDL; VSTLDEKNSVSVDLP;
STLDEKNSVSVDLPG; TLDEKNSVSVDLPGG; LDEKNSVSVDLPGGM;
DEKNSVSVDLPGGMT; EKNSVSVDLPGGMTE; KNSVSVDLPGGMTEL;
NSVSVDLPGGMTELV; SVSVDLPGGMTELVS; VSVDLPGGMTELVSK;
SVDLPGGMTELVSKE; VDLPGGMTELVSKEK; DLPGGMTELVSKEKD;
LPGGMTELVSKEKDK; PGGMTELVSKEKDKD; GGMTELVSKEKDKDG;
GMTELVSKEKDKDGK; MTELVSKEKDKDGKY; TELVSKEKDKDGKYS;
ELVSKEKDKDGKYSL; LVSKEKDKDGKYSLE; VSKEKDKDGKYSLEA;
SKEKDKDGKYSLEAT; KEKDKDGKYSLEATV; EKDKDGKYSLEATVD;
KDKDGKYSLEATVDK; DKDGKYSLEATVDKL; KDGKYSLEATVDKLE;
DGKYSLEATVDKLEL; GKYSLEATVDKLELK; KYSLEATVDKLELKG;
YSLEATVDKLELKGT; SLEATVDKLELKGTS; LEATVDKLELKGTSD;
EATVDKLELKGTSDK; ATVDKLELKGTSDKN; TVDKLELKGTSDKNN;
VDKLELKGTSDKNNG; DKLELKGTSDKNNGS; KLELKGTSDKNNGSG;
LELKGTSDKNNGSGT; ELKGTSDKNNGSGTL; LKGTSDKNNGSGTLE;
KGTSDKNNGSGTLEG; GTSDKNNGSGTLEGE; TSDKNNGSGTLEGEK;
SDKNNGSGTLEGEKT; DKNNGSGTLEGEKTD; KNNGSGTLEGEKTDK;
NNGSGTLEGEKTDKS; NGSGTLEGEKTDKSK; GSGTLEGEKTDKSKV;
SGTLEGEKTDKSKVK; GTLEGEKTDKSKVKL; TLEGEKTDKSKVKLT;
LEGEKTDKSKVKLTI; EGEKTDKSKVKLTIA; GEKTDKSKVKLTIAD;
EKTDKSKVKLTIADD; KTDKSKVKLTIADDL; TDKSKVKLTIADDLS;
DKSKVKLTIADDLSQ; KSKVKLTIADDLSQT; SKVKLTIADDLSQTK;
KVKLTIADDLSQTKF; VKLTIADDLSQTKFE; KLTIADDLSQTKFEI;

	LTIADDLSQTKFEIF; TIADDLSQTKFEIFK; IADDLSQTKFEIFKE; ADDLSQTKFEIFKED; DDLSQTKFEIFKEDA; DLSQTKFEIFKEDAK; LSQTKFEIFKEDAKT; SQTKFEIFKEDAKTL; QTKFEIFKEDAKTLV; TKFEIFKEDAKTLVS; KFEIFKEDAKTLVSK; FEIFKEDAKTLVSKK; EIFKEDAKTLVSKKV; IFKEDAKTLVSKKVT; FKEDAKTLVSKKVTL; KEDAKTLVSKKVTLK; EDAKTLVSKKVTLKD; DAKTLVSKKVTLKDK; AKTLVSKKVTLKDKS; KTLVSKKVTLKDKSS; TLVSKKVTLKDKSST; LVSKKVTLKDKSSTE; VSKKVTLKDKSSTEE; SKKVTLKDKSSTEEK; KKVTLKDKSSTEEKF; KVTLKDKSSTEEKFN; VTLKDKSSTEEKFNE; TLKDKSSTEEKFNEK; LKDKSSTEEKFNEKG; KDKSSTEEKFNEKGE; DKSSTEEKFNEKGET; KSSTEEKFNEKGETS; SSTEEKFNEKGETSE; STEEKFNEKGETSEK; TEEKFNEKGETSEKT; EEKFNEKGETSEKTI; EKFNEKGETSEKTIV; KFNEKGETSEKTIVR; FNEKGETSEKTIVRA; NEKGETSEKTIVRAN; EKGETSEKTIVRANG; KGETSEKTIVRANGT; GETSEKTIVRANGTR; ETSEKTIVRANGTRL; TSEKTIVRANGTRLE; SEKTIVRANGTRLEY; EKTIVRANGTRLEYT; KTIVRANGTRLEYTD; TIVRANGTRLEYTDI; IVRANGTRLEYTDIK; VRANGTRLEYTDIKS; RANGTRLEYTDIKSD; ANGTRLEYTDIKSDG; NGTRLEYTDIKSDGS; GTRLEYTDIKSDGSG; TRLEYTDIKSDGSGK; RLEYTDIKSDGSGKA; LEYTDIKSDGSGKAK; EYTDIKSDGSGKAKE; YTDIKSDGSGKAKEV; TDIKSDGSGKAKEVL; DIKSDGSGKAKEVLK; IKSDGSGKAKEVLKD; KSDGSGKAKEVLKDF; SDGSGKAKEVLKDFT; DGSGKAKEVLKDFTL; GSGKAKEVLKDFTLE; SGKAKEVLKDFTLEG; GKAKEVLKDFTLEGT; KAKEVLKDFTLEGTL; AKEVLKDFTLEGTLA; KEVLKDFTLEGTLAA; EVLKDFTLEGTLAAD; VLKDFTLEGTLAADG; LKDFTLEGTLAADGK; KDFTLEGTLAADGKT; DFTLEGTLAADGKTT; FTLEGTLAADGKTTL; TLEGTLAADGKTTLK; LEGTLAADGKTTLKV; EGTLAADGKTTLKVT; GTLAADGKTTLKVTE; TLAADGKTTLKVTEG; LAADGKTTLKVTEGT; AADGKTTLKVTEGTV; ADGKTTLKVTEGTVV; DGKTTLKVTEGTVVL; GKTTLKVTEGTVVLS; KTTLKVTEGTVVLSK; TTLKVTEGTVVLSKN; TLKVTEGTVVLSKNI; LKVTEGTVVLSKNIL; KVTEGTVVLSKNILK; VTEGTVVLSKNILKS; TEGTVVLSKNILKSG; EGTVVLSKNILKSGE; GTVVLSKNILKSGEI; TVVLSKNILKSGEIT; VVLSKNILKSGEITV; VLSKNILKSGEITVA; LSKNILKSGEITVAL; SKNILKSGEITVALD; KNILKSGEITVALDD; NILKSGEITVALDDS; ILKSGEITVALDDSD; LKSGEITVALDDSDT; KSGEITVALDDSDTT; SGEITVALDDSDTTQ; GEITVALDDSDTTQA; EITVALDDSDTTQAT; ITVALDDSDTTQATK; TVALDDSDTTQATKK; VALDDSDTTQATKKT; ALDDSDTTQATKKTG; LDDSDTTQATKKTGK; DDSDTTQATKKTGKW; DSDTTQATKKTGKWD; SDTTQATKKTGKWDS; DTTQATKKTGKWDSK; TTQATKKTGKWDSKT; TQATKKTGKWDSKTS; QATKKTGKWDSKTST; ATKKTGKWDSKTSTL; TKKTGKWDSKTSTLT; KKTGKWDSKTSTLTI; KTGKWDSKTSTLTIS; TGKWDSKTSTLTISV; GKWDSKTSTLTISVN; KWDSKTSTLTISVNS; WDSKTSTLTISVNSQ; DSKTSTLTISVNSQK; SKTSTLTISVNSQKT; KTSTLTISVNSQKTK; TSTLTISVNSQKTKN; STLTISVNSQKTKNL; TLTISVNSQKTKNLV; LTISVNSQKTKNLVF; TISVNSQKTKNLVFT; ISVNSQKTKNLVFTK; SVNSQKTKNLVFTKE; VNSQKTKNLVFTKED; NSQKTKNLVFTKEDT; SQKTKNLVFTKEDTI; QKTKNLVFTKEDTIT; KTKNLVFTKEDTITV; TKNLVFTKEDTITVQ; KNLVFTKEDTITVQK; NLVFTKEDTITVQKY; LVFTKEDTITVQKYD; VFTKEDTITVQKYDS; FTKEDTITVQKYDSA; TKEDTITVQKYDSAG; KEDTITVQKYDSAGT; EDTITVQKYDSAGTN; DTITVQKYDSAGTNL; TITVQKYDSAGTNLE; ITVQKYDSAGTNLEG; TVQKYDSAGTNLEGK; VQKYDSAGTNLEGKA; QKYDSAGTNLEGKAV; KYDSAGTNLEGKAVE; YDSAGTNLEGKAVEI; DSAGTNLEGKAVEIT; SAGTNLEGKAVEITT; AGTNLEGKAVEITTL; GTNLEGKAVEITTLK; TNLEGKAVEITTLKE; NLEGKAVEITTLKEL; LEGKAVEITTLKELK; EGKAVEITTLKELKN; GKAVEITTLKELKNA;

KAVEITTLKELKNAL; AVEITTLKELKNALK;

16 mers:
MKKYLLGIGLILALIA; KKYLLGIGLILALIAC; KYLLGIGLILALIACK;
YLLGIGLILALIACKQ; LLGIGLILALIACKQN; LGIGLILALIACKQNV;
GIGLILALIACKQNVS; IGLILALIACKQNVST; GLILALIACKQNVSTL;
LILALIACKQNVSTLD; ILALIACKQNVSTLDE; LALIACKQNVSTLDEK;
ALIACKQNVSTLDEKN; LIACKQNVSTLDEKNS; IACKQNVSTLDEKNSV;
ACKQNVSTLDEKNSVS; CKQNVSTLDEKNSVSV; KQNVSTLDEKNSVSVD;
QNVSTLDEKNSVSVDL; NVSTLDEKNSVSVDLP; VSTLDEKNSVSVDLPG;
STLDEKNSVSVDLPGG; TLDEKNSVSVDLPGGM; LDEKNSVSVDLPGGMT;
DEKNSVSVDLPGGMTE; EKNSVSVDLPGGMTEL; KNSVSVDLPGGMTELV;
NSVSVDLPGGMTELVS; SVSVDLPGGMTELVSK; VSVDLPGGMTELVSKE;
SVDLPGGMTELVSKEK; VDLPGGMTELVSKEKD; DLPGGMTELVSKEKDK;
LPGGMTELVSKEKDKD; PGGMTELVSKEKDKDG; GGMTELVSKEKDKDGK;
GMTELVSKEKDKDGKY; MTELVSKEKDKDGKYS; TELVSKEKDKDGKYSL;
ELVSKEKDKDGKYSLE; LVSKEKDKDGKYSLEA; VSKEKDKDGKYSLEAT;
SKEKDKDGKYSLEATV; KEKDKDGKYSLEATVD; EKDKDGKYSLEATVDK;
KDKDGKYSLEATVDKL; DKDGKYSLEATVDKLE; KDGKYSLEATVDKLEL;
DGKYSLEATVDKLELK; GKYSLEATVDKLELKG; KYSLEATVDKLELKGT;
YSLEATVDKLELKGTS; SLEATVDKLELKGTSD; LEATVDKLELKGTSDK;
EATVDKLELKGTSDKN; ATVDKLELKGTSDKNN; TVDKLELKGTSDKNNG;
VDKLELKGTSDKNNGS; DKLELKGTSDKNNGSG; KLELKGTSDKNNGSGT;
LELKGTSDKNNGSGTL; ELKGTSDKNNGSGTLE; LKGTSDKNNGSGTLEG;
KGTSDKNNGSGTLEGE; GTSDKNNGSGTLEGEK; TSDKNNGSGTLEGEKT;
SDKNNGSGTLEGEKTD; DKNNGSGTLEGEKTDK; KNNGSGTLEGEKTDKS;
NNGSGTLEGEKTDKSK; NGSGTLEGEKTDKSKV; GSGTLEGEKTDKSKVK;
SGTLEGEKTDKSKVKL; GTLEGEKTDKSKVKLT; TLEGEKTDKSKVKLTI;
LEGEKTDKSKVKLTIA; EGEKTDKSKVKLTIAD; GEKTDKSKVKLTIADD;
EKTDKSKVKLTIADDL; KTDKSKVKLTIADDLS; TDKSKVKLTIADDLSQ;
DKSKVKLTIADDLSQT; KSKVKLTIADDLSQTK; SKVKLTIADDLSQTKF;
KVKLTIADDLSQTKFE; VKLTIADDLSQTKFEI; KLTIADDLSQTKFEIF;
LTIADDLSQTKFEIFK; TIADDLSQTKFEIFKE; IADDLSQTKFEIFKED;
ADDLSQTKFEIFKEDA; DDLSQTKFEIFKEDAK; DLSQTKFEIFKEDAKT;
LSQTKFEIFKEDAKTL; SQTKFEIFKEDAKTLV; QTKFEIFKEDAKTLVS;
TKFEIFKEDAKTLVSK; KFEIFKEDAKTLVSKK; FEIFKEDAKTLVSKKV;
EIFKEDAKTLVSKKVT; IFKEDAKTLVSKKVTL; FKEDAKTLVSKKVTLK;
KEDAKTLVSKKVTLKD; EDAKTLVSKKVTLKDK; DAKTLVSKKVTLKDKS;
AKTLVSKKVTLKDKSS; KTLVSKKVTLKDKSST; TLVSKKVTLKDKSSTE;
LVSKKVTLKDKSSTEE; VSKKVTLKDKSSTEEK; SKKVTLKDKSSTEEKF;
KKVTLKDKSSTEEKFN; KVTLKDKSSTEEKFNE; VTLKDKSSTEEKFNEK;
TLKDKSSTEEKFNEKG; LKDKSSTEEKFNEKGE; KDKSSTEEKFNEKGET;
DKSSTEEKFNEKGETS; KSSTEEKFNEKGETSE; SSTEEKFNEKGETSEK;
STEEKFNEKGETSEKT; TEEKFNEKGETSEKTI; EEKFNEKGETSEKTIV;
EKFNEKGETSEKTIVR; KFNEKGETSEKTIVRA; FNEKGETSEKTIVRAN;
NEKGETSEKTIVRANG; EKGETSEKTIVRANGT; KGETSEKTIVRANGTR;
GETSEKTIVRANGTRL; ETSEKTIVRANGTRLE; TSEKTIVRANGTRLEY;
SEKTIVRANGTRLEYT; EKTIVRANGTRLEYTD; KTIVRANGTRLEYTDI;
TIVRANGTRLEYTDIK; IVRANGTRLEYTDIKS; VRANGTRLEYTDIKSD;
RANGTRLEYTDIKSDG; ANGTRLEYTDIKSDGS; NGTRLEYTDIKSDGSG;
GTRLEYTDIKSDGSGK; TRLEYTDIKSDGSGKA; RLEYTDIKSDGSGKAK;
LEYTDIKSDGSGKAKE; EYTDIKSDGSGKAKEV; YTDIKSDGSGKAKEVL;
TDIKSDGSGKAKEVLK; DIKSDGSGKAKEVLKD; IKSDGSGKAKEVLKDF;
KSDGSGKAKEVLKDFT; SDGSGKAKEVLKDFTL; DGSGKAKEVLKDFTLE;
GSGKAKEVLKDFTLEG; SGKAKEVLKDFTLEGT; GKAKEVLKDFTLEGTL;
KAKEVLKDFTLEGTLA; AKEVLKDFTLEGTLAA; KEVLKDFTLEGTLAAD;
EVLKDFTLEGTLAADG; VLKDFTLEGTLAADGK; LKDFTLEGTLAADGKT;

	KDFTLEGTLAADGKTT; DFTLEGTLAADGKTTL; FTLEGTLAADGKTTLK; TLEGTLAADGKTTLKV; LEGTLAADGKTTLKVT; EGTLAADGKTTLKVTE; GTLAADGKTTLKVTEG; TLAADGKTTLKVTEGT; LAADGKTTLKVTEGTV; AADGKTTLKVTEGTVV; ADGKTTLKVTEGTVVL; DGKTTLKVTEGTVVLS; GKTTLKVTEGTVVLSK; KTTLKVTEGTVVLSKN; TTLKVTEGTVVLSKNI; TLKVTEGTVVLSKNIL; LKVTEGTVVLSKNILK; KVTEGTVVLSKNILKS; VTEGTVVLSKNILKSG; TEGTVVLSKNILKSGE; EGTVVLSKNILKSGEI; GTVVLSKNILKSGEIT; TVVLSKNILKSGEITV; VVLSKNILKSGEITVA; VLSKNILKSGEITVAL; LSKNILKSGEITVALD; SKNILKSGEITVALDD; KNILKSGEITVALDDS; NILKSGEITVALDDSD; ILKSGEITVALDDSDT; LKSGEITVALDDSDTT; KSGEITVALDDSDTTQ; SGEITVALDDSDTTQA; GEITVALDDSDTTQAT; EITVALDDSDTTQATK; ITVALDDSDTTQATKK; TVALDDSDTTQATKKT; VALDDSDTTQATKKTG; ALDDSDTTQATKKTGK; LDDSDTTQATKKTGKW; DDSDTTQATKKTGKWD; DSDTTQATKKTGKWDS; SDTTQATKKTGKWDSK; DTTQATKKTGKWDSKT; TTQATKKTGKWDSKTS; TQATKKTGKWDSKTST; QATKKTGKWDSKTSTL; ATKKTGKWDSKTSTLT; TKKTGKWDSKTSTLTI; KKTGKWDSKTSTLTIS; KTGKWDSKTSTLTISV; TGKWDSKTSTLTISVN; GKWDSKTSTLTISVNS; KWDSKTSTLTISVNSQ; WDSKTSTLTISVNSQK; DSKTSTLTISVNSQKT; SKTSTLTISVNSQKTK; KTSTLTISVNSQKTKN; TSTLTISVNSQKTKNL; STLTISVNSQKTKNLV; TLTISVNSQKTKNLVF; LTISVNSQKTKNLVFT; TISVNSQKTKNLVFTK; ISVNSQKTKNLVFTKE; SVNSQKTKNLVFTKED; VNSQKTKNLVFTKEDT; NSQKTKNLVFTKEDTI; SQKTKNLVFTKEDTIT; QKTKNLVFTKEDTITV; KTKNLVFTKEDTITVQ; TKNLVFTKEDTITVQK; KNLVFTKEDTITVQKY; NLVFTKEDTITVQKYD; LVFTKEDTITVQKYDS; VFTKEDTITVQKYDSA; FTKEDTITVQKYDSAG; TKEDTITVQKYDSAGT; KEDTITVQKYDSAGTN; EDTITVQKYDSAGTNL; DTITVQKYDSAGTNLE; TITVQKYDSAGTNLEG; ITVQKYDSAGTNLEGK; TVQKYDSAGTNLEGKA; VQKYDSAGTNLEGKAV; QKYDSAGTNLEGKAVE; KYDSAGTNLEGKAVEI; YDSAGTNLEGKAVEIT; DSAGTNLEGKAVEITT; SAGTNLEGKAVEITTL; AGTNLEGKAVEITTLK; GTNLEGKAVEITTLKE; TNLEGKAVEITTLKEL; NLEGKAVEITTLKELK; LEGKAVEITTLKELKN; EGKAVEITTLKELKNA; GKAVEITTLKELKNAL; KAVEITTLKELKNALK; AVEITTLKELKNALK□;
|BAA22351.1| Outer surface protein B [Borrelia garinii]	13 mers: MKKYLLGFALVLA; KKYLLGFALVLAL; KYLLGFALVLALI; YLLGFALVLALIA; LLGFALVLALIAC; LGFALVLALIACG; GFALVLALIACGQ; FALVLALIACGQK; ALVLALIACGQKG; LVLALIACGQKGA; VLALIACGQKGAE; LALIACGQKGAEP; ALIACGQKGAEPK; LIACGQKGAEPKH; IACGQKGAEPKHN; ACGQKGAEPKHND; CGQKGAEPKHNDQ; GQKGAEPKHNDQE; QKGAEPKHNDQEV; KGAEPKHNDQEVE; GAEPKHNDQEVED; AEPKHNDQEVEDS; EPKHNDQEVEDSK; PKHNDQEVEDSKK; KHNDQEVEDSKKD; HNDQEVEDSKKDQ; NDQEVEDSKKDQK; DQEVEDSKKDQKD; QEVEDSKKDQKDA; EVEDSKKDQKDAS; VEDSKKDQKDASK; EDSKKDQKDASKK; DSKKDQKDASKKD; SKKDQKDASKKDL; KKDQKDASKKDLP; KDQKDASKKDLPL; DQKDASKKDLPLV; QKDASKKDLPLVT; KDASKKDLPLVTE; DASKKDLPLVTED; ASKKDLPLVTEDT; SKKDLPLVTEDTV; KKDLPLVTEDTVK; KDLPLVTEDTVKL; DLPLVTEDTVKLF; LPLVTEDTVKLFN; PLVTEDTVKLFND; LVTEDTVKLFNDT; VTEDTVKLFNDTK; TEDTVKLFNDTKI; EDTVKLFNDTKIF; DTVKLFNDTKIFI; TVKLFNDTKIFIS; VKLFNDTKIFISK; KLFNDTKIFISKE; LFNDTKIFISKEK; FNDTKIFISKEKN; NDTKIFISKEKNK; DTKIFISKEKNKD; TKIFISKEKNKDG; KIFISKEKNKDGK; IFISKEKNKDGKY; FISKEKNKDGKYE; ISKEKNKDGKYEL; SKEKNKDGKYELR; KEKNKDGKYELRA; EKNKDGKYELRAT; KNKDGKYELRATV; NKDGKYELRATVD; KDGKYELRATVDT; DGKYELRATVDTV; GKYELRATVDTVE; KYELRATVDTVEL; YELRATVDTVELK; ELRATVDTVELKG; LRATVDTVELKGV; RATVDTVELKGVA; ATVDTVELKGVAD; TVDTVELKGVADK; VDTVELKGVADKN; DTVELKGVADKND; TVELKGVADKNDG; VELKGVADKNDGS; ELKGVADKNDGSG; LKGVADKNDGSGG; KGVADKNDGSGGK; GVADKNDGSGGKL; VADKNDGSGGKLE;

ADKNDGSGGKLEG; DKNDGSGGKLEGV; KNDGSGGKLEGVK; NDGSGGKLEGVKS;
DGSGGKLEGVKSD; GSGGKLEGVKSDQ; SGGKLEGVKSDQS; GGKLEGVKSDQSK;
GKLEGVKSDQSKV; KLEGVKSDQSKVT; LEGVKSDQSKVTM; EGVKSDQSKVTMS;
GVKSDQSKVTMSI; VKSDQSKVTMSIT; KSDQSKVTMSITD; SDQSKVTMSITDD;
DQSKVTMSITDDL; QSKVTMSITDDLN; SKVTMSITDDLNT; KVTMSITDDLNTI;
VTMSITDDLNTIT; TMSITDDLNTITV; MSITDDLNTITVE; SITDDLNTITVET;
ITDDLNTITVETY; TDDLNTITVETYD; DDLNTITVETYDS; DLNTITVETYDSS;
LNTITVETYDSSN; NTITVETYDSSNT; TITVETYDSSNTK; ITVETYDSSNTKV;
TVETYDSSNTKVA; VETYDSSNTKVAS; ETYDSSNTKVASK; TYDSSNTKVASKV;
YDSSNTKVASKVF; DSSNTKVASKVFK; SSNTKVASKVFKK; SNTKVASKVFKKQ;
NTKVASKVFKKQG; TKVASKVFKKQGS; KVASKVFKKQGSL; VASKVFKKQGSLT;
ASKVFKKQGSLTE; SKVFKKQGSLTEE; KVFKKQGSLTEET; VFKKQGSLTEETE;
FKKQGSLTEETEE; KKQGSLTEETEET; KQGSLTEETEETY; QGSLTEETEETYK;
GSLTEETEETYKT; SLTEETEETYKTG; LTEETEETYKTGK; TEETEETYKTGKL;
EETEETYKTGKLS; ETEETYKTGKLST; TEETYKTGKLSTK; EETYKTGKLSTKK;
ETYKTGKLSTKKI; TYKTGKLSTKKIT; YKTGKLSTKKITR; KTGKLSTKKITRT;
TGKLSTKKITRTN; GKLSTKKITRTNG; KLSTKKITRTNGT; LSTKKITRTNGTT;
STKKITRTNGTTL; TKKITRTNGTTLE; KKITRTNGTTLEY; KITRTNGTTLEYS;
ITRTNGTTLEYSD; TRTNGTTLEYSDM; RTNGTTLEYSDMT; TNGTTLEYSDMTN;
NGTTLEYSDMTND; GTTLEYSDMTNDE; TTLEYSDMTNDEN; TLEYSDMTNDENA;
LEYSDMTNDENAT; EYSDMTNDENATK; YSDMTNDENATKA; SDMTNDENATKAV;
DMTNDENATKAVE; MTNDENATKAVET; TNDENATKAVETL; NDENATKAVETLK;
DENATKAVETLKN; ENATKAVETLKNG; NATKAVETLKNGI; ATKAVETLKNGIM;
TKAVETLKNGIML; KAVETLKNGIMLE; AVETLKNGIMLEG; VETLKNGIMLEGN;
ETLKNGIMLEGNL; TLKNGIMLEGNLV; LKNGIMLEGNLVG; KNGIMLEGNLVGG;
NGIMLEGNLVGGK; GIMLEGNLVGGKT; IMLEGNLVGGKTS; MLEGNLVGGKTSV;
LEGNLVGGKTSVE; EGNLVGGKTSVEI; GNLVGGKTSVEIK; NLVGGKTSVEIKE;
LVGGKTSVEIKEG; VGGKTSVEIKEGT; GGKTSVEIKEGTV; GKTSVEIKEGTVT;
KTSVEIKEGTVTL; TSVEIKEGTVTLK; SVEIKEGTVTLKK; VEIKEGTVTLKKE;
EIKEGTVTLKKEI; IKEGTVTLKKEIE; KEGTVTLKKEIEK; EGTVTLKKEIEKA;
GTVTLKKEIEKAG; TVTLKKEIEKAGT; VTLKKEIEKAGTV; TLKKEIEKAGTVK;
LKKEIEKAGTVKL; KKEIEKAGTVKLF; KEIEKAGTVKLFL; EIEKAGTVKLFLD;
IEKAGTVKLFLDD; EKAGTVKLFLDDT; KAGTVKLFLDDTS; AGTVKLFLDDTSS;
GTVKLFLDDTSSG; TVKLFLDDTSSGS; VKLFLDDTSSGST; KLFLDDTSSGSTK;
LFLDDTSSGSTKK; FLDDTSSGSTKKT; LDDTSSGSTKKTA; DDTSSGSTKKTAV;
DTSSGSTKKTAVW; TSSGSTKKTAVWS; SSGSTKKTAVWSD; SGSTKKTAVWSDT;
GSTKKTAVWSDTS; STKKTAVWSDTSN; TKKTAVWSDTSNT; KKTAVWSDTSNTL;
KTAVWSDTSNTLT; TAVWSDTSNTLTV; AVWSDTSNTLTVS; VWSDTSNTLTVSA;
WSDTSNTLTVSAD; SDTSNTLTVSADS; DTSNTLTVSADSK; TSNTLTVSADSKK;
SNTLTVSADSKKI; NTLTVSADSKKIK; TLTVSADSKKIKD; LTVSADSKKIKDF;
TVSADSKKIKDFV; VSADSKKIKDFVF; SADSKKIKDFVFL; ADSKKIKDFVFLT;
DSKKIKDFVFLTD; SKKIKDFVFLTDG; KKIKDFVFLTDGT; KIKDFVFLTDGTI;
IKDFVFLTDGTIT; KDFVFLTDGTITV; DFVFLTDGTITVQ; FVFLTDGTITVQN;
VFLTDGTITVQNY; FLTDGTITVQNYD; LTDGTITVQNYDT; TDGTITVQNYDTA;
DGTITVQNYDTAG; GTITVQNYDTAGT; TITVQNYDTAGTK; ITVQNYDTAGTKL;
TVQNYDTAGTKLA; VQNYDTAGTKLAG; QNYDTAGTKLAGT; NYDTAGTKLAGTA;
YDTAGTKLAGTAT; DTAGTKLAGTATE; TAGTKLAGTATEI; AGTKLAGTATEIK;
GTKLAGTATEIKD; TKLAGTATEIKDL; KLAGTATEIKDLE; LAGTATEIKDLEA;
AGTATEIKDLEAL; GTATEIKDLEALK; TATEIKDLEALKA; ATEIKDLEALKAA;
TEIKDLEALKAAL; EIKDLEALKAALK;

14 mers:
MKKYLLGFALVLAL; KKYLLGFALVLALI; KYLLGFALVLALIA;
YLLGFALVLALIAC; LLGFALVLALIACG; LGFALVLALIACGQ;
GFALVLALIACGQK; FALVLALIACGQKG; ALVLALIACGQKGA;
LVLALIACGQKGAE; VLALIACGQKGAEP; LALIACGQKGAEPK;
ALIACGQKGAEPKH; LIACGQKGAEPKHN; IACGQKGAEPKHND;

	ACGQKGAEPKHNDQ; CGQKGAEPKHNDQE; GQKGAEPKHNDQEV; QKGAEPKHNDQEVE; KGAEPKHNDQEVED; GAEPKHNDQEVEDS; AEPKHNDQEVEDSK; EPKHNDQEVEDSKK; PKHNDQEVEDSKKD; KHNDQEVEDSKKDQ; HNDQEVEDSKKDQK; NDQEVEDSKKDQKD; DQEVEDSKKDQKDA; QEVEDSKKDQKDAS; EVEDSKKDQKDASK; VEDSKKDQKDASKK; EDSKKDQKDASKKD; DSKKDQKDASKKDL; SKKDQKDASKKDLP; KKDQKDASKKDLPL; KDQKDASKKDLPLV; DQKDASKKDLPLVT; QKDASKKDLPLVTE; KDASKKDLPLVTED; DASKKDLPLVTEDT; ASKKDLPLVTEDTV; SKKDLPLVTEDTVK; KKDLPLVTEDTVKL; KDLPLVTEDTVKLF; DLPLVTEDTVKLFN; LPLVTEDTVKLFND; PLVTEDTVKLFNDT; LVTEDTVKLFNDTK; VTEDTVKLFNDTKI; TEDTVKLFNDTKIF; EDTVKLFNDTKIFI; DTVKLFNDTKIFIS; TVKLFNDTKIFISK; VKLFNDTKIFISKE; KLFNDTKIFISKEK; LFNDTKIFISKEKN; FNDTKIFISKEKNK; NDTKIFISKEKNKD; DTKIFISKEKNKDG; TKIFISKEKNKDGK; KIFISKEKNKDGKY; IFISKEKNKDGKYE; FISKEKNKDGKYEL; ISKEKNKDGKYELR; SKEKNKDGKYELRA; KEKNKDGKYELRAT; EKNKDGKYELRATV; KNKDGKYELRATVD; NKDGKYELRATVDT; KDGKYELRATVDTV; DGKYELRATVDTVE; GKYELRATVDTVEL; KYELRATVDTVELK; YELRATVDTVELKG; ELRATVDTVELKGV; LRATVDTVELKGVA; RATVDTVELKGVAD; ATVDTVELKGVADK; TVDTVELKGVADKN; VDTVELKGVADKND; DTVELKGVADKNDG; TVELKGVADKNDGS; VELKGVADKNDGSG; ELKGVADKNDGSGG; LKGVADKNDGSGGK; KGVADKNDGSGGKL; GVADKNDGSGGKLE; VADKNDGSGGKLEG; ADKNDGSGGKLEGV; DKNDGSGGKLEGVK; KNDGSGGKLEGVKS; NDGSGGKLEGVKSD; DGSGGKLEGVKSDQ; GSGGKLEGVKSDQS; SGGKLEGVKSDQSK; GGKLEGVKSDQSKV; GKLEGVKSDQSKVT; KLEGVKSDQSKVTM; LEGVKSDQSKVTMS; EGVKSDQSKVTMSI; GVKSDQSKVTMSIT; VKSDQSKVTMSITD; KSDQSKVTMSITDD; SDQSKVTMSITDDL; DQSKVTMSITDDLN; QSKVTMSITDDLNT; SKVTMSITDDLNTI; KVTMSITDDLNTIT; VTMSITDDLNTITV; TMSITDDLNTITVE; MSITDDLNTITVET; SITDDLNTITVETY; ITDDLNTITVETYD; TDDLNTITVETYDS; DDLNTITVETYDSS; DLNTITVETYDSSN; LNTITVETYDSSNT; NTITVETYDSSNTK; TITVETYDSSNTKV; ITVETYDSSNTKVA; TVETYDSSNTKVAS; VETYDSSNTKVASK; ETYDSSNTKVASKV; TYDSSNTKVASKVF; YDSSNTKVASKVFK; DSSNTKVASKVFKK; SSNTKVASKVFKKQ; SNTKVASKVFKKQG; NTKVASKVFKKQGS; TKVASKVFKKQGSL; KVASKVFKKQGSLT; VASKVFKKQGSLTE; ASKVFKKQGSLTEE; SKVFKKQGSLTEET; KVFKKQGSLTEETE; VFKKQGSLTEETEE; FKKQGSLTEETEET; KKQGSLTEETEETY; KQGSLTEETEETYK; QGSLTEETEETYKT; GSLTEETEETYKTG; SLTEETEETYKTGK; LTEETEETYKTGKL; TEETEETYKTGKLS; EETEETYKTGKLST; ETEETYKTGKLSTK; TEETYKTGKLSTKK; EETYKTGKLSTKKI; ETYKTGKLSTKKIT; TYKTGKLSTKKITR; YKTGKLSTKKITRT; KTGKLSTKKITRTN; TGKLSTKKITRTNG; GKLSTKKITRTNGT; KLSTKKITRTNGTT; LSTKKITRTNGTTL; STKKITRTNGTTLE; TKKITRTNGTTLEY; KKITRTNGTTLEYS; KITRTNGTTLEYSD; ITRTNGTTLEYSDM; TRTNGTTLEYSDMT; RTNGTTLEYSDMTN; TNGTTLEYSDMTND; NGTTLEYSDMTNDE; GTTLEYSDMTNDEN; TTLEYSDMTNDENA; TLEYSDMTNDENAT; LEYSDMTNDENATK; EYSDMTNDENATKA; YSDMTNDENATKAV; SDMTNDENATKAVE; DMTNDENATKAVET; MTNDENATKAVETL; TNDENATKAVETLK; NDENATKAVETLKN; DENATKAVETLKNG; ENATKAVETLKNGI; NATKAVETLKNGIM; ATKAVETLKNGIML; TKAVETLKNGIMLE; KAVETLKNGIMLEG; AVETLKNGIMLEGN; VETLKNGIMLEGNL; ETLKNGIMLEGNLV; TLKNGIMLEGNLVG;

LKNGIMLEGNLVGG; KNGIMLEGNLVGGK; NGIMLEGNLVGGKT;
GIMLEGNLVGGKTS; IMLEGNLVGGKTSV; MLEGNLVGGKTSVE;
LEGNLVGGKTSVEI; EGNLVGGKTSVEIK; GNLVGGKTSVEIKE;
NLVGGKTSVEIKEG; LVGGKTSVEIKEGT; VGGKTSVEIKEGTV;
GGKTSVEIKEGTVT; GKTSVEIKEGTVTL; KTSVEIKEGTVTLK;
TSVEIKEGTVTLKK; SVEIKEGTVTLKKE; VEIKEGTVTLKKEI;
EIKEGTVTLKKEIE; IKEGTVTLKKEIEK; KEGTVTLKKEIEKA;
EGTVTLKKEIEKAG; GTVTLKKEIEKAGT; TVTLKKEIEKAGTV;
VTLKKEIEKAGTVK; TLKKEIEKAGTVKL; LKKEIEKAGTVKLF;
KKEIEKAGTVKLFL; KEIEKAGTVKLFLD; EIEKAGTVKLFLDD;
IEKAGTVKLFLDDT; EKAGTVKLFLDDTS; KAGTVKLFLDDTSS;
AGTVKLFLDDTSSG; GTVKLFLDDTSSGS; TVKLFLDDTSSGST;
VKLFLDDTSSGSTK; KLFLDDTSSGSTKK; LFLDDTSSGSTKKT;
FLDDTSSGSTKKTA; LDDTSSGSTKKTAV; DDTSSGSTKKTAVW;
DTSSGSTKKTAVWS; TSSGSTKKTAVWSD; SSGSTKKTAVWSDT;
SGSTKKTAVWSDTS; GSTKKTAVWSDTSN; STKKTAVWSDTSNT;
TKKTAVWSDTSNTL; KKTAVWSDTSNTLT; KTAVWSDTSNTLTV;
TAVWSDTSNTLTVS; AVWSDTSNTLTVSA; VWSDTSNTLTVSAD;
WSDTSNTLTVSADS; SDTSNTLTVSADSK; DTSNTLTVSADSKK;
TSNTLTVSADSKKI; SNTLTVSADSKKIK; NTLTVSADSKKIKD;
TLTVSADSKKIKDF; LTVSADSKKIKDFV; TVSADSKKIKDFVF;
VSADSKKIKDFVFL; SADSKKIKDFVFLT; ADSKKIKDFVFLTD;
DSKKIKDFVFLTDG; SKKIKDFVFLTDGT; KKIKDFVFLTDGTI;
KIKDFVFLTDGTIT; IKDFVFLTDGTITV; KDFVFLTDGTITVQ;
DFVFLTDGTITVQN; FVFLTDGTITVQNY; VFLTDGTITVQNYD;
FLTDGTITVQNYDT; LTDGTITVQNYDTA; TDGTITVQNYDTAG;
DGTITVQNYDTAGT; GTITVQNYDTAGTK; TITVQNYDTAGTKL;
ITVQNYDTAGTKLA; TVQNYDTAGTKLAG; VQNYDTAGTKLAGT;
QNYDTAGTKLAGTA; NYDTAGTKLAGTAT; YDTAGTKLAGTATE;
DTAGTKLAGTATEI; TAGTKLAGTATEIK; AGTKLAGTATEIKD;
GTKLAGTATEIKDL; TKLAGTATEIKDLE; KLAGTATEIKDLEA;
LAGTATEIKDLEAL; AGTATEIKDLEALK; GTATEIKDLEALKA;
TATEIKDLEALKAA; ATEIKDLEALKAAL; TEIKDLEALKAALK;

15 mers:
MKKYLLGFALVLALI; KKYLLGFALVLALIA; KYLLGFALVLALIAC;
YLLGFALVLALIACG; LLGFALVLALIACGQ; LGFALVLALIACGQK;
GFALVLALIACGQKG; FALVLALIACGQKGA; ALVLALIACGQKGAE;
LVLALIACGQKGAEP; VLALIACGQKGAEPK; LALIACGQKGAEPKH;
ALIACGQKGAEPKHN; LIACGQKGAEPKHND; IACGQKGAEPKHNDQ;
ACGQKGAEPKHNDQE; CGQKGAEPKHNDQEV; GQKGAEPKHNDQEVE;
QKGAEPKHNDQEVED; KGAEPKHNDQEVEDS; GAEPKHNDQEVEDSK;
AEPKHNDQEVEDSKK; EPKHNDQEVEDSKKD; PKHNDQEVEDSKKDQ;
KHNDQEVEDSKKDQK; HNDQEVEDSKKDQKD; NDQEVEDSKKDQKDA;
DQEVEDSKKDQKDAS; QEVEDSKKDQKDASK; EVEDSKKDQKDASKK;
VEDSKKDQKDASKKD; EDSKKDQKDASKKDL; DSKKDQKDASKKDLP;
SKKDQKDASKKDLPL; KKDQKDASKKDLPLV; KDQKDASKKDLPLVT;
DQKDASKKDLPLVTE; QKDASKKDLPLVTED; KDASKKDLPLVTEDT;
DASKKDLPLVTEDTV; ASKKDLPLVTEDTVK; SKKDLPLVTEDTVKL;
KKDLPLVTEDTVKLF; KDLPLVTEDTVKLFN; DLPLVTEDTVKLFND;
LPLVTEDTVKLFNDT; PLVTEDTVKLFNDTK; LVTEDTVKLFNDTKI;
VTEDTVKLFNDTKIF; TEDTVKLFNDTKIFI; EDTVKLFNDTKIFIS;
DTVKLFNDTKIFISK; TVKLFNDTKIFISKE; VKLFNDTKIFISKEK;
KLFNDTKIFISKEKN; LFNDTKIFISKEKNK; FNDTKIFISKEKNKD;
NDTKIFISKEKNKDG; DTKIFISKEKNKDGK; TKIFISKEKNKDGKY;
KIFISKEKNKDGKYE; IFISKEKNKDGKYEL; FISKEKNKDGKYELR;
ISKEKNKDGKYELRA; SKEKNKDGKYELRAT; KEKNKDGKYELRATV;

	EKNKDGKYELRATVD; KNKDGKYELRATVDT; NKDGKYELRATVDTV; KDGKYELRATVDTVE; DGKYELRATVDTVEL; GKYELRATVDTVELK; KYELRATVDTVELKG; YELRATVDTVELKGV; ELRATVDTVELKGVA; LRATVDTVELKGVAD; RATVDTVELKGVADK; ATVDTVELKGVADKN; TVDTVELKGVADKND; VDTVELKGVADKNDG; DTVELKGVADKNDGS; TVELKGVADKNDGSG; VELKGVADKNDGSGG; ELKGVADKNDGSGGK; LKGVADKNDGSGGKL; KGVADKNDGSGGKLE; GVADKNDGSGGKLEG; VADKNDGSGGKLEGV; ADKNDGSGGKLEGVK; DKNDGSGGKLEGVKS; KNDGSGGKLEGVKSD; NDGSGGKLEGVKSDQ; DGSGGKLEGVKSDQS; GSGGKLEGVKSDQSK; SGGKLEGVKSDQSKV; GGKLEGVKSDQSKVT; GKLEGVKSDQSKVTM; KLEGVKSDQSKVTMS; LEGVKSDQSKVTMSI; EGVKSDQSKVTMSIT; GVKSDQSKVTMSITD; VKSDQSKVTMSITDD; KSDQSKVTMSITDDL; SDQSKVTMSITDDLN; DQSKVTMSITDDLNT; QSKVTMSITDDLNTI; SKVTMSITDDLNTIT; KVTMSITDDLNTITV; VTMSITDDLNTITVE; TMSITDDLNTITVET; MSITDDLNTITVETY; SITDDLNTITVETYD; ITDDLNTITVETYDS; TDDLNTITVETYDSS; DDLNTITVETYDSSN; DLNTITVETYDSSNT; LNTITVETYDSSNTK; NTITVETYDSSNTKV; TITVETYDSSNTKVA; ITVETYDSSNTKVAS; TVETYDSSNTKVASK; VETYDSSNTKVASKV; ETYDSSNTKVASKVF; TYDSSNTKVASKVFK; YDSSNTKVASKVFKK; DSSNTKVASKVFKKQ; SSNTKVASKVFKKQG; SNTKVASKVFKKQGS; NTKVASKVFKKQGSL; TKVASKVFKKQGSLT; KVASKVFKKQGSLTE; VASKVFKKQGSLTEE; ASKVFKKQGSLTEET; SKVFKKQGSLTEETE; KVFKKQGSLTEETEE; VFKKQGSLTEETEET; FKKQGSLTEETEETY; KKQGSLTEETEETYK; KQGSLTEETEETYKT; QGSLTEETEETYKTG; GSLTEETEETYKTGK; SLTEETEETYKTGKL; LTEETEETYKTGKLS; TEETEETYKTGKLST; EETEETYKTGKLSTK; ETEETYKTGKLSTKK; TEETYKTGKLSTKKI; EETYKTGKLSTKKIT; ETYKTGKLSTKKITR; TYKTGKLSTKKITRT; YKTGKLSTKKITRTN; KTGKLSTKKITRTNG; TGKLSTKKITRTNGT; GKLSTKKITRTNGTT; KLSTKKITRTNGTTL; LSTKKITRTNGTTLE; STKKITRTNGTTLEY; TKKITRTNGTTLEYS; KKITRTNGTTLEYSD; KITRTNGTTLEYSDM; ITRTNGTTLEYSDMT; TRTNGTTLEYSDMTN; RTNGTTLEYSDMTND; TNGTTLEYSDMTNDE; NGTTLEYSDMTNDEN; GTTLEYSDMTNDENA; TTLEYSDMTNDENAT; TLEYSDMTNDENATK; LEYSDMTNDENATKA; EYSDMTNDENATKAV; YSDMTNDENATKAVE; SDMTNDENATKAVET; DMTNDENATKAVETL; MTNDENATKAVETLK; TNDENATKAVETLKN; NDENATKAVETLKNG; DENATKAVETLKNGI; ENATKAVETLKNGIM; NATKAVETLKNGIML; ATKAVETLKNGIMLE; TKAVETLKNGIMLEG; KAVETLKNGIMLEGN; AVETLKNGIMLEGNL; VETLKNGIMLEGNLV; ETLKNGIMLEGNLVG; TLKNGIMLEGNLVGG; LKNGIMLEGNLVGGK; KNGIMLEGNLVGGKT; NGIMLEGNLVGGKTS; GIMLEGNLVGGKTSV; IMLEGNLVGGKTSVE; MLEGNLVGGKTSVEI; LEGNLVGGKTSVEIK; EGNLVGGKTSVEIKE; GNLVGGKTSVEIKEG; NLVGGKTSVEIKEGT; LVGGKTSVEIKEGTV; VGGKTSVEIKEGTVT; GGKTSVEIKEGTVTL; GKTSVEIKEGTVTLK; KTSVEIKEGTVTLKK; TSVEIKEGTVTLKKE; SVEIKEGTVTLKKEI; VEIKEGTVTLKKEIE; EIKEGTVTLKKEIEK; IKEGTVTLKKEIEKA; KEGTVTLKKEIEKAG; EGTVTLKKEIEKAGT; GTVTLKKEIEKAGTV; TVTLKKEIEKAGTVK; VTLKKEIEKAGTVKL; TLKKEIEKAGTVKLF; LKKEIEKAGTVKLFL; KKEIEKAGTVKLFLD; KEIEKAGTVKLFLDD; EIEKAGTVKLFLDDT; IEKAGTVKLFLDDTS; EKAGTVKLFLDDTSS; KAGTVKLFLDDTSSG; AGTVKLFLDDTSSGS; GTVKLFLDDTSSGST; TVKLFLDDTSSGSTK; VKLFLDDTSSGSTKK; KLFLDDTSSGSTKKT; LFLDDTSSGSTKKTA; FLDDTSSGSTKKTAV; LDDTSSGSTKKTAVW; DDTSSGSTKKTAVWS; DTSSGSTKKTAVWSD; TSSGSTKKTAVWSDT; SSGSTKKTAVWSDTS; SGSTKKTAVWSDTSN; GSTKKTAVWSDTSNT; STKKTAVWSDTSNTL; TKKTAVWSDTSNTLT; KKTAVWSDTSNTLTV; KTAVWSDTSNTLTVS;

TAVWSDTSNTLTVSA; AVWSDTSNTLTVSAD; VWSDTSNTLTVSADS;
WSDTSNTLTVSADSK; SDTSNTLTVSADSKK; DTSNTLTVSADSKKI;
TSNTLTVSADSKKIK; SNTLTVSADSKKIKD; NTLTVSADSKKIKDF;
TLTVSADSKKIKDFV; LTVSADSKKIKDFVF; TVSADSKKIKDFVFL;
VSADSKKIKDFVFLT; SADSKKIKDFVFLTD; ADSKKIKDFVFLTDG;
DSKKIKDFVFLTDGT; SKKIKDFVFLTDGTI; KKIKDFVFLTDGTIT;
KIKDFVFLTDGTITV; IKDFVFLTDGTITVQ; KDFVFLTDGTITVQN;
DFVFLTDGTITVQNY; FVFLTDGTITVQNYD; VFLTDGTITVQNYDT;
FLTDGTITVQNYDTA; LTDGTITVQNYDTAG; TDGTITVQNYDTAGT;
DGTITVQNYDTAGTK; GTITVQNYDTAGTKL; TITVQNYDTAGTKLA;
ITVQNYDTAGTKLAG; TVQNYDTAGTKLAGT; VQNYDTAGTKLAGTA;
QNYDTAGTKLAGTAT; NYDTAGTKLAGTATE; YDTAGTKLAGTATEI;
DTAGTKLAGTATEIK; TAGTKLAGTATEIKD; AGTKLAGTATEIKDL;
GTKLAGTATEIKDLE; TKLAGTATEIKDLEA; KLAGTATEIKDLEAL;
LAGTATEIKDLEALK; AGTATEIKDLEALKA; GTATEIKDLEALKAA;
TATEIKDLEALKAAL; ATEIKDLEALKAALK;

16 mers:
MKKYLLGFALVLALIA; KKYLLGFALVLALIAC; KYLLGFALVLALIACG;
YLLGFALVLALIACGQ; LLGFALVLALIACGQK; LGFALVLALIACGQKG;
GFALVLALIACGQKGA; FALVLALIACGQKGAE; ALVLALIACGQKGAEP;
LVLALIACGQKGAEPK; VLALIACGQKGAEPKH; LALIACGQKGAEPKHN;
ALIACGQKGAEPKHND; LIACGQKGAEPKHNDQ; IACGQKGAEPKHNDQE;
ACGQKGAEPKHNDQEV; CGQKGAEPKHNDQEVE; GQKGAEPKHNDQEVED;
QKGAEPKHNDQEVEDS; KGAEPKHNDQEVEDSK; GAEPKHNDQEVEDSKK;
AEPKHNDQEVEDSKKD; EPKHNDQEVEDSKKDQ; PKHNDQEVEDSKKDQK;
KHNDQEVEDSKKDQKD; HNDQEVEDSKKDQKDA; NDQEVEDSKKDQKDAS;
DQEVEDSKKDQKDASK; QEVEDSKKDQKDASKK; EVEDSKKDQKDASKKD;
VEDSKKDQKDASKKDL; EDSKKDQKDASKKDLP; DSKKDQKDASKKDLPL;
SKKDQKDASKKDLPLV; KKDQKDASKKDLPLVT; KDQKDASKKDLPLVTE;
DQKDASKKDLPLVTED; QKDASKKDLPLVTEDT; KDASKKDLPLVTEDTV;
DASKKDLPLVTEDTVK; ASKKDLPLVTEDTVKL; SKKDLPLVTEDTVKLF;
KKDLPLVTEDTVKLFN; KDLPLVTEDTVKLFND; DLPLVTEDTVKLFNDT;
LPLVTEDTVKLFNDTK; PLVTEDTVKLFNDTKI; LVTEDTVKLFNDTKIF;
VTEDTVKLFNDTKIFI; TEDTVKLFNDTKIFIS; EDTVKLFNDTKIFISK;
DTVKLFNDTKIFISKE; TVKLFNDTKIFISKEK; VKLFNDTKIFISKEKN;
KLFNDTKIFISKEKNK; LFNDTKIFISKEKNKD; FNDTKIFISKEKNKDG;
NDTKIFISKEKNKDGK; DTKIFISKEKNKDGKY; TKIFISKEKNKDGKYE;
KIFISKEKNKDGKYEL; IFISKEKNKDGKYELR; FISKEKNKDGKYELRA;
ISKEKNKDGKYELRAT; SKEKNKDGKYELRATV; KEKNKDGKYELRATVD;
EKNKDGKYELRATVDT; KNKDGKYELRATVDTV; NKDGKYELRATVDTVE;
KDGKYELRATVDTVEL; DGKYELRATVDTVELK; GKYELRATVDTVELKG;
KYELRATVDTVELKGV; YELRATVDTVELKGVA; ELRATVDTVELKGVAD;
LRATVDTVELKGVADK; RATVDTVELKGVADKN; ATVDTVELKGVADKND;
TVDTVELKGVADKNDG; VDTVELKGVADKNDGS; DTVELKGVADKNDGSG;
TVELKGVADKNDGSGG; VELKGVADKNDGSGGK; ELKGVADKNDGSGGKL;
LKGVADKNDGSGGKLE; KGVADKNDGSGGKLEG; GVADKNDGSGGKLEGV;
VADKNDGSGGKLEGVK; ADKNDGSGGKLEGVKS; DKNDGSGGKLEGVKSD;
KNDGSGGKLEGVKSDQ; NDGSGGKLEGVKSDQS; DGSGGKLEGVKSDQSK;
GSGGKLEGVKSDQSKV; SGGKLEGVKSDQSKVT; GGKLEGVKSDQSKVTM;
GKLEGVKSDQSKVTMS; KLEGVKSDQSKVTMSI; LEGVKSDQSKVTMSIT;
EGVKSDQSKVTMSITD; GVKSDQSKVTMSITDD; VKSDQSKVTMSITDDL;
KSDQSKVTMSITDDLN; SDQSKVTMSITDDLNT; DQSKVTMSITDDLNTI;
QSKVTMSITDDLNTIT; SKVTMSITDDLNTITV; KVTMSITDDLNTITVE;
VTMSITDDLNTITVET; TMSITDDLNTITVETY; MSITDDLNTITVETYD;
SITDDLNTITVETYDS; ITDDLNTITVETYDSS; TDDLNTITVETYDSSN;
DDLNTITVETYDSSNT; DLNTITVETYDSSNTK; LNTITVETYDSSNTKV;

	NTITVETYDSSNTKVA; TITVETYDSSNTKVAS; ITVETYDSSNTKVASK; TVETYDSSNTKVASKV; VETYDSSNTKVASKVF; ETYDSSNTKVASKVFK; TYDSSNTKVASKVFKK; YDSSNTKVASKVFKKQ; DSSNTKVASKVFKKQG; SSNTKVASKVFKKQGS; SNTKVASKVFKKQGSL; NTKVASKVFKKQGSLT; TKVASKVFKKQGSLTE; KVASKVFKKQGSLTEE; VASKVFKKQGSLTEET; ASKVFKKQGSLTEETE; SKVFKKQGSLTEETEE; KVFKKQGSLTEETEET; VFKKQGSLTEETEETY; FKKQGSLTEETEETYK; KKQGSLTEETEETYKT; KQGSLTEETEETYKTG; QGSLTEETEETYKTGK; GSLTEETEETYKTGKL; SLTEETEETYKTGKLS; LTEETEETYKTGKLST; TEETEETYKTGKLSTK; EETEETYKTGKLSTKK; ETEETYKTGKLSTKKI; TEETYKTGKLSTKKIT; EETYKTGKLSTKKITR; ETYKTGKLSTKKITRT; TYKTGKLSTKKITRTN; YKTGKLSTKKITRTNG; KTGKLSTKKITRTNGT; TGKLSTKKITRTNGTT; GKLSTKKITRTNGTTL; KLSTKKITRTNGTTLE; LSTKKITRTNGTTLEY; STKKITRTNGTTLEYS; TKKITRTNGTTLEYSD; KKITRTNGTTLEYSDM; KITRTNGTTLEYSDMT; ITRTNGTTLEYSDMTN; TRTNGTTLEYSDMTND; RTNGTTLEYSDMTNDE; TNGTTLEYSDMTNDEN; NGTTLEYSDMTNDENA; GTTLEYSDMTNDENAT; TTLEYSDMTNDENATK; TLEYSDMTNDENATKA; LEYSDMTNDENATKAV; EYSDMTNDENATKAVE; YSDMTNDENATKAVET; SDMTNDENATKAVETL; DMTNDENATKAVETLK; MTNDENATKAVETLKN; TNDENATKAVETLKNG; NDENATKAVETLKNGI; DENATKAVETLKNGIM; ENATKAVETLKNGIML; NATKAVETLKNGIMLE; ATKAVETLKNGIMLEG; TKAVETLKNGIMLEGN; KAVETLKNGIMLEGNL; AVETLKNGIMLEGNLV; VETLKNGIMLEGNLVG; ETLKNGIMLEGNLVGG; TLKNGIMLEGNLVGGK; LKNGIMLEGNLVGGKT; KNGIMLEGNLVGGKTS; NGIMLEGNLVGGKTSV; GIMLEGNLVGGKTSVE; IMLEGNLVGGKTSVEI; MLEGNLVGGKTSVEIK; LEGNLVGGKTSVEIKE; EGNLVGGKTSVEIKEG; GNLVGGKTSVEIKEGT; NLVGGKTSVEIKEGTV; LVGGKTSVEIKEGTVT; VGGKTSVEIKEGTVTL; GGKTSVEIKEGTVTLK; GKTSVEIKEGTVTLKK; KTSVEIKEGTVTLKKE; TSVEIKEGTVTLKKEI; SVEIKEGTVTLKKEIE; VEIKEGTVTLKKEIEK; EIKEGTVTLKKEIEKA; IKEGTVTLKKEIEKAG; KEGTVTLKKEIEKAGT; EGTVTLKKEIEKAGTV; GTVTLKKEIEKAGTVK; TVTLKKEIEKAGTVKL; VTLKKEIEKAGTVKLF; TLKKEIEKAGTVKLFL; LKKEIEKAGTVKLFLD; KKEIEKAGTVKLFLDD; KEIEKAGTVKLFLDDT; EIEKAGTVKLFLDDTS; IEKAGTVKLFLDDTSS; EKAGTVKLFLDDTSSG; KAGTVKLFLDDTSSGS; AGTVKLFLDDTSSGST; GTVKLFLDDTSSGSTK; TVKLFLDDTSSGSTKK; VKLFLDDTSSGSTKKT; KLFLDDTSSGSTKKTA; LFLDDTSSGSTKKTAV; FLDDTSSGSTKKTAVW; LDDTSSGSTKKTAVWS; DDTSSGSTKKTAVWSD; DTSSGSTKKTAVWSDT; TSSGSTKKTAVWSDTS; SSGSTKKTAVWSDTSN; SGSTKKTAVWSDTSNT; GSTKKTAVWSDTSNTL; STKKTAVWSDTSNTLT; TKKTAVWSDTSNTLTV; KKTAVWSDTSNTLTVS; KTAVWSDTSNTLTVSA; TAVWSDTSNTLTVSAD; AVWSDTSNTLTVSADS; VWSDTSNTLTVSADSK; WSDTSNTLTVSADSKK; SDTSNTLTVSADSKKI; DTSNTLTVSADSKKIK; TSNTLTVSADSKKIKD; SNTLTVSADSKKIKDF; NTLTVSADSKKIKDFV; TLTVSADSKKIKDFVF; LTVSADSKKIKDFVFL; TVSADSKKIKDFVFLT; VSADSKKIKDFVFLTD; SADSKKIKDFVFLTDG; ADSKKIKDFVFLTDGT; DSKKIKDFVFLTDGTI; SKKIKDFVFLTDGTIT; KKIKDFVFLTDGTITV; KIKDFVFLTDGTITVQ; IKDFVFLTDGTITVQN; KDFVFLTDGTITVQNY; DFVFLTDGTITVQNYD; FVFLTDGTITVQNYDT; VFLTDGTITVQNYDTA; FLTDGTITVQNYDTAG; LTDGTITVQNYDTAGT; TDGTITVQNYDTAGTK; DGTITVQNYDTAGTKL; GTITVQNYDTAGTKLA; TITVQNYDTAGTKLAG; ITVQNYDTAGTKLAGT; TVQNYDTAGTKLAGTA; VQNYDTAGTKLAGTAT; QNYDTAGTKLAGTATE; NYDTAGTKLAGTATEI; YDTAGTKLAGTATEIK; DTAGTKLAGTATEIKD; TAGTKLAGTATEIKDL; AGTKLAGTATEIKDLE; GTKLAGTATEIKDLEA; TKLAGTATEIKDLEAL; KLAGTATEIKDLEALK; LAGTATEIKDLEALKA; AGTATEIKDLEALKAA; GTATEIKDLEALKAAL; TATEIKDLEALKAALK;

AAM22469.1| Outer surface protein C [Borrelia afzelii]	13 mers: MKKNTLSAILMTL; KKNTLSAILMTLF; KNTLSAILMTLFL; NTLSAILMTLFLF; TLSAILMTLFLFI; LSAILMTLFLFIS; SAILMTLFLFISC; AILMTLFLFISCN; ILMTLFLFISCNN; LMTLFLFISCNNS; MTLFLFISCNNSG; TLFLFISCNNSGK; LFLFISCNNSGKG; FLFISCNNSGKGG; LFISCNNSGKGGD; FISCNNSGKGGDS; ISCNNSGKGGDSA; SCNNSGKGGDSAS; CNNSGKGGDSAST; NNSGKGGDSASTN; NSGKGGDSASTNP; SGKGGDSASTNPA; GKGGDSASTNPAD; KGGDSASTNPADE; GGDSASTNPADES; GDSASTNPADESA; DSASTNPADESAK; SASTNPADESAKG; ASTNPADESAKGP; STNPADESAKGPN; TNPADESAKGPNL; NPADESAKGPNLT; PADESAKGPNLTE; ADESAKGPNLTEI; DESAKGPNLTEIS; ESAKGPNLTEISK; SAKGPNLTEISKK; AKGPNLTEISKKI; KGPNLTEISKKIT; GPNLTEISKKITD; PNLTEISKKITDS; NLTEISKKITDSN; LTEISKKITDSNA; TEISKKITDSNAF; EISKKITDSNAFV; ISKKITDSNAFVL; SKKITDSNAFVLA; KKITDSNAFVLAV; KITDSNAFVLAVK; ITDSNAFVLAVKE; TDSNAFVLAVKEV; DSNAFVLAVKEVE; SNAFVLAVKEVET; NAFVLAVKEVETL; AFVLAVKEVETLV; FVLAVKEVETLVS; VLAVKEVETLVSS; LAVKEVETLVSSI; AVKEVETLVSSID; VKEVETLVSSIDE; KEVETLVSSIDEL; EVETLVSSIDELA; VETLVSSIDELAN; ETLVSSIDELANK; TLVSSIDELANKA; LVSSIDELANKAI; VSSIDELANKAIG; SSIDELANKAIGK; SIDELANKAIGKK; IDELANKAIGKKI; DELANKAIGKKIQ; ELANKAIGKKIQQ; LANKAIGKKIQQN; ANKAIGKKIQQNG; NKAIGKKIQQNGL; KAIGKKIQQNGLG; AIGKKIQQNGLGA; IGKKIQQNGLGAE; GKKIQQNGLGAEA; KKIQQNGLGAEAN; KIQQNGLGAEANR; IQQNGLGAEANRN; QQNGLGAEANRNE; QNGLGAEANRNES; NGLGAEANRNESL; GLGAEANRNESLL; LGAEANRNESLLA; GAEANRNESLLAG; AEANRNESLLAGV; EANRNESLLAGVH; ANRNESLLAGVHE; NRNESLLAGVHEI; RNESLLAGVHEIS; NESLLAGVHEIST; ESLLAGVHEISTL; SLLAGVHEISTLI; LLAGVHEISTLIT; LAGVHEISTLITE; AGVHEISTLITEK; GVHEISTLITEKL; VHEISTLITEKLS; HEISTLITEKLSK; EISTLITEKLSKL; ISTLITEKLSKLK; STLITEKLSKLKN; TLITEKLSKLKNS; LITEKLSKLKNSG; ITEKLSKLKNSGE; TEKLSKLKNSGEL; EKLSKLKNSGELK; KLSKLKNSGELKA; LSKLKNSGELKAK; SKLKNSGELKAKI; KLKNSGELKAKIE; LKNSGELKAKIED; KNSGELKAKIEDA; NSGELKAKIEDAK; SGELKAKIEDAKK; GELKAKIEDAKKC; ELKAKIEDAKKCS; LKAKIEDAKKCSE; KAKIEDAKKCSEE; AKIEDAKKCSEEF; KIEDAKKCSEEFT; IEDAKKCSEEFTN; EDAKKCSEEFTNK; DAKKCSEEFTNKL; AKKCSEEFTNKLR; KKCSEEFTNKLRV; KCSEEFTNKLRVS; CSEEFTNKLRVSH; SEEFTNKLRVSHA; EEFTNKLRVSHAD; EFTNKLRVSHADL; FTNKLRVSHADLG; TNKLRVSHADLGK; NKLRVSHADLGKQ; KLRVSHADLGKQG; LRVSHADLGKQGV; RVSHADLGKQGVN; VSHADLGKQGVND; SHADLGKQGVNDD; HADLGKQGVNDDD; ADLGKQGVNDDDA; DLGKQGVNDDDAK; LGKQGVNDDDAKK; GKQGVNDDDAKKA; KQGVNDDDAKKAI; QGVNDDDAKKAIL; GVNDDDAKKAILK; VNDDDAKKAILKT; NDDDAKKAILKTN; DDDAKKAILKTNA; DDAKKAILKTNAD; DAKKAILKTNADK; AKKAILKTNADKT; KKAILKTNADKTK; KAILKTNADKTKG; AILKTNADKTKGA; ILKTNADKTKGAE; LKTNADKTKGAEE; KTNADKTKGAEEL; TNADKTKGAEELG; NADKTKGAEELGK; ADKTKGAEELGKL; DKTKGAEELGKLF; KTKGAEELGKLFK; TKGAEELGKLFKS; KGAEELGKLFKSV; GAEELGKLFKSVE; AEELGKLFKSVEG; EELGKLFKSVEGL; ELGKLFKSVEGLV; LGKLFKSVEGLVK; GKLFKSVEGLVKA; KLFKSVEGLVKAA; LFKSVEGLVKAAQ; FKSVEGLVKAAQE; KSVEGLVKAAQEA; SVEGLVKAAQEAL; VEGLVKAAQEALT; EGLVKAAQEALTN; GLVKAAQEALTNS; LVKAAQEALTNSV; VKAAQEALTNSVK; KAAQEALTNSVKE; AAQEALTNSVKEL; AQEALTNSVKELT; QEALTNSVKELTS; EALTNSVKELTSP; ALTNSVKELTSPV; LTNSVKELTSPVV; TNSVKELTSPVVA; NSVKELTSPVVAE; SVKELTSPVVAES; VKELTSPVVAESP; KELTSPVVAESPK; ELTSPVVAESPKK; LTSPVVAESPKKP; 14 mers: MKKNTLSAILMTLF; KKNTLSAILMTLFL; KNTLSAILMTLFLF; NTLSAILMTLFLFI; TLSAILMTLFLFIS; LSAILMTLFLFISC; SAILMTLFLFISCN; AILMTLFLFISCNN; ILMTLFLFISCNNS;

	LMTLFLFISCNNSG; MTLFLFISCNNSGK; TLFLFISCNNSGKG; LFLFISCNNSGKGG; FLFISCNNSGKGGD; LFISCNNSGKGGDS; FISCNNSGKGGDSA; ISCNNSGKGGDSAS; SCNNSGKGGDSAST; CNNSGKGGDSASTN; NNSGKGGDSASTNP; NSGKGGDSASTNPA; SGKGGDSASTNPAD; GKGGDSASTNPADE; KGGDSASTNPADES; GGDSASTNPADESA; GDSASTNPADESAK; DSASTNPADESAKG; SASTNPADESAKGP; ASTNPADESAKGPN; STNPADESAKGPNL; TNPADESAKGPNLT; NPADESAKGPNLTE; PADESAKGPNLTEI; ADESAKGPNLTEIS; DESAKGPNLTEISK; ESAKGPNLTEISKK; SAKGPNLTEISKKI; AKGPNLTEISKKIT; KGPNLTEISKKITD; GPNLTEISKKITDS; PNLTEISKKITDSN; NLTEISKKITDSNA; LTEISKKITDSNAF; TEISKKITDSNAFV; EISKKITDSNAFVL; ISKKITDSNAFVLA; SKKITDSNAFVLAV; KKITDSNAFVLAVK; KITDSNAFVLAVKE; ITDSNAFVLAVKEV; TDSNAFVLAVKEVE; DSNAFVLAVKEVET; SNAFVLAVKEVETL; NAFVLAVKEVETLV; AFVLAVKEVETLVS; FVLAVKEVETLVSS; VLAVKEVETLVSSI; LAVKEVETLVSSID; AVKEVETLVSSIDE; VKEVETLVSSIDEL; KEVETLVSSIDELA; EVETLVSSIDELAN; VETLVSSIDELANK; ETLVSSIDELANKA; TLVSSIDELANKAI; LVSSIDELANKAIG; VSSIDELANKAIGK; SSIDELANKAIGKK; SIDELANKAIGKKI; IDELANKAIGKKIQ; DELANKAIGKKIQQ; ELANKAIGKKIQQN; LANKAIGKKIQQNG; ANKAIGKKIQQNGL; NKAIGKKIQQNGLG; KAIGKKIQQNGLGA; AIGKKIQQNGLGAE; IGKKIQQNGLGAEA; GKKIQQNGLGAEAN; KKIQQNGLGAEANR; KIQQNGLGAEANRN; IQQNGLGAEANRNE; QQNGLGAEANRNES; QNGLGAEANRNESL; NGLGAEANRNESLL; GLGAEANRNESLLA; LGAEANRNESLLAG; GAEANRNESLLAGV; AEANRNESLLAGVH; EANRNESLLAGVHE; ANRNESLLAGVHEI; NRNESLLAGVHEIS; RNESLLAGVHEIST; NESLLAGVHEISTL; ESLLAGVHEISTLI; SLLAGVHEISTLIT; LLAGVHEISTLITE; LAGVHEISTLITEK; AGVHEISTLITEKL; GVHEISTLITEKLS; VHEISTLITEKLSK; HEISTLITEKLSKL; EISTLITEKLSKLK; ISTLITEKLSKLKN; STLITEKLSKLKNS; TLITEKLSKLKNSG; LITEKLSKLKNSGE; ITEKLSKLKNSGEL; TEKLSKLKNSGELK; EKLSKLKNSGELKA; KLSKLKNSGELKAK; LSKLKNSGELKAKI; SKLKNSGELKAKIE; KLKNSGELKAKIED; LKNSGELKAKIEDA; KNSGELKAKIEDAK; NSGELKAKIEDAKK; SGELKAKIEDAKKC; GELKAKIEDAKKCS; ELKAKIEDAKKCSE; LKAKIEDAKKCSEE; KAKIEDAKKCSEEF; AKIEDAKKCSEEFT; KIEDAKKCSEEFTN; IEDAKKCSEEFTNK; EDAKKCSEEFTNKL; DAKKCSEEFTNKLR; AKKCSEEFTNKLRV; KKCSEEFTNKLRVS; KCSEEFTNKLRVSH; CSEEFTNKLRVSHA; SEEFTNKLRVSHAD; EEFTNKLRVSHADL; EFTNKLRVSHADLG; FTNKLRVSHADLGK; TNKLRVSHADLGKQ; NKLRVSHADLGKQG; KLRVSHADLGKQGV; LRVSHADLGKQGVN; RVSHADLGKQGVND; VSHADLGKQGVNDD; SHADLGKQGVNDDD; HADLGKQGVNDDDA; ADLGKQGVNDDDAK; DLGKQGVNDDDAKK; LGKQGVNDDDAKKA; GKQGVNDDDAKKAI; KQGVNDDDAKKAIL; QGVNDDDAKKAILK; GVNDDDAKKAILKT; VNDDDAKKAILKTN; NDDDAKKAILKTNA; DDDAKKAILKTNAD; DDAKKAILKTNADK; DAKKAILKTNADKT; AKKAILKTNADKTK; KKAILKTNADKTKG; KAILKTNADKTKGA; AILKTNADKTKGAE; ILKTNADKTKGAEE; LKTNADKTKGAEEL; KTNADKTKGAEELG; TNADKTKGAEELGK; NADKTKGAEELGKL; ADKTKGAEELGKLF; DKTKGAEELGKLFK; KTKGAEELGKLFKS; TKGAEELGKLFKSV; KGAEELGKLFKSVE; GAEELGKLFKSVEG; AEELGKLFKSVEGL; EELGKLFKSVEGLV; ELGKLFKSVEGLVK; LGKLFKSVEGLVKA; GKLFKSVEGLVKAA; KLFKSVEGLVKAAQ; LFKSVEGLVKAAQE; FKSVEGLVKAAQEA; KSVEGLVKAAQEAL; SVEGLVKAAQEALT;

VEGLVKAAQEALTN; EGLVKAAQEALTNS; GLVKAAQEALTNSV;
LVKAAQEALTNSVK; VKAAQEALTNSVKE; KAAQEALTNSVKEL;
AAQEALTNSVKELT; AQEALTNSVKELTS; QEALTNSVKELTSP;
EALTNSVKELTSPV; ALTNSVKELTSPVV; LTNSVKELTSPVVA;
TNSVKELTSPVVAE; NSVKELTSPVVAES; SVKELTSPVVAESP;
VKELTSPVVAESPK; KELTSPVVAESPKK; ELTSPVVAESPKKP;

15 mers:
MKKNTLSAILMTLFL; KKNTLSAILMTLFLF; KNTLSAILMTLFLFI;
NTLSAILMTLFLFIS; TLSAILMTLFLFISC; LSAILMTLFLFISCN;
SAILMTLFLFISCNN; AILMTLFLFISCNNS; ILMTLFLFISCNNSG;
LMTLFLFISCNNSGK; MTLFLFISCNNSGKG; TLFLFISCNNSGKGG;
LFLFISCNNSGKGGD; FLFISCNNSGKGGDS; LFISCNNSGKGGDSA;
FISCNNSGKGGDSAS; ISCNNSGKGGDSAST; SCNNSGKGGDSASTN;
CNNSGKGGDSASTNP; NNSGKGGDSASTNPA; NSGKGGDSASTNPAD;
SGKGGDSASTNPADE; GKGGDSASTNPADES; KGGDSASTNPADESA;
GGDSASTNPADESAK; GDSASTNPADESAKG; DSASTNPADESAKGP;
SASTNPADESAKGPN; ASTNPADESAKGPNL; STNPADESAKGPNLT;
TNPADESAKGPNLTE; NPADESAKGPNLTEI; PADESAKGPNLTEIS;
ADESAKGPNLTEISK; DESAKGPNLTEISKK; ESAKGPNLTEISKKI;
SAKGPNLTEISKKIT; AKGPNLTEISKKITD; KGPNLTEISKKITDS;
GPNLTEISKKITDSN; PNLTEISKKITDSNA; NLTEISKKITDSNAF;
LTEISKKITDSNAFV; TEISKKITDSNAFVL; EISKKITDSNAFVLA;
ISKKITDSNAFVLAV; SKKITDSNAFVLAVK; KKITDSNAFVLAVKE;
KITDSNAFVLAVKEV; ITDSNAFVLAVKEVE; TDSNAFVLAVKEVET;
DSNAFVLAVKEVETL; SNAFVLAVKEVETLV; NAFVLAVKEVETLVS;
AFVLAVKEVETLVSS; FVLAVKEVETLVSSI; VLAVKEVETLVSSID;
LAVKEVETLVSSIDE; AVKEVETLVSSIDEL; VKEVETLVSSIDELA;
KEVETLVSSIDELAN; EVETLVSSIDELANK; VETLVSSIDELANKA;
ETLVSSIDELANKAI; TLVSSIDELANKAIG; LVSSIDELANKAIGK;
VSSIDELANKAIGKK; SSIDELANKAIGKKI; SIDELANKAIGKKIQ;
IDELANKAIGKKIQQ; DELANKAIGKKIQQN; ELANKAIGKKIQQNG;
LANKAIGKKIQQNGL; ANKAIGKKIQQNGLG; NKAIGKKIQQNGLGA;
KAIGKKIQQNGLGAE; AIGKKIQQNGLGAEA; IGKKIQQNGLGAEAN;
GKKIQQNGLGAEANR; KKIQQNGLGAEANRN; KIQQNGLGAEANRNE;
IQQNGLGAEANRNES; QQNGLGAEANRNESL; QNGLGAEANRNESLL;
NGLGAEANRNESLLA; GLGAEANRNESLLAG; LGAEANRNESLLAGV;
GAEANRNESLLAGVH; AEANRNESLLAGVHE; EANRNESLLAGVHEI;
ANRNESLLAGVHEIS; NRNESLLAGVHEIST; RNESLLAGVHEISTL;
NESLLAGVHEISTLI; ESLLAGVHEISTLIT; SLLAGVHEISTLITE;
LLAGVHEISTLITEK; LAGVHEISTLITEKL; AGVHEISTLITEKLS;
GVHEISTLITEKLSK; VHEISTLITEKLSKL; HEISTLITEKLSKLK;
EISTLITEKLSKLKN; ISTLITEKLSKLKNS; STLITEKLSKLKNSG;
TLITEKLSKLKNSGE; LITEKLSKLKNSGEL; ITEKLSKLKNSGELK;
TEKLSKLKNSGELKA; EKLSKLKNSGELKAK; KLSKLKNSGELKAKI;
LSKLKNSGELKAKIE; SKLKNSGELKAKIED; KLKNSGELKAKIEDA;
LKNSGELKAKIEDAK; KNSGELKAKIEDAKK; NSGELKAKIEDAKKC;
SGELKAKIEDAKKCS; GELKAKIEDAKKCSE; ELKAKIEDAKKCSEE;
LKAKIEDAKKCSEEF; KAKIEDAKKCSEEFT; AKIEDAKKCSEEFTN;
KIEDAKKCSEEFTNK; IEDAKKCSEEFTNKL; EDAKKCSEEFTNKLR;
DAKKCSEEFTNKLRV; AKKCSEEFTNKLRVS; KKCSEEFTNKLRVSH;
KCSEEFTNKLRVSHA; CSEEFTNKLRVSHAD; SEEFTNKLRVSHADL;
EEFTNKLRVSHADLG; EFTNKLRVSHADLGK; FTNKLRVSHADLGKQ;
TNKLRVSHADLGKQG; NKLRVSHADLGKQGV; KLRVSHADLGKQGVN;
LRVSHADLGKQGVND; RVSHADLGKQGVNDD; VSHADLGKQGVNDDD;
SHADLGKQGVNDDDA; HADLGKQGVNDDDAK; ADLGKQGVNDDDAKK;
DLGKQGVNDDDAKKA; LGKQGVNDDDAKKAI; GKQGVNDDDAKKAIL;

KQGVNDDDAKKAILK; QGVNDDDAKKAILKT; GVNDDDAKKAILKTN;
VNDDDAKKAILKTNA; NDDDAKKAILKTNAD; DDDAKKAILKTNADK;
DDAKKAILKTNADKT; DAKKAILKTNADKTK; AKKAILKTNADKTKG;
KKAILKTNADKTKGA; KAILKTNADKTKGAE; AILKTNADKTKGAEE;
ILKTNADKTKGAEEL; LKTNADKTKGAEELG; KTNADKTKGAEELGK;
TNADKTKGAEELGKL; NADKTKGAEELGKLF; ADKTKGAEELGKLFK;
DKTKGAEELGKLFKS; KTKGAEELGKLFKSV; TKGAEELGKLFKSVE;
KGAEELGKLFKSVEG; GAEELGKLFKSVEGL; AEELGKLFKSVEGLV;
EELGKLFKSVEGLVK; ELGKLFKSVEGLVKA; LGKLFKSVEGLVKAA;
GKLFKSVEGLVKAAQ; KLFKSVEGLVKAAQE; LFKSVEGLVKAAQEA;
FKSVEGLVKAAQEAL; KSVEGLVKAAQEALT; SVEGLVKAAQEALTN;
VEGLVKAAQEALTNS; EGLVKAAQEALTNSV; GLVKAAQEALTNSVK;
LVKAAQEALTNSVKE; VKAAQEALTNSVKEL; KAAQEALTNSVKELT;
AAQEALTNSVKELTS; AQEALTNSVKELTSP; QEALTNSVKELTSPV;
EALTNSVKELTSPVV; ALTNSVKELTSPVVA; LTNSVKELTSPVVAE;
TNSVKELTSPVVAES; NSVKELTSPVVAESP; SVKELTSPVVAESPK;
VKELTSPVVAESPKK; KELTSPVVAESPKKP;

16 mers:
MKKNTLSAILMTLFLF; KKNTLSAILMTLFLFI; KNTLSAILMTLFLFIS;
NTLSAILMTLFLFISC; TLSAILMTLFLFISCN; LSAILMTLFLFISCNN;
SAILMTLFLFISCNNS; AILMTLFLFISCNNSG; ILMTLFLFISCNNSGK;
LMTLFLFISCNNSGKG; MTLFLFISCNNSGKGG; TLFLFISCNNSGKGGD;
LFLFISCNNSGKGGDS; FLFISCNNSGKGGDSA; LFISCNNSGKGGDSAS;
FISCNNSGKGGDSAST; ISCNNSGKGGDSASTN; SCNNSGKGGDSASTNP;
CNNSGKGGDSASTNPA; NNSGKGGDSASTNPAD; NSGKGGDSASTNPADE;
SGKGGDSASTNPADES; GKGGDSASTNPADESA; KGGDSASTNPADESAK;
GGDSASTNPADESAKG; GDSASTNPADESAKGP; DSASTNPADESAKGPN;
SASTNPADESAKGPNL; ASTNPADESAKGPNLT; STNPADESAKGPNLTE;
TNPADESAKGPNLTEI; NPADESAKGPNLTEIS; PADESAKGPNLTEISK;
ADESAKGPNLTEISKK; DESAKGPNLTEISKKI; ESAKGPNLTEISKKIT;
SAKGPNLTEISKKITD; AKGPNLTEISKKITDS; KGPNLTEISKKITDSN;
GPNLTEISKKITDSNA; PNLTEISKKITDSNAF; NLTEISKKITDSNAFV;
LTEISKKITDSNAFVL; TEISKKITDSNAFVLA; EISKKITDSNAFVLAV;
ISKKITDSNAFVLAVK; SKKITDSNAFVLAVKE; KKITDSNAFVLAVKEV;
KITDSNAFVLAVKEVE; ITDSNAFVLAVKEVET; TDSNAFVLAVKEVETL;
DSNAFVLAVKEVETLV; SNAFVLAVKEVETLVS; NAFVLAVKEVETLVSS;
AFVLAVKEVETLVSSI; FVLAVKEVETLVSSID; VLAVKEVETLVSSIDE;
LAVKEVETLVSSIDEL; AVKEVETLVSSIDELA; VKEVETLVSSIDELAN;
KEVETLVSSIDELANK; EVETLVSSIDELANKA; VETLVSSIDELANKAI;
ETLVSSIDELANKAIG; TLVSSIDELANKAIGK; LVSSIDELANKAIGKK;
VSSIDELANKAIGKKI; SSIDELANKAIGKKIQ; SIDELANKAIGKKIQQ;
IDELANKAIGKKIQQN; DELANKAIGKKIQQNG; ELANKAIGKKIQQNGL;
LANKAIGKKIQQNGLG; ANKAIGKKIQQNGLGA; NKAIGKKIQQNGLGAE;
KAIGKKIQQNGLGAEA; AIGKKIQQNGLGAEAN; IGKKIQQNGLGAEANR;
GKKIQQNGLGAEANRN; KKIQQNGLGAEANRNE; KIQQNGLGAEANRNES;
IQQNGLGAEANRNESL; QQNGLGAEANRNESLL; QNGLGAEANRNESLLA;
NGLGAEANRNESLLAG; GLGAEANRNESLLAGV; LGAEANRNESLLAGVH;
GAEANRNESLLAGVHE; AEANRNESLLAGVHEI; EANRNESLLAGVHEIS;
ANRNESLLAGVHEIST; NRNESLLAGVHEISTL; RNESLLAGVHEISTLI;
NESLLAGVHEISTLIT; ESLLAGVHEISTLITE; SLLAGVHEISTLITEK;
LLAGVHEISTLITEKL; LAGVHEISTLITEKLS; AGVHEISTLITEKLSK;
GVHEISTLITEKLSKL; VHEISTLITEKLSKLK; HEISTLITEKLSKLKN;
EISTLITEKLSKLKNS; ISTLITEKLSKLKNSG; STLITEKLSKLKNSGE;
TLITEKLSKLKNSGEL; LITEKLSKLKNSGELK; ITEKLSKLKNSGELKA;
TEKLSKLKNSGELKAK; EKLSKLKNSGELKAKI; KLSKLKNSGELKAKIE;
LSKLKNSGELKAKIED; SKLKNSGELKAKIEDA; KLKNSGELKAKIEDAK;

	LKNSGELKAKIEDAKK; KNSGELKAKIEDAKKC; NSGELKAKIEDAKKCS; SGELKAKIEDAKKCSE; GELKAKIEDAKKCSEE; ELKAKIEDAKKCSEEF; LKAKIEDAKKCSEEFT; KAKIEDAKKCSEEFTN; AKIEDAKKCSEEFTNK; KIEDAKKCSEEFTNKL; IEDAKKCSEEFTNKLR; EDAKKCSEEFTNKLRV; DAKKCSEEFTNKLRVS; AKKCSEEFTNKLRVSH; KKCSEEFTNKLRVSHA; KCSEEFTNKLRVSHAD; CSEEFTNKLRVSHADL; SEEFTNKLRVSHADLG; EEFTNKLRVSHADLGK; EFTNKLRVSHADLGKQ; FTNKLRVSHADLGKQG; TNKLRVSHADLGKQGV; NKLRVSHADLGKQGVN; KLRVSHADLGKQGVND; LRVSHADLGKQGVNDD; RVSHADLGKQGVNDDD; VSHADLGKQGVNDDDA; SHADLGKQGVNDDDAK; HADLGKQGVNDDDAKK; ADLGKQGVNDDDAKKA; DLGKQGVNDDDAKKAI; LGKQGVNDDDAKKAIL; GKQGVNDDDAKKAILK; KQGVNDDDAKKAILKT; QGVNDDDAKKAILKTN; GVNDDDAKKAILKTNA; VNDDDAKKAILKTNAD; NDDDAKKAILKTNADK; DDDAKKAILKTNADKT; DDAKKAILKTNADKTK; DAKKAILKTNADKTKG; AKKAILKTNADKTKGA; KKAILKTNADKTKGAE; KAILKTNADKTKGAEE; AILKTNADKTKGAEEL; ILKTNADKTKGAEELG; LKTNADKTKGAEELGK; KTNADKTKGAEELGKL; TNADKTKGAEELGKLF; NADKTKGAEELGKLFK; ADKTKGAEELGKLFKS; DKTKGAEELGKLFKSV; KTKGAEELGKLFKSVE; TKGAEELGKLFKSVEG; KGAEELGKLFKSVEGL; GAEELGKLFKSVEGLV; AEELGKLFKSVEGLVK; EELGKLFKSVEGLVKA; ELGKLFKSVEGLVKAA; LGKLFKSVEGLVKAAQ; GKLFKSVEGLVKAAQE; KLFKSVEGLVKAAQEA; LFKSVEGLVKAAQEAL; FKSVEGLVKAAQEALT; KSVEGLVKAAQEALTN; SVEGLVKAAQEALTNS; VEGLVKAAQEALTNSV; EGLVKAAQEALTNSVK; GLVKAAQEALTNSVKE; LVKAAQEALTNSVKEL; VKAAQEALTNSVKELT; KAAQEALTNSVKELTS; AAQEALTNSVKELTSP; AQEALTNSVKELTSPV; QEALTNSVKELTSPVV; EALTNSVKELTSPVVA; ALTNSVKELTSPVVAE; LTNSVKELTSPVVAES; TNSVKELTSPVVAESP; NSVKELTSPVVAESPK; SVKELTSPVVAESPKK; VKELTSPVVAESPKKP;
AAC62927.1| OspE-related lipoprotein [Borrelia garinii]	13 mers: MNKKMKMFIICAV; NKKMKMFIICAVF; KKMKMFIICAVFV; KMKMFIICAVFVL; MKMFIICAVFVLI; KMFIICAVFVLIS; MFIICAVFVLISS; FIICAVFVLISSC; IICAVFVLISSCG; ICAVFVLISSCGN; CAVFVLISSCGNF; AVFVLISSCGNFR; VFVLISSCGNFRS; FVLISSCGNFRSS; VLISSCGNFRSSL; LISSCGNFRSSLS; ISSCGNFRSSLSD; SSCGNFRSSLSDQ; SCGNFRSSLSDQG; CGNFRSSLSDQGS; GNFRSSLSDQGSL; NFRSSLSDQGSLS; FRSSLSDQGSLSD; RSSLSDQGSLSDQ; SSLSDQGSLSDQG; SLSDQGSLSDQGS; LSDQGSLSDQGSL; SDQGSLSDQGSLS; DQGSLSDQGSLSD; QGSLSDQGSLSDQ; GSLSDQGSLSDQG; SLSDQGSLSDQGS; LSDQGSLSDQGSL; SDQGSLSDQGSLS; DQGSLSDQGSLSD; QGSLSDQGSLSDQ; GSLSDQGSLSDQG; SLSDQGSLSDQGG; LSDQGSLSDQGGL; SDQGSLSDQGGLS; DQGSLSDQGGLSG; QGSLSDQGGLSGQ; GSLSDQGGLSGQA; SLSDQGGLSGQAS; LSDQGGLSGQASS; SDQGGLSGQASSD; DQGGLSGQASSDT; QGGLSGQASSDTI; GGLSGQASSDTIK; GLSGQASSDTIKF; LSGQASSDTIKFS; SGQASSDTIKFSE; GQASSDTIKFSEF; QASSDTIKFSEFT; ASSDTIKFSEFTV; SSDTIKFSEFTVN; SDTIKFSEFTVNI; DTIKFSEFTVNIK; TIKFSEFTVNIKN; IKFSEFTVNIKNK; KFSEFTVNIKNKK; FSEFTVNIKNKKD; SEFTVNIKNKKDN; EFTVNIKNKKDNN; FTVNIKNKKDNNG; TVNIKNKKDNNGD; VNIKNKKDNNGDW; NIKNKKDNNGDWS; IKNKKDNNGDWSN; KNKKDNNGDWSNL; NKKDNNGDWSNLG; KKDNNGDWSNLGT; KDNNGDWSNLGTL; DNNGDWSNLGTLV; NNGDWSNLGTLVI; NGDWSNLGTLVIR; GDWSNLGTLVIRK; DWSNLGTLVIRKE; WSNLGTLVIRKEQ; SNLGTLVIRKEQD; NLGTLVIRKEQDG; LGTLVIRKEQDGV; GTLVIRKEQDGVE; TLVIRKEQDGVET; LVIRKEQDGVETG; VIRKEQDGVETGL; IRKEQDGVETGLN; RKEQDGVETGLNV; KEQDGVETGLNVI; EQDGVETGLNVIG; QDGVETGLNVIGT; DGVETGLNVIGTI; GVETGLNVIGTIN; VETGLNVIGTING; ETGLNVIGTINGQ; TGLNVIGTINGQL; GLNVIGTINGQLR; LNVIGTINGQLRG; NVIGTINGQLRGH; VIGTINGQLRGHS; IGTINGQLRGHSA; GTINGQLRGHSAT; TINGQLRGHSATF; INGQLRGHSATFF;

NGQLRGHSATFFC; GQLRGHSATFFCI; QLRGHSATFFCIE; LRGHSATFFCIEE;
RGHSATFFCIEEA; GHSATFFCIEEAE; HSATFFCIEEAEV; SATFFCIEEAEVN;
ATFFCIEEAEVNN; TFFCIEEAEVNNF; FFCIEEAEVNNFV; FCIEEAEVNNFVK;
CIEEAEVNNFVKA; IEEAEVNNFVKAM; EEAEVNNFVKAMT; EAEVNNFVKAMTN;
AEVNNFVKAMTNV; EVNNFVKAMTNVG; VNNFVKAMTNVGS; NNFVKAMTNVGSF;
NFVKAMTNVGSFK; FVKAMTNVGSFKT; VKAMTNVGSFKTS; KAMTNVGSFKTSL;
AMTNVGSFKTSLY; MTNVGSFKTSLYY; TNVGSFKTSLYYG; NVGSFKTSLYYGY;
VGSFKTSLYYGYK; GSFKTSLYYGYKE; SFKTSLYYGYKEE; FKTSLYYGYKEEQ;
KTSLYYGYKEEQS; TSLYYGYKEEQSS; SLYYGYKEEQSST; LYYGYKEEQSSTN;
YYGYKEEQSSTNG; YGYKEEQSSTNGI; GYKEEQSSTNGIK; YKEEQSSTNGIKG;
KEEQSSTNGIKGK; EEQSSTNGIKGKE; EQSSTNGIKGKEI; QSSTNGIKGKEIT;
SSTNGIKGKEITT; STNGIKGKEITTK; TNGIKGKEITTKI; NGIKGKEITTKIE;
GIKGKEITTKIET; IKGKEITTKIETI; KGKEITTKIETIN; GKEITTKIETINN;
KEITTKIETINNS; EITTKIETINNSE; ITTKIETINNSEH; TTKIETINNSEHI;
TKIETINNSEHIT; KIETINNSEHITF; IETINNSEHITFS; ETINNSEHITFSG;
TINNSEHITFSGD; INNSEHITFSGDK; NNSEHITFSGDKI;

14 mers:
MNKKMKMFIICAVF; NKKMKMFIICAVFV; KKMKMFIICAVFVL;
KMKMFIICAVFVLI; MKMFIICAVFVLIS; KMFIICAVFVLISS;
MFIICAVFVLISSC; FIICAVFVLISSCG; IICAVFVLISSCGN;
ICAVFVLISSCGNF; CAVFVLISSCGNFR; AVFVLISSCGNFRS;
VFVLISSCGNFRSS; FVLISSCGNFRSSL; VLISSCGNFRSSLS;
LISSCGNFRSSLSD; ISSCGNFRSSLSDQ; SSCGNFRSSLSDQG;
SCGNFRSSLSDQGS; CGNFRSSLSDQGSL; GNFRSSLSDQGSLS;
NFRSSLSDQGSLSD; FRSSLSDQGSLSDQ; RSSLSDQGSLSDQG;
SSLSDQGSLSDQGS; SLSDQGSLSDQGSL; LSDQGSLSDQGSLS;
SDQGSLSDQGSLSD; DQGSLSDQGSLSDQ; QGSLSDQGSLSDQG;
GSLSDQGSLSDQGS; SLSDQGSLSDQGSL; LSDQGSLSDQGSLS;
SDQGSLSDQGSLSD; DQGSLSDQGSLSDQ; QGSLSDQGSLSDQG;
GSLSDQGSLSDQGG; SLSDQGSLSDQGGL; LSDQGSLSDQGGLS;
SDQGSLSDQGGLSG; DQGSLSDQGGLSGQ; QGSLSDQGGLSGQA;
GSLSDQGGLSGQAS; SLSDQGGLSGQASS; LSDQGGLSGQASSD;
SDQGGLSGQASSDT; DQGGLSGQASSDTI; QGGLSGQASSDTIK;
GGLSGQASSDTIKF; GLSGQASSDTIKFS; LSGQASSDTIKFSE;
SGQASSDTIKFSEF; GQASSDTIKFSEFT; QASSDTIKFSEFTV;
ASSDTIKFSEFTVN; SSDTIKFSEFTVNI; SDTIKFSEFTVNIK;
DTIKFSEFTVNIKN; TIKFSEFTVNIKNK; IKFSEFTVNIKNKK;
KFSEFTVNIKNKKD; FSEFTVNIKNKKDN; SEFTVNIKNKKDNN;
EFTVNIKNKKDNNG; FTVNIKNKKDNNGD; TVNIKNKKDNNGDW;
VNIKNKKDNNGDWS; NIKNKKDNNGDWSN; IKNKKDNNGDWSNL;
KNKKDNNGDWSNLG; NKKDNNGDWSNLGT; KKDNNGDWSNLGTL;
KDNNGDWSNLGTLV; DNNGDWSNLGTLVI; NNGDWSNLGTLVIR;
NGDWSNLGTLVIRK; GDWSNLGTLVIRKE; DWSNLGTLVIRKEQ;
WSNLGTLVIRKEQD; SNLGTLVIRKEQDG; NLGTLVIRKEQDGV;
LGTLVIRKEQDGVE; GTLVIRKEQDGVET; TLVIRKEQDGVETG;
LVIRKEQDGVETGL; VIRKEQDGVETGLN; IRKEQDGVETGLNV;
RKEQDGVETGLNVI; KEQDGVETGLNVIG; EQDGVETGLNVIGT;
QDGVETGLNVIGTI; DGVETGLNVIGTIN; GVETGLNVIGTING;
VETGLNVIGTINGQ; ETGLNVIGTINGQL; TGLNVIGTINGQLR;
GLNVIGTINGQLRG; LNVIGTINGQLRGH; NVIGTINGQLRGHS;
VIGTINGQLRGHSA; IGTINGQLRGHSAT; GTINGQLRGHSATF;
TINGQLRGHSATFF; INGQLRGHSATFFC; NGQLRGHSATFFCI;
GQLRGHSATFFCIE; QLRGHSATFFCIEE; LRGHSATFFCIEEA;
RGHSATFFCIEEAE; GHSATFFCIEEAEV; HSATFFCIEEAEVN;
SATFFCIEEAEVNN; ATFFCIEEAEVNNF; TFFCIEEAEVNNFV;
FFCIEEAEVNNFVK; FCIEEAEVNNFVKA; CIEEAEVNNFVKAM;

IEEAEVNNFVKAMT; EEAEVNNFVKAMTN; EAEVNNFVKAMTNV;
AEVNNFVKAMTNVG; EVNNFVKAMTNVGS; VNNFVKAMTNVGSF;
NNFVKAMTNVGSFK; NFVKAMTNVGSFKT; FVKAMTNVGSFKTS;
VKAMTNVGSFKTSL; KAMTNVGSFKTSLY; AMTNVGSFKTSLYY;
MTNVGSFKTSLYYG; TNVGSFKTSLYYGY; NVGSFKTSLYYGYK;
VGSFKTSLYYGYKE; GSFKTSLYYGYKEE; SFKTSLYYGYKEEQ;
FKTSLYYGYKEEQS; KTSLYYGYKEEQSS; TSLYYGYKEEQSST;
SLYYGYKEEQSSTN; LYYGYKEEQSSTNG; YYGYKEEQSSTNGI;
YGYKEEQSSTNGIK; GYKEEQSSTNGIKG; YKEEQSSTNGIKGK;
KEEQSSTNGIKGKE; EEQSSTNGIKGKEI; EQSSTNGIKGKEIT;
QSSTNGIKGKEITT; SSTNGIKGKEITTK; STNGIKGKEITTKI;
TNGIKGKEITTKIE; NGIKGKEITTKIET; GIKGKEITTKIETI;
IKGKEITTKIETIN; KGKEITTKIETINN; GKEITTKIETINNS;
KEITTKIETINNSE; EITTKIETINNSEH; ITTKIETINNSEHI;
TTKIETINNSEHIT; TKIETINNSEHITF; KIETINNSEHITFS;
IETINNSEHITFSG; ETINNSEHITFSGD; TINNSEHITFSGDK;
INNSEHITFSGDKI;

15 mers:
MNKKMKMFIICAVFV; NKKMKMFIICAVFVL; KKMKMFIICAVFVLI;
KMKMFIICAVFVLIS; MKMFIICAVFVLISS; KMFIICAVFVLISSC;
MFIICAVFVLISSCG; FIICAVFVLISSCGN; IICAVFVLISSCGNF;
ICAVFVLISSCGNFR; CAVFVLISSCGNFRS; AVFVLISSCGNFRSS;
VFVLISSCGNFRSSL; FVLISSCGNFRSSLS; VLISSCGNFRSSLSD;
LISSCGNFRSSLSDQ; ISSCGNFRSSLSDQG; SSCGNFRSSLSDQGS;
SCGNFRSSLSDQGSL; CGNFRSSLSDQGSLS; GNFRSSLSDQGSLSD;
NFRSSLSDQGSLSDQ; FRSSLSDQGSLSDQG; RSSLSDQGSLSDQGS;
SSLSDQGSLSDQGSL; SLSDQGSLSDQGSLS; LSDQGSLSDQGSLSD;
SDQGSLSDQGSLSDQ; DQGSLSDQGSLSDQG; QGSLSDQGSLSDQGS;
GSLSDQGSLSDQGSL; SLSDQGSLSDQGSLS; LSDQGSLSDQGSLSD;
SDQGSLSDQGSLSDQ; DQGSLSDQGSLSDQG; QGSLSDQGSLSDQGG;
GSLSDQGSLSDQGGL; SLSDQGSLSDQGGLS; LSDQGSLSDQGGLSG;
SDQGSLSDQGGLSGQ; DQGSLSDQGGLSGQA; QGSLSDQGGLSGQAS;
GSLSDQGGLSGQASS; SLSDQGGLSGQASSD; LSDQGGLSGQASSDT;
SDQGGLSGQASSDTI; DQGGLSGQASSDTIK; QGGLSGQASSDTIKF;
GGLSGQASSDTIKFS; GLSGQASSDTIKFSE; LSGQASSDTIKFSEF;
SGQASSDTIKFSEFT; GQASSDTIKFSEFTV; QASSDTIKFSEFTVN;
ASSDTIKFSEFTVNI; SSDTIKFSEFTVNIK; SDTIKFSEFTVNIKN;
DTIKFSEFTVNIKNK; TIKFSEFTVNIKNKK; IKFSEFTVNIKNKKD;
KFSEFTVNIKNKKDN; FSEFTVNIKNKKDNN; SEFTVNIKNKKDNNG;
EFTVNIKNKKDNNGD; FTVNIKNKKDNNGDW; TVNIKNKKDNNGDWS;
VNIKNKKDNNGDWSN; NIKNKKDNNGDWSNL; IKNKKDNNGDWSNLG;
KNKKDNNGDWSNLGT; NKKDNNGDWSNLGTL; KKDNNGDWSNLGTLV;
KDNNGDWSNLGTLVI; DNNGDWSNLGTLVIR; NNGDWSNLGTLVIRK;
NGDWSNLGTLVIRKE; GDWSNLGTLVIRKEQ; DWSNLGTLVIRKEQD;
WSNLGTLVIRKEQDG; SNLGTLVIRKEQDGV; NLGTLVIRKEQDGVE;
LGTLVIRKEQDGVET; GTLVIRKEQDGVETG; TLVIRKEQDGVETGL;
LVIRKEQDGVETGLN; VIRKEQDGVETGLNV; IRKEQDGVETGLNVI;
RKEQDGVETGLNVIG; KEQDGVETGLNVIGT; EQDGVETGLNVIGTI;
QDGVETGLNVIGTIN; DGVETGLNVIGTING; GVETGLNVIGTINGQ;
VETGLNVIGTINGQL; ETGLNVIGTINGQLR; TGLNVIGTINGQLRG;
GLNVIGTINGQLRGH; LNVIGTINGQLRGHS; NVIGTINGQLRGHSA;
VIGTINGQLRGHSAT; IGTINGQLRGHSATF; GTINGQLRGHSATFF;
TINGQLRGHSATFFC; INGQLRGHSATFFCI; NGQLRGHSATFFCIE;
GQLRGHSATFFCIEE; QLRGHSATFFCIEEA; LRGHSATFFCIEEAE;
RGHSATFFCIEEAEV; GHSATFFCIEEAEVN; HSATFFCIEEAEVNN;
SATFFCIEEAEVNNF; ATFFCIEEAEVNNFV; TFFCIEEAEVNNFVK;

FFCIEEAEVNNFVKA; FCIEEAEVNNFVKAM; CIEEAEVNNFVKAMT;
IEEAEVNNFVKAMTN; EEAEVNNFVKAMTNV; EAEVNNFVKAMTNVG;
AEVNNFVKAMTNVGS; EVNNFVKAMTNVGSF; VNNFVKAMTNVGSFK;
NNFVKAMTNVGSFKT; NFVKAMTNVGSFKTS; FVKAMTNVGSFKTSL;
VKAMTNVGSFKTSLY; KAMTNVGSFKTSLYY; AMTNVGSFKTSLYYG;
MTNVGSFKTSLYYGY; TNVGSFKTSLYYGYK; NVGSFKTSLYYGYKE;
VGSFKTSLYYGYKEE; GSFKTSLYYGYKEEQ; SFKTSLYYGYKEEQS;
FKTSLYYGYKEEQSS; KTSLYYGYKEEQSST; TSLYYGYKEEQSSTN;
SLYYGYKEEQSSTNG; LYYGYKEEQSSTNGI; YYGYKEEQSSTNGIK;
YGYKEEQSSTNGIKG; GYKEEQSSTNGIKGK; YKEEQSSTNGIKGKE;
KEEQSSTNGIKGKEI; EEQSSTNGIKGKEIT; EQSSTNGIKGKEITT;
QSSTNGIKGKEITTK; SSTNGIKGKEITTKI; STNGIKGKEITTKIE;
TNGIKGKEITTKIET; NGIKGKEITTKIETI; GIKGKEITTKIETIN;
IKGKEITTKIETINN; KGKEITTKIETINNS; GKEITTKIETINNSE;
KEITTKIETINNSEH; EITTKIETINNSEHI; ITTKIETINNSEHIT;
TTKIETINNSEHITF; TKIETINNSEHITFS; KIETINNSEHITFSG;
IETINNSEHITFSGD; ETINNSEHITFSGDK; TINNSEHITFSGDKI;

16 mers:
MNKKMKMFIICAVFVL; NKKMKMFIICAVFVLI; KKMKMFIICAVFVLIS;
KMKMFIICAVFVLISS; MKMFIICAVFVLISSC; KMFIICAVFVLISSCG;
MFIICAVFVLISSCGN; FIICAVFVLISSCGNF; IICAVFVLISSCGNFR;
ICAVFVLISSCGNFRS; CAVFVLISSCGNFRSS; AVFVLISSCGNFRSSL;
VFVLISSCGNFRSSLS; FVLISSCGNFRSSLSD; VLISSCGNFRSSLSDQ;
LISSCGNFRSSLSDQG; ISSCGNFRSSLSDQGS; SSCGNFRSSLSDQGSL;
SCGNFRSSLSDQGSLS; CGNFRSSLSDQGSLSD; GNFRSSLSDQGSLSDQ;
NFRSSLSDQGSLSDQG; FRSSLSDQGSLSDQGS; RSSLSDQGSLSDQGSL;
SSLSDQGSLSDQGSLS; SLSDQGSLSDQGSLSD; LSDQGSLSDQGSLSDQ;
SDQGSLSDQGSLSDQG; DQGSLSDQGSLSDQGS; QGSLSDQGSLSDQGSL;
GSLSDQGSLSDQGSLS; SLSDQGSLSDQGSLSD; LSDQGSLSDQGSLSDQ;
SDQGSLSDQGSLSDQG; DQGSLSDQGSLSDQGG; QGSLSDQGSLSDQGGL;
GSLSDQGSLSDQGGLS; SLSDQGSLSDQGGLSG; LSDQGSLSDQGGLSGQ;
SDQGSLSDQGGLSGQA; DQGSLSDQGGLSGQAS; QGSLSDQGGLSGQASS;
GSLSDQGGLSGQASSD; SLSDQGGLSGQASSDT; LSDQGGLSGQASSDTI;
SDQGGLSGQASSDTIK; DQGGLSGQASSDTIKF; QGGLSGQASSDTIKFS;
GGLSGQASSDTIKFSE; GLSGQASSDTIKFSEF; LSGQASSDTIKFSEFT;
SGQASSDTIKFSEFTV; GQASSDTIKFSEFTVN; QASSDTIKFSEFTVNI;
ASSDTIKFSEFTVNIK; SSDTIKFSEFTVNIKN; SDTIKFSEFTVNIKNK;
DTIKFSEFTVNIKNKK; TIKFSEFTVNIKNKKD; IKFSEFTVNIKNKKDN;
KFSEFTVNIKNKKDNN; FSEFTVNIKNKKDNNG; SEFTVNIKNKKDNNGD;
EFTVNIKNKKDNNGDW; FTVNIKNKKDNNGDWS; TVNIKNKKDNNGDWSN;
VNIKNKKDNNGDWSNL; NIKNKKDNNGDWSNLG; IKNKKDNNGDWSNLGT;
KNKKDNNGDWSNLGTL; NKKDNNGDWSNLGTLV; KKDNNGDWSNLGTLVI;
KDNNGDWSNLGTLVIR; DNNGDWSNLGTLVIRK; NNGDWSNLGTLVIRKE;
NGDWSNLGTLVIRKEQ; GDWSNLGTLVIRKEQD; DWSNLGTLVIRKEQDG;
WSNLGTLVIRKEQDGV; SNLGTLVIRKEQDGVE; NLGTLVIRKEQDGVET;
LGTLVIRKEQDGVETG; GTLVIRKEQDGVETGL; TLVIRKEQDGVETGLN;
LVIRKEQDGVETGLNV; VIRKEQDGVETGLNVI; IRKEQDGVETGLNVIG;
RKEQDGVETGLNVIGT; KEQDGVETGLNVIGTI; EQDGVETGLNVIGTIN;
QDGVETGLNVIGTING; DGVETGLNVIGTINGQ; GVETGLNVIGTINGQL;
VETGLNVIGTINGQLR; ETGLNVIGTINGQLRG; TGLNVIGTINGQLRGH;
GLNVIGTINGQLRGHS; LNVIGTINGQLRGHSA; NVIGTINGQLRGHSAT;
VIGTINGQLRGHSATF; IGTINGQLRGHSATFF; GTINGQLRGHSATFFC;
TINGQLRGHSATFFCI; INGQLRGHSATFFCIE; NGQLRGHSATFFCIEE;
GQLRGHSATFFCIEEA; QLRGHSATFFCIEEAE; LRGHSATFFCIEEAEV;
RGHSATFFCIEEAEVN; GHSATFFCIEEAEVNN; HSATFFCIEEAEVNNF;
SATFFCIEEAEVNNFV; ATFFCIEEAEVNNFVK; TFFCIEEAEVNNFVKA;

	FFCIEEAEVNNFVKAM; FCIEEAEVNNFVKAMT; CIEEAEVNNFVKAMTN; IEEAEVNNFVKAMTNV; EEAEVNNFVKAMTNVG; EAEVNNFVKAMTNVGS; AEVNNFVKAMTNVGSF; EVNNFVKAMTNVGSFK; VNNFVKAMTNVGSFKT; NNFVKAMTNVGSFKTS; NFVKAMTNVGSFKTSL; FVKAMTNVGSFKTSLY; VKAMTNVGSFKTSLYY; KAMTNVGSFKTSLYYG; AMTNVGSFKTSLYYGY; MTNVGSFKTSLYYGYK; TNVGSFKTSLYYGYKE; NVGSFKTSLYYGYKEE; VGSFKTSLYYGYKEEQ; GSFKTSLYYGYKEEQS; SFKTSLYYGYKEEQSS; FKTSLYYGYKEEQSST; KTSLYYGYKEEQSSTN; TSLYYGYKEEQSSTNG; SLYYGYKEEQSSTNGI; LYYGYKEEQSSTNGIK; YYGYKEEQSSTNGIKG; YGYKEEQSSTNGIKGK; GYKEEQSSTNGIKGKE; YKEEQSSTNGIKGKEI; KEEQSSTNGIKGKEIT; EEQSSTNGIKGKEITT; EQSSTNGIKGKEITTK; QSSTNGIKGKEITTKI; SSTNGIKGKEITTKIE; STNGIKGKEITTKIET; TNGIKGKEITTKIETI; NGIKGKEITTKIETIN; GIKGKEITTKIETINN; IKGKEITTKIETINNS; KGKEITTKIETINNSE; GKEITTKIETINNSEH; KEITTKIETINNSEHI; EITTKIETINNSEHIT; ITTKIETINNSEHITF; TTKIETINNSEHITFS; TKIETINNSEHITFSG; KIETINNSEHITFSGD; IETINNSEHITFSGDK; ETINNSEHITFSGDKI;
CAA57806.1| Outer surface protein G [Borrelia burgdorferi]	13 mers: MNKKMKNLIICAV; NKKMKNLIICAVF; KKMKNLIICAVFV; KMKNLIICAVFVL; MKNLIICAVFVLI; KNLIICAVFVLII; NLIICAVFVLIIS; LIICAVFVLIISC; IICAVFVLIISCK; ICAVFVLIISCKI; CAVFVLIISCKID; AVFVLIISCKIDA; VFVLIISCKIDAS; FVLIISCKIDASS; VLIISCKIDASSE; LIISCKIDASSED; IISCKIDASSEDL; ISCKIDASSEDLK; SCKIDASSEDLKQ; CKIDASSEDLKQN; KIDASSEDLKQNV; IDASSEDLKQNVK; DASSEDLKQNVKE; ASSEDLKQNVKEK; SSEDLKQNVKEKV; SEDLKQNVKEKVE; EDLKQNVKEKVEG; DLKQNVKEKVEGF; LKQNVKEKVEGFL; KQNVKEKVEGFLD; QNVKEKVEGFLDK; NVKEKVEGFLDKE; VKEKVEGFLDKEL; KEKVEGFLDKELM; EKVEGFLDKELMQ; KVEGFLDKELMQG; VEGFLDKELMQGD; EGFLDKELMQGDD; GFLDKELMQGDDP; FLDKELMQGDDPN; LDKELMQGDDPNN; DKELMQGDDPNNS; KELMQGDDPNNSL; ELMQGDDPNNSLF; LMQGDDPNNSLFN; MQGDDPNNSLFNP; QGDDPNNSLFNPP; GDDPNNSLFNPPP; DDPNNSLFNPPPV; DPNNSLFNPPPVL; PNNSLFNPPPVLP; NNSLFNPPPVLPA; NSLFNPPPVLPAS; SLFNPPPVLPASS; LFNPPPVLPASSH; FNPPPVLPASSHD; NPPPVLPASSHDN; PPPVLPASSHDNT; PPVLPASSHDNTP; PVLPASSHDNTPV; VLPASSHDNTPVL; LPASSHDNTPVLK; PASSHDNTPVLKA; ASSHDNTPVLKAV; SSHDNTPVLKAVQ; SHDNTPVLKAVQA; HDNTPVLKAVQAK; DNTPVLKAVQAKD; NTPVLKAVQAKDG; TPVLKAVQAKDGG; PVLKAVQAKDGGQ; VLKAVQAKDGGQQ; LKAVQAKDGGQQE; KAVQAKDGGQQEG; AVQAKDGGQQEGK; VQAKDGGQQEGKE; QAKDGGQQEGKEE; AKDGGQQEGKEEK; KDGGQQEGKEEKE; DGGQQEGKEEKEK; GGQQEGKEEKEKE; GQQEGKEEKEKEI; QQEGKEEKEKEIQ; QEGKEEKEKEIQE; EGKEEKEKEIQEL; GKEEKEKEIQELK; KEEKEKEIQELKD; EEKEKEIQELKDK; EKEKEIQELKDKI; KEKEIQELKDKID; EKEIQELKDKIDK; KEIQELKDKIDKR; EIQELKDKIDKRK; IQELKDKIDKRKK; QELKDKIDKRKKE; ELKDKIDKRKKEL; LKDKIDKRKKELE; KDKIDKRKKELEE; DKIDKRKKELEEA; KIDKRKKELEEAR; IDKRKKELEEARK; DKRKKELEEARKK; KRKKELEEARKKF; RKKELEEARKKFQ; KKELEEARKKFQE; KELEEARKKFQEF; ELEEARKKFQEFK; LEEARKKFQEFKE; EEARKKFQEFKEQ; EARKKFQEFKEQV; ARKKFQEFKEQVE; RKKFQEFKEQVES; KKFQEFKEQVESA; KFQEFKEQVESAT; FQEFKEQVESATG; QEFKEQVESATGE; EFKEQVESATGES; FKEQVESATGEST; KEQVESATGESTE; EQVESATGESTEK; QVESATGESTEKV; VESATGESTEKVK; ESATGESTEKVKK; SATGESTEKVKKQ; ATGESTEKVKKQG; TGESTEKVKKQGN; GESTEKVKKQGNI; ESTEKVKKQGNIG; STEKVKKQGNIGQ; TEKVKKQGNIGQK; EKVKKQGNIGQKA; KVKKQGNIGQKAL; VKKQGNIGQKALK; KKQGNIGQKALKY; KQGNIGQKALKYA; QGNIGQKALKYAK; GNIGQKALKYAKE; NIGQKALKYAKEL; IGQKALKYAKELG; GQKALKYAKELGV; QKALKYAKELGVN; KALKYAKELGVNG; ALKYAKELGVNGS; LKYAKELGVNGSY; KYAKELGVNGSYS; YAKELGVNGSYSV; AKELGVNGSYSVN; KELGVNGSYSVND;

ELGVNGSYSVNDG; LGVNGSYSVNDGT; GVNGSYSVNDGTN; VNGSYSVNDGTNT;
NGSYSVNDGTNTN; GSYSVNDGTNTND; SYSVNDGTNTNDF; YSVNDGTNTNDFV;
SVNDGTNTNDFVK; VNDGTNTNDFVKK; NDGTNTNDFVKKV; DGTNTNDFVKKVI;
GTNTNDFVKKVID; TNTNDFVKKVIDD; NTNDFVKKVIDDA; TNDFVKKVIDDAL;
NDFVKKVIDDALK; DFVKKVIDDALKN; FVKKVIDDALKNI; VKKVIDDALKNIE;
KKVIDDALKNIEE; KVIDDALKNIEEE; VIDDALKNIEEEL; IDDALKNIEEELE;
DDALKNIEEELEK; DALKNIEEELEKL; ALKNIEEELEKLA; LKNIEEELEKLAE;
KNIEEELEKLAEP; NIEEELEKLAEPQ; IEEELEKLAEPQN; EEELEKLAEPQNI;
EELEKLAEPQNIE; ELEKLAEPQNIED; LEKLAEPQNIEDK; EKLAEPQNIEDKK;

14 mers:
MNKKMKNLIICAVF; NKKMKNLIICAVFV; KKMKNLIICAVFVL;
KMKNLIICAVFVLI; MKNLIICAVFVLII; KNLIICAVFVLIIS;
NLIICAVFVLIISC; LIICAVFVLIISCK; IICAVFVLIISCKI;
ICAVFVLIISCKID; CAVFVLIISCKIDA; AVFVLIISCKIDAS;
VFVLIISCKIDASS; FVLIISCKIDASSE; VLIISCKIDASSED;
LIISCKIDASSEDL; IISCKIDASSEDLK; ISCKIDASSEDLKQ;
SCKIDASSEDLKQN; CKIDASSEDLKQNV; KIDASSEDLKQNVK;
IDASSEDLKQNVKE; DASSEDLKQNVKEK; ASSEDLKQNVKEKV;
SSEDLKQNVKEKVE; SEDLKQNVKEKVEG; EDLKQNVKEKVEGF;
DLKQNVKEKVEGFL; LKQNVKEKVEGFLD; KQNVKEKVEGFLDK;
QNVKEKVEGFLDKE; NVKEKVEGFLDKEL; VKEKVEGFLDKELM;
KEKVEGFLDKELMQ; EKVEGFLDKELMQG; KVEGFLDKELMQGD;
VEGFLDKELMQGDD; EGFLDKELMQGDDP; GFLDKELMQGDDPN;
FLDKELMQGDDPNN; LDKELMQGDDPNNS; DKELMQGDDPNNSL;
KELMQGDDPNNSLF; ELMQGDDPNNSLFN; LMQGDDPNNSLFNP;
MQGDDPNNSLFNPP; QGDDPNNSLFNPPP; GDDPNNSLFNPPPV;
DDPNNSLFNPPPVL; DPNNSLFNPPPVLP; PNNSLFNPPPVLPA;
NNSLFNPPPVLPAS; NSLFNPPPVLPASS; SLFNPPPVLPASSH;
LFNPPPVLPASSHD; FNPPPVLPASSHDN; NPPPVLPASSHDNT;
PPPVLPASSHDNTP; PPVLPASSHDNTPV; PVLPASSHDNTPVL;
VLPASSHDNTPVLK; LPASSHDNTPVLKA; PASSHDNTPVLKAV;
ASSHDNTPVLKAVQ; SSHDNTPVLKAVQA; SHDNTPVLKAVQAK;
HDNTPVLKAVQAKD; DNTPVLKAVQAKDG; NTPVLKAVQAKDGG;
TPVLKAVQAKDGGQ; PVLKAVQAKDGGQQ; VLKAVQAKDGGQQE;
LKAVQAKDGGQQEG; KAVQAKDGGQQEGK; AVQAKDGGQQEGKE;
VQAKDGGQQEGKEE; QAKDGGQQEGKEEK; AKDGGQQEGKEEKE;
KDGGQQEGKEEKEK; DGGQQEGKEEKEKE; GGQQEGKEEKEKEI;
GQQEGKEEKEKEIQ; QQEGKEEKEKEIQE; QEGKEEKEKEIQEL;
EGKEEKEKEIQELK; GKEEKEKEIQELKD; KEEKEKEIQELKDK;
EEKEKEIQELKDKI; EKEKEIQELKDKID; KEKEIQELKDKIDK;
EKEIQELKDKIDKR; KEIQELKDKIDKRK; EIQELKDKIDKRKK;
IQELKDKIDKRKKE; QELKDKIDKRKKEL; ELKDKIDKRKKELE;
LKDKIDKRKKELEE; KDKIDKRKKELEEA; DKIDKRKKELEEAR;
KIDKRKKELEEARK; IDKRKKELEEARKK; DKRKKELEEARKKF;
KRKKELEEARKKFQ; RKKELEEARKKFQE; KKELEEARKKFQEF;
KELEEARKKFQEFK; ELEEARKKFQEFKE; LEEARKKFQEFKEQ;
EEARKKFQEFKEQV; EARKKFQEFKEQVE; ARKKFQEFKEQVES;
RKKFQEFKEQVESA; KKFQEFKEQVESAT; KFQEFKEQVESATG;
FQEFKEQVESATGE; QEFKEQVESATGES; EFKEQVESATGEST;
FKEQVESATGESTE; KEQVESATGESTEK; EQVESATGESTEKV;
QVESATGESTEKVK; VESATGESTEKVKK; ESATGESTEKVKKQ;
SATGESTEKVKKQG; ATGESTEKVKKQGN; TGESTEKVKKQGNI;
GESTEKVKKQGNIG; ESTEKVKKQGNIGQ; STEKVKKQGNIGQK;
TEKVKKQGNIGQKA; EKVKKQGNIGQKAL; KVKKQGNIGQKALK;
VKKQGNIGQKALKY; KKQGNIGQKALKYA; KQGNIGQKALKYAK;
QGNIGQKALKYAKE; GNIGQKALKYAKEL; NIGQKALKYAKELG;

IGQKALKYAKELGV; GQKALKYAKELGVN; QKALKYAKELGVNG;
KALKYAKELGVNGS; ALKYAKELGVNGSY; LKYAKELGVNGSYS;
KYAKELGVNGSYSV; YAKELGVNGSYSVN; AKELGVNGSYSVND;
KELGVNGSYSVNDG; ELGVNGSYSVNDGT; LGVNGSYSVNDGTN;
GVNGSYSVNDGTNT; VNGSYSVNDGTNTN; NGSYSVNDGTNTND;
GSYSVNDGTNTNDF; SYSVNDGTNTNDFV; YSVNDGTNTNDFVK;
SVNDGTNTNDFVKK; VNDGTNTNDFVKKV; NDGTNTNDFVKKVI;
DGTNTNDFVKKVID; GTNTNDFVKKVIDD; TNTNDFVKKVIDDA;
NTNDFVKKVIDDAL; TNDFVKKVIDDALK; NDFVKKVIDDALKN;
DFVKKVIDDALKNI; FVKKVIDDALKNIE; VKKVIDDALKNIEE;
KKVIDDALKNIEEE; KVIDDALKNIEEEL; VIDDALKNIEEELE;
IDDALKNIEEELEK; DDALKNIEEELEKL; DALKNIEEELEKLA;
ALKNIEEELEKLAE; LKNIEEELEKLAEP; KNIEEELEKLAEPQ;
NIEEELEKLAEPQN; IEEELEKLAEPQNI; EEELEKLAEPQNIE;
EELEKLAEPQNIED; ELEKLAEPQNIEDK; LEKLAEPQNIEDKK;

15 mers:
MNKKMKNLIICAVFV; NKKMKNLIICAVFVL; KKMKNLIICAVFVLI;
KMKNLIICAVFVLII; MKNLIICAVFVLIIS; KNLIICAVFVLIISC;
NLIICAVFVLIISCK; LIICAVFVLIISCKI; IICAVFVLIISCKID;
ICAVFVLIISCKIDA; CAVFVLIISCKIDAS; AVFVLIISCKIDASS;
VFVLIISCKIDASSE; FVLIISCKIDASSED; VLIISCKIDASSEDL;
LIISCKIDASSEDLK; IISCKIDASSEDLKQ; ISCKIDASSEDLKQN;
SCKIDASSEDLKQNV; CKIDASSEDLKQNVK; KIDASSEDLKQNVKE;
IDASSEDLKQNVKEK; DASSEDLKQNVKEKV; ASSEDLKQNVKEKVE;
SSEDLKQNVKEKVEG; SEDLKQNVKEKVEGF; EDLKQNVKEKVEGFL;
DLKQNVKEKVEGFLD; LKQNVKEKVEGFLDK; KQNVKEKVEGFLDKE;
QNVKEKVEGFLDKEL; NVKEKVEGFLDKELM; VKEKVEGFLDKELMQ;
KEKVEGFLDKELMQG; EKVEGFLDKELMQGD; KVEGFLDKELMQGDD;
VEGFLDKELMQGDDP; EGFLDKELMQGDDPN; GFLDKELMQGDDPNN;
FLDKELMQGDDPNNS; LDKELMQGDDPNNSL; DKELMQGDDPNNSLF;
KELMQGDDPNNSLFN; ELMQGDDPNNSLFNP; LMQGDDPNNSLFNPP;
MQGDDPNNSLFNPPP; QGDDPNNSLFNPPPV; GDDPNNSLFNPPPVL;
DDPNNSLFNPPPVLP; DPNNSLFNPPPVLPA; PNNSLFNPPPVLPAS;
NNSLFNPPPVLPASS; NSLFNPPPVLPASSH; SLFNPPPVLPASSHD;
LFNPPPVLPASSHDN; FNPPPVLPASSHDNT; NPPPVLPASSHDNTP;
PPPVLPASSHDNTPV; PPVLPASSHDNTPVL; PVLPASSHDNTPVLK;
VLPASSHDNTPVLKA; LPASSHDNTPVLKAV; PASSHDNTPVLKAVQ;
ASSHDNTPVLKAVQA; SSHDNTPVLKAVQAK; SHDNTPVLKAVQAKD;
HDNTPVLKAVQAKDG; DNTPVLKAVQAKDGG; NTPVLKAVQAKDGGQ;
TPVLKAVQAKDGGQQ; PVLKAVQAKDGGQQE; VLKAVQAKDGGQQEG;
LKAVQAKDGGQQEGK; KAVQAKDGGQQEGKE; AVQAKDGGQQEGKEE;
VQAKDGGQQEGKEEK; QAKDGGQQEGKEEKE; AKDGGQQEGKEEKEK;
KDGGQQEGKEEKEKE; DGGQQEGKEEKEKEI; GGQQEGKEEKEKEIQ;
GQQEGKEEKEKEIQE; QQEGKEEKEKEIQEL; QEGKEEKEKEIQELK;
EGKEEKEKEIQELKD; GKEEKEKEIQELKDK; KEEKEKEIQELKDKI;
EEKEKEIQELKDKID; EKEKEIQELKDKIDK; KEKEIQELKDKIDKR;
EKEIQELKDKIDKRK; KEIQELKDKIDKRKK; EIQELKDKIDKRKKE;
IQELKDKIDKRKKEL; QELKDKIDKRKKELE; ELKDKIDKRKKELEE;
LKDKIDKRKKELEEA; KDKIDKRKKELEEAR; DKIDKRKKELEEARK;
KIDKRKKELEEARKK; IDKRKKELEEARKKF; DKRKKELEEARKKFQ;
KRKKELEEARKKFQE; RKKELEEARKKFQEF; KKELEEARKKFQEFK;
KELEEARKKFQEFKE; ELEEARKKFQEFKEQ; LEEARKKFQEFKEQV;
EEARKKFQEFKEQVE; EARKKFQEFKEQVES; ARKKFQEFKEQVESA;
RKKFQEFKEQVESAT; KKFQEFKEQVESATG; KFQEFKEQVESATGE;
FQEFKEQVESATGES; QEFKEQVESATGEST; EFKEQVESATGESTE;
FKEQVESATGESTEK; KEQVESATGESTEKV; EQVESATGESTEKVK;

QVESATGESTEKVKK; VESATGESTEKVKKQ; ESATGESTEKVKKQG;
SATGESTEKVKKQGN; ATGESTEKVKKQGNI; TGESTEKVKKQGNIG;
GESTEKVKKQGNIGQ; ESTEKVKKQGNIGQK; STEKVKKQGNIGQKA;
TEKVKKQGNIGQKAL; EKVKKQGNIGQKALK; KVKKQGNIGQKALKY;
VKKQGNIGQKALKYA; KKQGNIGQKALKYAK; KQGNIGQKALKYAKE;
QGNIGQKALKYAKEL; GNIGQKALKYAKELG; NIGQKALKYAKELGV;
IGQKALKYAKELGVN; GQKALKYAKELGVNG; QKALKYAKELGVNGS;
KALKYAKELGVNGSY; ALKYAKELGVNGSYS; LKYAKELGVNGSYSV;
KYAKELGVNGSYSVN; YAKELGVNGSYSVND; AKELGVNGSYSVNDG;
KELGVNGSYSVNDGT; ELGVNGSYSVNDGTN; LGVNGSYSVNDGTNT;
GVNGSYSVNDGTNTN; VNGSYSVNDGTNTND; NGSYSVNDGTNTNDF;
GSYSVNDGTNTNDFV; SYSVNDGTNTNDFVK; YSVNDGTNTNDFVKK;
SVNDGTNTNDFVKKV; VNDGTNTNDFVKKVI; NDGTNTNDFVKKVID;
DGTNTNDFVKKVIDD; GTNTNDFVKKVIDDA; TNTNDFVKKVIDDAL;
NTNDFVKKVIDDALK; TNDFVKKVIDDALKN; NDFVKKVIDDALKNI;
DFVKKVIDDALKNIE; FVKKVIDDALKNIEE; VKKVIDDALKNIEEE;
KKVIDDALKNIEEEL; KVIDDALKNIEEELE; VIDDALKNIEEELEK;
IDDALKNIEEELEKL; DDALKNIEEELEKLA; DALKNIEEELEKLAE;
ALKNIEEELEKLAEP; LKNIEEELEKLAEPQ; KNIEEELEKLAEPQN;
NIEEELEKLAEPQNI; IEEELEKLAEPQNIE; EEELEKLAEPQNIED;
EELEKLAEPQNIEDK; ELEKLAEPQNIEDKK;

16 mers:
MNKKMKNLIICAVFVL; NKKMKNLIICAVFVLI; KKMKNLIICAVFVLII;
KMKNLIICAVFVLIIS; MKNLIICAVFVLIISC; KNLIICAVFVLIISCK;
NLIICAVFVLIISCKI; LIICAVFVLIISCKID; IICAVFVLIISCKIDA;
ICAVFVLIISCKIDAS; CAVFVLIISCKIDASS; AVFVLIISCKIDASSE;
VFVLIISCKIDASSED; FVLIISCKIDASSEDL; VLIISCKIDASSEDLK;
LIISCKIDASSEDLKQ; IISCKIDASSEDLKQN; ISCKIDASSEDLKQNV;
SCKIDASSEDLKQNVK; CKIDASSEDLKQNVKE; KIDASSEDLKQNVKEK;
IDASSEDLKQNVKEKV; DASSEDLKQNVKEKVE; ASSEDLKQNVKEKVEG;
SSEDLKQNVKEKVEGF; SEDLKQNVKEKVEGFL; EDLKQNVKEKVEGFLD;
DLKQNVKEKVEGFLDK; LKQNVKEKVEGFLDKE; KQNVKEKVEGFLDKEL;
QNVKEKVEGFLDKELM; NVKEKVEGFLDKELMQ; VKEKVEGFLDKELMQG;
KEKVEGFLDKELMQGD; EKVEGFLDKELMQGDD; KVEGFLDKELMQGDDP;
VEGFLDKELMQGDDPN; EGFLDKELMQGDDPNN; GFLDKELMQGDDPNNS;
FLDKELMQGDDPNNSL; LDKELMQGDDPNNSLF; DKELMQGDDPNNSLFN;
KELMQGDDPNNSLFNP; ELMQGDDPNNSLFNPP; LMQGDDPNNSLFNPPP;
MQGDDPNNSLFNPPPV; QGDDPNNSLFNPPPVL; GDDPNNSLFNPPPVLP;
DDPNNSLFNPPPVLPA; DPNNSLFNPPPVLPAS; PNNSLFNPPPVLPASS;
NNSLFNPPPVLPASSH; NSLFNPPPVLPASSHD; SLFNPPPVLPASSHDN;
LFNPPPVLPASSHDNT; FNPPPVLPASSHDNTP; NPPPVLPASSHDNTPV;
PPPVLPASSHDNTPVL; PPVLPASSHDNTPVLK; PVLPASSHDNTPVLKA;
VLPASSHDNTPVLKAV; LPASSHDNTPVLKAVQ; PASSHDNTPVLKAVQA;
ASSHDNTPVLKAVQAK; SSHDNTPVLKAVQAKD; SHDNTPVLKAVQAKDG;
HDNTPVLKAVQAKDGG; DNTPVLKAVQAKDGGQ; NTPVLKAVQAKDGGQQ;
TPVLKAVQAKDGGQQE; PVLKAVQAKDGGQQEG; VLKAVQAKDGGQQEGK;
LKAVQAKDGGQQEGKE; KAVQAKDGGQQEGKEE; AVQAKDGGQQEGKEEK;
VQAKDGGQQEGKEEKE; QAKDGGQQEGKEEKEK; AKDGGQQEGKEEKEKE;
KDGGQQEGKEEKEKEI; DGGQQEGKEEKEKEIQ; GGQQEGKEEKEKEIQE;
GQQEGKEEKEKEIQEL; QQEGKEEKEKEIQELK; QEGKEEKEKEIQELKD;
EGKEEKEKEIQELKDK; GKEEKEKEIQELKDKI; KEEKEKEIQELKDKID;
EEKEKEIQELKDKIDK; EKEKEIQELKDKIDKR; KEKEIQELKDKIDKRK;
EKEIQELKDKIDKRKK; KEIQELKDKIDKRKKE; EIQELKDKIDKRKKEL;
IQELKDKIDKRKKELE; QELKDKIDKRKKELEE; ELKDKIDKRKKELEEA;
LKDKIDKRKKELEEAR; KDKIDKRKKELEEARK; DKIDKRKKELEEARKK;
KIDKRKKELEEARKKF; IDKRKKELEEARKKFQ; DKRKKELEEARKKFQE;

	KRKKELEEARKKFQEF; RKKELEEARKKFQEFK; KKELEEARKKFQEFKE; KELEEARKKFQEFKEQ; ELEEARKKFQEFKEQV; LEEARKKFQEFKEQVE; EEARKKFQEFKEQVES; EARKKFQEFKEQVESA; ARKKFQEFKEQVESAT; RKKFQEFKEQVESATG; KKFQEFKEQVESATGE; KFQEFKEQVESATGES; FQEFKEQVESATGEST; QEFKEQVESATGESTE; EFKEQVESATGESTEK; FKEQVESATGESTEKV; KEQVESATGESTEKVK; EQVESATGESTEKVKK; QVESATGESTEKVKKQ; VESATGESTEKVKKQG; ESATGESTEKVKKQGN; SATGESTEKVKKQGNI; ATGESTEKVKKQGNIG; TGESTEKVKKQGNIGQ; GESTEKVKKQGNIGQK; ESTEKVKKQGNIGQKA; STEKVKKQGNIGQKAL; TEKVKKQGNIGQKALK; EKVKKQGNIGQKALKY; KVKKQGNIGQKALKYA; VKKQGNIGQKALKYAK; KKQGNIGQKALKYAKE; KQGNIGQKALKYAKEL; QGNIGQKALKYAKELG; GNIGQKALKYAKELGV; NIGQKALKYAKELGVN; IGQKALKYAKELGVNG; GQKALKYAKELGVNGS; QKALKYAKELGVNGSY; KALKYAKELGVNGSYS; ALKYAKELGVNGSYSV; LKYAKELGVNGSYSVN; KYAKELGVNGSYSVND; YAKELGVNGSYSVNDG; AKELGVNGSYSVNDGT; KELGVNGSYSVNDGTN; ELGVNGSYSVNDGTNT; LGVNGSYSVNDGTNTN; GVNGSYSVNDGTNTND; VNGSYSVNDGTNTNDF; NGSYSVNDGTNTNDFV; GSYSVNDGTNTNDFVK; SYSVNDGTNTNDFVKK; YSVNDGTNTNDFVKKV; SVNDGTNTNDFVKKVI; VNDGTNTNDFVKKVID; NDGTNTNDFVKKVIDD; DGTNTNDFVKKVIDDA; GTNTNDFVKKVIDDAL; TNTNDFVKKVIDDALK; NTNDFVKKVIDDALKN; TNDFVKKVIDDALKNI; NDFVKKVIDDALKNIE; DFVKKVIDDALKNIEE; FVKKVIDDALKNIEEE; VKKVIDDALKNIEEEL; KKVIDDALKNIEEELE; KVIDDALKNIEEELEK; VIDDALKNIEEELEKL; IDDALKNIEEELEKLA; DDALKNIEEELEKLAE; DALKNIEEELEKLAEP; ALKNIEEELEKLAEPQ; LKNIEEELEKLAEPQN; KNIEEELEKLAEPQNI; NIEEELEKLAEPQNIE; IEEELEKLAEPQNIED; EEELEKLAEPQNIEDK; EELEKLAEPQNIEDKK;
AAC44770.1| FlaA protein (Borrelia burgdorferi)	13 mers: MKRKAKSILFFLL; KRKAKSILFFLLS; RKAKSILFFLLST; KAKSILFFLLSTV; AKSILFFLLSTVL; KSILFFLLSTVLF; SILFFLLSTVLFA; ILFFLLSTVLFAQ; LFFLLSTVLFAQE; FFLLSTVLFAQET; FLLSTVLFAQETD; LLSTVLFAQETDG; LSTVLFAQETDGL; STVLFAQETDGLA; TVLFAQETDGLAE; VLFAQETDGLAEG; LFAQETDGLAEGS; FAQETDGLAEGSK; AQETDGLAEGSKR; QETDGLAEGSKRA; ETDGLAEGSKRAE; TDGLAEGSKRAEP; DGLAEGSKRAEPG; GLAEGSKRAEPGE; LAEGSKRAEPGEL; AEGSKRAEPGELV; EGSKRAEPGELVL; GSKRAEPGELVLD; SKRAEPGELVLDF; KRAEPGELVLDFA; RAEPGELVLDFAE; AEPGELVLDFAEL; EPGELVLDFAELA; PGELVLDFAELAR; GELVLDFAELARD; ELVLDFAELARDP; LVLDFAELARDPS; VLDFAELARDPSS; LDFAELARDPSST; DFAELARDPSSTR; FAELARDPSSTRL; AELARDPSSTRLD; ELARDPSSTRLDL; LARDPSSTRLDLT; ARDPSSTRLDLTN; RDPSSTRLDLTNY; DPSSTRLDLTNYV; PSSTRLDLTNYVD; SSTRLDLTNYVDY; STRLDLTNYVDYV; TRLDLTNYVDYVY; RLDLTNYVDYVYS; LDLTNYVDYVYSG; DLTNYVDYVYSGA; LTNYVDYVYSGAS; TNYVDYVYSGASG; NYVDYVYSGASGI; YVDYVYSGASGIV; VDYVYSGASGIVK; DYVYSGASGIVKP; YVYSGASGIVKPE; VYSGASGIVKPED; YSGASGIVKPEDM; SGASGIVKPEDMV; GASGIVKPEDMVV; ASGIVKPEDMVVD; SGIVKPEDMVVDL; GIVKPEDMVVDLG; IVKPEDMVVDLGI; VKPEDMVVDLGIN; KPEDMVVDLGINN; PEDMVVDLGINNW; EDMVVDLGINNWS; DMVVDLGINNWSV; MVVDLGINNWSVL; VVDLGINNWSVLL; VDLGINNWSVLLT; DLGINNWSVLLTP; LGINNWSVLLTPS; GINNWSVLLTPSA; INNWSVLLTPSAR; NNWSVLLTPSARL; NWSVLLTPSARLQ; WSVLLTPSARLQA; SVLLTPSARLQAY; VLLTPSARLQAYV; LLTPSARLQAYVK; LTPSARLQAYVKN; TPSARLQAYVKNS; PSARLQAYVKNSV; SARLQAYVKNSVV; ARLQAYVKNSVVA; RLQAYVKNSVVAP; LQAYVKNSVVAPA; QAYVKNSVVAPAV; AYVKNSVVAPAVV; YVKNSVVAPAVVK; VKNSVVAPAVVKS; KNSVVAPAVVKSE; NSVVAPAVVKSES; SVVAPAVVKSESK; VVAPAVVKSESKR; VAPAVVKSESKRY; APAVVKSESKRYA; PAVVKSESKRYAG; AVVKSESKRYAGD; VVKSESKRYAGDT; VKSESKRYAGDTI;

	KSESKRYAGDTIL; SESKRYAGDTILG; ESKRYAGDTILGV; SKRYAGDTILGVR; KRYAGDTILGVRV; RYAGDTILGVRVL; YAGDTILGVRVLF; AGDTILGVRVLFP; GDTILGVRVLFPS; DTILGVRVLFPSY; TILGVRVLFPSYS; ILGVRVLFPSYSQ; LGVRVLFPSYSQS; GVRVLFPSYSQSS; VRVLFPSYSQSSA; RVLFPSYSQSSAM; VLFPSYSQSSAMI; LFPSYSQSSAMIM; FPSYSQSSAMIMP; PSYSQSSAMIMPP; SYSQSSAMIMPPF; YSQSSAMIMPPFK; SQSSAMIMPPFKI; QSSAMIMPPFKIP; SSAMIMPPFKIPF; SAMIMPPFKIPFY; AMIMPPFKIPFYS; MIMPPFKIPFYSG; IMPPFKIPFYSGE; MPPFKIPFYSGES; PPFKIPFYSGESG; PFKIPFYSGESGN; FKIPFYSGESGNQ; KIPFYSGESGNQF; IPFYSGESGNQFL; PFYSGESGNQFLG; FYSGESGNQFLGK; YSGESGNQFLGKG; SGESGNQFLGKGL; GESGNQFLGKGLI; ESGNQFLGKGLID; SGNQFLGKGLIDN; GNQFLGKGLIDNI; NQFLGKGLIDNIK; QFLGKGLIDNIKT; FLGKGLIDNIKTM; LGKGLIDNIKTMK; GKGLIDNIKTMKE; KGLIDNIKTMKEI; GLIDNIKTMKEIK; LIDNIKTMKEIKV; IDNIKTMKEIKVS; DNIKTMKEIKVSV; NIKTMKEIKVSVY; IKTMKEIKVSVYS; KTMKEIKVSVYSL; TMKEIKVSVYSLG; MKEIKVSVYSLGY; KEIKVSVYSLGYE; EIKVSVYSLGYEI; IKVSVYSLGYEID; KVSVYSLGYEIDL; VSVYSLGYEIDLE; SVYSLGYEIDLEV; VYSLGYEIDLEVL; YSLGYEIDLEVLF; SLGYEIDLEVLFE; LGYEIDLEVLFED; GYEIDLEVLFEDM; YEIDLEVLFEDMN; EIDLEVLFEDMNG; IDLEVLFEDMNGM; DLEVLFEDMNGME; LEVLFEDMNGMEY; EVLFEDMNGMEYA; VLFEDMNGMEYAY; LFEDMNGMEYAYS; FEDMNGMEYAYSM; EDMNGMEYAYSMG; DMNGMEYAYSMGT; MNGMEYAYSMGTL; NGMEYAYSMGTLK; GMEYAYSMGTLKF; MEYAYSMGTLKFK; EYAYSMGTLKFKG; YAYSMGTLKFKGW; AYSMGTLKFKGWA; YSMGTLKFKGWAD; SMGTLKFKGWADL; MGTLKFKGWADLI; GTLKFKGWADLIW; TLKFKGWADLIWS; LKFKGWADLIWSN; KFKGWADLIWSNP; FKGWADLIWSNPN; KGWADLIWSNPNY; GWADLIWSNPNYI; WADLIWSNPNYIP; ADLIWSNPNYIPN; DLIWSNPNYIPNI; LIWSNPNYIPNIS; IWSNPNYIPNISS; WSNPNYIPNISSR; SNPNYIPNISSRI; NPNYIPNISSRII; PNYIPNISSRIIK; NYIPNISSRIIKD; YIPNISSRIIKDD; IPNISSRIIKDDV; PNISSRIIKDDVP; NISSRIIKDDVPN; ISSRIIKDDVPNY; SSRIIKDDVPNYP; SRIIKDDVPNYPL; RIIKDDVPNYPLA; IIKDDVPNYPLAS; IKDDVPNYPLASS; KDDVPNYPLASSK; DDVPNYPLASSKM; DVPNYPLASSKMR; VPNYPLASSKMRF; PNYPLASSKMRFK; NYPLASSKMRFKA; YPLASSKMRFKAF; PLASSKMRFKAFR; LASSKMRFKAFRV; ASSKMRFKAFRVS; SSKMRFKAFRVSK; SKMRFKAFRVSKS; KMRFKAFRVSKSH; MRFKAFRVSKSHS; RFKAFRVSKSHSS; FKAFRVSKSHSSK; KAFRVSKSHSSKV; AFRVSKSHSSKVK; FRVSKSHSSKVKN; RVSKSHSSKVKNF; VSKSHSSKVKNFI; SKSHSSKVKNFIF; KSHSSKVKNFIFY; SHSSKVKNFIFYV; HSSKVKNFIFYVK; SSKVKNFIFYVKD; SKVKNFIFYVKDL; KVKNFIFYVKDLR; VKNFIFYVKDLRV; KNFIFYVKDLRVL; NFIFYVKDLRVLY; FIFYVKDLRVLYD; IFYVKDLRVLYDK; FYVKDLRVLYDKL; YVKDLRVLYDKLS; VKDLRVLYDKLSV; KDLRVLYDKLSVS; DLRVLYDKLSVSI; LRVLYDKLSVSID; RVLYDKLSVSIDS; VLYDKLSVSIDSD; LYDKLSVSIDSDI; YDKLSVSIDSDID; DKLSVSIDSDIDS; KLSVSIDSDIDSE; LSVSIDSDIDSES; SVSIDSDIDSESV; VSIDSDIDSESVF; SIDSDIDSESVFK; IDSDIDSESVFKV; DSDIDSESVFKVY; SDIDSESVFKVYE; DIDSESVFKVYET; IDSESVFKVYETS; DSESVFKVYETSG; SESVFKVYETSGT; ESVFKVYETSGTE; SVFKVYETSGTES; VFKVYETSGTESL; FKVYETSGTESLR; KVYETSGTESLRK; VYETSGTESLRKL; YETSGTESLRKLK; ETSGTESLRKLKA; TSGTESLRKLKAH; SGTESLRKLKAHE; GTESLRKLKAHET; TESLRKLKAHETF; ESLRKLKAHETFK; SLRKLKAHETFKR; LRKLKAHETFKRV; RKLKAHETFKRVL; KLKAHETFKRVLK; LKAHETFKRVLKL; KAHETFKRVLKLR; AHETFKRVLKLRE; HETFKRVLKLREK; ETFKRVLKLREKI; TFKRVLKLREKIS; FKRVLKLREKISI; KRVLKLREKISIA; RVLKLREKISIAE; VLKLREKISIAEG; LKLREKISIAEGS; KLREKISIAEGSF; LREKISIAEGSFQ; REKISIAEGSFQN; EKISIAEGSFQNF; KISIAEGSFQNFV; ISIAEGSFQNFVE; SIAEGSFQNFVEK; IAEGSFQNFVEKI; AEGSFQNFVEKIE; EGSFQNFVEKIES; GSFQNFVEKIESE; SFQNFVEKIESEK; FQNFVEKIESEKP; QNFVEKIESEKPE; NFVEKIESEKPEE; FVEKIESEKPEES; VEKIESEKPEESS; EKIESEKPEESSP; KIESEKPEESSPK; IESEKPEESSPKN;

14 mers:
MKRKAKSILFFLLS; KRKAKSILFFLLST; RKAKSILFFLLSTV;
KAKSILFFLLSTVL; AKSILFFLLSTVLF; KSILFFLLSTVLFA;
SILFFLLSTVLFAQ; ILFFLLSTVLFAQE; LFFLLSTVLFAQET;
FFLLSTVLFAQETD; FLLSTVLFAQETDG; LLSTVLFAQETDGL;
LSTVLFAQETDGLA; STVLFAQETDGLAE; TVLFAQETDGLAEG;
VLFAQETDGLAEGS; LFAQETDGLAEGSK; FAQETDGLAEGSKR;
AQETDGLAEGSKRA; QETDGLAEGSKRAE; ETDGLAEGSKRAEP;
TDGLAEGSKRAEPG; DGLAEGSKRAEPGE; GLAEGSKRAEPGEL;
LAEGSKRAEPGELV; AEGSKRAEPGELVL; EGSKRAEPGELVLD;
GSKRAEPGELVLDF; SKRAEPGELVLDFA; KRAEPGELVLDFAE;
RAEPGELVLDFAEL; AEPGELVLDFAELA; EPGELVLDFAELAR;
PGELVLDFAELARD; GELVLDFAELARDP; ELVLDFAELARDPS;
LVLDFAELARDPSS; VLDFAELARDPSST; LDFAELARDPSSTR;
DFAELARDPSSTRL; FAELARDPSSTRLD; AELARDPSSTRLDL;
ELARDPSSTRLDLT; LARDPSSTRLDLTN; ARDPSSTRLDLTNY;
RDPSSTRLDLTNYV; DPSSTRLDLTNYVD; PSSTRLDLTNYVDY;
SSTRLDLTNYVDYV; STRLDLTNYVDYVY; TRLDLTNYVDYVYS;
RLDLTNYVDYVYSG; LDLTNYVDYVYSGA; DLTNYVDYVYSGAS;
LTNYVDYVYSGASG; TNYVDYVYSGASGI; NYVDYVYSGASGIV;
YVDYVYSGASGIVK; VDYVYSGASGIVKP; DYVYSGASGIVKPE;
YVYSGASGIVKPED; VYSGASGIVKPEDM; YSGASGIVKPEDMV;
SGASGIVKPEDMVV; GASGIVKPEDMVVD; ASGIVKPEDMVVDL;
SGIVKPEDMVVDLG; GIVKPEDMVVDLGI; IVKPEDMVVDLGIN;
VKPEDMVVDLGINN; KPEDMVVDLGINNW; PEDMVVDLGINNWS;
EDMVVDLGINNWSV; DMVVDLGINNWSVL; MVVDLGINNWSVLL;
VVDLGINNWSVLLT; VDLGINNWSVLLTP; DLGINNWSVLLTPS;
LGINNWSVLLTPSA; GINNWSVLLTPSAR; INNWSVLLTPSARL;
NNWSVLLTPSARLQ; NWSVLLTPSARLQA; WSVLLTPSARLQAY;
SVLLTPSARLQAYV; VLLTPSARLQAYVK; LLTPSARLQAYVKN;
LTPSARLQAYVKNS; TPSARLQAYVKNSV; PSARLQAYVKNSVV;
SARLQAYVKNSVVA; ARLQAYVKNSVVAP; RLQAYVKNSVVAPA;
LQAYVKNSVVAPAV; QAYVKNSVVAPAVV; AYVKNSVVAPAVVK;
YVKNSVVAPAVVKS; VKNSVVAPAVVKSE; KNSVVAPAVVKSES;
NSVVAPAVVKSESK; SVVAPAVVKSESKR; VVAPAVVKSESKRY;
VAPAVVKSESKRYA; APAVVKSESKRYAG; PAVVKSESKRYAGD;
AVVKSESKRYAGDT; VVKSESKRYAGDTI; VKSESKRYAGDTIL;
KSESKRYAGDTILG; SESKRYAGDTILGV; ESKRYAGDTILGVR;
SKRYAGDTILGVRV; KRYAGDTILGVRVL; RYAGDTILGVRVLF;
YAGDTILGVRVLFP; AGDTILGVRVLFPS; GDTILGVRVLFPSY;
DTILGVRVLFPSYS; TILGVRVLFPSYSQ; ILGVRVLFPSYSQS;
LGVRVLFPSYSQSS; GVRVLFPSYSQSSA; VRVLFPSYSQSSAM;
RVLFPSYSQSSAMI; VLFPSYSQSSAMIM; LFPSYSQSSAMIMP;
FPSYSQSSAMIMPP; PSYSQSSAMIMPPF; SYSQSSAMIMPPFK;
YSQSSAMIMPPFKI; SQSSAMIMPPFKIP; QSSAMIMPPFKIPF;
SSAMIMPPFKIPFY; SAMIMPPFKIPFYS; AMIMPPFKIPFYSG;
MIMPPFKIPFYSGE; IMPPFKIPFYSGES; MPPFKIPFYSGESG;
PPFKIPFYSGESGN; PFKIPFYSGESGNQ; FKIPFYSGESGNQF;
KIPFYSGESGNQFL; IPFYSGESGNQFLG; PFYSGESGNQFLGK;
FYSGESGNQFLGKG; YSGESGNQFLGKGL; SGESGNQFLGKGLI;
GESGNQFLGKGLID; ESGNQFLGKGLIDN; SGNQFLGKGLIDNI;
GNQFLGKGLIDNIK; NQFLGKGLIDNIKT; QFLGKGLIDNIKTM;
FLGKGLIDNIKTMK; LGKGLIDNIKTMKE; GKGLIDNIKTMKEI;
KGLIDNIKTMKEIK; GLIDNIKTMKEIKV; LIDNIKTMKEIKVS;
IDNIKTMKEIKVSV; DNIKTMKEIKVSVY; NIKTMKEIKVSVYS;
IKTMKEIKVSVYSL; KTMKEIKVSVYSLG; TMKEIKVSVYSLGY;
MKEIKVSVYSLGYE; KEIKVSVYSLGYEI; EIKVSVYSLGYEID;

IKVSVYSLGYEIDL; KVSVYSLGYEIDLE; VSVYSLGYEIDLEV;
SVYSLGYEIDLEVL; VYSLGYEIDLEVLF; YSLGYEIDLEVLFE;
SLGYEIDLEVLFED; LGYEIDLEVLFEDM; GYEIDLEVLFEDMN;
YEIDLEVLFEDMNG; EIDLEVLFEDMNGM; IDLEVLFEDMNGME;
DLEVLFEDMNGMEY; LEVLFEDMNGMEYA; EVLFEDMNGMEYAY;
VLFEDMNGMEYAYS; LFEDMNGMEYAYSM; FEDMNGMEYAYSMG;
EDMNGMEYAYSMGT; DMNGMEYAYSMGTL; MNGMEYAYSMGTLK;
NGMEYAYSMGTLKF; GMEYAYSMGTLKFK; MEYAYSMGTLKFKG;
EYAYSMGTLKFKGW; YAYSMGTLKFKGWA; AYSMGTLKFKGWAD;
YSMGTLKFKGWADL; SMGTLKFKGWADLI; MGTLKFKGWADLIW;
GTLKFKGWADLIWS; TLKFKGWADLIWSN; LKFKGWADLIWSNP;
KFKGWADLIWSNPN; FKGWADLIWSNPNY; KGWADLIWSNPNYI;
GWADLIWSNPNYIP; WADLIWSNPNYIPN; ADLIWSNPNYIPNI;
DLIWSNPNYIPNIS; LIWSNPNYIPNISS; IWSNPNYIPNISSR;
WSNPNYIPNISSRI; SNPNYIPNISSRII; NPNYIPNISSRIIK;
PNYIPNISSRIIKD; NYIPNISSRIIKDD; YIPNISSRIIKDDV;
IPNISSRIIKDDVP; PNISSRIIKDDVPN; NISSRIIKDDVPNY;
ISSRIIKDDVPNYP; SSRIIKDDVPNYPL; SRIIKDDVPNYPLA;
RIIKDDVPNYPLAS; IIKDDVPNYPLASS; IKDDVPNYPLASSK;
KDDVPNYPLASSKM; DDVPNYPLASSKMR; DVPNYPLASSKMRF;
VPNYPLASSKMRFK; PNYPLASSKMRFKA; NYPLASSKMRFKAF;
YPLASSKMRFKAFR; PLASSKMRFKAFRV; LASSKMRFKAFRVS;
ASSKMRFKAFRVSK; SSKMRFKAFRVSKS; SKMRFKAFRVSKSH;
KMRFKAFRVSKSHS; MRFKAFRVSKSHSS; RFKAFRVSKSHSSK;
FKAFRVSKSHSSKV; KAFRVSKSHSSKVK; AFRVSKSHSSKVKN;
FRVSKSHSSKVKNF; RVSKSHSSKVKNFI; VSKSHSSKVKNFIF;
SKSHSSKVKNFIFY; KSHSSKVKNFIFYV; SHSSKVKNFIFYVK;
HSSKVKNFIFYVKD; SSKVKNFIFYVKDL; SKVKNFIFYVKDLR;
KVKNFIFYVKDLRV; VKNFIFYVKDLRVL; KNFIFYVKDLRVLY;
NFIFYVKDLRVLYD; FIFYVKDLRVLYDK; IFYVKDLRVLYDKL;
FYVKDLRVLYDKLS; YVKDLRVLYDKLSV; VKDLRVLYDKLSVS;
KDLRVLYDKLSVSI; DLRVLYDKLSVSID; LRVLYDKLSVSIDS;
RVLYDKLSVSIDSD; VLYDKLSVSIDSDI; LYDKLSVSIDSDID;
YDKLSVSIDSDIDS; DKLSVSIDSDIDSE; KLSVSIDSDIDSES;
LSVSIDSDIDSESV; SVSIDSDIDSESVF; VSIDSDIDSESVFK;
SIDSDIDSESVFKV; IDSDIDSESVFKVY; DSDIDSESVFKVYE;
SDIDSESVFKVYET; DIDSESVFKVYETS; IDSESVFKVYETSG;
DSESVFKVYETSGT; SESVFKVYETSGTE; ESVFKVYETSGTES;
SVFKVYETSGTESL; VFKVYETSGTESLR; FKVYETSGTESLRK;
KVYETSGTESLRKL; VYETSGTESLRKLK; YETSGTESLRKLKA;
ETSGTESLRKLKAH; TSGTESLRKLKAHE; SGTESLRKLKAHET;
GTESLRKLKAHETF; TESLRKLKAHETFK; ESLRKLKAHETFKR;
SLRKLKAHETFKRV; LRKLKAHETFKRVL; RKLKAHETFKRVLK;
KLKAHETFKRVLKL; LKAHETFKRVLKLR; KAHETFKRVLKLRE;
AHETFKRVLKLREK; HETFKRVLKLREKI; ETFKRVLKLREKIS;
TFKRVLKLREKISI; FKRVLKLREKISIA; KRVLKLREKISIAE;
RVLKLREKISIAEG; VLKLREKISIAEGS; LKLREKISIAEGSF;
KLREKISIAEGSFQ; LREKISIAEGSFQN; REKISIAEGSFQNF;
EKISIAEGSFQNFV; KISIAEGSFQNFVE; ISIAEGSFQNFVEK;
SIAEGSFQNFVEKI; IAEGSFQNFVEKIE; AEGSFQNFVEKIES;
EGSFQNFVEKIESE; GSFQNFVEKIESEK; SFQNFVEKIESEKP;
FQNFVEKIESEKPE; QNFVEKIESEKPEE; NFVEKIESEKPEES;
FVEKIESEKPEESS; VEKIESEKPEESSP; EKIESEKPEESSPK;
KIESEKPEESSPKN;

15 mers:
MKRKAKSILFFLLST; KRKAKSILFFLLSTV; RKAKSILFFLLSTVL;

	KAKSILFFLLSTVLF; AKSILFFLLSTVLFA; KSILFFLLSTVLFAQ; SILFFLLSTVLFAQE; ILFFLLSTVLFAQET; LFFLLSTVLFAQETD; FFLLSTVLFAQETDG; FLLSTVLFAQETDGL; LLSTVLFAQETDGLA; LSTVLFAQETDGLAE; STVLFAQETDGLAEG; TVLFAQETDGLAEGS; VLFAQETDGLAEGSK; LFAQETDGLAEGSKR; FAQETDGLAEGSKRA; AQETDGLAEGSKRAE; QETDGLAEGSKRAEP; ETDGLAEGSKRAEPG; TDGLAEGSKRAEPGE; DGLAEGSKRAEPGEL; GLAEGSKRAEPGELV; LAEGSKRAEPGELVL; AEGSKRAEPGELVLD; EGSKRAEPGELVLDF; GSKRAEPGELVLDFA; SKRAEPGELVLDFAE; KRAEPGELVLDFAEL; RAEPGELVLDFAELA; AEPGELVLDFAELAR; EPGELVLDFAELARD; PGELVLDFAELARDP; GELVLDFAELARDPS; ELVLDFAELARDPSS; LVLDFAELARDPSST; VLDFAELARDPSSTR; LDFAELARDPSSTRL; DFAELARDPSSTRLD; FAELARDPSSTRLDL; AELARDPSSTRLDLT; ELARDPSSTRLDLTN; LARDPSSTRLDLTNY; ARDPSSTRLDLTNYV; RDPSSTRLDLTNYVD; DPSSTRLDLTNYVDY; PSSTRLDLTNYVDYV; SSTRLDLTNYVDYVY; STRLDLTNYVDYVYS; TRLDLTNYVDYVYSG; RLDLTNYVDYVYSGA; LDLTNYVDYVYSGAS; DLTNYVDYVYSGASG; LTNYVDYVYSGASGI; TNYVDYVYSGASGIV; NYVDYVYSGASGIVK; YVDYVYSGASGIVKP; VDYVYSGASGIVKPE; DYVYSGASGIVKPED; YVYSGASGIVKPEDM; VYSGASGIVKPEDMV; YSGASGIVKPEDMVV; SGASGIVKPEDMVVD; GASGIVKPEDMVVDL; ASGIVKPEDMVVDLG; SGIVKPEDMVVDLGI; GIVKPEDMVVDLGIN; IVKPEDMVVDLGINN; VKPEDMVVDLGINNW; KPEDMVVDLGINNWS; PEDMVVDLGINNWSV; EDMVVDLGINNWSVL; DMVVDLGINNWSVLL; MVVDLGINNWSVLLT; VVDLGINNWSVLLTP; VDLGINNWSVLLTPS; DLGINNWSVLLTPSA; LGINNWSVLLTPSAR; GINNWSVLLTPSARL; INNWSVLLTPSARLQ; NNWSVLLTPSARLQA; NWSVLLTPSARLQAY; WSVLLTPSARLQAYV; SVLLTPSARLQAYVK; VLLTPSARLQAYVKN; LLTPSARLQAYVKNS; LTPSARLQAYVKNSV; TPSARLQAYVKNSVV; PSARLQAYVKNSVVA; SARLQAYVKNSVVAP; ARLQAYVKNSVVAPA; RLQAYVKNSVVAPAV; LQAYVKNSVVAPAVV; QAYVKNSVVAPAVVK; AYVKNSVVAPAVVKS; YVKNSVVAPAVVKSE; VKNSVVAPAVVKSES; KNSVVAPAVVKSESK; NSVVAPAVVKSESKR; SVVAPAVVKSESKRY; VVAPAVVKSESKRYA; VAPAVVKSESKRYAG; APAVVKSESKRYAGD; PAVVKSESKRYAGDT; AVVKSESKRYAGDTI; VVKSESKRYAGDTIL; VKSESKRYAGDTILG; KSESKRYAGDTILGV; SESKRYAGDTILGVR; ESKRYAGDTILGVRV; SKRYAGDTILGVRVL; KRYAGDTILGVRVLF; RYAGDTILGVRVLFP; YAGDTILGVRVLFPS; AGDTILGVRVLFPSY; GDTILGVRVLFPSYS; DTILGVRVLFPSYSQ; TILGVRVLFPSYSQS; ILGVRVLFPSYSQSS; LGVRVLFPSYSQSSA; GVRVLFPSYSQSSAM; VRVLFPSYSQSSAMI; RVLFPSYSQSSAMIM; VLFPSYSQSSAMIMP; LFPSYSQSSAMIMPP; FPSYSQSSAMIMPPF; PSYSQSSAMIMPPFK; SYSQSSAMIMPPFKI; YSQSSAMIMPPFKIP; SQSSAMIMPPFKIPF; QSSAMIMPPFKIPFY; SSAMIMPPFKIPFYS; SAMIMPPFKIPFYSG; AMIMPPFKIPFYSGE; MIMPPFKIPFYSGES; IMPPFKIPFYSGESG; MPPFKIPFYSGESGN; PPFKIPFYSGESGNQ; PFKIPFYSGESGNQF; FKIPFYSGESGNQFL; KIPFYSGESGNQFLG; IPFYSGESGNQFLGK; PFYSGESGNQFLGKG; FYSGESGNQFLGKGL; YSGESGNQFLGKGLI; SGESGNQFLGKGLID; GESGNQFLGKGLIDN; ESGNQFLGKGLIDNI; SGNQFLGKGLIDNIK; GNQFLGKGLIDNIKT; NQFLGKGLIDNIKTM; QFLGKGLIDNIKTMK; FLGKGLIDNIKTMKE; LGKGLIDNIKTMKEI; GKGLIDNIKTMKEIK; KGLIDNIKTMKEIKV; GLIDNIKTMKEIKVS; LIDNIKTMKEIKVSV; IDNIKTMKEIKVSVY; DNIKTMKEIKVSVYS; NIKTMKEIKVSVYSL; IKTMKEIKVSVYSLG; KTMKEIKVSVYSLGY; TMKEIKVSVYSLGYE; MKEIKVSVYSLGYEI; KEIKVSVYSLGYEID; EIKVSVYSLGYEIDL; IKVSVYSLGYEIDLE; KVSVYSLGYEIDLEV; VSVYSLGYEIDLEVL; SVYSLGYEIDLEVLF; VYSLGYEIDLEVLFE; YSLGYEIDLEVLFED;

SLGYEIDLEVLFEDM; LGYEIDLEVLFEDMN; GYEIDLEVLFEDMNG;
YEIDLEVLFEDMNGM; EIDLEVLFEDMNGME; IDLEVLFEDMNGMEY;
DLEVLFEDMNGMEYA; LEVLFEDMNGMEYAY; EVLFEDMNGMEYAYS;
VLFEDMNGMEYAYSM; LFEDMNGMEYAYSMG; FEDMNGMEYAYSMGT;
EDMNGMEYAYSMGTL; DMNGMEYAYSMGTLK; MNGMEYAYSMGTLKF;
NGMEYAYSMGTLKFK; GMEYAYSMGTLKFKG; MEYAYSMGTLKFKGW;
EYAYSMGTLKFKGWA; YAYSMGTLKFKGWAD; AYSMGTLKFKGWADL;
YSMGTLKFKGWADLI; SMGTLKFKGWADLIW; MGTLKFKGWADLIWS;
GTLKFKGWADLIWSN; TLKFKGWADLIWSNP; LKFKGWADLIWSNPN;
KFKGWADLIWSNPNY; FKGWADLIWSNPNYI; KGWADLIWSNPNYIP;
GWADLIWSNPNYIPN; WADLIWSNPNYIPNI; ADLIWSNPNYIPNIS;
DLIWSNPNYIPNISS; LIWSNPNYIPNISSR; IWSNPNYIPNISSRI;
WSNPNYIPNISSRII; SNPNYIPNISSRIIK; NPNYIPNISSRIIKD;
PNYIPNISSRIIKDD; NYIPNISSRIIKDDV; YIPNISSRIIKDDVP;
IPNISSRIIKDDVPN; PNISSRIIKDDVPNY; NISSRIIKDDVPNYP;
ISSRIIKDDVPNYPL; SSRIIKDDVPNYPLA; SRIIKDDVPNYPLAS;
RIIKDDVPNYPLASS; IIKDDVPNYPLASSK; IKDDVPNYPLASSKM;
KDDVPNYPLASSKMR; DDVPNYPLASSKMRF; DVPNYPLASSKMRFK;
VPNYPLASSKMRFKA; PNYPLASSKMRFKAF; NYPLASSKMRFKAFR;
YPLASSKMRFKAFRV; PLASSKMRFKAFRVS; LASSKMRFKAFRVSK;
ASSKMRFKAFRVSKS; SSKMRFKAFRVSKSH; SKMRFKAFRVSKSHS;
KMRFKAFRVSKSHSS; MRFKAFRVSKSHSSK; RFKAFRVSKSHSSKV;
FKAFRVSKSHSSKVK; KAFRVSKSHSSKVKN; AFRVSKSHSSKVKNF;
FRVSKSHSSKVKNFI; RVSKSHSSKVKNFIF; VSKSHSSKVKNFIFY;
SKSHSSKVKNFIFYV; KSHSSKVKNFIFYVK; SHSSKVKNFIFYVKD;
HSSKVKNFIFYVKDL; SSKVKNFIFYVKDLR; SKVKNFIFYVKDLRV;
KVKNFIFYVKDLRVL; VKNFIFYVKDLRVLY; KNFIFYVKDLRVLYD;
NFIFYVKDLRVLYDK; FIFYVKDLRVLYDKL; IFYVKDLRVLYDKLS;
FYVKDLRVLYDKLSV; YVKDLRVLYDKLSVS; VKDLRVLYDKLSVSI;
KDLRVLYDKLSVSID; DLRVLYDKLSVSIDS; LRVLYDKLSVSIDSD;
RVLYDKLSVSIDSDI; VLYDKLSVSIDSDID; LYDKLSVSIDSDIDS;
YDKLSVSIDSDIDSE; DKLSVSIDSDIDSES; KLSVSIDSDIDSESV;
LSVSIDSDIDSESVF; SVSIDSDIDSESVFK; VSIDSDIDSESVFKV;
SIDSDIDSESVFKVY; IDSDIDSESVFKVYE; DSDIDSESVFKVYET;
SDIDSESVFKVYETS; DIDSESVFKVYETSG; IDSESVFKVYETSGT;
DSESVFKVYETSGTE; SESVFKVYETSGTES; ESVFKVYETSGTESL;
SVFKVYETSGTESLR; VFKVYETSGTESLRK; FKVYETSGTESLRKL;
KVYETSGTESLRKLK; VYETSGTESLRKLKA; YETSGTESLRKLKAH;
ETSGTESLRKLKAHE; TSGTESLRKLKAHET; SGTESLRKLKAHETF;
GTESLRKLKAHETFK; TESLRKLKAHETFKR; ESLRKLKAHETFKRV;
SLRKLKAHETFKRVL; LRKLKAHETFKRVLK; RKLKAHETFKRVLKL;
KLKAHETFKRVLKLR; LKAHETFKRVLKLRE; KAHETFKRVLKLREK;
AHETFKRVLKLREKI; HETFKRVLKLREKIS; ETFKRVLKLREKISI;
TFKRVLKLREKISIA; FKRVLKLREKISIAE; KRVLKLREKISIAEG;
RVLKLREKISIAEGS; VLKLREKISIAEGSF; LKLREKISIAEGSFQ;
KLREKISIAEGSFQN; LREKISIAEGSFQNF; REKISIAEGSFQNFV;
EKISIAEGSFQNFVE; KISIAEGSFQNFVEK; ISIAEGSFQNFVEKI;
SIAEGSFQNFVEKIE; IAEGSFQNFVEKIES; AEGSFQNFVEKIESE;
EGSFQNFVEKIESEK; GSFQNFVEKIESEKP; SFQNFVEKIESEKPE;
FQNFVEKIESEKPEE; QNFVEKIESEKPEES; NFVEKIESEKPEESS;
FVEKIESEKPEESSP; VEKIESEKPEESSPK; EKIESEKPEESSPKN;

16 mers:
MKRKAKSILFFLLSTV; KRKAKSILFFLLSTVL; RKAKSILFFLLSTVLF;
KAKSILFFLLSTVLFA; AKSILFFLLSTVLFAQ; KSILFFLLSTVLFAQE;
SILFFLLSTVLFAQET; ILFFLLSTVLFAQETD; LFFLLSTVLFAQETDG;
FFLLSTVLFAQETDGL; FLLSTVLFAQETDGLA; LLSTVLFAQETDGLAE;

	LSTVLFAQETDGLAEG; STVLFAQETDGLAEGS; TVLFAQETDGLAEGSK; VLFAQETDGLAEGSKR; LFAQETDGLAEGSKRA; FAQETDGLAEGSKRAE; AQETDGLAEGSKRAEP; QETDGLAEGSKRAEPG; ETDGLAEGSKRAEPGE; TDGLAEGSKRAEPGEL; DGLAEGSKRAEPGELV; GLAEGSKRAEPGELVL; LAEGSKRAEPGELVLD; AEGSKRAEPGELVLDF; EGSKRAEPGELVLDFA; GSKRAEPGELVLDFAE; SKRAEPGELVLDFAEL; KRAEPGELVLDFAELA; RAEPGELVLDFAELAR; AEPGELVLDFAELARD; EPGELVLDFAELARDP; PGELVLDFAELARDPS; GELVLDFAELARDPSS; ELVLDFAELARDPSST; LVLDFAELARDPSSTR; VLDFAELARDPSSTRL; LDFAELARDPSSTRLD; DFAELARDPSSTRLDL; FAELARDPSSTRLDLT; AELARDPSSTRLDLTN; ELARDPSSTRLDLTNY; LARDPSSTRLDLTNYV; ARDPSSTRLDLTNYVD; RDPSSTRLDLTNYVDY; DPSSTRLDLTNYVDYV; PSSTRLDLTNYVDYVY; SSTRLDLTNYVDYVYS; STRLDLTNYVDYVYSG; TRLDLTNYVDYVYSGA; RLDLTNYVDYVYSGAS; LDLTNYVDYVYSGASG; DLTNYVDYVYSGASGI; LTNYVDYVYSGASGIV; TNYVDYVYSGASGIVK; NYVDYVYSGASGIVKP; YVDYVYSGASGIVKPE; VDYVYSGASGIVKPED; DYVYSGASGIVKPEDM; YVYSGASGIVKPEDMV; VYSGASGIVKPEDMVV; YSGASGIVKPEDMVVD; SGASGIVKPEDMVVDL; GASGIVKPEDMVVDLG; ASGIVKPEDMVVDLGI; SGIVKPEDMVVDLGIN; GIVKPEDMVVDLGINN; IVKPEDMVVDLGINNW; VKPEDMVVDLGINNWS; KPEDMVVDLGINNWSV; PEDMVVDLGINNWSVL; EDMVVDLGINNWSVLL; DMVVDLGINNWSVLLT; MVVDLGINNWSVLLTP; VVDLGINNWSVLLTPS; VDLGINNWSVLLTPSA; DLGINNWSVLLTPSAR; LGINNWSVLLTPSARL; GINNWSVLLTPSARLQ; INNWSVLLTPSARLQA; NNWSVLLTPSARLQAY; NWSVLLTPSARLQAYV; WSVLLTPSARLQAYVK; SVLLTPSARLQAYVKN; VLLTPSARLQAYVKNS; LLTPSARLQAYVKNSV; LTPSARLQAYVKNSVV; TPSARLQAYVKNSVVA; PSARLQAYVKNSVVAP; SARLQAYVKNSVVAPA; ARLQAYVKNSVVAPAV; RLQAYVKNSVVAPAVV; LQAYVKNSVVAPAVVK; QAYVKNSVVAPAVVKS; AYVKNSVVAPAVVKSE; YVKNSVVAPAVVKSES; VKNSVVAPAVVKSESK; KNSVVAPAVVKSESKR; NSVVAPAVVKSESKRY; SVVAPAVVKSESKRYA; VVAPAVVKSESKRYAG; VAPAVVKSESKRYAGD; APAVVKSESKRYAGDT; PAVVKSESKRYAGDTI; AVVKSESKRYAGDTIL; VVKSESKRYAGDTILG; VKSESKRYAGDTILGV; KSESKRYAGDTILGVR; SESKRYAGDTILGVRV; ESKRYAGDTILGVRVL; SKRYAGDTILGVRVLF; KRYAGDTILGVRVLFP; RYAGDTILGVRVLFPS; YAGDTILGVRVLFPSY; AGDTILGVRVLFPSYS; GDTILGVRVLFPSYSQ; DTILGVRVLFPSYSQS; TILGVRVLFPSYSQSS; ILGVRVLFPSYSQSSA; LGVRVLFPSYSQSSAM; GVRVLFPSYSQSSAMI; VRVLFPSYSQSSAMIM; RVLFPSYSQSSAMIMP; VLFPSYSQSSAMIMPP; LFPSYSQSSAMIMPPF; FPSYSQSSAMIMPPFK; PSYSQSSAMIMPPFKI; SYSQSSAMIMPPFKIP; YSQSSAMIMPPFKIPF; SQSSAMIMPPFKIPFY; QSSAMIMPPFKIPFYS; SSAMIMPPFKIPFYSG; SAMIMPPFKIPFYSGE; AMIMPPFKIPFYSGES; MIMPPFKIPFYSGESG; IMPPFKIPFYSGESGN; MPPFKIPFYSGESGNQ; PPFKIPFYSGESGNQF; PFKIPFYSGESGNQFL; FKIPFYSGESGNQFLG; KIPFYSGESGNQFLGK; IPFYSGESGNQFLGKG; PFYSGESGNQFLGKGL; FYSGESGNQFLGKGLI; YSGESGNQFLGKGLID; SGESGNQFLGKGLIDN; GESGNQFLGKGLIDNI; ESGNQFLGKGLIDNIK; SGNQFLGKGLIDNIKT; GNQFLGKGLIDNIKTM; NQFLGKGLIDNIKTMK; QFLGKGLIDNIKTMKE; FLGKGLIDNIKTMKEI; LGKGLIDNIKTMKEIK; GKGLIDNIKTMKEIKV; KGLIDNIKTMKEIKVS; GLIDNIKTMKEIKVSV; LIDNIKTMKEIKVSVY; IDNIKTMKEIKVSVYS; DNIKTMKEIKVSVYSL; NIKTMKEIKVSVYSLG; IKTMKEIKVSVYSLGY; KTMKEIKVSVYSLGYE; TMKEIKVSVYSLGYEI; MKEIKVSVYSLGYEID; KEIKVSVYSLGYEIDL; EIKVSVYSLGYEIDLE; IKVSVYSLGYEIDLEV; KVSVYSLGYEIDLEVL; VSVYSLGYEIDLEVLF; SVYSLGYEIDLEVLFE; VYSLGYEIDLEVLFED; YSLGYEIDLEVLFEDM; SLGYEIDLEVLFEDMN; LGYEIDLEVLFEDMNG; GYEIDLEVLFEDMNGM; YEIDLEVLFEDMNGME; EIDLEVLFEDMNGMEY; IDLEVLFEDMNGMEYA; DLEVLFEDMNGMEYAY; LEVLFEDMNGMEYAYS; EVLFEDMNGMEYAYSM;

	VLFEDMNGMEYAYSMG; LFEDMNGMEYAYSMGT; FEDMNGMEYAYSMGTL; EDMNGMEYAYSMGTLK; DMNGMEYAYSMGTLKF; MNGMEYAYSMGTLKFK; NGMEYAYSMGTLKFKG; GMEYAYSMGTLKFKGW; MEYAYSMGTLKFKGWA; EYAYSMGTLKFKGWAD; YAYSMGTLKFKGWADL; AYSMGTLKFKGWADLI; YSMGTLKFKGWADLIW; SMGTLKFKGWADLIWS; MGTLKFKGWADLIWSN; GTLKFKGWADLIWSNP; TLKFKGWADLIWSNPN; LKFKGWADLIWSNPNY; KFKGWADLIWSNPNYI; FKGWADLIWSNPNYIP; KGWADLIWSNPNYIPN; GWADLIWSNPNYIPNI; WADLIWSNPNYIPNIS; ADLIWSNPNYIPNISS; DLIWSNPNYIPNISSR; LIWSNPNYIPNISSRI; IWSNPNYIPNISSRII; WSNPNYIPNISSRIIK; SNPNYIPNISSRIIKD; NPNYIPNISSRIIKDD; PNYIPNISSRIIKDDV; NYIPNISSRIIKDDVP; YIPNISSRIIKDDVPN; IPNISSRIIKDDVPNY; PNISSRIIKDDVPNYP; NISSRIIKDDVPNYPL; ISSRIIKDDVPNYPLA; SSRIIKDDVPNYPLAS; SRIIKDDVPNYPLASS; RIIKDDVPNYPLASSK; IIKDDVPNYPLASSKM; IKDDVPNYPLASSKMR; KDDVPNYPLASSKMRF; DDVPNYPLASSKMRFK; DVPNYPLASSKMRFKA; VPNYPLASSKMRFKAF; PNYPLASSKMRFKAFR; NYPLASSKMRFKAFRV; YPLASSKMRFKAFRVS; PLASSKMRFKAFRVSK; LASSKMRFKAFRVSKS; ASSKMRFKAFRVSKSH; SSKMRFKAFRVSKSHS; SKMRFKAFRVSKSHSS; KMRFKAFRVSKSHSSK; MRFKAFRVSKSHSSKV; RFKAFRVSKSHSSKVK; FKAFRVSKSHSSKVKN; KAFRVSKSHSSKVKNF; AFRVSKSHSSKVKNFI; FRVSKSHSSKVKNFIF; RVSKSHSSKVKNFIFY; VSKSHSSKVKNFIFYV; SKSHSSKVKNFIFYVK; KSHSSKVKNFIFYVKD; SHSSKVKNFIFYVKDL; HSSKVKNFIFYVKDLR; SSKVKNFIFYVKDLRV; SKVKNFIFYVKDLRVL; KVKNFIFYVKDLRVLY; VKNFIFYVKDLRVLYD; KNFIFYVKDLRVLYDK; NFIFYVKDLRVLYDKL; FIFYVKDLRVLYDKLS; IFYVKDLRVLYDKLSV; FYVKDLRVLYDKLSVS; YVKDLRVLYDKLSVSI; VKDLRVLYDKLSVSID; KDLRVLYDKLSVSIDS; DLRVLYDKLSVSIDSD; LRVLYDKLSVSIDSDI; RVLYDKLSVSIDSDID; VLYDKLSVSIDSDIDS; LYDKLSVSIDSDIDSE; YDKLSVSIDSDIDSES; DKLSVSIDSDIDSESV; KLSVSIDSDIDSESVF; LSVSIDSDIDSESVFK; SVSIDSDIDSESVFKV; VSIDSDIDSESVFKVY; SIDSDIDSESVFKVYE; IDSDIDSESVFKVYET; DSDIDSESVFKVYETS; SDIDSESVFKVYETSG; DIDSESVFKVYETSGT; IDSESVFKVYETSGTE; DSESVFKVYETSGTES; SESVFKVYETSGTESL; ESVFKVYETSGTESLR; SVFKVYETSGTESLRK; VFKVYETSGTESLRKL; FKVYETSGTESLRKLK; KVYETSGTESLRKLKA; VYETSGTESLRKLKAH; YETSGTESLRKLKAHE; ETSGTESLRKLKAHET; TSGTESLRKLKAHETF; SGTESLRKLKAHETFK; GTESLRKLKAHETFKR; TESLRKLKAHETFKRV; ESLRKLKAHETFKRVL; SLRKLKAHETFKRVLK; LRKLKAHETFKRVLKL; RKLKAHETFKRVLKLR; KLKAHETFKRVLKLRE; LKAHETFKRVLKLREK; KAHETFKRVLKLREKI; AHETFKRVLKLREKIS; HETFKRVLKLREKISI; ETFKRVLKLREKISIA; TFKRVLKLREKISIAE; FKRVLKLREKISIAEG; KRVLKLREKISIAEGS; RVLKLREKISIAEGSF; VLKLREKISIAEGSFQ; LKLREKISIAEGSFQN; KLREKISIAEGSFQNF; LREKISIAEGSFQNFV; REKISIAEGSFQNFVE; EKISIAEGSFQNFVEK; KISIAEGSFQNFVEKI; ISIAEGSFQNFVEKIE; SIAEGSFQNFVEKIES; IAEGSFQNFVEKIESE; AEGSFQNFVEKIESEK; EGSFQNFVEKIESEKP; GSFQNFVEKIESEKPE; SFQNFVEKIESEKPEE; FQNFVEKIESEKPEES; QNFVEKIESEKPEESS; NFVEKIESEKPEESSP; FVEKIESEKPEESSPK; VEKIESEKPEESSPKN;
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi]	13 mers: MIINHNTSAINAS; IINHNTSAINASR; INHNTSAINASRN; NHNTSAINASRNN; HNTSAINASRNNS; NTSAINASRNNSI; TSAINASRNNSIN; SAINASRNNSINA; AINASRNNSINAA; INASRNNSINAAN; NASRNNSINAANL; ASRNNSINAANLS; SRNNSINAANLSK; RNNSINAANLSKT; NNSINAANLSKTQ; NSINAANLSKTQE; SINAANLSKTQEK; INAANLSKTQEKL; NAANLSKTQEKLS; AANLSKTQEKLSS; ANLSKTQEKLSSG; NLSKTQEKLSSGY; LSKTQEKLSSGYR; SKTQEKLSSGYRI;

	KTQEKLSSGYRIN; TQEKLSSGYRINR; QEKLSSGYRINRA; EKLSSGYRINRAS; KLSSGYRINRASD; LSSGYRINRASDD; SSGYRINRASDDA; SGYRINRASDDAA; GYRINRASDDAAG; YRINRASDDAAGM; RINRASDDAAGMG; INRASDDAAGMGV; NRASDDAAGMGVS; RASDDAAGMGVSG; ASDDAAGMGVSGK; SDDAAGMGVSGKI; DDAAGMGVSGKIN; DAAGMGVSGKINA; AAGMGVSGKINAQ; AGMGVSGKINAQI; GMGVSGKINAQIR; MGVSGKINAQIRG; GVSGKINAQIRGL; VSGKINAQIRGLS; SGKINAQIRGLSQ; GKINAQIRGLSQA; KINAQIRGLSQAS; INAQIRGLSQASR; NAQIRGLSQASRN; AQIRGLSQASRNT; QIRGLSQASRNTS; IRGLSQASRNTSK; RGLSQASRNTSKA; GLSQASRNTSKAI; LSQASRNTSKAIN; SQASRNTSKAINF; QASRNTSKAINFI; ASRNTSKAINFIQ; SRNTSKAINFIQT; RNTSKAINFIQTT; NTSKAINFIQTTE; TSKAINFIQTTEG; SKAINFIQTTEGN; KAINFIQTTEGNL; AINFIQTTEGNLN; INFIQTTEGNLNE; NFIQTTEGNLNEV; FIQTTEGNLNEVE; IQTTEGNLNEVEK; QTTEGNLNEVEKV; TTEGNLNEVEKVL; TEGNLNEVEKVLV; EGNLNEVEKVLVR; GNLNEVEKVLVRM; NLNEVEKVLVRMK; LNEVEKVLVRMKE; NEVEKVLVRMKEL; EVEKVLVRMKELA; VEKVLVRMKELAV; EKVLVRMKELAVQ; KVLVRMKELAVQS; VLVRMKELAVQSG; LVRMKELAVQSGN; VRMKELAVQSGNG; RMKELAVQSGNGT; MKELAVQSGNGTY; KELAVQSGNGTYS; ELAVQSGNGTYSD; LAVQSGNGTYSDA; AVQSGNGTYSDAD; VQSGNGTYSDADR; QSGNGTYSDADRG; SGNGTYSDADRGS; GNGTYSDADRGSI; NGTYSDADRGSIQ; GTYSDADRGSIQI; TYSDADRGSIQIE; YSDADRGSIQIEI; SDADRGSIQIEIE; DADRGSIQIEIEQ; ADRGSIQIEIEQL; DRGSIQIEIEQLT; RGSIQIEIEQLTD; GSIQIEIEQLTDE; SIQIEIEQLTDEI; IQIEIEQLTDEIN; QIEIEQLTDEINR; IEIEQLTDEINRI; EIEQLTDEINRIA; IEQLTDEINRIAD; EQLTDEINRIADQ; QLTDEINRIADQA; LTDEINRIADQAQ; TDEINRIADQAQY; DEINRIADQAQYN; EINRIADQAQYNQ; INRIADQAQYNQM; NRIADQAQYNQMH; RIADQAQYNQMHM; IADQAQYNQMHML; ADQAQYNQMHMLS; DQAQYNQMHMLSN; QAQYNQMHMLSNK; AQYNQMHMLSNKS; QYNQMHMLSNKSA; YNQMHMLSNKSAS; NQMHMLSNKSASQ; QMHMLSNKSASQN; MHMLSNKSASQNV; HMLSNKSASQNVR; MLSNKSASQNVRT; LSNKSASQNVRTA; SNKSASQNVRTAE; NKSASQNVRTAEE; KSASQNVRTAEEL; SASQNVRTAEELG; ASQNVRTAEELGM; SQNVRTAEELGMQ; QNVRTAEELGMQP; NVRTAEELGMQPA; VRTAEELGMQPAK; RTAEELGMQPAKI; TAEELGMQPAKIN; AEELGMQPAKINT; EELGMQPAKINTP; ELGMQPAKINTPA; LGMQPAKINTPAS; GMQPAKINTPASL; MQPAKINTPASLS; QPAKINTPASLSG; PAKINTPASLSGS; AKINTPASLSGSQ; KINTPASLSGSQA; INTPASLSGSQAS; NTPASLSGSQASW; TPASLSGSQASWT; PASLSGSQASWTL; ASLSGSQASWTLR; SLSGSQASWTLRV; LSGSQASWTLRVH; SGSQASWTLRVHV; GSQASWTLRVHVG; SQASWTLRVHVGA; QASWTLRVHVGAN; ASWTLRVHVGANQ; SWTLRVHVGANQD; WTLRVHVGANQDE; TLRVHVGANQDEA; LRVHVGANQDEAI; RVHVGANQDEAIA; VHVGANQDEAIAV; HVGANQDEAIAVN; VGANQDEAIAVNI; GANQDEAIAVNIY; ANQDEAIAVNIYA; NQDEAIAVNIYAA; QDEAIAVNIYAAN; DEAIAVNIYAANV; EAIAVNIYAANVA; AIAVNIYAANVAN; IAVNIYAANVANL; AVNIYAANVANLF; VNIYAANVANLFS; NIYAANVANLFSG; IYAANVANLFSGE; YAANVANLFSGEG; AANVANLFSGEGS; ANVANLFSGEGSQ; NVANLFSGEGSQA; VANLFSGEGSQAA; ANLFSGEGSQAAQ; NLFSGEGSQAAQT; LFSGEGSQAAQTA; FSGEGSQAAQTAP; SGEGSQAAQTAPV; GEGSQAAQTAPVQ; EGSQAAQTAPVQE; GSQAAQTAPVQEG; SQAAQTAPVQEGA; QAAQTAPVQEGAQ; AAQTAPVQEGAQQ; AQTAPVQEGAQQE; QTAPVQEGAQQEG; TAPVQEGAQQEGA; APVQEGAQQEGAQ; PVQEGAQQEGAQQ; VQEGAQQEGAQQP; QEGAQQEGAQQPA; EGAQQEGAQQPAP; GAQQEGAQQPAPA; AQQEGAQQPAPAT; QQEGAQQPAPATA; QEGAQQPAPATAP; EGAQQPAPATAPS; GAQQPAPATAPSQ; AQQPAPATAPSQG; QQPAPATAPSQGG; QPAPATAPSQGGV; PAPATAPSQGGVN; APATAPSQGGVNS; PATAPSQGGVNSP; ATAPSQGGVNSPV; TAPSQGGVNSPVN; APSQGGVNSPVNV; PSQGGVNSPVNVT; SQGGVNSPVNVTT; QGGVNSPVNVTTT; GGVNSPVNVTTTV; GVNSPVNVTTTVD; VNSPVNVTTTVDA; NSPVNVTTTVDAN; SPVNVTTTVDANT; PVNVTTTVDANTS; VNVTTTVDANTSL; NVTTTVDANTSLA; VTTTVDANTSLAK; TTTVDANTSLAKI; TTVDANTSLAKIE; TVDANTSLAKIEN; VDANTSLAKIENA; DANTSLAKIENAI; ANTSLAKIENAIR; NTSLAKIENAIRM; TSLAKIENAIRMI; SLAKIENAIRMIS; LAKIENAIRMISD; AKIENAIRMISDQ; KIENAIRMISDQR;

IENAIRMISDQRA; ENAIRMISDQRAN; NAIRMISDQRANL; AIRMISDQRANLG;
IRMISDQRANLGA; RMISDQRANLGAF; MISDQRANLGAFQ; ISDQRANLGAFQN;
SDQRANLGAFQNR; DQRANLGAFQNRL; QRANLGAFQNRLE; RANLGAFQNRLES;
ANLGAFQNRLESI; NLGAFQNRLESIK; LGAFQNRLESIKD; GAFQNRLESIKDS;
AFQNRLESIKDST; FQNRLESIKDSTE; QNRLESIKDSTEY; NRLESIKDSTEYA;
RLESIKDSTEYAI; LESIKDSTEYAIE; ESIKDSTEYAIEN; SIKDSTEYAIENL;
IKDSTEYAIENLK; KDSTEYAIENLKA; DSTEYAIENLKAS; STEYAIENLKASY;
TEYAIENLKASYA; EYAIENLKASYAQ; YAIENLKASYAQI; AIENLKASYAQIK;
IENLKASYAQIKD; ENLKASYAQIKDA; NLKASYAQIKDAT; LKASYAQIKDATM;
KASYAQIKDATMT; ASYAQIKDATMTD; SYAQIKDATMTDE; YAQIKDATMTDEV;
AQIKDATMTDEVV; QIKDATMTDEVVA; IKDATMTDEVVAS; KDATMTDEVVAST;
DATMTDEVVASTT; ATMTDEVVASTTN; TMTDEVVASTTNS; MTDEVVASTTNSI;
TDEVVASTTNSIL; DEVVASTTNSILT; EVVASTTNSILTQ; VVASTTNSILTQS;
VASTTNSILTQSA; ASTTNSILTQSAM; STTNSILTQSAMA; TTNSILTQSAMAM;
TNSILTQSAMAMI; NSILTQSAMAMIA; SILTQSAMAMIAQ; ILTQSAMAMIAQA;
LTQSAMAMIAQAN; TQSAMAMIAQANQ; QSAMAMIAQANQV; SAMAMIAQANQVP;
AMAMIAQANQVPQ; MAMIAQANQVPQY; AMIAQANQVPQYV; MIAQANQVPQYVL;
IAQANQVPQYVLS; AQANQVPQYVLSL; QANQVPQYVLSLL; ANQVPQYVLSLLR;

14 mers:
MIINHNTSAINASR; IINHNTSAINASRN; INHNTSAINASRNN;
NHNTSAINASRNNS; HNTSAINASRNNSI; NTSAINASRNNSIN;
TSAINASRNNSINA; SAINASRNNSINAA; AINASRNNSINAAN;
INASRNNSINAANL; NASRNNSINAANLS; ASRNNSINAANLSK;
SRNNSINAANLSKT; RNNSINAANLSKTQ; NNSINAANLSKTQE;
NSINAANLSKTQEK; SINAANLSKTQEKL; INAANLSKTQEKLS;
NAANLSKTQEKLSS; AANLSKTQEKLSSG; ANLSKTQEKLSSGY;
NLSKTQEKLSSGYR; LSKTQEKLSSGYRI; SKTQEKLSSGYRIN;
KTQEKLSSGYRINR; TQEKLSSGYRINRA; QEKLSSGYRINRAS;
EKLSSGYRINRASD; KLSSGYRINRASDD; LSSGYRINRASDDA;
SSGYRINRASDDAA; SGYRINRASDDAAG; GYRINRASDDAAGM;
YRINRASDDAAGMG; RINRASDDAAGMGV; INRASDDAAGMGVS;
NRASDDAAGMGVSG; RASDDAAGMGVSGK; ASDDAAGMGVSGKI;
SDDAAGMGVSGKIN; DDAAGMGVSGKINA; DAAGMGVSGKINAQ;
AAGMGVSGKINAQI; AGMGVSGKINAQIR; GMGVSGKINAQIRG;
MGVSGKINAQIRGL; GVSGKINAQIRGLS; VSGKINAQIRGLSQ;
SGKINAQIRGLSQA; GKINAQIRGLSQAS; KINAQIRGLSQASR;
INAQIRGLSQASRN; NAQIRGLSQASRNT; AQIRGLSQASRNTS;
QIRGLSQASRNTSK; IRGLSQASRNTSKA; RGLSQASRNTSKAI;
GLSQASRNTSKAIN; LSQASRNTSKAINF; SQASRNTSKAINFI;
QASRNTSKAINFIQ; ASRNTSKAINFIQT; SRNTSKAINFIQTT;
RNTSKAINFIQTTE; NTSKAINFIQTTEG; TSKAINFIQTTEGN;
SKAINFIQTTEGNL; KAINFIQTTEGNLN; AINFIQTTEGNLNE;
INFIQTTEGNLNEV; NFIQTTEGNLNEVE; FIQTTEGNLNEVEK;
IQTTEGNLNEVEKV; QTTEGNLNEVEKVL; TTEGNLNEVEKVLV;
TEGNLNEVEKVLVR; EGNLNEVEKVLVRM; GNLNEVEKVLVRMK;
NLNEVEKVLVRMKE; LNEVEKVLVRMKEL; NEVEKVLVRMKELA;
EVEKVLVRMKELAV; VEKVLVRMKELAVQ; EKVLVRMKELAVQS;
KVLVRMKELAVQSG; VLVRMKELAVQSGN; LVRMKELAVQSGNG;
VRMKELAVQSGNGT; RMKELAVQSGNGTY; MKELAVQSGNGTYS;
KELAVQSGNGTYSD; ELAVQSGNGTYSDA; LAVQSGNGTYSDAD;
AVQSGNGTYSDADR; VQSGNGTYSDADRG; QSGNGTYSDADRGS;
SGNGTYSDADRGSI; GNGTYSDADRGSIQ; NGTYSDADRGSIQI;
GTYSDADRGSIQIE; TYSDADRGSIQIEI; YSDADRGSIQIEIE;
SDADRGSIQIEIEQ; DADRGSIQIEIEQL; ADRGSIQIEIEQLT;
DRGSIQIEIEQLTD; RGSIQIEIEQLTDE; GSIQIEIEQLTDEI;
SIQIEIEQLTDEIN; IQIEIEQLTDEINR; QIEIEQLTDEINRI;

	IEIEQLTDEINRIA; EIEQLTDEINRIAD; IEQLTDEINRIADQ; EQLTDEINRIADQA; QLTDEINRIADQAQ; LTDEINRIADQAQY; TDEINRIADQAQYN; DEINRIADQAQYNQ; EINRIADQAQYNQM; INRIADQAQYNQMH; NRIADQAQYNQMHM; RIADQAQYNQMHML; IADQAQYNQMHMLS; ADQAQYNQMHMLSN; DQAQYNQMHMLSNK; QAQYNQMHMLSNKS; AQYNQMHMLSNKSA; QYNQMHMLSNKSAS; YNQMHMLSNKSASQ; NQMHMLSNKSASQN; QMHMLSNKSASQNV; MHMLSNKSASQNVR; HMLSNKSASQNVRT; MLSNKSASQNVRTA; LSNKSASQNVRTAE; SNKSASQNVRTAEE; NKSASQNVRTAEEL; KSASQNVRTAEELG; SASQNVRTAEELGM; ASQNVRTAEELGMQ; SQNVRTAEELGMQP; QNVRTAEELGMQPA; NVRTAEELGMQPAK; VRTAEELGMQPAKI; RTAEELGMQPAKIN; TAEELGMQPAKINT; AEELGMQPAKINTP; EELGMQPAKINTPA; ELGMQPAKINTPAS; LGMQPAKINTPASL; GMQPAKINTPASLS; MQPAKINTPASLSG; QPAKINTPASLSGS; PAKINTPASLSGSQ; AKINTPASLSGSQA; KINTPASLSGSQAS; INTPASLSGSQASW; NTPASLSGSQASWT; TPASLSGSQASWTL; PASLSGSQASWTLR; ASLSGSQASWTLRV; SLSGSQASWTLRVH; LSGSQASWTLRVHV; SGSQASWTLRVHVG; GSQASWTLRVHVGA; SQASWTLRVHVGAN; QASWTLRVHVGANQ; ASWTLRVHVGANQD; SWTLRVHVGANQDE; WTLRVHVGANQDEA; TLRVHVGANQDEAI; LRVHVGANQDEAIA; RVHVGANQDEAIAV; VHVGANQDEAIAVN; HVGANQDEAIAVNI; VGANQDEAIAVNIY; GANQDEAIAVNIYA; ANQDEAIAVNIYAA; NQDEAIAVNIYAAN; QDEAIAVNIYAANV; DEAIAVNIYAANVA; EAIAVNIYAANVAN; AIAVNIYAANVANL; IAVNIYAANVANLF; AVNIYAANVANLFS; VNIYAANVANLFSG; NIYAANVANLFSGE; IYAANVANLFSGEG; YAANVANLFSGEGS; AANVANLFSGEGSQ; ANVANLFSGEGSQA; NVANLFSGEGSQAA; VANLFSGEGSQAAQ; ANLFSGEGSQAAQT; NLFSGEGSQAAQTA; LFSGEGSQAAQTAP; FSGEGSQAAQTAPV; SGEGSQAAQTAPVQ; GEGSQAAQTAPVQE; EGSQAAQTAPVQEG; GSQAAQTAPVQEGA; SQAAQTAPVQEGAQ; QAAQTAPVQEGAQQ; AAQTAPVQEGAQQE; AQTAPVQEGAQQEG; QTAPVQEGAQQEGA; TAPVQEGAQQEGAQ; APVQEGAQQEGAQQ; PVQEGAQQEGAQQP; VQEGAQQEGAQQPA; QEGAQQEGAQQPAP; EGAQQEGAQQPAPA; GAQQEGAQQPAPAT; AQQEGAQQPAPATA; QQEGAQQPAPATAP; QEGAQQPAPATAPS; EGAQQPAPATAPSQ; GAQQPAPATAPSQG; AQQPAPATAPSQGG; QQPAPATAPSQGGV; QPAPATAPSQGGVN; PAPATAPSQGGVNS; APATAPSQGGVNSP; PATAPSQGGVNSPV; ATAPSQGGVNSPVN; TAPSQGGVNSPVNV; APSQGGVNSPVNVT; PSQGGVNSPVNVTT; SQGGVNSPVNVTTT; QGGVNSPVNVTTTV; GGVNSPVNVTTTVD; GVNSPVNVTTTVDA; VNSPVNVTTTVDAN; NSPVNVTTTVDANT; SPVNVTTTVDANTS; PVNVTTTVDANTSL; VNVTTTVDANTSLA; NVTTTVDANTSLAK; VTTTVDANTSLAKI; TTTVDANTSLAKIE; TTVDANTSLAKIEN; TVDANTSLAKIENA; VDANTSLAKIENAI; DANTSLAKIENAIR; ANTSLAKIENAIRM; NTSLAKIENAIRMI; TSLAKIENAIRMIS; SLAKIENAIRMISD; LAKIENAIRMISDQ; AKIENAIRMISDQR; KIENAIRMISDQRA; IENAIRMISDQRAN; ENAIRMISDQRANL; NAIRMISDQRANLG; AIRMISDQRANLGA; IRMISDQRANLGAF; RMISDQRANLGAFQ; MISDQRANLGAFQN; ISDQRANLGAFQNR; SDQRANLGAFQNRL; DQRANLGAFQNRLE; QRANLGAFQNRLES; RANLGAFQNRLESI; ANLGAFQNRLESIK; NLGAFQNRLESIKD; LGAFQNRLESIKDS; GAFQNRLESIKDST; AFQNRLESIKDSTE; FQNRLESIKDSTEY; QNRLESIKDSTEYA; NRLESIKDSTEYAI; RLESIKDSTEYAIE; LESIKDSTEYAIEN; ESIKDSTEYAIENL; SIKDSTEYAIENLK; IKDSTEYAIENLKA; KDSTEYAIENLKAS; DSTEYAIENLKASY; STEYAIENLKASYA; TEYAIENLKASYAQ; EYAIENLKASYAQI;

YAIENLKASYAQIK; AIENLKASYAQIKD; IENLKASYAQIKDA;
ENLKASYAQIKDAT; NLKASYAQIKDATM; LKASYAQIKDATMT;
KASYAQIKDATMTD; ASYAQIKDATMTDE; SYAQIKDATMTDEV;
YAQIKDATMTDEVV; AQIKDATMTDEVVA; QIKDATMTDEVVAS;
IKDATMTDEVVAST; KDATMTDEVVASTT; DATMTDEVVASTTN;
ATMTDEVVASTTNS; TMTDEVVASTTNSI; MTDEVVASTTNSIL;
TDEVVASTTNSILT; DEVVASTTNSILTQ; EVVASTTNSILTQS;
VVASTTNSILTQSA; VASTTNSILTQSAM; ASTTNSILTQSAMA;
STTNSILTQSAMAM; TTNSILTQSAMAMI; TNSILTQSAMAMIA;
NSILTQSAMAMIAQ; SILTQSAMAMIAQA; ILTQSAMAMIAQAN;
LTQSAMAMIAQANQ; TQSAMAMIAQANQV; QSAMAMIAQANQVP;
SAMAMIAQANQVPQ; AMAMIAQANQVPQY; MAMIAQANQVPQYV;
AMIAQANQVPQYVL; MIAQANQVPQYVLS; IAQANQVPQYVLSL;
AQANQVPQYVLSLL; QANQVPQYVLSLLR;

15 mers:
MIINHNTSAINASRN; IINHNTSAINASRNN; INHNTSAINASRNNS;
NHNTSAINASRNNSI; HNTSAINASRNNSIN; NTSAINASRNNSINA;
TSAINASRNNSINAA; SAINASRNNSINAAN; AINASRNNSINAANL;
INASRNNSINAANLS; NASRNNSINAANLSK; ASRNNSINAANLSKT;
SRNNSINAANLSKTQ; RNNSINAANLSKTQE; NNSINAANLSKTQEK;
NSINAANLSKTQEKL; SINAANLSKTQEKLS; INAANLSKTQEKLSS;
NAANLSKTQEKLSSG; AANLSKTQEKLSSGY; ANLSKTQEKLSSGYR;
NLSKTQEKLSSGYRI; LSKTQEKLSSGYRIN; SKTQEKLSSGYRINR;
KTQEKLSSGYRINRA; TQEKLSSGYRINRAS; QEKLSSGYRINRASD;
EKLSSGYRINRASDD; KLSSGYRINRASDDA; LSSGYRINRASDDAA;
SSGYRINRASDDAAG; SGYRINRASDDAAGM; GYRINRASDDAAGMG;
YRINRASDDAAGMGV; RINRASDDAAGMGVS; INRASDDAAGMGVSG;
NRASDDAAGMGVSGK; RASDDAAGMGVSGKI; ASDDAAGMGVSGKIN;
SDDAAGMGVSGKINA; DDAAGMGVSGKINAQ; DAAGMGVSGKINAQI;
AAGMGVSGKINAQIR; AGMGVSGKINAQIRG; GMGVSGKINAQIRGL;
MGVSGKINAQIRGLS; GVSGKINAQIRGLSQ; VSGKINAQIRGLSQA;
SGKINAQIRGLSQAS; GKINAQIRGLSQASR; KINAQIRGLSQASRN;
INAQIRGLSQASRNT; NAQIRGLSQASRNTS; AQIRGLSQASRNTSK;
QIRGLSQASRNTSKA; IRGLSQASRNTSKAI; RGLSQASRNTSKAIN;
GLSQASRNTSKAINF; LSQASRNTSKAINFI; SQASRNTSKAINFIQ;
QASRNTSKAINFIQT; ASRNTSKAINFIQTT; SRNTSKAINFIQTTE;
RNTSKAINFIQTTEG; NTSKAINFIQTTEGN; TSKAINFIQTTEGNL;
SKAINFIQTTEGNLN; KAINFIQTTEGNLNE; AINFIQTTEGNLNEV;
INFIQTTEGNLNEVE; NFIQTTEGNLNEVEK; FIQTTEGNLNEVEKV;
IQTTEGNLNEVEKVL; QTTEGNLNEVEKVLV; TTEGNLNEVEKVLVR;
TEGNLNEVEKVLVRM; EGNLNEVEKVLVRMK; GNLNEVEKVLVRMKE;
NLNEVEKVLVRMKEL; LNEVEKVLVRMKELA; NEVEKVLVRMKELAV;
EVEKVLVRMKELAVQ; VEKVLVRMKELAVQS; EKVLVRMKELAVQSG;
KVLVRMKELAVQSGN; VLVRMKELAVQSGNG; LVRMKELAVQSGNGT;
VRMKELAVQSGNGTY; RMKELAVQSGNGTYS; MKELAVQSGNGTYSD;
KELAVQSGNGTYSDA; ELAVQSGNGTYSDAD; LAVQSGNGTYSDADR;
AVQSGNGTYSDADRG; VQSGNGTYSDADRGS; QSGNGTYSDADRGSI;
SGNGTYSDADRGSIQ; GNGTYSDADRGSIQI; NGTYSDADRGSIQIE;
GTYSDADRGSIQIEI; TYSDADRGSIQIEIE; YSDADRGSIQIEIEQ;
SDADRGSIQIEIEQL; DADRGSIQIEIEQLT; ADRGSIQIEIEQLTD;
DRGSIQIEIEQLTDE; RGSIQIEIEQLTDEI; GSIQIEIEQLTDEIN;
SIQIEIEQLTDEINR; IQIEIEQLTDEINRI; QIEIEQLTDEINRIA;
IEIEQLTDEINRIAD; EIEQLTDEINRIADQ; IEQLTDEINRIADQA;
EQLTDEINRIADQAQ; QLTDEINRIADQAQY; LTDEINRIADQAQYN;
TDEINRIADQAQYNQ; DEINRIADQAQYNQM; EINRIADQAQYNQMH;
INRIADQAQYNQMHM; NRIADQAQYNQMHML; RIADQAQYNQMHMLS;

	IADQAQYNQMHMLSN; ADQAQYNQMHMLSNK; DQAQYNQMHMLSNKS; QAQYNQMHMLSNKSA; AQYNQMHMLSNKSAS; QYNQMHMLSNKSASQ; YNQMHMLSNKSASQN; NQMHMLSNKSASQNV; QMHMLSNKSASQNVR; MHMLSNKSASQNVRT; HMLSNKSASQNVRTA; MLSNKSASQNVRTAE; LSNKSASQNVRTAEE; SNKSASQNVRTAEEL; NKSASQNVRTAEELG; KSASQNVRTAEELGM; SASQNVRTAEELGMQ; ASQNVRTAEELGMQP; SQNVRTAEELGMQPA; QNVRTAEELGMQPAK; NVRTAEELGMQPAKI; VRTAEELGMQPAKIN; RTAEELGMQPAKINT; TAEELGMQPAKINTP; AEELGMQPAKINTPA; EELGMQPAKINTPAS; ELGMQPAKINTPASL; LGMQPAKINTPASLS; GMQPAKINTPASLSG; MQPAKINTPASLSGS; QPAKINTPASLSGSQ; PAKINTPASLSGSQA; AKINTPASLSGSQAS; KINTPASLSGSQASW; INTPASLSGSQASWT; NTPASLSGSQASWTL; TPASLSGSQASWTLR; PASLSGSQASWTLRV; ASLSGSQASWTLRVH; SLSGSQASWTLRVHV; LSGSQASWTLRVHVG; SGSQASWTLRVHVGA; GSQASWTLRVHVGAN; SQASWTLRVHVGANQ; QASWTLRVHVGANQD; ASWTLRVHVGANQDE; SWTLRVHVGANQDEA; WTLRVHVGANQDEAI; TLRVHVGANQDEAIA; LRVHVGANQDEAIAV; RVHVGANQDEAIAVN; VHVGANQDEAIAVNI; HVGANQDEAIAVNIY; VGANQDEAIAVNIYA; GANQDEAIAVNIYAA; ANQDEAIAVNIYAAN; NQDEAIAVNIYAANV; QDEAIAVNIYAANVA; DEAIAVNIYAANVAN; EAIAVNIYAANVANL; AIAVNIYAANVANLF; IAVNIYAANVANLFS; AVNIYAANVANLFSG; VNIYAANVANLFSGE; NIYAANVANLFSGEG; IYAANVANLFSGEGS; YAANVANLFSGEGSQ; AANVANLFSGEGSQA; ANVANLFSGEGSQAA; NVANLFSGEGSQAAQ; VANLFSGEGSQAAQT; ANLFSGEGSQAAQTA; NLFSGEGSQAAQTAP; LFSGEGSQAAQTAPV; FSGEGSQAAQTAPVQ; SGEGSQAAQTAPVQE; GEGSQAAQTAPVQEG; EGSQAAQTAPVQEGA; GSQAAQTAPVQEGAQ; SQAAQTAPVQEGAQQ; QAAQTAPVQEGAQQE; AAQTAPVQEGAQQEG; AQTAPVQEGAQQEGA; QTAPVQEGAQQEGAQ; TAPVQEGAQQEGAQQ; APVQEGAQQEGAQQP; PVQEGAQQEGAQQPA; VQEGAQQEGAQQPAP; QEGAQQEGAQQPAPA; EGAQQEGAQQPAPAT; GAQQEGAQQPAPATA; AQQEGAQQPAPATAP; QQEGAQQPAPATAPS; QEGAQQPAPATAPSQ; EGAQQPAPATAPSQG; GAQQPAPATAPSQGG; AQQPAPATAPSQGGV; QQPAPATAPSQGGVN; QPAPATAPSQGGVNS; PAPATAPSQGGVNSP; APATAPSQGGVNSPV; PATAPSQGGVNSPVN; ATAPSQGGVNSPVNV; TAPSQGGVNSPVNVT; APSQGGVNSPVNVTT; PSQGGVNSPVNVTTT; SQGGVNSPVNVTTTV; QGGVNSPVNVTTTVD; GGVNSPVNVTTTVDA; GVNSPVNVTTTVDAN; VNSPVNVTTTVDANT; NSPVNVTTTVDANTS; SPVNVTTTVDANTSL; PVNVTTTVDANTSLA; VNVTTTVDANTSLAK; NVTTTVDANTSLAKI; VTTTVDANTSLAKIE; TTTVDANTSLAKIEN; TTVDANTSLAKIENA; TVDANTSLAKIENAI; VDANTSLAKIENAIR; DANTSLAKIENAIRM; ANTSLAKIENAIRMI; NTSLAKIENAIRMIS; TSLAKIENAIRMISD; SLAKIENAIRMISDQ; LAKIENAIRMISDQR; AKIENAIRMISDQRA; KIENAIRMISDQRAN; IENAIRMISDQRANL; ENAIRMISDQRANLG; NAIRMISDQRANLGA; AIRMISDQRANLGAF; IRMISDQRANLGAFQ; RMISDQRANLGAFQN; MISDQRANLGAFQNR; ISDQRANLGAFQNRL; SDQRANLGAFQNRLE; DQRANLGAFQNRLES; QRANLGAFQNRLESI; RANLGAFQNRLESIK; ANLGAFQNRLESIKD; NLGAFQNRLESIKDS; LGAFQNRLESIKDST; GAFQNRLESIKDSTE; AFQNRLESIKDSTEY; FQNRLESIKDSTEYA; QNRLESIKDSTEYAI; NRLESIKDSTEYAIE; RLESIKDSTEYAIEN; LESIKDSTEYAIENL; ESIKDSTEYAIENLK; SIKDSTEYAIENLKA; IKDSTEYAIENLKAS; KDSTEYAIENLKASY; DSTEYAIENLKASYA; STEYAIENLKASYAQ; TEYAIENLKASYAQI; EYAIENLKASYAQIK; YAIENLKASYAQIKD; AIENLKASYAQIKDA; IENLKASYAQIKDAT; ENLKASYAQIKDATM; NLKASYAQIKDATMT; LKASYAQIKDATMTD; KASYAQIKDATMTDE; ASYAQIKDATMTDEV; SYAQIKDATMTDEVV; YAQIKDATMTDEVVA; AQIKDATMTDEVVAS; QIKDATMTDEVVAST;

IKDATMTDEVVASTT; KDATMTDEVVASTTN; DATMTDEVVASTTNS;
ATMTDEVVASTTNSI; TMTDEVVASTTNSIL; MTDEVVASTTNSILT;
TDEVVASTTNSILTQ; DEVVASTTNSILTQS; EVVASTTNSILTQSA;
VVASTTNSILTQSAM; VASTTNSILTQSAMA; ASTTNSILTQSAMAM;
STTNSILTQSAMAMI; TTNSILTQSAMAMIA; TNSILTQSAMAMIAQ;
NSILTQSAMAMIAQA; SILTQSAMAMIAQAN; ILTQSAMAMIAQANQ;
LTQSAMAMIAQANQV; TQSAMAMIAQANQVP; QSAMAMIAQANQVPQ;
SAMAMIAQANQVPQY; AMAMIAQANQVPQYV; MAMIAQANQVPQYVL;
AMIAQANQVPQYVLS; MIAQANQVPQYVLSL; IAQANQVPQYVLSLL;
AQANQVPQYVLSLLR;

16 mers:
MIINHNTSAINASRNN; IINHNTSAINASRNNS; INHNTSAINASRNNSI;
NHNTSAINASRNNSIN; HNTSAINASRNNSINA; NTSAINASRNNSINAA;
TSAINASRNNSINAAN; SAINASRNNSINAANL; AINASRNNSINAANLS;
INASRNNSINAANLSK; NASRNNSINAANLSKT; ASRNNSINAANLSKTQ;
SRNNSINAANLSKTQE; RNNSINAANLSKTQEK; NNSINAANLSKTQEKL;
NSINAANLSKTQEKLS; SINAANLSKTQEKLSS; INAANLSKTQEKLSSG;
NAANLSKTQEKLSSGY; AANLSKTQEKLSSGYR; ANLSKTQEKLSSGYRI;
NLSKTQEKLSSGYRIN; LSKTQEKLSSGYRINR; SKTQEKLSSGYRINRA;
KTQEKLSSGYRINRAS; TQEKLSSGYRINRASD; QEKLSSGYRINRASDD;
EKLSSGYRINRASDDA; KLSSGYRINRASDDAA; LSSGYRINRASDDAAG;
SSGYRINRASDDAAGM; SGYRINRASDDAAGMG; GYRINRASDDAAGMGV;
YRINRASDDAAGMGVS; RINRASDDAAGMGVSG; INRASDDAAGMGVSGK;
NRASDDAAGMGVSGKI; RASDDAAGMGVSGKIN; ASDDAAGMGVSGKINA;
SDDAAGMGVSGKINAQ; DDAAGMGVSGKINAQI; DAAGMGVSGKINAQIR;
AAGMGVSGKINAQIRG; AGMGVSGKINAQIRGL; GMGVSGKINAQIRGLS;
MGVSGKINAQIRGLSQ; GVSGKINAQIRGLSQA; VSGKINAQIRGLSQAS;
SGKINAQIRGLSQASR; GKINAQIRGLSQASRN; KINAQIRGLSQASRNT;
INAQIRGLSQASRNTS; NAQIRGLSQASRNTSK; AQIRGLSQASRNTSKA;
QIRGLSQASRNTSKAI; IRGLSQASRNTSKAIN; RGLSQASRNTSKAINF;
GLSQASRNTSKAINFI; LSQASRNTSKAINFIQ; SQASRNTSKAINFIQT;
QASRNTSKAINFIQTT; ASRNTSKAINFIQTTE; SRNTSKAINFIQTTEG;
RNTSKAINFIQTTEGN; NTSKAINFIQTTEGNL; TSKAINFIQTTEGNLN;
SKAINFIQTTEGNLNE; KAINFIQTTEGNLNEV; AINFIQTTEGNLNEVE;
INFIQTTEGNLNEVEK; NFIQTTEGNLNEVEKV; FIQTTEGNLNEVEKVL;
IQTTEGNLNEVEKVLV; QTTEGNLNEVEKVLVR; TTEGNLNEVEKVLVRM;
TEGNLNEVEKVLVRMK; EGNLNEVEKVLVRMKE; GNLNEVEKVLVRMKEL;
NLNEVEKVLVRMKELA; LNEVEKVLVRMKELAV; NEVEKVLVRMKELAVQ;
EVEKVLVRMKELAVQS; VEKVLVRMKELAVQSG; EKVLVRMKELAVQSGN;
KVLVRMKELAVQSGNG; VLVRMKELAVQSGNGT; LVRMKELAVQSGNGTY;
VRMKELAVQSGNGTYS; RMKELAVQSGNGTYSD; MKELAVQSGNGTYSDA;
KELAVQSGNGTYSDAD; ELAVQSGNGTYSDADR; LAVQSGNGTYSDADRG;
AVQSGNGTYSDADRGS; VQSGNGTYSDADRGSI; QSGNGTYSDADRGSIQ;
SGNGTYSDADRGSIQI; GNGTYSDADRGSIQIE; NGTYSDADRGSIQIEI;
GTYSDADRGSIQIEIE; TYSDADRGSIQIEIEQ; YSDADRGSIQIEIEQL;
SDADRGSIQIEIEQLT; DADRGSIQIEIEQLTD; ADRGSIQIEIEQLTDE;
DRGSIQIEIEQLTDEI; RGSIQIEIEQLTDEIN; GSIQIEIEQLTDEINR;
SIQIEIEQLTDEINRI; IQIEIEQLTDEINRIA; QIEIEQLTDEINRIAD;
IEIEQLTDEINRIADQ; EIEQLTDEINRIADQA; IEQLTDEINRIADQAQ;
EQLTDEINRIADQAQY; QLTDEINRIADQAQYN; LTDEINRIADQAQYNQ;
TDEINRIADQAQYNQM; DEINRIADQAQYNQMH; EINRIADQAQYNQMHM;
INRIADQAQYNQMHML; NRIADQAQYNQMHMLS; RIADQAQYNQMHMLSN;
IADQAQYNQMHMLSNK; ADQAQYNQMHMLSNKS; DQAQYNQMHMLSNKSA;
QAQYNQMHMLSNKSAS; AQYNQMHMLSNKSASQ; QYNQMHMLSNKSASQN;
YNQMHMLSNKSASQNV; NQMHMLSNKSASQNVR; QMHMLSNKSASQNVRT;
MHMLSNKSASQNVRTA; HMLSNKSASQNVRTAE; MLSNKSASQNVRTAEE;

	LSNKSASQNVRTAEEL; SNKSASQNVRTAEELG; NKSASQNVRTAEELGM; KSASQNVRTAEELGMQ; SASQNVRTAEELGMQP; ASQNVRTAEELGMQPA; SQNVRTAEELGMQPAK; QNVRTAEELGMQPAKI; NVRTAEELGMQPAKIN; VRTAEELGMQPAKINT; RTAEELGMQPAKINTP; TAEELGMQPAKINTPA; AEELGMQPAKINTPAS; EELGMQPAKINTPASL; ELGMQPAKINTPASLS; LGMQPAKINTPASLSG; GMQPAKINTPASLSGS; MQPAKINTPASLSGSQ; QPAKINTPASLSGSQA; PAKINTPASLSGSQAS; AKINTPASLSGSQASW; KINTPASLSGSQASWT; INTPASLSGSQASWTL; NTPASLSGSQASWTLR; TPASLSGSQASWTLRV; PASLSGSQASWTLRVH; ASLSGSQASWTLRVHV; SLSGSQASWTLRVHVG; LSGSQASWTLRVHVGA; SGSQASWTLRVHVGAN; GSQASWTLRVHVGANQ; SQASWTLRVHVGANQD; QASWTLRVHVGANQDE; ASWTLRVHVGANQDEA; SWTLRVHVGANQDEAI; WTLRVHVGANQDEAIA; TLRVHVGANQDEAIAV; LRVHVGANQDEAIAVN; RVHVGANQDEAIAVNI; VHVGANQDEAIAVNIY; HVGANQDEAIAVNIYA; VGANQDEAIAVNIYAA; GANQDEAIAVNIYAAN; ANQDEAIAVNIYAANV; NQDEAIAVNIYAANVA; QDEAIAVNIYAANVAN; DEAIAVNIYAANVANL; EAIAVNIYAANVANLF; AIAVNIYAANVANLFS; IAVNIYAANVANLFSG; AVNIYAANVANLFSGE; VNIYAANVANLFSGEG; NIYAANVANLFSGEGS; IYAANVANLFSGEGSQ; YAANVANLFSGEGSQA; AANVANLFSGEGSQAA; ANVANLFSGEGSQAAQ; NVANLFSGEGSQAAQT; VANLFSGEGSQAAQTA; ANLFSGEGSQAAQTAP; NLFSGEGSQAAQTAPV; LFSGEGSQAAQTAPVQ; FSGEGSQAAQTAPVQE; SGEGSQAAQTAPVQEG; GEGSQAAQTAPVQEGA; EGSQAAQTAPVQEGAQ; GSQAAQTAPVQEGAQQ; SQAAQTAPVQEGAQQE; QAAQTAPVQEGAQQEG; AAQTAPVQEGAQQEGA; AQTAPVQEGAQQEGAQ; QTAPVQEGAQQEGAQQ; TAPVQEGAQQEGAQQP; APVQEGAQQEGAQQPA; PVQEGAQQEGAQQPAP; VQEGAQQEGAQQPAPA; QEGAQQEGAQQPAPAT; EGAQQEGAQQPAPATA; GAQQEGAQQPAPATAP; AQQEGAQQPAPATAPS; QQEGAQQPAPATAPSQ; QEGAQQPAPATAPSQG; EGAQQPAPATAPSQGG; GAQQPAPATAPSQGGV; AQQPAPATAPSQGGVN; QQPAPATAPSQGGVNS; QPAPATAPSQGGVNSP; PAPATAPSQGGVNSPV; APATAPSQGGVNSPVN; PATAPSQGGVNSPVNV; ATAPSQGGVNSPVNVT; TAPSQGGVNSPVNVTT; APSQGGVNSPVNVTTT; PSQGGVNSPVNVTTTV; SQGGVNSPVNVTTTVD; QGGVNSPVNVTTTVDA; GGVNSPVNVTTTVDAN; GVNSPVNVTTTVDANT; VNSPVNVTTTVDANTS; NSPVNVTTTVDANTSL; SPVNVTTTVDANTSLA; PVNVTTTVDANTSLAK; VNVTTTVDANTSLAKI; NVTTTVDANTSLAKIE; VTTTVDANTSLAKIEN; TTTVDANTSLAKIENA; TTVDANTSLAKIENAI; TVDANTSLAKIENAIR; VDANTSLAKIENAIRM; DANTSLAKIENAIRMI; ANTSLAKIENAIRMIS; NTSLAKIENAIRMISD; TSLAKIENAIRMISDQ; SLAKIENAIRMISDQR; LAKIENAIRMISDQRA; AKIENAIRMISDQRAN; KIENAIRMISDQRANL; IENAIRMISDQRANLG; ENAIRMISDQRANLGA; NAIRMISDQRANLGAF; AIRMISDQRANLGAFQ; IRMISDQRANLGAFQN; RMISDQRANLGAFQNR; MISDQRANLGAFQNRL; ISDQRANLGAFQNRLE; SDQRANLGAFQNRLES; DQRANLGAFQNRLESI; QRANLGAFQNRLESIK; RANLGAFQNRLESIKD; ANLGAFQNRLESIKDS; NLGAFQNRLESIKDST; LGAFQNRLESIKDSTE; GAFQNRLESIKDSTEY; AFQNRLESIKDSTEYA; FQNRLESIKDSTEYAI; QNRLESIKDSTEYAIE; NRLESIKDSTEYAIEN; RLESIKDSTEYAIENL; LESIKDSTEYAIENLK; ESIKDSTEYAIENLKA; SIKDSTEYAIENLKAS; IKDSTEYAIENLKASY; KDSTEYAIENLKASYA; DSTEYAIENLKASYAQ; STEYAIENLKASYAQI; TEYAIENLKASYAQIK; EYAIENLKASYAQIKD; YAIENLKASYAQIKDA; AIENLKASYAQIKDAT; IENLKASYAQIKDATM; ENLKASYAQIKDATMT; NLKASYAQIKDATMTD; LKASYAQIKDATMTDE; KASYAQIKDATMTDEV; ASYAQIKDATMTDEVV; SYAQIKDATMTDEVVA; YAQIKDATMTDEVVAS; AQIKDATMTDEVVAST; QIKDATMTDEVVASTT; IKDATMTDEVVASTTN; KDATMTDEVVASTTNS; DATMTDEVVASTTNSI; ATMTDEVVASTTNSIL; TMTDEVVASTTNSILT; MTDEVVASTTNSILTQ; TDEVVASTTNSILTQS; DEVVASTTNSILTQSA; EVVASTTNSILTQSAM; VVASTTNSILTQSAMA; VASTTNSILTQSAMAM; ASTTNSILTQSAMAMI;

	STTNSILTQSAMAMIA; TTNSILTQSAMAMIAQ; TNSILTQSAMAMIAQA; NSILTQSAMAMIAQAN; SILTQSAMAMIAQANQ; ILTQSAMAMIAQANQV; LTQSAMAMIAQANQVP; TQSAMAMIAQANQVPQ; QSAMAMIAQANQVPQY; SAMAMIAQANQVPQYV; AMAMIAQANQVPQYVL; MAMIAQANQVPQYVLS; AMIAQANQVPQYVLSL; MIAQANQVPQYVLSLL; IAQANQVPQYVLSLLR;
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen Vlse Of Borrelia Burgdorferi	13 mers: MRGSHHHHHHGSS; RGSHHHHHHGSSQ; GSHHHHHHGSSQV; SHHHHHHGSSQVA; HHHHHHGSSQVAD; HHHHHGSSQVADK; HHHHGSSQVADKD; HHHGSSQVADKDD; HHGSSQVADKDDP; HGSSQVADKDDPT; GSSQVADKDDPTN; SSQVADKDDPTNK; SQVADKDDPTNKF; QVADKDDPTNKFY; VADKDDPTNKFYQ; ADKDDPTNKFYQS; DKDDPTNKFYQSV; KDDPTNKFYQSVI; DDPTNKFYQSVIQ; DPTNKFYQSVIQL; PTNKFYQSVIQLG; TNKFYQSVIQLGN; NKFYQSVIQLGNG; KFYQSVIQLGNGF; FYQSVIQLGNGFL; YQSVIQLGNGFLD; QSVIQLGNGFLDV; SVIQLGNGFLDVF; VIQLGNGFLDVFT; IQLGNGFLDVFTS; QLGNGFLDVFTSF; LGNGFLDVFTSFG; GNGFLDVFTSFGG; NGFLDVFTSFGGL; GFLDVFTSFGGLV; FLDVFTSFGGLVA; LDVFTSFGGLVAE; DVFTSFGGLVAEA; VFTSFGGLVAEAF; FTSFGGLVAEAFG; TSFGGLVAEAFGF; SFGGLVAEAFGFK; FGGLVAEAFGFKS; GGLVAEAFGFKSD; GLVAEAFGFKSDP; LVAEAFGFKSDPK; VAEAFGFKSDPKK; AEAFGFKSDPKKS; EAFGFKSDPKKSD; AFGFKSDPKKSDV; FGFKSDPKKSDVK; GFKSDPKKSDVKT; FKSDPKKSDVKTY; KSDPKKSDVKTYF; SDPKKSDVKTYFT; DPKKSDVKTYFTT; PKKSDVKTYFTTV; KKSDVKTYFTTVA; KSDVKTYFTTVAA; SDVKTYFTTVAAK; DVKTYFTTVAAKL; VKTYFTTVAAKLE; KTYFTTVAAKLEK; TYFTTVAAKLEKT; YFTTVAAKLEKTK; FTTVAAKLEKTKT; TTVAAKLEKTKTD; TVAAKLEKTKTDL; VAAKLEKTKTDLN; AAKLEKTKTDLNS; AKLEKTKTDLNSL; KLEKTKTDLNSLP; LEKTKTDLNSLPK; EKTKTDLNSLPKE; KTKTDLNSLPKEK; TKTDLNSLPKEKS; KTDLNSLPKEKSD; TDLNSLPKEKSDI; DLNSLPKEKSDIS; LNSLPKEKSDISS; NSLPKEKSDISST; SLPKEKSDISSTT; LPKEKSDISSTTG; PKEKSDISSTTGK; KEKSDISSTTGKP; EKSDISSTTGKPD; KSDISSTTGKPDS; SDISSTTGKPDST; DISSTTGKPDSTG; ISSTTGKPDSTGS; SSTTGKPDSTGSV; STTGKPDSTGSVG; TTGKPDSTGSVGT; TGKPDSTGSVGTA; GKPDSTGSVGTAV; KPDSTGSVGTAVE; PDSTGSVGTAVEG; DSTGSVGTAVEGA; STGSVGTAVEGAI; TGSVGTAVEGAIK; GSVGTAVEGAIKE; SVGTAVEGAIKEV; VGTAVEGAIKEVS; GTAVEGAIKEVSE; TAVEGAIKEVSEL; AVEGAIKEVSELL; VEGAIKEVSELLD; EGAIKEVSELLDK; GAIKEVSELLDKL; AIKEVSELLDKLV; IKEVSELLDKLVK; KEVSELLDKLVKA; EVSELLDKLVKAV; VSELLDKLVKAVK; SELLDKLVKAVKT; ELLDKLVKAVKTA; LLDKLVKAVKTAE; LDKLVKAVKTAEG; DKLVKAVKTAEGA; KLVKAVKTAEGAS; LVKAVKTAEGASS; VKAVKTAEGASSG; KAVKTAEGASSGT; AVKTAEGASSGTA; VKTAEGASSGTAA; KTAEGASSGTAAI; TAEGASSGTAAIG; AEGASSGTAAIGE; EGASSGTAAIGEV; GASSGTAAIGEVV; ASSGTAAIGEVVA; SSGTAAIGEVVAD; SGTAAIGEVVADA; GTAAIGEVVADAD; TAAIGEVVADADA; AAIGEVVADADAA; AIGEVVADADAAK; IGEVVADADAAKV; GEVVADADAAKVA; EVVADADAAKVAD; VVADADAAKVADK; VADADAAKVADKA; ADADAAKVADKAS; DADAAKVADKASV; ADAAKVADKASVK; DAAKVADKASVKG; AAKVADKASVKGI; AKVADKASVKGIA; KVADKASVKGIAK; VADKASVKGIAKG; ADKASVKGIAKGI; DKASVKGIAKGIK; KASVKGIAKGIKE; ASVKGIAKGIKEI; SVKGIAKGIKEIV; VKGIAKGIKEIVE; KGIAKGIKEIVEA; GIAKGIKEIVEAA; IAKGIKEIVEAAG; AKGIKEIVEAAGG; KGIKEIVEAAGGS; GIKEIVEAAGGSE; IKEIVEAAGGSEK; KEIVEAAGGSEKL; EIVEAAGGSEKLK; IVEAAGGSEKLKA; VEAAGGSEKLKAV; EAAGGSEKLKAVA; AAGGSEKLKAVAA; AGGSEKLKAVAAA; GGSEKLKAVAAAK; GSEKLKAVAAAKG; SEKLKAVAAAKGE; EKLKAVAAAKGEN; KLKAVAAAKGENN; LKAVAAAKGENNK; KAVAAAKGENNKG; AVAAAKGENNKGA; VAAAKGENNKGAG; AAAKGENNKGAGK; AAKGENNKGAGKL; AKGENNKGAGKLF; KGENNKGAGKLFG; GENNKGAGKLFGK; ENNKGAGKLFGKA; NNKGAGKLFGKAG; NKGAGKLFGKAGA; KGAGKLFGKAGAA; GAGKLFGKAGAAA; AGKLFGKAGAAAH; GKLFGKAGAAAHG; KLFGKAGAAAHGD; LFGKAGAAAHGDS; FGKAGAAAHGDSE; GKAGAAAHGDSEA; KAGAAAHGDSEAA;

AGAAAHGDSEAAS; GAAAHGDSEAASK; AAAHGDSEAASKA; AAHGDSEAASKAA;
AHGDSEAASKAAG; HGDSEAASKAAGA; GDSEAASKAAGAV; DSEAASKAAGAVS;
SEAASKAAGAVSA; EAASKAAGAVSAV; AASKAAGAVSAVS; ASKAAGAVSAVSG;
SKAAGAVSAVSGE; KAAGAVSAVSGEQ; AAGAVSAVSGEQI; AGAVSAVSGEQIL;
GAVSAVSGEQILS; AVSAVSGEQILSA; VSAVSGEQILSAI; SAVSGEQILSAIV;
AVSGEQILSAIVT; VSGEQILSAIVTA; SGEQILSAIVTAA; GEQILSAIVTAAD;
EQILSAIVTAADA; QILSAIVTAADAA; ILSAIVTAADAAE; LSAIVTAADAAEQ;
SAIVTAADAAEQD; AIVTAADAAEQDG; IVTAADAAEQDGK; VTAADAAEQDGKK;
TAADAAEQDGKKP; AADAAEQDGKKPE; ADAAEQDGKKPEE; DAAEQDGKKPEEA;
AAEQDGKKPEEAK; AEQDGKKPEEAKN; EQDGKKPEEAKNP; QDGKKPEEAKNPI;
DGKKPEEAKNPIA; GKKPEEAKNPIAA; KKPEEAKNPIAAA; KPEEAKNPIAAAI;
PEEAKNPIAAAIG; EEAKNPIAAAIGD; EAKNPIAAAIGDK; AKNPIAAAIGDKD;
KNPIAAAIGDKDG; NPIAAAIGDKDGG; PIAAAIGDKDGGA; IAAAIGDKDGGAE;
AAAIGDKDGGAEF; AAIGDKDGGAEFG; AIGDKDGGAEFGQ; IGDKDGGAEFGQD;
GDKDGGAEFGQDE; DKDGGAEFGQDEX; KDGGAEFGQDEXK; DGGAEFGQDEXKK;
GGAEFGQDEXKKD; GAEFGQDEXKKDD; AEFGQDEXKKDDQ; EFGQDEXKKDDQI;
FGQDEXKKDDQIA; GQDEXKKDDQIAA; QDEXKKDDQIAAA; DEXKKDDQIAAAI;
EXKKDDQIAAAIA; XKKDDQIAAAIAL; KKDDQIAAAIALR; KDDQIAAAIALRG;
DDQIAAAIALRGX; DQIAAAIALRGXA; QIAAAIALRGXAK; IAAAIALRGXAKD;
AAAIALRGXAKDG; AAIALRGXAKDGK; AIALRGXAKDGKF; IALRGXAKDGKFA;
ALRGXAKDGKFAV; LRGXAKDGKFAVK; RGXAKDGKFAVKD; GXAKDGKFAVKDG;
XAKDGKFAVKDGE; AKDGKFAVKDGEK; KDGKFAVKDGEKE; DGKFAVKDGEKEK;
GKFAVKDGEKEKA; KFAVKDGEKEKAE; FAVKDGEKEKAEG; AVKDGEKEKAEGA;
VKDGEKEKAEGAI; KDGEKEKAEGAIK; DGEKEKAEGAIKG; GEKEKAEGAIKGA;
EKEKAEGAIKGAA; KEKAEGAIKGAAE; EKAEGAIKGAAES; KAEGAIKGAAESA;
AEGAIKGAAESAV; EGAIKGAAESAVR; GAIKGAAESAVRK; AIKGAAESAVRKV;
IKGAAESAVRKVL; KGAAESAVRKVLG; GAAESAVRKVLGA; AAESAVRKVLGAI;
AESAVRKVLGAIT; ESAVRKVLGAITG; SAVRKVLGAITGL; AVRKVLGAITGLI;
VRKVLGAITGLIG; RKVLGAITGLIGD; KVLGAITGLIGDA; VLGAITGLIGDAV;
LGAITGLIGDAVS; GAITGLIGDAVSS; AITGLIGDAVSSG; ITGLIGDAVSSGL;
TGLIGDAVSSGLR; GLIGDAVSSGLRK; LIGDAVSSGLRKV; IGDAVSSGLRKVG;
GDAVSSGLRKVGD; DAVSSGLRKVGDS; AVSSGLRKVGDSV; VSSGLRKVGDSVK;
SSGLRKVGDSVKA; SGLRKVGDSVKAA; GLRKVGDSVKAAS; LRKVGDSVKAASK;
RKVGDSVKAASKE; KVGDSVKAASKET; VGDSVKAASKETP; GDSVKAASKETPP;
DSVKAASKETPPA; SVKAASKETPPAL; VKAASKETPPALN; KAASKETPPALNK;

14 mers:
MRGSHHHHHHGSSQ; RGSHHHHHHGSSQV; GSHHHHHHGSSQVA;
SHHHHHHGSSQVAD; HHHHHHGSSQVADK; HHHHHGSSQVADKD;
HHHHGSSQVADKDD; HHHGSSQVADKDDP; HHGSSQVADKDDPT;
HGSSQVADKDDPTN; GSSQVADKDDPTNK; SSQVADKDDPTNKF;
SQVADKDDPTNKFY; QVADKDDPTNKFYQ; VADKDDPTNKFYQS;
ADKDDPTNKFYQSV; DKDDPTNKFYQSVI; KDDPTNKFYQSVIQ;
DDPTNKFYQSVIQL; DPTNKFYQSVIQLG; PTNKFYQSVIQLGN;
TNKFYQSVIQLGNG; NKFYQSVIQLGNGF; KFYQSVIQLGNGFL;
FYQSVIQLGNGFLD; YQSVIQLGNGFLDV; QSVIQLGNGFLDVF;
SVIQLGNGFLDVFT; VIQLGNGFLDVFTS; IQLGNGFLDVFTSF;
QLGNGFLDVFTSFG; LGNGFLDVFTSFGG; GNGFLDVFTSFGGL;
NGFLDVFTSFGGLV; GFLDVFTSFGGLVA; FLDVFTSFGGLVAE;
LDVFTSFGGLVAEA; DVFTSFGGLVAEAF; VFTSFGGLVAEAFG;
FTSFGGLVAEAFGF; TSFGGLVAEAFGFK; SFGGLVAEAFGFKS;
FGGLVAEAFGFKSD; GGLVAEAFGFKSDP; GLVAEAFGFKSDPK;
LVAEAFGFKSDPKK; VAEAFGFKSDPKKS; AEAFGFKSDPKKSD;
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GFKSDPKKSDVKTY; FKSDPKKSDVKTYF; KSDPKKSDVKTYFT;
SDPKKSDVKTYFTT; DPKKSDVKTYFTTV; PKKSDVKTYFTTVA;
KKSDVKTYFTTVAA; KSDVKTYFTTVAAK; SDVKTYFTTVAAKL;

	DVKTYFTTVAAKLE; VKTYFTTVAAKLEK; KTYFTTVAAKLEKT; TYFTTVAAKLEKTK; YFTTVAAKLEKTKT; FTTVAAKLEKTKTD; TTVAAKLEKTKTDL; TVAAKLEKTKTDLN; VAAKLEKTKTDLNS; AAKLEKTKTDLNSL; AKLEKTKTDLNSLP; KLEKTKTDLNSLPK; LEKTKTDLNSLPKE; EKTKTDLNSLPKEK; KTKTDLNSLPKEKS; TKTDLNSLPKEKSD; KTDLNSLPKEKSDI; TDLNSLPKEKSDIS; DLNSLPKEKSDISS; LNSLPKEKSDISST; NSLPKEKSDISSTT; SLPKEKSDISSTTG; LPKEKSDISSTTGK; PKEKSDISSTTGKP; KEKSDISSTTGKPD; EKSDISSTTGKPDS; KSDISSTTGKPDST; SDISSTTGKPDSTG; DISSTTGKPDSTGS; ISSTTGKPDSTGSV; SSTTGKPDSTGSVG; STTGKPDSTGSVGT; TTGKPDSTGSVGTA; TGKPDSTGSVGTAV; GKPDSTGSVGTAVE; KPDSTGSVGTAVEG; PDSTGSVGTAVEGA; DSTGSVGTAVEGAI; STGSVGTAVEGAIK; TGSVGTAVEGAIKE; GSVGTAVEGAIKEV; SVGTAVEGAIKEVS; VGTAVEGAIKEVSE; GTAVEGAIKEVSEL; TAVEGAIKEVSELL; AVEGAIKEVSELLD; VEGAIKEVSELLDK; EGAIKEVSELLDKL; GAIKEVSELLDKLV; AIKEVSELLDKLVK; IKEVSELLDKLVKA; KEVSELLDKLVKAV; EVSELLDKLVKAVK; VSELLDKLVKAVKT; SELLDKLVKAVKTA; ELLDKLVKAVKTAE; LLDKLVKAVKTAEG; LDKLVKAVKTAEGA; DKLVKAVKTAEGAS; KLVKAVKTAEGASS; LVKAVKTAEGASSG; VKAVKTAEGASSGT; KAVKTAEGASSGTA; AVKTAEGASSGTAA; VKTAEGASSGTAAI; KTAEGASSGTAAIG; TAEGASSGTAAIGE; AEGASSGTAAIGEV; EGASSGTAAIGEVV; GASSGTAAIGEVVA; ASSGTAAIGEVVAD; SSGTAAIGEVVADA; SGTAAIGEVVADAD; GTAAIGEVVADADA; TAAIGEVVADADAA; AAIGEVVADADAAK; AIGEVVADADAAKV; IGEVVADADAAKVA; GEVVADADAAKVAD; EVVADADAAKVADK; VVADADAAKVADKA; VADADAAKVADKAS; ADADAAKVADKASV; DADAAKVADKASVK; ADAAKVADKASVKG; DAAKVADKASVKGI; AAKVADKASVKGIA; AKVADKASVKGIAK; KVADKASVKGIAKG; VADKASVKGIAKGI; ADKASVKGIAKGIK; DKASVKGIAKGIKE; KASVKGIAKGIKEI; ASVKGIAKGIKEIV; SVKGIAKGIKEIVE; VKGIAKGIKEIVEA; KGIAKGIKEIVEAA; GIAKGIKEIVEAAG; IAKGIKEIVEAAGG; AKGIKEIVEAAGGS; KGIKEIVEAAGGSE; GIKEIVEAAGGSEK; IKEIVEAAGGSEKL; KEIVEAAGGSEKLK; EIVEAAGGSEKLKA; IVEAAGGSEKLKAV; VEAAGGSEKLKAVA; EAAGGSEKLKAVAA; AAGGSEKLKAVAAA; AGGSEKLKAVAAAK; GGSEKLKAVAAAKG; GSEKLKAVAAAKGE; SEKLKAVAAAKGEN; EKLKAVAAAKGENN; KLKAVAAAKGENNK; LKAVAAAKGENNKG; KAVAAAKGENNKGA; AVAAAKGENNKGAG; VAAAKGENNKGAGK; AAAKGENNKGAGKL; AAKGENNKGAGKLF; AKGENNKGAGKLFG; KGENNKGAGKLFGK; GENNKGAGKLFGKA; ENNKGAGKLFGKAG; NNKGAGKLFGKAGA; NKGAGKLFGKAGAA; KGAGKLFGKAGAAA; GAGKLFGKAGAAAH; AGKLFGKAGAAAHG; GKLFGKAGAAAHGD; KLFGKAGAAAHGDS; LFGKAGAAAHGDSE; FGKAGAAAHGDSEA; GKAGAAAHGDSEAA; KAGAAAHGDSEAAS; AGAAAHGDSEAASK; GAAAHGDSEAASKA; AAAHGDSEAASKAA; AAHGDSEAASKAAG; AHGDSEAASKAAGA; HGDSEAASKAAGAV; GDSEAASKAAGAVS; DSEAASKAAGAVSA; SEAASKAAGAVSAV; EAASKAAGAVSAVS; AASKAAGAVSAVSG; ASKAAGAVSAVSGE; SKAAGAVSAVSGEQ; KAAGAVSAVSGEQI; AAGAVSAVSGEQIL; AGAVSAVSGEQILS; GAVSAVSGEQILSA; AVSAVSGEQILSAI; VSAVSGEQILSAIV; SAVSGEQILSAIVT; AVSGEQILSAIVTA; VSGEQILSAIVTAA; SGEQILSAIVTAAD; GEQILSAIVTAADA; EQILSAIVTAADAA; QILSAIVTAADAAE; ILSAIVTAADAAEQ; LSAIVTAADAAEQD; SAIVTAADAAEQDG; AIVTAADAAEQDGK; IVTAADAAEQDGKK; VTAADAAEQDGKKP; TAADAAEQDGKKPE; AADAAEQDGKKPEE; ADAAEQDGKKPEEA;

DAAEQDGKKPEEAK; AAEQDGKKPEEAKN; AEQDGKKPEEAKNP;
EQDGKKPEEAKNPI; QDGKKPEEAKNPIA; DGKKPEEAKNPIAA;
GKKPEEAKNPIAAA; KKPEEAKNPIAAAI; KPEEAKNPIAAAIG;
PEEAKNPIAAAIGD; EEAKNPIAAAIGDK; EAKNPIAAAIGDKD;
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PIAAAIGDKDGGAE; IAAAIGDKDGGAEF; AAAIGDKDGGAEFG;
AAIGDKDGGAEFGQ; AIGDKDGGAEFGQD; IGDKDGGAEFGQDE;
GDKDGGAEFGQDEX; DKDGGAEFGQDEXK; KDGGAEFGQDEXKK;
DGGAEFGQDEXKKD; GGAEFGQDEXKKDD; GAEFGQDEXKKDDQ;
AEFGQDEXKKDDQI; EFGQDEXKKDDQIA; FGQDEXKKDDQIAA;
GQDEXKKDDQIAAA; QDEXKKDDQIAAAI; DEXKKDDQIAAAIA;
EXKKDDQIAAAIAL; XKKDDQIAAAIALR; KKDDQIAAAIALRG;
KDDQIAAAIALRGX; DDQIAAAIALRGXA; DQIAAAIALRGXAK;
QIAAAIALRGXAKD; IAAAIALRGXAKDG; AAAIALRGXAKDGK;
AAIALRGXAKDGKF; AIALRGXAKDGKFA; IALRGXAKDGKFAV;
ALRGXAKDGKFAVK; LRGXAKDGKFAVKD; RGXAKDGKFAVKDG;
GXAKDGKFAVKDGE; XAKDGKFAVKDGEK; AKDGKFAVKDGEKE;
KDGKFAVKDGEKEK; DGKFAVKDGEKEKA; GKFAVKDGEKEKAE;
KFAVKDGEKEKAEG; FAVKDGEKEKAEGA; AVKDGEKEKAEGAI;
VKDGEKEKAEGAIK; KDGEKEKAEGAIKG; DGEKEKAEGAIKGA;
GEKEKAEGAIKGAA; EKEKAEGAIKGAAE; KEKAEGAIKGAAES;
EKAEGAIKGAAESA; KAEGAIKGAAESAV; AEGAIKGAAESAVR;
EGAIKGAAESAVRK; GAIKGAAESAVRKV; AIKGAAESAVRKVL;
IKGAAESAVRKVLG; KGAAESAVRKVLGA; GAAESAVRKVLGAI;
AAESAVRKVLGAIT; AESAVRKVLGAITG; ESAVRKVLGAITGL;
SAVRKVLGAITGLI; AVRKVLGAITGLIG; VRKVLGAITGLIGD;
RKVLGAITGLIGDA; KVLGAITGLIGDAV; VLGAITGLIGDAVS;
LGAITGLIGDAVSS; GAITGLIGDAVSSG; AITGLIGDAVSSGL;
ITGLIGDAVSSGLR; TGLIGDAVSSGLRK; GLIGDAVSSGLRKV;
LIGDAVSSGLRKVG; IGDAVSSGLRKVGD; GDAVSSGLRKVGDS;
DAVSSGLRKVGDSV; AVSSGLRKVGDSVK; VSSGLRKVGDSVKA;
SSGLRKVGDSVKAA; SGLRKVGDSVKAAS; GLRKVGDSVKAASK;
LRKVGDSVKAASKE; RKVGDSVKAASKET; KVGDSVKAASKETP;
VGDSVKAASKETPP; GDSVKAASKETPPA; DSVKAASKETPPAL;
SVKAASKETPPALN; VKAASKETPPALNK;

15 mers:
MRGSHHHHHHGSSQV; RGSHHHHHHGSSQVA; GSHHHHHHGSSQVAD;
SHHHHHHGSSQVADK; HHHHHHGSSQVADKD; HHHHHGSSQVADKDD;
HHHHGSSQVADKDDP; HHHGSSQVADKDDPT; HHGSSQVADKDDPTN;
HGSSQVADKDDPTNK; GSSQVADKDDPTNKF; SSQVADKDDPTNKFY;
SQVADKDDPTNKFYQ; QVADKDDPTNKFYQS; VADKDDPTNKFYQSV;
ADKDDPTNKFYQSVI; DKDDPTNKFYQSVIQ; KDDPTNKFYQSVIQL;
DDPTNKFYQSVIQLG; DPTNKFYQSVIQLGN; PTNKFYQSVIQLGNG;
TNKFYQSVIQLGNGF; NKFYQSVIQLGNGFL; KFYQSVIQLGNGFLD;
FYQSVIQLGNGFLDV; YQSVIQLGNGFLDVF; QSVIQLGNGFLDVFT;
SVIQLGNGFLDVFTS; VIQLGNGFLDVFTSF; IQLGNGFLDVFTSFG;
QLGNGFLDVFTSFGG; LGNGFLDVFTSFGGL; GNGFLDVFTSFGGLV;
NGFLDVFTSFGGLVA; GFLDVFTSFGGLVAE; FLDVFTSFGGLVAEA;
LDVFTSFGGLVAEAF; DVFTSFGGLVAEAFG; VFTSFGGLVAEAFGF;
FTSFGGLVAEAFGFK; TSFGGLVAEAFGFKS; SFGGLVAEAFGFKSD;
FGGLVAEAFGFKSDP; GGLVAEAFGFKSDPK; GLVAEAFGFKSDPKK;
LVAEAFGFKSDPKKS; VAEAFGFKSDPKKSD; AEAFGFKSDPKKSDV;
EAFGFKSDPKKSDVK; AFGFKSDPKKSDVKT; FGFKSDPKKSDVKTY;
GFKSDPKKSDVKTYF; FKSDPKKSDVKTYFT; KSDPKKSDVKTYFTT;
SDPKKSDVKTYFTTV; DPKKSDVKTYFTTVA; PKKSDVKTYFTTVAA;
KKSDVKTYFTTVAAK; KSDVKTYFTTVAAKL; SDVKTYFTTVAAKLE;

	DVKTYFTTVAAKLEK; VKTYFTTVAAKLEKT; KTYFTTVAAKLEKTK; TYFTTVAAKLEKTKT; YFTTVAAKLEKTKTD; FTTVAAKLEKTKTDL; TTVAAKLEKTKTDLN; TVAAKLEKTKTDLNS; VAAKLEKTKTDLNSL; AAKLEKTKTDLNSLP; AKLEKTKTDLNSLPK; KLEKTKTDLNSLPKE; LEKTKTDLNSLPKEK; EKTKTDLNSLPKEKS; KTKTDLNSLPKEKSD; TKTDLNSLPKEKSDI; KTDLNSLPKEKSDIS; TDLNSLPKEKSDISS; DLNSLPKEKSDISST; LNSLPKEKSDISSTT; NSLPKEKSDISSTTG; SLPKEKSDISSTTGK; LPKEKSDISSTTGKP; PKEKSDISSTTGKPD; KEKSDISSTTGKPDS; EKSDISSTTGKPDST; KSDISSTTGKPDSTG; SDISSTTGKPDSTGS; DISSTTGKPDSTGSV; ISSTTGKPDSTGSVG; SSTTGKPDSTGSVGT; STTGKPDSTGSVGTA; TTGKPDSTGSVGTAV; TGKPDSTGSVGTAVE; GKPDSTGSVGTAVEG; KPDSTGSVGTAVEGA; PDSTGSVGTAVEGAI; DSTGSVGTAVEGAIK; STGSVGTAVEGAIKE; TGSVGTAVEGAIKEV; GSVGTAVEGAIKEVS; SVGTAVEGAIKEVSE; VGTAVEGAIKEVSEL; GTAVEGAIKEVSELL; TAVEGAIKEVSELLD; AVEGAIKEVSELLDK; VEGAIKEVSELLDKL; EGAIKEVSELLDKLV; GAIKEVSELLDKLVK; AIKEVSELLDKLVKA; IKEVSELLDKLVKAV; KEVSELLDKLVKAVK; EVSELLDKLVKAVKT; VSELLDKLVKAVKTA; SELLDKLVKAVKTAE; ELLDKLVKAVKTAEG; LLDKLVKAVKTAEGA; LDKLVKAVKTAEGAS; DKLVKAVKTAEGASS; KLVKAVKTAEGASSG; LVKAVKTAEGASSGT; VKAVKTAEGASSGTA; KAVKTAEGASSGTAA; AVKTAEGASSGTAAI; VKTAEGASSGTAAIG; KTAEGASSGTAAIGE; TAEGASSGTAAIGEV; AEGASSGTAAIGEVV; EGASSGTAAIGEVVA; GASSGTAAIGEVVAD; ASSGTAAIGEVVADA; SSGTAAIGEVVADAD; SGTAAIGEVVADADA; GTAAIGEVVADADAA; TAAIGEVVADADAAK; AAIGEVVADADAAKV; AIGEVVADADAAKVA; IGEVVADADAAKVAD; GEVVADADAAKVADK; EVVADADAAKVADKA; VVADADAAKVADKAS; VADADAAKVADKASV; ADADAAKVADKASVK; DADAAKVADKASVKG; ADAAKVADKASVKGI; DAAKVADKASVKGIA; AAKVADKASVKGIAK; AKVADKASVKGIAKG; KVADKASVKGIAKGI; VADKASVKGIAKGIK; ADKASVKGIAKGIKE; DKASVKGIAKGIKEI; KASVKGIAKGIKEIV; ASVKGIAKGIKEIVE; SVKGIAKGIKEIVEA; VKGIAKGIKEIVEAA; KGIAKGIKEIVEAAG; GIAKGIKEIVEAAGG; IAKGIKEIVEAAGGS; AKGIKEIVEAAGGSE; KGIKEIVEAAGGSEK; GIKEIVEAAGGSEKL; IKEIVEAAGGSEKLK; KEIVEAAGGSEKLKA; EIVEAAGGSEKLKAV; IVEAAGGSEKLKAVA; VEAAGGSEKLKAVAA; EAAGGSEKLKAVAAA; AAGGSEKLKAVAAAK; AGGSEKLKAVAAAKG; GGSEKLKAVAAAKGE; GSEKLKAVAAAKGEN; SEKLKAVAAAKGENN; EKLKAVAAAKGENNK; KLKAVAAAKGENNKG; LKAVAAAKGENNKGA; KAVAAAKGENNKGAG; AVAAAKGENNKGAGK; VAAAKGENNKGAGKL; AAAKGENNKGAGKLF; AAKGENNKGAGKLFG; AKGENNKGAGKLFGK; KGENNKGAGKLFGKA; GENNKGAGKLFGKAG; ENNKGAGKLFGKAGA; NNKGAGKLFGKAGAA; NKGAGKLFGKAGAAA; KGAGKLFGKAGAAAH; GAGKLFGKAGAAAHG; AGKLFGKAGAAAHGD; GKLFGKAGAAAHGDS; KLFGKAGAAAHGDSE; LFGKAGAAAHGDSEA; FGKAGAAAHGDSEAA; GKAGAAAHGDSEAAS; KAGAAAHGDSEAASK; AGAAAHGDSEAASKA; GAAAHGDSEAASKAA; AAAHGDSEAASKAAG; AAHGDSEAASKAAGA; AHGDSEAASKAAGAV; HGDSEAASKAAGAVS; GDSEAASKAAGAVSA; DSEAASKAAGAVSAV; SEAASKAAGAVSAVS; EAASKAAGAVSAVSG; AASKAAGAVSAVSGE; ASKAAGAVSAVSGEQ; SKAAGAVSAVSGEQI; KAAGAVSAVSGEQIL; AAGAVSAVSGEQILS; AGAVSAVSGEQILSA; GAVSAVSGEQILSAI; AVSAVSGEQILSAIV; VSAVSGEQILSAIVT; SAVSGEQILSAIVTA; AVSGEQILSAIVTAA; VSGEQILSAIVTAAD; SGEQILSAIVTAADA; GEQILSAIVTAADAA; EQILSAIVTAADAAE; QILSAIVTAADAAEQ; ILSAIVTAADAAEQD; LSAIVTAADAAEQDG; SAIVTAADAAEQDGK; AIVTAADAAEQDGKK; IVTAADAAEQDGKKP; VTAADAAEQDGKKPE; TAADAAEQDGKKPEE; AADAAEQDGKKPEEA; ADAAEQDGKKPEEAK;

DAAEQDGKKPEEAKN; AAEQDGKKPEEAKNP; AEQDGKKPEEAKNPI;
EQDGKKPEEAKNPIA; QDGKKPEEAKNPIAA; DGKKPEEAKNPIAAA;
GKKPEEAKNPIAAAI; KKPEEAKNPIAAAIG; KPEEAKNPIAAAIGD;
PEEAKNPIAAAIGDK; EEAKNPIAAAIGDKD; EAKNPIAAAIGDKDG;
AKNPIAAAIGDKDGG; KNPIAAAIGDKDGGA; NPIAAAIGDKDGGAE;
PIAAAIGDKDGGAEF; IAAAIGDKDGGAEFG; AAAIGDKDGGAEFGQ;
AAIGDKDGGAEFGQD; AIGDKDGGAEFGQDE; IGDKDGGAEFGQDEX;
GDKDGGAEFGQDEXK; DKDGGAEFGQDEXKK; KDGGAEFGQDEXKKD;
DGGAEFGQDEXKKDD; GGAEFGQDEXKKDDQ; GAEFGQDEXKKDDQI;
AEFGQDEXKKDDQIA; EFGQDEXKKDDQIAA; FGQDEXKKDDQIAAA;
GQDEXKKDDQIAAAI; QDEXKKDDQIAAAIA; DEXKKDDQIAAAIAL;
EXKKDDQIAAAIALR; XKKDDQIAAAIALRG; KKDDQIAAAIALRGX;
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QIAAAIALRGXAKDG; IAAAIALRGXAKDGK; AAAIALRGXAKDGKF;
AAIALRGXAKDGKFA; AIALRGXAKDGKFAV; IALRGXAKDGKFAVK;
ALRGXAKDGKFAVKD; LRGXAKDGKFAVKDG; RGXAKDGKFAVKDGE;
GXAKDGKFAVKDGEK; XAKDGKFAVKDGEKE; AKDGKFAVKDGEKEK;
KDGKFAVKDGEKEKA; DGKFAVKDGEKEKAE; GKFAVKDGEKEKAEG;
KFAVKDGEKEKAEGA; FAVKDGEKEKAEGAI; AVKDGEKEKAEGAIK;
VKDGEKEKAEGAIKG; KDGEKEKAEGAIKGA; DGEKEKAEGAIKGAA;
GEKEKAEGAIKGAAE; EKEKAEGAIKGAAES; KEKAEGAIKGAAESA;
EKAEGAIKGAAESAV; KAEGAIKGAAESAVR; AEGAIKGAAESAVRK;
EGAIKGAAESAVRKV; GAIKGAAESAVRKVL; AIKGAAESAVRKVLG;
IKGAAESAVRKVLGA; KGAAESAVRKVLGAI; GAAESAVRKVLGAIT;
AAESAVRKVLGAITG; AESAVRKVLGAITGL; ESAVRKVLGAITGLI;
SAVRKVLGAITGLIG; AVRKVLGAITGLIGD; VRKVLGAITGLIGDA;
RKVLGAITGLIGDAV; KVLGAITGLIGDAVS; VLGAITGLIGDAVSS;
LGAITGLIGDAVSSG; GAITGLIGDAVSSGL; AITGLIGDAVSSGLR;
ITGLIGDAVSSGLRK; TGLIGDAVSSGLRKV; GLIGDAVSSGLRKVG;
LIGDAVSSGLRKVGD; IGDAVSSGLRKVGDS; GDAVSSGLRKVGDSV;
DAVSSGLRKVGDSVK; AVSSGLRKVGDSVKA; VSSGLRKVGDSVKAA;
SSGLRKVGDSVKAAS; SGLRKVGDSVKAASK; GLRKVGDSVKAASKE;
LRKVGDSVKAASKET; RKVGDSVKAASKETP; KVGDSVKAASKETPP;
VGDSVKAASKETPPA; GDSVKAASKETPPAL; DSVKAASKETPPALN;
SVKAASKETPPALNK;

16 mers:
MRGSHHHHHHGSSQVA; RGSHHHHHHGSSQVAD; GSHHHHHHGSSQVADK;
SHHHHHHGSSQVADKD; HHHHHHGSSQVADKDD; HHHHHGSSQVADKDDP;
HHHHGSSQVADKDDPT; HHHGSSQVADKDDPTN; HHGSSQVADKDDPTNK;
HGSSQVADKDDPTNKF; GSSQVADKDDPTNKFY; SSQVADKDDPTNKFYQ;
SQVADKDDPTNKFYQS; QVADKDDPTNKFYQSV; VADKDDPTNKFYQSVI;
ADKDDPTNKFYQSVIQ; DKDDPTNKFYQSVIQL; KDDPTNKFYQSVIQLG;
DDPTNKFYQSVIQLGN; DPTNKFYQSVIQLGNG; PTNKFYQSVIQLGNGF;
TNKFYQSVIQLGNGFL; NKFYQSVIQLGNGFLD; KFYQSVIQLGNGFLDV;
FYQSVIQLGNGFLDVF; YQSVIQLGNGFLDVFT; QSVIQLGNGFLDVFTS;
SVIQLGNGFLDVFTSF; VIQLGNGFLDVFTSFG; IQLGNGFLDVFTSFGG;
QLGNGFLDVFTSFGGL; LGNGFLDVFTSFGGLV; GNGFLDVFTSFGGLVA;
NGFLDVFTSFGGLVAE; GFLDVFTSFGGLVAEA; FLDVFTSFGGLVAEAF;
LDVFTSFGGLVAEAFG; DVFTSFGGLVAEAFGF; VFTSFGGLVAEAFGFK;
FTSFGGLVAEAFGFKS; TSFGGLVAEAFGFKSD; SFGGLVAEAFGFKSDP;
FGGLVAEAFGFKSDPK; GGLVAEAFGFKSDPKK; GLVAEAFGFKSDPKKS;
LVAEAFGFKSDPKKSD; VAEAFGFKSDPKKSDV; AEAFGFKSDPKKSDVK;
EAFGFKSDPKKSDVKT; AFGFKSDPKKSDVKTY; FGFKSDPKKSDVKTYF;
GFKSDPKKSDVKTYFT; FKSDPKKSDVKTYFTT; KSDPKKSDVKTYFTTV;
SDPKKSDVKTYFTTVA; DPKKSDVKTYFTTVAA; PKKSDVKTYFTTVAAK;
KKSDVKTYFTTVAAKL; KSDVKTYFTTVAAKLE; SDVKTYFTTVAAKLEK;

	DVKTYFTTVAAKLEKT; VKTYFTTVAAKLEKTK; KTYFTTVAAKLEKTKT; TYFTTVAAKLEKTKTD; YFTTVAAKLEKTKTDL; FTTVAAKLEKTKTDLN; TTVAAKLEKTKTDLNS; TVAAKLEKTKTDLNSL; VAAKLEKTKTDLNSLP; AAKLEKTKTDLNSLPK; AKLEKTKTDLNSLPKE; KLEKTKTDLNSLPKEK; LEKTKTDLNSLPKEKS; EKTKTDLNSLPKEKSD; KTKTDLNSLPKEKSDI; TKTDLNSLPKEKSDIS; KTDLNSLPKEKSDISS; TDLNSLPKEKSDISST; DLNSLPKEKSDISSTT; LNSLPKEKSDISSTTG; NSLPKEKSDISSTTGK; SLPKEKSDISSTTGKP; LPKEKSDISSTTGKPD; PKEKSDISSTTGKPDS; KEKSDISSTTGKPDST; EKSDISSTTGKPDSTG; KSDISSTTGKPDSTGS; SDISSTTGKPDSTGSV; DISSTTGKPDSTGSVG; ISSTTGKPDSTGSVGT; SSTTGKPDSTGSVGTA; STTGKPDSTGSVGTAV; TTGKPDSTGSVGTAVE; TGKPDSTGSVGTAVEG; GKPDSTGSVGTAVEGA; KPDSTGSVGTAVEGAI; PDSTGSVGTAVEGAIK; DSTGSVGTAVEGAIKE; STGSVGTAVEGAIKEV; TGSVGTAVEGAIKEVS; GSVGTAVEGAIKEVSE; SVGTAVEGAIKEVSEL; VGTAVEGAIKEVSELL; GTAVEGAIKEVSELLD; TAVEGAIKEVSELLDK; AVEGAIKEVSELLDKL; VEGAIKEVSELLDKLV; EGAIKEVSELLDKLVK; GAIKEVSELLDKLVKA; AIKEVSELLDKLVKAV; IKEVSELLDKLVKAVK; KEVSELLDKLVKAVKT; EVSELLDKLVKAVKTA; VSELLDKLVKAVKTAE; SELLDKLVKAVKTAEG; ELLDKLVKAVKTAEGA; LLDKLVKAVKTAEGAS; LDKLVKAVKTAEGASS; DKLVKAVKTAEGASSG; KLVKAVKTAEGASSGT; LVKAVKTAEGASSGTA; VKAVKTAEGASSGTAA; KAVKTAEGASSGTAAI; AVKTAEGASSGTAAIG; VKTAEGASSGTAAIGE; KTAEGASSGTAAIGEV; TAEGASSGTAAIGEVV; AEGASSGTAAIGEVVA; EGASSGTAAIGEVVAD; GASSGTAAIGEVVADA; ASSGTAAIGEVVADAD; SSGTAAIGEVVADADA; SGTAAIGEVVADADAA; GTAAIGEVVADADAAK; TAAIGEVVADADAAKV; AAIGEVVADADAAKVA; AIGEVVADADAAKVAD; IGEVVADADAAKVADK; GEVVADADAAKVADKA; EVVADADAAKVADKAS; VVADADAAKVADKASV; VADADAAKVADKASVK; ADADAAKVADKASVKG; DADAAKVADKASVKGI; ADAAKVADKASVKGIA; DAAKVADKASVKGIAK; AAKVADKASVKGIAKG; AKVADKASVKGIAKGI; KVADKASVKGIAKGIK; VADKASVKGIAKGIKE; ADKASVKGIAKGIKEI; DKASVKGIAKGIKEIV; KASVKGIAKGIKEIVE; ASVKGIAKGIKEIVEA; SVKGIAKGIKEIVEAA; VKGIAKGIKEIVEAAG; KGIAKGIKEIVEAAGG; GIAKGIKEIVEAAGGS; IAKGIKEIVEAAGGSE; AKGIKEIVEAAGGSEK; KGIKEIVEAAGGSEKL; GIKEIVEAAGGSEKLK; IKEIVEAAGGSEKLKA; KEIVEAAGGSEKLKAV; EIVEAAGGSEKLKAVA; IVEAAGGSEKLKAVAA; VEAAGGSEKLKAVAAA; EAAGGSEKLKAVAAAK; AAGGSEKLKAVAAAKG; AGGSEKLKAVAAAKGE; GGSEKLKAVAAAKGEN; GSEKLKAVAAAKGENN; SEKLKAVAAAKGENNK; EKLKAVAAAKGENNKG; KLKAVAAAKGENNKGA; LKAVAAAKGENNKGAG; KAVAAAKGENNKGAGK; AVAAAKGENNKGAGKL; VAAAKGENNKGAGKLF; AAAKGENNKGAGKLFG; AAKGENNKGAGKLFGK; AKGENNKGAGKLFGKA; KGENNKGAGKLFGKAG; GENNKGAGKLFGKAGA; ENNKGAGKLFGKAGAA; NNKGAGKLFGKAGAAA; NKGAGKLFGKAGAAAH; KGAGKLFGKAGAAAHG; GAGKLFGKAGAAAHGD; AGKLFGKAGAAAHGDS; GKLFGKAGAAAHGDSE; KLFGKAGAAAHGDSEA; LFGKAGAAAHGDSEAA; FGKAGAAAHGDSEAAS; GKAGAAAHGDSEAASK; KAGAAAHGDSEAASKA; AGAAAHGDSEAASKAA; GAAAHGDSEAASKAAG; AAAHGDSEAASKAAGA; AAHGDSEAASKAAGAV; AHGDSEAASKAAGAVS; HGDSEAASKAAGAVSA; GDSEAASKAAGAVSAV; DSEAASKAAGAVSAVS; SEAASKAAGAVSAVSG; EAASKAAGAVSAVSGE; AASKAAGAVSAVSGEQ; ASKAAGAVSAVSGEQI; SKAAGAVSAVSGEQIL; KAAGAVSAVSGEQILS; AAGAVSAVSGEQILSA; AGAVSAVSGEQILSAI; GAVSAVSGEQILSAIV; AVSAVSGEQILSAIVT; VSAVSGEQILSAIVTA; SAVSGEQILSAIVTAA; AVSGEQILSAIVTAAD; VSGEQILSAIVTAADA; SGEQILSAIVTAADAA; GEQILSAIVTAADAAE; EQILSAIVTAADAAEQ; QILSAIVTAADAAEQD; ILSAIVTAADAAEQDG; LSAIVTAADAAEQDGK; SAIVTAADAAEQDGKK; AIVTAADAAEQDGKKP; IVTAADAAEQDGKKPE; VTAADAAEQDGKKPEE; TAADAAEQDGKKPEEA; AADAAEQDGKKPEEAK; ADAAEQDGKKPEEAKN;

	DAAEQDGKKPEEAKNP; AAEQDGKKPEEAKNPI; AEQDGKKPEEAKNPIA; EQDGKKPEEAKNPIAA; QDGKKPEEAKNPIAAA; DGKKPEEAKNPIAAAI; GKKPEEAKNPIAAAIG; KKPEEAKNPIAAAIGD; KPEEAKNPIAAAIGDK; PEEAKNPIAAAIGDKD; EEAKNPIAAAIGDKDG; EAKNPIAAAIGDKDGG; AKNPIAAAIGDKDGGA; KNPIAAAIGDKDGGAE; NPIAAAIGDKDGGAEF; PIAAAIGDKDGGAEFG; IAAAIGDKDGGAEFGQ; AAAIGDKDGGAEFGQD; AAIGDKDGGAEFGQDE; AIGDKDGGAEFGQDEX; IGDKDGGAEFGQDEXK; GDKDGGAEFGQDEXKK; DKDGGAEFGQDEXKKD; KDGGAEFGQDEXKKDD; DGGAEFGQDEXKKDDQ; GGAEFGQDEXKKDDQI; GAEFGQDEXKKDDQIA; AEFGQDEXKKDDQIAA; EFGQDEXKKDDQIAAA; FGQDEXKKDDQIAAAI; GQDEXKKDDQIAAAIA; QDEXKKDDQIAAAIAL; DEXKKDDQIAAAIALR; EXKKDDQIAAAIALRG; XKKDDQIAAAIALRGX; KKDDQIAAAIALRGXA; KDDQIAAAIALRGXAK; DDQIAAAIALRGXAKD; DQIAAAIALRGXAKDG; QIAAAIALRGXAKDGK; IAAAIALRGXAKDGKF; AAAIALRGXAKDGKFA; AAIALRGXAKDGKFAV; AIALRGXAKDGKFAVK; IALRGXAKDGKFAVKD; ALRGXAKDGKFAVKDG; LRGXAKDGKFAVKDGE; RGXAKDGKFAVKDGEK; GXAKDGKFAVKDGEKE; XAKDGKFAVKDGEKEK; AKDGKFAVKDGEKEKA; KDGKFAVKDGEKEKAE; DGKFAVKDGEKEKAEG; GKFAVKDGEKEKAEGA; KFAVKDGEKEKAEGAI; FAVKDGEKEKAEGAIK; AVKDGEKEKAEGAIKG; VKDGEKEKAEGAIKGA; KDGEKEKAEGAIKGAA; DGEKEKAEGAIKGAAE; GEKEKAEGAIKGAAES; EKEKAEGAIKGAAESA; KEKAEGAIKGAAESAV; EKAEGAIKGAAESAVR; KAEGAIKGAAESAVRK; AEGAIKGAAESAVRKV; EGAIKGAAESAVRKVL; GAIKGAAESAVRKVLG; AIKGAAESAVRKVLGA; IKGAAESAVRKVLGAI; KGAAESAVRKVLGAIT; GAAESAVRKVLGAITG; AAESAVRKVLGAITGL; AESAVRKVLGAITGLI; ESAVRKVLGAITGLIG; SAVRKVLGAITGLIGD; AVRKVLGAITGLIGDA; VRKVLGAITGLIGDAV; RKVLGAITGLIGDAVS; KVLGAITGLIGDAVSS; VLGAITGLIGDAVSSG; LGAITGLIGDAVSSGL; GAITGLIGDAVSSGLR; AITGLIGDAVSSGLRK; ITGLIGDAVSSGLRKV; TGLIGDAVSSGLRKVG; GLIGDAVSSGLRKVGD; LIGDAVSSGLRKVGDS; IGDAVSSGLRKVGDSV; GDAVSSGLRKVGDSVK; DAVSSGLRKVGDSVKA; AVSSGLRKVGDSVKAA; VSSGLRKVGDSVKAAS; SSGLRKVGDSVKAASK; SGLRKVGDSVKAASKE; GLRKVGDSVKAASKET; LRKVGDSVKAASKETP; RKVGDSVKAASKETPP; KVGDSVKAASKETPPA; VGDSVKAASKETPPAL; GDSVKAASKETPPALN; DSVKAASKETPPALNK;
CAA57807.1 Associated protein A (BapA)[Borrelia burgdorferi]	13 mers: MKKISLLIFLFLF; KKISLLIFLFLFV; KISLLIFLFLFVV; ISLLIFLFLFVVS; SLLIFLFLFVVSL; LLIFLFLFVVSLS; LIFLFLFVVSLSA; IFLFLFVVSLSAN; FLFLFVVSLSANI; LFLFVVSLSANIE; LFLFVVSLSANIEE; LFVVSLSANIEEN; FVVSLSANIEENY; VVSLSANIEENYT; VSLSANIEENYTE; SLSANIEENYTET; LSANIEENYTETK; SANIEENYTETKR; ANIEENYTETKRA; NIEENYTETKRAF; IEENYTETKRAFS; EENYTETKRAFSK; ENYTETKRAFSKE; NYTETKRAFSKED; YTETKRAFSKEDF; TETKRAFSKEDFN; ETKRAFSKEDFNL; TKRAFSKEDFNLI; KRAFSKEDFNLIN; RAFSKEDFNLINK; AFSKEDFNLINKR; FSKEDFNLINKRL; SKEDFNLINKRLD; KEDFNLINKRLDN; EDFNLINKRLDNY; DFNLINKRLDNYD; FNLINKRLDNYDF; NLINKRLDNYDFK; LINKRLDNYDFKN; INKRLDNYDFKNE; NKRLDNYDFKNEY; KRLDNYDFKNEYE; RLDNYDFKNEYEK; LDNYDFKNEYEKS; DNYDFKNEYEKSH; NYDFKNEYEKSHV; YDFKNEYEKSHVF; DFKNEYEKSHVFS; FKNEYEKSHVFSD; KNEYEKSHVFSDA; NEYEKSHVFSDAP; EYEKSHVFSDAPR; YEKSHVFSDAPRI; EKSHVFSDAPRIR; KSHVFSDAPRIRG; SHVFSDAPRIRGD; HVFSDAPRIRGDL; VFSDAPRIRGDLR; FSDAPRIRGDLRK; SDAPRIRGDLRKI; DAPRIRGDLRKIG; APRIRGDLRKIGI; PRIRGDLRKIGIK; RIRGDLRKIGIKE; IRGDLRKIGIKEK; RGDLRKIGIKEKS; GDLRKIGIKEKSV; DLRKIGIKEKSVF; LRKIGIKEKSVFL; RKIGIKEKSVFLD; KIGIKEKSVFLDA; IGIKEKSVFLDAL; GIKEKSVFLDALE; IKEKSVFLDALEA; KEKSVFLDALEAI; EKSVFLDALEAIE; KSVFLDALEAIEY; SVFLDALEAIEYL; VFLDALEAIEYLI; FLDALEAIEYLIK;

LDALEAIEYLIKI; DALEAIEYLIKIK; ALEAIEYLIKIKI; LEAIEYLIKIKIS;
EAIEYLIKIKIST; AIEYLIKIKISTD; IEYLIKIKISTDS; EYLIKIKISTDSI;
YLIKIKISTDSIF; LIKIKISTDSIFL; IKIKISTDSIFLS; KIKISTDSIFLSE;
IKISTDSIFLSED; KISTDSIFLSEDM; ISTDSIFLSEDMI; STDSIFLSEDMIR;
TDSIFLSEDMIRL; DSIFLSEDMIRLI; SIFLSEDMIRLIG; IFLSEDMIRLIGS;
FLSEDMIRLIGSY; LSEDMIRLIGSYP; SEDMIRLIGSYPD; EDMIRLIGSYPDS;
DMIRLIGSYPDSI; MIRLIGSYPDSIF; IRLIGSYPDSIFN; RLIGSYPDSIFNY;
LIGSYPDSIFNYL; IGSYPDSIFNYLI; GSYPDSIFNYLIQ; SYPDSIFNYLIQL;
YPDSIFNYLIQLN; PDSIFNYLIQLNS; DSIFNYLIQLNSD; SIFNYLIQLNSDK;
IFNYLIQLNSDKI; FNYLIQLNSDKID; NYLIQLNSDKIDY; YLIQLNSDKIDYA;
LIQLNSDKIDYAE; IQLNSDKIDYAEK; QLNSDKIDYAEKY; LNSDKIDYAEKYG;
NSDKIDYAEKYGD; SDKIDYAEKYGDN; DKIDYAEKYGDNA; KIDYAEKYGDNAR;
IDYAEKYGDNARN; DYAEKYGDNARNN; YAEKYGDNARNNF; AEKYGDNARNNFK;
EKYGDNARNNFKK; KYGDNARNNFKKD; YGDNARNNFKKDY; GDNARNNFKKDYS;
DNARNNFKKDYSE; NARNNFKKDYSED; ARNNFKKDYSEDK; RNNFKKDYSEDKA;
NNFKKDYSEDKAN; NFKKDYSEDKANT; FKKDYSEDKANTV; KKDYSEDKANTVK;
KDYSEDKANTVKQ; DYSEDKANTVKQI; YSEDKANTVKQIL; SEDKANTVKQILK;
EDKANTVKQILKQ; DKANTVKQILKQI; KANTVKQILKQIL; ANTVKQILKQILA;
NTVKQILKQILAD; TVKQILKQILADL; VKQILKQILADLP; KQILKQILADLPK;
QILKQILADLPKD;

14 mers:
MKKISLLIFLFLFV; KKISLLIFLFLFVV; KISLLIFLFLFVVS;
ISLLIFLFLFVVSL; SLLIFLFLFVVSLS; LLIFLFLFVVSLSA;
LIFLFLFVVSLSAN; IFLFLFVVSLSANI; FLFLFVVSLSANIE;
LFLFVVSLSANIEE; FLFVVSLSANIEEN; LFVVSLSANIEENY;
FVVSLSANIEENYT; VVSLSANIEENYTE; VSLSANIEENYTET;
SLSANIEENYTETK; LSANIEENYTETKR; SANIEENYTETKRA;
ANIEENYTETKRAF; NIEENYTETKRAFS; IEENYTETKRAFSK;
EENYTETKRAFSKE; ENYTETKRAFSKED; NYTETKRAFSKEDF;
YTETKRAFSKEDFN; TETKRAFSKEDFNL; ETKRAFSKEDFNLI;
TKRAFSKEDFNLIN; KRAFSKEDFNLINK; RAFSKEDFNLINKR;
AFSKEDFNLINKRL; FSKEDFNLINKRLD; SKEDFNLINKRLDN;
KEDFNLINKRLDNY; EDFNLINKRLDNYD; DFNLINKRLDNYDF;
FNLINKRLDNYDFK; NLINKRLDNYDFKN; LINKRLDNYDFKNE;
INKRLDNYDFKNEY; NKRLDNYDFKNEYE; KRLDNYDFKNEYEK;
RLDNYDFKNEYEKS; LDNYDFKNEYEKSH; DNYDFKNEYEKSHV;
NYDFKNEYEKSHVF; YDFKNEYEKSHVFS; DFKNEYEKSHVFSD;
FKNEYEKSHVFSDA; KNEYEKSHVFSDAP; NEYEKSHVFSDAPR;
EYEKSHVFSDAPRI; YEKSHVFSDAPRIR; EKSHVFSDAPRIRG;
KSHVFSDAPRIRGD; SHVFSDAPRIRGDL; HVFSDAPRIRGDLR;
VFSDAPRIRGDLRK; FSDAPRIRGDLRKI; SDAPRIRGDLRKIG;
DAPRIRGDLRKIGI; APRIRGDLRKIGIK; PRIRGDLRKIGIKE;
RIRGDLRKIGIKEK; IRGDLRKIGIKEKS; RGDLRKIGIKEKSV;
GDLRKIGIKEKSVF; DLRKIGIKEKSVFL; LRKIGIKEKSVFLD;
RKIGIKEKSVFLDA; KIGIKEKSVFLDAL; IGIKEKSVFLDALE;
GIKEKSVFLDALEA; IKEKSVFLDALEAI; KEKSVFLDALEAIE;
EKSVFLDALEAIEY; KSVFLDALEAIEYL; SVFLDALEAIEYLI;
VFLDALEAIEYLIK; FLDALEAIEYLIKI; LDALEAIEYLIKIK;
DALEAIEYLIKIKI; ALEAIEYLIKIKIS; LEAIEYLIKIKIST;
EAIEYLIKIKISTD; AIEYLIKIKISTDS; IEYLIKIKISTDSI;
EYLIKIKISTDSIF; YLIKIKISTDSIFL; LIKIKISTDSIFLS;
IKIKISTDSIFLSE; KIKISTDSIFLSED; IKISTDSIFLSEDM;
KISTDSIFLSEDMI; ISTDSIFLSEDMIR; STDSIFLSEDMIRL;
TDSIFLSEDMIRLI; DSIFLSEDMIRLIG; SIFLSEDMIRLIGS;
IFLSEDMIRLIGSY; FLSEDMIRLIGSYP; LSEDMIRLIGSYPD;
SEDMIRLIGSYPDS; EDMIRLIGSYPDSI; DMIRLIGSYPDSIF;

MIRLIGSYPDSIFN; IRLIGSYPDSIFNY; RLIGSYPDSIFNYL;
LIGSYPDSIFNYLI; IGSYPDSIFNYLIQ; GSYPDSIFNYLIQL;
SYPDSIFNYLIQLN; YPDSIFNYLIQLNS; PDSIFNYLIQLNSD;
DSIFNYLIQLNSDK; SIFNYLIQLNSDKI; IFNYLIQLNSDKID;
FNYLIQLNSDKIDY; NYLIQLNSDKIDYA; YLIQLNSDKIDYAE;
LIQLNSDKIDYAEK; IQLNSDKIDYAEKY; QLNSDKIDYAEKYG;
LNSDKIDYAEKYGD; NSDKIDYAEKYGDN; SDKIDYAEKYGDNA;
DKIDYAEKYGDNAR; KIDYAEKYGDNARN; IDYAEKYGDNARNN;
DYAEKYGDNARNNF; YAEKYGDNARNNFK; AEKYGDNARNNFKK;
EKYGDNARNNFKKD; KYGDNARNNFKKDY; YGDNARNNFKKDYS;
GDNARNNFKKDYSE; DNARNNFKKDYSED; NARNNFKKDYSEDK;
ARNNFKKDYSEDKA; RNNFKKDYSEDKAN; NNFKKDYSEDKANT;
NFKKDYSEDKANTV; FKKDYSEDKANTVK; KKDYSEDKANTVKQ;
KDYSEDKANTVKQI; DYSEDKANTVKQIL; YSEDKANTVKQILK;
SEDKANTVKQILKQ; EDKANTVKQILKQI; DKANTVKQILKQIL;
KANTVKQILKQILA; ANTVKQILKQILAD; NTVKQILKQILADL;
TVKQILKQILADLP; VKQILKQILADLPK; KQILKQILADLPKD;

15 mers:
MKKISLLIFLFLFVV; KKISLLIFLFLFVVS; KISLLIFLFLFVVSL;
ISLLIFLFLFVVSLS; SLLIFLFLFVVSLSA; LLIFLFLFVVSLSAN;
LIFLFLFVVSLSANI; IFLFLFVVSLSANIE; FLFLFVVSLSANIEE;
LFLFVVSLSANIEEN; FLFVVSLSANIEENY; LFVVSLSANIEENYT;
FVVSLSANIEENYTE; VVSLSANIEENYTET; VSLSANIEENYTETK;
SLSANIEENYTETKR; LSANIEENYTETKRA; SANIEENYTETKRAF;
ANIEENYTETKRAFS; NIEENYTETKRAFSK; IEENYTETKRAFSKE;
EENYTETKRAFSKED; ENYTETKRAFSKEDF; NYTETKRAFSKEDFN;
YTETKRAFSKEDFNL; TETKRAFSKEDFNLI; ETKRAFSKEDFNLIN;
TKRAFSKEDFNLINK; KRAFSKEDFNLINKR; RAFSKEDFNLINKRL;
AFSKEDFNLINKRLD; FSKEDFNLINKRLDN; SKEDFNLINKRLDNY;
KEDFNLINKRLDNYD; EDFNLINKRLDNYDF; DFNLINKRLDNYDFK;
FNLINKRLDNYDFKN; NLINKRLDNYDFKNE; LINKRLDNYDFKNEY;
INKRLDNYDFKNEYE; NKRLDNYDFKNEYEK; KRLDNYDFKNEYEKS;
RLDNYDFKNEYEKSH; LDNYDFKNEYEKSHV; DNYDFKNEYEKSHVF;
NYDFKNEYEKSHVFS; YDFKNEYEKSHVFSD; DFKNEYEKSHVFSDA;
FKNEYEKSHVFSDAP; KNEYEKSHVFSDAPR; NEYEKSHVFSDAPRI;
EYEKSHVFSDAPRIR; YEKSHVFSDAPRIRG; EKSHVFSDAPRIRGD;
KSHVFSDAPRIRGDL; SHVFSDAPRIRGDLR; HVFSDAPRIRGDLRK;
VFSDAPRIRGDLRKI; FSDAPRIRGDLRKIG; SDAPRIRGDLRKIGI;
DAPRIRGDLRKIGIK; APRIRGDLRKIGIKE; PRIRGDLRKIGIKEK;
RIRGDLRKIGIKEKS; IRGDLRKIGIKEKSV; RGDLRKIGIKEKSVF;
GDLRKIGIKEKSVFL; DLRKIGIKEKSVFLD; LRKIGIKEKSVFLDA;
RKIGIKEKSVFLDAL; KIGIKEKSVFLDALE; IGIKEKSVFLDALEA;
GIKEKSVFLDALEAI; IKEKSVFLDALEAIE; KEKSVFLDALEAIEY;
EKSVFLDALEAIEYL; KSVFLDALEAIEYLI; SVFLDALEAIEYLIK;
VFLDALEAIEYLIKI; FLDALEAIEYLIKIK; LDALEAIEYLIKIKI;
DALEAIEYLIKIKIS; ALEAIEYLIKIKIST; LEAIEYLIKIKISTD;
EAIEYLIKIKISTDS; AIEYLIKIKISTDSI; IEYLIKIKISTDSIF;
EYLIKIKISTDSIFL; YLIKIKISTDSIFLS; LIKIKISTDSIFLSE;
IKIKISTDSIFLSED; KIKISTDSIFLSEDM; IKISTDSIFLSEDMI;
KISTDSIFLSEDMIR; ISTDSIFLSEDMIRL; STDSIFLSEDMIRLI;
TDSIFLSEDMIRLIG; DSIFLSEDMIRLIGS; SIFLSEDMIRLIGSY;
IFLSEDMIRLIGSYP; FLSEDMIRLIGSYPD; LSEDMIRLIGSYPDS;
SEDMIRLIGSYPDSI; EDMIRLIGSYPDSIF; DMIRLIGSYPDSIFN;
MIRLIGSYPDSIFNY; IRLIGSYPDSIFNYL; RLIGSYPDSIFNYLI;
LIGSYPDSIFNYLIQ; IGSYPDSIFNYLIQL; GSYPDSIFNYLIQLN;
SYPDSIFNYLIQLNS; YPDSIFNYLIQLNSD; PDSIFNYLIQLNSDK;

DSIFNYLIQLNSDKI; SIFNYLIQLNSDKID; IFNYLIQLNSDKIDY;
FNYLIQLNSDKIDYA; NYLIQLNSDKIDYAE; YLIQLNSDKIDYAEK;
LIQLNSDKIDYAEKY; IQLNSDKIDYAEKYG; QLNSDKIDYAEKYGD;
LNSDKIDYAEKYGDN; NSDKIDYAEKYGDNA; SDKIDYAEKYGDNAR;
DKIDYAEKYGDNARN; KIDYAEKYGDNARNN; IDYAEKYGDNARNNF;
DYAEKYGDNARNNFK; YAEKYGDNARNNFKK; AEKYGDNARNNFKKD;
EKYGDNARNNFKKDY; KYGDNARNNFKKDYS; YGDNARNNFKKDYSE;
GDNARNNFKKDYSED; DNARNNFKKDYSEDK; NARNNFKKDYSEDKA;
ARNNFKKDYSEDKAN; RNNFKKDYSEDKANT; NNFKKDYSEDKANTV;
NFKKDYSEDKANTVK; FKKDYSEDKANTVKQ; KKDYSEDKANTVKQI;
KDYSEDKANTVKQIL; DYSEDKANTVKQILK; YSEDKANTVKQILKQ;
SEDKANTVKQILKQI; EDKANTVKQILKQIL; DKANTVKQILKQILA;
KANTVKQILKQILAD; ANTVKQILKQILADL; NTVKQILKQILADLP;
TVKQILKQILADLPK; VKQILKQILADLPKD;

16 mers:
MKKISLLIFLFLFVVS; KKISLLIFLFLFVVSL; KISLLIFLFLFVVSLS;
ISLLIFLFLFVVSLSA; SLLIFLFLFVVSLSAN; LLIFLFLFVVSLSANI;
LIFLFLFVVSLSANIE; IFLFLFVVSLSANIEE; FLFLFVVSLSANIEEN;
LFLFVVSLSANIEENY; FLFVVSLSANIEENYT; LFVVSLSANIEENYTE;
FVVSLSANIEENYTET; VVSLSANIEENYTETK; VSLSANIEENYTETKR;
SLSANIEENYTETKRA; LSANIEENYTETKRAF; SANIEENYTETKRAFS;
ANIEENYTETKRAFSK; NIEENYTETKRAFSKE; IEENYTETKRAFSKED;
EENYTETKRAFSKEDF; ENYTETKRAFSKEDFN; NYTETKRAFSKEDFNL;
YTETKRAFSKEDFNLI; TETKRAFSKEDFNLIN; ETKRAFSKEDFNLINK;
TKRAFSKEDFNLINKR; KRAFSKEDFNLINKRL; RAFSKEDFNLINKRLD;
AFSKEDFNLINKRLDN; FSKEDFNLINKRLDNY; SKEDFNLINKRLDNYD;
KEDFNLINKRLDNYDF; EDFNLINKRLDNYDFK; DFNLINKRLDNYDFKN;
FNLINKRLDNYDFKNE; NLINKRLDNYDFKNEY; LINKRLDNYDFKNEYE;
INKRLDNYDFKNEYEK; NKRLDNYDFKNEYEKS; KRLDNYDFKNEYEKSH;
RLDNYDFKNEYEKSHV; LDNYDFKNEYEKSHVF; DNYDFKNEYEKSHVFS;
NYDFKNEYEKSHVFSD; YDFKNEYEKSHVFSDA; DFKNEYEKSHVFSDAP;
FKNEYEKSHVFSDAPR; KNEYEKSHVFSDAPRI; NEYEKSHVFSDAPRIR;
EYEKSHVFSDAPRIRG; YEKSHVFSDAPRIRGD; EKSHVFSDAPRIRGDL;
KSHVFSDAPRIRGDLR; SHVFSDAPRIRGDLRK; HVFSDAPRIRGDLRKI;
VFSDAPRIRGDLRKIG; FSDAPRIRGDLRKIGI; SDAPRIRGDLRKIGIK;
DAPRIRGDLRKIGIKE; APRIRGDLRKIGIKEK; PRIRGDLRKIGIKEKS;
RIRGDLRKIGIKEKSV; IRGDLRKIGIKEKSVF; RGDLRKIGIKEKSVFL;
GDLRKIGIKEKSVFLD; DLRKIGIKEKSVFLDA; LRKIGIKEKSVFLDAL;
RKIGIKEKSVFLDALE; KIGIKEKSVFLDALEA; IGIKEKSVFLDALEAI;
GIKEKSVFLDALEAIE; IKEKSVFLDALEAIEY; KEKSVFLDALEAIEYL;
EKSVFLDALEAIEYLI; KSVFLDALEAIEYLIK; SVFLDALEAIEYLIKI;
VFLDALEAIEYLIKIK; FLDALEAIEYLIKIKI; LDALEAIEYLIKIKIS;
DALEAIEYLIKIKIST; ALEAIEYLIKIKISTD; LEAIEYLIKIKISTDS;
EAIEYLIKIKISTDSI; AIEYLIKIKISTDSIF; IEYLIKIKISTDSIFL;
EYLIKIKISTDSIFLS; YLIKIKISTDSIFLSE; LIKIKISTDSIFLSED;
IKIKISTDSIFLSEDM; KIKISTDSIFLSEDMI; IKISTDSIFLSEDMIR;
KISTDSIFLSEDMIRL; ISTDSIFLSEDMIRLI; STDSIFLSEDMIRLIG;
TDSIFLSEDMIRLIGS; DSIFLSEDMIRLIGSY; SIFLSEDMIRLIGSYP;
IFLSEDMIRLIGSYPD; FLSEDMIRLIGSYPDS; LSEDMIRLIGSYPDSI;
SEDMIRLIGSYPDSIF; EDMIRLIGSYPDSIFN; DMIRLIGSYPDSIFNY;
MIRLIGSYPDSIFNYL; IRLIGSYPDSIFNYLI; RLIGSYPDSIFNYLIQ;
LIGSYPDSIFNYLIQL; IGSYPDSIFNYLIQLN; GSYPDSIFNYLIQLNS;
SYPDSIFNYLIQLNSD; YPDSIFNYLIQLNSDK; PDSIFNYLIQLNSDKI;
DSIFNYLIQLNSDKID; SIFNYLIQLNSDKIDY; IFNYLIQLNSDKIDYA;
FNYLIQLNSDKIDYAE; NYLIQLNSDKIDYAEK; YLIQLNSDKIDYAEKY;
LIQLNSDKIDYAEKYG; IQLNSDKIDYAEKYGD; QLNSDKIDYAEKYGDN;

	LNSDKIDYAEKYGDNA; NSDKIDYAEKYGDNAR; SDKIDYAEKYGDNARN; DKIDYAEKYGDNARNN; KIDYAEKYGDNARNNF; IDYAEKYGDNARNNFK; DYAEKYGDNARNNFKK; YAEKYGDNARNNFKKD; AEKYGDNARNNFKKDY; EKYGDNARNNFKKDYS; KYGDNARNNFKKDYSE; YGDNARNNFKKDYSED; GDNARNNFKKDYSEDK; DNARNNFKKDYSEDKA; NARNNFKKDYSEDKAN; ARNNFKKDYSEDKANT; RNNFKKDYSEDKANTV; NNFKKDYSEDKANTVK; NFKKDYSEDKANTVKQ; FKKDYSEDKANTVKQI; KKDYSEDKANTVKQIL; KDYSEDKANTVKQILK; DYSEDKANTVKQILKQ; YSEDKANTVKQILKQI; SEDKANTVKQILKQIL; EDKANTVKQILKQILA; DKANTVKQILKQILAD; KANTVKQILKQILADL; ANTVKQILKQILADLP; NTVKQILKQILADLPK; TVKQILKQILADLPKD;
Seq19	13 mers: MCAFLLLNLVNCK; CAFLLLNLVNCKF; AFLLLNLVNCKFD; FLLLNLVNCKFDS; LLLNLVNCKFDSL; LLNLVNCKFDSLN; LNLVNCKFDSLNL; NLVNCKFDSLNLS; LVNCKFDSLNLST; VNCKFDSLNLSTK; NCKFDSLNLSTKS; CKFDSLNLSTKSV; KFDSLNLSTKSVD; FDSLNLSTKSVDD; DSLNLSTKSVDDK; SLNLSTKSVDDKN; LNLSTKSVDDKNN; NLSTKSVDDKNNS; LSTKSVDDKNNSI; STKSVDDKNNSIA; TKSVDDKNNSIAK; KSVDDKNNSIAKL; SVDDKNNSIAKLL; VDDKNNSIAKLLQ; DDKNNSIAKLLQH; DKNNSIAKLLQHL; KNNSIAKLLQHLS; NNSIAKLLQHLSK; NSIAKLLQHLSKS; SIAKLLQHLSKSE; IAKLLQHLSKSED; AKLLQHLSKSEDQ; KLLQHLSKSEDQA; LLQHLSKSEDQAN; LQHLSKSEDQANK; QHLSKSEDQANKT; HLSKSEDQANKTS; LSKSEDQANKTST; SKSEDQANKTSTS; KSEDQANKTSTSE; SEDQANKTSTSED; EDQANKTSTSEDQ; DQANKTSTSEDQK; QANKTSTSEDQKE; ANKTSTSEDQKEL; NKTSTSEDQKELE; KTSTSEDQKELEI; TSTSEDQKELEIT; STSEDQKELEITE; TSEDQKELEITEN; SEDQKELEITENK; EDQKELEITENKE; DQKELEITENKEQ; QKELEITENKEQE; KELEITENKEQEH; ELEITENKEQEHE; LEITENKEQEHEK; EITENKEQEHEKL; ITENKEQEHEKLS; TENKEQEHEKLSQ; ENKEQEHEKLSQV; NKEQEHEKLSQVA; KEQEHEKLSQVAQ; EQEHEKLSQVAQH; QEHEKLSQVAQHA; EHEKLSQVAQHAP; HEKLSQVAQHAPN; EKLSQVAQHAPNS; KLSQVAQHAPNSK; LSQVAQHAPNSKI; SQVAQHAPNSKIE; QVAQHAPNSKIEK; VAQHAPNSKIEKV; AQHAPNSKIEKVK; QHAPNSKIEKVKS; HAPNSKIEKVKSD; APNSKIEKVKSDG; PNSKIEKVKSDGK; NSKIEKVKSDGKP; SKIEKVKSDGKPV; KIEKVKSDGKPVP; IEKVKSDGKPVPG; EKVKSDGKPVPGD; KVKSDGKPVPGDK; VKSDGKPVPGDKI; KSDGKPVPGDKIL; SDGKPVPGDKILS; DGKPVPGDKILSS; GKPVPGDKILSSN; KPVPGDKILSSNK; PVPGDKILSSNKD; VPGDKILSSNKDI; PGDKILSSNKDIY; GDKILSSNKDIYN; DKILSSNKDIYNS; KILSSNKDIYNSY; ILSSNKDIYNSYI; LSSNKDIYNSYIP; SSNKDIYNSYIPE; SNKDIYNSYIPEV; NKDIYNSYIPEVK; KDIYNSYIPEVKE; DIYNSYIPEVKEE; IYNSYIPEVKEEI; YNSYIPEVKEEIV; NSYIPEVKEEIVY; SYIPEVKEEIVYE; YIPEVKEEIVYEI; IPEVKEEIVYEIL; PEVKEEIVYEILE; EVKEEIVYEILEE; VKEEIVYEILEEV; KEEIVYEILEEVI; EEIVYEILEEVII;

	EIVYEILEEVIIP; IVYEILEEVIIPE; VYEILEEVIIPET; YEILEEVIIPETK; EILEEVIIPETKI; ILEEVIIPETKIP; LEEVIIPETKIPE; EEVIIPETKIPEI; EVIIPETKIPEIT; VIIPETKIPEITE; IIPETKIPEITEE; IPETKIPEITEEV; PETKIPEITEEVI; ETKIPEITEEVIM; TKIPEITEEVIMP; KIPEITEEVIMPI; IPEITEEVIMPIP; PEITEEVIMPIPQ; EITEEVIMPIPQT; ITEEVIMPIPQTI; TEEVIMPIPQTID; EEVIMPIPQTIDF; EVIMPIPQTIDFY; VIMPIPQTIDFYI; IMPIPQTIDFYIE; MPIPQTIDFYIEP; PIPQTIDFYIEPR; IPQTIDFYIEPRP; PQTIDFYIEPRPI; QTIDFYIEPRPIS; TIDFYIEPRPISS; IDFYIEPRPISSF; DFYIEPRPISSFL; FYIEPRPISSFLT; YIEPRPISSFLTQ; IEPRPISSFLTQG; EPRPISSFLTQGT; PRPISSFLTQGTS; RPISSFLTQGTSP; PISSFLTQGTSPS; ISSFLTQGTSPSI; SSFLTQGTSPSIT; SFLTQGTSPSITS; FLTQGTSPSITST; LTQGTSPSITSTI; TQGTSPSITSTIK; QGTSPSITSTIKS; GTSPSITSTIKSY; TSPSITSTIKSYK; SPSITSTIKSYKE; PSITSTIKSYKEL; SITSTIKSYKELA; ITSTIKSYKELAK; TSTIKSYKELAKE; STIKSYKELAKEK; TIKSYKELAKEKI; IKSYKELAKEKIN; KSYKELAKEKINN; SYKELAKEKINNG; YKELAKEKINNGL; KELAKEKINNGLN; ELAKEKINNGLNI; LAKEKINNGLNIV; AKEKINNGLNIVQ; KEKINNGLNIVQK; EKINNGLNIVQKI; KINNGLNIVQKIT; INNGLNIVQKITQ; NNGLNIVQKITQN; NGLNIVQKITQNI; GLNIVQKITQNID; LNIVQKITQNIDN; NIVQKITQNIDNI; IVQKITQNIDNIT; VQKITQNIDNITE; QKITQNIDNITEN; KITQNIDNITENL; ITQNIDNITENLN; TQNIDNITENLNS; QNIDNITENLNSK; NIDNITENLNSKE; IDNITENLNSKET; DNITENLNSKETP; NITENLNSKETPK; ITENLNSKETPKE; TENLNSKETPKEI; ENLNSKETPKEIS; NLNSKETPKEISG; LNSKETPKEISGK; NSKETPKEISGKE; SKETPKEISGKEV; KETPKEISGKEVE; ETPKEISGKEVEE; TPKEISGKEVEEK; PKEISGKEVEEKI; KEISGKEVEEKIT; EISGKEVEEKITH; ISGKEVEEKITHP; SGKEVEEKITHPI; GKEVEEKITHPIF; KEVEEKITHPIFD; EVEEKITHPIFDH; VEEKITHPIFDHI; EEKITHPIFDHIT; EKITHPIFDHITG; KITHPIFDHITGS; ITHPIFDHITGSG; THPIFDHITGSGN; HPIFDHITGSGNN; PIFDHITGSGNNP; IFDHITGSGNNPG; FDHITGSGNNPGQ; DHITGSGNNPGQD; HITGSGNNPGQDS; ITGSGNNPGQDSI; TGSGNNPGQDSIS; GSGNNPGQDSISN; SGNNPGQDSISNT; GNNPGQDSISNTW; NNPGQDSISNTWG; NPGQDSISNTWGE; PGQDSISNTWGEG; GQDSISNTWGEGL; QDSISNTWGEGLE; DSISNTWGEGLEI; SISNTWGEGLEIG; ISNTWGEGLEIGG; SNTWGEGLEIGGD; NTWGEGLEIGGDS; TWGEGLEIGGDSN; WGEGLEIGGDSNF; GEGLEIGGDSNFF; EGLEIGGDSNFFT; GLEIGGDSNFFTN; LEIGGDSNFFTNL; EIGGDSNFFTNLE; IGGDSNFFTNLEE; GGDSNFFTNLEEV; GDSNFFTNLEEVR; DSNFFTNLEEVRS; SNFFTNLEEVRSS; NFFTNLEEVRSSI; FFTNLEEVRSSIR; FTNLEEVRSSIRT; TNLEEVRSSIRTK; NLEEVRSSIRTKI; LEEVRSSIRTKIK; EEVRSSIRTKIKV; EVRSSIRTKIKVS; VRSSIRTKIKVSD; RSSIRTKIKVSDG; SSIRTKIKVSDGT; SIRTKIKVSDGTE;

IRTKIKVSDGTEQ; RTKIKVSDGTEQT; TKIKVSDGTEQTK;
KIKVSDGTEQTKD; IKVSDGTEQTKDK; KVSDGTEQTKDKV;
VSDGTEQTKDKVE; SDGTEQTKDKVEI; DGTEQTKDKVEID;
GTEQTKDKVEIDE; TEQTKDKVEIDEI; EQTKDKVEIDEII;
QTKDKVEIDEIIE; TKDKVEIDEIIED; KDKVEIDEIIEDL;
DKVEIDEIIEDLQ; KVEIDEIIEDLQK; VEIDEIIEDLQKL;
EIDEIIEDLQKLK; IDEIIEDLQKLKE; DEIIEDLQKLKEF;
EIIEDLQKLKEFL; IIEDLQKLKEFLE; IEDLQKLKEFLEK;
EDLQKLKEFLEKL; DLQKLKEFLEKLK; LQKLKEFLEKLKK;
QKLKEFLEKLKKY; KLKEFLEKLKKYL; LKEFLEKLKKYLK;
KEFLEKLKKYLKD; EFLEKLKKYLKDT; FLEKLKKYLKDTN;
LEKLKKYLKDTNN; EKLKKYLKDTNNL; KLKKYLKDTNNLS;
LKKYLKDTNNLSA; KKYLKDTNNLSAI; KYLKDTNNLSAIE;
YLKDTNNLSAIEE; LKDTNNLSAIEES; KDTNNLSAIEESV;
DTNNLSAIEESVK; TNNLSAIEESVKG; NNLSAIEESVKGL;
NLSAIEESVKGLS;

14 mers:
MCAFLLLNLVNCKF; CAFLLLNLVNCKFD; AFLLLNLVNCKFDS;
FLLLNLVNCKFDSL; LLLNLVNCKFDSLN; LLNLVNCKFDSLNL;
LNLVNCKFDSLNLS; NLVNCKFDSLNLST; LVNCKFDSLNLSTK;
VNCKFDSLNLSTKS; NCKFDSLNLSTKSV; CKFDSLNLSTKSVD;
KFDSLNLSTKSVDD; FDSLNLSTKSVDDK; DSLNLSTKSVDDKN;
SLNLSTKSVDDKNN; LNLSTKSVDDKNNS; NLSTKSVDDKNNSI;
LSTKSVDDKNNSIA; STKSVDDKNNSIAK; TKSVDDKNNSIAKL;
KSVDDKNNSIAKLL; SVDDKNNSIAKLLQ; VDDKNNSIAKLLQH;
DDKNNSIAKLLQHL; DKNNSIAKLLQHLS; KNNSIAKLLQHLSK;
NNSIAKLLQHLSKS; NSIAKLLQHLSKSE; SIAKLLQHLSKSED;
IAKLLQHLSKSEDQ; AKLLQHLSKSEDQA; KLLQHLSKSEDQAN;
LLQHLSKSEDQANK; LQHLSKSEDQANKT; QHLSKSEDQANKTS;
HLSKSEDQANKTST; LSKSEDQANKTSTS; SKSEDQANKTSTSE;
KSEDQANKTSTSED; SEDQANKTSTSEDQ; EDQANKTSTSEDQK;
DQANKTSTSEDQKE; QANKTSTSEDQKEL; ANKTSTSEDQKELE;
NKTSTSEDQKELEI; KTSTSEDQKELEIT; TSTSEDQKELEITE;
STSEDQKELEITEN; TSEDQKELEITENK; SEDQKELEITENKE;
EDQKELEITENKEQ; DQKELEITENKEQE; QKELEITENKEQEH;
KELEITENKEQEHE; ELEITENKEQEHEK; LEITENKEQEHEKL;
EITENKEQEHEKLS; ITENKEQEHEKLSQ; TENKEQEHEKLSQV;
ENKEQEHEKLSQVA; NKEQEHEKLSQVAQ; KEQEHEKLSQVAQH;
EQEHEKLSQVAQHA; QEHEKLSQVAQHAP; EHEKLSQVAQHAPN;
HEKLSQVAQHAPNS; EKLSQVAQHAPNSK; KLSQVAQHAPNSKI;
LSQVAQHAPNSKIE; SQVAQHAPNSKIEK; QVAQHAPNSKIEKV;
VAQHAPNSKIEKVK; AQHAPNSKIEKVKS; QHAPNSKIEKVKSD;
HAPNSKIEKVKSDG; APNSKIEKVKSDGK; PNSKIEKVKSDGKP;
NSKIEKVKSDGKPV; SKIEKVKSDGKPVP; KIEKVKSDGKPVPG;
IEKVKSDGKPVPGD; EKVKSDGKPVPGDK; KVKSDGKPVPGDKI;
VKSDGKPVPGDKIL; KSDGKPVPGDKILS; SDGKPVPGDKILSS;
DGKPVPGDKILSSN; GKPVPGDKILSSNK; KPVPGDKILSSNKD;
PVPGDKILSSNKDI; VPGDKILSSNKDIY; PGDKILSSNKDIYN;
GDKILSSNKDIYNS; DKILSSNKDIYNSY; KILSSNKDIYNSYI;
ILSSNKDIYNSYIP; LSSNKDIYNSYIPE; SSNKDIYNSYIPEV;

	SNKDIYNSYIPEVK; NKDIYNSYIPEVKE; KDIYNSYIPEVKEE; DIYNSYIPEVKEEI; IYNSYIPEVKEEIV; YNSYIPEVKEEIVY; NSYIPEVKEEIVYE; SYIPEVKEEIVYEI; YIPEVKEEIVYEIL; IPEVKEEIVYEILE; PEVKEEIVYEILEE; EVKEEIVYEILEEV; VKEEIVYEILEEVI; KEEIVYEILEEVII; EEIVYEILEEVIIP; EIVYEILEEVIIPE; IVYEILEEVIIPET; VYEILEEVIIPETK; YEILEEVIIPETKI; EILEEVIIPETKIP; ILEEVIIPETKIPE; LEEVIIPETKIPEI; EEVIIPETKIPEIT; EVIIPETKIPEITE; VIIPETKIPEITEE; IIPETKIPEITEEV; IPETKIPEITEEVI; PETKIPEITEEVIM; ETKIPEITEEVIMP; TKIPEITEEVIMPI; KIPEITEEVIMPIP; IPEITEEVIMPIPQ; PEITEEVIMPIPQT; EITEEVIMPIPQTI; ITEEVIMPIPQTID; TEEVIMPIPQTIDF; EEVIMPIPQTIDFY; EVIMPIPQTIDFYI; VIMPIPQTIDFYIE; IMPIPQTIDFYIEP; MPIPQTIDFYIEPR; PIPQTIDFYIEPRP; IPQTIDFYIEPRPI; PQTIDFYIEPRPIS; QTIDFYIEPRPISS; TIDFYIEPRPISSF; IDFYIEPRPISSFL; DFYIEPRPISSFLT; FYIEPRPISSFLTQ; YIEPRPISSFLTQG; IEPRPISSFLTQGT; EPRPISSFLTQGTS; PRPISSFLTQGTSP; RPISSFLTQGTSPS; PISSFLTQGTSPSI; ISSFLTQGTSPSIT; SSFLTQGTSPSITS; SFLTQGTSPSITST; FLTQGTSPSITSTI; LTQGTSPSITSTIK; TQGTSPSITSTIKS; QGTSPSITSTIKSY; GTSPSITSTIKSYK; TSPSITSTIKSYKE; SPSITSTIKSYKEL; PSITSTIKSYKELA; SITSTIKSYKELAK; ITSTIKSYKELAKE; TSTIKSYKELAKEK; STIKSYKELAKEKI; TIKSYKELAKEKIN; IKSYKELAKEKINN; KSYKELAKEKINNG; SYKELAKEKINNGL; YKELAKEKINNGLN; KELAKEKINNGLNI; ELAKEKINNGLNIV; LAKEKINNGLNIVQ; AKEKINNGLNIVQK; KEKINNGLNIVQKI; EKINNGLNIVQKIT; KINNGLNIVQKITQ; INNGLNIVQKITQN; NNGLNIVQKITQNI; NGLNIVQKITQNID; GLNIVQKITQNIDN; LNIVQKITQNIDNI; NIVQKITQNIDNIT; IVQKITQNIDNITE; VQKITQNIDNITEN; QKITQNIDNITENL; KITQNIDNITENLN; ITQNIDNITENLNS; TQNIDNITENLNSK; QNIDNITENLNSKE; NIDNITENLNSKET; IDNITENLNSKETP; DNITENLNSKETPK; NITENLNSKETPKE; ITENLNSKETPKEI; TENLNSKETPKEIS; ENLNSKETPKEISG; NLNSKETPKEISGK; LNSKETPKEISGKE; NSKETPKEISGKEV; SKETPKEISGKEVE; KETPKEISGKEVEE; ETPKEISGKEVEEK; TPKEISGKEVEEKI; PKEISGKEVEEKIT; KEISGKEVEEKITH; EISGKEVEEKITHP; ISGKEVEEKITHPI; SGKEVEEKITHPIF; GKEVEEKITHPIFD; KEVEEKITHPIFDH; EVEEKITHPIFDHI; VEEKITHPIFDHIT; EEKITHPIFDHITG; EKITHPIFDHITGS; KITHPIFDHITGSG; ITHPIFDHITGSGN; THPIFDHITGSGNN; HPIFDHITGSGNNP; PIFDHITGSGNNPG; IFDHITGSGNNPGQ; FDHITGSGNNPGQD; DHITGSGNNPGQDS; HITGSGNNPGQDSI; ITGSGNNPGQDSIS; TGSGNNPGQDSISN; GSGNNPGQDSISNT; SGNNPGQDSISNTW; GNNPGQDSISNTWG; NNPGQDSISNTWGE; NPGQDSISNTWGEG; PGQDSISNTWGEGL; GQDSISNTWGEGLE; QDSISNTWGEGLEI; DSISNTWGEGLEIG; SISNTWGEGLEIGG; ISNTWGEGLEIGGD; SNTWGEGLEIGGDS; NTWGEGLEIGGDSN; TWGEGLEIGGDSNF; WGEGLEIGGDSNFF; GEGLEIGGDSNFFT; EGLEIGGDSNFFTN; GLEIGGDSNFFTNL; LEIGGDSNFFTNLE; EIGGDSNFFTNLEE; IGGDSNFFTNLEEV; GGDSNFFTNLEEVR;

	GDSNFFTNLEEVRS; DSNFFTNLEEVRSS; SNFFTNLEEVRSSI; NFFTNLEEVRSSIR; FFTNLEEVRSSIRT; FTNLEEVRSSIRTK; TNLEEVRSSIRTKI; NLEEVRSSIRTKIK; LEEVRSSIRTKIKV; EEVRSSIRTKIKVS; EVRSSIRTKIKVSD; VRSSIRTKIKVSDG; RSSIRTKIKVSDGT; SSIRTKIKVSDGTE; SIRTKIKVSDGTEQ; IRTKIKVSDGTEQT; RTKIKVSDGTEQTK; TKIKVSDGTEQTKD; KIKVSDGTEQTKDK; IKVSDGTEQTKDKV; KVSDGTEQTKDKVE; VSDGTEQTKDKVEI; SDGTEQTKDKVEID; DGTEQTKDKVEIDE; GTEQTKDKVEIDEI; TEQTKDKVEIDEII; EQTKDKVEIDEIIE; QTKDKVEIDEIIED; TKDKVEIDEIIEDL; KDKVEIDEIIEDLQ; DKVEIDEIIEDLQK; KVEIDEIIEDLQKL; VEIDEIIEDLQKLK; EIDEIIEDLQKLKE; IDEIIEDLQKLKEF; DEIIEDLQKLKEFL; EIIEDLQKLKEFLE; IIEDLQKLKEFLEK; IEDLQKLKEFLEKL; EDLQKLKEFLEKLK; DLQKLKEFLEKLKK; LQKLKEFLEKLKKY; QKLKEFLEKLKKYL; KLKEFLEKLKKYLK; LKEFLEKLKKYLKD; KEFLEKLKKYLKDT; EFLEKLKKYLKDTN; FLEKLKKYLKDTNN; LEKLKKYLKDTNNL; EKLKKYLKDTNNLS; KLKKYLKDTNNLSA; LKKYLKDTNNLSAI; KKYLKDTNNLSAIE; KYLKDTNNLSAIEE; YLKDTNNLSAIEES; LKDTNNLSAIEESV; KDTNNLSAIEESVK; DTNNLSAIEESVKG; TNNLSAIEESVKGL; NNLSAIEESVKGLS; 15 mers: MCAFLLLNLVNCKFD; CAFLLLNLVNCKFDS; AFLLLNLVNCKFDSL; FLLLNLVNCKFDSLN; LLLNLVNCKFDSLNL; LLNLVNCKFDSLNLS; LNLVNCKFDSLNLST; NLVNCKFDSLNLSTK; LVNCKFDSLNLSTKS; VNCKFDSLNLSTKSV; NCKFDSLNLSTKSVD; CKFDSLNLSTKSVDD; KFDSLNLSTKSVDDK; FDSLNLSTKSVDDKN; DSLNLSTKSVDDKNN; SLNLSTKSVDDKNNS; LNLSTKSVDDKNNSI; NLSTKSVDDKNNSIA; LSTKSVDDKNNSIAK; STKSVDDKNNSIAKL; TKSVDDKNNSIAKLL; KSVDDKNNSIAKLLQ; SVDDKNNSIAKLLQH; VDDKNNSIAKLLQHL; DDKNNSIAKLLQHLS; DKNNSIAKLLQHLSK; KNNSIAKLLQHLSKS; NNSIAKLLQHLSKSE; NSIAKLLQHLSKSED; SIAKLLQHLSKSEDQ; IAKLLQHLSKSEDQA; AKLLQHLSKSEDQAN; KLLQHLSKSEDQANK; LLQHLSKSEDQANKT; LQHLSKSEDQANKTS; QHLSKSEDQANKTST; HLSKSEDQANKTSTS; LSKSEDQANKTSTSE; SKSEDQANKTSTSED; KSEDQANKTSTSEDQ; SEDQANKTSTSEDQK; EDQANKTSTSEDQKE; DQANKTSTSEDQKEL; QANKTSTSEDQKELE; ANKTSTSEDQKELEI; NKTSTSEDQKELEIT; KTSTSEDQKELEITE; TSTSEDQKELEITEN; STSEDQKELEITENK; TSEDQKELEITENKE; SEDQKELEITENKEQ; EDQKELEITENKEQE; DQKELEITENKEQEH; QKELEITENKEQEHE; KELEITENKEQEHEK; ELEITENKEQEHEKL; LEITENKEQEHEKLS; EITENKEQEHEKLSQ; ITENKEQEHEKLSQV; TENKEQEHEKLSQVA; ENKEQEHEKLSQVAQ; NKEQEHEKLSQVAQH; KEQEHEKLSQVAQHA; EQEHEKLSQVAQHAP; QEHEKLSQVAQHAPN; EHEKLSQVAQHAPNS; HEKLSQVAQHAPNSK; EKLSQVAQHAPNSKI; KLSQVAQHAPNSKIE; LSQVAQHAPNSKIEK; SQVAQHAPNSKIEKV; QVAQHAPNSKIEKVK; VAQHAPNSKIEKVKS; AQHAPNSKIEKVKSD; QHAPNSKIEKVKSDG; HAPNSKIEKVKSDGK; APNSKIEKVKSDGKP; PNSKIEKVKSDGKPV; NSKIEKVKSDGKPVP; SKIEKVKSDGKPVPG; KIEKVKSDGKPVPGD; IEKVKSDGKPVPGDK; EKVKSDGKPVPGDKI; KVKSDGKPVPGDKIL; VKSDGKPVPGDKILS; KSDGKPVPGDKILSS; SDGKPVPGDKILSSN;

	DGKPVPGDKILSSNK; GKPVPGDKILSSNKD; KPVPGDKILSSNKDI; PVPGDKILSSNKDIY; VPGDKILSSNKDIYN; PGDKILSSNKDIYNS; GDKILSSNKDIYNSY; DKILSSNKDIYNSYI; KILSSNKDIYNSYIP; ILSSNKDIYNSYIPE; LSSNKDIYNSYIPEV; SSNKDIYNSYIPEVK; SNKDIYNSYIPEVKE; NKDIYNSYIPEVKEE; KDIYNSYIPEVKEEI; DIYNSYIPEVKEEIV; IYNSYIPEVKEEIVY; YNSYIPEVKEEIVYE; NSYIPEVKEEIVYEI; SYIPEVKEEIVYEIL; YIPEVKEEIVYEILE; IPEVKEEIVYEILEE; PEVKEEIVYEILEEV; EVKEEIVYEILEEVI; VKEEIVYEILEEVII; KEEIVYEILEEVIIP; EEIVYEILEEVIIPE; EIVYEILEEVIIPET; IVYEILEEVIIPETK; VYEILEEVIIPETKI; YEILEEVIIPETKIP; EILEEVIIPETKIPE; ILEEVIIPETKIPEI; LEEVIIPETKIPEIT; EEVIIPETKIPEITE; EVIIPETKIPEITEE; VIIPETKIPEITEEV; IIPETKIPEITEEVI; IPETKIPEITEEVIM; PETKIPEITEEVIMP; ETKIPEITEEVIMPI; TKIPEITEEVIMPIP; KIPEITEEVIMPIPQ; IPEITEEVIMPIPQT; PEITEEVIMPIPQTI; EITEEVIMPIPQTID; ITEEVIMPIPQTIDF; TEEVIMPIPQTIDFY; EEVIMPIPQTIDFYI; EVIMPIPQTIDFYIE; VIMPIPQTIDFYIEP; IMPIPQTIDFYIEPR; MPIPQTIDFYIEPRP; PIPQTIDFYIEPRPI; IPQTIDFYIEPRPIS; PQTIDFYIEPRPISS; QTIDFYIEPRPISSF; TIDFYIEPRPISSFL; IDFYIEPRPISSFLT; DFYIEPRPISSFLTQ; FYIEPRPISSFLTQG; YIEPRPISSFLTQGT; IEPRPISSFLTQGTS; EPRPISSFLTQGTSP; PRPISSFLTQGTSPS; RPISSFLTQGTSPSI; PISSFLTQGTSPSIT; ISSFLTQGTSPSITS; SSFLTQGTSPSITST; SFLTQGTSPSITSTI; FLTQGTSPSITSTIK; LTQGTSPSITSTIKS; TQGTSPSITSTIKSY; QGTSPSITSTIKSYK; GTSPSITSTIKSYKE; TSPSITSTIKSYKEL; SPSITSTIKSYKELA; PSITSTIKSYKELAK; SITSTIKSYKELAKE; ITSTIKSYKELAKEK; TSTIKSYKELAKEKI; STIKSYKELAKEKIN; TIKSYKELAKEKINN; IKSYKELAKEKINNG; KSYKELAKEKINNGL; SYKELAKEKINNGLN; YKELAKEKINNGLNI; KELAKEKINNGLNIV; ELAKEKINNGLNIVQ; LAKEKINNGLNIVQK; AKEKINNGLNIVQKI; KEKINNGLNIVQKIT; EKINNGLNIVQKITQ; KINNGLNIVQKITQN; INNGLNIVQKITQNI; NNGLNIVQKITQNID; NGLNIVQKITQNIDN; GLNIVQKITQNIDNI; LNIVQKITQNIDNIT; NIVQKITQNIDNITE; IVQKITQNIDNITEN; VQKITQNIDNITENL; QKITQNIDNITENLN; KITQNIDNITENLNS; ITQNIDNITENLNSK; TQNIDNITENLNSKE; QNIDNITENLNSKET; NIDNITENLNSKETP; IDNITENLNSKETPK; DNITENLNSKETPKE; NITENLNSKETPKEI; ITENLNSKETPKEIS; TENLNSKETPKEISG; ENLNSKETPKEISGK; NLNSKETPKEISGKE; LNSKETPKEISGKEV; NSKETPKEISGKEVE; SKETPKEISGKEVEE; KETPKEISGKEVEEK; ETPKEISGKEVEEKI; TPKEISGKEVEEKIT; PKEISGKEVEEKITH; KEISGKEVEEKITHP; EISGKEVEEKITHPI; ISGKEVEEKITHPIF; SGKEVEEKITHPIFD; GKEVEEKITHPIFDH; KEVEEKITHPIFDHI; EVEEKITHPIFDHIT; VEEKITHPIFDHITG; EEKITHPIFDHITGS; EKITHPIFDHITGSG; KITHPIFDHITGSGN; ITHPIFDHITGSGNN; THPIFDHITGSGNNP; HPIFDHITGSGNNPG; PIFDHITGSGNNPGQ; IFDHITGSGNNPGQD; FDHITGSGNNPGQDS; DHITGSGNNPGQDSI; HITGSGNNPGQDSIS; ITGSGNNPGQDSISN; TGSGNNPGQDSISNT; GSGNNPGQDSISNTW; SGNNPGQDSISNTWG; GNNPGQDSISNTWGE; NNPGQDSISNTWGEG; NPGQDSISNTWGEGL; PGQDSISNTWGEGLE; GQDSISNTWGEGLEI; QDSISNTWGEGLEIG; DSISNTWGEGLEIGG; SISNTWGEGLEIGGD;

	ISNTWGEGLEIGGDS; SNTWGEGLEIGGDSN; NTWGEGLEIGGDSNF; TWGEGLEIGGDSNFF; WGEGLEIGGDSNFFT; GEGLEIGGDSNFFTN; EGLEIGGDSNFFTNL; GLEIGGDSNFFTNLE; LEIGGDSNFFTNLEE; EIGGDSNFFTNLEEV; IGGDSNFFTNLEEVR; GGDSNFFTNLEEVRS; GDSNFFTNLEEVRSS; DSNFFTNLEEVRSSI; SNFFTNLEEVRSSIR; NFFTNLEEVRSSIRT; FFTNLEEVRSSIRTK; FTNLEEVRSSIRTKI; TNLEEVRSSIRTKIK; NLEEVRSSIRTKIKV; LEEVRSSIRTKIKVS; EEVRSSIRTKIKVSD; EVRSSIRTKIKVSDG; VRSSIRTKIKVSDGT; RSSIRTKIKVSDGTE; SSIRTKIKVSDGTEQ; SIRTKIKVSDGTEQT; IRTKIKVSDGTEQTK; RTKIKVSDGTEQTKD; TKIKVSDGTEQTKDK; KIKVSDGTEQTKDKV; IKVSDGTEQTKDKVE; KVSDGTEQTKDKVEI; VSDGTEQTKDKVEID; SDGTEQTKDKVEIDE; DGTEQTKDKVEIDEI; GTEQTKDKVEIDEII; TEQTKDKVEIDEIIE; EQTKDKVEIDEIIED; QTKDKVEIDEIIEDL; TKDKVEIDEIIEDLQ; KDKVEIDEIIEDLQK; DKVEIDEIIEDLQKL; KVEIDEIIEDLQKLK; VEIDEIIEDLQKLKE; EIDEIIEDLQKLKEF; IDEIIEDLQKLKEFL; DEIIEDLQKLKEFLE; EIIEDLQKLKEFLEK; IIEDLQKLKEFLEKL; IEDLQKLKEFLEKLK; EDLQKLKEFLEKLKK; DLQKLKEFLEKLKKY; LQKLKEFLEKLKKYL; QKLKEFLEKLKKYLK; KLKEFLEKLKKYLKD; LKEFLEKLKKYLKDT; KEFLEKLKKYLKDTN; EFLEKLKKYLKDTNN; FLEKLKKYLKDTNNL; LEKLKKYLKDTNNLS; EKLKKYLKDTNNLSA; KLKKYLKDTNNLSAI; LKKYLKDTNNLSAIE; KKYLKDTNNLSAIEE; KYLKDTNNLSAIEES; YLKDTNNLSAIEESV; LKDTNNLSAIEESVK; KDTNNLSAIEESVKG; DTNNLSAIEESVKGL; TNNLSAIEESVKGLS; 16 mers: MCAFLLLNLVNCKFDS; CAFLLLNLVNCKFDSL; AFLLLNLVNCKFDSLN; FLLLNLVNCKFDSLNL; LLLNLVNCKFDSLNLS; LLNLVNCKFDSLNLST; LNLVNCKFDSLNLSTK; NLVNCKFDSLNLSTKS; LVNCKFDSLNLSTKSV; VNCKFDSLNLSTKSVD; NCKFDSLNLSTKSVDD; CKFDSLNLSTKSVDDK; KFDSLNLSTKSVDDKN; FDSLNLSTKSVDDKNN; DSLNLSTKSVDDKNNS; SLNLSTKSVDDKNNSI; LNLSTKSVDDKNNSIA; NLSTKSVDDKNNSIAK; LSTKSVDDKNNSIAKL; STKSVDDKNNSIAKLL; TKSVDDKNNSIAKLLQ; KSVDDKNNSIAKLLQH; SVDDKNNSIAKLLQHL; VDDKNNSIAKLLQHLS; DDKNNSIAKLLQHLSK; DKNNSIAKLLQHLSKS; KNNSIAKLLQHLSKSE; NNSIAKLLQHLSKSED; NSIAKLLQHLSKSEDQ; SIAKLLQHLSKSEDQA; IAKLLQHLSKSEDQAN; AKLLQHLSKSEDQANK; KLLQHLSKSEDQANKT; LLQHLSKSEDQANKTS; LQHLSKSEDQANKTST; QHLSKSEDQANKTSTS; HLSKSEDQANKTSTSE; LSKSEDQANKTSTSED; SKSEDQANKTSTSEDQ; KSEDQANKTSTSEDQK; SEDQANKTSTSEDQKE; EDQANKTSTSEDQKEL; DQANKTSTSEDQKELE; QANKTSTSEDQKELEI; ANKTSTSEDQKELEIT; NKTSTSEDQKELEITE; KTSTSEDQKELEITEN; TSTSEDQKELEITENK; STSEDQKELEITENKE; TSEDQKELEITENKEQ; SEDQKELEITENKEQE; EDQKELEITENKEQEH; DQKELEITENKEQEHE; QKELEITENKEQEHEK; KELEITENKEQEHEKL; ELEITENKEQEHEKLS; LEITENKEQEHEKLSQ; EITENKEQEHEKLSQV; ITENKEQEHEKLSQVA; TENKEQEHEKLSQVAQ; ENKEQEHEKLSQVAQH; NKEQEHEKLSQVAQHA; KEQEHEKLSQVAQHAP; EQEHEKLSQVAQHAPN; QEHEKLSQVAQHAPNS; EHEKLSQVAQHAPNSK; HEKLSQVAQHAPNSKI; EKLSQVAQHAPNSKIE; KLSQVAQHAPNSKIEK; LSQVAQHAPNSKIEKV; SQVAQHAPNSKIEKVK; QVAQHAPNSKIEKVKS; VAQHAPNSKIEKVKSD; AQHAPNSKIEKVKSDG; QHAPNSKIEKVKSDGK;

	HAPNSKIEKVKSDGKP; APNSKIEKVKSDGKPV; PNSKIEKVKSDGKPVP; NSKIEKVKSDGKPVPG; SKIEKVKSDGKPVPGD; KIEKVKSDGKPVPGDK; IEKVKSDGKPVPGDKI; EKVKSDGKPVPGDKIL; KVKSDGKPVPGDKILS; VKSDGKPVPGDKILSS; KSDGKPVPGDKILSSN; SDGKPVPGDKILSSNK; DGKPVPGDKILSSNKD; GKPVPGDKILSSNKDI; KPVPGDKILSSNKDIY; PVPGDKILSSNKDIYN; VPGDKILSSNKDIYNS; PGDKILSSNKDIYNSY; GDKILSSNKDIYNSYI; DKILSSNKDIYNSYIP; KILSSNKDIYNSYIPE; ILSSNKDIYNSYIPEV; LSSNKDIYNSYIPEVK; SSNKDIYNSYIPEVKE; SNKDIYNSYIPEVKEE; NKDIYNSYIPEVKEEI; KDIYNSYIPEVKEEIV; DIYNSYIPEVKEEIVY; IYNSYIPEVKEEIVYE; YNSYIPEVKEEIVYEI; NSYIPEVKEEIVYEIL; SYIPEVKEEIVYEILE; YIPEVKEEIVYEILEE; IPEVKEEIVYEILEEV; PEVKEEIVYEILEEVI; EVKEEIVYEILEEVII; VKEEIVYEILEEVIIP; KEEIVYEILEEVIIPE; EEIVYEILEEVIIPET; EIVYEILEEVIIPETK; IVYEILEEVIIPETKI; VYEILEEVIIPETKIP; YEILEEVIIPETKIPE; EILEEVIIPETKIPEI; ILEEVIIPETKIPEIT; LEEVIIPETKIPEITE; EEVIIPETKIPEITEE; EVIIPETKIPEITEEV; VIIPETKIPEITEEVI; IIPETKIPEITEEVIM; IPETKIPEITEEVIMP; PETKIPEITEEVIMPI; ETKIPEITEEVIMPIP; TKIPEITEEVIMPIPQ; KIPEITEEVIMPIPQT; IPEITEEVIMPIPQTI; PEITEEVIMPIPQTID; EITEEVIMPIPQTIDF; ITEEVIMPIPQTIDFY; TEEVIMPIPQTIDFYI; EEVIMPIPQTIDFYIE; EVIMPIPQTIDFYIEP; VIMPIPQTIDFYIEPR; IMPIPQTIDFYIEPRP; MPIPQTIDFYIEPRPI; PIPQTIDFYIEPRPIS; IPQTIDFYIEPRPISS; PQTIDFYIEPRPISSF; QTIDFYIEPRPISSFL; TIDFYIEPRPISSFLT; IDFYIEPRPISSFLTQ; DFYIEPRPISSFLTQG; FYIEPRPISSFLTQGT; YIEPRPISSFLTQGTS; IEPRPISSFLTQGTSP; EPRPISSFLTQGTSPS; PRPISSFLTQGTSPSI; RPISSFLTQGTSPSIT; PISSFLTQGTSPSITS; ISSFLTQGTSPSITST; SSFLTQGTSPSITSTI; SFLTQGTSPSITSTIK; FLTQGTSPSITSTIKS; LTQGTSPSITSTIKSY; TQGTSPSITSTIKSYK; QGTSPSITSTIKSYKE; GTSPSITSTIKSYKEL; TSPSITSTIKSYKELA; SPSITSTIKSYKELAK; PSITSTIKSYKELAKE; SITSTIKSYKELAKEK; ITSTIKSYKELAKEKI; TSTIKSYKELAKEKIN; STIKSYKELAKEKINN; TIKSYKELAKEKINNG; IKSYKELAKEKINNGL; KSYKELAKEKINNGLN; SYKELAKEKINNGLNI; YKELAKEKINNGLNIV; KELAKEKINNGLNIVQ; ELAKEKINNGLNIVQK; LAKEKINNGLNIVQKI; AKEKINNGLNIVQKIT; KEKINNGLNIVQKITQ; EKINNGLNIVQKITQN; KINNGLNIVQKITQNI; INNGLNIVQKITQNID; NNGLNIVQKITQNIDN; NGLNIVQKITQNIDNI; GLNIVQKITQNIDNIT; LNIVQKITQNIDNITE; NIVQKITQNIDNITEN; IVQKITQNIDNITENL; VQKITQNIDNITENLN; QKITQNIDNITENLNS; KITQNIDNITENLNSK; ITQNIDNITENLNSKE; TQNIDNITENLNSKET; QNIDNITENLNSKETP; NIDNITENLNSKETPK; IDNITENLNSKETPKE; DNITENLNSKETPKEI; NITENLNSKETPKEIS; ITENLNSKETPKEISG; TENLNSKETPKEISGK; ENLNSKETPKEISGKE; NLNSKETPKEISGKEV; LNSKETPKEISGKEVE; NSKETPKEISGKEVEE; SKETPKEISGKEVEEK; KETPKEISGKEVEEKI; ETPKEISGKEVEEKIT; TPKEISGKEVEEKITH; PKEISGKEVEEKITHP; KEISGKEVEEKITHPI; EISGKEVEEKITHPIF; ISGKEVEEKITHPIFD; SGKEVEEKITHPIFDH; GKEVEEKITHPIFDHI; KEVEEKITHPIFDHIT; EVEEKITHPIFDHITG; VEEKITHPIFDHITGS; EEKITHPIFDHITGSG; EKITHPIFDHITGSGN; KITHPIFDHITGSGNN; ITHPIFDHITGSGNNP; THPIFDHITGSGNNPG; HPIFDHITGSGNNPGQ; PIFDHITGSGNNPGQD; IFDHITGSGNNPGQDS; FDHITGSGNNPGQDSI; DHITGSGNNPGQDSIS; HITGSGNNPGQDSISN;

	ITGSGNNPGQDSISNT; TGSGNNPGQDSISNTW; GSGNNPGQDSISNTWG; SGNNPGQDSISNTWGE; GNNPGQDSISNTWGEG; NNPGQDSISNTWGEGL; NPGQDSISNTWGEGLE; PGQDSISNTWGEGLEI; GQDSISNTWGEGLEIG; QDSISNTWGEGLEIGG; DSISNTWGEGLEIGGD; SISNTWGEGLEIGGDS; ISNTWGEGLEIGGDSN; SNTWGEGLEIGGDSNF; NTWGEGLEIGGDSNFF; TWGEGLEIGGDSNFFT; WGEGLEIGGDSNFFTN; GEGLEIGGDSNFFTNL; EGLEIGGDSNFFTNLE; GLEIGGDSNFFTNLEE; LEIGGDSNFFTNLEEV; EIGGDSNFFTNLEEVR; IGGDSNFFTNLEEVRS; GGDSNFFTNLEEVRSS; GDSNFFTNLEEVRSSI; DSNFFTNLEEVRSSIR; SNFFTNLEEVRSSIRT; NFFTNLEEVRSSIRTK; FFTNLEEVRSSIRTKI; FTNLEEVRSSIRTKIK; TNLEEVRSSIRTKIKV; NLEEVRSSIRTKIKVS; LEEVRSSIRTKIKVSD; EEVRSSIRTKIKVSDG; EVRSSIRTKIKVSDGT; VRSSIRTKIKVSDGTE; RSSIRTKIKVSDGTEQ; SSIRTKIKVSDGTEQT; SIRTKIKVSDGTEQTK; IRTKIKVSDGTEQTKD; RTKIKVSDGTEQTKDK; TKIKVSDGTEQTKDKV; KIKVSDGTEQTKDKVE; IKVSDGTEQTKDKVEI; KVSDGTEQTKDKVEID; VSDGTEQTKDKVEIDE; SDGTEQTKDKVEIDEI; DGTEQTKDKVEIDEII; GTEQTKDKVEIDEIIE; TEQTKDKVEIDEIIED; EQTKDKVEIDEIIEDL; QTKDKVEIDEIIEDLQ; TKDKVEIDEIIEDLQK; KDKVEIDEIIEDLQKL; DKVEIDEIIEDLQKLK; KVEIDEIIEDLQKLKE; VEIDEIIEDLQKLKEF; EIDEIIEDLQKLKEFL; IDEIIEDLQKLKEFLE; DEIIEDLQKLKEFLEK; EIIEDLQKLKEFLEKL; IIEDLQKLKEFLEKLK; IEDLQKLKEFLEKLKK; EDLQKLKEFLEKLKKY; DLQKLKEFLEKLKKYL; LQKLKEFLEKLKKYLK; QKLKEFLEKLKKYLKD; KLKEFLEKLKKYLKDT; LKEFLEKLKKYLKDTN; KEFLEKLKKYLKDTNN; EFLEKLKKYLKDTNNL; FLEKLKKYLKDTNNLS; LEKLKKYLKDTNNLSA; EKLKKYLKDTNNLSAI; KLKKYLKDTNNLSAIE; LKKYLKDTNNLSAIEE; KKYLKDTNNLSAIEES; KYLKDTNNLSAIEESV; YLKDTNNLSAIEESVK; LKDTNNLSAIEESVKG; KDTNNLSAIEESVKGL; DTNNLSAIEESVKGLS;
Seq 20	13 mers: MIKMSLNYTEINT; IKMSLNYTEINTL; KMSLNYTEINTLI; MSLNYTEINTLIK; SLNYTEINTLIKE; LNYTEINTLIKEI; NYTEINTLIKEIP; YTEINTLIKEIPF; TEINTLIKEIPFT; EINTLIKEIPFTN; INTLIKEIPFTNS; NTLIKEIPFTNSL; TLIKEIPFTNSLI; LIKEIPFTNSLIT; IKEIPFTNSLITK; KEIPFTNSLITKI; EIPFTNSLITKII; IPFTNSLITKIIQ; PFTNSLITKIIQP; FTNSLITKIIQPD; TNSLITKIIQPDY; NSLITKIIQPDYK; SLITKIIQPDYKS; LITKIIQPDYKSL; ITKIIQPDYKSLV; TKIIQPDYKSLVL; KIIQPDYKSLVLE; IIQPDYKSLVLEI; IQPDYKSLVLEIY; QPDYKSLVLEIYN; PDYKSLVLEIYNK; DYKSLVLEIYNKI; YKSLVLEIYNKID; KSLVLEIYNKIDN; SLVLEIYNKIDNK; LVLEIYNKIDNKK; VLEIYNKIDNKKF; LEIYNKIDNKKFK; EIYNKIDNKKFKI; IYNKIDNKKFKIL; YNKIDNKKFKILI; NKIDNKKFKILIC; KIDNKKFKILICL; IDNKKFKILICLN; DNKKFKILICLNP; NKKFKILICLNPN; KKFKILICLNPNT; KFKILICLNPNTT; FKILICLNPNTTR; KILICLNPNTTRF; ILICLNPNTTRFH; LICLNPNTTRFHI; ICLNPNTTRFHIT; CLNPNTTRFHITK; LNPNTTRFHITKK; NPNTTRFHITKKN; PNTTRFHITKKNF; NTTRFHITKKNFK; TTRFHITKKNFKK; TRFHITKKNFKKN;

	RFHITKKNFKKNA; FHITKKNFKKNAL; HITKKNFKKNALK; ITKKNFKKNALKL; TKKNFKKNALKLR; KKNFKKNALKLRF; KNFKKNALKLRFS; NFKKNALKLRFSD; FKKNALKLRFSDF; KKNALKLRFSDFL; KNALKLRFSDFLK; NALKLRFSDFLKS; ALKLRFSDFLKSK; LKLRFSDFLKSKI; KLRFSDFLKSKIQ; LRFSDFLKSKIQN; RFSDFLKSKIQNG; FSDFLKSKIQNGK; SDFLKSKIQNGKI; DFLKSKIQNGKII; FLKSKIQNGKIIK; LKSKIQNGKIIKA; KSKIQNGKIIKAF; SKIQNGKIIKAFQ; KIQNGKIIKAFQM; IQNGKIIKAFQMK; QNGKIIKAFQMKN; NGKIIKAFQMKNE; GKIIKAFQMKNER; KIIKAFQMKNERI; IIKAFQMKNERII; IKAFQMKNERIIS; KAFQMKNERIISL; AFQMKNERIISLE; FQMKNERIISLEI; QMKNERIISLEIL; MKNERIISLEILQ; KNERIISLEILQK; NERIISLEILQKD; ERIISLEILQKDM; RIISLEILQKDMI; IISLEILQKDMII; ISLEILQKDMIIL; SLEILQKDMIILF; LEILQKDMIILFI; EILQKDMIILFIK; ILQKDMIILFIKL; LQKDMIILFIKLW; QKDMIILFIKLWP; KDMIILFIKLWPS; DMIILFIKLWPSS; MIILFIKLWPSSP; IILFIKLWPSSPN; ILFIKLWPSSPNI; LFIKLWPSSPNII; FIKLWPSSPNIIA; IKLWPSSPNIIAT; KLWPSSPNIIATN; LWPSSPNIIATNS; WPSSPNIIATNSN; PSSPNIIATNSNF; SSPNIIATNSNFK; SPNIIATNSNFKI; PNIIATNSNFKIL; NIIATNSNFKILD; IIATNSNFKILDA; IATNSNFKILDAY; ATNSNFKILDAYY; TNSNFKILDAYYR; NSNFKILDAYYRR; SNFKILDAYYRRP; NFKILDAYYRRPK; FKILDAYYRRPKI; KILDAYYRRPKIK; ILDAYYRRPKIKE; LDAYYRRPKIKET; DAYYRRPKIKETT; AYYRRPKIKETTG; YYRRPKIKETTGE; YRRPKIKETTGEI; RRPKIKETTGEIF; RPKIKETTGEIFL; PKIKETTGEIFLK; KIKETTGEIFLKA; IKETTGEIFLKAK; KETTGEIFLKAKE; ETTGEIFLKAKEI; TTGEIFLKAKEIH; TGEIFLKAKEIHE; GEIFLKAKEIHES; EIFLKAKEIHESN; IFLKAKEIHESNK; FLKAKEIHESNKM; LKAKEIHESNKMS; KAKEIHESNKMSD; AKEIHESNKMSDK; KEIHESNKMSDKK; EIHESNKMSDKKI; IHESNKMSDKKIM; HESNKMSDKKIME; ESNKMSDKKIMEL; SNKMSDKKIMELK; NKMSDKKIMELKE; KMSDKKIMELKEE; MSDKKIMELKEEY; SDKKIMELKEEYN; DKKIMELKEEYNN; KKIMELKEEYNNT; KIMELKEEYNNTS; IMELKEEYNNTSY; MELKEEYNNTSYT; ELKEEYNNTSYTS; LKEEYNNTSYTSY; KEEYNNTSYTSYS; EEYNNTSYTSYSE; EYNNTSYTSYSEF; YNNTSYTSYSEFL; NNTSYTSYSEFLE; NTSYTSYSEFLEN; TSYTSYSEFLENY; SYTSYSEFLENYY; YTSYSEFLENYYE; TSYSEFLENYYES; SYSEFLENYYESL; YSEFLENYYESLN; SEFLENYYESLND; EFLENYYESLNDQ; FLENYYESLNDQI; LENYYESLNDQIK; ENYYESLNDQIKK; NYYESLNDQIKKT; YYESLNDQIKKTN; YESLNDQIKKTNI; ESLNDQIKKTNIK; SLNDQIKKTNIKE; LNDQIKKTNIKEL; NDQIKKTNIKELL; DQIKKTNIKELLI; QIKKTNIKELLIE; IKKTNIKELLIEK; KKTNIKELLIEKY; KTNIKELLIEKYK; TNIKELLIEKYKK; NIKELLIEKYKKE; IKELLIEKYKKEL; KELLIEKYKKELI; ELLIEKYKKELIV; LLIEKYKKELIVL; LIEKYKKELIVLE; IEKYKKELIVLEK; EKYKKELIVLEKR; KYKKELIVLEKRI; YKKELIVLEKRID;

	KKELIVLEKRIDS; KELIVLEKRIDSL; ELIVLEKRIDSLK; LIVLEKRIDSLKQ; IVLEKRIDSLKQQ; VLEKRIDSLKQQI; LEKRIDSLKQQIK; EKRIDSLKQQIKL; KRIDSLKQQIKLL; RIDSLKQQIKLLE; IDSLKQQIKLLEN; DSLKQQIKLLENI; SLKQQIKLLENIE; LKQQIKLLENIEN; KQQIKLLENIENE; QQIKLLENIENEK; QIKLLENIENEKE; IKLLENIENEKEK; KLLENIENEKEKG; LLENIENEKEKGE; LENIENEKEKGEL; ENIENEKEKGELI; NIENEKEKGELIL; IENEKEKGELILL; ENEKEKGELILLN; NEKEKGELILLNI; EKEKGELILLNIN; KEKGELILLNINK; EKGELILLNINKI; KGELILLNINKIQ; GELILLNINKIQK; ELILLNINKIQKG; LILLNINKIQKGI; ILLNINKIQKGIK; LLNINKIQKGIKE; LNINKIQKGIKEI; NINKIQKGIKEIN; INKIQKGIKEINL; NKIQKGIKEINLL; KIQKGIKEINLLN; IQKGIKEINLLNY; QKGIKEINLLNYK; KGIKEINLLNYKE; GIKEINLLNYKEE; IKEINLLNYKEEK; KEINLLNYKEEKI; EINLLNYKEEKIK; INLLNYKEEKIKI; NLLNYKEEKIKIS; LLNYKEEKIKISL; LNYKEEKIKISLN; NYKEEKIKISLNQ; YKEEKIKISLNQS; KEEKIKISLNQSL; EEKIKISLNQSLS; EKIKISLNQSLSP; KIKISLNQSLSPK; IKISLNQSLSPKE; KISLNQSLSPKEN; ISLNQSLSPKENA; SLNQSLSPKENAL; LNQSLSPKENALQ; NQSLSPKENALQY; QSLSPKENALQYF; SLSPKENALQYFK; LSPKENALQYFKA; SPKENALQYFKAY; PKENALQYFKAYK; KENALQYFKAYKK; ENALQYFKAYKKG; NALQYFKAYKKGK; ALQYFKAYKKGKN; LQYFKAYKKGKNS; QYFKAYKKGKNSF; YFKAYKKGKNSFK; FKAYKKGKNSFKT; KAYKKGKNSFKTI; AYKKGKNSFKTIQ; YKKGKNSFKTIQN; KKGKNSFKTIQNQ; KGKNSFKTIQNQL; GKNSFKTIQNQLK; KNSFKTIQNQLKD; NSFKTIQNQLKDN; SFKTIQNQLKDNL; FKTIQNQLKDNLD; KTIQNQLKDNLDK; TIQNQLKDNLDKF; IQNQLKDNLDKFN; QNQLKDNLDKFNL; NQLKDNLDKFNLI; QLKDNLDKFNLIQ; LKDNLDKFNLIQS; KDNLDKFNLIQSK; DNLDKFNLIQSKI; NLDKFNLIQSKIT; LDKFNLIQSKITM; DKFNLIQSKITML; KFNLIQSKITMLK; FNLIQSKITMLKV; NLIQSKITMLKVE; LIQSKITMLKVEN; IQSKITMLKVENL; QSKITMLKVENLI; SKITMLKVENLIP; KITMLKVENLIPE; ITMLKVENLIPEE; TMLKVENLIPEEE; MLKVENLIPEEEY; LKVENLIPEEEYN; KVENLIPEEEYNQ; VENLIPEEEYNQE; ENLIPEEEYNQEK; NLIPEEEYNQEKT; LIPEEEYNQEKTA; IPEEEYNQEKTAI; PEEEYNQEKTAIK; EEEYNQEKTAIKE; EEYNQEKTAIKEK; EYNQEKTAIKEKE; YNQEKTAIKEKEK; NQEKTAIKEKEKT; QEKTAIKEKEKTP; EKTAIKEKEKTPK; KTAIKEKEKTPKI; TAIKEKEKTPKIG; AIKEKEKTPKIGL; IKEKEKTPKIGLH; KEKEKTPKIGLHF; EKEKTPKIGLHFT; KEKTPKIGLHFTY; EKTPKIGLHFTYC; KTPKIGLHFTYCG; TPKIGLHFTYCGF; PKIGLHFTYCGFE; KIGLHFTYCGFEI; IGLHFTYCGFEIL; GLHFTYCGFEILI; LHFTYCGFEILIG; HFTYCGFEILIGR; FTYCGFEILIGRN; TYCGFEILIGRNA; YCGFEILIGRNAK; CGFEILIGRNAKE; GFEILIGRNAKEN; FEILIGRNAKEND; EILIGRNAKENDK; ILIGRNAKENDKL; LIGRNAKENDKLL; IGRNAKENDKLLR; GRNAKENDKLLRH; RNAKENDKLLRHC; NAKENDKLLRHCV;

AKENDKLLRHCVK; KENDKLLRHCVKG; ENDKLLRHCVKGN;
NDKLLRHCVKGND; DKLLRHCVKGNDY; KLLRHCVKGNDYW;
LLRHCVKGNDYWL; LRHCVKGNDYWLH; RHCVKGNDYWLHT;
HCVKGNDYWLHTR; CVKGNDYWLHTRD; VKGNDYWLHTRDY;
KGNDYWLHTRDYP; GNDYWLHTRDYPG; NDYWLHTRDYPGA;
DYWLHTRDYPGAY; YWLHTRDYPGAYV; WLHTRDYPGAYVF;
LHTRDYPGAYVFI; HTRDYPGAYVFIK; TRDYPGAYVFIKN;
RDYPGAYVFIKNQ; DYPGAYVFIKNQK; YPGAYVFIKNQKN;
PGAYVFIKNQKNK; GAYVFIKNQKNKT; AYVFIKNQKNKTP;
YVFIKNQKNKTPS; VFIKNQKNKTPSL; FIKNQKNKTPSLD;
IKNQKNKTPSLDV; KNQKNKTPSLDVL; NQKNKTPSLDVLL;
QKNKTPSLDVLLG; KNKTPSLDVLLGA; NKTPSLDVLLGAG;
KTPSLDVLLGAGN; TPSLDVLLGAGNL; PSLDVLLGAGNLC;
SLDVLLGAGNLCV; LDVLLGAGNLCVF; DVLLGAGNLCVFY;
VLLGAGNLCVFYT; LLGAGNLCVFYTK; LGAGNLCVFYTKL;
GAGNLCVFYTKLA; AGNLCVFYTKLAK; GNLCVFYTKLAKK;
NLCVFYTKLAKKS; LCVFYTKLAKKSG; CVFYTKLAKKSGK;
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AKKSGKADLYYTQ; KKSGKADLYYTQV; KSGKADLYYTQVK;
SGKADLYYTQVKN; GKADLYYTQVKNL; KADLYYTQVKNLR;
ADLYYTQVKNLRR; DLYYTQVKNLRRV; LYYTQVKNLRRVK;
YYTQVKNLRRVKN; YTQVKNLRRVKNK; TQVKNLRRVKNKK;
QVKNLRRVKNKKL; VKNLRRVKNKKLG; KNLRRVKNKKLGL;
NLRRVKNKKLGLV; LRRVKNKKLGLVI; RRVKNKKLGLVIP;
RVKNKKLGLVIPK; VKNKKLGLVIPKA; KNKKLGLVIPKAE;
NKKLGLVIPKAEK; KKLGLVIPKAEKN; KLGLVIPKAEKNL;
LGLVIPKAEKNLH; GLVIPKAEKNLHI; LVIPKAEKNLHIK;
VIPKAEKNLHIKL; IPKAEKNLHIKLD; PKAEKNLHIKLDE;
KAEKNLHIKLDEN; AEKNLHIKLDENL; EKNLHIKLDENLI;
KNLHIKLDENLIK; NLHIKLDENLIKK; LHIKLDENLIKKI;
HIKLDENLIKKIK; IKLDENLIKKIKN; KLDENLIKKIKNQ;
LDENLIKKIKNQT;

14 mers:
MIKMSLNYTEINTL; IKMSLNYTEINTLI; KMSLNYTEINTLIK;
MSLNYTEINTLIKE; SLNYTEINTLIKEI; LNYTEINTLIKEIP;
NYTEINTLIKEIPF; YTEINTLIKEIPFT; TEINTLIKEIPFTN;
EINTLIKEIPFTNS; INTLIKEIPFTNSL; NTLIKEIPFTNSLI;
TLIKEIPFTNSLIT; LIKEIPFTNSLITK; IKEIPFTNSLITKI;
KEIPFTNSLITKII; EIPFTNSLITKIIQ; IPFTNSLITKIIQP;
PFTNSLITKIIQPD; FTNSLITKIIQPDY; TNSLITKIIQPDYK;
NSLITKIIQPDYKS; SLITKIIQPDYKSL; LITKIIQPDYKSLV;
ITKIIQPDYKSLVL; TKIIQPDYKSLVLE; KIIQPDYKSLVLEI;
IIQPDYKSLVLEIY; IQPDYKSLVLEIYN; QPDYKSLVLEIYNK;
PDYKSLVLEIYNKI; DYKSLVLEIYNKID; YKSLVLEIYNKIDN;
KSLVLEIYNKIDNK; SLVLEIYNKIDNKK; LVLEIYNKIDNKKF;
VLEIYNKIDNKKFK; LEIYNKIDNKKFKI; EIYNKIDNKKFKIL;
IYNKIDNKKFKILI; YNKIDNKKFKILIC; NKIDNKKFKILICL;
KIDNKKFKILICLN; IDNKKFKILICLNP; DNKKFKILICLNPN;
NKKFKILICLNPNT; KKFKILICLNPNTT; KFKILICLNPNTTR;

	FKILICLNPNTTRF; KILICLNPNTTRFH; ILICLNPNTTRFHI; LICLNPNTTRFHIT; ICLNPNTTRFHITK; CLNPNTTRFHITKK; LNPNTTRFHITKKN; NPNTTRFHITKKNF; PNTTRFHITKKNFK; NTTRFHITKKNFKK; TTRFHITKKNFKKN; TRFHITKKNFKKNA; RFHITKKNFKKNAL; FHITKKNFKKNALK; HITKKNFKKNALKL; ITKKNFKKNALKLR; TKKNFKKNALKLRF; KKNFKKNALKLRFS; KNFKKNALKLRFSD; NFKKNALKLRFSDF; FKKNALKLRFSDFL; KKNALKLRFSDFLK; KNALKLRFSDFLKS; NALKLRFSDFLKSK; ALKLRFSDFLKSKI; LKLRFSDFLKSKIQ; KLRFSDFLKSKIQN; LRFSDFLKSKIQNG; RFSDFLKSKIQNGK; FSDFLKSKIQNGKI; SDFLKSKIQNGKII; DFLKSKIQNGKIIK; FLKSKIQNGKIIKA; LKSKIQNGKIIKAF; KSKIQNGKIIKAFQ; SKIQNGKIIKAFQM; KIQNGKIIKAFQMK; IQNGKIIKAFQMKN; QNGKIIKAFQMKNE; NGKIIKAFQMKNER; GKIIKAFQMKNERI; KIIKAFQMKNERII; IIKAFQMKNERIIS; IKAFQMKNERIISL; KAFQMKNERIISLE; AFQMKNERIISLEI; FQMKNERIISLEIL; QMKNERIISLEILQ; MKNERIISLEILQK; KNERIISLEILQKD; NERIISLEILQKDM; ERIISLEILQKDMI; RIISLEILQKDMII; IISLEILQKDMIIL; ISLEILQKDMIILF; SLEILQKDMIILFI; LEILQKDMIILFIK; EILQKDMIILFIKL; ILQKDMIILFIKLW; LQKDMIILFIKLWP; QKDMIILFIKLWPS; KDMIILFIKLWPSS; DMIILFIKLWPSSP; MIILFIKLWPSSPN; IILFIKLWPSSPNI; ILFIKLWPSSPNII; LFIKLWPSSPNIIA; FIKLWPSSPNIIAT; IKLWPSSPNIIATN; KLWPSSPNIIATNS; LWPSSPNIIATNSN; WPSSPNIIATNSNF; PSSPNIIATNSNFK; SSPNIIATNSNFKI; SPNIIATNSNFKIL; PNIIATNSNFKILD; NIIATNSNFKILDA; IIATNSNFKILDAY; IATNSNFKILDAYY; ATNSNFKILDAYYR; TNSNFKILDAYYRR; NSNFKILDAYYRRP; SNFKILDAYYRRPK; NFKILDAYYRRPKI; FKILDAYYRRPKIK; KILDAYYRRPKIKE; ILDAYYRRPKIKET; LDAYYRRPKIKETT; DAYYRRPKIKETTG; AYYRRPKIKETTGE; YYRRPKIKETTGEI; YRRPKIKETTGEIF; RRPKIKETTGEIFL; RPKIKETTGEIFLK; PKIKETTGEIFLKA; KIKETTGEIFLKAK; IKETTGEIFLKAKE; KETTGEIFLKAKEI; ETTGEIFLKAKEIH; TTGEIFLKAKEIHE; TGEIFLKAKEIHES; GEIFLKAKEIHESN; EIFLKAKEIHESNK; IFLKAKEIHESNKM; FLKAKEIHESNKMS; LKAKEIHESNKMSD; KAKEIHESNKMSDK; AKEIHESNKMSDKK; KEIHESNKMSDKKI; EIHESNKMSDKKIM; IHESNKMSDKKIME; HESNKMSDKKIMEL; ESNKMSDKKIMELK; SNKMSDKKIMELKE; NKMSDKKIMELKEE; KMSDKKIMELKEEY; MSDKKIMELKEEYN; SDKKIMELKEEYNN; DKKIMELKEEYNNT; KKIMELKEEYNNTS; KIMELKEEYNNTSY; IMELKEEYNNTSYT; MELKEEYNNTSYTS; ELKEEYNNTSYTSY; LKEEYNNTSYTSYS; KEEYNNTSYTSYSE; EEYNNTSYTSYSEF; EYNNTSYTSYSEFL; YNNTSYTSYSEFLE; NNTSYTSYSEFLEN; NTSYTSYSEFLENY; TSYTSYSEFLENYY; SYTSYSEFLENYYE; YTSYSEFLENYYES; TSYSEFLENYYESL; SYSEFLENYYESLN; YSEFLENYYESLND; SEFLENYYESLNDQ; EFLENYYESLNDQI; FLENYYESLNDQIK; LENYYESLNDQIKK; ENYYESLNDQIKKT; NYYESLNDQIKKTN; YYESLNDQIKKTNI; YESLNDQIKKTNIK; ESLNDQIKKTNIKE; SLNDQIKKTNIKEL; LNDQIKKTNIKELL; NDQIKKTNIKELLI; DQIKKTNIKELLIE; QIKKTNIKELLIEK; IKKTNIKELLIEKY; KKTNIKELLIEKYK;

	KTNIKELLIEKYKK; TNIKELLIEKYKKE; NIKELLIEKYKKEL; IKELLIEKYKKELI; KELLIEKYKKELIV; ELLIEKYKKELIVL; LLIEKYKKELIVLE; LIEKYKKELIVLEK; IEKYKKELIVLEKR; EKYKKELIVLEKRI; KYKKELIVLEKRID; YKKELIVLEKRIDS; KKELIVLEKRIDSL; KELIVLEKRIDSLK; ELIVLEKRIDSLKQ; LIVLEKRIDSLKQQ; IVLEKRIDSLKQQI; VLEKRIDSLKQQIK; LEKRIDSLKQQIKL; EKRIDSLKQQIKLL; KRIDSLKQQIKLLE; RIDSLKQQIKLLEN; IDSLKQQIKLLENI; DSLKQQIKLLENIE; SLKQQIKLLENIEN; LKQQIKLLENIENE; KQQIKLLENIENEK; QQIKLLENIENEKE; QIKLLENIENEKEK; IKLLENIENEKEKG; KLLENIENEKEKGE; LLENIENEKEKGEL; LENIENEKEKGELI; ENIENEKEKGELIL; NIENEKEKGELILL; IENEKEKGELILLN; ENEKEKGELILLNI; NEKEKGELILLNIN; EKEKGELILLNINK; KEKGELILLNINKI; EKGELILLNINKIQ; KGELILLNINKIQK; GELILLNINKIQKG; ELILLNINKIQKGI; LILLNINKIQKGIK; ILLNINKIQKGIKE; LLNINKIQKGIKEI; LNINKIQKGIKEIN; NINKIQKGIKEINL; INKIQKGIKEINLL; NKIQKGIKEINLLN; KIQKGIKEINLLNY; IQKGIKEINLLNYK; QKGIKEINLLNYKE; KGIKEINLLNYKEE; GIKEINLLNYKEEK; IKEINLLNYKEEKI; KEINLLNYKEEKIK; EINLLNYKEEKIKI; INLLNYKEEKIKIS; NLLNYKEEKIKISL; LLNYKEEKIKISLN; LNYKEEKIKISLNQ; NYKEEKIKISLNQS; YKEEKIKISLNQSL; KEEKIKISLNQSLS; EEKIKISLNQSLSP; EKIKISLNQSLSPK; KIKISLNQSLSPKE; IKISLNQSLSPKEN; KISLNQSLSPKENA; ISLNQSLSPKENAL; SLNQSLSPKENALQ; LNQSLSPKENALQY; NQSLSPKENALQYF; QSLSPKENALQYFK; SLSPKENALQYFKA; LSPKENALQYFKAY; SPKENALQYFKAYK; PKENALQYFKAYKK; KENALQYFKAYKKG; ENALQYFKAYKKGK; NALQYFKAYKKGKN; ALQYFKAYKKGKNS; LQYFKAYKKGKNSF; QYFKAYKKGKNSFK; YFKAYKKGKNSFKT; FKAYKKGKNSFKTI; KAYKKGKNSFKTIQ; AYKKGKNSFKTIQN; YKKGKNSFKTIQNQ; KKGKNSFKTIQNQL; KGKNSFKTIQNQLK; GKNSFKTIQNQLKD; KNSFKTIQNQLKDN; NSFKTIQNQLKDNL; SFKTIQNQLKDNLD; FKTIQNQLKDNLDK; KTIQNQLKDNLDKF; TIQNQLKDNLDKFN; IQNQLKDNLDKFNL; QNQLKDNLDKFNLI; NQLKDNLDKFNLIQ; QLKDNLDKFNLIQS; LKDNLDKFNLIQSK; KDNLDKFNLIQSKI; DNLDKFNLIQSKIT; NLDKFNLIQSKITM; LDKFNLIQSKITML; DKFNLIQSKITMLK; KFNLIQSKITMLKV; FNLIQSKITMLKVE; NLIQSKITMLKVEN; LIQSKITMLKVENL; IQSKITMLKVENLI; QSKITMLKVENLIP; SKITMLKVENLIPE; KITMLKVENLIPEE; ITMLKVENLIPEEE; TMLKVENLIPEEEY; MLKVENLIPEEEYN; LKVENLIPEEEYNQ; KVENLIPEEEYNQE; VENLIPEEEYNQEK; ENLIPEEEYNQEKT; NLIPEEEYNQEKTA; LIPEEEYNQEKTAI; IPEEEYNQEKTAIK; PEEEYNQEKTAIKE; EEEYNQEKTAIKEK; EEYNQEKTAIKEKE; EYNQEKTAIKEKEK; YNQEKTAIKEKEKT; NQEKTAIKEKEKTP; QEKTAIKEKEKTPK; EKTAIKEKEKTPKI; KTAIKEKEKTPKIG; TAIKEKEKTPKIGL; AIKEKEKTPKIGLH; IKEKEKTPKIGLHF; KEKEKTPKIGLHFT; EKEKTPKIGLHFTY; KEKTPKIGLHFTYC; EKTPKIGLHFTYCG; KTPKIGLHFTYCGF; TPKIGLHFTYCGFE; PKIGLHFTYCGFEI; KIGLHFTYCGFEIL; IGLHFTYCGFEILI; GLHFTYCGFEILIG; LHFTYCGFEILIGR; HFTYCGFEILIGRN; FTYCGFEILIGRNA;

	TYCGFEILIGRNAK; YCGFEILIGRNAKE; CGFEILIGRNAKEN; GFEILIGRNAKEND; FEILIGRNAKENDK; EILIGRNAKENDKL; ILIGRNAKENDKLL; LIGRNAKENDKLLR; IGRNAKENDKLLRH; GRNAKENDKLLRHC; RNAKENDKLLRHCV; NAKENDKLLRHCVK; AKENDKLLRHCVKG; KENDKLLRHCVKGN; ENDKLLRHCVKGND; NDKLLRHCVKGNDY; DKLLRHCVKGNDYW; KLLRHCVKGNDYWL; LLRHCVKGNDYWLH; LRHCVKGNDYWLHT; RHCVKGNDYWLHTR; HCVKGNDYWLHTRD; CVKGNDYWLHTRDY; VKGNDYWLHTRDYP; KGNDYWLHTRDYPG; GNDYWLHTRDYPGA; NDYWLHTRDYPGAY; DYWLHTRDYPGAYV; YWLHTRDYPGAYVF; WLHTRDYPGAYVFI; LHTRDYPGAYVFIK; HTRDYPGAYVFIKN; TRDYPGAYVFIKNQ; RDYPGAYVFIKNQK; DYPGAYVFIKNQKN; YPGAYVFIKNQKNK; PGAYVFIKNQKNKT; GAYVFIKNQKNKTP; AYVFIKNQKNKTPS; YVFIKNQKNKTPSL; VFIKNQKNKTPSLD; FIKNQKNKTPSLDV; IKNQKNKTPSLDVL; KNQKNKTPSLDVLL; NQKNKTPSLDVLLG; QKNKTPSLDVLLGA; KNKTPSLDVLLGAG; NKTPSLDVLLGAGN; KTPSLDVLLGAGNL; TPSLDVLLGAGNLC; PSLDVLLGAGNLCV; SLDVLLGAGNLCVF; LDVLLGAGNLCVFY; DVLLGAGNLCVFYT; VLLGAGNLCVFYTK; LLGAGNLCVFYTKL; LGAGNLCVFYTKLA; GAGNLCVFYTKLAK; AGNLCVFYTKLAKK; GNLCVFYTKLAKKS; NLCVFYTKLAKKSG; LCVFYTKLAKKSGK; CVFYTKLAKKSGKA; VFYTKLAKKSGKAD; FYTKLAKKSGKADL; YTKLAKKSGKADLY; TKLAKKSGKADLYY; KLAKKSGKADLYYT; LAKKSGKADLYYTQ; AKKSGKADLYYTQV; KKSGKADLYYTQVK; KSGKADLYYTQVKN; SGKADLYYTQVKNL; GKADLYYTQVKNLR; KADLYYTQVKNLRR; ADLYYTQVKNLRRV; DLYYTQVKNLRRVK; LYYTQVKNLRRVKN; YYTQVKNLRRVKNK; YTQVKNLRRVKNKK; TQVKNLRRVKNKKL; QVKNLRRVKNKKLG; VKNLRRVKNKKLGL; KNLRRVKNKKLGLV; NLRRVKNKKLGLVI; LRRVKNKKLGLVIP; RRVKNKKLGLVIPK; RVKNKKLGLVIPKA; VKNKKLGLVIPKAE; KNKKLGLVIPKAEK; NKKLGLVIPKAEKN; KKLGLVIPKAEKNL; KLGLVIPKAEKNLH; LGLVIPKAEKNLHI; GLVIPKAEKNLHIK; LVIPKAEKNLHIKL; VIPKAEKNLHIKLD; IPKAEKNLHIKLDE; PKAEKNLHIKLDEN; KAEKNLHIKLDENL; AEKNLHIKLDENLI; EKNLHIKLDENLIK; KNLHIKLDENLIKK; NLHIKLDENLIKKI; LHIKLDENLIKKIK; HIKLDENLIKKIKN; IKLDENLIKKIKNQ; KLDENLIKKIKNQT; 15 mers: MIKMSLNYTEINTLI; IKMSLNYTEINTLIK; KMSLNYTEINTLIKE; MSLNYTEINTLIKEI; SLNYTEINTLIKEIP; LNYTEINTLIKEIPF; NYTEINTLIKEIPFT; YTEINTLIKEIPFTN; TEINTLIKEIPFTNS; EINTLIKEIPFTNSL; INTLIKEIPFTNSLI; NTLIKEIPFTNSLIT; TLIKEIPFTNSLITK; LIKEIPFTNSLITKI; IKEIPFTNSLITKII; KEIPFTNSLITKIIQ; EIPFTNSLITKIIQP; IPFTNSLITKIIQPD; PFTNSLITKIIQPDY; FTNSLITKIIQPDYK; TNSLITKIIQPDYKS; NSLITKIIQPDYKSL; SLITKIIQPDYKSLV; LITKIIQPDYKSLVL; ITKIIQPDYKSLVLE; TKIIQPDYKSLVLEI; KIIQPDYKSLVLEIY; IIQPDYKSLVLEIYN; IQPDYKSLVLEIYNK; QPDYKSLVLEIYNKI; PDYKSLVLEIYNKID; DYKSLVLEIYNKIDN; YKSLVLEIYNKIDNK; KSLVLEIYNKIDNKK; SLVLEIYNKIDNKKF; LVLEIYNKIDNKKFK; VLEIYNKIDNKKFKI; LEIYNKIDNKKFKIL; EIYNKIDNKKFKILI;

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	YESLNDQIKKTNIKE; ESLNDQIKKTNIKEL; SLNDQIKKTNIKELL; LNDQIKKTNIKELLI; NDQIKKTNIKELLIE; DQIKKTNIKELLIEK; QIKKTNIKELLIEKY; IKKTNIKELLIEKYK; KKTNIKELLIEKYKK; KTNIKELLIEKYKKE; TNIKELLIEKYKKEL; NIKELLIEKYKKELI; IKELLIEKYKKELIV; KELLIEKYKKELIVL; ELLIEKYKKELIVLE; LLIEKYKKELIVLEK; LIEKYKKELIVLEKR; IEKYKKELIVLEKRI; EKYKKELIVLEKRID; KYKKELIVLEKRIDS; YKKELIVLEKRIDSL; KKELIVLEKRIDSLK; KELIVLEKRIDSLKQ; ELIVLEKRIDSLKQQ; LIVLEKRIDSLKQQI; IVLEKRIDSLKQQIK; VLEKRIDSLKQQIKL; LEKRIDSLKQQIKLL; EKRIDSLKQQIKLLE; KRIDSLKQQIKLLEN; RIDSLKQQIKLLENI; IDSLKQQIKLLENIE; DSLKQQIKLLENIEN; SLKQQIKLLENIENE; LKQQIKLLENIENEK; KQQIKLLENIENEKE; QQIKLLENIENEKEK; QIKLLENIENEKEKG; IKLLENIENEKEKGE; KLLENIENEKEKGEL; LLENIENEKEKGELI; LENIENEKEKGELIL; ENIENEKEKGELILL; NIENEKEKGELILLN; IENEKEKGELILLNI; ENEKEKGELILLNIN; NEKEKGELILLNINK; EKEKGELILLNINKI; KEKGELILLNINKIQ; EKGELILLNINKIQK; KGELILLNINKIQKG; GELILLNINKIQKGI; ELILLNINKIQKGIK; LILLNINKIQKGIKE; ILLNINKIQKGIKEI; LLNINKIQKGIKEIN; LNINKIQKGIKEINL; NINKIQKGIKEINLL; INKIQKGIKEINLLN; NKIQKGIKEINLLNY; KIQKGIKEINLLNYK; IQKGIKEINLLNYKE; QKGIKEINLLNYKEE; KGIKEINLLNYKEEK; GIKEINLLNYKEEKI; IKEINLLNYKEEKIK; KEINLLNYKEEKIKI; EINLLNYKEEKIKIS; INLLNYKEEKIKISL; NLLNYKEEKIKISLN; LLNYKEEKIKISLNQ; LNYKEEKIKISLNQS; NYKEEKIKISLNQSL; YKEEKIKISLNQSLS; KEEKIKISLNQSLSP; EEKIKISLNQSLSPK; EKIKISLNQSLSPKE; KIKISLNQSLSPKEN; IKISLNQSLSPKENA; KISLNQSLSPKENAL; ISLNQSLSPKENALQ; SLNQSLSPKENALQY; LNQSLSPKENALQYF; NQSLSPKENALQYFK; QSLSPKENALQYFKA; SLSPKENALQYFKAY; LSPKENALQYFKAYK; SPKENALQYFKAYKK; PKENALQYFKAYKKG; KENALQYFKAYKKGK; ENALQYFKAYKKGKN; NALQYFKAYKKGKNS; ALQYFKAYKKGKNSF; LQYFKAYKKGKNSFK; QYFKAYKKGKNSFKT; YFKAYKKGKNSFKTI; FKAYKKGKNSFKTIQ; KAYKKGKNSFKTIQN; AYKKGKNSFKTIQNQ; YKKGKNSFKTIQNQL; KKGKNSFKTIQNQLK; KGKNSFKTIQNQLKD; GKNSFKTIQNQLKDN; KNSFKTIQNQLKDNL; NSFKTIQNQLKDNLD; SFKTIQNQLKDNLDK; FKTIQNQLKDNLDKF; KTIQNQLKDNLDKFN; TIQNQLKDNLDKFNL; IQNQLKDNLDKFNLI; QNQLKDNLDKFNLIQ; NQLKDNLDKFNLIQS; QLKDNLDKFNLIQSK; LKDNLDKFNLIQSKI; KDNLDKFNLIQSKIT; DNLDKFNLIQSKITM; NLDKFNLIQSKITML; LDKFNLIQSKITMLK; DKFNLIQSKITMLKV; KFNLIQSKITMLKVE; FNLIQSKITMLKVEN; NLIQSKITMLKVENL; LIQSKITMLKVENLI; IQSKITMLKVENLIP; QSKITMLKVENLIPE; SKITMLKVENLIPEE; KITMLKVENLIPEEE; ITMLKVENLIPEEEY; TMLKVENLIPEEEYN; MLKVENLIPEEEYNQ; LKVENLIPEEEYNQE; KVENLIPEEEYNQEK; VENLIPEEEYNQEKT; ENLIPEEEYNQEKTA; NLIPEEEYNQEKTAI; LIPEEEYNQEKTAIK; IPEEEYNQEKTAIKE; PEEEYNQEKTAIKEK; EEEYNQEKTAIKEKE; EEYNQEKTAIKEKEK; EYNQEKTAIKEKEKT; YNQEKTAIKEKEKTP; NQEKTAIKEKEKTPK; QEKTAIKEKEKTPKI; EKTAIKEKEKTPKIG; KTAIKEKEKTPKIGL; TAIKEKEKTPKIGLH; AIKEKEKTPKIGLHF; IKEKEKTPKIGLHFT; KEKEKTPKIGLHFTY; EKEKTPKIGLHFTYC; KEKTPKIGLHFTYCG; EKTPKIGLHFTYCGF;

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KIGLHFTYCGFEILI; IGLHFTYCGFEILIG; GLHFTYCGFEILIGR;
LHFTYCGFEILIGRN; HFTYCGFEILIGRNA; FTYCGFEILIGRNAK;
TYCGFEILIGRNAKE; YCGFEILIGRNAKEN; CGFEILIGRNAKEND;
GFEILIGRNAKENDK; FEILIGRNAKENDKL; EILIGRNAKENDKLL;
ILIGRNAKENDKLLR; LIGRNAKENDKLLRH; IGRNAKENDKLLRHC;
GRNAKENDKLLRHCV; RNAKENDKLLRHCVK; NAKENDKLLRHCVKG;
AKENDKLLRHCVKGN; KENDKLLRHCVKGND; ENDKLLRHCVKGNDY;
NDKLLRHCVKGNDYW; DKLLRHCVKGNDYWL; KLLRHCVKGNDYWLH;
LLRHCVKGNDYWLHT; LRHCVKGNDYWLHTR; RHCVKGNDYWLHTRD;
HCVKGNDYWLHTRDY; CVKGNDYWLHTRDYP; VKGNDYWLHTRDYPG;
KGNDYWLHTRDYPGA; GNDYWLHTRDYPGAY; NDYWLHTRDYPGAYV;
DYWLHTRDYPGAYVF; YWLHTRDYPGAYVFI; WLHTRDYPGAYVFIK;
LHTRDYPGAYVFIKN; HTRDYPGAYVFIKNQ; TRDYPGAYVFIKNQK;
RDYPGAYVFIKNQKN; DYPGAYVFIKNQKNK; YPGAYVFIKNQKNKT;
PGAYVFIKNQKNKTP; GAYVFIKNQKNKTPS; AYVFIKNQKNKTPSL;
YVFIKNQKNKTPSLD; VFIKNQKNKTPSLDV; FIKNQKNKTPSLDVL;
IKNQKNKTPSLDVLL; KNQKNKTPSLDVLLG; NQKNKTPSLDVLLGA;
QKNKTPSLDVLLGAG; KNKTPSLDVLLGAGN; NKTPSLDVLLGAGNL;
KTPSLDVLLGAGNLC; TPSLDVLLGAGNLCV; PSLDVLLGAGNLCVF;
SLDVLLGAGNLCVFY; LDVLLGAGNLCVFYT; DVLLGAGNLCVFYTK;
VLLGAGNLCVFYTKL; LLGAGNLCVFYTKLA; LGAGNLCVFYTKLAK;
GAGNLCVFYTKLAKK; AGNLCVFYTKLAKKS; GNLCVFYTKLAKKSG;
NLCVFYTKLAKKSGK; LCVFYTKLAKKSGKA; CVFYTKLAKKSGKAD;
VFYTKLAKKSGKADL; FYTKLAKKSGKADLY; YTKLAKKSGKADLYY;
TKLAKKSGKADLYYT; KLAKKSGKADLYYTQ; LAKKSGKADLYYTQV;
AKKSGKADLYYTQVK; KKSGKADLYYTQVKN; KSGKADLYYTQVKNL;
SGKADLYYTQVKNLR; GKADLYYTQVKNLRR; KADLYYTQVKNLRRV;
ADLYYTQVKNLRRVK; DLYYTQVKNLRRVKN; LYYTQVKNLRRVKNK;
YYTQVKNLRRVKNKK; YTQVKNLRRVKNKKL; TQVKNLRRVKNKKLG;
QVKNLRRVKNKKLGL; VKNLRRVKNKKLGLV; KNLRRVKNKKLGLVI;
NLRRVKNKKLGLVIP; LRRVKNKKLGLVIPK; RRVKNKKLGLVIPKA;
RVKNKKLGLVIPKAE; VKNKKLGLVIPKAEK; KNKKLGLVIPKAEKN;
NKKLGLVIPKAEKNL; KKLGLVIPKAEKNLH; KLGLVIPKAEKNLHI;
LGLVIPKAEKNLHIK; GLVIPKAEKNLHIKL; LVIPKAEKNLHIKLD;
VIPKAEKNLHIKLDE; IPKAEKNLHIKLDEN; PKAEKNLHIKLDENL;
KAEKNLHIKLDENLI; AEKNLHIKLDENLIK; EKNLHIKLDENLIKK;
KNLHIKLDENLIKKI; NLHIKLDENLIKKIK; LHIKLDENLIKKIKN;
HIKLDENLIKKIKNQ; IKLDENLIKKIKNQT;

16 mers:
MIKMSLNYTEINTLIK; IKMSLNYTEINTLIKE; KMSLNYTEINTLIKEI;
MSLNYTEINTLIKEIP; SLNYTEINTLIKEIPF; LNYTEINTLIKEIPFT;
NYTEINTLIKEIPFTN; YTEINTLIKEIPFTNS; TEINTLIKEIPFTNSL;
EINTLIKEIPFTNSLI; INTLIKEIPFTNSLIT; NTLIKEIPFTNSLITK;
TLIKEIPFTNSLITKI; LIKEIPFTNSLITKII; IKEIPFTNSLITKIIQ;
KEIPFTNSLITKIIQP; EIPFTNSLITKIIQPD; IPFTNSLITKIIQPDY;
PFTNSLITKIIQPDYK; FTNSLITKIIQPDYKS; TNSLITKIIQPDYKSL;
NSLITKIIQPDYKSLV; SLITKIIQPDYKSLVL; LITKIIQPDYKSLVLE;
ITKIIQPDYKSLVLEI; TKIIQPDYKSLVLEIY; KIIQPDYKSLVLEIYN;
IIQPDYKSLVLEIYNK; IQPDYKSLVLEIYNKI; QPDYKSLVLEIYNKID;

	PDYKSLVLEIYNKIDN; DYKSLVLEIYNKIDNK; YKSLVLEIYNKIDNKK; KSLVLEIYNKIDNKKF; SLVLEIYNKIDNKKFK; LVLEIYNKIDNKKFKI; VLEIYNKIDNKKFKIL; LEIYNKIDNKKFKILI; EIYNKIDNKKFKILIC; IYNKIDNKKFKILICL; YNKIDNKKFKILICLN; NKIDNKKFKILICLNP; KIDNKKFKILICLNPN; IDNKKFKILICLNPNT; DNKKFKILICLNPNTT; NKKFKILICLNPNTTR; KKFKILICLNPNTTRF; KFKILICLNPNTTRFH; FKILICLNPNTTRFHI; KILICLNPNTTRFHIT; ILICLNPNTTRFHITK; LICLNPNTTRFHITKK; ICLNPNTTRFHITKKN; CLNPNTTRFHITKKNF; LNPNTTRFHITKKNFK; NPNTTRFHITKKNFKK; PNTTRFHITKKNFKKN; NTTRFHITKKNFKKNA; TTRFHITKKNFKKNAL; TRFHITKKNFKKNALK; RFHITKKNFKKNALKL; FHITKKNFKKNALKLR; HITKKNFKKNALKLRF; ITKKNFKKNALKLRFS; TKKNFKKNALKLRFSD; KKNFKKNALKLRFSDF; KNFKKNALKLRFSDFL; NFKKNALKLRFSDFLK; FKKNALKLRFSDFLKS; KKNALKLRFSDFLKSK; KNALKLRFSDFLKSKI; NALKLRFSDFLKSKIQ; ALKLRFSDFLKSKIQN; LKLRFSDFLKSKIQNG; KLRFSDFLKSKIQNGK; LRFSDFLKSKIQNGKI; RFSDFLKSKIQNGKII; FSDFLKSKIQNGKIIK; SDFLKSKIQNGKIIKA; DFLKSKIQNGKIIKAF; FLKSKIQNGKIIKAFQ; LKSKIQNGKIIKAFQM; KSKIQNGKIIKAFQMK; SKIQNGKIIKAFQMKN; KIQNGKIIKAFQMKNE; IQNGKIIKAFQMKNER; QNGKIIKAFQMKNERI; NGKIIKAFQMKNERII; GKIIKAFQMKNERIIS; KIIKAFQMKNERIISL; IIKAFQMKNERIISLE; IKAFQMKNERIISLEI; KAFQMKNERIISLEIL; AFQMKNERIISLEILQ; FQMKNERIISLEILQK; QMKNERIISLEILQKD; MKNERIISLEILQKDM; KNERIISLEILQKDMI; NERIISLEILQKDMII; ERIISLEILQKDMIIL; RIISLEILQKDMIILF; IISLEILQKDMIILFI; ISLEILQKDMIILFIK; SLEILQKDMIILFIKL; LEILQKDMIILFIKLW; EILQKDMIILFIKLWP; ILQKDMIILFIKLWPS; LQKDMIILFIKLWPSS; QKDMIILFIKLWPSSP; KDMIILFIKLWPSSPN; DMIILFIKLWPSSPNI; MIILFIKLWPSSPNII; IILFIKLWPSSPNIIA; ILFIKLWPSSPNIIAT; LFIKLWPSSPNIIATN; FIKLWPSSPNIIATNS; IKLWPSSPNIIATNSN; KLWPSSPNIIATNSNF; LWPSSPNIIATNSNFK; WPSSPNIIATNSNFKI; PSSPNIIATNSNFKIL; SSPNIIATNSNFKILD; SPNIIATNSNFKILDA; PNIIATNSNFKILDAY; NIIATNSNFKILDAYY; IIATNSNFKILDAYYR; IATNSNFKILDAYYRR; ATNSNFKILDAYYRRP; TNSNFKILDAYYRRPK; NSNFKILDAYYRRPKI; SNFKILDAYYRRPKIK; NFKILDAYYRRPKIKE; FKILDAYYRRPKIKET; KILDAYYRRPKIKETT; ILDAYYRRPKIKETTG; LDAYYRRPKIKETTGE; DAYYRRPKIKETTGEI; AYYRRPKIKETTGEIF; YYRRPKIKETTGEIFL; YRRPKIKETTGEIFLK; RRPKIKETTGEIFLKA; RPKIKETTGEIFLKAK; PKIKETTGEIFLKAKE; KIKETTGEIFLKAKEI; IKETTGEIFLKAKEIH; KETTGEIFLKAKEIHE; ETTGEIFLKAKEIHES; TTGEIFLKAKEIHESN; TGEIFLKAKEIHESNK; GEIFLKAKEIHESNKM; EIFLKAKEIHESNKMS; IFLKAKEIHESNKMSD; FLKAKEIHESNKMSDK; LKAKEIHESNKMSDKK; KAKEIHESNKMSDKKI; AKEIHESNKMSDKKIM; KEIHESNKMSDKKIME; EIHESNKMSDKKIMEL; IHESNKMSDKKIMELK; HESNKMSDKKIMELKE; ESNKMSDKKIMELKEE; SNKMSDKKIMELKEEY; NKMSDKKIMELKEEYN; KMSDKKIMELKEEYNN; MSDKKIMELKEEYNNT; SDKKIMELKEEYNNTS; DKKIMELKEEYNNTSY; KKIMELKEEYNNTSYT; KIMELKEEYNNTSYTS; IMELKEEYNNTSYTSY; MELKEEYNNTSYTSYS; ELKEEYNNTSYTSYSE; LKEEYNNTSYTSYSEF; KEEYNNTSYTSYSEFL; EEYNNTSYTSYSEFLE; EYNNTSYTSYSEFLEN; YNNTSYTSYSEFLENY; NNTSYTSYSEFLENYY; NTSYTSYSEFLENYYE; TSYTSYSEFLENYYES; SYTSYSEFLENYYESL; YTSYSEFLENYYESLN; TSYSEFLENYYESLND;

	SYSEFLENYYESLNDQ; YSEFLENYYESLNDQI; SEFLENYYESLNDQIK; EFLENYYESLNDQIKK; FLENYYESLNDQIKKT; LENYYESLNDQIKKTN; ENYYESLNDQIKKTNI; NYYESLNDQIKKTNIK; YYESLNDQIKKTNIKE; YESLNDQIKKTNIKEL; ESLNDQIKKTNIKELL; SLNDQIKKTNIKELLI; LNDQIKKTNIKELLIE; NDQIKKTNIKELLIEK; DQIKKTNIKELLIEKY; QIKKTNIKELLIEKYK; IKKTNIKELLIEKYKK; KKTNIKELLIEKYKKE; KTNIKELLIEKYKKEL; TNIKELLIEKYKKELI; NIKELLIEKYKKELIV; IKELLIEKYKKELIVL; KELLIEKYKKELIVLE; ELLIEKYKKELIVLEK; LLIEKYKKELIVLEKR; LIEKYKKELIVLEKRI; IEKYKKELIVLEKRID; EKYKKELIVLEKRIDS; KYKKELIVLEKRIDSL; YKKELIVLEKRIDSLK; KKELIVLEKRIDSLKQ; KELIVLEKRIDSLKQQ; ELIVLEKRIDSLKQQI; LIVLEKRIDSLKQQIK; IVLEKRIDSLKQQIKL; VLEKRIDSLKQQIKLL; LEKRIDSLKQQIKLLE; EKRIDSLKQQIKLLEN; KRIDSLKQQIKLLENI; RIDSLKQQIKLLENIE; IDSLKQQIKLLENIEN; DSLKQQIKLLENIENE; SLKQQIKLLENIENEK; LKQQIKLLENIENEKE; KQQIKLLENIENEKEK; QQIKLLENIENEKEKG; QIKLLENIENEKEKGE; IKLLENIENEKEKGEL; KLLENIENEKEKGELI; LLENIENEKEKGELIL; LENIENEKEKGELILL; ENIENEKEKGELILLN; NIENEKEKGELILLNI; IENEKEKGELILLNIN; ENEKEKGELILLNINK; NEKEKGELILLNINKI; EKEKGELILLNINKIQ; KEKGELILLNINKIQK; EKGELILLNINKIQKG; KGELILLNINKIQKGI; GELILLNINKIQKGIK; ELILLNINKIQKGIKE; LILLNINKIQKGIKEI; ILLNINKIQKGIKEIN; LLNINKIQKGIKEINL; LNINKIQKGIKEINLL; NINKIQKGIKEINLLN; INKIQKGIKEINLLNY; NKIQKGIKEINLLNYK; KIQKGIKEINLLNYKE; IQKGIKEINLLNYKEE; QKGIKEINLLNYKEEK; KGIKEINLLNYKEEKI; GIKEINLLNYKEEKIK; IKEINLLNYKEEKIKI; KEINLLNYKEEKIKIS; EINLLNYKEEKIKISL; INLLNYKEEKIKISLN; NLLNYKEEKIKISLNQ; LLNYKEEKIKISLNQS; LNYKEEKIKISLNQSL; NYKEEKIKISLNQSLS; YKEEKIKISLNQSLSP; KEEKIKISLNQSLSPK; EEKIKISLNQSLSPKE; EKIKISLNQSLSPKEN; KIKISLNQSLSPKENA; IKISLNQSLSPKENAL; KISLNQSLSPKENALQ; ISLNQSLSPKENALQY; SLNQSLSPKENALQYF; LNQSLSPKENALQYFK; NQSLSPKENALQYFKA; QSLSPKENALQYFKAY; SLSPKENALQYFKAYK; LSPKENALQYFKAYKK; SPKENALQYFKAYKKG; PKENALQYFKAYKKGK; KENALQYFKAYKKGKN; ENALQYFKAYKKGKNS; NALQYFKAYKKGKNSF; ALQYFKAYKKGKNSFK; LQYFKAYKKGKNSFKT; QYFKAYKKGKNSFKTI; YFKAYKKGKNSFKTIQ; FKAYKKGKNSFKTIQN; KAYKKGKNSFKTIQNQ; AYKKGKNSFKTIQNQL; YKKGKNSFKTIQNQLK; KKGKNSFKTIQNQLKD; KGKNSFKTIQNQLKDN; GKNSFKTIQNQLKDNL; KNSFKTIQNQLKDNLD; NSFKTIQNQLKDNLDK; SFKTIQNQLKDNLDKF; FKTIQNQLKDNLDKFN; KTIQNQLKDNLDKFNL; TIQNQLKDNLDKFNLI; IQNQLKDNLDKFNLIQ; QNQLKDNLDKFNLIQS; NQLKDNLDKFNLIQSK; QLKDNLDKFNLIQSKI; LKDNLDKFNLIQSKIT; KDNLDKFNLIQSKITM; DNLDKFNLIQSKITML; NLDKFNLIQSKITMLK; LDKFNLIQSKITMLKV; DKFNLIQSKITMLKVE; KFNLIQSKITMLKVEN; FNLIQSKITMLKVENL; NLIQSKITMLKVENLI; LIQSKITMLKVENLIP; IQSKITMLKVENLIPE; QSKITMLKVENLIPEE; SKITMLKVENLIPEEE; KITMLKVENLIPEEEY; ITMLKVENLIPEEEYN; TMLKVENLIPEEEYNQ; MLKVENLIPEEEYNQE; LKVENLIPEEEYNQEK; KVENLIPEEEYNQEKT; VENLIPEEEYNQEKTA; ENLIPEEEYNQEKTAI; NLIPEEEYNQEKTAIK; LIPEEEYNQEKTAIKE; IPEEEYNQEKTAIKEK; PEEEYNQEKTAIKEKE; EEEYNQEKTAIKEKEK; EEYNQEKTAIKEKEKT; EYNQEKTAIKEKEKTP; YNQEKTAIKEKEKTPK; NQEKTAIKEKEKTPKI; QEKTAIKEKEKTPKIG;

	EKTAIKEKEKTPKIGL; KTAIKEKEKTPKIGLH; TAIKEKEKTPKIGLHF; AIKEKEKTPKIGLHFT; IKEKEKTPKIGLHFTY; KEKEKTPKIGLHFTYC; EKEKTPKIGLHFTYCG; KEKTPKIGLHFTYCGF; EKTPKIGLHFTYCGFE; KTPKIGLHFTYCGFEI; TPKIGLHFTYCGFEIL; PKIGLHFTYCGFEILI; KIGLHFTYCGFEILIG; IGLHFTYCGFEILIGR; GLHFTYCGFEILIGRN; LHFTYCGFEILIGRNA; HFTYCGFEILIGRNAK; FTYCGFEILIGRNAKE; TYCGFEILIGRNAKEN; YCGFEILIGRNAKEND; CGFEILIGRNAKENDK; GFEILIGRNAKENDKL; FEILIGRNAKENDKLL; EILIGRNAKENDKLLR; ILIGRNAKENDKLLRH; LIGRNAKENDKLLRHC; IGRNAKENDKLLRHCV; GRNAKENDKLLRHCVK; RNAKENDKLLRHCVKG; NAKENDKLLRHCVKGN; AKENDKLLRHCVKGND; KENDKLLRHCVKGNDY; ENDKLLRHCVKGNDYW; NDKLLRHCVKGNDYWL; DKLLRHCVKGNDYWLH; KLLRHCVKGNDYWLHT; LLRHCVKGNDYWLHTR; LRHCVKGNDYWLHTRD; RHCVKGNDYWLHTRDY; HCVKGNDYWLHTRDYP; CVKGNDYWLHTRDYPG; VKGNDYWLHTRDYPGA; KGNDYWLHTRDYPGAY; GNDYWLHTRDYPGAYV; NDYWLHTRDYPGAYVF; DYWLHTRDYPGAYVFI; YWLHTRDYPGAYVFIK; WLHTRDYPGAYVFIKN; LHTRDYPGAYVFIKNQ; HTRDYPGAYVFIKNQK; TRDYPGAYVFIKNQKN; RDYPGAYVFIKNQKNK; DYPGAYVFIKNQKNKT; YPGAYVFIKNQKNKTP; PGAYVFIKNQKNKTPS; GAYVFIKNQKNKTPSL; AYVFIKNQKNKTPSLD; YVFIKNQKNKTPSLDV; VFIKNQKNKTPSLDVL; FIKNQKNKTPSLDVLL; IKNQKNKTPSLDVLLG; KNQKNKTPSLDVLLGA; NQKNKTPSLDVLLGAG; QKNKTPSLDVLLGAGN; KNKTPSLDVLLGAGNL; NKTPSLDVLLGAGNLC; KTPSLDVLLGAGNLCV; TPSLDVLLGAGNLCVF; PSLDVLLGAGNLCVFY; SLDVLLGAGNLCVFYT; LDVLLGAGNLCVFYTK; DVLLGAGNLCVFYTKL; VLLGAGNLCVFYTKLA; LLGAGNLCVFYTKLAK; LGAGNLCVFYTKLAKK; GAGNLCVFYTKLAKKS; AGNLCVFYTKLAKKSG; GNLCVFYTKLAKKSGK; NLCVFYTKLAKKSGKA; LCVFYTKLAKKSGKAD; CVFYTKLAKKSGKADL; VFYTKLAKKSGKADLY; FYTKLAKKSGKADLYY; YTKLAKKSGKADLYYT; TKLAKKSGKADLYYTQ; KLAKKSGKADLYYTQV; LAKKSGKADLYYTQVK; AKKSGKADLYYTQVKN; KKSGKADLYYTQVKNL; KSGKADLYYTQVKNLR; SGKADLYYTQVKNLRR; GKADLYYTQVKNLRRV; KADLYYTQVKNLRRVK; ADLYYTQVKNLRRVKN; DLYYTQVKNLRRVKNK; LYYTQVKNLRRVKNKK; YYTQVKNLRRVKNKKL; YTQVKNLRRVKNKKLG; TQVKNLRRVKNKKLGL; QVKNLRRVKNKKLGLV; VKNLRRVKNKKLGLVI; KNLRRVKNKKLGLVIP; NLRRVKNKKLGLVIPK; LRRVKNKKLGLVIPKA; RRVKNKKLGLVIPKAE; RVKNKKLGLVIPKAEK; VKNKKLGLVIPKAEKN; KNKKLGLVIPKAEKNL; NKKLGLVIPKAEKNLH; KKLGLVIPKAEKNLHI; KLGLVIPKAEKNLHIK; LGLVIPKAEKNLHIKL; GLVIPKAEKNLHIKLD; LVIPKAEKNLHIKLDE; VIPKAEKNLHIKLDEN; IPKAEKNLHIKLDENL; PKAEKNLHIKLDENLI; KAEKNLHIKLDENLIK; AEKNLHIKLDENLIKK; EKNLHIKLDENLIKKI; KNLHIKLDENLIKKIK; NLHIKLDENLIKKIKN; LHIKLDENLIKKIKNQ; HIKLDENLIKKIKNQT;
Seq 21	13 mers: MKLQRSLSLIIFS; KLQRSLSLIIFSL; LQRSLSLIIFSLT; QRSLSLIIFSLTV; RSLSLIIFSLTVL; SLSLIIFSLTVLC; LSLIIFSLTVLCC; SLIIFSLTVLCCD; LIIFSLTVLCCDN; IIFSLTVLCCDNK; IFSLTVLCCDNKE; FSLTVLCCDNKER; SLTVLCCDNKERK; LTVLCCDNKERKE; TVLCCDNKERKEG; VLCCDNKERKEGV; LCCDNKERKEGVS; CCDNKERKEGVST;

	CDNKERKEGVSTK; DNKERKEGVSTKI; NKERKEGVSTKIS; KERKEGVSTKISL; ERKEGVSTKISLG; RKEGVSTKISLGA; KEGVSTKISLGAE; EGVSTKISLGAEP; GVSTKISLGAEPR; VSTKISLGAEPRS; STKISLGAEPRSL; TKISLGAEPRSLD; KISLGAEPRSLDP; ISLGAEPRSLDPQ; SLGAEPRSLDPQL; LGAEPRSLDPQLA; GAEPRSLDPQLAE; AEPRSLDPQLAED; EPRSLDPQLAEDN; PRSLDPQLAEDNV; RSLDPQLAEDNVA; SLDPQLAEDNVAS; LDPQLAEDNVASK; DPQLAEDNVASKM; PQLAEDNVASKMI; QLAEDNVASKMID; LAEDNVASKMIDT; AEDNVASKMIDTL; EDNVASKMIDTLY; DNVASKMIDTLYR; NVASKMIDTLYRG; VASKMIDTLYRGI; ASKMIDTLYRGIV; SKMIDTLYRGIVT; KMIDTLYRGIVTG; MIDTLYRGIVTGD; IDTLYRGIVTGDP; DTLYRGIVTGDPN; TLYRGIVTGDPNT; LYRGIVTGDPNTG; YRGIVTGDPNTGG; RGIVTGDPNTGGH; GIVTGDPNTGGHK; IVTGDPNTGGHKP; VTGDPNTGGHKPG; TGDPNTGGHKPGL; GDPNTGGHKPGLA; DPNTGGHKPGLAK; PNTGGHKPGLAKG; NTGGHKPGLAKGW; TGGHKPGLAKGWE; GGHKPGLAKGWET; GHKPGLAKGWETS; HKPGLAKGWETSS; KPGLAKGWETSSD; PGLAKGWETSSDG; GLAKGWETSSDGT; LAKGWETSSDGTA; AKGWETSSDGTAY; KGWETSSDGTAYP; GWETSSDGTAYPF; WETSSDGTAYPFY; ETSSDGTAYPFYL; TSSDGTAYPFYLR; SSDGTAYPFYLRD; SDGTAYPFYLRDN; DGTAYPFYLRDNL; GTAYPFYLRDNLT; TAYPFYLRDNLTW; AYPFYLRDNLTWS; YPFYLRDNLTWSD; PFYLRDNLTWSDG; FYLRDNLTWSDGV; YLRDNLTWSDGVA; LRDNLTWSDGVAI; RDNLTWSDGVAIT; DNLTWSDGVAITA; NLTWSDGVAITAE; LTWSDGVAITAEG; TWSDGVAITAEGI; WSDGVAITAEGIR; SDGVAITAEGIRK; DGVAITAEGIRKS; GVAITAEGIRKSY; VAITAEGIRKSYL; AITAEGIRKSYLR; ITAEGIRKSYLRI; TAEGIRKSYLRIL; AEGIRKSYLRILN; EGIRKSYLRILNK; GIRKSYLRILNKE; IRKSYLRILNKET; RKSYLRILNKETG; KSYLRILNKETGS; SYLRILNKETGST; YLRILNKETGSTY; LRILNKETGSTYV; RILNKETGSTYVD; ILNKETGSTYVDM; LNKETGSTYVDMV; NKETGSTYVDMVK; KETGSTYVDMVKS; ETGSTYVDMVKSI; TGSTYVDMVKSII; GSTYVDMVKSIIK; STYVDMVKSIIKN; TYVDMVKSIIKNG; YVDMVKSIIKNGQ; VDMVKSIIKNGQE; DMVKSIIKNGQEY; MVKSIIKNGQEYF; VKSIIKNGQEYFD; KSIIKNGQEYFDG; SIIKNGQEYFDGQ; IIKNGQEYFDGQV; IKNGQEYFDGQVT; KNGQEYFDGQVTD; NGQEYFDGQVTDS; GQEYFDGQVTDSE; QEYFDGQVTDSEL; EYFDGQVTDSELG; YFDGQVTDSELGI; FDGQVTDSELGIR; DGQVTDSELGIRA; GQVTDSELGIRAI; QVTDSELGIRAID; VTDSELGIRAIDS; TDSELGIRAIDSK; DSELGIRAIDSKT; SELGIRAIDSKTL; ELGIRAIDSKTLE; LGIRAIDSKTLEI; GIRAIDSKTLEIT; IRAIDSKTLEITL; RAIDSKTLEITLA; AIDSKTLEITLAS; IDSKTLEITLASP; DSKTLEITLASPK; SKTLEITLASPKP; KTLEITLASPKPY; TLEITLASPKPYF; LEITLASPKPYFI; EITLASPKPYFID; ITLASPKPYFIDL; TLASPKPYFIDLL; LASPKPYFIDLLV; ASPKPYFIDLLVH; SPKPYFIDLLVHQ; PKPYFIDLLVHQS; KPYFIDLLVHQSF; PYFIDLLVHQSFI; YFIDLLVHQSFIP; FIDLLVHQSFIPV;

IDLLVHQSFIPVP; DLLVHQSFIPVPV; LLVHQSFIPVPVH;
LVHQSFIPVPVHV; VHQSFIPVPVHVT; HQSFIPVPVHVTD;
QSFIPVPVHVTDK; SFIPVPVHVTDKY; FIPVPVHVTDKYG;
IPVPVHVTDKYGQ; PVPVHVTDKYGQN; VPVHVTDKYGQNW;
PVHVTDKYGQNWT; VHVTDKYGQNWTS; HVTDKYGQNWTSP;
VTDKYGQNWTSPE; TDKYGQNWTSPEN; DKYGQNWTSPENM;
KYGQNWTSPENMV; YGQNWTSPENMVT; GQNWTSPENMVTS;
QNWTSPENMVTSG; NWTSPENMVTSGP; WTSPENMVTSGPF;
TSPENMVTSGPFK; SPENMVTSGPFKL; PENMVTSGPFKLK;
ENMVTSGPFKLKE; NMVTSGPFKLKER; MVTSGPFKLKERI;
VTSGPFKLKERIP; TSGPFKLKERIPS; SGPFKLKERIPSE;
GPFKLKERIPSEK; PFKLKERIPSEKY; FKLKERIPSEKYV;
KLKERIPSEKYVF; LKERIPSEKYVFE; KERIPSEKYVFEK;
ERIPSEKYVFEKD; RIPSEKYVFEKDN; IPSEKYVFEKDNK;
PSEKYVFEKDNKY; SEKYVFEKDNKYY; EKYVFEKDNKYYD;
KYVFEKDNKYYDS; YVFEKDNKYYDSN; VFEKDNKYYDSNE;
FEKDNKYYDSNEV; EKDNKYYDSNEVE; KDNKYYDSNEVEL;
DNKYYDSNEVELE; NKYYDSNEVELEE; KYYDSNEVELEEI;
YYDSNEVELEEIT; YDSNEVELEEITF; DSNEVELEEITFY;
SNEVELEEITFYT; NEVELEEITFYTT; EVELEEITFYTTN;
VELEEITFYTTND; ELEEITFYTTNDS; LEEITFYTTNDSS;
EEITFYTTNDSST; EITFYTTNDSSTA; ITFYTTNDSSTAY;
TFYTTNDSSTAYK; FYTTNDSSTAYKM; YTTNDSSTAYKMY;
TTNDSSTAYKMYV; TNDSSTAYKMYVN; NDSSTAYKMYVNE;
DSSTAYKMYVNEE; SSTAYKMYVNEEL; STAYKMYVNEELD;
TAYKMYVNEELDA; AYKMYVNEELDAI; YKMYVNEELDAIL;
KMYVNEELDAILV; MYVNEELDAILVP; YVNEELDAILVPY;
VNEELDAILVPYP; NEELDAILVPYPQ; EELDAILVPYPQI;

14 mers:
MKLQRSLSLIIFSL; KLQRSLSLIIFSLT; LQRSLSLIIFSLTV;
QRSLSLIIFSLTVL; RSLSLIIFSLTVLC; SLSLIIFSLTVLCC;
LSLIIFSLTVLCCD; SLIIFSLTVLCCDN; LIIFSLTVLCCDNK;
IIFSLTVLCCDNKE; IFSLTVLCCDNKER; FSLTVLCCDNKERK;
SLTVLCCDNKERKE; LTVLCCDNKERKEG; TVLCCDNKERKEGV;
VLCCDNKERKEGVS; LCCDNKERKEGVST; CCDNKERKEGVSTK;
CDNKERKEGVSTKI; DNKERKEGVSTKIS; NKERKEGVSTKISL;
KERKEGVSTKISLG; ERKEGVSTKISLGA; RKEGVSTKISLGAE;
KEGVSTKISLGAEP; EGVSTKISLGAEPR; GVSTKISLGAEPRS;
VSTKISLGAEPRSL; STKISLGAEPRSLD; TKISLGAEPRSLDP;
KISLGAEPRSLDPQ; ISLGAEPRSLDPQL; SLGAEPRSLDPQLA;
LGAEPRSLDPQLAE; GAEPRSLDPQLAED; AEPRSLDPQLAEDN;
EPRSLDPQLAEDNV; PRSLDPQLAEDNVA; RSLDPQLAEDNVAS;
SLDPQLAEDNVASK; LDPQLAEDNVASKM; DPQLAEDNVASKMI;
PQLAEDNVASKMID; QLAEDNVASKMIDT; LAEDNVASKMIDTL;
AEDNVASKMIDTLY; EDNVASKMIDTLYR; DNVASKMIDTLYRG;
NVASKMIDTLYRGI; VASKMIDTLYRGIV; ASKMIDTLYRGIVT;
SKMIDTLYRGIVTG; KMIDTLYRGIVTGD; MIDTLYRGIVTGDP;
IDTLYRGIVTGDPN; DTLYRGIVTGDPNT; TLYRGIVTGDPNTG;
LYRGIVTGDPNTGG; YRGIVTGDPNTGGH; RGIVTGDPNTGGHK;
GIVTGDPNTGGHKP; IVTGDPNTGGHKPG; VTGDPNTGGHKPGL;

	TGDPNTGGHKPGLA; GDPNTGGHKPGLAK; DPNTGGHKPGLAKG; PNTGGHKPGLAKGW; NTGGHKPGLAKGWE; TGGHKPGLAKGWET; GGHKPGLAKGWETS; GHKPGLAKGWETSS; HKPGLAKGWETSSD; KPGLAKGWETSSDG; PGLAKGWETSSDGT; GLAKGWETSSDGTA; LAKGWETSSDGTAY; AKGWETSSDGTAYP; KGWETSSDGTAYPF; GWETSSDGTAYPFY; WETSSDGTAYPFYL; ETSSDGTAYPFYLR; TSSDGTAYPFYLRD; SSDGTAYPFYLRDN; SDGTAYPFYLRDNL; DGTAYPFYLRDNLT; GTAYPFYLRDNLTW; TAYPFYLRDNLTWS; AYPFYLRDNLTWSD; YPFYLRDNLTWSDG; PFYLRDNLTWSDGV; FYLRDNLTWSDGVA; YLRDNLTWSDGVAI; LRDNLTWSDGVAIT; RDNLTWSDGVAITA; DNLTWSDGVAITAE; NLTWSDGVAITAEG; LTWSDGVAITAEGI; TWSDGVAITAEGIR; WSDGVAITAEGIRK; SDGVAITAEGIRKS; DGVAITAEGIRKSY; GVAITAEGIRKSYL; VAITAEGIRKSYLR; AITAEGIRKSYLRI; ITAEGIRKSYLRIL; TAEGIRKSYLRILN; AEGIRKSYLRILNK; EGIRKSYLRILNKE; GIRKSYLRILNKET; IRKSYLRILNKETG; RKSYLRILNKETGS; KSYLRILNKETGST; SYLRILNKETGSTY; YLRILNKETGSTYV; LRILNKETGSTYVD; RILNKETGSTYVDM; ILNKETGSTYVDMV; LNKETGSTYVDMVK; NKETGSTYVDMVKS; KETGSTYVDMVKSI; ETGSTYVDMVKSII; TGSTYVDMVKSIIK; GSTYVDMVKSIIKN; STYVDMVKSIIKNG; TYVDMVKSIIKNGQ; YVDMVKSIIKNGQE; VDMVKSIIKNGQEY; DMVKSIIKNGQEYF; MVKSIIKNGQEYFD; VKSIIKNGQEYFDG; KSIIKNGQEYFDGQ; SIIKNGQEYFDGQV; IIKNGQEYFDGQVT; IKNGQEYFDGQVTD; KNGQEYFDGQVTDS; NGQEYFDGQVTDSE; GQEYFDGQVTDSEL; QEYFDGQVTDSELG; EYFDGQVTDSELGI; YFDGQVTDSELGIR; FDGQVTDSELGIRA; DGQVTDSELGIRAI; GQVTDSELGIRAID; QVTDSELGIRAIDS; VTDSELGIRAIDSK; TDSELGIRAIDSKT; DSELGIRAIDSKTL; SELGIRAIDSKTLE; ELGIRAIDSKTLEI; LGIRAIDSKTLEIT; GIRAIDSKTLEITL; IRAIDSKTLEITLA; RAIDSKTLEITLAS; AIDSKTLEITLASP; IDSKTLEITLASPK; DSKTLEITLASPKP; SKTLEITLASPKPY; KTLEITLASPKPYF; TLEITLASPKPYFI; LEITLASPKPYFID; EITLASPKPYFIDL; ITLASPKPYFIDLL; TLASPKPYFIDLLV; LASPKPYFIDLLVH; ASPKPYFIDLLVHQ; SPKPYFIDLLVHQS; PKPYFIDLLVHQSF; KPYFIDLLVHQSFI; PYFIDLLVHQSFIP; YFIDLLVHQSFIPV; FIDLLVHQSFIPVP; IDLLVHQSFIPVPV; DLLVHQSFIPVPVH; LLVHQSFIPVPVHV; LVHQSFIPVPVHVT; VHQSFIPVPVHVTD; HQSFIPVPVHVTDK; QSFIPVPVHVTDKY; SFIPVPVHVTDKYG; FIPVPVHVTDKYGQ; IPVPVHVTDKYGQN; PVPVHVTDKYGQNW; VPVHVTDKYGQNWT; PVHVTDKYGQNWTS; VHVTDKYGQNWTSP; HVTDKYGQNWTSPE; VTDKYGQNWTSPEN; TDKYGQNWTSPENM; DKYGQNWTSPENMV; KYGQNWTSPENMVT; YGQNWTSPENMVTS; GQNWTSPENMVTSG; QNWTSPENMVTSGP; NWTSPENMVTSGPF; WTSPENMVTSGPFK; TSPENMVTSGPFKL; SPENMVTSGPFKLK; PENMVTSGPFKLKE; ENMVTSGPFKLKER; NMVTSGPFKLKERI; MVTSGPFKLKERIP; VTSGPFKLKERIPS; TSGPFKLKERIPSE; SGPFKLKERIPSEK; GPFKLKERIPSEKY; PFKLKERIPSEKYV; FKLKERIPSEKYVF; KLKERIPSEKYVFE; LKERIPSEKYVFEK; KERIPSEKYVFEKD; ERIPSEKYVFEKDN; RIPSEKYVFEKDNK; IPSEKYVFEKDNKY; PSEKYVFEKDNKYY; SEKYVFEKDNKYYD; EKYVFEKDNKYYDS;

KYVFEKDNKYYDSN; YVFEKDNKYYDSNE; VFEKDNKYYDSNEV;
FEKDNKYYDSNEVE; EKDNKYYDSNEVEL; KDNKYYDSNEVELE;
DNKYYDSNEVELEE; NKYYDSNEVELEEI; KYYDSNEVELEEIT;
YYDSNEVELEEITF; YDSNEVELEEITFY; DSNEVELEEITFYT;
SNEVELEEITFYTT; NEVELEEITFYTTN; EVELEEITFYTTND;
VELEEITFYTTNDS; ELEEITFYTTNDSS; LEEITFYTTNDSST;
EEITFYTTNDSSTA; EITFYTTNDSSTAY; ITFYTTNDSSTAYK;
TFYTTNDSSTAYKM; FYTTNDSSTAYKMY; YTTNDSSTAYKMYV;
TTNDSSTAYKMYVN; TNDSSTAYKMYVNE; NDSSTAYKMYVNEE;
DSSTAYKMYVNEEL; SSTAYKMYVNEELD; STAYKMYVNEELDA;
TAYKMYVNEELDAI; AYKMYVNEELDAIL; YKMYVNEELDAILV;
KMYVNEELDAILVP; MYVNEELDAILVPY; YVNEELDAILVPYP;
VNEELDAILVPYPQ; NEELDAILVPYPQI;

15 mers:
MKLQRSLSLIIFSLT; KLQRSLSLIIFSLTV; LQRSLSLIIFSLTVL;
QRSLSLIIFSLTVLC; RSLSLIIFSLTVLCC; SLSLIIFSLTVLCCD;
LSLIIFSLTVLCCDN; SLIIFSLTVLCCDNK; LIIFSLTVLCCDNKE;
IIFSLTVLCCDNKER; IFSLTVLCCDNKERK; FSLTVLCCDNKERKE;
SLTVLCCDNKERKEG; LTVLCCDNKERKEGV; TVLCCDNKERKEGVS;
VLCCDNKERKEGVST; LCCDNKERKEGVSTK; CCDNKERKEGVSTKI;
CDNKERKEGVSTKIS; DNKERKEGVSTKISL; NKERKEGVSTKISLG;
KERKEGVSTKISLGA; ERKEGVSTKISLGAE; RKEGVSTKISLGAEP;
KEGVSTKISLGAEPR; EGVSTKISLGAEPRS; GVSTKISLGAEPRSL;
VSTKISLGAEPRSLD; STKISLGAEPRSLDP; TKISLGAEPRSLDPQ;
KISLGAEPRSLDPQL; ISLGAEPRSLDPQLA; SLGAEPRSLDPQLAE;
LGAEPRSLDPQLAED; GAEPRSLDPQLAEDN; AEPRSLDPQLAEDNV;
EPRSLDPQLAEDNVA; PRSLDPQLAEDNVAS; RSLDPQLAEDNVASK;
SLDPQLAEDNVASKM; LDPQLAEDNVASKMI; DPQLAEDNVASKMID;
PQLAEDNVASKMIDT; QLAEDNVASKMIDTL; LAEDNVASKMIDTLY;
AEDNVASKMIDTLYR; EDNVASKMIDTLYRG; DNVASKMIDTLYRGI;
NVASKMIDTLYRGIV; VASKMIDTLYRGIVT; ASKMIDTLYRGIVTG;
SKMIDTLYRGIVTGD; KMIDTLYRGIVTGDP; MIDTLYRGIVTGDPN;
IDTLYRGIVTGDPNT; DTLYRGIVTGDPNTG; TLYRGIVTGDPNTGG;
LYRGIVTGDPNTGGH; YRGIVTGDPNTGGHK; RGIVTGDPNTGGHKP;
GIVTGDPNTGGHKPG; IVTGDPNTGGHKPGL; VTGDPNTGGHKPGLA;
TGDPNTGGHKPGLAK; GDPNTGGHKPGLAKG; DPNTGGHKPGLAKGW;
PNTGGHKPGLAKGWE; NTGGHKPGLAKGWET; TGGHKPGLAKGWETS;
GGHKPGLAKGWETSS; GHKPGLAKGWETSSD; HKPGLAKGWETSSDG;
KPGLAKGWETSSDGT; PGLAKGWETSSDGTA; GLAKGWETSSDGTAY;
LAKGWETSSDGTAYP; AKGWETSSDGTAYPF; KGWETSSDGTAYPFY;
GWETSSDGTAYPFYL; WETSSDGTAYPFYLR; ETSSDGTAYPFYLRD;
TSSDGTAYPFYLRDN; SSDGTAYPFYLRDNL; SDGTAYPFYLRDNLT;
DGTAYPFYLRDNLTW; GTAYPFYLRDNLTWS; TAYPFYLRDNLTWSD;
AYPFYLRDNLTWSDG; YPFYLRDNLTWSDGV; PFYLRDNLTWSDGVA;
FYLRDNLTWSDGVAI; YLRDNLTWSDGVAIT; LRDNLTWSDGVAITA;
RDNLTWSDGVAITAE; DNLTWSDGVAITAEG; NLTWSDGVAITAEGI;
LTWSDGVAITAEGIR; TWSDGVAITAEGIRK; WSDGVAITAEGIRKS;
SDGVAITAEGIRKSY; DGVAITAEGIRKSYL; GVAITAEGIRKSYLR;
VAITAEGIRKSYLRI; AITAEGIRKSYLRIL; ITAEGIRKSYLRILN;
TAEGIRKSYLRILNK; AEGIRKSYLRILNKE; EGIRKSYLRILNKET;

	GIRKSYLRILNKETG; IRKSYLRILNKETGS; RKSYLRILNKETGST; KSYLRILNKETGSTY; SYLRILNKETGSTYV; YLRILNKETGSTYVD; LRILNKETGSTYVDM; RILNKETGSTYVDMV; ILNKETGSTYVDMVK; LNKETGSTYVDMVKS; NKETGSTYVDMVKSI; KETGSTYVDMVKSII; ETGSTYVDMVKSIIK; TGSTYVDMVKSIIKN; GSTYVDMVKSIIKNG; STYVDMVKSIIKNGQ; TYVDMVKSIIKNGQE; YVDMVKSIIKNGQEY; VDMVKSIIKNGQEYF; DMVKSIIKNGQEYFD; MVKSIIKNGQEYFDG; VKSIIKNGQEYFDGQ; KSIIKNGQEYFDGQV; SIIKNGQEYFDGQVT; IIKNGQEYFDGQVTD; IKNGQEYFDGQVTDS; KNGQEYFDGQVTDSE; NGQEYFDGQVTDSEL; GQEYFDGQVTDSELG; QEYFDGQVTDSELGI; EYFDGQVTDSELGIR; YFDGQVTDSELGIRA; FDGQVTDSELGIRAI; DGQVTDSELGIRAID; GQVTDSELGIRAIDS; QVTDSELGIRAIDSK; VTDSELGIRAIDSKT; TDSELGIRAIDSKTL; DSELGIRAIDSKTLE; SELGIRAIDSKTLEI; ELGIRAIDSKTLEIT; LGIRAIDSKTLEITL; GIRAIDSKTLEITLA; IRAIDSKTLEITLAS; RAIDSKTLEITLASP; AIDSKTLEITLASPK; IDSKTLEITLASPKP; DSKTLEITLASPKPY; SKTLEITLASPKPYF; KTLEITLASPKPYFI; TLEITLASPKPYFID; LEITLASPKPYFIDL; EITLASPKPYFIDLL; ITLASPKPYFIDLLV; TLASPKPYFIDLLVH; LASPKPYFIDLLVHQ; ASPKPYFIDLLVHQS; SPKPYFIDLLVHQSF; PKPYFIDLLVHQSFI; KPYFIDLLVHQSFIP; PYFIDLLVHQSFIPV; YFIDLLVHQSFIPVP; FIDLLVHQSFIPVPV; IDLLVHQSFIPVPVH; DLLVHQSFIPVPVHV; LLVHQSFIPVPVHVT; LVHQSFIPVPVHVTD; VHQSFIPVPVHVTDK; HQSFIPVPVHVTDKY; QSFIPVPVHVTDKYG; SFIPVPVHVTDKYGQ; FIPVPVHVTDKYGQN; IPVPVHVTDKYGQNW; PVPVHVTDKYGQNWT; VPVHVTDKYGQNWTS; PVHVTDKYGQNWTSP; VHVTDKYGQNWTSPE; HVTDKYGQNWTSPEN; VTDKYGQNWTSPENM; TDKYGQNWTSPENMV; DKYGQNWTSPENMVT; KYGQNWTSPENMVTS; YGQNWTSPENMVTSG; GQNWTSPENMVTSGP; QNWTSPENMVTSGPF; NWTSPENMVTSGPFK; WTSPENMVTSGPFKL; TSPENMVTSGPFKLK; SPENMVTSGPFKLKE; PENMVTSGPFKLKER; ENMVTSGPFKLKERI; NMVTSGPFKLKERIP; MVTSGPFKLKERIPS; VTSGPFKLKERIPSE; TSGPFKLKERIPSEK; SGPFKLKERIPSEKY; GPFKLKERIPSEKYV; PFKLKERIPSEKYVF; FKLKERIPSEKYVFE; KLKERIPSEKYVFEK; LKERIPSEKYVFEKD; KERIPSEKYVFEKDN; ERIPSEKYVFEKDNK; RIPSEKYVFEKDNKY; IPSEKYVFEKDNKYY; PSEKYVFEKDNKYYD; SEKYVFEKDNKYYDS; EKYVFEKDNKYYDSN; KYVFEKDNKYYDSNE; YVFEKDNKYYDSNEV; VFEKDNKYYDSNEVE; FEKDNKYYDSNEVEL; EKDNKYYDSNEVELE; KDNKYYDSNEVELEE; DNKYYDSNEVELEEI; NKYYDSNEVELEEIT; KYYDSNEVELEEITF; YYDSNEVELEEITFY; YDSNEVELEEITFYT; DSNEVELEEITFYTT; SNEVELEEITFYTTN; NEVELEEITFYTTND; EVELEEITFYTTNDS; VELEEITFYTTNDSS; ELEEITFYTTNDSST; LEEITFYTTNDSSTA; EEITFYTTNDSSTAY; EITFYTTNDSSTAYK; ITFYTTNDSSTAYKM; TFYTTNDSSTAYKMY; FYTTNDSSTAYKMYV; YTTNDSSTAYKMYVN; TTNDSSTAYKMYVNE; TNDSSTAYKMYVNEE; NDSSTAYKMYVNEEL; DSSTAYKMYVNEELD; SSTAYKMYVNEELDA; STAYKMYVNEELDAI; TAYKMYVNEELDAIL; AYKMYVNEELDAILV; YKMYVNEELDAILVP; KMYVNEELDAILVPY; MYVNEELDAILVPYP; YVNEELDAILVPYPQ; VNEELDAILVPYPQI; 16 mers:

	MKLQRSLSLIIFSLTV; KLQRSLSLIIFSLTVL; LQRSLSLIIFSLTVLC; QRSLSLIIFSLTVLCC; RSLSLIIFSLTVLCCD; SLSLIIFSLTVLCCDN; LSLIIFSLTVLCCDNK; SLIIFSLTVLCCDNKE; LIIFSLTVLCCDNKER; IIFSLTVLCCDNKERK; IFSLTVLCCDNKERKE; FSLTVLCCDNKERKEG; SLTVLCCDNKERKEGV; LTVLCCDNKERKEGVS; TVLCCDNKERKEGVST; VLCCDNKERKEGVSTK; LCCDNKERKEGVSTKI; CCDNKERKEGVSTKIS; CDNKERKEGVSTKISL; DNKERKEGVSTKISLG; NKERKEGVSTKISLGA; KERKEGVSTKISLGAE; ERKEGVSTKISLGAEP; RKEGVSTKISLGAEPR; KEGVSTKISLGAEPRS; EGVSTKISLGAEPRSL; GVSTKISLGAEPRSLD; VSTKISLGAEPRSLDP; STKISLGAEPRSLDPQ; TKISLGAEPRSLDPQL; KISLGAEPRSLDPQLA; ISLGAEPRSLDPQLAE; SLGAEPRSLDPQLAED; LGAEPRSLDPQLAEDN; GAEPRSLDPQLAEDNV; AEPRSLDPQLAEDNVA; EPRSLDPQLAEDNVAS; PRSLDPQLAEDNVASK; RSLDPQLAEDNVASKM; SLDPQLAEDNVASKMI; LDPQLAEDNVASKMID; DPQLAEDNVASKMIDT; PQLAEDNVASKMIDTL; QLAEDNVASKMIDTLY; LAEDNVASKMIDTLYR; AEDNVASKMIDTLYRG; EDNVASKMIDTLYRGI; DNVASKMIDTLYRGIV; NVASKMIDTLYRGIVT; VASKMIDTLYRGIVTG; ASKMIDTLYRGIVTGD; SKMIDTLYRGIVTGDP; KMIDTLYRGIVTGDPN; MIDTLYRGIVTGDPNT; IDTLYRGIVTGDPNTG; DTLYRGIVTGDPNTGG; TLYRGIVTGDPNTGGH; LYRGIVTGDPNTGGHK; YRGIVTGDPNTGGHKP; RGIVTGDPNTGGHKPG; GIVTGDPNTGGHKPGL; IVTGDPNTGGHKPGLA; VTGDPNTGGHKPGLAK; TGDPNTGGHKPGLAKG; GDPNTGGHKPGLAKGW; DPNTGGHKPGLAKGWE; PNTGGHKPGLAKGWET; NTGGHKPGLAKGWETS; TGGHKPGLAKGWETSS; GGHKPGLAKGWETSSD; GHKPGLAKGWETSSDG; HKPGLAKGWETSSDGT; KPGLAKGWETSSDGTA; PGLAKGWETSSDGTAY; GLAKGWETSSDGTAYP; LAKGWETSSDGTAYPF; AKGWETSSDGTAYPFY; KGWETSSDGTAYPFYL; GWETSSDGTAYPFYLR; WETSSDGTAYPFYLRD; ETSSDGTAYPFYLRDN; TSSDGTAYPFYLRDNL; SSDGTAYPFYLRDNLT; SDGTAYPFYLRDNLTW; DGTAYPFYLRDNLTWS; GTAYPFYLRDNLTWSD; TAYPFYLRDNLTWSDG; AYPFYLRDNLTWSDGV; YPFYLRDNLTWSDGVA; PFYLRDNLTWSDGVAI; FYLRDNLTWSDGVAIT; YLRDNLTWSDGVAITA; LRDNLTWSDGVAITAE; RDNLTWSDGVAITAEG; DNLTWSDGVAITAEGI; NLTWSDGVAITAEGIR; LTWSDGVAITAEGIRK; TWSDGVAITAEGIRKS; WSDGVAITAEGIRKSY; SDGVAITAEGIRKSYL; DGVAITAEGIRKSYLR; GVAITAEGIRKSYLRI; VAITAEGIRKSYLRIL; AITAEGIRKSYLRILN; ITAEGIRKSYLRILNK; TAEGIRKSYLRILNKE; AEGIRKSYLRILNKET; EGIRKSYLRILNKETG; GIRKSYLRILNKETGS; IRKSYLRILNKETGST; RKSYLRILNKETGSTY; KSYLRILNKETGSTYV; SYLRILNKETGSTYVD; YLRILNKETGSTYVDM; LRILNKETGSTYVDMV; RILNKETGSTYVDMVK; ILNKETGSTYVDMVKS; LNKETGSTYVDMVKSI; NKETGSTYVDMVKSII; KETGSTYVDMVKSIIK; ETGSTYVDMVKSIIKN; TGSTYVDMVKSIIKNG; GSTYVDMVKSIIKNGQ; STYVDMVKSIIKNGQE; TYVDMVKSIIKNGQEY; YVDMVKSIIKNGQEYF; VDMVKSIIKNGQEYFD; DMVKSIIKNGQEYFDG; MVKSIIKNGQEYFDGQ; VKSIIKNGQEYFDGQV; KSIIKNGQEYFDGQVT; SIIKNGQEYFDGQVTD; IIKNGQEYFDGQVTDS; IKNGQEYFDGQVTDSE; KNGQEYFDGQVTDSEL; NGQEYFDGQVTDSELG; GQEYFDGQVTDSELGI; QEYFDGQVTDSELGIR; EYFDGQVTDSELGIRA; YFDGQVTDSELGIRAI; FDGQVTDSELGIRAID; DGQVTDSELGIRAIDS; GQVTDSELGIRAIDSK; QVTDSELGIRAIDSKT; VTDSELGIRAIDSKTL; TDSELGIRAIDSKTLE; DSELGIRAIDSKTLEI; SELGIRAIDSKTLEIT; ELGIRAIDSKTLEITL; LGIRAIDSKTLEITLA; GIRAIDSKTLEITLAS; IRAIDSKTLEITLASP; RAIDSKTLEITLASPK;

	AIDSKTLEITLASPKP; IDSKTLEITLASPKPY; DSKTLEITLASPKPYF; SKTLEITLASPKPYFI; KTLEITLASPKPYFID; TLEITLASPKPYFIDL; LEITLASPKPYFIDLL; EITLASPKPYFIDLLV; ITLASPKPYFIDLLVH; TLASPKPYFIDLLVHQ; LASPKPYFIDLLVHQS; ASPKPYFIDLLVHQSF; SPKPYFIDLLVHQSFI; PKPYFIDLLVHQSFIP; KPYFIDLLVHQSFIPV; PYFIDLLVHQSFIPVP; YFIDLLVHQSFIPVPV; FIDLLVHQSFIPVPVH; IDLLVHQSFIPVPVHV; DLLVHQSFIPVPVHVT; LLVHQSFIPVPVHVTD; LVHQSFIPVPVHVTDK; VHQSFIPVPVHVTDKY; HQSFIPVPVHVTDKYG; QSFIPVPVHVTDKYGQ; SFIPVPVHVTDKYGQN; FIPVPVHVTDKYGQNW; IPVPVHVTDKYGQNWT; PVPVHVTDKYGQNWTS; VPVHVTDKYGQNWTSP; PVHVTDKYGQNWTSPE; VHVTDKYGQNWTSPEN; HVTDKYGQNWTSPENM; VTDKYGQNWTSPENMV; TDKYGQNWTSPENMVT; DKYGQNWTSPENMVTS; KYGQNWTSPENMVTSG; YGQNWTSPENMVTSGP; GQNWTSPENMVTSGPF; QNWTSPENMVTSGPFK; NWTSPENMVTSGPFKL; WTSPENMVTSGPFKLK; TSPENMVTSGPFKLKE; SPENMVTSGPFKLKER; PENMVTSGPFKLKERI; ENMVTSGPFKLKERIP; NMVTSGPFKLKERIPS; MVTSGPFKLKERIPSE; VTSGPFKLKERIPSEK; TSGPFKLKERIPSEKY; SGPFKLKERIPSEKYV; GPFKLKERIPSEKYVF; PFKLKERIPSEKYVFE; FKLKERIPSEKYVFEK; KLKERIPSEKYVFEKD; LKERIPSEKYVFEKDN; KERIPSEKYVFEKDNK; ERIPSEKYVFEKDNKY; RIPSEKYVFEKDNKYY; IPSEKYVFEKDNKYYD; PSEKYVFEKDNKYYDS; SEKYVFEKDNKYYDSN; EKYVFEKDNKYYDSNE; KYVFEKDNKYYDSNEV; YVFEKDNKYYDSNEVE; VFEKDNKYYDSNEVEL; FEKDNKYYDSNEVELE; EKDNKYYDSNEVELEE; KDNKYYDSNEVELEEI; DNKYYDSNEVELEEIT; NKYYDSNEVELEEITF; KYYDSNEVELEEITFY; YYDSNEVELEEITFYT; YDSNEVELEEITFYTT; DSNEVELEEITFYTTN; SNEVELEEITFYTTND; NEVELEEITFYTTNDS; EVELEEITFYTTNDSS; VELEEITFYTTNDSST; ELEEITFYTTNDSSTA; LEEITFYTTNDSSTAY; EEITFYTTNDSSTAYK; EITFYTTNDSSTAYKM; ITFYTTNDSSTAYKMY; TFYTTNDSSTAYKMYV; FYTTNDSSTAYKMYVN; YTTNDSSTAYKMYVNE; TTNDSSTAYKMYVNEE; TNDSSTAYKMYVNEEL; NDSSTAYKMYVNEELD; DSSTAYKMYVNEELDA; SSTAYKMYVNEELDAI; STAYKMYVNEELDAIL; TAYKMYVNEELDAILV; AYKMYVNEELDAILVP; YKMYVNEELDAILVPY; KMYVNEELDAILVPYP; MYVNEELDAILVPYPQ; YVNEELDAILVPYPQI;
Seq 22	13 mers: MNLINKLFILTIL; NLINKLFILTILF; LINKLFILTILFS; INKLFILTILFSS; NKLFILTILFSSV; KLFILTILFSSVI; LFILTILFSSVIS; FILTILFSSVISC; ILTILFSSVISCK; LTILFSSVISCKL; TILFSSVISCKLY; ILFSSVISCKLYK; LFSSVISCKLYKK; FSSVISCKLYKKI; SSVISCKLYKKIT; SVISCKLYKKITY; VISCKLYKKITYN; ISCKLYKKITYNA; SCKLYKKITYNAD; CKLYKKITYNADQ; KLYKKITYNADQV; LYKKITYNADQVI; YKKITYNADQVID; KKITYNADQVIDK; KITYNADQVIDKL; ITYNADQVIDKLK; TYNADQVIDKLKS; YNADQVIDKLKSN; NADQVIDKLKSNN; ADQVIDKLKSNNG; DQVIDKLKSNNGS; QVIDKLKSNNGSF; VIDKLKSNNGSFN; IDKLKSNNGSFNT; DKLKSNNGSFNTL; KLKSNNGSFNTLK; LKSNNGSFNTLKS; KSNNGSFNTLKSN; SNNGSFNTLKSND; NNGSFNTLKSNDD; NGSFNTLKSNDDS; GSFNTLKSNDDSK; SFNTLKSNDDSKR; FNTLKSNDDSKRS; NTLKSNDDSKRSG;

	TLKSNDDSKRSGR; LKSNDDSKRSGRK; KSNDDSKRSGRKP; SNDDSKRSGRKPR; NDDSKRSGRKPRS; DDSKRSGRKPRSV; DSKRSGRKPRSVD; SKRSGRKPRSVDN; KRSGRKPRSVDNT; RSGRKPRSVDNTY; SGRKPRSVDNTYM; GRKPRSVDNTYMD; RKPRSVDNTYMDQ; KPRSVDNTYMDQD; PRSVDNTYMDQDT; RSVDNTYMDQDTG; SVDNTYMDQDTGK; VDNTYMDQDTGKK; DNTYMDQDTGKKP; NTYMDQDTGKKPL; TYMDQDTGKKPLM; YMDQDTGKKPLMA; MDQDTGKKPLMAD; DQDTGKKPLMADM; QDTGKKPLMADMQ; DTGKKPLMADMQP; TGKKPLMADMQPD; GKKPLMADMQPDM; KKPLMADMQPDMQ; KPLMADMQPDMQN; PLMADMQPDMQND; LMADMQPDMQNDN; MADMQPDMQNDNS; ADMQPDMQNDNSS; DMQPDMQNDNSSS; MQPDMQNDNSSSN; QPDMQNDNSSSNH; PDMQNDNSSSNHT; DMQNDNSSSNHTL; MQNDNSSSNHTLQ; QNDNSSSNHTLQV; NDNSSSNHTLQVN; DNSSSNHTLQVNI; NSSSNHTLQVNIQ; SSSNHTLQVNIQD; SSNHTLQVNIQDN; SNHTLQVNIQDNE; NHTLQVNIQDNEA; HTLQVNIQDNEAS; TLQVNIQDNEASE; LQVNIQDNEASEA; QVNIQDNEASEAR; VNIQDNEASEARN; NIQDNEASEARNI; IQDNEASEARNIM; QDNEASEARNIMT; DNEASEARNIMTE; NEASEARNIMTEI; EASEARNIMTEIE; ASEARNIMTEIES; SEARNIMTEIESS; EARNIMTEIESSK; ARNIMTEIESSKE; RNIMTEIESSKEE; NIMTEIESSKEEY; IMTEIESSKEEYN; MTEIESSKEEYNR; TEIESSKEEYNRI; EIESSKEEYNRIN; IESSKEEYNRINE; ESSKEEYNRINED; SSKEEYNRINEDL; SKEEYNRINEDLA; KEEYNRINEDLAK; EEYNRINEDLAKV; EYNRINEDLAKVK; YNRINEDLAKVKA; NRINEDLAKVKAS; RINEDLAKVKASL; INEDLAKVKASLD; NEDLAKVKASLDK; EDLAKVKASLDKI; DLAKVKASLDKIK; LAKVKASLDKIKS; AKVKASLDKIKSL; KVKASLDKIKSLL; VKASLDKIKSLLS; KASLDKIKSLLST; ASLDKIKSLLSTA; SLDKIKSLLSTAK; LDKIKSLLSTAKS; DKIKSLLSTAKSY; KIKSLLSTAKSYL; IKSLLSTAKSYLE; KSLLSTAKSYLEQ; SLLSTAKSYLEQT; LLSTAKSYLEQTR; LSTAKSYLEQTRR; STAKSYLEQTRRG; TAKSYLEQTRRGV; AKSYLEQTRRGVG; KSYLEQTRRGVGS; SYLEQTRRGVGSS; YLEQTRRGVGSSK; LEQTRRGVGSSKA; EQTRRGVGSSKAN; QTRRGVGSSKANL; TRRGVGSSKANLA; RRGVGSSKANLAL; RGVGSSKANLALL; GVGSSKANLALLP; VGSSKANLALLPS; GSSKANLALLPSL; SSKANLALLPSLE; SKANLALLPSLEE; KANLALLPSLEEA; ANLALLPSLEEAI; NLALLPSLEEAIA; LALLPSLEEAIAK; ALLPSLEEAIAKV; LLPSLEEAIAKVK; LPSLEEAIAKVKS; PSLEEAIAKVKSN; SLEEAIAKVKSNH; LEEAIAKVKSNHA; EEAIAKVKSNHAS; EAIAKVKSNHASA; AIAKVKSNHASAD; IAKVKSNHASADT; AKVKSNHASADTH; KVKSNHASADTHC; VKSNHASADTHCN; KSNHASADTHCND; SNHASADTHCNDA; NHASADTHCNDAI; HASADTHCNDAIA; ASADTHCNDAIAA; SADTHCNDAIAAL; ADTHCNDAIAALK; DTHCNDAIAALKR; THCNDAIAALKRA; HCNDAIAALKRAK; CNDAIAALKRAKN; NDAIAALKRAKND; DAIAALKRAKNDF; AIAALKRAKNDFE; IAALKRAKNDFEY; AALKRAKNDFEYA; ALKRAKNDFEYAQ; LKRAKNDFEYAQR; KRAKNDFEYAQRK; RAKNDFEYAQRKA; AKNDFEYAQRKAD;

KNDFEYAQRKADR; NDFEYAQRKADRA; DFEYAQRKADRAL;
FEYAQRKADRALE; EYAQRKADRALEE; YAQRKADRALEEA;
AQRKADRALEEAL; QRKADRALEEALS; RKADRALEEALSN;
KADRALEEALSNS; ADRALEEALSNSN; DRALEEALSNSNA;
RALEEALSNSNAS; ALEEALSNSNASR; LEEALSNSNASRH;
EEALSNSNASRHE; EALSNSNASRHES; ALSNSNASRHESY;
LSNSNASRHESYY; SNSNASRHESYYY; NSNASRHESYYYA;
SNASRHESYYYAG; NASRHESYYYAGY; ASRHESYYYAGYH;
SRHESYYYAGYHQ; RHESYYYAGYHQF; HESYYYAGYHQFM;
ESYYYAGYHQFMA; SYYYAGYHQFMAD; YYYAGYHQFMADA;
YYAGYHQFMADAK; YAGYHQFMADAKA; AGYHQFMADAKAS;
GYHQFMADAKASM; YHQFMADAKASMS; HQFMADAKASMSS;
QFMADAKASMSST; FMADAKASMSSTK; MADAKASMSSTKS;
ADAKASMSSTKSL; DAKASMSSTKSLL; AKASMSSTKSLLE;
KASMSSTKSLLEV; ASMSSTKSLLEVA; SMSSTKSLLEVAK;
MSSTKSLLEVAKN; SSTKSLLEVAKNK; STKSLLEVAKNKQ;
TKSLLEVAKNKQK; KSLLEVAKNKQKE; SLLEVAKNKQKEL;
LLEVAKNKQKELN; LEVAKNKQKELNE; EVAKNKQKELNEN;
VAKNKQKELNENM; AKNKQKELNENMT; KNKQKELNENMTK;
NKQKELNENMTKT; KQKELNENMTKTN; QKELNENMTKTNK;
KELNENMTKTNKD; ELNENMTKTNKDF; LNENMTKTNKDFQ;
NENMTKTNKDFQE; ENMTKTNKDFQEL; NMTKTNKDFQELN;
MTKTNKDFQELND; TKTNKDFQELNDI; KTNKDFQELNDIY;
TNKDFQELNDIYK; NKDFQELNDIYKK; KDFQELNDIYKKL;
DFQELNDIYKKLQ; FQELNDIYKKLQD; QELNDIYKKLQDM;
ELNDIYKKLQDMD; LNDIYKKLQDMDS; NDIYKKLQDMDSR;

14 mers:
MNLINKLFILTILF; NLINKLFILTILFS; LINKLFILTILFSS;
INKLFILTILFSSV; NKLFILTILFSSVI; KLFILTILFSSVIS;
LFILTILFSSVISC; FILTILFSSVISCK; ILTILFSSVISCKL;
LTILFSSVISCKLY; TILFSSVISCKLYK; ILFSSVISCKLYKK;
LFSSVISCKLYKKI; FSSVISCKLYKKIT; SSVISCKLYKKITY;
SVISCKLYKKITYN; VISCKLYKKITYNA; ISCKLYKKITYNAD;
SCKLYKKITYNADQ; CKLYKKITYNADQV; KLYKKITYNADQVI;
LYKKITYNADQVID; YKKITYNADQVIDK; KKITYNADQVIDKL;
KITYNADQVIDKLK; ITYNADQVIDKLKS; TYNADQVIDKLKSN;
YNADQVIDKLKSNN; NADQVIDKLKSNNG; ADQVIDKLKSNNGS;
DQVIDKLKSNNGSF; QVIDKLKSNNGSFN; VIDKLKSNNGSFNT;
IDKLKSNNGSFNTL; DKLKSNNGSFNTLK; KLKSNNGSFNTLKS;
LKSNNGSFNTLKSN; KSNNGSFNTLKSND; SNNGSFNTLKSNDD;
NNGSFNTLKSNDDS; NGSFNTLKSNDDSK; GSFNTLKSNDDSKR;
SFNTLKSNDDSKRS; FNTLKSNDDSKRSG; NTLKSNDDSKRSGR;
TLKSNDDSKRSGRK; LKSNDDSKRSGRKP; KSNDDSKRSGRKPR;
SNDDSKRSGRKPRS; NDDSKRSGRKPRSV; DDSKRSGRKPRSVD;
DSKRSGRKPRSVDN; SKRSGRKPRSVDNT; KRSGRKPRSVDNTY;
RSGRKPRSVDNTYM; SGRKPRSVDNTYMD; GRKPRSVDNTYMDQ;
RKPRSVDNTYMDQD; KPRSVDNTYMDQDT; PRSVDNTYMDQDTG;
RSVDNTYMDQDTGK; SVDNTYMDQDTGKK; VDNTYMDQDTGKKP;
DNTYMDQDTGKKPL; NTYMDQDTGKKPLM; TYMDQDTGKKPLMA;
YMDQDTGKKPLMAD; MDQDTGKKPLMADM; DQDTGKKPLMADMQ;

	QDTGKKPLMADMQP; DTGKKPLMADMQPD; TGKKPLMADMQPDM; GKKPLMADMQPDMQ; KKPLMADMQPDMQN; KPLMADMQPDMQND; PLMADMQPDMQNDN; LMADMQPDMQNDNS; MADMQPDMQNDNSS; ADMQPDMQNDNSSS; DMQPDMQNDNSSSN; MQPDMQNDNSSSNH; QPDMQNDNSSSNHT; PDMQNDNSSSNHTL; DMQNDNSSSNHTLQ; MQNDNSSSNHTLQV; QNDNSSSNHTLQVN; NDNSSSNHTLQVNI; DNSSSNHTLQVNIQ; NSSSNHTLQVNIQD; SSSNHTLQVNIQDN; SSNHTLQVNIQDNE; SNHTLQVNIQDNEA; NHTLQVNIQDNEAS; HTLQVNIQDNEASE; TLQVNIQDNEASEA; LQVNIQDNEASEAR; QVNIQDNEASEARN; VNIQDNEASEARNI; NIQDNEASEARNIM; IQDNEASEARNIMT; QDNEASEARNIMTE; DNEASEARNIMTEI; NEASEARNIMTEIE; EASEARNIMTEIES; ASEARNIMTEIESS; SEARNIMTEIESSK; EARNIMTEIESSKE; ARNIMTEIESSKEE; RNIMTEIESSKEEY; NIMTEIESSKEEYN; IMTEIESSKEEYNR; MTEIESSKEEYNRI; TEIESSKEEYNRIN; EIESSKEEYNRINE; IESSKEEYNRINED; ESSKEEYNRINEDL; SSKEEYNRINEDLA; SKEEYNRINEDLAK; KEEYNRINEDLAKV; EEYNRINEDLAKVK; EYNRINEDLAKVKA; YNRINEDLAKVKAS; NRINEDLAKVKASL; RINEDLAKVKASLD; INEDLAKVKASLDK; NEDLAKVKASLDKI; EDLAKVKASLDKIK; DLAKVKASLDKIKS; LAKVKASLDKIKSL; AKVKASLDKIKSLL; KVKASLDKIKSLLS; VKASLDKIKSLLST; KASLDKIKSLLSTA; ASLDKIKSLLSTAK; SLDKIKSLLSTAKS; LDKIKSLLSTAKSY; DKIKSLLSTAKSYL; KIKSLLSTAKSYLE; IKSLLSTAKSYLEQ; KSLLSTAKSYLEQT; SLLSTAKSYLEQTR; LLSTAKSYLEQTRR; LSTAKSYLEQTRRG; STAKSYLEQTRRGV; TAKSYLEQTRRGVG; AKSYLEQTRRGVGS; KSYLEQTRRGVGSS; SYLEQTRRGVGSSK; YLEQTRRGVGSSKA; LEQTRRGVGSSKAN; EQTRRGVGSSKANL; QTRRGVGSSKANLA; TRRGVGSSKANLAL; RRGVGSSKANLALL; RGVGSSKANLALLP; GVGSSKANLALLPS; VGSSKANLALLPSL; GSSKANLALLPSLE; SSKANLALLPSLEE; SKANLALLPSLEEA; KANLALLPSLEEAI; ANLALLPSLEEAIA; NLALLPSLEEAIAK; LALLPSLEEAIAKV; ALLPSLEEAIAKVK; LLPSLEEAIAKVKS; LPSLEEAIAKVKSN; PSLEEAIAKVKSNH; SLEEAIAKVKSNHA; LEEAIAKVKSNHAS; EEAIAKVKSNHASA; EAIAKVKSNHASAD; AIAKVKSNHASADT; IAKVKSNHASADTH; AKVKSNHASADTHC; KVKSNHASADTHCN; VKSNHASADTHCND; KSNHASADTHCNDA; SNHASADTHCNDAI; NHASADTHCNDAIA; HASADTHCNDAIAA; ASADTHCNDAIAAL; SADTHCNDAIAALK; ADTHCNDAIAALKR; DTHCNDAIAALKRA; THCNDAIAALKRAK; HCNDAIAALKRAKN; CNDAIAALKRAKND; NDAIAALKRAKNDF; DAIAALKRAKNDFE; AIAALKRAKNDFEY; IAALKRAKNDFEYA; AALKRAKNDFEYAQ; ALKRAKNDFEYAQR; LKRAKNDFEYAQRK; KRAKNDFEYAQRKA; RAKNDFEYAQRKAD; AKNDFEYAQRKADR; KNDFEYAQRKADRA; NDFEYAQRKADRAL; DFEYAQRKADRALE; FEYAQRKADRALEE; EYAQRKADRALEEA; YAQRKADRALEEAL; AQRKADRALEEALS; QRKADRALEEALSN; RKADRALEEALSNS; KADRALEEALSNSN; ADRALEEALSNSNA; DRALEEALSNSNAS; RALEEALSNSNASR; ALEEALSNSNASRH; LEEALSNSNASRHE; EEALSNSNASRHES; EALSNSNASRHESY; ALSNSNASRHESYY; LSNSNASRHESYYY; SNSNASRHESYYYA; NSNASRHESYYYAG; SNASRHESYYYAGY; NASRHESYYYAGYH; ASRHESYYYAGYHQ;

	SRHESYYYAGYHQF; RHESYYYAGYHQFM; HESYYYAGYHQFMA; ESYYYAGYHQFMAD; SYYYAGYHQFMADA; YYYAGYHQFMADAK; YYAGYHQFMADAKA; YAGYHQFMADAKAS; AGYHQFMADAKASM; GYHQFMADAKASMS; YHQFMADAKASMSS; HQFMADAKASMSST; QFMADAKASMSSTK; FMADAKASMSSTKS; MADAKASMSSTKSL; ADAKASMSSTKSLL; DAKASMSSTKSLLE; AKASMSSTKSLLEV; KASMSSTKSLLEVA; ASMSSTKSLLEVAK; SMSSTKSLLEVAKN; MSSTKSLLEVAKNK; SSTKSLLEVAKNKQ; STKSLLEVAKNKQK; TKSLLEVAKNKQKE; KSLLEVAKNKQKEL; SLLEVAKNKQKELN; LLEVAKNKQKELNE; LEVAKNKQKELNEN; EVAKNKQKELNENM; VAKNKQKELNENMT; AKNKQKELNENMTK; KNKQKELNENMTKT; NKQKELNENMTKTN; KQKELNENMTKTNK; QKELNENMTKTNKD; KELNENMTKTNKDF; ELNENMTKTNKDFQ; LNENMTKTNKDFQE; NENMTKTNKDFQEL; ENMTKTNKDFQELN; NMTKTNKDFQELND; MTKTNKDFQELNDI; TKTNKDFQELNDIY; KTNKDFQELNDIYK; TNKDFQELNDIYKK; NKDFQELNDIYKKL; KDFQELNDIYKKLQ; DFQELNDIYKKLQD; FQELNDIYKKLQDM; QELNDIYKKLQDMD; ELNDIYKKLQDMDS; LNDIYKKLQDMDSR; 15 mers: MNLINKLFILTILFS; NLINKLFILTILFSS; LINKLFILTILFSSV; INKLFILTILFSSVI; NKLFILTILFSSVIS; KLFILTILFSSVISC; LFILTILFSSVISCK; FILTILFSSVISCKL; ILTILFSSVISCKLY; LTILFSSVISCKLYK; TILFSSVISCKLYKK; ILFSSVISCKLYKKI; LFSSVISCKLYKKIT; FSSVISCKLYKKITY; SSVISCKLYKKITYN; SVISCKLYKKITYNA; VISCKLYKKITYNAD; ISCKLYKKITYNADQ; SCKLYKKITYNADQV; CKLYKKITYNADQVI; KLYKKITYNADQVID; LYKKITYNADQVIDK; YKKITYNADQVIDKL; KKITYNADQVIDKLK; KITYNADQVIDKLKS; ITYNADQVIDKLKSN; TYNADQVIDKLKSNN; YNADQVIDKLKSNNG; NADQVIDKLKSNNGS; ADQVIDKLKSNNGSF; DQVIDKLKSNNGSFN; QVIDKLKSNNGSFNT; VIDKLKSNNGSFNTL; IDKLKSNNGSFNTLK; DKLKSNNGSFNTLKS; KLKSNNGSFNTLKSN; LKSNNGSFNTLKSND; KSNNGSFNTLKSNDD; SNNGSFNTLKSNDDS; NNGSFNTLKSNDDSK; NGSFNTLKSNDDSKR; GSFNTLKSNDDSKRS; SFNTLKSNDDSKRSG; FNTLKSNDDSKRSGR; NTLKSNDDSKRSGRK; TLKSNDDSKRSGRKP; LKSNDDSKRSGRKPR; KSNDDSKRSGRKPRS; SNDDSKRSGRKPRSV; NDDSKRSGRKPRSVD; DDSKRSGRKPRSVDN; DSKRSGRKPRSVDNT; SKRSGRKPRSVDNTY; KRSGRKPRSVDNTYM; RSGRKPRSVDNTYMD; SGRKPRSVDNTYMDQ; GRKPRSVDNTYMDQD; RKPRSVDNTYMDQDT; KPRSVDNTYMDQDTG; PRSVDNTYMDQDTGK; RSVDNTYMDQDTGKK; SVDNTYMDQDTGKKP; VDNTYMDQDTGKKPL; DNTYMDQDTGKKPLM; NTYMDQDTGKKPLMA; TYMDQDTGKKPLMAD; YMDQDTGKKPLMADM; MDQDTGKKPLMADMQ; DQDTGKKPLMADMQP; QDTGKKPLMADMQPD; DTGKKPLMADMQPDM; TGKKPLMADMQPDMQ; GKKPLMADMQPDMQN; KKPLMADMQPDMQND; KPLMADMQPDMQNDN; PLMADMQPDMQNDNS; LMADMQPDMQNDNSS; MADMQPDMQNDNSSS; ADMQPDMQNDNSSSN; DMQPDMQNDNSSSNH; MQPDMQNDNSSSNHT; QPDMQNDNSSSNHTL; PDMQNDNSSSNHTLQ; DMQNDNSSSNHTLQV; MQNDNSSSNHTLQVN; QNDNSSSNHTLQVNI; NDNSSSNHTLQVNIQ; DNSSSNHTLQVNIQD; NSSSNHTLQVNIQDN; SSSNHTLQVNIQDNE; SSNHTLQVNIQDNEA; SNHTLQVNIQDNEAS; NHTLQVNIQDNEASE;

	HTLQVNIQDNEASEA; TLQVNIQDNEASEAR; LQVNIQDNEASEARN; QVNIQDNEASEARNI; VNIQDNEASEARNIM; NIQDNEASEARNIMT; IQDNEASEARNIMTE; QDNEASEARNIMTEI; DNEASEARNIMTEIE; NEASEARNIMTEIES; EASEARNIMTEIESS; ASEARNIMTEIESSK; SEARNIMTEIESSKE; EARNIMTEIESSKEE; ARNIMTEIESSKEEY; RNIMTEIESSKEEYN; NIMTEIESSKEEYNR; IMTEIESSKEEYNRI; MTEIESSKEEYNRIN; TEIESSKEEYNRINE; EIESSKEEYNRINED; IESSKEEYNRINEDL; ESSKEEYNRINEDLA; SSKEEYNRINEDLAK; SKEEYNRINEDLAKV; KEEYNRINEDLAKVK; EEYNRINEDLAKVKA; EYNRINEDLAKVKAS; YNRINEDLAKVKASL; NRINEDLAKVKASLD; RINEDLAKVKASLDK; INEDLAKVKASLDKI; NEDLAKVKASLDKIK; EDLAKVKASLDKIKS; DLAKVKASLDKIKSL; LAKVKASLDKIKSLL; AKVKASLDKIKSLLS; KVKASLDKIKSLLST; VKASLDKIKSLLSTA; KASLDKIKSLLSTAK; ASLDKIKSLLSTAKS; SLDKIKSLLSTAKSY; LDKIKSLLSTAKSYL; DKIKSLLSTAKSYLE; KIKSLLSTAKSYLEQ; IKSLLSTAKSYLEQT; KSLLSTAKSYLEQTR; SLLSTAKSYLEQTRR; LLSTAKSYLEQTRRG; LSTAKSYLEQTRRGV; STAKSYLEQTRRGVG; TAKSYLEQTRRGVGS; AKSYLEQTRRGVGSS; KSYLEQTRRGVGSSK; SYLEQTRRGVGSSKA; YLEQTRRGVGSSKAN; LEQTRRGVGSSKANL; EQTRRGVGSSKANLA; QTRRGVGSSKANLAL; TRRGVGSSKANLALL; RRGVGSSKANLALLP; RGVGSSKANLALLPS; GVGSSKANLALLPSL; VGSSKANLALLPSLE; GSSKANLALLPSLEE; SSKANLALLPSLEEA; SKANLALLPSLEEAI; KANLALLPSLEEAIA; ANLALLPSLEEAIAK; NLALLPSLEEAIAKV; LALLPSLEEAIAKVK; ALLPSLEEAIAKVKS; LLPSLEEAIAKVKSN; LPSLEEAIAKVKSNH; PSLEEAIAKVKSNHA; SLEEAIAKVKSNHAS; LEEAIAKVKSNHASA; EEAIAKVKSNHASAD; EAIAKVKSNHASADT; AIAKVKSNHASADTH; IAKVKSNHASADTHC; AKVKSNHASADTHCN; KVKSNHASADTHCND; VKSNHASADTHCNDA; KSNHASADTHCNDAI; SNHASADTHCNDAIA; NHASADTHCNDAIAA; HASADTHCNDAIAAL; ASADTHCNDAIAALK; SADTHCNDAIAALKR; ADTHCNDAIAALKRA; DTHCNDAIAALKRAK; THCNDAIAALKRAKN; HCNDAIAALKRAKND; CNDAIAALKRAKNDF; NDAIAALKRAKNDFE; DAIAALKRAKNDFEY; AIAALKRAKNDFEYA; IAALKRAKNDFEYAQ; AALKRAKNDFEYAQR; ALKRAKNDFEYAQRK; LKRAKNDFEYAQRKA; KRAKNDFEYAQRKAD; RAKNDFEYAQRKADR; AKNDFEYAQRKADRA; KNDFEYAQRKADRAL; NDFEYAQRKADRALE; DFEYAQRKADRALEE; FEYAQRKADRALEEA; EYAQRKADRALEEAL; YAQRKADRALEEALS; AQRKADRALEEALSN; QRKADRALEEALSNS; RKADRALEEALSNSN; KADRALEEALSNSNA; ADRALEEALSNSNAS; DRALEEALSNSNASR; RALEEALSNSNASRH; ALEEALSNSNASRHE; LEEALSNSNASRHES; EEALSNSNASRHESY; EALSNSNASRHESYY; ALSNSNASRHESYYY; LSNSNASRHESYYYA; SNSNASRHESYYYAG; NSNASRHESYYYAGY; SNASRHESYYYAGYH; NASRHESYYYAGYHQ; ASRHESYYYAGYHQF; SRHESYYYAGYHQFM; RHESYYYAGYHQFMA; HESYYYAGYHQFMAD; ESYYYAGYHQFMADA; SYYYAGYHQFMADAK; YYYAGYHQFMADAKA; YYAGYHQFMADAKAS; YAGYHQFMADAKASM; AGYHQFMADAKASMS; GYHQFMADAKASMSS; YHQFMADAKASMSST; HQFMADAKASMSSTK; QFMADAKASMSSTKS; FMADAKASMSSTKSL; MADAKASMSSTKSLL; ADAKASMSSTKSLLE; DAKASMSSTKSLLEV; AKASMSSTKSLLEVA; KASMSSTKSLLEVAK; ASMSSTKSLLEVAKN; SMSSTKSLLEVAKNK; MSSTKSLLEVAKNKQ; SSTKSLLEVAKNKQK; STKSLLEVAKNKQKE;

	TKSLLEVAKNKQKEL; KSLLEVAKNKQKELN; SLLEVAKNKQKELNE; LLEVAKNKQKELNEN; LEVAKNKQKELNENM; EVAKNKQKELNENMT; VAKNKQKELNENMTK; AKNKQKELNENMTKT; KNKQKELNENMTKTN; NKQKELNENMTKTNK; KQKELNENMTKTNKD; QKELNENMTKTNKDF; KELNENMTKTNKDFQ; ELNENMTKTNKDFQE; LNENMTKTNKDFQEL; NENMTKTNKDFQELN; ENMTKTNKDFQELND; NMTKTNKDFQELNDI; MTKTNKDFQELNDIY; TKTNKDFQELNDIYK; KTNKDFQELNDIYKK; TNKDFQELNDIYKKL; NKDFQELNDIYKKLQ; KDFQELNDIYKKLQD; DFQELNDIYKKLQDM; FQELNDIYKKLQDMD; QELNDIYKKLQDMDS; ELNDIYKKLQDMDSR; 16 mers: MNLINKLFILTILFSS; NLINKLFILTILFSSV; LINKLFILTILFSSVI; INKLFILTILFSSVIS; NKLFILTILFSSVISC; KLFILTILFSSVISCK; LFILTILFSSVISCKL; FILTILFSSVISCKLY; ILTILFSSVISCKLYK; LTILFSSVISCKLYKK; TILFSSVISCKLYKKI; ILFSSVISCKLYKKIT; LFSSVISCKLYKKITY; FSSVISCKLYKKITYN; SSVISCKLYKKITYNA; SVISCKLYKKITYNAD; VISCKLYKKITYNADQ; ISCKLYKKITYNADQV; SCKLYKKITYNADQVI; CKLYKKITYNADQVID; KLYKKITYNADQVIDK; LYKKITYNADQVIDKL; YKKITYNADQVIDKLK; KKITYNADQVIDKLKS; KITYNADQVIDKLKSN; ITYNADQVIDKLKSNN; TYNADQVIDKLKSNNG; YNADQVIDKLKSNNGS; NADQVIDKLKSNNGSF; ADQVIDKLKSNNGSFN; DQVIDKLKSNNGSFNT; QVIDKLKSNNGSFNTL; VIDKLKSNNGSFNTLK; IDKLKSNNGSFNTLKS; DKLKSNNGSFNTLKSN; KLKSNNGSFNTLKSND; LKSNNGSFNTLKSNDD; KSNNGSFNTLKSNDDS; SNNGSFNTLKSNDDSK; NNGSFNTLKSNDDSKR; NGSFNTLKSNDDSKRS; GSFNTLKSNDDSKRSG; SFNTLKSNDDSKRSGR; FNTLKSNDDSKRSGRK; NTLKSNDDSKRSGRKP; TLKSNDDSKRSGRKPR; LKSNDDSKRSGRKPRS; KSNDDSKRSGRKPRSV; SNDDSKRSGRKPRSVD; NDDSKRSGRKPRSVDN; DDSKRSGRKPRSVDNT; DSKRSGRKPRSVDNTY; SKRSGRKPRSVDNTYM; KRSGRKPRSVDNTYMD; RSGRKPRSVDNTYMDQ; SGRKPRSVDNTYMDQD; GRKPRSVDNTYMDQDT; RKPRSVDNTYMDQDTG; KPRSVDNTYMDQDTGK; PRSVDNTYMDQDTGKK; RSVDNTYMDQDTGKKP; SVDNTYMDQDTGKKPL; VDNTYMDQDTGKKPLM; DNTYMDQDTGKKPLMA; NTYMDQDTGKKPLMAD; TYMDQDTGKKPLMADM; YMDQDTGKKPLMADMQ; MDQDTGKKPLMADMQP; DQDTGKKPLMADMQPD; QDTGKKPLMADMQPDM; DTGKKPLMADMQPDMQ; TGKKPLMADMQPDMQN; GKKPLMADMQPDMQND; KKPLMADMQPDMQNDN; KPLMADMQPDMQNDNS; PLMADMQPDMQNDNSS; LMADMQPDMQNDNSSS; MADMQPDMQNDNSSSN; ADMQPDMQNDNSSSNH; DMQPDMQNDNSSSNHT; MQPDMQNDNSSSNHTL; QPDMQNDNSSSNHTLQ; PDMQNDNSSSNHTLQV; DMQNDNSSSNHTLQVN; MQNDNSSSNHTLQVNI; QNDNSSSNHTLQVNIQ; NDNSSSNHTLQVNIQD; DNSSSNHTLQVNIQDN; NSSSNHTLQVNIQDNE; SSSNHTLQVNIQDNEA; SSNHTLQVNIQDNEAS; SNHTLQVNIQDNEASE; NHTLQVNIQDNEASEA; HTLQVNIQDNEASEAR; TLQVNIQDNEASEARN; LQVNIQDNEASEARNI; QVNIQDNEASEARNIM; VNIQDNEASEARNIMT; NIQDNEASEARNIMTE; IQDNEASEARNIMTEI; QDNEASEARNIMTEIE; DNEASEARNIMTEIES; NEASEARNIMTEIESS; EASEARNIMTEIESSK; ASEARNIMTEIESSKE; SEARNIMTEIESSKEE; EARNIMTEIESSKEEY; ARNIMTEIESSKEEYN; RNIMTEIESSKEEYNR; NIMTEIESSKEEYNRI; IMTEIESSKEEYNRIN; MTEIESSKEEYNRINE; TEIESSKEEYNRINED; EIESSKEEYNRINEDL; IESSKEEYNRINEDLA; ESSKEEYNRINEDLAK; SSKEEYNRINEDLAKV;

	SKEEYNRINEDLAKVK; KEEYNRINEDLAKVKA; EEYNRINEDLAKVKAS; EYNRINEDLAKVKASL; YNRINEDLAKVKASLD; NRINEDLAKVKASLDK; RINEDLAKVKASLDKI; INEDLAKVKASLDKIK; NEDLAKVKASLDKIKS; EDLAKVKASLDKIKSL; DLAKVKASLDKIKSLL; LAKVKASLDKIKSLLS; AKVKASLDKIKSLLST; KVKASLDKIKSLLSTA; VKASLDKIKSLLSTAK; KASLDKIKSLLSTAKS; ASLDKIKSLLSTAKSY; SLDKIKSLLSTAKSYL; LDKIKSLLSTAKSYLE; DKIKSLLSTAKSYLEQ; KIKSLLSTAKSYLEQT; IKSLLSTAKSYLEQTR; KSLLSTAKSYLEQTRR; SLLSTAKSYLEQTRRG; LLSTAKSYLEQTRRGV; LSTAKSYLEQTRRGVG; STAKSYLEQTRRGVGS; TAKSYLEQTRRGVGSS; AKSYLEQTRRGVGSSK; KSYLEQTRRGVGSSKA; SYLEQTRRGVGSSKAN; YLEQTRRGVGSSKANL; LEQTRRGVGSSKANLA; EQTRRGVGSSKANLAL; QTRRGVGSSKANLALL; TRRGVGSSKANLALLP; RRGVGSSKANLALLPS; RGVGSSKANLALLPSL; GVGSSKANLALLPSLE; VGSSKANLALLPSLEE; GSSKANLALLPSLEEA; SSKANLALLPSLEEAI; SKANLALLPSLEEAIA; KANLALLPSLEEAIAK; ANLALLPSLEEAIAKV; NLALLPSLEEAIAKVK; LALLPSLEEAIAKVKS; ALLPSLEEAIAKVKSN; LLPSLEEAIAKVKSNH; LPSLEEAIAKVKSNHA; PSLEEAIAKVKSNHAS; SLEEAIAKVKSNHASA; LEEAIAKVKSNHASAD; EEAIAKVKSNHASADT; EAIAKVKSNHASADTH; AIAKVKSNHASADTHC; IAKVKSNHASADTHCN; AKVKSNHASADTHCND; KVKSNHASADTHCNDA; VKSNHASADTHCNDAI; KSNHASADTHCNDAIA; SNHASADTHCNDAIAA; NHASADTHCNDAIAAL; HASADTHCNDAIAALK; ASADTHCNDAIAALKR; SADTHCNDAIAALKRA; ADTHCNDAIAALKRAK; DTHCNDAIAALKRAKN; THCNDAIAALKRAKND; HCNDAIAALKRAKNDF; CNDAIAALKRAKNDFE; NDAIAALKRAKNDFEY; DAIAALKRAKNDFEYA; AIAALKRAKNDFEYAQ; IAALKRAKNDFEYAQR; AALKRAKNDFEYAQRK; ALKRAKNDFEYAQRKA; LKRAKNDFEYAQRKAD; KRAKNDFEYAQRKADR; RAKNDFEYAQRKADRA; AKNDFEYAQRKADRAL; KNDFEYAQRKADRALE; NDFEYAQRKADRALEE; DFEYAQRKADRALEEA; FEYAQRKADRALEEAL; EYAQRKADRALEEALS; YAQRKADRALEEALSN; AQRKADRALEEALSNS; QRKADRALEEALSNSN; RKADRALEEALSNSNA; KADRALEEALSNSNAS; ADRALEEALSNSNASR; DRALEEALSNSNASRH; RALEEALSNSNASRHE; ALEEALSNSNASRHES; LEEALSNSNASRHESY; EEALSNSNASRHESYY; EALSNSNASRHESYYY; ALSNSNASRHESYYYA; LSNSNASRHESYYYAG; SNSNASRHESYYYAGY; NSNASRHESYYYAGYH; SNASRHESYYYAGYHQ; NASRHESYYYAGYHQF; ASRHESYYYAGYHQFM; SRHESYYYAGYHQFMA; RHESYYYAGYHQFMAD; HESYYYAGYHQFMADA; ESYYYAGYHQFMADAK; SYYYAGYHQFMADAKA; YYYAGYHQFMADAKAS; YYAGYHQFMADAKASM; YAGYHQFMADAKASMS; AGYHQFMADAKASMSS; GYHQFMADAKASMSST; YHQFMADAKASMSSTK; HQFMADAKASMSSTKS; QFMADAKASMSSTKSL; FMADAKASMSSTKSLL; MADAKASMSSTKSLLE; ADAKASMSSTKSLLEV; DAKASMSSTKSLLEVA; AKASMSSTKSLLEVAK; KASMSSTKSLLEVAKN; ASMSSTKSLLEVAKNK; SMSSTKSLLEVAKNKQ; MSSTKSLLEVAKNKQK; SSTKSLLEVAKNKQKE; STKSLLEVAKNKQKEL; TKSLLEVAKNKQKELN; KSLLEVAKNKQKELNE; SLLEVAKNKQKELNEN; LLEVAKNKQKELNENM; LEVAKNKQKELNENMT; EVAKNKQKELNENMTK; VAKNKQKELNENMTKT; AKNKQKELNENMTKTN; KNKQKELNENMTKTNK; NKQKELNENMTKTNKD; KQKELNENMTKTNKDF; QKELNENMTKTNKDFQ; KELNENMTKTNKDFQE; ELNENMTKTNKDFQEL; LNENMTKTNKDFQELN; NENMTKTNKDFQELND; ENMTKTNKDFQELNDI; NMTKTNKDFQELNDIY; MTKTNKDFQELNDIYK; TKTNKDFQELNDIYKK; KTNKDFQELNDIYKKL; TNKDFQELNDIYKKLQ; NKDFQELNDIYKKLQD; KDFQELNDIYKKLQDM;

	DFQELNDIYKKLQDMD; FQELNDIYKKLQDMDS; QELNDIYKKLQDMDSR;
Seq 23	13 mers: MIINHNTSAINAS; IINHNTSAINASR; INHNTSAINASRN; NHNTSAINASRNN; HNTSAINASRNNG; NTSAINASRNNGI; TSAINASRNNGIN; SAINASRNNGINA; AINASRNNGINAA; INASRNNGINAAN; NASRNNGINAANL; ASRNNGINAANLS; SRNNGINAANLSK; RNNGINAANLSKT; NNGINAANLSKTQ; NGINAANLSKTQE; GINAANLSKTQEK; INAANLSKTQEKL; NAANLSKTQEKLS; AANLSKTQEKLSS; ANLSKTQEKLSSG; NLSKTQEKLSSGY; LSKTQEKLSSGYR; SKTQEKLSSGYRI; KTQEKLSSGYRIN; TQEKLSSGYRINR; QEKLSSGYRINRA; EKLSSGYRINRAS; KLSSGYRINRASD; LSSGYRINRASDD; SSGYRINRASDDA; SGYRINRASDDAA; GYRINRASDDAAG; YRINRASDDAAGM; RINRASDDAAGMG; INRASDDAAGMGV; NRASDDAAGMGVS; RASDDAAGMGVSG; ASDDAAGMGVSGK; SDDAAGMGVSGKI; DDAAGMGVSGKIN; DAAGMGVSGKINA; AAGMGVSGKINAQ; AGMGVSGKINAQI; GMGVSGKINAQIR; MGVSGKINAQIRG; GVSGKINAQIRGL; VSGKINAQIRGLS; SGKINAQIRGLSQ; GKINAQIRGLSQA; KINAQIRGLSQAS; INAQIRGLSQASR; NAQIRGLSQASRN; AQIRGLSQASRNT; QIRGLSQASRNTS; IRGLSQASRNTSK; RGLSQASRNTSKA; GLSQASRNTSKAI; LSQASRNTSKAIN; SQASRNTSKAINF; QASRNTSKAINFI; ASRNTSKAINFIQ; SRNTSKAINFIQT; RNTSKAINFIQTT; NTSKAINFIQTTE; TSKAINFIQTTEG; SKAINFIQTTEGN; KAINFIQTTEGNL; AINFIQTTEGNLN; INFIQTTEGNLNE; NFIQTTEGNLNEV; FIQTTEGNLNEVE; IQTTEGNLNEVEK; QTTEGNLNEVEKV; TTEGNLNEVEKVL; TEGNLNEVEKVLV; EGNLNEVEKVLVR; GNLNEVEKVLVRM; NLNEVEKVLVRMK; LNEVEKVLVRMKE; NEVEKVLVRMKEL; EVEKVLVRMKELA; VEKVLVRMKELAV; EKVLVRMKELAVQ; KVLVRMKELAVQS; VLVRMKELAVQSG; LVRMKELAVQSGN; VRMKELAVQSGNG; RMKELAVQSGNGT; MKELAVQSGNGTY; KELAVQSGNGTYS; ELAVQSGNGTYSD; LAVQSGNGTYSDA; AVQSGNGTYSDAD; VQSGNGTYSDADR; QSGNGTYSDADRG; SGNGTYSDADRGS; GNGTYSDADRGSI; NGTYSDADRGSIQ; GTYSDADRGSIQI; TYSDADRGSIQIE; YSDADRGSIQIEI; SDADRGSIQIEIE; DADRGSIQIEIEQ; ADRGSIQIEIEQL; DRGSIQIEIEQLT; RGSIQIEIEQLTD; GSIQIEIEQLTDE; SIQIEIEQLTDEI; IQIEIEQLTDEIN; QIEIEQLTDEINR; IEIEQLTDEINRI; EIEQLTDEINRIA; IEQLTDEINRIAD; EQLTDEINRIADQ; QLTDEINRIADQA; LTDEINRIADQAQ; TDEINRIADQAQY; DEINRIADQAQYN; EINRIADQAQYNQ; INRIADQAQYNQM; NRIADQAQYNQMH; RIADQAQYNQMHM; IADQAQYNQMHML; ADQAQYNQMHMLS; DQAQYNQMHMLSN; QAQYNQMHMLSNK; AQYNQMHMLSNKS; QYNQMHMLSNKSA; YNQMHMLSNKSAS; NQMHMLSNKSASQ; QMHMLSNKSASQN; MHMLSNKSASQNV; HMLSNKSASQNVR; MLSNKSASQNVRT; LSNKSASQNVRTA; SNKSASQNVRTAE; NKSASQNVRTAEE; KSASQNVRTAEEL; SASQNVRTAEELG; ASQNVRTAEELGM;

	SQNVRTAEELGMQ; QNVRTAEELGMQP; NVRTAEELGMQPA; VRTAEELGMQPAK; RTAEELGMQPAKI; TAEELGMQPAKIN; AEELGMQPAKINT; EELGMQPAKINTP; ELGMQPAKINTPA; LGMQPAKINTPAS; GMQPAKINTPASL; MQPAKINTPASLS; QPAKINTPASLSG; PAKINTPASLSGS; AKINTPASLSGSQ; KINTPASLSGSQA; INTPASLSGSQAS; NTPASLSGSQASW; TPASLSGSQASWT; PASLSGSQASWTL; ASLSGSQASWTLR; SLSGSQASWTLRV; LSGSQASWTLRVH; SGSQASWTLRVHV; GSQASWTLRVHVG; SQASWTLRVHVGA; QASWTLRVHVGAN; ASWTLRVHVGANQ; SWTLRVHVGANQD; WTLRVHVGANQDE; TLRVHVGANQDEA; LRVHVGANQDEAI; RVHVGANQDEAIA; VHVGANQDEAIAV; HVGANQDEAIAVN; VGANQDEAIAVNI; GANQDEAIAVNIY; ANQDEAIAVNIYA; NQDEAIAVNIYAA; QDEAIAVNIYAAN; DEAIAVNIYAANV; EAIAVNIYAANVA; AIAVNIYAANVAN; IAVNIYAANVANL; AVNIYAANVANLF; VNIYAANVANLFS; NIYAANVANLFSG; IYAANVANLFSGE; YAANVANLFSGEG; AANVANLFSGEGA; ANVANLFSGEGAQ; NVANLFSGEGAQT; VANLFSGEGAQTA; ANLFSGEGAQTAQ; NLFSGEGAQTAQA; LFSGEGAQTAQAA; FSGEGAQTAQAAP; SGEGAQTAQAAPV; GEGAQTAQAAPVQ; EGAQTAQAAPVQE; GAQTAQAAPVQEG; AQTAQAAPVQEGV; QTAQAAPVQEGVQ; TAQAAPVQEGVQQ; AQAAPVQEGVQQE; QAAPVQEGVQQEG; AAPVQEGVQQEGA; APVQEGVQQEGAQ; PVQEGVQQEGAQQ; VQEGVQQEGAQQP; QEGVQQEGAQQPA; EGVQQEGAQQPAP; GVQQEGAQQPAPA; VQQEGAQQPAPAT; QQEGAQQPAPATA; QEGAQQPAPATAP; EGAQQPAPATAPS; GAQQPAPATAPSQ; AQQPAPATAPSQG; QQPAPATAPSQGG; QPAPATAPSQGGV; PAPATAPSQGGVN; APATAPSQGGVNS; PATAPSQGGVNSP; ATAPSQGGVNSPV; TAPSQGGVNSPVN; APSQGGVNSPVNV; PSQGGVNSPVNVT; SQGGVNSPVNVTT; QGGVNSPVNVTTT; GGVNSPVNVTTTV; GVNSPVNVTTTVD; VNSPVNVTTTVDA; NSPVNVTTTVDAN; SPVNVTTTVDANT; PVNVTTTVDANTS; VNVTTTVDANTSL; NVTTTVDANTSLA; VTTTVDANTSLAK; TTTVDANTSLAKI; TTVDANTSLAKIE; TVDANTSLAKIEN; VDANTSLAKIENA; DANTSLAKIENAI; ANTSLAKIENAIR; NTSLAKIENAIRM; TSLAKIENAIRMI; SLAKIENAIRMIS; LAKIENAIRMISD; AKIENAIRMISDQ; KIENAIRMISDQR; IENAIRMISDQRA; ENAIRMISDQRAN; NAIRMISDQRANL; AIRMISDQRANLG; IRMISDQRANLGA; RMISDQRANLGAF; MISDQRANLGAFQ; ISDQRANLGAFQN; SDQRANLGAFQNR; DQRANLGAFQNRL; QRANLGAFQNRLE; RANLGAFQNRLES; ANLGAFQNRLESI; NLGAFQNRLESIK; LGAFQNRLESIKN; GAFQNRLESIKNS; AFQNRLESIKNST; FQNRLESIKNSTE; QNRLESIKNSTEY; NRLESIKNSTEYA; RLESIKNSTEYAI; LESIKNSTEYAIE; ESIKNSTEYAIEN; SIKNSTEYAIENL; IKNSTEYAIENLK; KNSTEYAIENLKA; NSTEYAIENLKAS; STEYAIENLKASY; TEYAIENLKASYA; EYAIENLKASYAQ; YAIENLKASYAQI; AIENLKASYAQIK; IENLKASYAQIKD; ENLKASYAQIKDA; NLKASYAQIKDAT; LKASYAQIKDATM; KASYAQIKDATMT; ASYAQIKDATMTD; SYAQIKDATMTDE; YAQIKDATMTDEV; AQIKDATMTDEVV; QIKDATMTDEVVA;

IKDATMTDEVVAA; KDATMTDEVVAAT; DATMTDEVVAATT;
ATMTDEVVAATTN; TMTDEVVAATTNS; MTDEVVAATTNSI;
TDEVVAATTNSIL; DEVVAATTNSILT; EVVAATTNSILTQ;
VVAATTNSILTQS; VAATTNSILTQSA; AATTNSILTQSAM;
ATTNSILTQSAMA; TTNSILTQSAMAM; TNSILTQSAMAMI;
NSILTQSAMAMIA; SILTQSAMAMIAQ; ILTQSAMAMIAQA;
LTQSAMAMIAQAN; TQSAMAMIAQANQ; QSAMAMIAQANQV;
SAMAMIAQANQVP; AMAMIAQANQVPQ; MAMIAQANQVPQY;
AMIAQANQVPQYV; MIAQANQVPQYVL; IAQANQVPQYVLS;
AQANQVPQYVLSL; QANQVPQYVLSLL; ANQVPQYVLSLLR;

14 mers:
MIINHNTSAINASR; IINHNTSAINASRN; INHNTSAINASRNN;
NHNTSAINASRNNG; HNTSAINASRNNGI; NTSAINASRNNGIN;
TSAINASRNNGINA; SAINASRNNGINAA; AINASRNNGINAAN;
INASRNNGINAANL; NASRNNGINAANLS; ASRNNGINAANLSK;
SRNNGINAANLSKT; RNNGINAANLSKTQ; NNGINAANLSKTQE;
NGINAANLSKTQEK; GINAANLSKTQEKL; INAANLSKTQEKLS;
NAANLSKTQEKLSS; AANLSKTQEKLSSG; ANLSKTQEKLSSGY;
NLSKTQEKLSSGYR; LSKTQEKLSSGYRI; SKTQEKLSSGYRIN;
KTQEKLSSGYRINR; TQEKLSSGYRINRA; QEKLSSGYRINRAS;
EKLSSGYRINRASD; KLSSGYRINRASDD; LSSGYRINRASDDA;
SSGYRINRASDDAA; SGYRINRASDDAAG; GYRINRASDDAAGM;
YRINRASDDAAGMG; RINRASDDAAGMGV; INRASDDAAGMGVS;
NRASDDAAGMGVSG; RASDDAAGMGVSGK; ASDDAAGMGVSGKI;
SDDAAGMGVSGKIN; DDAAGMGVSGKINA; DAAGMGVSGKINAQ;
AAGMGVSGKINAQI; AGMGVSGKINAQIR; GMGVSGKINAQIRG;
MGVSGKINAQIRGL; GVSGKINAQIRGLS; VSGKINAQIRGLSQ;
SGKINAQIRGLSQA; GKINAQIRGLSQAS; KINAQIRGLSQASR;
INAQIRGLSQASRN; NAQIRGLSQASRNT; AQIRGLSQASRNTS;
QIRGLSQASRNTSK; IRGLSQASRNTSKA; RGLSQASRNTSKAI;
GLSQASRNTSKAIN; LSQASRNTSKAINF; SQASRNTSKAINFI;
QASRNTSKAINFIQ; ASRNTSKAINFIQT; SRNTSKAINFIQTT;
RNTSKAINFIQTTE; NTSKAINFIQTTEG; TSKAINFIQTTEGN;
SKAINFIQTTEGNL; KAINFIQTTEGNLN; AINFIQTTEGNLNE;
INFIQTTEGNLNEV; NFIQTTEGNLNEVE; FIQTTEGNLNEVEK;
IQTTEGNLNEVEKV; QTTEGNLNEVEKVL; TTEGNLNEVEKVLV;
TEGNLNEVEKVLVR; EGNLNEVEKVLVRM; GNLNEVEKVLVRMK;
NLNEVEKVLVRMKE; LNEVEKVLVRMKEL; NEVEKVLVRMKELA;
EVEKVLVRMKELAV; VEKVLVRMKELAVQ; EKVLVRMKELAVQS;
KVLVRMKELAVQSG; VLVRMKELAVQSGN; LVRMKELAVQSGNG;
VRMKELAVQSGNGT; RMKELAVQSGNGTY; MKELAVQSGNGTYS;
KELAVQSGNGTYSD; ELAVQSGNGTYSDA; LAVQSGNGTYSDAD;
AVQSGNGTYSDADR; VQSGNGTYSDADRG; QSGNGTYSDADRGS;
SGNGTYSDADRGSI; GNGTYSDADRGSIQ; NGTYSDADRGSIQI;
GTYSDADRGSIQIE; TYSDADRGSIQIEI; YSDADRGSIQIEIE;
SDADRGSIQIEIEQ; DADRGSIQIEIEQL; ADRGSIQIEIEQLT;
DRGSIQIEIEQLTD; RGSIQIEIEQLTDE; GSIQIEIEQLTDEI;
SIQIEIEQLTDEIN; IQIEIEQLTDEINR; QIEIEQLTDEINRI;
IEIEQLTDEINRIA; EIEQLTDEINRIAD; IEQLTDEINRIADQ;
EQLTDEINRIADQA; QLTDEINRIADQAQ; LTDEINRIADQAQY;

	TDEINRIADQAQYN; DEINRIADQAQYNQ; EINRIADQAQYNQM; INRIADQAQYNQMH; NRIADQAQYNQMHM; RIADQAQYNQMHML; IADQAQYNQMHMLS; ADQAQYNQMHMLSN; DQAQYNQMHMLSNK; QAQYNQMHMLSNKS; AQYNQMHMLSNKSA; QYNQMHMLSNKSAS; YNQMHMLSNKSASQ; NQMHMLSNKSASQN; QMHMLSNKSASQNV; MHMLSNKSASQNVR; HMLSNKSASQNVRT; MLSNKSASQNVRTA; LSNKSASQNVRTAE; SNKSASQNVRTAEE; NKSASQNVRTAEEL; KSASQNVRTAEELG; SASQNVRTAEELGM; ASQNVRTAEELGMQ; SQNVRTAEELGMQP; QNVRTAEELGMQPA; NVRTAEELGMQPAK; VRTAEELGMQPAKI; RTAEELGMQPAKIN; TAEELGMQPAKINT; AEELGMQPAKINTP; EELGMQPAKINTPA; ELGMQPAKINTPAS; LGMQPAKINTPASL; GMQPAKINTPASLS; MQPAKINTPASLSG; QPAKINTPASLSGS; PAKINTPASLSGSQ; AKINTPASLSGSQA; KINTPASLSGSQAS; INTPASLSGSQASW; NTPASLSGSQASWT; TPASLSGSQASWTL; PASLSGSQASWTLR; ASLSGSQASWTLRV; SLSGSQASWTLRVH; LSGSQASWTLRVHV; SGSQASWTLRVHVG; GSQASWTLRVHVGA; SQASWTLRVHVGAN; QASWTLRVHVGANQ; ASWTLRVHVGANQD; SWTLRVHVGANQDE; WTLRVHVGANQDEA; TLRVHVGANQDEAI; LRVHVGANQDEAIA; RVHVGANQDEAIAV; VHVGANQDEAIAVN; HVGANQDEAIAVNI; VGANQDEAIAVNIY; GANQDEAIAVNIYA; ANQDEAIAVNIYAA; NQDEAIAVNIYAAN; QDEAIAVNIYAANV; DEAIAVNIYAANVA; EAIAVNIYAANVAN; AIAVNIYAANVANL; IAVNIYAANVANLF; AVNIYAANVANLFS; VNIYAANVANLFSG; NIYAANVANLFSGE; IYAANVANLFSGEG; YAANVANLFSGEGA; AANVANLFSGEGAQ; ANVANLFSGEGAQT; NVANLFSGEGAQTA; VANLFSGEGAQTAQ; ANLFSGEGAQTAQA; NLFSGEGAQTAQAA; LFSGEGAQTAQAAP; FSGEGAQTAQAAPV; SGEGAQTAQAAPVQ; GEGAQTAQAAPVQE; EGAQTAQAAPVQEG; GAQTAQAAPVQEGV; AQTAQAAPVQEGVQ; QTAQAAPVQEGVQQ; TAQAAPVQEGVQQE; AQAAPVQEGVQQEG; QAAPVQEGVQQEGA; AAPVQEGVQQEGAQ; APVQEGVQQEGAQQ; PVQEGVQQEGAQQP; VQEGVQQEGAQQPA; QEGVQQEGAQQPAP; EGVQQEGAQQPAPA; GVQQEGAQQPAPAT; VQQEGAQQPAPATA; QQEGAQQPAPATAP; QEGAQQPAPATAPS; EGAQQPAPATAPSQ; GAQQPAPATAPSQG; AQQPAPATAPSQGG; QQPAPATAPSQGGV; QPAPATAPSQGGVN; PAPATAPSQGGVNS; APATAPSQGGVNSP; PATAPSQGGVNSPV; ATAPSQGGVNSPVN; TAPSQGGVNSPVNV; APSQGGVNSPVNVT; PSQGGVNSPVNVTT; SQGGVNSPVNVTTT; QGGVNSPVNVTTTV; GGVNSPVNVTTTVD; GVNSPVNVTTTVDA; VNSPVNVTTTVDAN; NSPVNVTTTVDANT; SPVNVTTTVDANTS; PVNVTTTVDANTSL; VNVTTTVDANTSLA; NVTTTVDANTSLAK; VTTTVDANTSLAKI; TTTVDANTSLAKIE; TTVDANTSLAKIEN; TVDANTSLAKIENA; VDANTSLAKIENAI; DANTSLAKIENAIR; ANTSLAKIENAIRM; NTSLAKIENAIRMI; TSLAKIENAIRMIS; SLAKIENAIRMISD; LAKIENAIRMISDQ; AKIENAIRMISDQR; KIENAIRMISDQRA; IENAIRMISDQRAN; ENAIRMISDQRANL; NAIRMISDQRANLG; AIRMISDQRANLGA; IRMISDQRANLGAF; RMISDQRANLGAFQ; MISDQRANLGAFQN; ISDQRANLGAFQNR; SDQRANLGAFQNRL; DQRANLGAFQNRLE; QRANLGAFQNRLES; RANLGAFQNRLESI; ANLGAFQNRLESIK; NLGAFQNRLESIKN; LGAFQNRLESIKNS; GAFQNRLESIKNST; AFQNRLESIKNSTE; FQNRLESIKNSTEY;

	QNRLESIKNSTEYA; NRLESIKNSTEYAI; RLESIKNSTEYAIE; LESIKNSTEYAIEN; ESIKNSTEYAIENL; SIKNSTEYAIENLK; IKNSTEYAIENLKA; KNSTEYAIENLKAS; NSTEYAIENLKASY; STEYAIENLKASYA; TEYAIENLKASYAQ; EYAIENLKASYAQI; YAIENLKASYAQIK; AIENLKASYAQIKD; IENLKASYAQIKDA; ENLKASYAQIKDAT; NLKASYAQIKDATM; LKASYAQIKDATMT; KASYAQIKDATMTD; ASYAQIKDATMTDE; SYAQIKDATMTDEV; YAQIKDATMTDEVV; AQIKDATMTDEVVA; QIKDATMTDEVVAA; IKDATMTDEVVAAT; KDATMTDEVVAATT; DATMTDEVVAATTN; ATMTDEVVAATTNS; TMTDEVVAATTNSI; MTDEVVAATTNSIL; TDEVVAATTNSILT; DEVVAATTNSILTQ; EVVAATTNSILTQS; VVAATTNSILTQSA; VAATTNSILTQSAM; AATTNSILTQSAMA; ATTNSILTQSAMAM; TTNSILTQSAMAMI; TNSILTQSAMAMIA; NSILTQSAMAMIAQ; SILTQSAMAMIAQA; ILTQSAMAMIAQAN; LTQSAMAMIAQANQ; TQSAMAMIAQANQV; QSAMAMIAQANQVP; SAMAMIAQANQVPQ; AMAMIAQANQVPQY; MAMIAQANQVPQYV; AMIAQANQVPQYVL; MIAQANQVPQYVLS; IAQANQVPQYVLSL; AQANQVPQYVLSLL; QANQVPQYVLSLLR; 15 mers: MIINHNTSAINASRN; IINHNTSAINASRNN; INHNTSAINASRNNG; NHNTSAINASRNNGI; HNTSAINASRNNGIN; NTSAINASRNNGINA; TSAINASRNNGINAA; SAINASRNNGINAAN; AINASRNNGINAANL; INASRNNGINAANLS; NASRNNGINAANLSK; ASRNNGINAANLSKT; SRNNGINAANLSKTQ; RNNGINAANLSKTQE; NNGINAANLSKTQEK; NGINAANLSKTQEKL; GINAANLSKTQEKLS; INAANLSKTQEKLSS; NAANLSKTQEKLSSG; AANLSKTQEKLSSGY; ANLSKTQEKLSSGYR; NLSKTQEKLSSGYRI; LSKTQEKLSSGYRIN; SKTQEKLSSGYRINR; KTQEKLSSGYRINRA; TQEKLSSGYRINRAS; QEKLSSGYRINRASD; EKLSSGYRINRASDD; KLSSGYRINRASDDA; LSSGYRINRASDDAA; SSGYRINRASDDAAG; SGYRINRASDDAAGM; GYRINRASDDAAGMG; YRINRASDDAAGMGV; RINRASDDAAGMGVS; INRASDDAAGMGVSG; NRASDDAAGMGVSGK; RASDDAAGMGVSGKI; ASDDAAGMGVSGKIN; SDDAAGMGVSGKINA; DDAAGMGVSGKINAQ; DAAGMGVSGKINAQI; AAGMGVSGKINAQIR; AGMGVSGKINAQIRG; GMGVSGKINAQIRGL; MGVSGKINAQIRGLS; GVSGKINAQIRGLSQ; VSGKINAQIRGLSQA; SGKINAQIRGLSQAS; GKINAQIRGLSQASR; KINAQIRGLSQASRN; INAQIRGLSQASRNT; NAQIRGLSQASRNTS; AQIRGLSQASRNTSK; QIRGLSQASRNTSKA; IRGLSQASRNTSKAI; RGLSQASRNTSKAIN; GLSQASRNTSKAINF; LSQASRNTSKAINFI; SQASRNTSKAINFIQ; QASRNTSKAINFIQT; ASRNTSKAINFIQTT; SRNTSKAINFIQTTE; RNTSKAINFIQTTEG; NTSKAINFIQTTEGN; TSKAINFIQTTEGNL; SKAINFIQTTEGNLN; KAINFIQTTEGNLNE; AINFIQTTEGNLNEV; INFIQTTEGNLNEVE; NFIQTTEGNLNEVEK; FIQTTEGNLNEVEKV; IQTTEGNLNEVEKVL; QTTEGNLNEVEKVLV; TTEGNLNEVEKVLVR; TEGNLNEVEKVLVRM; EGNLNEVEKVLVRMK; GNLNEVEKVLVRMKE; NLNEVEKVLVRMKEL; LNEVEKVLVRMKELA; NEVEKVLVRMKELAV; EVEKVLVRMKELAVQ; VEKVLVRMKELAVQS; EKVLVRMKELAVQSG; KVLVRMKELAVQSGN; VLVRMKELAVQSGNG; LVRMKELAVQSGNGT; VRMKELAVQSGNGTY; RMKELAVQSGNGTYS; MKELAVQSGNGTYSD; KELAVQSGNGTYSDA; ELAVQSGNGTYSDAD; LAVQSGNGTYSDADR;

	AVQSGNGTYSDADRG; VQSGNGTYSDADRGS; QSGNGTYSDADRGSI; SGNGTYSDADRGSIQ; GNGTYSDADRGSIQI; NGTYSDADRGSIQIE; GTYSDADRGSIQIEI; TYSDADRGSIQIEIE; YSDADRGSIQIEIEQ; SDADRGSIQIEIEQL; DADRGSIQIEIEQLT; ADRGSIQIEIEQLTD; DRGSIQIEIEQLTDE; RGSIQIEIEQLTDEI; GSIQIEIEQLTDEIN; SIQIEIEQLTDEINR; IQIEIEQLTDEINRI; QIEIEQLTDEINRIA; IEIEQLTDEINRIAD; EIEQLTDEINRIADQ; IEQLTDEINRIADQA; EQLTDEINRIADQAQ; QLTDEINRIADQAQY; LTDEINRIADQAQYN; TDEINRIADQAQYNQ; DEINRIADQAQYNQM; EINRIADQAQYNQMH; INRIADQAQYNQMHM; NRIADQAQYNQMHML; RIADQAQYNQMHMLS; IADQAQYNQMHMLSN; ADQAQYNQMHMLSNK; DQAQYNQMHMLSNKS; QAQYNQMHMLSNKSA; AQYNQMHMLSNKSAS; QYNQMHMLSNKSASQ; YNQMHMLSNKSASQN; NQMHMLSNKSASQNV; QMHMLSNKSASQNVR; MHMLSNKSASQNVRT; HMLSNKSASQNVRTA; MLSNKSASQNVRTAE; LSNKSASQNVRTAEE; SNKSASQNVRTAEEL; NKSASQNVRTAEELG; KSASQNVRTAEELGM; SASQNVRTAEELGMQ; ASQNVRTAEELGMQP; SQNVRTAEELGMQPA; QNVRTAEELGMQPAK; NVRTAEELGMQPAKI; VRTAEELGMQPAKIN; RTAEELGMQPAKINT; TAEELGMQPAKINTP; AEELGMQPAKINTPA; EELGMQPAKINTPAS; ELGMQPAKINTPASL; LGMQPAKINTPASLS; GMQPAKINTPASLSG; MQPAKINTPASLSGS; QPAKINTPASLSGSQ; PAKINTPASLSGSQA; AKINTPASLSGSQAS; KINTPASLSGSQASW; INTPASLSGSQASWT; NTPASLSGSQASWTL; TPASLSGSQASWTLR; PASLSGSQASWTLRV; ASLSGSQASWTLRVH; SLSGSQASWTLRVHV; LSGSQASWTLRVHVG; SGSQASWTLRVHVGA; GSQASWTLRVHVGAN; SQASWTLRVHVGANQ; QASWTLRVHVGANQD; ASWTLRVHVGANQDE; SWTLRVHVGANQDEA; WTLRVHVGANQDEAI; TLRVHVGANQDEAIA; LRVHVGANQDEAIAV; RVHVGANQDEAIAVN; VHVGANQDEAIAVNI; HVGANQDEAIAVNIY; VGANQDEAIAVNIYA; GANQDEAIAVNIYAA; ANQDEAIAVNIYAAN; NQDEAIAVNIYAANV; QDEAIAVNIYAANVA; DEAIAVNIYAANVAN; EAIAVNIYAANVANL; AIAVNIYAANVANLF; IAVNIYAANVANLFS; AVNIYAANVANLFSG; VNIYAANVANLFSGE; NIYAANVANLFSGEG; IYAANVANLFSGEGA; YAANVANLFSGEGAQ; AANVANLFSGEGAQT; ANVANLFSGEGAQTA; NVANLFSGEGAQTAQ; VANLFSGEGAQTAQA; ANLFSGEGAQTAQAA; NLFSGEGAQTAQAAP; LFSGEGAQTAQAAPV; FSGEGAQTAQAAPVQ; SGEGAQTAQAAPVQE; GEGAQTAQAAPVQEG; EGAQTAQAAPVQEGV; GAQTAQAAPVQEGVQ; AQTAQAAPVQEGVQQ; QTAQAAPVQEGVQQE; TAQAAPVQEGVQQEG; AQAAPVQEGVQQEGA; QAAPVQEGVQQEGAQ; AAPVQEGVQQEGAQQ; APVQEGVQQEGAQQP; PVQEGVQQEGAQQPA; VQEGVQQEGAQQPAP; QEGVQQEGAQQPAPA; EGVQQEGAQQPAPAT; GVQQEGAQQPAPATA; VQQEGAQQPAPATAP; QQEGAQQPAPATAPS; QEGAQQPAPATAPSQ; EGAQQPAPATAPSQG; GAQQPAPATAPSQGG; AQQPAPATAPSQGGV; QQPAPATAPSQGGVN; QPAPATAPSQGGVNS; PAPATAPSQGGVNSP; APATAPSQGGVNSPV; PATAPSQGGVNSPVN; ATAPSQGGVNSPVNV; TAPSQGGVNSPVNVT; APSQGGVNSPVNVTT; PSQGGVNSPVNVTTT; SQGGVNSPVNVTTTV; QGGVNSPVNVTTTVD; GGVNSPVNVTTTVDA; GVNSPVNVTTTVDAN; VNSPVNVTTTVDANT; NSPVNVTTTVDANTS; SPVNVTTTVDANTSL; PVNVTTTVDANTSLA; VNVTTTVDANTSLAK; NVTTTVDANTSLAKI; VTTTVDANTSLAKIE; TTTVDANTSLAKIEN; TTVDANTSLAKIENA; TVDANTSLAKIENAI; VDANTSLAKIENAIR; DANTSLAKIENAIRM; ANTSLAKIENAIRMI;

	NTSLAKIENAIRMIS; TSLAKIENAIRMISD; SLAKIENAIRMISDQ; LAKIENAIRMISDQR; AKIENAIRMISDQRA; KIENAIRMISDQRAN; IENAIRMISDQRANL; ENAIRMISDQRANLG; NAIRMISDQRANLGA; AIRMISDQRANLGAF; IRMISDQRANLGAFQ; RMISDQRANLGAFQN; MISDQRANLGAFQNR; ISDQRANLGAFQNRL; SDQRANLGAFQNRLE; DQRANLGAFQNRLES; QRANLGAFQNRLESI; RANLGAFQNRLESIK; ANLGAFQNRLESIKN; NLGAFQNRLESIKNS; LGAFQNRLESIKNST; GAFQNRLESIKNSTE; AFQNRLESIKNSTEY; FQNRLESIKNSTEYA; QNRLESIKNSTEYAI; NRLESIKNSTEYAIE; RLESIKNSTEYAIEN; LESIKNSTEYAIENL; ESIKNSTEYAIENLK; SIKNSTEYAIENLKA; IKNSTEYAIENLKAS; KNSTEYAIENLKASY; NSTEYAIENLKASYA; STEYAIENLKASYAQ; TEYAIENLKASYAQI; EYAIENLKASYAQIK; YAIENLKASYAQIKD; AIENLKASYAQIKDA; IENLKASYAQIKDAT; ENLKASYAQIKDATM; NLKASYAQIKDATMT; LKASYAQIKDATMTD; KASYAQIKDATMTDE; ASYAQIKDATMTDEV; SYAQIKDATMTDEVV; YAQIKDATMTDEVVA; AQIKDATMTDEVVAA; QIKDATMTDEVVAAT; IKDATMTDEVVAATT; KDATMTDEVVAATTN; DATMTDEVVAATTNS; ATMTDEVVAATTNSI; TMTDEVVAATTNSIL; MTDEVVAATTNSILT; TDEVVAATTNSILTQ; DEVVAATTNSILTQS; EVVAATTNSILTQSA; VVAATTNSILTQSAM; VAATTNSILTQSAMA; AATTNSILTQSAMAM; ATTNSILTQSAMAMI; TTNSILTQSAMAMIA; TNSILTQSAMAMIAQ; NSILTQSAMAMIAQA; SILTQSAMAMIAQAN; ILTQSAMAMIAQANQ; LTQSAMAMIAQANQV; TQSAMAMIAQANQVP; QSAMAMIAQANQVPQ; SAMAMIAQANQVPQY; AMAMIAQANQVPQYV; MAMIAQANQVPQYVL; AMIAQANQVPQYVLS; MIAQANQVPQYVLSL; IAQANQVPQYVLSLL; AQANQVPQYVLSLLR; 16 mers: MIINHNTSAINASRNN; IINHNTSAINASRNNG; INHNTSAINASRNNGI; NHNTSAINASRNNGIN; HNTSAINASRNNGINA; NTSAINASRNNGINAA; TSAINASRNNGINAAN; SAINASRNNGINAANL; AINASRNNGINAANLS; INASRNNGINAANLSK; NASRNNGINAANLSKT; ASRNNGINAANLSKTQ; SRNNGINAANLSKTQE; RNNGINAANLSKTQEK; NNGINAANLSKTQEKL; NGINAANLSKTQEKLS; GINAANLSKTQEKLSS; INAANLSKTQEKLSSG; NAANLSKTQEKLSSGY; AANLSKTQEKLSSGYR; ANLSKTQEKLSSGYRI; NLSKTQEKLSSGYRIN; LSKTQEKLSSGYRINR; SKTQEKLSSGYRINRA; KTQEKLSSGYRINRAS; TQEKLSSGYRINRASD; QEKLSSGYRINRASDD; EKLSSGYRINRASDDA; KLSSGYRINRASDDAA; LSSGYRINRASDDAAG; SSGYRINRASDDAAGM; SGYRINRASDDAAGMG; GYRINRASDDAAGMGV; YRINRASDDAAGMGVS; RINRASDDAAGMGVSG; INRASDDAAGMGVSGK; NRASDDAAGMGVSGKI; RASDDAAGMGVSGKIN; ASDDAAGMGVSGKINA; SDDAAGMGVSGKINAQ; DDAAGMGVSGKINAQI; DAAGMGVSGKINAQIR; AAGMGVSGKINAQIRG; AGMGVSGKINAQIRGL; GMGVSGKINAQIRGLS; MGVSGKINAQIRGLSQ; GVSGKINAQIRGLSQA; VSGKINAQIRGLSQAS; SGKINAQIRGLSQASR; GKINAQIRGLSQASRN; KINAQIRGLSQASRNT; INAQIRGLSQASRNTS; NAQIRGLSQASRNTSK; AQIRGLSQASRNTSKA; QIRGLSQASRNTSKAI; IRGLSQASRNTSKAIN; RGLSQASRNTSKAINF; GLSQASRNTSKAINFI; LSQASRNTSKAINFIQ; SQASRNTSKAINFIQT; QASRNTSKAINFIQTT; ASRNTSKAINFIQTTE; SRNTSKAINFIQTTEG; RNTSKAINFIQTTEGN; NTSKAINFIQTTEGNL; TSKAINFIQTTEGNLN; SKAINFIQTTEGNLNE; KAINFIQTTEGNLNEV; AINFIQTTEGNLNEVE;

	INFIQTTEGNLNEVEK; NFIQTTEGNLNEVEKV; FIQTTEGNLNEVEKVL; IQTTEGNLNEVEKVLV; QTTEGNLNEVEKVLVR; TTEGNLNEVEKVLVRM; TEGNLNEVEKVLVRMK; EGNLNEVEKVLVRMKE; GNLNEVEKVLVRMKEL; NLNEVEKVLVRMKELA; LNEVEKVLVRMKELAV; NEVEKVLVRMKELAVQ; EVEKVLVRMKELAVQS; VEKVLVRMKELAVQSG; EKVLVRMKELAVQSGN; KVLVRMKELAVQSGNG; VLVRMKELAVQSGNGT; LVRMKELAVQSGNGTY; VRMKELAVQSGNGTYS; RMKELAVQSGNGTYSD; MKELAVQSGNGTYSDA; KELAVQSGNGTYSDAD; ELAVQSGNGTYSDADR; LAVQSGNGTYSDADRG; AVQSGNGTYSDADRGS; VQSGNGTYSDADRGSI; QSGNGTYSDADRGSIQ; SGNGTYSDADRGSIQI; GNGTYSDADRGSIQIE; NGTYSDADRGSIQIEI; GTYSDADRGSIQIEIE; TYSDADRGSIQIEIEQ; YSDADRGSIQIEIEQL; SDADRGSIQIEIEQLT; DADRGSIQIEIEQLTD; ADRGSIQIEIEQLTDE; DRGSIQIEIEQLTDEI; RGSIQIEIEQLTDEIN; GSIQIEIEQLTDEINR; SIQIEIEQLTDEINRI; IQIEIEQLTDEINRIA; QIEIEQLTDEINRIAD; IEIEQLTDEINRIADQ; EIEQLTDEINRIADQA; IEQLTDEINRIADQAQ; EQLTDEINRIADQAQY; QLTDEINRIADQAQYN; LTDEINRIADQAQYNQ; TDEINRIADQAQYNQM; DEINRIADQAQYNQMH; EINRIADQAQYNQMHM; INRIADQAQYNQMHML; NRIADQAQYNQMHMLS; RIADQAQYNQMHMLSN; IADQAQYNQMHMLSNK; ADQAQYNQMHMLSNKS; DQAQYNQMHMLSNKSA; QAQYNQMHMLSNKSAS; AQYNQMHMLSNKSASQ; QYNQMHMLSNKSASQN; YNQMHMLSNKSASQNV; NQMHMLSNKSASQNVR; QMHMLSNKSASQNVRT; MHMLSNKSASQNVRTA; HMLSNKSASQNVRTAE; MLSNKSASQNVRTAEE; LSNKSASQNVRTAEEL; SNKSASQNVRTAEELG; NKSASQNVRTAEELGM; KSASQNVRTAEELGMQ; SASQNVRTAEELGMQP; ASQNVRTAEELGMQPA; SQNVRTAEELGMQPAK; QNVRTAEELGMQPAKI; NVRTAEELGMQPAKIN; VRTAEELGMQPAKINT; RTAEELGMQPAKINTP; TAEELGMQPAKINTPA; AEELGMQPAKINTPAS; EELGMQPAKINTPASL; ELGMQPAKINTPASLS; LGMQPAKINTPASLSG; GMQPAKINTPASLSGS; MQPAKINTPASLSGSQ; QPAKINTPASLSGSQA; PAKINTPASLSGSQAS; AKINTPASLSGSQASW; KINTPASLSGSQASWT; INTPASLSGSQASWTL; NTPASLSGSQASWTLR; TPASLSGSQASWTLRV; PASLSGSQASWTLRVH; ASLSGSQASWTLRVHV; SLSGSQASWTLRVHVG; LSGSQASWTLRVHVGA; SGSQASWTLRVHVGAN; GSQASWTLRVHVGANQ; SQASWTLRVHVGANQD; QASWTLRVHVGANQDE; ASWTLRVHVGANQDEA; SWTLRVHVGANQDEAI; WTLRVHVGANQDEAIA; TLRVHVGANQDEAIAV; LRVHVGANQDEAIAVN; RVHVGANQDEAIAVNI; VHVGANQDEAIAVNIY; HVGANQDEAIAVNIYA; VGANQDEAIAVNIYAA; GANQDEAIAVNIYAAN; ANQDEAIAVNIYAANV; NQDEAIAVNIYAANVA; QDEAIAVNIYAANVAN; DEAIAVNIYAANVANL; EAIAVNIYAANVANLF; AIAVNIYAANVANLFS; IAVNIYAANVANLFSG; AVNIYAANVANLFSGE; VNIYAANVANLFSGEG; NIYAANVANLFSGEGA; IYAANVANLFSGEGAQ; YAANVANLFSGEGAQT; AANVANLFSGEGAQTA; ANVANLFSGEGAQTAQ; NVANLFSGEGAQTAQA; VANLFSGEGAQTAQAA; ANLFSGEGAQTAQAAP; NLFSGEGAQTAQAAPV; LFSGEGAQTAQAAPVQ; FSGEGAQTAQAAPVQE; SGEGAQTAQAAPVQEG; GEGAQTAQAAPVQEGV; EGAQTAQAAPVQEGVQ; GAQTAQAAPVQEGVQQ; AQTAQAAPVQEGVQQE; QTAQAAPVQEGVQQEG; TAQAAPVQEGVQQEGA; AQAAPVQEGVQQEGAQ; QAAPVQEGVQQEGAQQ; AAPVQEGVQQEGAQQP; APVQEGVQQEGAQQPA; PVQEGVQQEGAQQPAP; VQEGVQQEGAQQPAPA; QEGVQQEGAQQPAPAT; EGVQQEGAQQPAPATA; GVQQEGAQQPAPATAP; VQQEGAQQPAPATAPS; QQEGAQQPAPATAPSQ; QEGAQQPAPATAPSQG; EGAQQPAPATAPSQGG; GAQQPAPATAPSQGGV; AQQPAPATAPSQGGVN; QQPAPATAPSQGGVNS; QPAPATAPSQGGVNSP;

	PAPATAPSQGGVNSPV; APATAPSQGGVNSPVN; PATAPSQGGVNSPVNV; ATAPSQGGVNSPVNVT; TAPSQGGVNSPVNVTT; APSQGGVNSPVNVTTT; PSQGGVNSPVNVTTTV; SQGGVNSPVNVTTTVD; QGGVNSPVNVTTTVDA; GGVNSPVNVTTTVDAN; GVNSPVNVTTTVDANT; VNSPVNVTTTVDANTS; NSPVNVTTTVDANTSL; SPVNVTTTVDANTSLA; PVNVTTTVDANTSLAK; VNVTTTVDANTSLAKI; NVTTTVDANTSLAKIE; VTTTVDANTSLAKIEN; TTTVDANTSLAKIENA; TTVDANTSLAKIENAI; TVDANTSLAKIENAIR; VDANTSLAKIENAIRM; DANTSLAKIENAIRMI; ANTSLAKIENAIRMIS; NTSLAKIENAIRMISD; TSLAKIENAIRMISDQ; SLAKIENAIRMISDQR; LAKIENAIRMISDQRA; AKIENAIRMISDQRAN; KIENAIRMISDQRANL; IENAIRMISDQRANLG; ENAIRMISDQRANLGA; NAIRMISDQRANLGAF; AIRMISDQRANLGAFQ; IRMISDQRANLGAFQN; RMISDQRANLGAFQNR; MISDQRANLGAFQNRL; ISDQRANLGAFQNRLE; SDQRANLGAFQNRLES; DQRANLGAFQNRLESI; QRANLGAFQNRLESIK; RANLGAFQNRLESIKN; ANLGAFQNRLESIKNS; NLGAFQNRLESIKNST; LGAFQNRLESIKNSTE; GAFQNRLESIKNSTEY; AFQNRLESIKNSTEYA; FQNRLESIKNSTEYAI; QNRLESIKNSTEYAIE; NRLESIKNSTEYAIEN; RLESIKNSTEYAIENL; LESIKNSTEYAIENLK; ESIKNSTEYAIENLKA; SIKNSTEYAIENLKAS; IKNSTEYAIENLKASY; KNSTEYAIENLKASYA; NSTEYAIENLKASYAQ; STEYAIENLKASYAQI; TEYAIENLKASYAQIK; EYAIENLKASYAQIKD; YAIENLKASYAQIKDA; AIENLKASYAQIKDAT; IENLKASYAQIKDATM; ENLKASYAQIKDATMT; NLKASYAQIKDATMTD; LKASYAQIKDATMTDE; KASYAQIKDATMTDEV; ASYAQIKDATMTDEVV; SYAQIKDATMTDEVVA; YAQIKDATMTDEVVAA; AQIKDATMTDEVVAAT; QIKDATMTDEVVAATT; IKDATMTDEVVAATTN; KDATMTDEVVAATTNS; DATMTDEVVAATTNSI; ATMTDEVVAATTNSIL; TMTDEVVAATTNSILT; MTDEVVAATTNSILTQ; TDEVVAATTNSILTQS; DEVVAATTNSILTQSA; EVVAATTNSILTQSAM; VVAATTNSILTQSAMA; VAATTNSILTQSAMAM; AATTNSILTQSAMAMI; ATTNSILTQSAMAMIA; TTNSILTQSAMAMIAQ; TNSILTQSAMAMIAQA; NSILTQSAMAMIAQAN; SILTQSAMAMIAQANQ; ILTQSAMAMIAQANQV; LTQSAMAMIAQANQVP; TQSAMAMIAQANQVPQ; QSAMAMIAQANQVPQY; SAMAMIAQANQVPQYV; AMAMIAQANQVPQYVL; MAMIAQANQVPQYVLS; AMIAQANQVPQYVLSL; MIAQANQVPQYVLSLL; IAQANQVPQYVLSLLR;
Seq 24	13 mers: MKLQRSLFLIIFF; KLQRSLFLIIFFL; LQRSLFLIIFFLT; QRSLFLIIFFLTF; RSLFLIIFFLTFL; SLFLIIFFLTFLC; LFLIIFFLTFLCC; FLIIFFLTFLCCN; LIIFFLTFLCCNN; IIFFLTFLCCNNK; IFFLTFLCCNNKE; FFLTFLCCNNKER; FLTFLCCNNKERK; LTFLCCNNKERKE; TFLCCNNKERKEG; FLCCNNKERKEGV; LCCNNKERKEGVS; CCNNKERKEGVSF; CNNKERKEGVSFK; NNKERKEGVSFKI; NKERKEGVSFKIS; KERKEGVSFKISL; ERKEGVSFKISLG; RKEGVSFKISLGA; KEGVSFKISLGAE; EGVSFKISLGAEP; GVSFKISLGAEPS; VSFKISLGAEPSS; SFKISLGAEPSSL; FKISLGAEPSSLD; KISLGAEPSSLDP; ISLGAEPSSLDPQ; SLGAEPSSLDPQL; LGAEPSSLDPQLA; GAEPSSLDPQLAE; AEPSSLDPQLAED; EPSSLDPQLAEDN; PSSLDPQLAEDNV; SSLDPQLAEDNVA; SLDPQLAEDNVAS; LDPQLAEDNVASK; DPQLAEDNVASKM; PQLAEDNVASKMI; QLAEDNVASKMID; LAEDNVASKMIDT;

	AEDNVASKMIDTM; EDNVASKMIDTMF; DNVASKMIDTMFR; NVASKMIDTMFRG; VASKMIDTMFRGI; ASKMIDTMFRGIV; SKMIDTMFRGIVT; KMIDTMFRGIVTG; MIDTMFRGIVTGD; IDTMFRGIVTGDP; DTMFRGIVTGDPN; TMFRGIVTGDPNT; MFRGIVTGDPNTG; FRGIVTGDPNTGG; RGIVTGDPNTGGN; GIVTGDPNTGGNK; IVTGDPNTGGNKP; VTGDPNTGGNKPG; TGDPNTGGNKPGL; GDPNTGGNKPGLA; DPNTGGNKPGLAK; PNTGGNKPGLAKG; NTGGNKPGLAKGW; TGGNKPGLAKGWD; GGNKPGLAKGWDI; GNKPGLAKGWDIS; NKPGLAKGWDISS; KPGLAKGWDISSD; PGLAKGWDISSDG; GLAKGWDISSDGT; LAKGWDISSDGTV; AKGWDISSDGTVY; KGWDISSDGTVYT; GWDISSDGTVYTF; WDISSDGTVYTFN; DISSDGTVYTFNL; ISSDGTVYTFNLR; SSDGTVYTFNLRE; SDGTVYTFNLREK; DGTVYTFNLREKI; GTVYTFNLREKIT; TVYTFNLREKITW; VYTFNLREKITWS; YTFNLREKITWSD; TFNLREKITWSDG; FNLREKITWSDGV; NLREKITWSDGVA; LREKITWSDGVAI; REKITWSDGVAIT; EKITWSDGVAITA; KITWSDGVAITAE; ITWSDGVAITAEG; TWSDGVAITAEGI; WSDGVAITAEGIR; SDGVAITAEGIRK; DGVAITAEGIRKS; GVAITAEGIRKSY; VAITAEGIRKSYL; AITAEGIRKSYLR; ITAEGIRKSYLRI; TAEGIRKSYLRIL; AEGIRKSYLRILN; EGIRKSYLRILNK; GIRKSYLRILNKE; IRKSYLRILNKET; RKSYLRILNKETG; KSYLRILNKETGS; SYLRILNKETGSK; YLRILNKETGSKY; LRILNKETGSKYV; RILNKETGSKYVE; ILNKETGSKYVEM; LNKETGSKYVEMV; NKETGSKYVEMVK; KETGSKYVEMVKS; ETGSKYVEMVKSV; TGSKYVEMVKSVI; GSKYVEMVKSVIK; SKYVEMVKSVIKN; KYVEMVKSVIKNG; YVEMVKSVIKNGQ; VEMVKSVIKNGQK; EMVKSVIKNGQKY; MVKSVIKNGQKYF; VKSVIKNGQKYFD; KSVIKNGQKYFDG; SVIKNGQKYFDGQ; VIKNGQKYFDGQV; IKNGQKYFDGQVT; KNGQKYFDGQVTD; NGQKYFDGQVTDS; GQKYFDGQVTDSE; QKYFDGQVTDSEL; KYFDGQVTDSELG; YFDGQVTDSELGI; FDGQVTDSELGIR; DGQVTDSELGIRA; GQVTDSELGIRAI; QVTDSELGIRAID; VTDSELGIRAIDE; TDSELGIRAIDEK; DSELGIRAIDEKT; SELGIRAIDEKTL; ELGIRAIDEKTLE; LGIRAIDEKTLEI; GIRAIDEKTLEIT; IRAIDEKTLEITL; RAIDEKTLEITLE; AIDEKTLEITLES; IDEKTLEITLESP; DEKTLEITLESPK; EKTLEITLESPKP; KTLEITLESPKPY; TLEITLESPKPYF; LEITLESPKPYFI; EITLESPKPYFID; ITLESPKPYFIDM; TLESPKPYFIDML; LESPKPYFIDMLV; ESPKPYFIDMLVH; SPKPYFIDMLVHQ; PKPYFIDMLVHQS; KPYFIDMLVHQSF; PYFIDMLVHQSFI; YFIDMLVHQSFIP; FIDMLVHQSFIPV; IDMLVHQSFIPVP; DMLVHQSFIPVPV; MLVHQSFIPVPVH; LVHQSFIPVPVHV; VHQSFIPVPVHVT; HQSFIPVPVHVTE; QSFIPVPVHVTEK; SFIPVPVHVTEKY; FIPVPVHVTEKYG; IPVPVHVTEKYGQ; PVPVHVTEKYGQN; VPVHVTEKYGQNW; PVHVTEKYGQNWT; VHVTEKYGQNWTS; HVTEKYGQNWTSP; VTEKYGQNWTSPE; TEKYGQNWTSPEN; EKYGQNWTSPENM; KYGQNWTSPENMV; YGQNWTSPENMVT; GQNWTSPENMVTS; QNWTSPENMVTSG; NWTSPENMVTSGP; WTSPENMVTSGPF; TSPENMVTSGPFK; SPENMVTSGPFKL; PENMVTSGPFKLK;

	ENMVTSGPFKLKE; NMVTSGPFKLKER; MVTSGPFKLKERI; VTSGPFKLKERIP; TSGPFKLKERIPN; SGPFKLKERIPNE; GPFKLKERIPNEK; PFKLKERIPNEKY; FKLKERIPNEKYV; KLKERIPNEKYVF; LKERIPNEKYVFE; KERIPNEKYVFEK; ERIPNEKYVFEKN; RIPNEKYVFEKNN; IPNEKYVFEKNNK; PNEKYVFEKNNKY; NEKYVFEKNNKYY; EKYVFEKNNKYYD; KYVFEKNNKYYDS; YVFEKNNKYYDSN; VFEKNNKYYDSNE; FEKNNKYYDSNEV; EKNNKYYDSNEVE; KNNKYYDSNEVEL; NNKYYDSNEVELE; NKYYDSNEVELEE; KYYDSNEVELEEI; YYDSNEVELEEIT; YDSNEVELEEITF; DSNEVELEEITFY; SNEVELEEITFYT; NEVELEEITFYTT; EVELEEITFYTTN; VELEEITFYTTND; ELEEITFYTTNDS; LEEITFYTTNDSS; EEITFYTTNDSST; EITFYTTNDSSTA; ITFYTTNDSSTAY; TFYTTNDSSTAYK; FYTTNDSSTAYKM; YTTNDSSTAYKMY; TTNDSSTAYKMYE; TNDSSTAYKMYEN; NDSSTAYKMYENE; DSSTAYKMYENEE; SSTAYKMYENEEL; STAYKMYENEELD; TAYKMYENEELDA; AYKMYENEELDAI; YKMYENEELDAIF; KMYENEELDAIFG; MYENEELDAIFGS; YENEELDAIFGSI; ENEELDAIFGSIP; NEELDAIFGSIPP; EELDAIFGSIPPD; ELDAIFGSIPPDL; LDAIFGSIPPDLI; DAIFGSIPPDLIK; AIFGSIPPDLIKN; IFGSIPPDLIKNL; FGSIPPDLIKNLK; GSIPPDLIKNLKL; SIPPDLIKNLKLR; IPPDLIKNLKLRS; PPDLIKNLKLRSD; PDLIKNLKLRSDY; DLIKNLKLRSDYY; LIKNLKLRSDYYS; IKNLKLRSDYYSS; KNLKLRSDYYSSA; NLKLRSDYYSSAV; LKLRSDYYSSAVN; KLRSDYYSSAVNA; LRSDYYSSAVNAI; RSDYYSSAVNAIY; SDYYSSAVNAIYF; DYYSSAVNAIYFY; YYSSAVNAIYFYA; YSSAVNAIYFYAF; SSAVNAIYFYAFN; SAVNAIYFYAFNT; AVNAIYFYAFNTH; VNAIYFYAFNTHI; NAIYFYAFNTHIK; AIYFYAFNTHIKP; IYFYAFNTHIKPL; YFYAFNTHIKPLD; FYAFNTHIKPLDN; YAFNTHIKPLDNV; AFNTHIKPLDNVK; FNTHIKPLDNVKI; NTHIKPLDNVKIR; THIKPLDNVKIRK; HIKPLDNVKIRKA; IKPLDNVKIRKAL; KPLDNVKIRKALT; PLDNVKIRKALTL; LDNVKIRKALTLA; DNVKIRKALTLAI; NVKIRKALTLAID; VKIRKALTLAIDR; KIRKALTLAIDRE; IRKALTLAIDRET; RKALTLAIDRETL; KALTLAIDRETLT; ALTLAIDRETLTY; LTLAIDRETLTYK; TLAIDRETLTYKV; LAIDRETLTYKVL; AIDRETLTYKVLD; IDRETLTYKVLDN; DRETLTYKVLDNG; RETLTYKVLDNGT; ETLTYKVLDNGTT; TLTYKVLDNGTTP; LTYKVLDNGTTPT; TYKVLDNGTTPTR; YKVLDNGTTPTRR; KVLDNGTTPTRRA; VLDNGTTPTRRAT; LDNGTTPTRRATP; DNGTTPTRRATPN; NGTTPTRRATPNF; GTTPTRRATPNFS; TTPTRRATPNFSS; TPTRRATPNFSSY; PTRRATPNFSSYS; TRRATPNFSSYSY; RRATPNFSSYSYA; RATPNFSSYSYAK; ATPNFSSYSYAKS; TPNFSSYSYAKSL; PNFSSYSYAKSLE; NFSSYSYAKSLEL; FSSYSYAKSLELF; SSYSYAKSLELFN; SYSYAKSLELFNP; YSYAKSLELFNPE; SYAKSLELFNPEI; YAKSLELFNPEIA; AKSLELFNPEIAK; KSLELFNPEIAKT; SLELFNPEIAKTL; LELFNPEIAKTLL; ELFNPEIAKTLLA; LFNPEIAKTLLAE; FNPEIAKTLLAEA; NPEIAKTLLAEAG; PEIAKTLLAEAGY; EIAKTLLAEAGYP; IAKTLLAEAGYPN;

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GYTQFSSHNYSNPE; YTQFSSHNYSNPEY; TQFSSHNYSNPEYN;
QFSSHNYSNPEYNE; FSSHNYSNPEYNEL; SSHNYSNPEYNELI;
SHNYSNPEYNELIK; HNYSNPEYNELIKK; NYSNPEYNELIKKS;
YSNPEYNELIKKSD; SNPEYNELIKKSDL; NPEYNELIKKSDLE;
PEYNELIKKSDLEL; EYNELIKKSDLELD; YNELIKKSDLELDP;
NELIKKSDLELDPI; ELIKKSDLELDPIK; LIKKSDLELDPIKR;
IKKSDLELDPIKRQ; KKSDLELDPIKRQD; KSDLELDPIKRQDI;
SDLELDPIKRQDIL; DLELDPIKRQDILR; LELDPIKRQDILRQ;
ELDPIKRQDILRQA; LDPIKRQDILRQAE; DPIKRQDILRQAEE;
PIKRQDILRQAEEI; IKRQDILRQAEEII; KRQDILRQAEEIII;
RQDILRQAEEIIIE; QDILRQAEEIIIEK; DILRQAEEIIIEKD;
ILRQAEEIIIEKDF; LRQAEEIIIEKDFP; RQAEEIIIEKDFPI;
QAEEIIIEKDFPIA; AEEIIIEKDFPIAP; EEIIIEKDFPIAPI;
EIIIEKDFPIAPIY; IIIEKDFPIAPIYI; IIEKDFPIAPIYIY;
IEKDFPIAPIYIYG; EKDFPIAPIYIYGN; KDFPIAPIYIYGNS;
DFPIAPIYIYGNSY; FPIAPIYIYGNSYL; PIAPIYIYGNSYLF;
IAPIYIYGNSYLFR; APIYIYGNSYLFRN; PIYIYGNSYLFRND;
IYIYGNSYLFRNDK; YIYGNSYLFRNDKW; IYGNSYLFRNDKWT;
YGNSYLFRNDKWTG; GNSYLFRNDKWTGW; NSYLFRNDKWTGWN;
SYLFRNDKWTGWNT; YLFRNDKWTGWNTN; LFRNDKWTGWNTNI;
FRNDKWTGWNTNIL; RNDKWTGWNTNILE; NDKWTGWNTNILER;
DKWTGWNTNILERF; KWTGWNTNILERFD; WTGWNTNILERFDL;
TGWNTNILERFDLS; GWNTNILERFDLSQ; WNTNILERFDLSQL;
NTNILERFDLSQLK; TNILERFDLSQLKL; NILERFDLSQLKLK;
ILERFDLSQLKLKN; LERFDLSQLKLKNK;

15 mers:
MKLQRSLFLIIFFLT; KLQRSLFLIIFFLTF; LQRSLFLIIFFLTFL;
QRSLFLIIFFLTFLC; RSLFLIIFFLTFLCC; SLFLIIFFLTFLCCN;
LFLIIFFLTFLCCNN; FLIIFFLTFLCCNNK; LIIFFLTFLCCNNKE;
IIFFLTFLCCNNKER; IFFLTFLCCNNKERK; FFLTFLCCNNKERKE;
FLTFLCCNNKERKEG; LTFLCCNNKERKEGV; TFLCCNNKERKEGVS;
FLCCNNKERKEGVSF; LCCNNKERKEGVSFK; CCNNKERKEGVSFKI;
CNNKERKEGVSFKIS; NNKERKEGVSFKISL; NKERKEGVSFKISLG;
KERKEGVSFKISLGA; ERKEGVSFKISLGAE; RKEGVSFKISLGAEP;
KEGVSFKISLGAEPS; EGVSFKISLGAEPSS; GVSFKISLGAEPSSL;
VSFKISLGAEPSSLD; SFKISLGAEPSSLDP; FKISLGAEPSSLDPQ;
KISLGAEPSSLDPQL; ISLGAEPSSLDPQLA; SLGAEPSSLDPQLAE;
LGAEPSSLDPQLAED; GAEPSSLDPQLAEDN; AEPSSLDPQLAEDNV;
EPSSLDPQLAEDNVA; PSSLDPQLAEDNVAS; SSLDPQLAEDNVASK;
SLDPQLAEDNVASKM; LDPQLAEDNVASKMI; DPQLAEDNVASKMID;
PQLAEDNVASKMIDT; QLAEDNVASKMIDTM; LAEDNVASKMIDTMF;
AEDNVASKMIDTMFR; EDNVASKMIDTMFRG; DNVASKMIDTMFRGI;
NVASKMIDTMFRGIV; VASKMIDTMFRGIVT; ASKMIDTMFRGIVTG;
SKMIDTMFRGIVTGD; KMIDTMFRGIVTGDP; MIDTMFRGIVTGDPN;
IDTMFRGIVTGDPNT; DTMFRGIVTGDPNTG; TMFRGIVTGDPNTGG;
MFRGIVTGDPNTGGN; FRGIVTGDPNTGGNK; RGIVTGDPNTGGNKP;
GIVTGDPNTGGNKPG; IVTGDPNTGGNKPGL; VTGDPNTGGNKPGLA;
TGDPNTGGNKPGLAK; GDPNTGGNKPGLAKG; DPNTGGNKPGLAKGW;
PNTGGNKPGLAKGWD; NTGGNKPGLAKGWDI; TGGNKPGLAKGWDIS;
GGNKPGLAKGWDISS; GNKPGLAKGWDISSD; NKPGLAKGWDISSDG;

	KPGLAKGWDISSDGT; PGLAKGWDISSDGTV; GLAKGWDISSDGTVY; LAKGWDISSDGTVYT; AKGWDISSDGTVYTF; KGWDISSDGTVYTFN; GWDISSDGTVYTFNL; WDISSDGTVYTFNLR; DISSDGTVYTFNLRE; ISSDGTVYTFNLREK; SSDGTVYTFNLREKI; SDGTVYTFNLREKIT; DGTVYTFNLREKITW; GTVYTFNLREKITWS; TVYTFNLREKITWSD; VYTFNLREKITWSDG; YTFNLREKITWSDGV; TFNLREKITWSDGVA; FNLREKITWSDGVAI; NLREKITWSDGVAIT; LREKITWSDGVAITA; REKITWSDGVAITAE; EKITWSDGVAITAEG; KITWSDGVAITAEGI; ITWSDGVAITAEGIR; TWSDGVAITAEGIRK; WSDGVAITAEGIRKS; SDGVAITAEGIRKSY; DGVAITAEGIRKSYL; GVAITAEGIRKSYLR; VAITAEGIRKSYLRI; AITAEGIRKSYLRIL; ITAEGIRKSYLRILN; TAEGIRKSYLRILNK; AEGIRKSYLRILNKE; EGIRKSYLRILNKET; GIRKSYLRILNKETG; IRKSYLRILNKETGS; RKSYLRILNKETGSK; KSYLRILNKETGSKY; SYLRILNKETGSKYV; YLRILNKETGSKYVE; LRILNKETGSKYVEM; RILNKETGSKYVEMV; ILNKETGSKYVEMVK; LNKETGSKYVEMVKS; NKETGSKYVEMVKSV; KETGSKYVEMVKSVI; ETGSKYVEMVKSVIK; TGSKYVEMVKSVIKN; GSKYVEMVKSVIKNG; SKYVEMVKSVIKNGQ; KYVEMVKSVIKNGQK; YVEMVKSVIKNGQKY; VEMVKSVIKNGQKYF; EMVKSVIKNGQKYFD; MVKSVIKNGQKYFDG; VKSVIKNGQKYFDGQ; KSVIKNGQKYFDGQV; SVIKNGQKYFDGQVT; VIKNGQKYFDGQVTD; IKNGQKYFDGQVTDS; KNGQKYFDGQVTDSE; NGQKYFDGQVTDSEL; GQKYFDGQVTDSELG; QKYFDGQVTDSELGI; KYFDGQVTDSELGIR; YFDGQVTDSELGIRA; FDGQVTDSELGIRAI; DGQVTDSELGIRAID; GQVTDSELGIRAIDE; QVTDSELGIRAIDEK; VTDSELGIRAIDEKT; TDSELGIRAIDEKTL; DSELGIRAIDEKTLE; SELGIRAIDEKTLEI; ELGIRAIDEKTLEIT; LGIRAIDEKTLEITL; GIRAIDEKTLEITLE; IRAIDEKTLEITLES; RAIDEKTLEITLESP; AIDEKTLEITLESPK; IDEKTLEITLESPKP; DEKTLEITLESPKPY; EKTLEITLESPKPYF; KTLEITLESPKPYFI; TLEITLESPKPYFID; LEITLESPKPYFIDM; EITLESPKPYFIDML; ITLESPKPYFIDMLV; TLESPKPYFIDMLVH; LESPKPYFIDMLVHQ; ESPKPYFIDMLVHQS; SPKPYFIDMLVHQSF; PKPYFIDMLVHQSFI; KPYFIDMLVHQSFIP; PYFIDMLVHQSFIPV; YFIDMLVHQSFIPVP; FIDMLVHQSFIPVPV; IDMLVHQSFIPVPVH; DMLVHQSFIPVPVHV; MLVHQSFIPVPVHVT; LVHQSFIPVPVHVTE; VHQSFIPVPVHVTEK; HQSFIPVPVHVTEKY; QSFIPVPVHVTEKYG; SFIPVPVHVTEKYGQ; FIPVPVHVTEKYGQN; IPVPVHVTEKYGQNW; PVPVHVTEKYGQNWT; VPVHVTEKYGQNWTS; PVHVTEKYGQNWTSP; VHVTEKYGQNWTSPE; HVTEKYGQNWTSPEN; VTEKYGQNWTSPENM; TEKYGQNWTSPENMV; EKYGQNWTSPENMVT; KYGQNWTSPENMVTS; YGQNWTSPENMVTSG; GQNWTSPENMVTSGP; QNWTSPENMVTSGPF; NWTSPENMVTSGPFK; WTSPENMVTSGPFKL; TSPENMVTSGPFKLK; SPENMVTSGPFKLKE; PENMVTSGPFKLKER; ENMVTSGPFKLKERI; NMVTSGPFKLKERIP; MVTSGPFKLKERIPN; VTSGPFKLKERIPNE; TSGPFKLKERIPNEK; SGPFKLKERIPNEKY; GPFKLKERIPNEKYV; PFKLKERIPNEKYVF; FKLKERIPNEKYVFE; KLKERIPNEKYVFEK; LKERIPNEKYVFEKN; KERIPNEKYVFEKNN; ERIPNEKYVFEKNNK; RIPNEKYVFEKNNKY; IPNEKYVFEKNNKYY; PNEKYVFEKNNKYYD; NEKYVFEKNNKYYDS; EKYVFEKNNKYYDSN; KYVFEKNNKYYDSNE; YVFEKNNKYYDSNEV; VFEKNNKYYDSNEVE; FEKNNKYYDSNEVEL; EKNNKYYDSNEVELE; KNNKYYDSNEVELEE; NNKYYDSNEVELEEI; NKYYDSNEVELEEIT; KYYDSNEVELEEITF;

	YYDSNEVELEEITFY; YDSNEVELEEITFYT; DSNEVELEEITFYTT; SNEVELEEITFYTTN; NEVELEEITFYTTND; EVELEEITFYTTNDS; VELEEITFYTTNDSS; ELEEITFYTTNDSST; LEEITFYTTNDSSTA; EEITFYTTNDSSTAY; EITFYTTNDSSTAYK; ITFYTTNDSSTAYKM; TFYTTNDSSTAYKMY; FYTTNDSSTAYKMYE; YTTNDSSTAYKMYEN; TTNDSSTAYKMYENE; TNDSSTAYKMYENEE; NDSSTAYKMYENEEL; DSSTAYKMYENEELD; SSTAYKMYENEELDA; STAYKMYENEELDAI; TAYKMYENEELDAIF; AYKMYENEELDAIFG; YKMYENEELDAIFGS; KMYENEELDAIFGSI; MYENEELDAIFGSIP; YENEELDAIFGSIPP; ENEELDAIFGSIPPD; NEELDAIFGSIPPDL; EELDAIFGSIPPDLI; ELDAIFGSIPPDLIK; LDAIFGSIPPDLIKN; DAIFGSIPPDLIKNL; AIFGSIPPDLIKNLK; IFGSIPPDLIKNLKL; FGSIPPDLIKNLKLR; GSIPPDLIKNLKLRS; SIPPDLIKNLKLRSD; IPPDLIKNLKLRSDY; PPDLIKNLKLRSDYY; PDLIKNLKLRSDYYS; DLIKNLKLRSDYYSS; LIKNLKLRSDYYSSA; IKNLKLRSDYYSSAV; KNLKLRSDYYSSAVN; NLKLRSDYYSSAVNA; LKLRSDYYSSAVNAI; KLRSDYYSSAVNAIY; LRSDYYSSAVNAIYF; RSDYYSSAVNAIYFY; SDYYSSAVNAIYFYA; DYYSSAVNAIYFYAF; YYSSAVNAIYFYAFN; YSSAVNAIYFYAFNT; SSAVNAIYFYAFNTH; SAVNAIYFYAFNTHI; AVNAIYFYAFNTHIK; VNAIYFYAFNTHIKP; NAIYFYAFNTHIKPL; AIYFYAFNTHIKPLD; IYFYAFNTHIKPLDN; YFYAFNTHIKPLDNV; FYAFNTHIKPLDNVK; YAFNTHIKPLDNVKI; AFNTHIKPLDNVKIR; FNTHIKPLDNVKIRK; NTHIKPLDNVKIRKA; THIKPLDNVKIRKAL; HIKPLDNVKIRKALT; IKPLDNVKIRKALTL; KPLDNVKIRKALTLA; PLDNVKIRKALTLAI; LDNVKIRKALTLAID; DNVKIRKALTLAIDR; NVKIRKALTLAIDRE; VKIRKALTLAIDRET; KIRKALTLAIDRETL; IRKALTLAIDRETLT; RKALTLAIDRETLTY; KALTLAIDRETLTYK; ALTLAIDRETLTYKV; LTLAIDRETLTYKVL; TLAIDRETLTYKVLD; LAIDRETLTYKVLDN; AIDRETLTYKVLDNG; IDRETLTYKVLDNGT; DRETLTYKVLDNGTT; RETLTYKVLDNGTTP; ETLTYKVLDNGTTPT; TLTYKVLDNGTTPTR; LTYKVLDNGTTPTRR; TYKVLDNGTTPTRRA; YKVLDNGTTPTRRAT; KVLDNGTTPTRRATP; VLDNGTTPTRRATPN; LDNGTTPTRRATPNF; DNGTTPTRRATPNFS; NGTTPTRRATPNFSS; GTTPTRRATPNFSSY; TTPTRRATPNFSSYS; TPTRRATPNFSSYSY; PTRRATPNFSSYSYA; TRRATPNFSSYSYAK; RRATPNFSSYSYAKS; RATPNFSSYSYAKSL; ATPNFSSYSYAKSLE; TPNFSSYSYAKSLEL; PNFSSYSYAKSLELF; NFSSYSYAKSLELFN; FSSYSYAKSLELFNP; SSYSYAKSLELFNPE; SYSYAKSLELFNPEI; YSYAKSLELFNPEIA; SYAKSLELFNPEIAK; YAKSLELFNPEIAKT; AKSLELFNPEIAKTL; KSLELFNPEIAKTLL; SLELFNPEIAKTLLA; LELFNPEIAKTLLAE; ELFNPEIAKTLLAEA; LFNPEIAKTLLAEAG; FNPEIAKTLLAEAGY; NPEIAKTLLAEAGYP; PEIAKTLLAEAGYPN; EIAKTLLAEAGYPNG; IAKTLLAEAGYPNGN; AKTLLAEAGYPNGNG; KTLLAEAGYPNGNGF; TLLAEAGYPNGNGFP; LLAEAGYPNGNGFPI; LAEAGYPNGNGFPIL; AEAGYPNGNGFPILK; EAGYPNGNGFPILKL; AGYPNGNGFPILKLK; GYPNGNGFPILKLKY; YPNGNGFPILKLKYN; PNGNGFPILKLKYNT; NGNGFPILKLKYNTN; GNGFPILKLKYNTNE; NGFPILKLKYNTNEA; GFPILKLKYNTNEAN; FPILKLKYNTNEANK; PILKLKYNTNEANKK; ILKLKYNTNEANKKI; LKLKYNTNEANKKIC; KLKYNTNEANKKICE; LKYNTNEANKKICEF; KYNTNEANKKICEFI; YNTNEANKKICEFIQ; NTNEANKKICEFIQN; TNEANKKICEFIQNQ; NEANKKICEFIQNQW; EANKKICEFIQNQWK;

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	PIKRQDILRQAEEIII; IKRQDILRQAEEIIIE; KRQDILRQAEEIIIEK; RQDILRQAEEIIIEKD; QDILRQAEEIIIEKDF; DILRQAEEIIIEKDFP; ILRQAEEIIIEKDFPI; LRQAEEIIIEKDFPIA; RQAEEIIIEKDFPIAP; QAEEIIIEKDFPIAPI; AEEIIIEKDFPIAPIY; EEIIIEKDFPIAPIYI; EIIIEKDFPIAPIYIY; IIIEKDFPIAPIYIYG; IIEKDFPIAPIYIYGN; IEKDFPIAPIYIYGNS; EKDFPIAPIYIYGNSY; KDFPIAPIYIYGNSYL; DFPIAPIYIYGNSYLF; FPIAPIYIYGNSYLFR; PIAPIYIYGNSYLFRN; IAPIYIYGNSYLFRND; APIYIYGNSYLFRNDK; PIYIYGNSYLFRNDKW; IYIYGNSYLFRNDKWT; YIYGNSYLFRNDKWTG; IYGNSYLFRNDKWTGW; YGNSYLFRNDKWTGWN; GNSYLFRNDKWTGWNT; NSYLFRNDKWTGWNTN; SYLFRNDKWTGWNTNI; YLFRNDKWTGWNTNIL; LFRNDKWTGWNTNILE; FRNDKWTGWNTNILER; RNDKWTGWNTNILERF; NDKWTGWNTNILERFD; DKWTGWNTNILERFDL; KWTGWNTNILERFDLS; WTGWNTNILERFDLSQ; TGWNTNILERFDLSQL; GWNTNILERFDLSQLK; WNTNILERFDLSQLKL; NTNILERFDLSQLKLK; TNILERFDLSQLKLKN; NILERFDLSQLKLKNK;
Seq 25	13 mers: MTKIFSNLIINGL; TKIFSNLIINGLL; KIFSNLIINGLLF; IFSNLIINGLLFG; FSNLIINGLLFGF; SNLIINGLLFGFV; NLIINGLLFGFVS; LIINGLLFGFVSL; IINGLLFGFVSLN; INGLLFGFVSLNV; NGLLFGFVSLNVF; GLLFGFVSLNVFA; LLFGFVSLNVFAD; LFGFVSLNVFADS; FGFVSLNVFADSN; GFVSLNVFADSNN; FVSLNVFADSNNA; VSLNVFADSNNAN; SLNVFADSNNANI; LNVFADSNNANIL; NVFADSNNANILK; VFADSNNANILKP; FADSNNANILKPQ; ADSNNANILKPQS; DSNNANILKPQSN; SNNANILKPQSNV; NNANILKPQSNVL; NANILKPQSNVLE; ANILKPQSNVLEH; NILKPQSNVLEHS; ILKPQSNVLEHSD; LKPQSNVLEHSDQ; KPQSNVLEHSDQK; PQSNVLEHSDQKD; QSNVLEHSDQKDN; SNVLEHSDQKDNK; NVLEHSDQKDNKK; VLEHSDQKDNKKL; LEHSDQKDNKKLD; EHSDQKDNKKLDQ; HSDQKDNKKLDQK; SDQKDNKKLDQKD; DQKDNKKLDQKDQ; QKDNKKLDQKDQV; KDNKKLDQKDQVN; DNKKLDQKDQVNQ; NKKLDQKDQVNQA; KKLDQKDQVNQAL; KLDQKDQVNQALD; LDQKDQVNQALDT; DQKDQVNQALDTI; QKDQVNQALDTIN; KDQVNQALDTINK; DQVNQALDTINKV; QVNQALDTINKVT; VNQALDTINKVTE; NQALDTINKVTED; QALDTINKVTEDV; ALDTINKVTEDVS; LDTINKVTEDVSS; DTINKVTEDVSSK; TINKVTEDVSSKL; INKVTEDVSSKLE; NKVTEDVSSKLEG; KVTEDVSSKLEGV; VTEDVSSKLEGVR; TEDVSSKLEGVRE; EDVSSKLEGVRES; DVSSKLEGVRESS; VSSKLEGVRESSL; SSKLEGVRESSLE; SKLEGVRESSLEL; KLEGVRESSLELV; LEGVRESSLELVE; EGVRESSLELVES; GVRESSLELVESN; VRESSLELVESND; RESSLELVESNDA; ESSLELVESNDAG; SSLELVESNDAGV; SLELVESNDAGVV; LELVESNDAGVVK; ELVESNDAGVVKK; LVESNDAGVVKKF; VESNDAGVVKKFV; ESNDAGVVKKFVG; SNDAGVVKKFVGS; NDAGVVKKFVGSM; DAGVVKKFVGSMS; AGVVKKFVGSMSL; GVVKKFVGSMSLM; VVKKFVGSMSLMS; VKKFVGSMSLMSD; KKFVGSMSLMSDV; KFVGSMSLMSDVA; FVGSMSLMSDVAK; VGSMSLMSDVAKG; GSMSLMSDVAKGT; SMSLMSDVAKGTV;

	MSLMSDVAKGTVV; SLMSDVAKGTVVA; LMSDVAKGTVVAS; MSDVAKGTVVASQ; SDVAKGTVVASQE; DVAKGTVVASQEA; VAKGTVVASQEAT; AKGTVVASQEATI; KGTVVASQEATIV; GTVVASQEATIVA; TVVASQEATIVAK; VVASQEATIVAKC; VASQEATIVAKCS; ASQEATIVAKCSG; SQEATIVAKCSGM; QEATIVAKCSGMV; EATIVAKCSGMVA; ATIVAKCSGMVAE; TIVAKCSGMVAEG; IVAKCSGMVAEGA; VAKCSGMVAEGAN; AKCSGMVAEGANK; KCSGMVAEGANKV; CSGMVAEGANKVV; SGMVAEGANKVVE; GMVAEGANKVVEM; MVAEGANKVVEMS; VAEGANKVVEMSK; AEGANKVVEMSKK; EGANKVVEMSKKA; GANKVVEMSKKAV; ANKVVEMSKKAVQ; NKVVEMSKKAVQE; KVVEMSKKAVQET; VVEMSKKAVQETQ; VEMSKKAVQETQK; EMSKKAVQETQKA; MSKKAVQETQKAV; SKKAVQETQKAVS; KKAVQETQKAVSV; KAVQETQKAVSVA; AVQETQKAVSVAG; VQETQKAVSVAGE; QETQKAVSVAGEA; ETQKAVSVAGEAT; TQKAVSVAGEATF; QKAVSVAGEATFL; KAVSVAGEATFLI; AVSVAGEATFLIE; VSVAGEATFLIEK; SVAGEATFLIEKQ; VAGEATFLIEKQI; AGEATFLIEKQIM; GEATFLIEKQIML; EATFLIEKQIMLN; ATFLIEKQIMLNK; TFLIEKQIMLNKS; FLIEKQIMLNKSP; LIEKQIMLNKSPN; IEKQIMLNKSPNN; EKQIMLNKSPNNK; KQIMLNKSPNNKE; QIMLNKSPNNKEL; IMLNKSPNNKELE; MLNKSPNNKELEL; LNKSPNNKELELT; NKSPNNKELELTK; KSPNNKELELTKE; SPNNKELELTKEE; PNNKELELTKEEF; NNKELELTKEEFA; NKELELTKEEFAK; KELELTKEEFAKV; ELELTKEEFAKVD; LELTKEEFAKVDE; ELTKEEFAKVDEV; LTKEEFAKVDEVK; TKEEFAKVDEVKE; KEEFAKVDEVKET; EEFAKVDEVKETL; EFAKVDEVKETLM; FAKVDEVKETLMA; AKVDEVKETLMAS; KVDEVKETLMASE; VDEVKETLMASER; DEVKETLMASERA; EVKETLMASERAL; VKETLMASERALD; KETLMASERALDE; ETLMASERALDET; TLMASERALDETV; LMASERALDETVQ; MASERALDETVQE; ASERALDETVQEA; SERALDETVQEAQ; ERALDETVQEAQK; RALDETVQEAQKV; ALDETVQEAQKVL; LDETVQEAQKVLN; DETVQEAQKVLNM; ETVQEAQKVLNMV; TVQEAQKVLNMVN; VQEAQKVLNMVNG; QEAQKVLNMVNGL; EAQKVLNMVNGLN; AQKVLNMVNGLNP; QKVLNMVNGLNPS; KVLNMVNGLNPSN; VLNMVNGLNPSNK; LNMVNGLNPSNKD; NMVNGLNPSNKDQ; MVNGLNPSNKDQV; VNGLNPSNKDQVL; NGLNPSNKDQVLA; GLNPSNKDQVLAK; LNPSNKDQVLAKK; NPSNKDQVLAKKD; PSNKDQVLAKKDV; SNKDQVLAKKDVR; NKDQVLAKKDVRK; KDQVLAKKDVRKA; DQVLAKKDVRKAI; QVLAKKDVRKAIS; VLAKKDVRKAISN; LAKKDVRKAISNV; AKKDVRKAISNVV; KKDVRKAISNVVK; KDVRKAISNVVKV; DVRKAISNVVKVA; VRKAISNVVKVAQ; RKAISNVVKVAQG; KAISNVVKVAQGA; AISNVVKVAQGAR; ISNVVKVAQGARD; SNVVKVAQGARDL; NVVKVAQGARDLT; VVKVAQGARDLTK; VKVAQGARDLTKV; KVAQGARDLTKVM; VAQGARDLTKVMA; AQGARDLTKVMAI; QGARDLTKVMAIS; GARDLTKVMAISL; ARDLTKVMAISLY; RDLTKVMAISLYM; DLTKVMAISLYMR; 14 mers:

	MTKIFSNLIINGLL; TKIFSNLIINGLLF; KIFSNLIINGLLFG; IFSNLIINGLLFGF; FSNLIINGLLFGFV; SNLIINGLLFGFVS; NLIINGLLFGFVSL; LIINGLLFGFVSLN; IINGLLFGFVSLNV; INGLLFGFVSLNVF; NGLLFGFVSLNVFA; GLLFGFVSLNVFAD; LLFGFVSLNVFADS; LFGFVSLNVFADSN; FGFVSLNVFADSNN; GFVSLNVFADSNNA; FVSLNVFADSNNAN; VSLNVFADSNNANI; SLNVFADSNNANIL; LNVFADSNNANILK; NVFADSNNANILKP; VFADSNNANILKPQ; FADSNNANILKPQS; ADSNNANILKPQSN; DSNNANILKPQSNV; SNNANILKPQSNVL; NNANILKPQSNVLE; NANILKPQSNVLEH; ANILKPQSNVLEHS; NILKPQSNVLEHSD; ILKPQSNVLEHSDQ; LKPQSNVLEHSDQK; KPQSNVLEHSDQKD; PQSNVLEHSDQKDN; QSNVLEHSDQKDNK; SNVLEHSDQKDNKK; NVLEHSDQKDNKKL; VLEHSDQKDNKKLD; LEHSDQKDNKKLDQ; EHSDQKDNKKLDQK; HSDQKDNKKLDQKD; SDQKDNKKLDQKDQ; DQKDNKKLDQKDQV; QKDNKKLDQKDQVN; KDNKKLDQKDQVNQ; DNKKLDQKDQVNQA; NKKLDQKDQVNQAL; KKLDQKDQVNQALD; KLDQKDQVNQALDT; LDQKDQVNQALDTI; DQKDQVNQALDTIN; QKDQVNQALDTINK; KDQVNQALDTINKV; DQVNQALDTINKVT; QVNQALDTINKVTE; VNQALDTINKVTED; NQALDTINKVTEDV; QALDTINKVTEDVS; ALDTINKVTEDVSS; LDTINKVTEDVSSK; DTINKVTEDVSSKL; TINKVTEDVSSKLE; INKVTEDVSSKLEG; NKVTEDVSSKLEGV; KVTEDVSSKLEGVR; VTEDVSSKLEGVRE; TEDVSSKLEGVRES; EDVSSKLEGVRESS; DVSSKLEGVRESSL; VSSKLEGVRESSLE; SSKLEGVRESSLEL; SKLEGVRESSLELV; KLEGVRESSLELVE; LEGVRESSLELVES; EGVRESSLELVESN; GVRESSLELVESND; VRESSLELVESNDA; RESSLELVESNDAG; ESSLELVESNDAGV; SSLELVESNDAGVV; SLELVESNDAGVVK; LELVESNDAGVVKK; ELVESNDAGVVKKF; LVESNDAGVVKKFV; VESNDAGVVKKFVG; ESNDAGVVKKFVGS; SNDAGVVKKFVGSM; NDAGVVKKFVGSMS; DAGVVKKFVGSMSL; AGVVKKFVGSMSLM; GVVKKFVGSMSLMS; VVKKFVGSMSLMSD; VKKFVGSMSLMSDV; KKFVGSMSLMSDVA; KFVGSMSLMSDVAK; FVGSMSLMSDVAKG; VGSMSLMSDVAKGT; GSMSLMSDVAKGTV; SMSLMSDVAKGTVV; MSLMSDVAKGTVVA; SLMSDVAKGTVVAS; LMSDVAKGTVVASQ; MSDVAKGTVVASQE; SDVAKGTVVASQEA; DVAKGTVVASQEAT; VAKGTVVASQEATI; AKGTVVASQEATIV; KGTVVASQEATIVA; GTVVASQEATIVAK; TVVASQEATIVAKC; VVASQEATIVAKCS; VASQEATIVAKCSG; ASQEATIVAKCSGM; SQEATIVAKCSGMV; QEATIVAKCSGMVA; EATIVAKCSGMVAE; ATIVAKCSGMVAEG; TIVAKCSGMVAEGA; IVAKCSGMVAEGAN; VAKCSGMVAEGANK; AKCSGMVAEGANKV; KCSGMVAEGANKVV; CSGMVAEGANKVVE; SGMVAEGANKVVEM; GMVAEGANKVVEMS; MVAEGANKVVEMSK; VAEGANKVVEMSKK; AEGANKVVEMSKKA; EGANKVVEMSKKAV; GANKVVEMSKKAVQ; ANKVVEMSKKAVQE; NKVVEMSKKAVQET; KVVEMSKKAVQETQ; VVEMSKKAVQETQK; VEMSKKAVQETQKA; EMSKKAVQETQKAV; MSKKAVQETQKAVS; SKKAVQETQKAVSV; KKAVQETQKAVSVA; KAVQETQKAVSVAG; AVQETQKAVSVAGE; VQETQKAVSVAGEA; QETQKAVSVAGEAT; ETQKAVSVAGEATF; TQKAVSVAGEATFL; QKAVSVAGEATFLI; KAVSVAGEATFLIE; AVSVAGEATFLIEK; VSVAGEATFLIEKQ; SVAGEATFLIEKQI; VAGEATFLIEKQIM; AGEATFLIEKQIML; GEATFLIEKQIMLN;

EATFLIEKQIMLNK; ATFLIEKQIMLNKS; TFLIEKQIMLNKSP;
FLIEKQIMLNKSPN; LIEKQIMLNKSPNN; IEKQIMLNKSPNNK;
EKQIMLNKSPNNKE; KQIMLNKSPNNKEL; QIMLNKSPNNKELE;
IMLNKSPNNKELEL; MLNKSPNNKELELT; LNKSPNNKELELTK;
NKSPNNKELELTKE; KSPNNKELELTKEE; SPNNKELELTKEEF;
PNNKELELTKEEFA; NNKELELTKEEFAK; NKELELTKEEFAKV;
KELELTKEEFAKVD; ELELTKEEFAKVDE; LELTKEEFAKVDEV;
ELTKEEFAKVDEVK; LTKEEFAKVDEVKE; TKEEFAKVDEVKET;
KEEFAKVDEVKETL; EEFAKVDEVKETLM; EFAKVDEVKETLMA;
FAKVDEVKETLMAS; AKVDEVKETLMASE; KVDEVKETLMASER;
VDEVKETLMASERA; DEVKETLMASERAL; EVKETLMASERALD;
VKETLMASERALDE; KETLMASERALDET; ETLMASERALDETV;
TLMASERALDETVQ; LMASERALDETVQE; MASERALDETVQEA;
ASERALDETVQEAQ; SERALDETVQEAQK; ERALDETVQEAQKV;
RALDETVQEAQKVL; ALDETVQEAQKVLN; LDETVQEAQKVLNM;
DETVQEAQKVLNMV; ETVQEAQKVLNMVN; TVQEAQKVLNMVNG;
VQEAQKVLNMVNGL; QEAQKVLNMVNGLN; EAQKVLNMVNGLNP;
AQKVLNMVNGLNPS; QKVLNMVNGLNPSN; KVLNMVNGLNPSNK;
VLNMVNGLNPSNKD; LNMVNGLNPSNKDQ; NMVNGLNPSNKDQV;
MVNGLNPSNKDQVL; VNGLNPSNKDQVLA; NGLNPSNKDQVLAK;
GLNPSNKDQVLAKK; LNPSNKDQVLAKKD; NPSNKDQVLAKKDV;
PSNKDQVLAKKDVR; SNKDQVLAKKDVRK; NKDQVLAKKDVRKA;
KDQVLAKKDVRKAI; DQVLAKKDVRKAIS; QVLAKKDVRKAISN;
VLAKKDVRKAISNV; LAKKDVRKAISNVV; AKKDVRKAISNVVK;
KKDVRKAISNVVKV; KDVRKAISNVVKVA; DVRKAISNVVKVAQ;
VRKAISNVVKVAQG; RKAISNVVKVAQGA; KAISNVVKVAQGAR;
AISNVVKVAQGARD; ISNVVKVAQGARDL; SNVVKVAQGARDLT;
NVVKVAQGARDLTK; VVKVAQGARDLTKV; VKVAQGARDLTKVM;
KVAQGARDLTKVMA; VAQGARDLTKVMAI; AQGARDLTKVMAIS;
QGARDLTKVMAISL; GARDLTKVMAISLY; ARDLTKVMAISLYM;
RDLTKVMAISLYMR;

15 mers:
MTKIFSNLIINGLLF; TKIFSNLIINGLLFG; KIFSNLIINGLLFGF;
IFSNLIINGLLFGFV; FSNLIINGLLFGFVS; SNLIINGLLFGFVSL;
NLIINGLLFGFVSLN; LIINGLLFGFVSLNV; IINGLLFGFVSLNVF;
INGLLFGFVSLNVFA; NGLLFGFVSLNVFAD; GLLFGFVSLNVFADS;
LLFGFVSLNVFADSN; LFGFVSLNVFADSNN; FGFVSLNVFADSNNA;
GFVSLNVFADSNNAN; FVSLNVFADSNNANI; VSLNVFADSNNANIL;
SLNVFADSNNANILK; LNVFADSNNANILKP; NVFADSNNANILKPQ;
VFADSNNANILKPQS; FADSNNANILKPQSN; ADSNNANILKPQSNV;
DSNNANILKPQSNVL; SNNANILKPQSNVLE; NNANILKPQSNVLEH;
NANILKPQSNVLEHS; ANILKPQSNVLEHSD; NILKPQSNVLEHSDQ;
ILKPQSNVLEHSDQK; LKPQSNVLEHSDQKD; KPQSNVLEHSDQKDN;
PQSNVLEHSDQKDNK; QSNVLEHSDQKDNKK; SNVLEHSDQKDNKKL;
NVLEHSDQKDNKKLD; VLEHSDQKDNKKLDQ; LEHSDQKDNKKLDQK;
EHSDQKDNKKLDQKD; HSDQKDNKKLDQKDQ; SDQKDNKKLDQKDQV;
DQKDNKKLDQKDQVN; QKDNKKLDQKDQVNQ; KDNKKLDQKDQVNQA;
DNKKLDQKDQVNQAL; NKKLDQKDQVNQALD; KKLDQKDQVNQALDT;
KLDQKDQVNQALDTI; LDQKDQVNQALDTIN; DQKDQVNQALDTINK;
QKDQVNQALDTINKV; KDQVNQALDTINKVT; DQVNQALDTINKVTE;

	QVNQALDTINKVTED; VNQALDTINKVTEDV; NQALDTINKVTEDVS; QALDTINKVTEDVSS; ALDTINKVTEDVSSK; LDTINKVTEDVSSKL; DTINKVTEDVSSKLE; TINKVTEDVSSKLEG; INKVTEDVSSKLEGV; NKVTEDVSSKLEGVR; KVTEDVSSKLEGVRE; VTEDVSSKLEGVRES; TEDVSSKLEGVRESS; EDVSSKLEGVRESSL; DVSSKLEGVRESSLE; VSSKLEGVRESSLEL; SSKLEGVRESSLELV; SKLEGVRESSLELVE; KLEGVRESSLELVES; LEGVRESSLELVESN; EGVRESSLELVESND; GVRESSLELVESNDA; VRESSLELVESNDAG; RESSLELVESNDAGV; ESSLELVESNDAGVV; SSLELVESNDAGVVK; SLELVESNDAGVVKK; LELVESNDAGVVKKF; ELVESNDAGVVKKFV; LVESNDAGVVKKFVG; VESNDAGVVKKFVGS; ESNDAGVVKKFVGSM; SNDAGVVKKFVGSMS; NDAGVVKKFVGSMSL; DAGVVKKFVGSMSLM; AGVVKKFVGSMSLMS; GVVKKFVGSMSLMSD; VVKKFVGSMSLMSDV; VKKFVGSMSLMSDVA; KKFVGSMSLMSDVAK; KFVGSMSLMSDVAKG; FVGSMSLMSDVAKGT; VGSMSLMSDVAKGTV; GSMSLMSDVAKGTVV; SMSLMSDVAKGTVVA; MSLMSDVAKGTVVAS; SLMSDVAKGTVVASQ; LMSDVAKGTVVASQE; MSDVAKGTVVASQEA; SDVAKGTVVASQEAT; DVAKGTVVASQEATI; VAKGTVVASQEATIV; AKGTVVASQEATIVA; KGTVVASQEATIVAK; GTVVASQEATIVAKC; TVVASQEATIVAKCS; VVASQEATIVAKCSG; VASQEATIVAKCSGM; ASQEATIVAKCSGMV; SQEATIVAKCSGMVA; QEATIVAKCSGMVAE; EATIVAKCSGMVAEG; ATIVAKCSGMVAEGA; TIVAKCSGMVAEGAN; IVAKCSGMVAEGANK; VAKCSGMVAEGANKV; AKCSGMVAEGANKVV; KCSGMVAEGANKVVE; CSGMVAEGANKVVEM; SGMVAEGANKVVEMS; GMVAEGANKVVEMSK; MVAEGANKVVEMSKK; VAEGANKVVEMSKKA; AEGANKVVEMSKKAV; EGANKVVEMSKKAVQ; GANKVVEMSKKAVQE; ANKVVEMSKKAVQET; NKVVEMSKKAVQETQ; KVVEMSKKAVQETQK; VVEMSKKAVQETQKA; VEMSKKAVQETQKAV; EMSKKAVQETQKAVS; MSKKAVQETQKAVSV; SKKAVQETQKAVSVA; KKAVQETQKAVSVAG; KAVQETQKAVSVAGE; AVQETQKAVSVAGEA; VQETQKAVSVAGEAT; QETQKAVSVAGEATF; ETQKAVSVAGEATFL; TQKAVSVAGEATFLI; QKAVSVAGEATFLIE; KAVSVAGEATFLIEK; AVSVAGEATFLIEKQ; VSVAGEATFLIEKQI; SVAGEATFLIEKQIM; VAGEATFLIEKQIML; AGEATFLIEKQIMLN; GEATFLIEKQIMLNK; EATFLIEKQIMLNKS; ATFLIEKQIMLNKSP; TFLIEKQIMLNKSPN; FLIEKQIMLNKSPNN; LIEKQIMLNKSPNNK; IEKQIMLNKSPNNKE; EKQIMLNKSPNNKEL; KQIMLNKSPNNKELE; QIMLNKSPNNKELEL; IMLNKSPNNKELELT; MLNKSPNNKELELTK; LNKSPNNKELELTKE; NKSPNNKELELTKEE; KSPNNKELELTKEEF; SPNNKELELTKEEFA; PNNKELELTKEEFAK; NNKELELTKEEFAKV; NKELELTKEEFAKVD; KELELTKEEFAKVDE; ELELTKEEFAKVDEV; LELTKEEFAKVDEVK; ELTKEEFAKVDEVKE; LTKEEFAKVDEVKET; TKEEFAKVDEVKETL; KEEFAKVDEVKETLM; EEFAKVDEVKETLMA; EFAKVDEVKETLMAS; FAKVDEVKETLMASE; AKVDEVKETLMASER; KVDEVKETLMASERA; VDEVKETLMASERAL; DEVKETLMASERALD; EVKETLMASERALDE; VKETLMASERALDET; KETLMASERALDETV; ETLMASERALDETVQ; TLMASERALDETVQE; LMASERALDETVQEA; MASERALDETVQEAQ; ASERALDETVQEAQK; SERALDETVQEAQKV; ERALDETVQEAQKVL; RALDETVQEAQKVLN; ALDETVQEAQKVLNM; LDETVQEAQKVLNMV; DETVQEAQKVLNMVN; ETVQEAQKVLNMVNG; TVQEAQKVLNMVNGL; VQEAQKVLNMVNGLN; QEAQKVLNMVNGLNP; EAQKVLNMVNGLNPS; AQKVLNMVNGLNPSN; QKVLNMVNGLNPSNK; KVLNMVNGLNPSNKD;

	VLNMVNGLNPSNKDQ; LNMVNGLNPSNKDQV; NMVNGLNPSNKDQVL; MVNGLNPSNKDQVLA; VNGLNPSNKDQVLAK; NGLNPSNKDQVLAKK; GLNPSNKDQVLAKKD; LNPSNKDQVLAKKDV; NPSNKDQVLAKKDVR; PSNKDQVLAKKDVRK; SNKDQVLAKKDVRKA; NKDQVLAKKDVRKAI; KDQVLAKKDVRKAIS; DQVLAKKDVRKAISN; QVLAKKDVRKAISNV; VLAKKDVRKAISNVV; LAKKDVRKAISNVVK; AKKDVRKAISNVVKV; KKDVRKAISNVVKVA; KDVRKAISNVVKVAQ; DVRKAISNVVKVAQG; VRKAISNVVKVAQGA; RKAISNVVKVAQGAR; KAISNVVKVAQGARD; AISNVVKVAQGARDL; ISNVVKVAQGARDLT; SNVVKVAQGARDLTK; NVVKVAQGARDLTKV; VVKVAQGARDLTKVM; VKVAQGARDLTKVMA; KVAQGARDLTKVMAI; VAQGARDLTKVMAIS; AQGARDLTKVMAISL; QGARDLTKVMAISLY; GARDLTKVMAISLYM; ARDLTKVMAISLYMR; 16 mers: MTKIFSNLIINGLLFG; TKIFSNLIINGLLFGF; KIFSNLIINGLLFGFV; IFSNLIINGLLFGFVS; FSNLIINGLLFGFVSL; SNLIINGLLFGFVSLN; NLIINGLLFGFVSLNV; LIINGLLFGFVSLNVF; IINGLLFGFVSLNVFA; INGLLFGFVSLNVFAD; NGLLFGFVSLNVFADS; GLLFGFVSLNVFADSN; LLFGFVSLNVFADSNN; LFGFVSLNVFADSNNA; FGFVSLNVFADSNNAN; GFVSLNVFADSNNANI; FVSLNVFADSNNANIL; VSLNVFADSNNANILK; SLNVFADSNNANILKP; LNVFADSNNANILKPQ; NVFADSNNANILKPQS; VFADSNNANILKPQSN; FADSNNANILKPQSNV; ADSNNANILKPQSNVL; DSNNANILKPQSNVLE; SNNANILKPQSNVLEH; NNANILKPQSNVLEHS; NANILKPQSNVLEHSD; ANILKPQSNVLEHSDQ; NILKPQSNVLEHSDQK; ILKPQSNVLEHSDQKD; LKPQSNVLEHSDQKDN; KPQSNVLEHSDQKDNK; PQSNVLEHSDQKDNKK; QSNVLEHSDQKDNKKL; SNVLEHSDQKDNKKLD; NVLEHSDQKDNKKLDQ; VLEHSDQKDNKKLDQK; LEHSDQKDNKKLDQKD; EHSDQKDNKKLDQKDQ; HSDQKDNKKLDQKDQV; SDQKDNKKLDQKDQVN; DQKDNKKLDQKDQVNQ; QKDNKKLDQKDQVNQA; KDNKKLDQKDQVNQAL; DNKKLDQKDQVNQALD; NKKLDQKDQVNQALDT; KKLDQKDQVNQALDTI; KLDQKDQVNQALDTIN; LDQKDQVNQALDTINK; DQKDQVNQALDTINKV; QKDQVNQALDTINKVT; KDQVNQALDTINKVTE; DQVNQALDTINKVTED; QVNQALDTINKVTEDV; VNQALDTINKVTEDVS; NQALDTINKVTEDVSS; QALDTINKVTEDVSSK; ALDTINKVTEDVSSKL; LDTINKVTEDVSSKLE; DTINKVTEDVSSKLEG; TINKVTEDVSSKLEGV; INKVTEDVSSKLEGVR; NKVTEDVSSKLEGVRE; KVTEDVSSKLEGVRES; VTEDVSSKLEGVRESS; TEDVSSKLEGVRESSL; EDVSSKLEGVRESSLE; DVSSKLEGVRESSLEL; VSSKLEGVRESSLELV; SSKLEGVRESSLELVE; SKLEGVRESSLELVES; KLEGVRESSLELVESN; LEGVRESSLELVESND; EGVRESSLELVESNDA; GVRESSLELVESNDAG; VRESSLELVESNDAGV; RESSLELVESNDAGVV; ESSLELVESNDAGVVK; SSLELVESNDAGVVKK; SLELVESNDAGVVKKF; LELVESNDAGVVKKFV; ELVESNDAGVVKKFVG; LVESNDAGVVKKFVGS; VESNDAGVVKKFVGSM; ESNDAGVVKKFVGSMS; SNDAGVVKKFVGSMSL; NDAGVVKKFVGSMSLM; DAGVVKKFVGSMSLMS; AGVVKKFVGSMSLMSD; GVVKKFVGSMSLMSDV; VVKKFVGSMSLMSDVA; VKKFVGSMSLMSDVAK; KKFVGSMSLMSDVAKG; KFVGSMSLMSDVAKGT; FVGSMSLMSDVAKGTV; VGSMSLMSDVAKGTVV; GSMSLMSDVAKGTVVA; SMSLMSDVAKGTVVAS; MSLMSDVAKGTVVASQ; SLMSDVAKGTVVASQE; LMSDVAKGTVVASQEA; MSDVAKGTVVASQEAT; SDVAKGTVVASQEATI; DVAKGTVVASQEATIV; VAKGTVVASQEATIVA; AKGTVVASQEATIVAK; KGTVVASQEATIVAKC; GTVVASQEATIVAKCS; TVVASQEATIVAKCSG; VVASQEATIVAKCSGM;

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Seq 26	13 mers: MKKMLLIFSFFLI; KKMLLIFSFFLIF; KMLLIFSFFLIFL; MLLIFSFFLIFLN; LLIFSFFLIFLNG; LIFSFFLIFLNGF; IFSFFLIFLNGFP; FSFFLIFLNGFPL; SFFLIFLNGFPLN; FFLIFLNGFPLNA; FLIFLNGFPLNAR; LIFLNGFPLNARK;

	IFLNGFPLNARKV; FLNGFPLNARKVD; LNGFPLNARKVDK; NGFPLNARKVDKE; GFPLNARKVDKEK; FPLNARKVDKEKL; PLNARKVDKEKLK; LNARKVDKEKLKD; NARKVDKEKLKDF; ARKVDKEKLKDFV; RKVDKEKLKDFVN; KVDKEKLKDFVNM; VDKEKLKDFVNMD; DKEKLKDFVNMDL; KEKLKDFVNMDLE; EKLKDFVNMDLEF; KLKDFVNMDLEFV; LKDFVNMDLEFVN; KDFVNMDLEFVNY; DFVNMDLEFVNYK; FVNMDLEFVNYKG; VNMDLEFVNYKGP; NMDLEFVNYKGPY; MDLEFVNYKGPYD; DLEFVNYKGPYDS; LEFVNYKGPYDST; EFVNYKGPYDSTN; FVNYKGPYDSTNT; VNYKGPYDSTNTY; NYKGPYDSTNTYE; YKGPYDSTNTYEQ; KGPYDSTNTYEQI; GPYDSTNTYEQIV; PYDSTNTYEQIVG; YDSTNTYEQIVGI; DSTNTYEQIVGIG; STNTYEQIVGIGE; TNTYEQIVGIGEF; NTYEQIVGIGEFL; TYEQIVGIGEFLA; YEQIVGIGEFLAR; EQIVGIGEFLARP; QIVGIGEFLARPL; IVGIGEFLARPLT; VGIGEFLARPLTN; GIGEFLARPLTNS; IGEFLARPLTNSN; GEFLARPLTNSNS; EFLARPLTNSNSN; FLARPLTNSNSNS; LARPLTNSNSNSS; ARPLTNSNSNSSY; RPLTNSNSNSSYY; PLTNSNSNSSYYG; LTNSNSNSSYYGK; TNSNSNSSYYGKY; NSNSNSSYYGKYF; SNSNSSYYGKYFI; NSNSSYYGKYFIN; SNSSYYGKYFINR; NSSYYGKYFINRF; SSYYGKYFINRFI; SYYGKYFINRFID; YYGKYFINRFIDD; YGKYFINRFIDDQ; GKYFINRFIDDQD; KYFINRFIDDQDK; YFINRFIDDQDKK; FINRFIDDQDKKA; INRFIDDQDKKAS; NRFIDDQDKKASV; RFIDDQDKKASVD; FIDDQDKKASVDV; IDDQDKKASVDVF; DDQDKKASVDVFS; DQDKKASVDVFSI; QDKKASVDVFSIS; DKKASVDVFSISS; KKASVDVFSISSK; KASVDVFSISSKS; ASVDVFSISSKSE; SVDVFSISSKSEL; VDVFSISSKSELD; DVFSISSKSELDS; VFSISSKSELDSI; FSISSKSELDSIL; SISSKSELDSILN; ISSKSELDSILNL; SSKSELDSILNLR; SKSELDSILNLRR; KSELDSILNLRRI; SELDSILNLRRIL; ELDSILNLRRILT; LDSILNLRRILTG; DSILNLRRILTGY; SILNLRRILTGYI; ILNLRRILTGYII; LNLRRILTGYIIK; NLRRILTGYIIKS; LRRILTGYIIKSF; RRILTGYIIKSFD; RILTGYIIKSFDY; ILTGYIIKSFDYD; LTGYIIKSFDYDR; TGYIIKSFDYDRS; GYIIKSFDYDRSS; YIIKSFDYDRSSA; IIKSFDYDRSSAE; IKSFDYDRSSAEL; KSFDYDRSSAELI; SFDYDRSSAELIA; FDYDRSSAELIAK; DYDRSSAELIAKV; YDRSSAELIAKVI; DRSSAELIAKVIT; RSSAELIAKVITI; SSAELIAKVITIY; SAELIAKVITIYN; AELIAKVITIYNA; ELIAKVITIYNAV; LIAKVITIYNAVY; IAKVITIYNAVYR; AKVITIYNAVYRG; KVITIYNAVYRGD; VITIYNAVYRGDL; ITIYNAVYRGDLD; TIYNAVYRGDLDY; IYNAVYRGDLDYY; YNAVYRGDLDYYK; NAVYRGDLDYYKG; AVYRGDLDYYKGF; VYRGDLDYYKGFY; YRGDLDYYKGFYI; RGDLDYYKGFYIE; GDLDYYKGFYIEP; DLDYYKGFYIEPA; LDYYKGFYIEPAL; DYYKGFYIEPALK; YYKGFYIEPALKS; YKGFYIEPALKSL; KGFYIEPALKSLT; GFYIEPALKSLTK; FYIEPALKSLTKE; YIEPALKSLTKEN; IEPALKSLTKENA; EPALKSLTKENAG; PALKSLTKENAGL; ALKSLTKENAGLS; LKSLTKENAGLSR; KSLTKENAGLSRV; SLTKENAGLSRVY; LTKENAGLSRVYS; TKENAGLSRVYSQ;

	KENAGLSRVYSQW; ENAGLSRVYSQWA; NAGLSRVYSQWAG; AGLSRVYSQWAGK; GLSRVYSQWAGKT; LSRVYSQWAGKTQ; SRVYSQWAGKTQI; RVYSQWAGKTQIF; VYSQWAGKTQIFI; YSQWAGKTQIFIP; SQWAGKTQIFIPL; QWAGKTQIFIPLK; WAGKTQIFIPLKK; AGKTQIFIPLKKD; GKTQIFIPLKKDI; KTQIFIPLKKDIL; TQIFIPLKKDILS; QIFIPLKKDILSG; IFIPLKKDILSGN; FIPLKKDILSGNI; IPLKKDILSGNIE; PLKKDILSGNIES; LKKDILSGNIESD; KKDILSGNIESDI; KDILSGNIESDID; DILSGNIESDIDI; ILSGNIESDIDID; LSGNIESDIDIDS; SGNIESDIDIDSL; GNIESDIDIDSLV; NIESDIDIDSLVT; IESDIDIDSLVTD; ESDIDIDSLVTDK; SDIDIDSLVTDKV; DIDIDSLVTDKVI; IDIDSLVTDKVIA; DIDSLVTDKVIAA; IDSLVTDKVIAAL; DSLVTDKVIAALL; SLVTDKVIAALLS; LVTDKVIAALLSE; VTDKVIAALLSEN; TDKVIAALLSENE; DKVIAALLSENEA; KVIAALLSENEAG; VIAALLSENEAGV; IAALLSENEAGVN; AALLSENEAGVNF; ALLSENEAGVNFA; LLSENEAGVNFAR; LSENEAGVNFARD; SENEAGVNFARDI; ENEAGVNFARDIT; NEAGVNFARDITD; EAGVNFARDITDI; AGVNFARDITDIQ; GVNFARDITDIQG; VNFARDITDIQGE; NFARDITDIQGET; FARDITDIQGETH; ARDITDIQGETHK; RDITDIQGETHKA; DITDIQGETHKAD; ITDIQGETHKADQ; TDIQGETHKADQD; DIQGETHKADQDK; IQGETHKADQDKI; QGETHKADQDKID; GETHKADQDKIDT; ETHKADQDKIDTE; THKADQDKIDTEL; HKADQDKIDTELD; KADQDKIDTELDN; ADQDKIDTELDNI; DQDKIDTELDNIH; QDKIDTELDNIHE; DKIDTELDNIHES; KIDTELDNIHESD; IDTELDNIHESDS; DTELDNIHESDSN; TELDNIHESDSNI; ELDNIHESDSNIT; LDNIHESDSNITE; DNIHESDSNITET; NIHESDSNITETI; IHESDSNITETIE; HESDSNITETIEN; ESDSNITETIENL; SDSNITETIENLR; DSNITETIENLRD; SNITETIENLRDQ; NITETIENLRDQL; ITETIENLRDQLE; TETIENLRDQLEK; ETIENLRDQLEKA; TIENLRDQLEKAT; IENLRDQLEKATD; ENLRDQLEKATDE; NLRDQLEKATDEE; LRDQLEKATDEEH; RDQLEKATDEEHK; DQLEKATDEEHKK; QLEKATDEEHKKE; LEKATDEEHKKEI; EKATDEEHKKEIE; KATDEEHKKEIES; ATDEEHKKEIESQ; TDEEHKKEIESQV; DEEHKKEIESQVD; EEHKKEIESQVDA; EHKKEIESQVDAK; HKKEIESQVDAKK; KKEIESQVDAKKK; KEIESQVDAKKKE; EIESQVDAKKKEK; IESQVDAKKKEKE; ESQVDAKKKEKEE; SQVDAKKKEKEEL; QVDAKKKEKEELD; VDAKKKEKEELDK; DAKKKEKEELDKK; AKKKEKEELDKKA; KKKEKEELDKKAI; KKEKEELDKKAIN; KEKEELDKKAINL; EKEELDKKAINLD; KEELDKKAINLDK; EELDKKAINLDKA; ELDKKAINLDKAQ; LDKKAINLDKAQQ; DKKAINLDKAQQK; KKAINLDKAQQKL; KAINLDKAQQKLD; AINLDKAQQKLDS; INLDKAQQKLDSA; NLDKAQQKLDSAE; LDKAQQKLDSAED; DKAQQKLDSAEDN; KAQQKLDSAEDNL; AQQKLDSAEDNLD; QQKLDSAEDNLDV; QKLDSAEDNLDVQ; KLDSAEDNLDVQR; LDSAEDNLDVQRD; DSAEDNLDVQRDT; SAEDNLDVQRDTV; AEDNLDVQRDTVR; EDNLDVQRDTVRE; DNLDVQRDTVREK; NLDVQRDTVREKI; LDVQRDTVREKIQ; DVQRDTVREKIQE; VQRDTVREKIQED;

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	NFEINKNSSLYVD; FEINKNSSLYVDS; EINKNSSLYVDSK; INKNSSLYVDSKM; NKNSSLYVDSKMI; KNSSLYVDSKMIL; NSSLYVDSKMILA; SSLYVDSKMILAA; SLYVDSKMILAAV; LYVDSKMILAAVR; YVDSKMILAAVRD; VDSKMILAAVRDK; DSKMILAAVRDKD; SKMILAAVRDKDD; KMILAAVRDKDDS; MILAAVRDKDDSN; ILAAVRDKDDSNA; LAAVRDKDDSNAW; AAVRDKDDSNAWR; AVRDKDDSNAWRL; VRDKDDSNAWRLA; RDKDDSNAWRLAK; DKDDSNAWRLAKF; KDDSNAWRLAKFS; DDSNAWRLAKFSP; DSNAWRLAKFSPK; SNAWRLAKFSPKN; NAWRLAKFSPKNL; AWRLAKFSPKNLD; WRLAKFSPKNLDE; RLAKFSPKNLDEF; LAKFSPKNLDEFI; AKFSPKNLDEFIL; KFSPKNLDEFILS; FSPKNLDEFILSE; SPKNLDEFILSEN; PKNLDEFILSENK; KNLDEFILSENKI; NLDEFILSENKIL; LDEFILSENKILP; DEFILSENKILPF; EFILSENKILPFT; FILSENKILPFTS; ILSENKILPFTSF; LSENKILPFTSFS; SENKILPFTSFSV; ENKILPFTSFSVR; NKILPFTSFSVRK; KILPFTSFSVRKN; ILPFTSFSVRKNF; LPFTSFSVRKNFI; PFTSFSVRKNFIY; FTSFSVRKNFIYL; TSFSVRKNFIYLQ; SFSVRKNFIYLQD; FSVRKNFIYLQDE; SVRKNFIYLQDEL; VRKNFIYLQDELK; RKNFIYLQDELKN; KNFIYLQDELKNL; NFIYLQDELKNLV; FIYLQDELKNLVI; IYLQDELKNLVIL; YLQDELKNLVILD; LQDELKNLVILDV; QDELKNLVILDVN; DELKNLVILDVNT; ELKNLVILDVNTL; LKNLVILDVNTLK; KNLVILDVNTLKK; NLVILDVNTLKKV; LVILDVNTLKKVK; 14 mers: MKKMLLIFSFFLIF; KKMLLIFSFFLIFL; KMLLIFSFFLIFLN; MLLIFSFFLIFLNG; LLIFSFFLIFLNGF; LIFSFFLIFLNGFP; IFSFFLIFLNGFPL; FSFFLIFLNGFPLN; SFFLIFLNGFPLNA; FFLIFLNGFPLNAR; FLIFLNGFPLNARK; LIFLNGFPLNARKV; IFLNGFPLNARKVD; FLNGFPLNARKVDK; LNGFPLNARKVDKE; NGFPLNARKVDKEK; GFPLNARKVDKEKL; FPLNARKVDKEKLK; PLNARKVDKEKLKD; LNARKVDKEKLKDF; NARKVDKEKLKDFV; ARKVDKEKLKDFVN; RKVDKEKLKDFVNM; KVDKEKLKDFVNMD; VDKEKLKDFVNMDL; DKEKLKDFVNMDLE; KEKLKDFVNMDLEF; EKLKDFVNMDLEFV; KLKDFVNMDLEFVN; LKDFVNMDLEFVNY; KDFVNMDLEFVNYK; DFVNMDLEFVNYKG; FVNMDLEFVNYKGP; VNMDLEFVNYKGPY; NMDLEFVNYKGPYD; MDLEFVNYKGPYDS; DLEFVNYKGPYDST; LEFVNYKGPYDSTN; EFVNYKGPYDSTNT; FVNYKGPYDSTNTY; VNYKGPYDSTNTYE; NYKGPYDSTNTYEQ; YKGPYDSTNTYEQI; KGPYDSTNTYEQIV; GPYDSTNTYEQIVG; PYDSTNTYEQIVGI; YDSTNTYEQIVGIG; DSTNTYEQIVGIGE; STNTYEQIVGIGEF; TNTYEQIVGIGEFL; NTYEQIVGIGEFLA; TYEQIVGIGEFLAR; YEQIVGIGEFLARP; EQIVGIGEFLARPL; QIVGIGEFLARPLT; IVGIGEFLARPLTN; VGIGEFLARPLTNS; GIGEFLARPLTNSN; IGEFLARPLTNSNS; GEFLARPLTNSNSN; EFLARPLTNSNSNS; FLARPLTNSNSNSS; LARPLTNSNSNSSY; ARPLTNSNSNSSYY; RPLTNSNSNSSYYG; PLTNSNSNSSYYGK; LTNSNSNSSYYGKY; TNSNSNSSYYGKYF; NSNSNSSYYGKYFI; SNSNSSYYGKYFIN; NSNSSYYGKYFINR; SNSSYYGKYFINRF; NSSYYGKYFINRFI; SSYYGKYFINRFID; SYYGKYFINRFIDD;

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	ITDIQGETHKADQD; TDIQGETHKADQDK; DIQGETHKADQDKI; IQGETHKADQDKID; QGETHKADQDKIDT; GETHKADQDKIDTE; ETHKADQDKIDTEL; THKADQDKIDTELD; HKADQDKIDTELDN; KADQDKIDTELDNI; ADQDKIDTELDNIH; DQDKIDTELDNIHE; QDKIDTELDNIHES; DKIDTELDNIHESD; KIDTELDNIHESDS; IDTELDNIHESDSN; DTELDNIHESDSNI; TELDNIHESDSNIT; ELDNIHESDSNITE; LDNIHESDSNITET; DNIHESDSNITETI; NIHESDSNITETIE; IHESDSNITETIEN; HESDSNITETIENL; ESDSNITETIENLR; SDSNITETIENLRD; DSNITETIENLRDQ; SNITETIENLRDQL; NITETIENLRDQLE; ITETIENLRDQLEK; TETIENLRDQLEKA; ETIENLRDQLEKAT; TIENLRDQLEKATD; IENLRDQLEKATDE; ENLRDQLEKATDEE; NLRDQLEKATDEEH; LRDQLEKATDEEHK; RDQLEKATDEEHKK; DQLEKATDEEHKKE; QLEKATDEEHKKEI; LEKATDEEHKKEIE; EKATDEEHKKEIES; KATDEEHKKEIESQ; ATDEEHKKEIESQV; TDEEHKKEIESQVD; DEEHKKEIESQVDA; EEHKKEIESQVDAK; EHKKEIESQVDAKK; HKKEIESQVDAKKK; KKEIESQVDAKKKE; KEIESQVDAKKKEK; EIESQVDAKKKEKE; IESQVDAKKKEKEE; ESQVDAKKKEKEEL; SQVDAKKKEKEELD; QVDAKKKEKEELDK; VDAKKKEKEELDKK; DAKKKEKEELDKKA; AKKKEKEELDKKAI; KKKEKEELDKKAIN; KKEKEELDKKAINL; KEKEELDKKAINLD; EKEELDKKAINLDK; KEELDKKAINLDKA; EELDKKAINLDKAQ; ELDKKAINLDKAQQ; LDKKAINLDKAQQK; DKKAINLDKAQQKL; KKAINLDKAQQKLD; KAINLDKAQQKLDS; AINLDKAQQKLDSA; INLDKAQQKLDSAE; NLDKAQQKLDSAED; LDKAQQKLDSAEDN; DKAQQKLDSAEDNL; KAQQKLDSAEDNLD; AQQKLDSAEDNLDV; QQKLDSAEDNLDVQ; QKLDSAEDNLDVQR; KLDSAEDNLDVQRD; LDSAEDNLDVQRDT; DSAEDNLDVQRDTV; SAEDNLDVQRDTVR; AEDNLDVQRDTVRE; EDNLDVQRDTVREK; DNLDVQRDTVREKI; NLDVQRDTVREKIQ; LDVQRDTVREKIQE; DVQRDTVREKIQED; VQRDTVREKIQEDI; QRDTVREKIQEDIN; RDTVREKIQEDINE; DTVREKIQEDINEI; TVREKIQEDINEIN; VREKIQEDINEINK; REKIQEDINEINKE; EKIQEDINEINKEK; KIQEDINEINKEKN; IQEDINEINKEKNL; QEDINEINKEKNLP; EDINEINKEKNLPK; DINEINKEKNLPKP; INEINKEKNLPKPG; NEINKEKNLPKPGD; EINKEKNLPKPGDV; INKEKNLPKPGDVS; NKEKNLPKPGDVSS; KEKNLPKPGDVSSP; EKNLPKPGDVSSPK; KNLPKPGDVSSPKV; NLPKPGDVSSPKVD; LPKPGDVSSPKVDK; PKPGDVSSPKVDKQ; KPGDVSSPKVDKQL; PGDVSSPKVDKQLQ; GDVSSPKVDKQLQI; DVSSPKVDKQLQIK; VSSPKVDKQLQIKE; SSPKVDKQLQIKES; SPKVDKQLQIKESL; PKVDKQLQIKESLE; KVDKQLQIKESLED; VDKQLQIKESLEDL; DKQLQIKESLEDLQ; KQLQIKESLEDLQE; QLQIKESLEDLQEQ; LQIKESLEDLQEQL; QIKESLEDLQEQLK; IKESLEDLQEQLKE; KESLEDLQEQLKEA; ESLEDLQEQLKEAG; SLEDLQEQLKEAGD; LEDLQEQLKEAGDE; EDLQEQLKEAGDEN; DLQEQLKEAGDENQ; LQEQLKEAGDENQK; QEQLKEAGDENQKR; EQLKEAGDENQKRE; QLKEAGDENQKREI; LKEAGDENQKREIE; KEAGDENQKREIEK; EAGDENQKREIEKQ; AGDENQKREIEKQI; GDENQKREIEKQIE; DENQKREIEKQIEI; ENQKREIEKQIEIK; NQKREIEKQIEIKK; QKREIEKQIEIKKR; KREIEKQIEIKKRD; REIEKQIEIKKRDE; EIEKQIEIKKRDEE; IEKQIEIKKRDEEL; EKQIEIKKRDEELL;

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	TIYNAVYRGDLDYYK; IYNAVYRGDLDYYKG; YNAVYRGDLDYYKGF; NAVYRGDLDYYKGFY; AVYRGDLDYYKGFYI; VYRGDLDYYKGFYIE; YRGDLDYYKGFYIEP; RGDLDYYKGFYIEPA; GDLDYYKGFYIEPAL; DLDYYKGFYIEPALK; LDYYKGFYIEPALKS; DYYKGFYIEPALKSL; YYKGFYIEPALKSLT; YKGFYIEPALKSLTK; KGFYIEPALKSLTKE; GFYIEPALKSLTKEN; FYIEPALKSLTKENA; YIEPALKSLTKENAG; IEPALKSLTKENAGL; EPALKSLTKENAGLS; PALKSLTKENAGLSR; ALKSLTKENAGLSRV; LKSLTKENAGLSRVY; KSLTKENAGLSRVYS; SLTKENAGLSRVYSQ; LTKENAGLSRVYSQW; TKENAGLSRVYSQWA; KENAGLSRVYSQWAG; ENAGLSRVYSQWAGK; NAGLSRVYSQWAGKT; AGLSRVYSQWAGKTQ; GLSRVYSQWAGKTQI; LSRVYSQWAGKTQIF; SRVYSQWAGKTQIFI; RVYSQWAGKTQIFIP; VYSQWAGKTQIFIPL; YSQWAGKTQIFIPLK; SQWAGKTQIFIPLKK; QWAGKTQIFIPLKKD; WAGKTQIFIPLKKDI; AGKTQIFIPLKKDIL; GKTQIFIPLKKDILS; KTQIFIPLKKDILSG; TQIFIPLKKDILSGN; QIFIPLKKDILSGNI; IFIPLKKDILSGNIE; FIPLKKDILSGNIES; IPLKKDILSGNIESD; PLKKDILSGNIESDI; LKKDILSGNIESDID; KKDILSGNIESDIDI; KDILSGNIESDIDID; DILSGNIESDIDIDS; ILSGNIESDIDIDSL; LSGNIESDIDIDSLV; SGNIESDIDIDSLVT; GNIESDIDIDSLVTD; NIESDIDIDSLVTDK; IESDIDIDSLVTDKV; ESDIDIDSLVTDKVI; SDIDIDSLVTDKVIA; DIDIDSLVTDKVIAA; IDIDSLVTDKVIAAL; DIDSLVTDKVIAALL; IDSLVTDKVIAALLS; DSLVTDKVIAALLSE; SLVTDKVIAALLSEN; LVTDKVIAALLSENE; VTDKVIAALLSENEA; TDKVIAALLSENEAG; DKVIAALLSENEAGV; KVIAALLSENEAGVN; VIAALLSENEAGVNF; IAALLSENEAGVNFA; AALLSENEAGVNFAR; ALLSENEAGVNFARD; LLSENEAGVNFARDI; LSENEAGVNFARDIT; SENEAGVNFARDITD; ENEAGVNFARDITDI; NEAGVNFARDITDIQ; EAGVNFARDITDIQG; AGVNFARDITDIQGE; GVNFARDITDIQGET; VNFARDITDIQGETH; NFARDITDIQGETHK; FARDITDIQGETHKA; ARDITDIQGETHKAD; RDITDIQGETHKADQ; DITDIQGETHKADQD; ITDIQGETHKADQDK; TDIQGETHKADQDKI; DIQGETHKADQDKID; IQGETHKADQDKIDT; QGETHKADQDKIDTE; GETHKADQDKIDTEL; ETHKADQDKIDTELD; THKADQDKIDTELDN; HKADQDKIDTELDNI; KADQDKIDTELDNIH; ADQDKIDTELDNIHE; DQDKIDTELDNIHES; QDKIDTELDNIHESD; DKIDTELDNIHESDS; KIDTELDNIHESDSN; IDTELDNIHESDSNI; DTELDNIHESDSNIT; TELDNIHESDSNITE; ELDNIHESDSNITET; LDNIHESDSNITETI; DNIHESDSNITETIE; NIHESDSNITETIEN; IHESDSNITETIENL; HESDSNITETIENLR; ESDSNITETIENLRD; SDSNITETIENLRDQ; DSNITETIENLRDQL; SNITETIENLRDQLE; NITETIENLRDQLEK; ITETIENLRDQLEKA; TETIENLRDQLEKAT; ETIENLRDQLEKATD; TIENLRDQLEKATDE; IENLRDQLEKATDEE; ENLRDQLEKATDEEH; NLRDQLEKATDEEHK; LRDQLEKATDEEHKK; RDQLEKATDEEHKKE; DQLEKATDEEHKKEI; QLEKATDEEHKKEIE; LEKATDEEHKKEIES; EKATDEEHKKEIESQ; KATDEEHKKEIESQV; ATDEEHKKEIESQVD; TDEEHKKEIESQVDA; DEEHKKEIESQVDAK; EEHKKEIESQVDAKK; EHKKEIESQVDAKKK; HKKEIESQVDAKKKE; KKEIESQVDAKKKEK; KEIESQVDAKKKEKE; EIESQVDAKKKEKEE; IESQVDAKKKEKEEL; ESQVDAKKKEKEELD; SQVDAKKKEKEELDK; QVDAKKKEKEELDKK; VDAKKKEKEELDKKA; DAKKKEKEELDKKAI; AKKKEKEELDKKAIN; KKKEKEELDKKAINL; KKEKEELDKKAINLD; KEKEELDKKAINLDK; EKEELDKKAINLDKA;

	KEELDKKAINLDKAQ; EELDKKAINLDKAQQ; ELDKKAINLDKAQQK; LDKKAINLDKAQQKL; DKKAINLDKAQQKLD; KKAINLDKAQQKLDS; KAINLDKAQQKLDSA; AINLDKAQQKLDSAE; INLDKAQQKLDSAED; NLDKAQQKLDSAEDN; LDKAQQKLDSAEDNL; DKAQQKLDSAEDNLD; KAQQKLDSAEDNLDV; AQQKLDSAEDNLDVQ; QQKLDSAEDNLDVQR; QKLDSAEDNLDVQRD; KLDSAEDNLDVQRDT; LDSAEDNLDVQRDTV; DSAEDNLDVQRDTVR; SAEDNLDVQRDTVRE; AEDNLDVQRDTVREK; EDNLDVQRDTVREKI; DNLDVQRDTVREKIQ; NLDVQRDTVREKIQE; LDVQRDTVREKIQED; DVQRDTVREKIQEDI; VQRDTVREKIQEDIN; QRDTVREKIQEDINE; RDTVREKIQEDINEI; DTVREKIQEDINEIN; TVREKIQEDINEINK; VREKIQEDINEINKE; REKIQEDINEINKEK; EKIQEDINEINKEKN; KIQEDINEINKEKNL; IQEDINEINKEKNLP; QEDINEINKEKNLPK; EDINEINKEKNLPKP; DINEINKEKNLPKPG; INEINKEKNLPKPGD; NEINKEKNLPKPGDV; EINKEKNLPKPGDVS; INKEKNLPKPGDVSS; NKEKNLPKPGDVSSP; KEKNLPKPGDVSSPK; EKNLPKPGDVSSPKV; KNLPKPGDVSSPKVD; NLPKPGDVSSPKVDK; LPKPGDVSSPKVDKQ; PKPGDVSSPKVDKQL; KPGDVSSPKVDKQLQ; PGDVSSPKVDKQLQI; GDVSSPKVDKQLQIK; DVSSPKVDKQLQIKE; VSSPKVDKQLQIKES; SSPKVDKQLQIKESL; SPKVDKQLQIKESLE; PKVDKQLQIKESLED; KVDKQLQIKESLEDL; VDKQLQIKESLEDLQ; DKQLQIKESLEDLQE; KQLQIKESLEDLQEQ; QLQIKESLEDLQEQL; LQIKESLEDLQEQLK; QIKESLEDLQEQLKE; IKESLEDLQEQLKEA; KESLEDLQEQLKEAG; ESLEDLQEQLKEAGD; SLEDLQEQLKEAGDE; LEDLQEQLKEAGDEN; EDLQEQLKEAGDENQ; DLQEQLKEAGDENQK; LQEQLKEAGDENQKR; QEQLKEAGDENQKRE; EQLKEAGDENQKREI; QLKEAGDENQKREIE; LKEAGDENQKREIEK; KEAGDENQKREIEKQ; EAGDENQKREIEKQI; AGDENQKREIEKQIE; GDENQKREIEKQIEI; DENQKREIEKQIEIK; ENQKREIEKQIEIKK; NQKREIEKQIEIKKR; QKREIEKQIEIKKRD; KREIEKQIEIKKRDE; REIEKQIEIKKRDEE; EIEKQIEIKKRDEEL; IEKQIEIKKRDEELL; EKQIEIKKRDEELLK; KQIEIKKRDEELLKS; QIEIKKRDEELLKSK; IEIKKRDEELLKSKD; EIKKRDEELLKSKDG; IKKRDEELLKSKDGK; KKRDEELLKSKDGKV; KRDEELLKSKDGKVS; RDEELLKSKDGKVSK; DEELLKSKDGKVSKD; EELLKSKDGKVSKDY; ELLKSKDGKVSKDYE; LLKSKDGKVSKDYEA; LKSKDGKVSKDYEAL; KSKDGKVSKDYEALD; SKDGKVSKDYEALDL; KDGKVSKDYEALDLD; DGKVSKDYEALDLDR; GKVSKDYEALDLDRE; KVSKDYEALDLDREL; VSKDYEALDLDRELS; SKDYEALDLDRELSK; KDYEALDLDRELSKA; DYEALDLDRELSKAS; YEALDLDRELSKASS; EALDLDRELSKASSK; ALDLDRELSKASSKE; LDLDRELSKASSKEK; DLDRELSKASSKEKS; LDRELSKASSKEKSK; DRELSKASSKEKSKV; RELSKASSKEKSKVK; ELSKASSKEKSKVKE; LSKASSKEKSKVKEE; SKASSKEKSKVKEEE; KASSKEKSKVKEEEI; ASSKEKSKVKEEEIT; SSKEKSKVKEEEITK; SKEKSKVKEEEITKG; KEKSKVKEEEITKGK; EKSKVKEEEITKGKS; KSKVKEEEITKGKSR; SKVKEEEITKGKSRA; KVKEEEITKGKSRAS; VKEEEITKGKSRASL; KEEEITKGKSRASLG; EEEITKGKSRASLGD; EEITKGKSRASLGDL; EITKGKSRASLGDLN; ITKGKSRASLGDLNN; TKGKSRASLGDLNND; KGKSRASLGDLNNDK; GKSRASLGDLNNDKN; KSRASLGDLNNDKNL; SRASLGDLNNDKNLM; RASLGDLNNDKNLML; ASLGDLNNDKNLMLP; SLGDLNNDKNLMLPE; LGDLNNDKNLMLPED; GDLNNDKNLMLPEDQ; DLNNDKNLMLPEDQK; LNNDKNLMLPEDQKL; NNDKNLMLPEDQKLP; NDKNLMLPEDQKLPE;

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	VVIKMDSGKAKLQIL; VIKMDSGKAKLQILN; IKMDSGKAKLQILNK; KMDSGKAKLQILNKL; MDSGKAKLQILNKLE; DSGKAKLQILNKLEN; SGKAKLQILNKLENL; GKAKLQILNKLENLK; KAKLQILNKLENLKV; AKLQILNKLENLKVV; KLQILNKLENLKVVS; LQILNKLENLKVVSE; QILNKLENLKVVSES; ILNKLENLKVVSESN; LNKLENLKVVSESNF; NKLENLKVVSESNFE; KLENLKVVSESNFEI; LENLKVVSESNFEIN; ENLKVVSESNFEINK; NLKVVSESNFEINKN; LKVVSESNFEINKNS; KVVSESNFEINKNSS; VVSESNFEINKNSSL; VSESNFEINKNSSLY; SESNFEINKNSSLYV; ESNFEINKNSSLYVD; SNFEINKNSSLYVDS; NFEINKNSSLYVDSK; FEINKNSSLYVDSKM; EINKNSSLYVDSKMI; INKNSSLYVDSKMIL; NKNSSLYVDSKMILA; KNSSLYVDSKMILAA; NSSLYVDSKMILAAV; SSLYVDSKMILAAVR; SLYVDSKMILAAVRD; LYVDSKMILAAVRDK; YVDSKMILAAVRDKD; VDSKMILAAVRDKDD; DSKMILAAVRDKDDS; SKMILAAVRDKDDSN; KMILAAVRDKDDSNA; MILAAVRDKDDSNAW; ILAAVRDKDDSNAWR; LAAVRDKDDSNAWRL; AAVRDKDDSNAWRLA; AVRDKDDSNAWRLAK; VRDKDDSNAWRLAKF; RDKDDSNAWRLAKFS; DKDDSNAWRLAKFSP; KDDSNAWRLAKFSPK; DDSNAWRLAKFSPKN; DSNAWRLAKFSPKNL; SNAWRLAKFSPKNLD; NAWRLAKFSPKNLDE; AWRLAKFSPKNLDEF; WRLAKFSPKNLDEFI; RLAKFSPKNLDEFIL; LAKFSPKNLDEFILS; AKFSPKNLDEFILSE; KFSPKNLDEFILSEN; FSPKNLDEFILSENK; SPKNLDEFILSENKI; PKNLDEFILSENKIL; KNLDEFILSENKILP; NLDEFILSENKILPF; LDEFILSENKILPFT; DEFILSENKILPFTS; EFILSENKILPFTSF; FILSENKILPFTSFS; ILSENKILPFTSFSV; LSENKILPFTSFSVR; SENKILPFTSFSVRK; ENKILPFTSFSVRKN; NKILPFTSFSVRKNF; KILPFTSFSVRKNFI; ILPFTSFSVRKNFIY; LPFTSFSVRKNFIYL; PFTSFSVRKNFIYLQ; FTSFSVRKNFIYLQD; TSFSVRKNFIYLQDE; SFSVRKNFIYLQDEL; FSVRKNFIYLQDELK; SVRKNFIYLQDELKN; VRKNFIYLQDELKNL; RKNFIYLQDELKNLV; KNFIYLQDELKNLVI; NFIYLQDELKNLVIL; FIYLQDELKNLVILD; IYLQDELKNLVILDV; YLQDELKNLVILDVN; LQDELKNLVILDVNT; QDELKNLVILDVNTL; DELKNLVILDVNTLK; ELKNLVILDVNTLKK; LKNLVILDVNTLKKV; KNLVILDVNTLKKVK; 16 mers: MKKMLLIFSFFLIFLN; KKMLLIFSFFLIFLNG; KMLLIFSFFLIFLNGF; MLLIFSFFLIFLNGFP; LLIFSFFLIFLNGFPL; LIFSFFLIFLNGFPLN; IFSFFLIFLNGFPLNA; FSFFLIFLNGFPLNAR; SFFLIFLNGFPLNARK; FFLIFLNGFPLNARKV; FLIFLNGFPLNARKVD; LIFLNGFPLNARKVDK; IFLNGFPLNARKVDKE; FLNGFPLNARKVDKEK; LNGFPLNARKVDKEKL; NGFPLNARKVDKEKLK; GFPLNARKVDKEKLKD; FPLNARKVDKEKLKDF; PLNARKVDKEKLKDFV; LNARKVDKEKLKDFVN; NARKVDKEKLKDFVNM; ARKVDKEKLKDFVNMD; RKVDKEKLKDFVNMDL; KVDKEKLKDFVNMDLE; VDKEKLKDFVNMDLEF; DKEKLKDFVNMDLEFV; KEKLKDFVNMDLEFVN; EKLKDFVNMDLEFVNY; KLKDFVNMDLEFVNYK; LKDFVNMDLEFVNYKG; KDFVNMDLEFVNYKGP; DFVNMDLEFVNYKGPY; FVNMDLEFVNYKGPYD; VNMDLEFVNYKGPYDS; NMDLEFVNYKGPYDST; MDLEFVNYKGPYDSTN; DLEFVNYKGPYDSTNT; LEFVNYKGPYDSTNTY; EFVNYKGPYDSTNTYE; FVNYKGPYDSTNTYEQ; VNYKGPYDSTNTYEQI; NYKGPYDSTNTYEQIV; YKGPYDSTNTYEQIVG; KGPYDSTNTYEQIVGI; GPYDSTNTYEQIVGIG; PYDSTNTYEQIVGIGE; YDSTNTYEQIVGIGEF; DSTNTYEQIVGIGEFL;

	STNTYEQIVGIGEFLA; TNTYEQIVGIGEFLAR; NTYEQIVGIGEFLARP; TYEQIVGIGEFLARPL; YEQIVGIGEFLARPLT; EQIVGIGEFLARPLTN; QIVGIGEFLARPLTNS; IVGIGEFLARPLTNSN; VGIGEFLARPLTNSNS; GIGEFLARPLTNSNSN; IGEFLARPLTNSNSNS; GEFLARPLTNSNSNSS; EFLARPLTNSNSNSSY; FLARPLTNSNSNSSYY; LARPLTNSNSNSSYYG; ARPLTNSNSNSSYYGK; RPLTNSNSNSSYYGKY; PLTNSNSNSSYYGKYF; LTNSNSNSSYYGKYFI; TNSNSNSSYYGKYFIN; NSNSNSSYYGKYFINR; SNSNSSYYGKYFINRF; NSNSSYYGKYFINRFI; SNSSYYGKYFINRFID; NSSYYGKYFINRFIDD; SSYYGKYFINRFIDDQ; SYYGKYFINRFIDDQD; YYGKYFINRFIDDQDK; YGKYFINRFIDDQDKK; GKYFINRFIDDQDKKA; KYFINRFIDDQDKKAS; YFINRFIDDQDKKASV; FINRFIDDQDKKASVD; INRFIDDQDKKASVDV; NRFIDDQDKKASVDVF; RFIDDQDKKASVDVFS; FIDDQDKKASVDVFSI; IDDQDKKASVDVFSIS; DDQDKKASVDVFSISS; DQDKKASVDVFSISSK; QDKKASVDVFSISSKS; DKKASVDVFSISSKSE; KKASVDVFSISSKSEL; KASVDVFSISSKSELD; ASVDVFSISSKSELDS; SVDVFSISSKSELDSI; VDVFSISSKSELDSIL; DVFSISSKSELDSILN; VFSISSKSELDSILNL; FSISSKSELDSILNLR; SISSKSELDSILNLRR; ISSKSELDSILNLRRI; SSKSELDSILNLRRIL; SKSELDSILNLRRILT; KSELDSILNLRRILTG; SELDSILNLRRILTGY; ELDSILNLRRILTGYI; LDSILNLRRILTGYII; DSILNLRRILTGYIIK; SILNLRRILTGYIIKS; ILNLRRILTGYIIKSF; LNLRRILTGYIIKSFD; NLRRILTGYIIKSFDY; LRRILTGYIIKSFDYD; RRILTGYIIKSFDYDR; RILTGYIIKSFDYDRS; ILTGYIIKSFDYDRSS; LTGYIIKSFDYDRSSA; TGYIIKSFDYDRSSAE; GYIIKSFDYDRSSAEL; YIIKSFDYDRSSAELI; IIKSFDYDRSSAELIA; IKSFDYDRSSAELIAK; KSFDYDRSSAELIAKV; SFDYDRSSAELIAKVI; FDYDRSSAELIAKVIT; DYDRSSAELIAKVITI; YDRSSAELIAKVITIY; DRSSAELIAKVITIYN; RSSAELIAKVITIYNA; SSAELIAKVITIYNAV; SAELIAKVITIYNAVY; AELIAKVITIYNAVYR; ELIAKVITIYNAVYRG; LIAKVITIYNAVYRGD; IAKVITIYNAVYRGDL; AKVITIYNAVYRGDLD; KVITIYNAVYRGDLDY; VITIYNAVYRGDLDYY; ITIYNAVYRGDLDYYK; TIYNAVYRGDLDYYKG; IYNAVYRGDLDYYKGF; YNAVYRGDLDYYKGFY; NAVYRGDLDYYKGFYI; AVYRGDLDYYKGFYIE; VYRGDLDYYKGFYIEP; YRGDLDYYKGFYIEPA; RGDLDYYKGFYIEPAL; GDLDYYKGFYIEPALK; DLDYYKGFYIEPALKS; LDYYKGFYIEPALKSL; DYYKGFYIEPALKSLT; YYKGFYIEPALKSLTK; YKGFYIEPALKSLTKE; KGFYIEPALKSLTKEN; GFYIEPALKSLTKENA; FYIEPALKSLTKENAG; YIEPALKSLTKENAGL; IEPALKSLTKENAGLS; EPALKSLTKENAGLSR; PALKSLTKENAGLSRV; ALKSLTKENAGLSRVY; LKSLTKENAGLSRVYS; KSLTKENAGLSRVYSQ; SLTKENAGLSRVYSQW; LTKENAGLSRVYSQWA; TKENAGLSRVYSQWAG; KENAGLSRVYSQWAGK; ENAGLSRVYSQWAGKT; NAGLSRVYSQWAGKTQ; AGLSRVYSQWAGKTQI; GLSRVYSQWAGKTQIF; LSRVYSQWAGKTQIFI; SRVYSQWAGKTQIFIP; RVYSQWAGKTQIFIPL; VYSQWAGKTQIFIPLK; YSQWAGKTQIFIPLKK; SQWAGKTQIFIPLKKD; QWAGKTQIFIPLKKDI; WAGKTQIFIPLKKDIL; AGKTQIFIPLKKDILS; GKTQIFIPLKKDILSG; KTQIFIPLKKDILSGN; TQIFIPLKKDILSGNI; QIFIPLKKDILSGNIE; IFIPLKKDILSGNIES; FIPLKKDILSGNIESD; IPLKKDILSGNIESDI; PLKKDILSGNIESDID; LKKDILSGNIESDIDI; KKDILSGNIESDIDID; KDILSGNIESDIDIDS; DILSGNIESDIDIDSL; ILSGNIESDIDIDSLV; LSGNIESDIDIDSLVT; SGNIESDIDIDSLVTD; GNIESDIDIDSLVTDK; NIESDIDIDSLVTDKV; IESDIDIDSLVTDKVI; ESDIDIDSLVTDKVIA; SDIDIDSLVTDKVIAA; DIDIDSLVTDKVIAAL; IDIDSLVTDKVIAALL;

	DIDSLVTDKVIAALLS; IDSLVTDKVIAALLSE; DSLVTDKVIAALLSEN; SLVTDKVIAALLSENE; LVTDKVIAALLSENEA; VTDKVIAALLSENEAG; TDKVIAALLSENEAGV; DKVIAALLSENEAGVN; KVIAALLSENEAGVNF; VIAALLSENEAGVNFA; IAALLSENEAGVNFAR; AALLSENEAGVNFARD; ALLSENEAGVNFARDI; LLSENEAGVNFARDIT; LSENEAGVNFARDITD; SENEAGVNFARDITDI; ENEAGVNFARDITDIQ; NEAGVNFARDITDIQG; EAGVNFARDITDIQGE; AGVNFARDITDIQGET; GVNFARDITDIQGETH; VNFARDITDIQGETHK; NFARDITDIQGETHKA; FARDITDIQGETHKAD; ARDITDIQGETHKADQ; RDITDIQGETHKADQD; DITDIQGETHKADQDK; ITDIQGETHKADQDKI; TDIQGETHKADQDKID; DIQGETHKADQDKIDT; IQGETHKADQDKIDTE; QGETHKADQDKIDTEL; GETHKADQDKIDTELD; ETHKADQDKIDTELDN; THKADQDKIDTELDNI; HKADQDKIDTELDNIH; KADQDKIDTELDNIHE; ADQDKIDTELDNIHES; DQDKIDTELDNIHESD; QDKIDTELDNIHESDS; DKIDTELDNIHESDSN; KIDTELDNIHESDSNI; IDTELDNIHESDSNIT; DTELDNIHESDSNITE; TELDNIHESDSNITET; ELDNIHESDSNITETI; LDNIHESDSNITETIE; DNIHESDSNITETIEN; NIHESDSNITETIENL; IHESDSNITETIENLR; HESDSNITETIENLRD; ESDSNITETIENLRDQ; SDSNITETIENLRDQL; DSNITETIENLRDQLE; SNITETIENLRDQLEK; NITETIENLRDQLEKA; ITETIENLRDQLEKAT; TETIENLRDQLEKATD; ETIENLRDQLEKATDE; TIENLRDQLEKATDEE; IENLRDQLEKATDEEH; ENLRDQLEKATDEEHK; NLRDQLEKATDEEHKK; LRDQLEKATDEEHKKE; RDQLEKATDEEHKKEI; DQLEKATDEEHKKEIE; QLEKATDEEHKKEIES; LEKATDEEHKKEIESQ; EKATDEEHKKEIESQV; KATDEEHKKEIESQVD; ATDEEHKKEIESQVDA; TDEEHKKEIESQVDAK; DEEHKKEIESQVDAKK; EEHKKEIESQVDAKKK; EHKKEIESQVDAKKKE; HKKEIESQVDAKKKEK; KKEIESQVDAKKKEKE; KEIESQVDAKKKEKEE; EIESQVDAKKKEKEEL; IESQVDAKKKEKEELD; ESQVDAKKKEKEELDK; SQVDAKKKEKEELDKK; QVDAKKKEKEELDKKA; VDAKKKEKEELDKKAI; DAKKKEKEELDKKAIN; AKKKEKEELDKKAINL; KKKEKEELDKKAINLD; KKEKEELDKKAINLDK; KEKEELDKKAINLDKA; EKEELDKKAINLDKAQ; KEELDKKAINLDKAQQ; EELDKKAINLDKAQQK; ELDKKAINLDKAQQKL; LDKKAINLDKAQQKLD; DKKAINLDKAQQKLDS; KKAINLDKAQQKLDSA; KAINLDKAQQKLDSAE; AINLDKAQQKLDSAED; INLDKAQQKLDSAEDN; NLDKAQQKLDSAEDNL; LDKAQQKLDSAEDNLD; DKAQQKLDSAEDNLDV; KAQQKLDSAEDNLDVQ; AQQKLDSAEDNLDVQR; QQKLDSAEDNLDVQRD; QKLDSAEDNLDVQRDT; KLDSAEDNLDVQRDTV; LDSAEDNLDVQRDTVR; DSAEDNLDVQRDTVRE; SAEDNLDVQRDTVREK; AEDNLDVQRDTVREKI; EDNLDVQRDTVREKIQ; DNLDVQRDTVREKIQE; NLDVQRDTVREKIQED; LDVQRDTVREKIQEDI; DVQRDTVREKIQEDIN; VQRDTVREKIQEDINE; QRDTVREKIQEDINEI; RDTVREKIQEDINEIN; DTVREKIQEDINEINK; TVREKIQEDINEINKE; VREKIQEDINEINKEK; REKIQEDINEINKEKN; EKIQEDINEINKEKNL; KIQEDINEINKEKNLP; IQEDINEINKEKNLPK; QEDINEINKEKNLPKP; EDINEINKEKNLPKPG; DINEINKEKNLPKPGD; INEINKEKNLPKPGDV; NEINKEKNLPKPGDVS; EINKEKNLPKPGDVSS; INKEKNLPKPGDVSSP; NKEKNLPKPGDVSSPK; KEKNLPKPGDVSSPKV; EKNLPKPGDVSSPKVD; KNLPKPGDVSSPKVDK; NLPKPGDVSSPKVDKQ; LPKPGDVSSPKVDKQL; PKPGDVSSPKVDKQLQ; KPGDVSSPKVDKQLQI; PGDVSSPKVDKQLQIK; GDVSSPKVDKQLQIKE; DVSSPKVDKQLQIKES; VSSPKVDKQLQIKESL; SSPKVDKQLQIKESLE; SPKVDKQLQIKESLED; PKVDKQLQIKESLEDL; KVDKQLQIKESLEDLQ; VDKQLQIKESLEDLQE; DKQLQIKESLEDLQEQ; KQLQIKESLEDLQEQL; QLQIKESLEDLQEQLK;

	LQIKESLEDLQEQLKE; QIKESLEDLQEQLKEA; IKESLEDLQEQLKEAG; KESLEDLQEQLKEAGD; ESLEDLQEQLKEAGDE; SLEDLQEQLKEAGDEN; LEDLQEQLKEAGDENQ; EDLQEQLKEAGDENQK; DLQEQLKEAGDENQKR; LQEQLKEAGDENQKRE; QEQLKEAGDENQKREI; EQLKEAGDENQKREIE; QLKEAGDENQKREIEK; LKEAGDENQKREIEKQ; KEAGDENQKREIEKQI; EAGDENQKREIEKQIE; AGDENQKREIEKQIEI; GDENQKREIEKQIEIK; DENQKREIEKQIEIKK; ENQKREIEKQIEIKKR; NQKREIEKQIEIKKRD; QKREIEKQIEIKKRDE; KREIEKQIEIKKRDEE; REIEKQIEIKKRDEEL; EIEKQIEIKKRDEELL; IEKQIEIKKRDEELLK; EKQIEIKKRDEELLKS; KQIEIKKRDEELLKSK; QIEIKKRDEELLKSKD; IEIKKRDEELLKSKDG; EIKKRDEELLKSKDGK; IKKRDEELLKSKDGKV; KKRDEELLKSKDGKVS; KRDEELLKSKDGKVSK; RDEELLKSKDGKVSKD; DEELLKSKDGKVSKDY; EELLKSKDGKVSKDYE; ELLKSKDGKVSKDYEA; LLKSKDGKVSKDYEAL; LKSKDGKVSKDYEALD; KSKDGKVSKDYEALDL; SKDGKVSKDYEALDLD; KDGKVSKDYEALDLDR; DGKVSKDYEALDLDRE; GKVSKDYEALDLDREL; KVSKDYEALDLDRELS; VSKDYEALDLDRELSK; SKDYEALDLDRELSKA; KDYEALDLDRELSKAS; DYEALDLDRELSKASS; YEALDLDRELSKASSK; EALDLDRELSKASSKE; ALDLDRELSKASSKEK; LDLDRELSKASSKEKS; DLDRELSKASSKEKSK; LDRELSKASSKEKSKV; DRELSKASSKEKSKVK; RELSKASSKEKSKVKE; ELSKASSKEKSKVKEE; LSKASSKEKSKVKEEE; SKASSKEKSKVKEEEI; KASSKEKSKVKEEEIT; ASSKEKSKVKEEEITK; SSKEKSKVKEEEITKG; SKEKSKVKEEEITKGK; KEKSKVKEEEITKGKS; EKSKVKEEEITKGKSR; KSKVKEEEITKGKSRA; SKVKEEEITKGKSRAS; KVKEEEITKGKSRASL; VKEEEITKGKSRASLG; KEEEITKGKSRASLGD; EEEITKGKSRASLGDL; EEITKGKSRASLGDLN; EITKGKSRASLGDLNN; ITKGKSRASLGDLNND; TKGKSRASLGDLNNDK; KGKSRASLGDLNNDKN; GKSRASLGDLNNDKNL; KSRASLGDLNNDKNLM; SRASLGDLNNDKNLML; RASLGDLNNDKNLMLP; ASLGDLNNDKNLMLPE; SLGDLNNDKNLMLPED; LGDLNNDKNLMLPEDQ; GDLNNDKNLMLPEDQK; DLNNDKNLMLPEDQKL; LNNDKNLMLPEDQKLP; NNDKNLMLPEDQKLPE; NDKNLMLPEDQKLPED; DKNLMLPEDQKLPEDK; KNLMLPEDQKLPEDKK; NLMLPEDQKLPEDKKL; LMLPEDQKLPEDKKLD; MLPEDQKLPEDKKLDS; LPEDQKLPEDKKLDSK; PEDQKLPEDKKLDSKL; EDQKLPEDKKLDSKLD; DQKLPEDKKLDSKLDG; QKLPEDKKLDSKLDGK; KLPEDKKLDSKLDGKK; LPEDKKLDSKLDGKKE; PEDKKLDSKLDGKKEF; EDKKLDSKLDGKKEFK; DKKLDSKLDGKKEFKP; KKLDSKLDGKKEFKPV; KLDSKLDGKKEFKPVS; LDSKLDGKKEFKPVSE; DSKLDGKKEFKPVSEV; SKLDGKKEFKPVSEVE; KLDGKKEFKPVSEVEK; LDGKKEFKPVSEVEKL; DGKKEFKPVSEVEKLD; GKKEFKPVSEVEKLDK; KKEFKPVSEVEKLDKI; KEFKPVSEVEKLDKIS; EFKPVSEVEKLDKISK; FKPVSEVEKLDKISKS; KPVSEVEKLDKISKSN; PVSEVEKLDKISKSNN; VSEVEKLDKISKSNNN; SEVEKLDKISKSNNNE; EVEKLDKISKSNNNEV; VEKLDKISKSNNNEVG; EKLDKISKSNNNEVGK; KLDKISKSNNNEVGKL; LDKISKSNNNEVGKLS; DKISKSNNNEVGKLSP; KISKSNNNEVGKLSPL; ISKSNNNEVGKLSPLD; SKSNNNEVGKLSPLDK; KSNNNEVGKLSPLDKP; SNNNEVGKLSPLDKPS; NNNEVGKLSPLDKPSY; NNEVGKLSPLDKPSYD; NEVGKLSPLDKPSYDD; EVGKLSPLDKPSYDDI; VGKLSPLDKPSYDDID; GKLSPLDKPSYDDIDS; KLSPLDKPSYDDIDSK; LSPLDKPSYDDIDSKE; SPLDKPSYDDIDSKEE; PLDKPSYDDIDSKEEV; LDKPSYDDIDSKEEVD; DKPSYDDIDSKEEVDN; KPSYDDIDSKEEVDNK; PSYDDIDSKEEVDNKA; SYDDIDSKEEVDNKAI; YDDIDSKEEVDNKAIN; DDIDSKEEVDNKAINL; DIDSKEEVDNKAINLQ; IDSKEEVDNKAINLQK; DSKEEVDNKAINLQKI;

	SKEEVDNKAINLQKID; KEEVDNKAINLQKIDP; EEVDNKAINLQKIDPK; EVDNKAINLQKIDPKV; VDNKAINLQKIDPKVK; DNKAINLQKIDPKVKD; NKAINLQKIDPKVKDQ; KAINLQKIDPKVKDQT; AINLQKIDPKVKDQTT; INLQKIDPKVKDQTTS; NLQKIDPKVKDQTTSL; LQKIDPKVKDQTTSLN; QKIDPKVKDQTTSLNE; KIDPKVKDQTTSLNED; IDPKVKDQTTSLNEDL; DPKVKDQTTSLNEDLD; PKVKDQTTSLNEDLDK; KVKDQTTSLNEDLDKD; VKDQTTSLNEDLDKDL; KDQTTSLNEDLDKDLT; DQTTSLNEDLDKDLTT; QTTSLNEDLDKDLTTM; TTSLNEDLDKDLTTMS; TSLNEDLDKDLTTMSI; SLNEDLDKDLTTMSID; LNEDLDKDLTTMSIDS; NEDLDKDLTTMSIDSS; EDLDKDLTTMSIDSSS; DLDKDLTTMSIDSSSP; LDKDLTTMSIDSSSPV; DKDLTTMSIDSSSPVF; KDLTTMSIDSSSPVFL; DLTTMSIDSSSPVFLE; LTTMSIDSSSPVFLEV; TTMSIDSSSPVFLEVI; TMSIDSSSPVFLEVID; MSIDSSSPVFLEVIDP; SIDSSSPVFLEVIDPI; IDSSSPVFLEVIDPIT; DSSSPVFLEVIDPITN; SSSPVFLEVIDPITNL; SSPVFLEVIDPITNLG; SPVFLEVIDPITNLGT; PVFLEVIDPITNLGTL; VFLEVIDPITNLGTLQ; FLEVIDPITNLGTLQL; LEVIDPITNLGTLQLI; EVIDPITNLGTLQLID; VIDPITNLGTLQLIDL; IDPITNLGTLQLIDLN; DPITNLGTLQLIDLNT; PITNLGTLQLIDLNTG; ITNLGTLQLIDLNTGV; TNLGTLQLIDLNTGVR; NLGTLQLIDLNTGVRL; LGTLQLIDLNTGVRLK; GTLQLIDLNTGVRLKE; TLQLIDLNTGVRLKES; LQLIDLNTGVRLKEST; QLIDLNTGVRLKESTQ; LIDLNTGVRLKESTQQ; IDLNTGVRLKESTQQG; DLNTGVRLKESTQQGI; LNTGVRLKESTQQGIQ; NTGVRLKESTQQGIQR; TGVRLKESTQQGIQRY; GVRLKESTQQGIQRYG; VRLKESTQQGIQRYGI; RLKESTQQGIQRYGIY; LKESTQQGIQRYGIYE; KESTQQGIQRYGIYER; ESTQQGIQRYGIYERE; STQQGIQRYGIYEREK; TQQGIQRYGIYEREKD; QQGIQRYGIYEREKDL; QGIQRYGIYEREKDLV; GIQRYGIYEREKDLVV; IQRYGIYEREKDLVVI; QRYGIYEREKDLVVIK; RYGIYEREKDLVVIKM; YGIYEREKDLVVIKMD; GIYEREKDLVVIKMDS; IYEREKDLVVIKMDSG; YEREKDLVVIKMDSGK; EREKDLVVIKMDSGKA; REKDLVVIKMDSGKAK; EKDLVVIKMDSGKAKL; KDLVVIKMDSGKAKLQ; DLVVIKMDSGKAKLQI; LVVIKMDSGKAKLQIL; VVIKMDSGKAKLQILN; VIKMDSGKAKLQILNK; IKMDSGKAKLQILNKL; KMDSGKAKLQILNKLE; MDSGKAKLQILNKLEN; DSGKAKLQILNKLENL; SGKAKLQILNKLENLK; GKAKLQILNKLENLKV; KAKLQILNKLENLKVV; AKLQILNKLENLKVVS; KLQILNKLENLKVVSE; LQILNKLENLKVVSES; QILNKLENLKVVSESN; ILNKLENLKVVSESNF; LNKLENLKVVSESNFE; NKLENLKVVSESNFEI; KLENLKVVSESNFEIN; LENLKVVSESNFEINK; ENLKVVSESNFEINKN; NLKVVSESNFEINKNS; LKVVSESNFEINKNSS; KVVSESNFEINKNSSL; VVSESNFEINKNSSLY; VSESNFEINKNSSLYV; SESNFEINKNSSLYVD; ESNFEINKNSSLYVDS; SNFEINKNSSLYVDSK; NFEINKNSSLYVDSKM; FEINKNSSLYVDSKMI; EINKNSSLYVDSKMIL; INKNSSLYVDSKMILA; NKNSSLYVDSKMILAA; KNSSLYVDSKMILAAV; NSSLYVDSKMILAAVR; SSLYVDSKMILAAVRD; SLYVDSKMILAAVRDK; LYVDSKMILAAVRDKD; YVDSKMILAAVRDKDD; VDSKMILAAVRDKDDS; DSKMILAAVRDKDDSN; SKMILAAVRDKDDSNA; KMILAAVRDKDDSNAW; MILAAVRDKDDSNAWR; ILAAVRDKDDSNAWRL; LAAVRDKDDSNAWRLA; AAVRDKDDSNAWRLAK; AVRDKDDSNAWRLAKF; VRDKDDSNAWRLAKFS; RDKDDSNAWRLAKFSP; DKDDSNAWRLAKFSPK; KDDSNAWRLAKFSPKN; DDSNAWRLAKFSPKNL; DSNAWRLAKFSPKNLD; SNAWRLAKFSPKNLDE; NAWRLAKFSPKNLDEF; AWRLAKFSPKNLDEFI; WRLAKFSPKNLDEFIL; RLAKFSPKNLDEFILS; LAKFSPKNLDEFILSE; AKFSPKNLDEFILSEN; KFSPKNLDEFILSENK; FSPKNLDEFILSENKI; SPKNLDEFILSENKIL;

	PKNLDEFILSENKILP; KNLDEFILSENKILPF; NLDEFILSENKILPFT; LDEFILSENKILPFTS; DEFILSENKILPFTSF; EFILSENKILPFTSFS; FILSENKILPFTSFSV; ILSENKILPFTSFSVR; LSENKILPFTSFSVRK; SENKILPFTSFSVRKN; ENKILPFTSFSVRKNF; NKILPFTSFSVRKNFI; KILPFTSFSVRKNFIY; ILPFTSFSVRKNFIYL; LPFTSFSVRKNFIYLQ; PFTSFSVRKNFIYLQD; FTSFSVRKNFIYLQDE; TSFSVRKNFIYLQDEL; SFSVRKNFIYLQDELK; FSVRKNFIYLQDELKN; SVRKNFIYLQDELKNL; VRKNFIYLQDELKNLV; RKNFIYLQDELKNLVI; KNFIYLQDELKNLVIL; NFIYLQDELKNLVILD; FIYLQDELKNLVILDV; IYLQDELKNLVILDVN; YLQDELKNLVILDVNT; LQDELKNLVILDVNTL; QDELKNLVILDVNTLK; DELKNLVILDVNTLKK; ELKNLVILDVNTLKKV; LKNLVILDVNTLKKVK;
Seq 27	13 mers: MKYILSIDQGTTS; KYILSIDQGTTSS; YILSIDQGTTSSR; ILSIDQGTTSSRA; LSIDQGTTSSRAM; SIDQGTTSSRAMV; IDQGTTSSRAMVF; DQGTTSSRAMVFD; QGTTSSRAMVFDK; GTTSSRAMVFDKN; TTSSRAMVFDKNA; TSSRAMVFDKNAN; SSRAMVFDKNANI; SRAMVFDKNANIK; RAMVFDKNANIKG; AMVFDKNANIKGF; MVFDKNANIKGFA; VFDKNANIKGFAQ; FDKNANIKGFAQK; DKNANIKGFAQKE; KNANIKGFAQKEF; NANIKGFAQKEFT; ANIKGFAQKEFTQ; NIKGFAQKEFTQI; IKGFAQKEFTQIY; KGFAQKEFTQIYP; GFAQKEFTQIYPQ; FAQKEFTQIYPQP; AQKEFTQIYPQPS; QKEFTQIYPQPSW; KEFTQIYPQPSWV; EFTQIYPQPSWVE; FTQIYPQPSWVEH; TQIYPQPSWVEHD; QIYPQPSWVEHDP; IYPQPSWVEHDPT; YPQPSWVEHDPTE; PQPSWVEHDPTEI; QPSWVEHDPTEIW; PSWVEHDPTEIWG; SWVEHDPTEIWGS; WVEHDPTEIWGSQ; VEHDPTEIWGSQL; EHDPTEIWGSQLG; HDPTEIWGSQLGV; DPTEIWGSQLGVI; PTEIWGSQLGVIT; TEIWGSQLGVITE; EIWGSQLGVITEA; IWGSQLGVITEAM; WGSQLGVITEAMA; GSQLGVITEAMAN; SQLGVITEAMANA; QLGVITEAMANAR; LGVITEAMANARI; GVITEAMANARIL; VITEAMANARILP; ITEAMANARILPN; TEAMANARILPNE; EAMANARILPNEI; AMANARILPNEID; MANARILPNEIDA; ANARILPNEIDAI; NARILPNEIDAIG; ARILPNEIDAIGI; RILPNEIDAIGIT; ILPNEIDAIGITN; LPNEIDAIGITNQ; PNEIDAIGITNQR; NEIDAIGITNQRE; EIDAIGITNQRET; IDAIGITNQRETT; DAIGITNQRETTV; AIGITNQRETTVI; IGITNQRETTVIW; GITNQRETTVIWE; ITNQRETTVIWEK; TNQRETTVIWEKN; NQRETTVIWEKNT; QRETTVIWEKNTG; RETTVIWEKNTGK; ETTVIWEKNTGKP; TTVIWEKNTGKPI; TVIWEKNTGKPIY; VIWEKNTGKPIYN; IWEKNTGKPIYNA; WEKNTGKPIYNAI; EKNTGKPIYNAIV; KNTGKPIYNAIVW; NTGKPIYNAIVWQ; TGKPIYNAIVWQD; GKPIYNAIVWQDR; KPIYNAIVWQDRR; PIYNAIVWQDRRT; IYNAIVWQDRRTA; YNAIVWQDRRTAK; NAIVWQDRRTAKI; AIVWQDRRTAKIC; IVWQDRRTAKICD; VWQDRRTAKICDQ; WQDRRTAKICDQL; QDRRTAKICDQLK; DRRTAKICDQLKK; RRTAKICDQLKKE; RTAKICDQLKKEG; TAKICDQLKKEGK; AKICDQLKKEGKD; KICDQLKKEGKDK; ICDQLKKEGKDKI; CDQLKKEGKDKII; DQLKKEGKDKIIL;

	QLKKEGKDKIILE; LKKEGKDKIILEK; KKEGKDKIILEKT; KEGKDKIILEKTG; EGKDKIILEKTGL; GKDKIILEKTGLV; KDKIILEKTGLVL; DKIILEKTGLVLD; KIILEKTGLVLDS; IILEKTGLVLDSY; ILEKTGLVLDSYF; LEKTGLVLDSYFS; EKTGLVLDSYFSG; KTGLVLDSYFSGT; TGLVLDSYFSGTK; GLVLDSYFSGTKI; LVLDSYFSGTKIM; VLDSYFSGTKIMW; LDSYFSGTKIMWI; DSYFSGTKIMWIL; SYFSGTKIMWILD; YFSGTKIMWILDN; FSGTKIMWILDNV; SGTKIMWILDNVE; GTKIMWILDNVEG; TKIMWILDNVEGA; KIMWILDNVEGAR; IMWILDNVEGARQ; MWILDNVEGARQR; WILDNVEGARQRA; ILDNVEGARQRAE; LDNVEGARQRAEN; DNVEGARQRAENG; NVEGARQRAENGE; VEGARQRAENGEL; EGARQRAENGELC; GARQRAENGELCF; ARQRAENGELCFG; RQRAENGELCFGT; QRAENGELCFGTI; RAENGELCFGTID; AENGELCFGTIDT; ENGELCFGTIDTW; NGELCFGTIDTWI; GELCFGTIDTWIL; ELCFGTIDTWILW; LCFGTIDTWILWN; CFGTIDTWILWNL; FGTIDTWILWNLT; GTIDTWILWNLTQ; TIDTWILWNLTQK; IDTWILWNLTQKK; DTWILWNLTQKKE; TWILWNLTQKKEH; WILWNLTQKKEHA; ILWNLTQKKEHAT; LWNLTQKKEHATD; WNLTQKKEHATDY; NLTQKKEHATDYS; LTQKKEHATDYSN; TQKKEHATDYSNA; QKKEHATDYSNAS; KKEHATDYSNASR; KEHATDYSNASRT; EHATDYSNASRTL; HATDYSNASRTLL; ATDYSNASRTLLL; TDYSNASRTLLLN; DYSNASRTLLLNI; YSNASRTLLLNIK; SNASRTLLLNIKT; NASRTLLLNIKTL; ASRTLLLNIKTLE; SRTLLLNIKTLEW; RTLLLNIKTLEWD; TLLLNIKTLEWDD; LLLNIKTLEWDDE; LLNIKTLEWDDEL; LNIKTLEWDDELL; NIKTLEWDDELLS; IKTLEWDDELLSI; KTLEWDDELLSIL; TLEWDDELLSILN; LEWDDELLSILNV; EWDDELLSILNVP; WDDELLSILNVPR; DDELLSILNVPRA; DELLSILNVPRAI; ELLSILNVPRAIL; LLSILNVPRAILP; LSILNVPRAILPE; SILNVPRAILPEL; ILNVPRAILPELK; LNVPRAILPELKE; NVPRAILPELKES; VPRAILPELKESS; PRAILPELKESST; RAILPELKESSTI; AILPELKESSTIY; ILPELKESSTIYG; LPELKESSTIYGK; PELKESSTIYGKT; ELKESSTIYGKTD; LKESSTIYGKTDK; KESSTIYGKTDKA; ESSTIYGKTDKAL; SSTIYGKTDKALF; STIYGKTDKALFG; TIYGKTDKALFGA; IYGKTDKALFGAE; YGKTDKALFGAEI; GKTDKALFGAEIP; KTDKALFGAEIPI; TDKALFGAEIPIA; DKALFGAEIPIAG; KALFGAEIPIAGI; ALFGAEIPIAGIA; LFGAEIPIAGIAG; FGAEIPIAGIAGD; GAEIPIAGIAGDQ; AEIPIAGIAGDQF; EIPIAGIAGDQFA; IPIAGIAGDQFAA; PIAGIAGDQFAAT; IAGIAGDQFAATF; AGIAGDQFAATFG; GIAGDQFAATFGQ; IAGDQFAATFGQA; AGDQFAATFGQAC; GDQFAATFGQACL; DQFAATFGQACLK; QFAATFGQACLKK; FAATFGQACLKKG; AATFGQACLKKGM; ATFGQACLKKGMA; TFGQACLKKGMAK; FGQACLKKGMAKN; GQACLKKGMAKNT; QACLKKGMAKNTY; ACLKKGMAKNTYG; CLKKGMAKNTYGT; LKKGMAKNTYGTG; KKGMAKNTYGTGC; KGMAKNTYGTGCF; GMAKNTYGTGCFL; MAKNTYGTGCFLT; AKNTYGTGCFLTV; KNTYGTGCFLTVN; NTYGTGCFLTVNI; TYGTGCFLTVNIG; YGTGCFLTVNIGK; GTGCFLTVNIGKE; TGCFLTVNIGKEP;

	GCFLTVNIGKEPI; CFLTVNIGKEPII; FLTVNIGKEPIIS; LTVNIGKEPIISH; TVNIGKEPIISHD; VNIGKEPIISHDK; NIGKEPIISHDKL; IGKEPIISHDKLL; GKEPIISHDKLLT; KEPIISHDKLLTS; EPIISHDKLLTSI; PIISHDKLLTSIA; IISHDKLLTSIAW; ISHDKLLTSIAWG; SHDKLLTSIAWGR; HDKLLTSIAWGRK; DKLLTSIAWGRKK; KLLTSIAWGRKKS; LLTSIAWGRKKSV; LTSIAWGRKKSVT; TSIAWGRKKSVTY; SIAWGRKKSVTYV; IAWGRKKSVTYVL; AWGRKKSVTYVLE; WGRKKSVTYVLEG; GRKKSVTYVLEGS; RKKSVTYVLEGSV; KKSVTYVLEGSVF; KSVTYVLEGSVFI; SVTYVLEGSVFIG; VTYVLEGSVFIGG; TYVLEGSVFIGGA; YVLEGSVFIGGAV; VLEGSVFIGGAVI; LEGSVFIGGAVIQ; EGSVFIGGAVIQW; GSVFIGGAVIQWL; SVFIGGAVIQWLR; VFIGGAVIQWLRD; FIGGAVIQWLRDG; IGGAVIQWLRDGL; GGAVIQWLRDGLE; GAVIQWLRDGLEF; AVIQWLRDGLEFF; VIQWLRDGLEFFR; IQWLRDGLEFFRK; QWLRDGLEFFRKS; WLRDGLEFFRKSS; LRDGLEFFRKSSD; RDGLEFFRKSSDA; DGLEFFRKSSDAE; GLEFFRKSSDAEA; LEFFRKSSDAEAL; EFFRKSSDAEALA; FFRKSSDAEALAS; FRKSSDAEALASS; RKSSDAEALASSV; KSSDAEALASSVS; SSDAEALASSVSD; SDAEALASSVSDN; DAEALASSVSDNG; AEALASSVSDNGG; EALASSVSDNGGV; ALASSVSDNGGVY; LASSVSDNGGVYF; ASSVSDNGGVYFV; SSVSDNGGVYFVP; SVSDNGGVYFVPA; VSDNGGVYFVPAF; SDNGGVYFVPAFV; DNGGVYFVPAFVG; NGGVYFVPAFVGL; GGVYFVPAFVGLG; GVYFVPAFVGLGA; VYFVPAFVGLGAP; YFVPAFVGLGAPH; FVPAFVGLGAPHW; VPAFVGLGAPHWD; PAFVGLGAPHWDS; AFVGLGAPHWDSY; FVGLGAPHWDSYA; VGLGAPHWDSYAR; GLGAPHWDSYARG; LGAPHWDSYARGT; GAPHWDSYARGTI; APHWDSYARGTII; PHWDSYARGTIIG; HWDSYARGTIIGI; WDSYARGTIIGIT; DSYARGTIIGITR; SYARGTIIGITRG; YARGTIIGITRGS; ARGTIIGITRGST; RGTIIGITRGSTK; GTIIGITRGSTKA; TIIGITRGSTKAH; IIGITRGSTKAHI; IGITRGSTKAHIT; GITRGSTKAHITR; ITRGSTKAHITRA; TRGSTKAHITRAA; RGSTKAHITRAAL; GSTKAHITRAALE; STKAHITRAALES; TKAHITRAALESI; KAHITRAALESIA; AHITRAALESIAF; HITRAALESIAFQ; ITRAALESIAFQS; TRAALESIAFQSF; RAALESIAFQSFD; AALESIAFQSFDI; ALESIAFQSFDIL; LESIAFQSFDILN; ESIAFQSFDILNT; SIAFQSFDILNTM; IAFQSFDILNTMK; AFQSFDILNTMKK; FQSFDILNTMKKS; QSFDILNTMKKSI; SFDILNTMKKSIP; FDILNTMKKSIPN; DILNTMKKSIPNF; ILNTMKKSIPNFE; LNTMKKSIPNFEI; NTMKKSIPNFEIQ; TMKKSIPNFEIQE; MKKSIPNFEIQEL; KKSIPNFEIQELR; KSIPNFEIQELRV; SIPNFEIQELRVD; IPNFEIQELRVDG; PNFEIQELRVDGG; NFEIQELRVDGGA; FEIQELRVDGGAS; EIQELRVDGGASQ; IQELRVDGGASQN; QELRVDGGASQNN; ELRVDGGASQNNL; LRVDGGASQNNLL; RVDGGASQNNLLM; VDGGASQNNLLMQ; DGGASQNNLLMQF; GGASQNNLLMQFQ; GASQNNLLMQFQA; ASQNNLLMQFQAD; SQNNLLMQFQADL; QNNLLMQFQADLL; NNLLMQFQADLLE; NLLMQFQADLLEC; LLMQFQADLLECK; LMQFQADLLECKV; MQFQADLLECKVV;

	QFQADLLECKVVR; FQADLLECKVVRP; QADLLECKVVRPK; ADLLECKVVRPKI; DLLECKVVRPKIT; LLECKVVRPKITE; LECKVVRPKITET; ECKVVRPKITETT; CKVVRPKITETTA; KVVRPKITETTAL; VVRPKITETTALG; VRPKITETTALGA; RPKITETTALGAA; PKITETTALGAAY; KITETTALGAAYL; ITETTALGAAYLA; TETTALGAAYLAG; ETTALGAAYLAGL; TTALGAAYLAGLA; TALGAAYLAGLAT; ALGAAYLAGLATG; LGAAYLAGLATGY; GAAYLAGLATGYW; AAYLAGLATGYWQ; AYLAGLATGYWQS; YLAGLATGYWQSA; LAGLATGYWQSAE; AGLATGYWQSAEE; GLATGYWQSAEEI; LATGYWQSAEEIV; ATGYWQSAEEIVS; TGYWQSAEEIVSL; GYWQSAEEIVSLW; YWQSAEEIVSLWQ; WQSAEEIVSLWQV; QSAEEIVSLWQVD; SAEEIVSLWQVDK; AEEIVSLWQVDKI; EEIVSLWQVDKIF; EIVSLWQVDKIFE; IVSLWQVDKIFEP; VSLWQVDKIFEPS; SLWQVDKIFEPSM; LWQVDKIFEPSMP; WQVDKIFEPSMPK; QVDKIFEPSMPKN; VDKIFEPSMPKNQ; DKIFEPSMPKNQK; KIFEPSMPKNQKE; IFEPSMPKNQKEK; FEPSMPKNQKEKL; EPSMPKNQKEKLL; PSMPKNQKEKLLE; SMPKNQKEKLLEN; MPKNQKEKLLENW; PKNQKEKLLENWN; KNQKEKLLENWNK; NQKEKLLENWNKA; QKEKLLENWNKAV; KEKLLENWNKAVG; EKLLENWNKAVGK; KLLENWNKAVGKA; LLENWNKAVGKAK; LENWNKAVGKAKS; ENWNKAVGKAKSW; NWNKAVGKAKSWI; WNKAVGKAKSWIQ; NKAVGKAKSWIQN; KAVGKAKSWIQNS; AVGKAKSWIQNSH; VGKAKSWIQNSHS; GKAKSWIQNSHSS; 14 mers: MKYILSIDQGTTSS; KYILSIDQGTTSSR; YILSIDQGTTSSRA; ILSIDQGTTSSRAM; LSIDQGTTSSRAMV; SIDQGTTSSRAMVF; IDQGTTSSRAMVFD; DQGTTSSRAMVFDK; QGTTSSRAMVFDKN; GTTSSRAMVFDKNA; TTSSRAMVFDKNAN; TSSRAMVFDKNANI; SSRAMVFDKNANIK; SRAMVFDKNANIKG; RAMVFDKNANIKGF; AMVFDKNANIKGFA; MVFDKNANIKGFAQ; VFDKNANIKGFAQK; FDKNANIKGFAQKE; DKNANIKGFAQKEF; KNANIKGFAQKEFT; NANIKGFAQKEFTQ; ANIKGFAQKEFTQI; NIKGFAQKEFTQIY; IKGFAQKEFTQIYP; KGFAQKEFTQIYPQ; GFAQKEFTQIYPQP; FAQKEFTQIYPQPS; AQKEFTQIYPQPSW; QKEFTQIYPQPSWV; KEFTQIYPQPSWVE; EFTQIYPQPSWVEH; FTQIYPQPSWVEHD; TQIYPQPSWVEHDP; QIYPQPSWVEHDPT; IYPQPSWVEHDPTE; YPQPSWVEHDPTEI; PQPSWVEHDPTEIW; QPSWVEHDPTEIWG; PSWVEHDPTEIWGS; SWVEHDPTEIWGSQ; WVEHDPTEIWGSQL; VEHDPTEIWGSQLG; EHDPTEIWGSQLGV; HDPTEIWGSQLGVI; DPTEIWGSQLGVIT; PTEIWGSQLGVITE; TEIWGSQLGVITEA; EIWGSQLGVITEAM; IWGSQLGVITEAMA; WGSQLGVITEAMAN; GSQLGVITEAMANA; SQLGVITEAMANAR; QLGVITEAMANARI; LGVITEAMANARIL; GVITEAMANARILP; VITEAMANARILPN; ITEAMANARILPNE; TEAMANARILPNEI; EAMANARILPNEID; AMANARILPNEIDA; MANARILPNEIDAI; ANARILPNEIDAIG; NARILPNEIDAIGI; ARILPNEIDAIGIT; RILPNEIDAIGITN; ILPNEIDAIGITNQ; LPNEIDAIGITNQR; PNEIDAIGITNQRE; NEIDAIGITNQRET; EIDAIGITNQRETT; IDAIGITNQRETTV; DAIGITNQRETTVI; AIGITNQRETTVIW; IGITNQRETTVIWE;

	GITNQRETTVIWEK; ITNQRETTVIWEKN; TNQRETTVIWEKNT; NQRETTVIWEKNTG; QRETTVIWEKNTGK; RETTVIWEKNTGKP; ETTVIWEKNTGKPI; TTVIWEKNTGKPIY; TVIWEKNTGKPIYN; VIWEKNTGKPIYNA; IWEKNTGKPIYNAI; WEKNTGKPIYNAIV; EKNTGKPIYNAIVW; KNTGKPIYNAIVWQ; NTGKPIYNAIVWQD; TGKPIYNAIVWQDR; GKPIYNAIVWQDRR; KPIYNAIVWQDRRT; PIYNAIVWQDRRTA; IYNAIVWQDRRTAK; YNAIVWQDRRTAKI; NAIVWQDRRTAKIC; AIVWQDRRTAKICD; IVWQDRRTAKICDQ; VWQDRRTAKICDQL; WQDRRTAKICDQLK; QDRRTAKICDQLKK; DRRTAKICDQLKKE; RRTAKICDQLKKEG; RTAKICDQLKKEGK; TAKICDQLKKEGKD; AKICDQLKKEGKDK; KICDQLKKEGKDKI; ICDQLKKEGKDKII; CDQLKKEGKDKIIL; DQLKKEGKDKIILE; QLKKEGKDKIILEK; LKKEGKDKIILEKT; KKEGKDKIILEKTG; KEGKDKIILEKTGL; EGKDKIILEKTGLV; GKDKIILEKTGLVL; KDKIILEKTGLVLD; DKIILEKTGLVLDS; KIILEKTGLVLDSY; IILEKTGLVLDSYF; ILEKTGLVLDSYFS; LEKTGLVLDSYFSG; EKTGLVLDSYFSGT; KTGLVLDSYFSGTK; TGLVLDSYFSGTKI; GLVLDSYFSGTKIM; LVLDSYFSGTKIMW; VLDSYFSGTKIMWI; LDSYFSGTKIMWIL; DSYFSGTKIMWILD; SYFSGTKIMWILDN; YFSGTKIMWILDNV; FSGTKIMWILDNVE; SGTKIMWILDNVEG; GTKIMWILDNVEGA; TKIMWILDNVEGAR; KIMWILDNVEGARQ; IMWILDNVEGARQR; MWILDNVEGARQRA; WILDNVEGARQRAE; ILDNVEGARQRAEN; LDNVEGARQRAENG; DNVEGARQRAENGE; NVEGARQRAENGEL; VEGARQRAENGELC; EGARQRAENGELCF; GARQRAENGELCFG; ARQRAENGELCFGT; RQRAENGELCFGTI; QRAENGELCFGTID; RAENGELCFGTIDT; AENGELCFGTIDTW; ENGELCFGTIDTWI; NGELCFGTIDTWIL; GELCFGTIDTWILW; ELCFGTIDTWILWN; LCFGTIDTWILWNL; CFGTIDTWILWNLT; FGTIDTWILWNLTQ; GTIDTWILWNLTQK; TIDTWILWNLTQKK; IDTWILWNLTQKKE; DTWILWNLTQKKEH; TWILWNLTQKKEHA; WILWNLTQKKEHAT; ILWNLTQKKEHATD; LWNLTQKKEHATDY; WNLTQKKEHATDYS; NLTQKKEHATDYSN; LTQKKEHATDYSNA; TQKKEHATDYSNAS; QKKEHATDYSNASR; KKEHATDYSNASRT; KEHATDYSNASRTL; EHATDYSNASRTLL; HATDYSNASRTLLL; ATDYSNASRTLLLN; TDYSNASRTLLLNI; DYSNASRTLLLNIK; YSNASRTLLLNIKT; SNASRTLLLNIKTL; NASRTLLLNIKTLE; ASRTLLLNIKTLEW; SRTLLLNIKTLEWD; RTLLLNIKTLEWDD; TLLLNIKTLEWDDE; LLLNIKTLEWDDEL; LLNIKTLEWDDELL; LNIKTLEWDDELLS; NIKTLEWDDELLSI; IKTLEWDDELLSIL; KTLEWDDELLSILN; TLEWDDELLSILNV; LEWDDELLSILNVP; EWDDELLSILNVPR; WDDELLSILNVPRA; DDELLSILNVPRAI; DELLSILNVPRAIL; ELLSILNVPRAILP; LLSILNVPRAILPE; LSILNVPRAILPEL; SILNVPRAILPELK; ILNVPRAILPELKE; LNVPRAILPELKES; NVPRAILPELKESS; VPRAILPELKESST; PRAILPELKESSTI; RAILPELKESSTIY; AILPELKESSTIYG; ILPELKESSTIYGK; LPELKESSTIYGKT; PELKESSTIYGKTD; ELKESSTIYGKTDK; LKESSTIYGKTDKA; KESSTIYGKTDKAL; ESSTIYGKTDKALF; SSTIYGKTDKALFG; STIYGKTDKALFGA; TIYGKTDKALFGAE; IYGKTDKALFGAEI; YGKTDKALFGAEIP; GKTDKALFGAEIPI; KTDKALFGAEIPIA; TDKALFGAEIPIAG; DKALFGAEIPIAGI; KALFGAEIPIAGIA; ALFGAEIPIAGIAG;

	LFGAEIPIAGIAGD; FGAEIPIAGIAGDQ; GAEIPIAGIAGDQF; AEIPIAGIAGDQFA; EIPIAGIAGDQFAA; IPIAGIAGDQFAAT; PIAGIAGDQFAATF; IAGIAGDQFAATFG; AGIAGDQFAATFGQ; GIAGDQFAATFGQA; IAGDQFAATFGQAC; AGDQFAATFGQACL; GDQFAATFGQACLK; DQFAATFGQACLKK; QFAATFGQACLKKG; FAATFGQACLKKGM; AATFGQACLKKGMA; ATFGQACLKKGMAK; TFGQACLKKGMAKN; FGQACLKKGMAKNT; GQACLKKGMAKNTY; QACLKKGMAKNTYG; ACLKKGMAKNTYGT; CLKKGMAKNTYGTG; LKKGMAKNTYGTGC; KKGMAKNTYGTGCF; KGMAKNTYGTGCFL; GMAKNTYGTGCFLT; MAKNTYGTGCFLTV; AKNTYGTGCFLTVN; KNTYGTGCFLTVNI; NTYGTGCFLTVNIG; TYGTGCFLTVNIGK; YGTGCFLTVNIGKE; GTGCFLTVNIGKEP; TGCFLTVNIGKEPI; GCFLTVNIGKEPII; CFLTVNIGKEPIIS; FLTVNIGKEPIISH; LTVNIGKEPIISHD; TVNIGKEPIISHDK; VNIGKEPIISHDKL; NIGKEPIISHDKLL; IGKEPIISHDKLLT; GKEPIISHDKLLTS; KEPIISHDKLLTSI; EPIISHDKLLTSIA; PIISHDKLLTSIAW; IISHDKLLTSIAWG; ISHDKLLTSIAWGR; SHDKLLTSIAWGRK; HDKLLTSIAWGRKK; DKLLTSIAWGRKKS; KLLTSIAWGRKKSV; LLTSIAWGRKKSVT; LTSIAWGRKKSVTY; TSIAWGRKKSVTYV; SIAWGRKKSVTYVL; IAWGRKKSVTYVLE; AWGRKKSVTYVLEG; WGRKKSVTYVLEGS; GRKKSVTYVLEGSV; RKKSVTYVLEGSVF; KKSVTYVLEGSVFI; KSVTYVLEGSVFIG; SVTYVLEGSVFIGG; VTYVLEGSVFIGGA; TYVLEGSVFIGGAV; YVLEGSVFIGGAVI; VLEGSVFIGGAVIQ; LEGSVFIGGAVIQW; EGSVFIGGAVIQWL; GSVFIGGAVIQWLR; SVFIGGAVIQWLRD; VFIGGAVIQWLRDG; FIGGAVIQWLRDGL; IGGAVIQWLRDGLE; GGAVIQWLRDGLEF; GAVIQWLRDGLEFF; AVIQWLRDGLEFFR; VIQWLRDGLEFFRK; IQWLRDGLEFFRKS; QWLRDGLEFFRKSS; WLRDGLEFFRKSSD; LRDGLEFFRKSSDA; RDGLEFFRKSSDAE; DGLEFFRKSSDAEA; GLEFFRKSSDAEAL; LEFFRKSSDAEALA; EFFRKSSDAEALAS; FFRKSSDAEALASS; FRKSSDAEALASSV; RKSSDAEALASSVS; KSSDAEALASSVSD; SSDAEALASSVSDN; SDAEALASSVSDNG; DAEALASSVSDNGG; AEALASSVSDNGGV; EALASSVSDNGGVY; ALASSVSDNGGVYF; LASSVSDNGGVYFV; ASSVSDNGGVYFVP; SSVSDNGGVYFVPA; SVSDNGGVYFVPAF; VSDNGGVYFVPAFV; SDNGGVYFVPAFVG; DNGGVYFVPAFVGL; NGGVYFVPAFVGLG; GGVYFVPAFVGLGA; GVYFVPAFVGLGAP; VYFVPAFVGLGAPH; YFVPAFVGLGAPHW; FVPAFVGLGAPHWD; VPAFVGLGAPHWDS; PAFVGLGAPHWDSY; AFVGLGAPHWDSYA; FVGLGAPHWDSYAR; VGLGAPHWDSYARG; GLGAPHWDSYARGT; LGAPHWDSYARGTI; GAPHWDSYARGTII; APHWDSYARGTIIG; PHWDSYARGTIIGI; HWDSYARGTIIGIT; WDSYARGTIIGITR; DSYARGTIIGITRG; SYARGTIIGITRGS; YARGTIIGITRGST; ARGTIIGITRGSTK; RGTIIGITRGSTKA; GTIIGITRGSTKAH; TIIGITRGSTKAHI; IIGITRGSTKAHIT; IGITRGSTKAHITR; GITRGSTKAHITRA; ITRGSTKAHITRAA; TRGSTKAHITRAAL; RGSTKAHITRAALE; GSTKAHITRAALES; STKAHITRAALESI; TKAHITRAALESIA; KAHITRAALESIAF; AHITRAALESIAFQ; HITRAALESIAFQS; ITRAALESIAFQSF; TRAALESIAFQSFD; RAALESIAFQSFDI; AALESIAFQSFDIL; ALESIAFQSFDILN; LESIAFQSFDILNT; ESIAFQSFDILNTM; SIAFQSFDILNTMK; IAFQSFDILNTMKK;

	AFQSFDILNTMKKS; FQSFDILNTMKKSI; QSFDILNTMKKSIP; SFDILNTMKKSIPN; FDILNTMKKSIPNF; DILNTMKKSIPNFE; ILNTMKKSIPNFEI; LNTMKKSIPNFEIQ; NTMKKSIPNFEIQE; TMKKSIPNFEIQEL; MKKSIPNFEIQELR; KKSIPNFEIQELRV; KSIPNFEIQELRVD; SIPNFEIQELRVDG; IPNFEIQELRVDGG; PNFEIQELRVDGGA; NFEIQELRVDGGAS; FEIQELRVDGGASQ; EIQELRVDGGASQN; IQELRVDGGASQNN; QELRVDGGASQNNL; ELRVDGGASQNNLL; LRVDGGASQNNLLM; RVDGGASQNNLLMQ; VDGGASQNNLLMQF; DGGASQNNLLMQFQ; GGASQNNLLMQFQA; GASQNNLLMQFQAD; ASQNNLLMQFQADL; SQNNLLMQFQADLL; QNNLLMQFQADLLE; NNLLMQFQADLLEC; NLLMQFQADLLECK; LLMQFQADLLECKV; LMQFQADLLECKVV; MQFQADLLECKVVR; QFQADLLECKVVRP; FQADLLECKVVRPK; QADLLECKVVRPKI; ADLLECKVVRPKIT; DLLECKVVRPKITE; LLECKVVRPKITET; LECKVVRPKITETT; ECKVVRPKITETTA; CKVVRPKITETTAL; KVVRPKITETTALG; VVRPKITETTALGA; VRPKITETTALGAA; RPKITETTALGAAY; PKITETTALGAAYL; KITETTALGAAYLA; ITETTALGAAYLAG; TETTALGAAYLAGL; ETTALGAAYLAGLA; TTALGAAYLAGLAT; TALGAAYLAGLATG; ALGAAYLAGLATGY; LGAAYLAGLATGYW; GAAYLAGLATGYWQ; AAYLAGLATGYWQS; AYLAGLATGYWQSA; YLAGLATGYWQSAE; LAGLATGYWQSAEE; AGLATGYWQSAEEI; GLATGYWQSAEEIV; LATGYWQSAEEIVS; ATGYWQSAEEIVSL; TGYWQSAEEIVSLW; GYWQSAEEIVSLWQ; YWQSAEEIVSLWQV; WQSAEEIVSLWQVD; QSAEEIVSLWQVDK; SAEEIVSLWQVDKI; AEEIVSLWQVDKIF; EEIVSLWQVDKIFE; EIVSLWQVDKIFEP; IVSLWQVDKIFEPS; VSLWQVDKIFEPSM; SLWQVDKIFEPSMP; LWQVDKIFEPSMPK; WQVDKIFEPSMPKN; QVDKIFEPSMPKNQ; VDKIFEPSMPKNQK; DKIFEPSMPKNQKE; KIFEPSMPKNQKEK; IFEPSMPKNQKEKL; FEPSMPKNQKEKLL; EPSMPKNQKEKLLE; PSMPKNQKEKLLEN; SMPKNQKEKLLENW; MPKNQKEKLLENWN; PKNQKEKLLENWNK; KNQKEKLLENWNKA; NQKEKLLENWNKAV; QKEKLLENWNKAVG; KEKLLENWNKAVGK; EKLLENWNKAVGKA; KLLENWNKAVGKAK; LLENWNKAVGKAKS; LENWNKAVGKAKSW; ENWNKAVGKAKSWI; NWNKAVGKAKSWIQ; WNKAVGKAKSWIQN; NKAVGKAKSWIQNS; KAVGKAKSWIQNSH; AVGKAKSWIQNSHS; VGKAKSWIQNSHSS; 15 mers: MKYILSIDQGTTSSR; KYILSIDQGTTSSRA; YILSIDQGTTSSRAM; ILSIDQGTTSSRAMV; LSIDQGTTSSRAMVF; SIDQGTTSSRAMVFD; IDQGTTSSRAMVFDK; DQGTTSSRAMVFDKN; QGTTSSRAMVFDKNA; GTTSSRAMVFDKNAN; TTSSRAMVFDKNANI; TSSRAMVFDKNANIK; SSRAMVFDKNANIKG; SRAMVFDKNANIKGF; RAMVFDKNANIKGFA; AMVFDKNANIKGFAQ; MVFDKNANIKGFAQK; VFDKNANIKGFAQKE; FDKNANIKGFAQKEF; DKNANIKGFAQKEFT; KNANIKGFAQKEFTQ; NANIKGFAQKEFTQI; ANIKGFAQKEFTQIY; NIKGFAQKEFTQIYP; IKGFAQKEFTQIYPQ; KGFAQKEFTQIYPQP; GFAQKEFTQIYPQPS; FAQKEFTQIYPQPSW; AQKEFTQIYPQPSWV; QKEFTQIYPQPSWVE; KEFTQIYPQPSWVEH; EFTQIYPQPSWVEHD; FTQIYPQPSWVEHDP; TQIYPQPSWVEHDPT; QIYPQPSWVEHDPTE; IYPQPSWVEHDPTEI; YPQPSWVEHDPTEIW; PQPSWVEHDPTEIWG; QPSWVEHDPTEIWGS;

	PSWVEHDPTEIWGSQ; SWVEHDPTEIWGSQL; WVEHDPTEIWGSQLG; VEHDPTEIWGSQLGV; EHDPTEIWGSQLGVI; HDPTEIWGSQLGVIT; DPTEIWGSQLGVITE; PTEIWGSQLGVITEA; TEIWGSQLGVITEAM; EIWGSQLGVITEAMA; IWGSQLGVITEAMAN; WGSQLGVITEAMANA; GSQLGVITEAMANAR; SQLGVITEAMANARI; QLGVITEAMANARIL; LGVITEAMANARILP; GVITEAMANARILPN; VITEAMANARILPNE; ITEAMANARILPNEI; TEAMANARILPNEID; EAMANARILPNEIDA; AMANARILPNEIDAI; MANARILPNEIDAIG; ANARILPNEIDAIGI; NARILPNEIDAIGIT; ARILPNEIDAIGITN; RILPNEIDAIGITNQ; ILPNEIDAIGITNQR; LPNEIDAIGITNQRE; PNEIDAIGITNQRET; NEIDAIGITNQRETT; EIDAIGITNQRETTV; IDAIGITNQRETTVI; DAIGITNQRETTVIW; AIGITNQRETTVIWE; IGITNQRETTVIWEK; GITNQRETTVIWEKN; ITNQRETTVIWEKNT; TNQRETTVIWEKNTG; NQRETTVIWEKNTGK; QRETTVIWEKNTGKP; RETTVIWEKNTGKPI; ETTVIWEKNTGKPIY; TTVIWEKNTGKPIYN; TVIWEKNTGKPIYNA; VIWEKNTGKPIYNAI; IWEKNTGKPIYNAIV; WEKNTGKPIYNAIVW; EKNTGKPIYNAIVWQ; KNTGKPIYNAIVWQD; NTGKPIYNAIVWQDR; TGKPIYNAIVWQDRR; GKPIYNAIVWQDRRT; KPIYNAIVWQDRRTA; PIYNAIVWQDRRTAK; IYNAIVWQDRRTAKI; YNAIVWQDRRTAKIC; NAIVWQDRRTAKICD; AIVWQDRRTAKICDQ; IVWQDRRTAKICDQL; VWQDRRTAKICDQLK; WQDRRTAKICDQLKK; QDRRTAKICDQLKKE; DRRTAKICDQLKKEG; RRTAKICDQLKKEGK; RTAKICDQLKKEGKD; TAKICDQLKKEGKDK; AKICDQLKKEGKDKI; KICDQLKKEGKDKII; ICDQLKKEGKDKIIL; CDQLKKEGKDKIILE; DQLKKEGKDKIILEK; QLKKEGKDKIILEKT; LKKEGKDKIILEKTG; KKEGKDKIILEKTGL; KEGKDKIILEKTGLV; EGKDKIILEKTGLVL; GKDKIILEKTGLVLD; KDKIILEKTGLVLDS; DKIILEKTGLVLDSY; KIILEKTGLVLDSYF; IILEKTGLVLDSYFS; ILEKTGLVLDSYFSG; LEKTGLVLDSYFSGT; EKTGLVLDSYFSGTK; KTGLVLDSYFSGTKI; TGLVLDSYFSGTKIM; GLVLDSYFSGTKIMW; LVLDSYFSGTKIMWI; VLDSYFSGTKIMWIL; LDSYFSGTKIMWILD; DSYFSGTKIMWILDN; SYFSGTKIMWILDNV; YFSGTKIMWILDNVE; FSGTKIMWILDNVEG; SGTKIMWILDNVEGA; GTKIMWILDNVEGAR; TKIMWILDNVEGARQ; KIMWILDNVEGARQR; IMWILDNVEGARQRA; MWILDNVEGARQRAE; WILDNVEGARQRAEN; ILDNVEGARQRAENG; LDNVEGARQRAENGE; DNVEGARQRAENGEL; NVEGARQRAENGELC; VEGARQRAENGELCF; EGARQRAENGELCFG; GARQRAENGELCFGT; ARQRAENGELCFGTI; RQRAENGELCFGTID; QRAENGELCFGTIDT; RAENGELCFGTIDTW; AENGELCFGTIDTWI; ENGELCFGTIDTWIL; NGELCFGTIDTWILW; GELCFGTIDTWILWN; ELCFGTIDTWILWNL; LCFGTIDTWILWNLT; CFGTIDTWILWNLTQ; FGTIDTWILWNLTQK; GTIDTWILWNLTQKK; TIDTWILWNLTQKKE; IDTWILWNLTQKKEH; DTWILWNLTQKKEHA; TWILWNLTQKKEHAT; WILWNLTQKKEHATD; ILWNLTQKKEHATDY; LWNLTQKKEHATDYS; WNLTQKKEHATDYSN; NLTQKKEHATDYSNA; LTQKKEHATDYSNAS; TQKKEHATDYSNASR; QKKEHATDYSNASRT; KKEHATDYSNASRTL; KEHATDYSNASRTLL; EHATDYSNASRTLLL; HATDYSNASRTLLLN; ATDYSNASRTLLLNI; TDYSNASRTLLLNIK; DYSNASRTLLLNIKT; YSNASRTLLLNIKTL; SNASRTLLLNIKTLE; NASRTLLLNIKTLEW; ASRTLLLNIKTLEWD; SRTLLLNIKTLEWDD; RTLLLNIKTLEWDDE; TLLLNIKTLEWDDEL; LLLNIKTLEWDDELL; LLNIKTLEWDDELLS; LNIKTLEWDDELLSI; NIKTLEWDDELLSIL; IKTLEWDDELLSILN;

	KTLEWDDELLSILNV; TLEWDDELLSILNVP; LEWDDELLSILNVPR; EWDDELLSILNVPRA; WDDELLSILNVPRAI; DDELLSILNVPRAIL; DELLSILNVPRAILP; ELLSILNVPRAILPE; LLSILNVPRAILPEL; LSILNVPRAILPELK; SILNVPRAILPELKE; ILNVPRAILPELKES; LNVPRAILPELKESS; NVPRAILPELKESST; VPRAILPELKESSTI; PRAILPELKESSTIY; RAILPELKESSTIYG; AILPELKESSTIYGK; ILPELKESSTIYGKT; LPELKESSTIYGKTD; PELKESSTIYGKTDK; ELKESSTIYGKTDKA; LKESSTIYGKTDKAL; KESSTIYGKTDKALF; ESSTIYGKTDKALFG; SSTIYGKTDKALFGA; STIYGKTDKALFGAE; TIYGKTDKALFGAEI; IYGKTDKALFGAEIP; YGKTDKALFGAEIPI; GKTDKALFGAEIPIA; KTDKALFGAEIPIAG; TDKALFGAEIPIAGI; DKALFGAEIPIAGIA; KALFGAEIPIAGIAG; ALFGAEIPIAGIAGD; LFGAEIPIAGIAGDQ; FGAEIPIAGIAGDQF; GAEIPIAGIAGDQFA; AEIPIAGIAGDQFAA; EIPIAGIAGDQFAAT; IPIAGIAGDQFAATF; PIAGIAGDQFAATFG; IAGIAGDQFAATFGQ; AGIAGDQFAATFGQA; GIAGDQFAATFGQAC; IAGDQFAATFGQACL; AGDQFAATFGQACLK; GDQFAATFGQACLKK; DQFAATFGQACLKKG; QFAATFGQACLKKGM; FAATFGQACLKKGMA; AATFGQACLKKGMAK; ATFGQACLKKGMAKN; TFGQACLKKGMAKNT; FGQACLKKGMAKNTY; GQACLKKGMAKNTYG; QACLKKGMAKNTYGT; ACLKKGMAKNTYGTG; CLKKGMAKNTYGTGC; LKKGMAKNTYGTGCF; KKGMAKNTYGTGCFL; KGMAKNTYGTGCFLT; GMAKNTYGTGCFLTV; MAKNTYGTGCFLTVN; AKNTYGTGCFLTVNI; KNTYGTGCFLTVNIG; NTYGTGCFLTVNIGK; TYGTGCFLTVNIGKE; YGTGCFLTVNIGKEP; GTGCFLTVNIGKEPI; TGCFLTVNIGKEPII; GCFLTVNIGKEPIIS; CFLTVNIGKEPIISH; FLTVNIGKEPIISHD; LTVNIGKEPIISHDK; TVNIGKEPIISHDKL; VNIGKEPIISHDKLL; NIGKEPIISHDKLLT; IGKEPIISHDKLLTS; GKEPIISHDKLLTSI; KEPIISHDKLLTSIA; EPIISHDKLLTSIAW; PIISHDKLLTSIAWG; IISHDKLLTSIAWGR; ISHDKLLTSIAWGRK; SHDKLLTSIAWGRKK; HDKLLTSIAWGRKKS; DKLLTSIAWGRKKSV; KLLTSIAWGRKKSVT; LLTSIAWGRKKSVTY; LTSIAWGRKKSVTYV; TSIAWGRKKSVTYVL; SIAWGRKKSVTYVLE; IAWGRKKSVTYVLEG; AWGRKKSVTYVLEGS; WGRKKSVTYVLEGSV; GRKKSVTYVLEGSVF; RKKSVTYVLEGSVFI; KKSVTYVLEGSVFIG; KSVTYVLEGSVFIGG; SVTYVLEGSVFIGGA; VTYVLEGSVFIGGAV; TYVLEGSVFIGGAVI; YVLEGSVFIGGAVIQ; VLEGSVFIGGAVIQW; LEGSVFIGGAVIQWL; EGSVFIGGAVIQWLR; GSVFIGGAVIQWLRD; SVFIGGAVIQWLRDG; VFIGGAVIQWLRDGL; FIGGAVIQWLRDGLE; IGGAVIQWLRDGLEF; GGAVIQWLRDGLEFF; GAVIQWLRDGLEFFR; AVIQWLRDGLEFFRK; VIQWLRDGLEFFRKS; IQWLRDGLEFFRKSS; QWLRDGLEFFRKSSD; WLRDGLEFFRKSSDA; LRDGLEFFRKSSDAE; RDGLEFFRKSSDAEA; DGLEFFRKSSDAEAL; GLEFFRKSSDAEALA; LEFFRKSSDAEALAS; EFFRKSSDAEALASS; FFRKSSDAEALASSV; FRKSSDAEALASSVS; RKSSDAEALASSVSD; KSSDAEALASSVSDN; SSDAEALASSVSDNG; SDAEALASSVSDNGG; DAEALASSVSDNGGV; AEALASSVSDNGGVY; EALASSVSDNGGVYF; ALASSVSDNGGVYFV; LASSVSDNGGVYFVP; ASSVSDNGGVYFVPA; SSVSDNGGVYFVPAF; SVSDNGGVYFVPAFV; VSDNGGVYFVPAFVG; SDNGGVYFVPAFVGL; DNGGVYFVPAFVGLG; NGGVYFVPAFVGLGA; GGVYFVPAFVGLGAP; GVYFVPAFVGLGAPH; VYFVPAFVGLGAPHW; YFVPAFVGLGAPHWD; FVPAFVGLGAPHWDS; VPAFVGLGAPHWDSY; PAFVGLGAPHWDSYA; AFVGLGAPHWDSYAR; FVGLGAPHWDSYARG;

	VGLGAPHWDSYARGT; GLGAPHWDSYARGTI; LGAPHWDSYARGTII; GAPHWDSYARGTIIG; APHWDSYARGTIIGI; PHWDSYARGTIIGIT; HWDSYARGTIIGITR; WDSYARGTIIGITRG; DSYARGTIIGITRGS; SYARGTIIGITRGST; YARGTIIGITRGSTK; ARGTIIGITRGSTKA; RGTIIGITRGSTKAH; GTIIGITRGSTKAHI; TIIGITRGSTKAHIT; IIGITRGSTKAHITR; IGITRGSTKAHITRA; GITRGSTKAHITRAA; ITRGSTKAHITRAAL; TRGSTKAHITRAALE; RGSTKAHITRAALES; GSTKAHITRAALESI; STKAHITRAALESIA; TKAHITRAALESIAF; KAHITRAALESIAFQ; AHITRAALESIAFQS; HITRAALESIAFQSF; ITRAALESIAFQSFD; TRAALESIAFQSFDI; RAALESIAFQSFDIL; AALESIAFQSFDILN; ALESIAFQSFDILNT; LESIAFQSFDILNTM; ESIAFQSFDILNTMK; SIAFQSFDILNTMKK; IAFQSFDILNTMKKS; AFQSFDILNTMKKSI; FQSFDILNTMKKSIP; QSFDILNTMKKSIPN; SFDILNTMKKSIPNF; FDILNTMKKSIPNFE; DILNTMKKSIPNFEI; ILNTMKKSIPNFEIQ; LNTMKKSIPNFEIQE; NTMKKSIPNFEIQEL; TMKKSIPNFEIQELR; MKKSIPNFEIQELRV; KKSIPNFEIQELRVD; KSIPNFEIQELRVDG; SIPNFEIQELRVDGG; IPNFEIQELRVDGGA; PNFEIQELRVDGGAS; NFEIQELRVDGGASQ; FEIQELRVDGGASQN; EIQELRVDGGASQNN; IQELRVDGGASQNNL; QELRVDGGASQNNLL; ELRVDGGASQNNLLM; LRVDGGASQNNLLMQ; RVDGGASQNNLLMQF; VDGGASQNNLLMQFQ; DGGASQNNLLMQFQA; GGASQNNLLMQFQAD; GASQNNLLMQFQADL; ASQNNLLMQFQADLL; SQNNLLMQFQADLLE; QNNLLMQFQADLLEC; NNLLMQFQADLLECK; NLLMQFQADLLECKV; LLMQFQADLLECKVV; LMQFQADLLECKVVR; MQFQADLLECKVVRP; QFQADLLECKVVRPK; FQADLLECKVVRPKI; QADLLECKVVRPKIT; ADLLECKVVRPKITE; DLLECKVVRPKITET; LLECKVVRPKITETT; LECKVVRPKITETTA; ECKVVRPKITETTAL; CKVVRPKITETTALG; KVVRPKITETTALGA; VVRPKITETTALGAA; VRPKITETTALGAAY; RPKITETTALGAAYL; PKITETTALGAAYLA; KITETTALGAAYLAG; ITETTALGAAYLAGL; TETTALGAAYLAGLA; ETTALGAAYLAGLAT; TTALGAAYLAGLATG; TALGAAYLAGLATGY; ALGAAYLAGLATGYW; LGAAYLAGLATGYWQ; GAAYLAGLATGYWQS; AAYLAGLATGYWQSA; AYLAGLATGYWQSAE; YLAGLATGYWQSAEE; LAGLATGYWQSAEEI; AGLATGYWQSAEEIV; GLATGYWQSAEEIVS; LATGYWQSAEEIVSL; ATGYWQSAEEIVSLW; TGYWQSAEEIVSLWQ; GYWQSAEEIVSLWQV; YWQSAEEIVSLWQVD; WQSAEEIVSLWQVDK; QSAEEIVSLWQVDKI; SAEEIVSLWQVDKIF; AEEIVSLWQVDKIFE; EEIVSLWQVDKIFEP; EIVSLWQVDKIFEPS; IVSLWQVDKIFEPSM; VSLWQVDKIFEPSMP; SLWQVDKIFEPSMPK; LWQVDKIFEPSMPKN; WQVDKIFEPSMPKNQ; QVDKIFEPSMPKNQK; VDKIFEPSMPKNQKE; DKIFEPSMPKNQKEK; KIFEPSMPKNQKEKL; IFEPSMPKNQKEKLL; FEPSMPKNQKEKLLE; EPSMPKNQKEKLLEN; PSMPKNQKEKLLENW; SMPKNQKEKLLENWN; MPKNQKEKLLENWNK; PKNQKEKLLENWNKA; KNQKEKLLENWNKAV; NQKEKLLENWNKAVG; QKEKLLENWNKAVGK; KEKLLENWNKAVGKA; EKLLENWNKAVGKAK; KLLENWNKAVGKAKS; LLENWNKAVGKAKSW; LENWNKAVGKAKSWI; ENWNKAVGKAKSWIQ; NWNKAVGKAKSWIQN; WNKAVGKAKSWIQNS; NKAVGKAKSWIQNSH; KAVGKAKSWIQNSHS; AVGKAKSWIQNSHSS; 16 mers: MKYILSIDQGTTSSRA; KYILSIDQGTTSSRAM; YILSIDQGTTSSRAMV;

	ILSIDQGTTSSRAMVF; LSIDQGTTSSRAMVFD; SIDQGTTSSRAMVFDK; IDQGTTSSRAMVFDKN; DQGTTSSRAMVFDKNA; QGTTSSRAMVFDKNAN; GTTSSRAMVFDKNANI; TTSSRAMVFDKNANIK; TSSRAMVFDKNANIKG; SSRAMVFDKNANIKGF; SRAMVFDKNANIKGFA; RAMVFDKNANIKGFAQ; AMVFDKNANIKGFAQK; MVFDKNANIKGFAQKE; VFDKNANIKGFAQKEF; FDKNANIKGFAQKEFT; DKNANIKGFAQKEFTQ; KNANIKGFAQKEFTQI; NANIKGFAQKEFTQIY; ANIKGFAQKEFTQIYP; NIKGFAQKEFTQIYPQ; IKGFAQKEFTQIYPQP; KGFAQKEFTQIYPQPS; GFAQKEFTQIYPQPSW; FAQKEFTQIYPQPSWV; AQKEFTQIYPQPSWVE; QKEFTQIYPQPSWVEH; KEFTQIYPQPSWVEHD; EFTQIYPQPSWVEHDP; FTQIYPQPSWVEHDPT; TQIYPQPSWVEHDPTE; QIYPQPSWVEHDPTEI; IYPQPSWVEHDPTEIW; YPQPSWVEHDPTEIWG; PQPSWVEHDPTEIWGS; QPSWVEHDPTEIWGSQ; PSWVEHDPTEIWGSQL; SWVEHDPTEIWGSQLG; WVEHDPTEIWGSQLGV; VEHDPTEIWGSQLGVI; EHDPTEIWGSQLGVIT; HDPTEIWGSQLGVITE; DPTEIWGSQLGVITEA; PTEIWGSQLGVITEAM; TEIWGSQLGVITEAMA; EIWGSQLGVITEAMAN; IWGSQLGVITEAMANA; WGSQLGVITEAMANAR; GSQLGVITEAMANARI; SQLGVITEAMANARIL; QLGVITEAMANARILP; LGVITEAMANARILPN; GVITEAMANARILPNE; VITEAMANARILPNEI; ITEAMANARILPNEID; TEAMANARILPNEIDA; EAMANARILPNEIDAI; AMANARILPNEIDAIG; MANARILPNEIDAIGI; ANARILPNEIDAIGIT; NARILPNEIDAIGITN; ARILPNEIDAIGITNQ; RILPNEIDAIGITNQR; ILPNEIDAIGITNQRE; LPNEIDAIGITNQRET; PNEIDAIGITNQRETT; NEIDAIGITNQRETTV; EIDAIGITNQRETTVI; IDAIGITNQRETTVIW; DAIGITNQRETTVIWE; AIGITNQRETTVIWEK; IGITNQRETTVIWEKN; GITNQRETTVIWEKNT; ITNQRETTVIWEKNTG; TNQRETTVIWEKNTGK; NQRETTVIWEKNTGKP; QRETTVIWEKNTGKPI; RETTVIWEKNTGKPIY; ETTVIWEKNTGKPIYN; TTVIWEKNTGKPIYNA; TVIWEKNTGKPIYNAI; VIWEKNTGKPIYNAIV; IWEKNTGKPIYNAIVW; WEKNTGKPIYNAIVWQ; EKNTGKPIYNAIVWQD; KNTGKPIYNAIVWQDR; NTGKPIYNAIVWQDRR; TGKPIYNAIVWQDRRT; GKPIYNAIVWQDRRTA; KPIYNAIVWQDRRTAK; PIYNAIVWQDRRTAKI; IYNAIVWQDRRTAKIC; YNAIVWQDRRTAKICD; NAIVWQDRRTAKICDQ; AIVWQDRRTAKICDQL; IVWQDRRTAKICDQLK; VWQDRRTAKICDQLKK; WQDRRTAKICDQLKKE; QDRRTAKICDQLKKEG; DRRTAKICDQLKKEGK; RRTAKICDQLKKEGKD; RTAKICDQLKKEGKDK; TAKICDQLKKEGKDKI; AKICDQLKKEGKDKII; KICDQLKKEGKDKIIL; ICDQLKKEGKDKIILE; CDQLKKEGKDKIILEK; DQLKKEGKDKIILEKT; QLKKEGKDKIILEKTG; LKKEGKDKIILEKTGL; KKEGKDKIILEKTGLV; KEGKDKIILEKTGLVL; EGKDKIILEKTGLVLD; GKDKIILEKTGLVLDS; KDKIILEKTGLVLDSY; DKIILEKTGLVLDSYF; KIILEKTGLVLDSYFS; IILEKTGLVLDSYFSG; ILEKTGLVLDSYFSGT; LEKTGLVLDSYFSGTK; EKTGLVLDSYFSGTKI; KTGLVLDSYFSGTKIM; TGLVLDSYFSGTKIMW; GLVLDSYFSGTKIMWI; LVLDSYFSGTKIMWIL; VLDSYFSGTKIMWILD; LDSYFSGTKIMWILDN; DSYFSGTKIMWILDNV; SYFSGTKIMWILDNVE; YFSGTKIMWILDNVEG; FSGTKIMWILDNVEGA; SGTKIMWILDNVEGAR; GTKIMWILDNVEGARQ; TKIMWILDNVEGARQR; KIMWILDNVEGARQRA; IMWILDNVEGARQRAE; MWILDNVEGARQRAEN; WILDNVEGARQRAENG; ILDNVEGARQRAENGE; LDNVEGARQRAENGEL; DNVEGARQRAENGELC; NVEGARQRAENGELCF; VEGARQRAENGELCFG; EGARQRAENGELCFGT; GARQRAENGELCFGTI; ARQRAENGELCFGTID; RQRAENGELCFGTIDT; QRAENGELCFGTIDTW; RAENGELCFGTIDTWI; AENGELCFGTIDTWIL; ENGELCFGTIDTWILW; NGELCFGTIDTWILWN; GELCFGTIDTWILWNL;

	ELCFGTIDTWILWNLT; LCFGTIDTWILWNLTQ; CFGTIDTWILWNLTQK; FGTIDTWILWNLTQKK; GTIDTWILWNLTQKKE; TIDTWILWNLTQKKEH; IDTWILWNLTQKKEHA; DTWILWNLTQKKEHAT; TWILWNLTQKKEHATD; WILWNLTQKKEHATDY; ILWNLTQKKEHATDYS; LWNLTQKKEHATDYSN; WNLTQKKEHATDYSNA; NLTQKKEHATDYSNAS; LTQKKEHATDYSNASR; TQKKEHATDYSNASRT; QKKEHATDYSNASRTL; KKEHATDYSNASRTLL; KEHATDYSNASRTLLL; EHATDYSNASRTLLLN; HATDYSNASRTLLLNI; ATDYSNASRTLLLNIK; TDYSNASRTLLLNIKT; DYSNASRTLLLNIKTL; YSNASRTLLLNIKTLE; SNASRTLLLNIKTLEW; NASRTLLLNIKTLEWD; ASRTLLLNIKTLEWDD; SRTLLLNIKTLEWDDE; RTLLLNIKTLEWDDEL; TLLLNIKTLEWDDELL; LLLNIKTLEWDDELLS; LLNIKTLEWDDELLSI; LNIKTLEWDDELLSIL; NIKTLEWDDELLSILN; IKTLEWDDELLSILNV; KTLEWDDELLSILNVP; TLEWDDELLSILNVPR; LEWDDELLSILNVPRA; EWDDELLSILNVPRAI; WDDELLSILNVPRAIL; DDELLSILNVPRAILP; DELLSILNVPRAILPE; ELLSILNVPRAILPEL; LLSILNVPRAILPELK; LSILNVPRAILPELKE; SILNVPRAILPELKES; ILNVPRAILPELKESS; LNVPRAILPELKESST; NVPRAILPELKESSTI; VPRAILPELKESSTIY; PRAILPELKESSTIYG; RAILPELKESSTIYGK; AILPELKESSTIYGKT; ILPELKESSTIYGKTD; LPELKESSTIYGKTDK; PELKESSTIYGKTDKA; ELKESSTIYGKTDKAL; LKESSTIYGKTDKALF; KESSTIYGKTDKALFG; ESSTIYGKTDKALFGA; SSTIYGKTDKALFGAE; STIYGKTDKALFGAEI; TIYGKTDKALFGAEIP; IYGKTDKALFGAEIPI; YGKTDKALFGAEIPIA; GKTDKALFGAEIPIAG; KTDKALFGAEIPIAGI; TDKALFGAEIPIAGIA; DKALFGAEIPIAGIAG; KALFGAEIPIAGIAGD; ALFGAEIPIAGIAGDQ; LFGAEIPIAGIAGDQF; FGAEIPIAGIAGDQFA; GAEIPIAGIAGDQFAA; AEIPIAGIAGDQFAAT; EIPIAGIAGDQFAATF; IPIAGIAGDQFAATFG; PIAGIAGDQFAATFGQ; IAGIAGDQFAATFGQA; AGIAGDQFAATFGQAC; GIAGDQFAATFGQACL; IAGDQFAATFGQACLK; AGDQFAATFGQACLKK; GDQFAATFGQACLKKG; DQFAATFGQACLKKGM; QFAATFGQACLKKGMA; FAATFGQACLKKGMAK; AATFGQACLKKGMAKN; ATFGQACLKKGMAKNT; TFGQACLKKGMAKNTY; FGQACLKKGMAKNTYG; GQACLKKGMAKNTYGT; QACLKKGMAKNTYGTG; ACLKKGMAKNTYGTGC; CLKKGMAKNTYGTGCF; LKKGMAKNTYGTGCFL; KKGMAKNTYGTGCFLT; KGMAKNTYGTGCFLTV; GMAKNTYGTGCFLTVN; MAKNTYGTGCFLTVNI; AKNTYGTGCFLTVNIG; KNTYGTGCFLTVNIGK; NTYGTGCFLTVNIGKE; TYGTGCFLTVNIGKEP; YGTGCFLTVNIGKEPI; GTGCFLTVNIGKEPII; TGCFLTVNIGKEPIIS; GCFLTVNIGKEPIISH; CFLTVNIGKEPIISHD; FLTVNIGKEPIISHDK; LTVNIGKEPIISHDKL; TVNIGKEPIISHDKLL; VNIGKEPIISHDKLLT; NIGKEPIISHDKLLTS; IGKEPIISHDKLLTSI; GKEPIISHDKLLTSIA; KEPIISHDKLLTSIAW; EPIISHDKLLTSIAWG; PIISHDKLLTSIAWGR; IISHDKLLTSIAWGRK; ISHDKLLTSIAWGRKK; SHDKLLTSIAWGRKKS; HDKLLTSIAWGRKKSV; DKLLTSIAWGRKKSVT; KLLTSIAWGRKKSVTY; LLTSIAWGRKKSVTYV; LTSIAWGRKKSVTYVL; TSIAWGRKKSVTYVLE; SIAWGRKKSVTYVLEG; IAWGRKKSVTYVLEGS; AWGRKKSVTYVLEGSV; WGRKKSVTYVLEGSVF; GRKKSVTYVLEGSVFI; RKKSVTYVLEGSVFIG; KKSVTYVLEGSVFIGG; KSVTYVLEGSVFIGGA; SVTYVLEGSVFIGGAV; VTYVLEGSVFIGGAVI; TYVLEGSVFIGGAVIQ; YVLEGSVFIGGAVIQW; VLEGSVFIGGAVIQWL; LEGSVFIGGAVIQWLR; EGSVFIGGAVIQWLRD; GSVFIGGAVIQWLRDG; SVFIGGAVIQWLRDGL; VFIGGAVIQWLRDGLE; FIGGAVIQWLRDGLEF; IGGAVIQWLRDGLEFF; GGAVIQWLRDGLEFFR; GAVIQWLRDGLEFFRK; AVIQWLRDGLEFFRKS; VIQWLRDGLEFFRKSS;

	IQWLRDGLEFFRKSSD; QWLRDGLEFFRKSSDA; WLRDGLEFFRKSSDAE; LRDGLEFFRKSSDAEA; RDGLEFFRKSSDAEAL; DGLEFFRKSSDAEALA; GLEFFRKSSDAEALAS; LEFFRKSSDAEALASS; EFFRKSSDAEALASSV; FFRKSSDAEALASSVS; FRKSSDAEALASSVSD; RKSSDAEALASSVSDN; KSSDAEALASSVSDNG; SSDAEALASSVSDNGG; SDAEALASSVSDNGGV; DAEALASSVSDNGGVY; AEALASSVSDNGGVYF; EALASSVSDNGGVYFV; ALASSVSDNGGVYFVP; LASSVSDNGGVYFVPA; ASSVSDNGGVYFVPAF; SSVSDNGGVYFVPAFV; SVSDNGGVYFVPAFVG; VSDNGGVYFVPAFVGL; SDNGGVYFVPAFVGLG; DNGGVYFVPAFVGLGA; NGGVYFVPAFVGLGAP; GGVYFVPAFVGLGAPH; GVYFVPAFVGLGAPHW; VYFVPAFVGLGAPHWD; YFVPAFVGLGAPHWDS; FVPAFVGLGAPHWDSY; VPAFVGLGAPHWDSYA; PAFVGLGAPHWDSYAR; AFVGLGAPHWDSYARG; FVGLGAPHWDSYARGT; VGLGAPHWDSYARGTI; GLGAPHWDSYARGTII; LGAPHWDSYARGTIIG; GAPHWDSYARGTIIGI; APHWDSYARGTIIGIT; PHWDSYARGTIIGITR; HWDSYARGTIIGITRG; WDSYARGTIIGITRGS; DSYARGTIIGITRGST; SYARGTIIGITRGSTK; YARGTIIGITRGSTKA; ARGTIIGITRGSTKAH; RGTIIGITRGSTKAHI; GTIIGITRGSTKAHIT; TIIGITRGSTKAHITR; IIGITRGSTKAHITRA; IGITRGSTKAHITRAA; GITRGSTKAHITRAAL; ITRGSTKAHITRAALE; TRGSTKAHITRAALES; RGSTKAHITRAALESI; GSTKAHITRAALESIA; STKAHITRAALESIAF; TKAHITRAALESIAFQ; KAHITRAALESIAFQS; AHITRAALESIAFQSF; HITRAALESIAFQSFD; ITRAALESIAFQSFDI; TRAALESIAFQSFDIL; RAALESIAFQSFDILN; AALESIAFQSFDILNT; ALESIAFQSFDILNTM; LESIAFQSFDILNTMK; ESIAFQSFDILNTMKK; SIAFQSFDILNTMKKS; IAFQSFDILNTMKKSI; AFQSFDILNTMKKSIP; FQSFDILNTMKKSIPN; QSFDILNTMKKSIPNF; SFDILNTMKKSIPNFE; FDILNTMKKSIPNFEI; DILNTMKKSIPNFEIQ; ILNTMKKSIPNFEIQE; LNTMKKSIPNFEIQEL; NTMKKSIPNFEIQELR; TMKKSIPNFEIQELRV; MKKSIPNFEIQELRVD; KKSIPNFEIQELRVDG; KSIPNFEIQELRVDGG; SIPNFEIQELRVDGGA; IPNFEIQELRVDGGAS; PNFEIQELRVDGGASQ; NFEIQELRVDGGASQN; FEIQELRVDGGASQNN; EIQELRVDGGASQNNL; IQELRVDGGASQNNLL; QELRVDGGASQNNLLM; ELRVDGGASQNNLLMQ; LRVDGGASQNNLLMQF; RVDGGASQNNLLMQFQ; VDGGASQNNLLMQFQA; DGGASQNNLLMQFQAD; GGASQNNLLMQFQADL; GASQNNLLMQFQADLL; ASQNNLLMQFQADLLE; SQNNLLMQFQADLLEC; QNNLLMQFQADLLECK; NNLLMQFQADLLECKV; NLLMQFQADLLECKVV; LLMQFQADLLECKVVR; LMQFQADLLECKVVRP; MQFQADLLECKVVRPK; QFQADLLECKVVRPKI; FQADLLECKVVRPKIT; QADLLECKVVRPKITE; ADLLECKVVRPKITET; DLLECKVVRPKITETT; LLECKVVRPKITETTA; LECKVVRPKITETTAL; ECKVVRPKITETTALG; CKVVRPKITETTALGA; KVVRPKITETTALGAA; VVRPKITETTALGAAY; VRPKITETTALGAAYL; RPKITETTALGAAYLA; PKITETTALGAAYLAG; KITETTALGAAYLAGL; ITETTALGAAYLAGLA; TETTALGAAYLAGLAT; ETTALGAAYLAGLATG; TTALGAAYLAGLATGY; TALGAAYLAGLATGYW; ALGAAYLAGLATGYWQ; LGAAYLAGLATGYWQS; GAAYLAGLATGYWQSA; AAYLAGLATGYWQSAE; AYLAGLATGYWQSAEE; YLAGLATGYWQSAEEI; LAGLATGYWQSAEEIV; AGLATGYWQSAEEIVS; GLATGYWQSAEEIVSL; LATGYWQSAEEIVSLW; ATGYWQSAEEIVSLWQ; TGYWQSAEEIVSLWQV; GYWQSAEEIVSLWQVD; YWQSAEEIVSLWQVDK; WQSAEEIVSLWQVDKI; QSAEEIVSLWQVDKIF; SAEEIVSLWQVDKIFE; AEEIVSLWQVDKIFEP; EEIVSLWQVDKIFEPS; EIVSLWQVDKIFEPSM; IVSLWQVDKIFEPSMP; VSLWQVDKIFEPSMPK; SLWQVDKIFEPSMPKN; LWQVDKIFEPSMPKNQ; WQVDKIFEPSMPKNQK;

	QVDKIFEPSMPKNQKE; VDKIFEPSMPKNQKEK; DKIFEPSMPKNQKEKL; KIFEPSMPKNQKEKLL; IFEPSMPKNQKEKLLE; FEPSMPKNQKEKLLEN; EPSMPKNQKEKLLENW; PSMPKNQKEKLLENWN; SMPKNQKEKLLENWNK; MPKNQKEKLLENWNKA; PKNQKEKLLENWNKAV; KNQKEKLLENWNKAVG; NQKEKLLENWNKAVGK; QKEKLLENWNKAVGKA; KEKLLENWNKAVGKAK; EKLLENWNKAVGKAKS; KLLENWNKAVGKAKSW; LLENWNKAVGKAKSWI; LENWNKAVGKAKSWIQ; ENWNKAVGKAKSWIQN; NWNKAVGKAKSWIQNS; WNKAVGKAKSWIQNSH; NKAVGKAKSWIQNSHS; KAVGKAKSWIQNSHSS;
Seq 28	13 mers: MKTIKKDSEFYDS; KTIKKDSEFYDSL; TIKKDSEFYDSLA; IKKDSEFYDSLAT; KKDSEFYDSLATL; KDSEFYDSLATLK; DSEFYDSLATLKK; SEFYDSLATLKKH; EFYDSLATLKKHI; FYDSLATLKKHIN; YDSLATLKKHINK; DSLATLKKHINKY; SLATLKKHINKYI; LATLKKHINKYIE; ATLKKHINKYIEE; TLKKHINKYIEEK; LKKHINKYIEEKV; KKHINKYIEEKVL; KHINKYIEEKVLK; HINKYIEEKVLKY; INKYIEEKVLKYS; NKYIEEKVLKYSI; KYIEEKVLKYSIS; YIEEKVLKYSISS; IEEKVLKYSISSQ; EEKVLKYSISSQL; EKVLKYSISSQLY; KVLKYSISSQLYK; VLKYSISSQLYKL; LKYSISSQLYKLE; KYSISSQLYKLEK; YSISSQLYKLEKP; SISSQLYKLEKPE; ISSQLYKLEKPEI; SSQLYKLEKPEII; SQLYKLEKPEIIE; QLYKLEKPEIIEL; LYKLEKPEIIELI; YKLEKPEIIELIK; KLEKPEIIELIKI; LEKPEIIELIKIS; EKPEIIELIKISN; KPEIIELIKISND; PEIIELIKISNDY; EIIELIKISNDYE; IIELIKISNDYEK; IELIKISNDYEKE; ELIKISNDYEKEK; LIKISNDYEKEKN; IKISNDYEKEKNA; KISNDYEKEKNAF; ISNDYEKEKNAFN; SNDYEKEKNAFNT; NDYEKEKNAFNTS; DYEKEKNAFNTSL; YEKEKNAFNTSLE; EKEKNAFNTSLEE; KEKNAFNTSLEEC; EKNAFNTSLEECY; KNAFNTSLEECYY; NAFNTSLEECYYK; AFNTSLEECYYKN; FNTSLEECYYKNT; NTSLEECYYKNTQ; TSLEECYYKNTQN; SLEECYYKNTQNE; LEECYYKNTQNEA; EECYYKNTQNEAI; ECYYKNTQNEAIK; CYYKNTQNEAIKK; YYKNTQNEAIKKW; YKNTQNEAIKKWI; KNTQNEAIKKWIL; NTQNEAIKKWILE; TQNEAIKKWILEI; QNEAIKKWILEIV; NEAIKKWILEIVR; EAIKKWILEIVRN; AIKKWILEIVRNK; IKKWILEIVRNKN; KKWILEIVRNKNF; KWILEIVRNKNFI; WILEIVRNKNFIQ; ILEIVRNKNFIQI; LEIVRNKNFIQIS; EIVRNKNFIQISK; IVRNKNFIQISKE; VRNKNFIQISKEA; RNKNFIQISKEAN; NKNFIQISKEANL; KNFIQISKEANLN; NFIQISKEANLNT; FIQISKEANLNTK; IQISKEANLNTKK; QISKEANLNTKKL; ISKEANLNTKKLG; SKEANLNTKKLGT; KEANLNTKKLGTT; EANLNTKKLGTTY; ANLNTKKLGTTYK; NLNTKKLGTTYKL; LNTKKLGTTYKLK; NTKKLGTTYKLKS; TKKLGTTYKLKSS; KKLGTTYKLKSSN; KLGTTYKLKSSNF; LGTTYKLKSSNFL; GTTYKLKSSNFLK; TTYKLKSSNFLKL; TYKLKSSNFLKLI; YKLKSSNFLKLIE; KLKSSNFLKLIEI; LKSSNFLKLIEIQ; KSSNFLKLIEIQN; SSNFLKLIEIQNS; SNFLKLIEIQNSP; NFLKLIEIQNSPY; FLKLIEIQNSPYY; LKLIEIQNSPYYS; KLIEIQNSPYYSQ;

	LIEIQNSPYYSQE; IEIQNSPYYSQEK; EIQNSPYYSQEKK; IQNSPYYSQEKKD; QNSPYYSQEKKDI; NSPYYSQEKKDIY; SPYYSQEKKDIYK; PYYSQEKKDIYKQ; YYSQEKKDIYKQI; YSQEKKDIYKQII; SQEKKDIYKQIIL; QEKKDIYKQIILN; EKKDIYKQIILNF; KKDIYKQIILNFS; KDIYKQIILNFSS; DIYKQIILNFSSN; IYKQIILNFSSNI; YKQIILNFSSNIN; KQIILNFSSNINI; QIILNFSSNINID; IILNFSSNINIDS; ILNFSSNINIDSL; LNFSSNINIDSLE; NFSSNINIDSLEQ; FSSNINIDSLEQT; SSNINIDSLEQTI; SNINIDSLEQTID; NINIDSLEQTIDI; INIDSLEQTIDIL; NIDSLEQTIDILV; IDSLEQTIDILVA; DSLEQTIDILVAV; SLEQTIDILVAVR; LEQTIDILVAVRN; EQTIDILVAVRNR; QTIDILVAVRNRN; TIDILVAVRNRNK; IDILVAVRNRNKI; DILVAVRNRNKIK; ILVAVRNRNKIKI; LVAVRNRNKIKIL; VAVRNRNKIKILN; AVRNRNKIKILNI; VRNRNKIKILNIL; RNRNKIKILNILN; NRNKIKILNILNK; RNKIKILNILNKN; NKIKILNILNKNL; KIKILNILNKNLK; IKILNILNKNLKY; KILNILNKNLKYR; ILNILNKNLKYRP; LNILNKNLKYRPE; NILNKNLKYRPEN; ILNKNLKYRPENQ; LNKNLKYRPENQK; NKNLKYRPENQKV; KNLKYRPENQKVF; NLKYRPENQKVFK; LKYRPENQKVFKS; KYRPENQKVFKSS; YRPENQKVFKSSL; RPENQKVFKSSLT; PENQKVFKSSLTN; ENQKVFKSSLTNK; NQKVFKSSLTNKE; QKVFKSSLTNKES; KVFKSSLTNKESR; VFKSSLTNKESRL; FKSSLTNKESRLI; KSSLTNKESRLIK; SSLTNKESRLIKL; SLTNKESRLIKLK; LTNKESRLIKLKR; TNKESRLIKLKRM; NKESRLIKLKRML; KESRLIKLKRMLI; ESRLIKLKRMLIL; SRLIKLKRMLILT; RLIKLKRMLILTY; LIKLKRMLILTYW; IKLKRMLILTYWP; KLKRMLILTYWPV; LKRMLILTYWPVG; KRMLILTYWPVGC; RMLILTYWPVGCL; MLILTYWPVGCLS; LILTYWPVGCLSK; ILTYWPVGCLSKN; LTYWPVGCLSKNI; TYWPVGCLSKNIF; YWPVGCLSKNIFI; WPVGCLSKNIFIK; PVGCLSKNIFIKI; VGCLSKNIFIKIL; GCLSKNIFIKILI; CLSKNIFIKILIK; LSKNIFIKILIKX; SKNIFIKILIKXY; KNIFIKILIKXYK; NIFIKILIKXYKY; IFIKILIKXYKYL; FIKILIKXYKYLE; IKILIKXYKYLEE; KILIKXYKYLEEE; ILIKXYKYLEEEI; LIKXYKYLEEEIL; IKXYKYLEEEILA; KXYKYLEEEILAL; XYKYLEEEILALK; YKYLEEEILALKY; KYLEEEILALKYN; YLEEEILALKYNE; LEEEILALKYNEI; EEEILALKYNEIL; EEILALKYNEILN; EILALKYNEILNY; ILALKYNEILNYL; LALKYNEILNYLR; ALKYNEILNYLRA; LKYNEILNYLRAL; KYNEILNYLRALK; YNEILNYLRALKT; NEILNYLRALKTL; EILNYLRALKTLS; ILNYLRALKTLSL; LNYLRALKTLSLN; NYLRALKTLSLNE; YLRALKTLSLNEI; LRALKTLSLNEIF; RALKTLSLNEIFY; ALKTLSLNEIFYK; LKTLSLNEIFYKG; KTLSLNEIFYKGS; TLSLNEIFYKGSS; LSLNEIFYKGSSK; SLNEIFYKGSSKN; LNEIFYKGSSKNI; NEIFYKGSSKNIS; EIFYKGSSKNISF; IFYKGSSKNISFN; FYKGSSKNISFNY; YKGSSKNISFNYF; KGSSKNISFNYFF; GSSKNISFNYFFS; SSKNISFNYFFSD; SKNISFNYFFSDF; KNISFNYFFSDFT; NISFNYFFSDFTQ; ISFNYFFSDFTQY; SFNYFFSDFTQYA; FNYFFSDFTQYAP; NYFFSDFTQYAPK;

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	KYLEEEILALKYNEIL; YLEEEILALKYNEILN; LEEEILALKYNEILNY; EEEILALKYNEILNYL; EEILALKYNEILNYLR; EILALKYNEILNYLRA; ILALKYNEILNYLRAL; LALKYNEILNYLRALK; ALKYNEILNYLRALKT; LKYNEILNYLRALKTL; KYNEILNYLRALKTLS; YNEILNYLRALKTLSL; NEILNYLRALKTLSLN; EILNYLRALKTLSLNE; ILNYLRALKTLSLNEI; LNYLRALKTLSLNEIF; NYLRALKTLSLNEIFY; YLRALKTLSLNEIFYK; LRALKTLSLNEIFYKG; RALKTLSLNEIFYKGS; ALKTLSLNEIFYKGSS; LKTLSLNEIFYKGSSK; KTLSLNEIFYKGSSKN; TLSLNEIFYKGSSKNI; LSLNEIFYKGSSKNIS; SLNEIFYKGSSKNISF; LNEIFYKGSSKNISFN; NEIFYKGSSKNISFNY; EIFYKGSSKNISFNYF; IFYKGSSKNISFNYFF; FYKGSSKNISFNYFFS; YKGSSKNISFNYFFSD; KGSSKNISFNYFFSDF; GSSKNISFNYFFSDFT; SSKNISFNYFFSDFTQ; SKNISFNYFFSDFTQY; KNISFNYFFSDFTQYA; NISFNYFFSDFTQYAP; ISFNYFFSDFTQYAPK; SFNYFFSDFTQYAPKD; FNYFFSDFTQYAPKDF; NYFFSDFTQYAPKDFQ; YFFSDFTQYAPKDFQD; FFSDFTQYAPKDFQDT; FSDFTQYAPKDFQDTL; SDFTQYAPKDFQDTLK; DFTQYAPKDFQDTLKC; FTQYAPKDFQDTLKCY; TQYAPKDFQDTLKCYL; QYAPKDFQDTLKCYLY; YAPKDFQDTLKCYLYV; APKDFQDTLKCYLYVI; PKDFQDTLKCYLYVIE; KDFQDTLKCYLYVIEK; DFQDTLKCYLYVIEKT; FQDTLKCYLYVIEKTI; QDTLKCYLYVIEKTIT; DTLKCYLYVIEKTITK; TLKCYLYVIEKTITKK; LKCYLYVIEKTITKKY; KCYLYVIEKTITKKYL; CYLYVIEKTITKKYLT; YLYVIEKTITKKYLTW; LYVIEKTITKKYLTWF; YVIEKTITKKYLTWFF; VIEKTITKKYLTWFFK; IEKTITKKYLTWFFKD; EKTITKKYLTWFFKDK; KTITKKYLTWFFKDKI; TITKKYLTWFFKDKIS; ITKKYLTWFFKDKISN; TKKYLTWFFKDKISNN; KKYLTWFFKDKISNNW; KYLTWFFKDKISNNWE; YLTWFFKDKISNNWES; LTWFFKDKISNNWESF; TWFFKDKISNNWESFI; WFFKDKISNNWESFID; FFKDKISNNWESFIDA; FKDKISNNWESFIDAL; KDKISNNWESFIDALE; DKISNNWESFIDALEY; KISNNWESFIDALEYI; ISNNWESFIDALEYIE; SNNWESFIDALEYIEK; NNWESFIDALEYIEKH; NWESFIDALEYIEKHK; WESFIDALEYIEKHKL; ESFIDALEYIEKHKLI; SFIDALEYIEKHKLIN; FIDALEYIEKHKLINI; IDALEYIEKHKLINIK; DALEYIEKHKLINIKE; ALEYIEKHKLINIKEK; LEYIEKHKLINIKEKI; EYIEKHKLINIKEKIK; YIEKHKLINIKEKIKE; IEKHKLINIKEKIKEI; EKHKLINIKEKIKEII; KHKLINIKEKIKEIIT; HKLINIKEKIKEIITA; KLINIKEKIKEIITAK; LINIKEKIKEIITAKF; INIKEKIKEIITAKFQ; NIKEKIKEIITAKFQT; IKEKIKEIITAKFQTE; KEKIKEIITAKFQTED; EKIKEIITAKFQTEDF; KIKEIITAKFQTEDFF; IKEIITAKFQTEDFFI; KEIITAKFQTEDFFIS; EIITAKFQTEDFFISF; IITAKFQTEDFFISFD; ITAKFQTEDFFISFDK; TAKFQTEDFFISFDKT; AKFQTEDFFISFDKTN; KFQTEDFFISFDKTNF; FQTEDFFISFDKTNFN; QTEDFFISFDKTNFNP; TEDFFISFDKTNFNPY; EDFFISFDKTNFNPYE; DFFISFDKTNFNPYES; FFISFDKTNFNPYESS; FISFDKTNFNPYESSI; ISFDKTNFNPYESSIF; SFDKTNFNPYESSIFK; FDKTNFNPYESSIFKE; DKTNFNPYESSIFKER; KTNFNPYESSIFKERY; TNFNPYESSIFKERYI; NFNPYESSIFKERYIK; FNPYESSIFKERYIKS; NPYESSIFKERYIKSA; PYESSIFKERYIKSAF; YESSIFKERYIKSAFL; ESSIFKERYIKSAFLE; SSIFKERYIKSAFLEI; SIFKERYIKSAFLEII; IFKERYIKSAFLEIIM; FKERYIKSAFLEIIMH; KERYIKSAFLEIIMHY; ERYIKSAFLEIIMHYV; RYIKSAFLEIIMHYVK; YIKSAFLEIIMHYVKK; IKSAFLEIIMHYVKKN; KSAFLEIIMHYVKKNS; SAFLEIIMHYVKKNSQ; AFLEIIMHYVKKNSQN; FLEIIMHYVKKNSQNI; LEIIMHYVKKNSQNIE; EIIMHYVKKNSQNIET; IIMHYVKKNSQNIETY; IMHYVKKNSQNIETYG;

	MHYVKKNSQNIETYGW; HYVKKNSQNIETYGWI; YVKKNSQNIETYGWIA; VKKNSQNIETYGWIAF; KKNSQNIETYGWIAFY; KNSQNIETYGWIAFYI; NSQNIETYGWIAFYIY; SQNIETYGWIAFYIYA; QNIETYGWIAFYIYAD; NIETYGWIAFYIYADN; IETYGWIAFYIYADNK; ETYGWIAFYIYADNKD; TYGWIAFYIYADNKDK; YGWIAFYIYADNKDKK; GWIAFYIYADNKDKKI; WIAFYIYADNKDKKIF; IAFYIYADNKDKKIFC; AFYIYADNKDKKIFCQ; FYIYADNKDKKIFCQR; YIYADNKDKKIFCQRM; IYADNKDKKIFCQRMK; YADNKDKKIFCQRMKE; ADNKDKKIFCQRMKEF; DNKDKKIFCQRMKEFF; NKDKKIFCQRMKEFFK; KDKKIFCQRMKEFFKS; DKKIFCQRMKEFFKSK; KKIFCQRMKEFFKSKT; KIFCQRMKEFFKSKTF; IFCQRMKEFFKSKTFE; FCQRMKEFFKSKTFEI; CQRMKEFFKSKTFEIQ; QRMKEFFKSKTFEIQN; RMKEFFKSKTFEIQNQ; MKEFFKSKTFEIQNQI; KEFFKSKTFEIQNQIF; EFFKSKTFEIQNQIFV; FFKSKTFEIQNQIFVY; FKSKTFEIQNQIFVYF; KSKTFEIQNQIFVYFL; SKTFEIQNQIFVYFLS; KTFEIQNQIFVYFLSF; TFEIQNQIFVYFLSFY; FEIQNQIFVYFLSFYP; EIQNQIFVYFLSFYPN; IQNQIFVYFLSFYPNI; QNQIFVYFLSFYPNIE; NQIFVYFLSFYPNIEY; QIFVYFLSFYPNIEYK; IFVYFLSFYPNIEYKH; FVYFLSFYPNIEYKHF; VYFLSFYPNIEYKHFK; YFLSFYPNIEYKHFKF; FLSFYPNIEYKHFKFI; LSFYPNIEYKHFKFIS; SFYPNIEYKHFKFISD; FYPNIEYKHFKFISDI; YPNIEYKHFKFISDIL; PNIEYKHFKFISDILL; NIEYKHFKFISDILLY; IEYKHFKFISDILLYL; EYKHFKFISDILLYLD; YKHFKFISDILLYLDE; KHFKFISDILLYLDEN; HFKFISDILLYLDENK; FKFISDILLYLDENKI; KFISDILLYLDENKIT; FISDILLYLDENKITI; ISDILLYLDENKITIP; SDILLYLDENKITIPK; DILLYLDENKITIPKK; ILLYLDENKITIPKKI; LLYLDENKITIPKKII; LYLDENKITIPKKIIK; YLDENKITIPKKIIKI; LDENKITIPKKIIKIQ; DENKITIPKKIIKIQK; ENKITIPKKIIKIQKI; NKITIPKKIIKIQKIN; KITIPKKIIKIQKINP; ITIPKKIIKIQKINPN; TIPKKIIKIQKINPNQ; IPKKIIKIQKINPNQL; PKKIIKIQKINPNQLD; KKIIKIQKINPNQLDY; KIIKIQKINPNQLDYQ; IIKIQKINPNQLDYQK; IKIQKINPNQLDYQKS; KIQKINPNQLDYQKSY; IQKINPNQLDYQKSYL; QKINPNQLDYQKSYLL; KINPNQLDYQKSYLLI; INPNQLDYQKSYLLIK; NPNQLDYQKSYLLIKS; PNQLDYQKSYLLIKSL; NQLDYQKSYLLIKSLK; QLDYQKSYLLIKSLKT; LDYQKSYLLIKSLKTR; DYQKSYLLIKSLKTRS; YQKSYLLIKSLKTRSR; QKSYLLIKSLKTRSRI; KSYLLIKSLKTRSRIL; SYLLIKSLKTRSRILK; YLLIKSLKTRSRILKI; LLIKSLKTRSRILKII; LIKSLKTRSRILKIII; IKSLKTRSRILKIIIK; KSLKTRSRILKIIIKN; SLKTRSRILKIIIKNI; LKTRSRILKIIIKNIR; KTRSRILKIIIKNIRF; TRSRILKIIIKNIRFN; RSRILKIIIKNIRFNL; SRILKIIIKNIRFNLI; RILKIIIKNIRFNLIE; ILKIIIKNIRFNLIEK; LKIIIKNIRFNLIEKL; KIIIKNIRFNLIEKLE; IIIKNIRFNLIEKLED; IIKNIRFNLIEKLEDE; IKNIRFNLIEKLEDEN; KNIRFNLIEKLEDENE; NIRFNLIEKLEDENEK; IRFNLIEKLEDENEKK; RFNLIEKLEDENEKKL; FNLIEKLEDENEKKLL; NLIEKLEDENEKKLLP; LIEKLEDENEKKLLPA; IEKLEDENEKKLLPAM; EKLEDENEKKLLPAMC; KLEDENEKKLLPAMCY; LEDENEKKLLPAMCYL; EDENEKKLLPAMCYLI; DENEKKLLPAMCYLIY; ENEKKLLPAMCYLIYC; NEKKLLPAMCYLIYCE; EKKLLPAMCYLIYCEN; KKLLPAMCYLIYCENL; KLLPAMCYLIYCENLV; LLPAMCYLIYCENLVE; LPAMCYLIYCENLVEL; PAMCYLIYCENLVELK; AMCYLIYCENLVELKN; MCYLIYCENLVELKNN; CYLIYCENLVELKNNR; YLIYCENLVELKNNRK; LIYCENLVELKNNRKI; IYCENLVELKNNRKIK; YCENLVELKNNRKIKS; CENLVELKNNRKIKSN; ENLVELKNNRKIKSNE; NLVELKNNRKIKSNEK; LVELKNNRKIKSNEKN;

	VELKNNRKIKSNEKNS; ELKNNRKIKSNEKNSL; LKNNRKIKSNEKNSLL; KNNRKIKSNEKNSLLE; NNRKIKSNEKNSLLEF; NRKIKSNEKNSLLEFI; RKIKSNEKNSLLEFIS; KIKSNEKNSLLEFISF; IKSNEKNSLLEFISFF; KSNEKNSLLEFISFFK; SNEKNSLLEFISFFKT; NEKNSLLEFISFFKTK; EKNSLLEFISFFKTKL; KNSLLEFISFFKTKLK; NSLLEFISFFKTKLKQ; SLLEFISFFKTKLKQK; LLEFISFFKTKLKQKI; LEFISFFKTKLKQKIN; EFISFFKTKLKQKINF; FISFFKTKLKQKINFK; ISFFKTKLKQKINFKK; SFFKTKLKQKINFKKE; FFKTKLKQKINFKKEL; FKTKLKQKINFKKELM; KTKLKQKINFKKELMK; TKLKQKINFKKELMKS; KLKQKINFKKELMKSK; LKQKINFKKELMKSKG; KQKINFKKELMKSKGI;
Seq 29	13 mers: MITQQDYTEIKKK; ITQQDYTEIKKKL; TQQDYTEIKKKLE; QQDYTEIKKKLEN; QDYTEIKKKLENT; DYTEIKKKLENTK; YTEIKKKLENTKT; TEIKKKLENTKTR; EIKKKLENTKTRI; IKKKLENTKTRIQ; KKKLENTKTRIQF; KKLENTKTRIQFR; KLENTKTRIQFRN; LENTKTRIQFRNG; ENTKTRIQFRNGN; NTKTRIQFRNGNK; TKTRIQFRNGNKI; KTRIQFRNGNKID; TRIQFRNGNKIDS; RIQFRNGNKIDSL; IQFRNGNKIDSLG; QFRNGNKIDSLGY; FRNGNKIDSLGYQ; RNGNKIDSLGYQG; NGNKIDSLGYQGS; GNKIDSLGYQGSL; NKIDSLGYQGSLG; KIDSLGYQGSLGE; IDSLGYQGSLGEP; DSLGYQGSLGEPI; SLGYQGSLGEPIL; LGYQGSLGEPILL; GYQGSLGEPILLK; YQGSLGEPILLKD; QGSLGEPILLKDK; GSLGEPILLKDKL; SLGEPILLKDKLT; LGEPILLKDKLTF; GEPILLKDKLTFS; EPILLKDKLTFSI; PILLKDKLTFSIC; ILLKDKLTFSICD; LLKDKLTFSICDG; LKDKLTFSICDGK; KDKLTFSICDGKN; DKLTFSICDGKNI; KLTFSICDGKNID; LTFSICDGKNIDN; TFSICDGKNIDNR; FSICDGKNIDNRK; SICDGKNIDNRKE; ICDGKNIDNRKEY; CDGKNIDNRKEYE; DGKNIDNRKEYEI; GKNIDNRKEYEIT; KNIDNRKEYEITK; NIDNRKEYEITKN; IDNRKEYEITKNA; DNRKEYEITKNAP; NRKEYEITKNAPS; RKEYEITKNAPSL; KEYEITKNAPSLD; EYEITKNAPSLDS; YEITKNAPSLDSL; EITKNAPSLDSLI; ITKNAPSLDSLIE; TKNAPSLDSLIEY; KNAPSLDSLIEYL; NAPSLDSLIEYLE; APSLDSLIEYLEH; PSLDSLIEYLEHM; SLDSLIEYLEHMI; LDSLIEYLEHMIL; DSLIEYLEHMILF; SLIEYLEHMILFF; LIEYLEHMILFFL; IEYLEHMILFFLE; EYLEHMILFFLEK; YLEHMILFFLEKT; LEHMILFFLEKTP; EHMILFFLEKTPV; HMILFFLEKTPVG; MILFFLEKTPVGT; ILFFLEKTPVGTL; LFFLEKTPVGTLT; FFLEKTPVGTLTA; FLEKTPVGTLTAK; LEKTPVGTLTAKF; EKTPVGTLTAKFA; KTPVGTLTAKFAM; TPVGTLTAKFAME; PVGTLTAKFAMEG; VGTLTAKFAMEGS; GTLTAKFAMEGSI; TLTAKFAMEGSIL; LTAKFAMEGSILT; TAKFAMEGSILTR; AKFAMEGSILTRS; KFAMEGSILTRSK; FAMEGSILTRSKL; AMEGSILTRSKLI; MEGSILTRSKLIQ; EGSILTRSKLIQA; GSILTRSKLIQAF; SILTRSKLIQAFT; ILTRSKLIQAFTN; LTRSKLIQAFTNT; TRSKLIQAFTNTN; RSKLIQAFTNTNK; SKLIQAFTNTNKF; KLIQAFTNTNKFC; LIQAFTNTNKFCI; IQAFTNTNKFCIP; QAFTNTNKFCIPD;

	AFTNTNKFCIPDG; FTNTNKFCIPDGR; TNTNKFCIPDGRS; NTNKFCIPDGRSL; TNKFCIPDGRSLP; NKFCIPDGRSLPS; KFCIPDGRSLPSN; FCIPDGRSLPSNC; CIPDGRSLPSNCY; IPDGRSLPSNCYA; PDGRSLPSNCYAY; DGRSLPSNCYAYK; GRSLPSNCYAYKV; RSLPSNCYAYKVL; SLPSNCYAYKVLG; LPSNCYAYKVLGI; PSNCYAYKVLGIS; SNCYAYKVLGISS; NCYAYKVLGISSA; CYAYKVLGISSAP; YAYKVLGISSAPK; AYKVLGISSAPKL; YKVLGISSAPKLS; KVLGISSAPKLSG; VLGISSAPKLSGR; LGISSAPKLSGRF; GISSAPKLSGRFL; ISSAPKLSGRFLR; SSAPKLSGRFLRH; SAPKLSGRFLRHY; APKLSGRFLRHYD; PKLSGRFLRHYDS; KLSGRFLRHYDSG; LSGRFLRHYDSGG; SGRFLRHYDSGGS; GRFLRHYDSGGST; RFLRHYDSGGSTD; FLRHYDSGGSTDS; LRHYDSGGSTDSD; RHYDSGGSTDSDG; HYDSGGSTDSDGT; YDSGGSTDSDGTR; DSGGSTDSDGTRS; SGGSTDSDGTRSL; GGSTDSDGTRSLG; GSTDSDGTRSLGH; STDSDGTRSLGHT; TDSDGTRSLGHTQ; DSDGTRSLGHTQE; SDGTRSLGHTQED; DGTRSLGHTQEDS; GTRSLGHTQEDSY; TRSLGHTQEDSYK; RSLGHTQEDSYKN; SLGHTQEDSYKNH; LGHTQEDSYKNHD; GHTQEDSYKNHDH; HTQEDSYKNHDHD; TQEDSYKNHDHDL; QEDSYKNHDHDLD; EDSYKNHDHDLDF; DSYKNHDHDLDFS; SYKNHDHDLDFSR; YKNHDHDLDFSRI; KNHDHDLDFSRIN; NHDHDLDFSRINF; HDHDLDFSRINFK; DHDLDFSRINFKG; HDLDFSRINFKGK; DLDFSRINFKGKL; LDFSRINFKGKLV; DFSRINFKGKLVK; FSRINFKGKLVKR; SRINFKGKLVKRM; RINFKGKLVKRMT; INFKGKLVKRMTM; NFKGKLVKRMTMI; FKGKLVKRMTMIY; KGKLVKRMTMIYR; GKLVKRMTMIYRS; KLVKRMTMIYRSA; LVKRMTMIYRSAD; VKRMTMIYRSADT; KRMTMIYRSADTW; RMTMIYRSADTWY; MTMIYRSADTWYT; TMIYRSADTWYTW; MIYRSADTWYTWY; IYRSADTWYTWYW; YRSADTWYTWYWA; RSADTWYTWYWAE; SADTWYTWYWAEE; ADTWYTWYWAEEI; DTWYTWYWAEEIM; TWYTWYWAEEIMS; WYTWYWAEEIMSP; YTWYWAEEIMSPF; TWYWAEEIMSPFI; WYWAEEIMSPFIT; YWAEEIMSPFITG; WAEEIMSPFITGY; AEEIMSPFITGYS; EEIMSPFITGYSY; EIMSPFITGYSYE; IMSPFITGYSYEE; MSPFITGYSYEEI; SPFITGYSYEEID; PFITGYSYEEIDP; FITGYSYEEIDPE; ITGYSYEEIDPEY; TGYSYEEIDPEYL; GYSYEEIDPEYLL; YSYEEIDPEYLLP; SYEEIDPEYLLPP; YEEIDPEYLLPPF; EEIDPEYLLPPFT; EIDPEYLLPPFTS; IDPEYLLPPFTSQ; DPEYLLPPFTSQS; PEYLLPPFTSQSG; EYLLPPFTSQSGS; YLLPPFTSQSGSK; LLPPFTSQSGSKE; LPPFTSQSGSKET; PPFTSQSGSKETK; PFTSQSGSKETKP; FTSQSGSKETKPK; TSQSGSKETKPKN; SQSGSKETKPKNT; QSGSKETKPKNTC; SGSKETKPKNTCY; GSKETKPKNTCYI; SKETKPKNTCYIS; KETKPKNTCYISF; ETKPKNTCYISFY; TKPKNTCYISFYR; KPKNTCYISFYRY; PKNTCYISFYRYD; KNTCYISFYRYDL; 14 mers: MITQQDYTEIKKKL; ITQQDYTEIKKKLE; TQQDYTEIKKKLEN; QQDYTEIKKKLENT; QDYTEIKKKLENTK; DYTEIKKKLENTKT;

	YTEIKKKLENTKTR; TEIKKKLENTKTRI; EIKKKLENTKTRIQ; IKKKLENTKTRIQF; KKKLENTKTRIQFR; KKLENTKTRIQFRN; KLENTKTRIQFRNG; LENTKTRIQFRNGN; ENTKTRIQFRNGNK; NTKTRIQFRNGNKI; TKTRIQFRNGNKID; KTRIQFRNGNKIDS; TRIQFRNGNKIDSL; RIQFRNGNKIDSLG; IQFRNGNKIDSLGY; QFRNGNKIDSLGYQ; FRNGNKIDSLGYQG; RNGNKIDSLGYQGS; NGNKIDSLGYQGSL; GNKIDSLGYQGSLG; NKIDSLGYQGSLGE; KIDSLGYQGSLGEP; IDSLGYQGSLGEPI; DSLGYQGSLGEPIL; SLGYQGSLGEPILL; LGYQGSLGEPILLK; GYQGSLGEPILLKD; YQGSLGEPILLKDK; QGSLGEPILLKDKL; GSLGEPILLKDKLT; SLGEPILLKDKLTF; LGEPILLKDKLTFS; GEPILLKDKLTFSI; EPILLKDKLTFSIC; PILLKDKLTFSICD; ILLKDKLTFSICDG; LLKDKLTFSICDGK; LKDKLTFSICDGKN; KDKLTFSICDGKNI; DKLTFSICDGKNID; KLTFSICDGKNIDN; LTFSICDGKNIDNR; TFSICDGKNIDNRK; FSICDGKNIDNRKE; SICDGKNIDNRKEY; ICDGKNIDNRKEYE; CDGKNIDNRKEYEI; DGKNIDNRKEYEIT; GKNIDNRKEYEITK; KNIDNRKEYEITKN; NIDNRKEYEITKNA; IDNRKEYEITKNAP; DNRKEYEITKNAPS; NRKEYEITKNAPSL; RKEYEITKNAPSLD; KEYEITKNAPSLDS; EYEITKNAPSLDSL; YEITKNAPSLDSLI; EITKNAPSLDSLIE; ITKNAPSLDSLIEY; TKNAPSLDSLIEYL; KNAPSLDSLIEYLE; NAPSLDSLIEYLEH; APSLDSLIEYLEHM; PSLDSLIEYLEHMI; SLDSLIEYLEHMIL; LDSLIEYLEHMILF; DSLIEYLEHMILFF; SLIEYLEHMILFFL; LIEYLEHMILFFLE; IEYLEHMILFFLEK; EYLEHMILFFLEKT; YLEHMILFFLEKTP; LEHMILFFLEKTPV; EHMILFFLEKTPVG; HMILFFLEKTPVGT; MILFFLEKTPVGTL; ILFFLEKTPVGTLT; LFFLEKTPVGTLTA; FFLEKTPVGTLTAK; FLEKTPVGTLTAKF; LEKTPVGTLTAKFA; EKTPVGTLTAKFAM; KTPVGTLTAKFAME; TPVGTLTAKFAMEG; PVGTLTAKFAMEGS; VGTLTAKFAMEGSI; GTLTAKFAMEGSIL; TLTAKFAMEGSILT; LTAKFAMEGSILTR; TAKFAMEGSILTRS; AKFAMEGSILTRSK; KFAMEGSILTRSKL; FAMEGSILTRSKLI; AMEGSILTRSKLIQ; MEGSILTRSKLIQA; EGSILTRSKLIQAF; GSILTRSKLIQAFT; SILTRSKLIQAFTN; ILTRSKLIQAFTNT; LTRSKLIQAFTNTN; TRSKLIQAFTNTNK; RSKLIQAFTNTNKF; SKLIQAFTNTNKFC; KLIQAFTNTNKFCI; LIQAFTNTNKFCIP; IQAFTNTNKFCIPD; QAFTNTNKFCIPDG; AFTNTNKFCIPDGR; FTNTNKFCIPDGRS; TNTNKFCIPDGRSL; NTNKFCIPDGRSLP; TNKFCIPDGRSLPS; NKFCIPDGRSLPSN; KFCIPDGRSLPSNC; FCIPDGRSLPSNCY; CIPDGRSLPSNCYA; IPDGRSLPSNCYAY; PDGRSLPSNCYAYK; DGRSLPSNCYAYKV; GRSLPSNCYAYKVL; RSLPSNCYAYKVLG; SLPSNCYAYKVLGI; LPSNCYAYKVLGIS; PSNCYAYKVLGISS; SNCYAYKVLGISSA; NCYAYKVLGISSAP; CYAYKVLGISSAPK; YAYKVLGISSAPKL; AYKVLGISSAPKLS; YKVLGISSAPKLSG; KVLGISSAPKLSGR; VLGISSAPKLSGRF; LGISSAPKLSGRFL; GISSAPKLSGRFLR; ISSAPKLSGRFLRH; SSAPKLSGRFLRHY; SAPKLSGRFLRHYD; APKLSGRFLRHYDS; PKLSGRFLRHYDSG; KLSGRFLRHYDSGG; LSGRFLRHYDSGGS; SGRFLRHYDSGGST; GRFLRHYDSGGSTD; RFLRHYDSGGSTDS; FLRHYDSGGSTDSD; LRHYDSGGSTDSDG; RHYDSGGSTDSDGT; HYDSGGSTDSDGTR; YDSGGSTDSDGTRS; DSGGSTDSDGTRSL; SGGSTDSDGTRSLG; GGSTDSDGTRSLGH;

GSTDSDGTRSLGHT; STDSDGTRSLGHTQ; TDSDGTRSLGHTQE;
DSDGTRSLGHTQED; SDGTRSLGHTQEDS; DGTRSLGHTQEDSY;
GTRSLGHTQEDSYK; TRSLGHTQEDSYKN; RSLGHTQEDSYKNH;
SLGHTQEDSYKNHD; LGHTQEDSYKNHDH; GHTQEDSYKNHDHD;
HTQEDSYKNHDHDL; TQEDSYKNHDHDLD; QEDSYKNHDHDLDF;
EDSYKNHDHDLDFS; DSYKNHDHDLDFSR; SYKNHDHDLDFSRI;
YKNHDHDLDFSRIN; KNHDHDLDFSRINF; NHDHDLDFSRINFK;
HDHDLDFSRINFKG; DHDLDFSRINFKGK; HDLDFSRINFKGKL;
DLDFSRINFKGKLV; LDFSRINFKGKLVK; DFSRINFKGKLVKR;
FSRINFKGKLVKRM; SRINFKGKLVKRMT; RINFKGKLVKRMTM;
INFKGKLVKRMTMI; NFKGKLVKRMTMIY; FKGKLVKRMTMIYR;
KGKLVKRMTMIYRS; GKLVKRMTMIYRSA; KLVKRMTMIYRSAD;
LVKRMTMIYRSADT; VKRMTMIYRSADTW; KRMTMIYRSADTWY;
RMTMIYRSADTWYT; MTMIYRSADTWYTW; TMIYRSADTWYTWY;
MIYRSADTWYTWYW; IYRSADTWYTWYWA; YRSADTWYTWYWAE;
RSADTWYTWYWAEE; SADTWYTWYWAEEI; ADTWYTWYWAEEIM;
DTWYTWYWAEEIMS; TWYTWYWAEEIMSP; WYTWYWAEEIMSPF;
YTWYWAEEIMSPFI; TWYWAEEIMSPFIT; WYWAEEIMSPFITG;
YWAEEIMSPFITGY; WAEEIMSPFITGYS; AEEIMSPFITGYSY;
EEIMSPFITGYSYE; EIMSPFITGYSYEE; IMSPFITGYSYEEI;
MSPFITGYSYEEID; SPFITGYSYEEIDP; PFITGYSYEEIDPE;
FITGYSYEEIDPEY; ITGYSYEEIDPEYL; TGYSYEEIDPEYLL;
GYSYEEIDPEYLLP; YSYEEIDPEYLLPP; SYEEIDPEYLLPPF;
YEEIDPEYLLPPFT; EEIDPEYLLPPFTS; EIDPEYLLPPFTSQ;
IDPEYLLPPFTSQS; DPEYLLPPFTSQSG; PEYLLPPFTSQSGS;
EYLLPPFTSQSGSK; YLLPPFTSQSGSKE; LLPPFTSQSGSKET;
LPPFTSQSGSKETK; PPFTSQSGSKETKP; PFTSQSGSKETKPK;
FTSQSGSKETKPKN; TSQSGSKETKPKNT; SQSGSKETKPKNTC;
QSGSKETKPKNTCY; SGSKETKPKNTCYI; GSKETKPKNTCYIS;
SKETKPKNTCYISF; KETKPKNTCYISFY; ETKPKNTCYISFYR;
TKPKNTCYISFYRY; KPKNTCYISFYRYD; PKNTCYISFYRYDL;

15 mers:
MITQQDYTEIKKKLE; ITQQDYTEIKKKLEN; TQQDYTEIKKKLENT;
QQDYTEIKKKLENTK; QDYTEIKKKLENTKT; DYTEIKKKLENTKTR;
YTEIKKKLENTKTRI; TEIKKKLENTKTRIQ; EIKKKLENTKTRIQF;
IKKKLENTKTRIQFR; KKKLENTKTRIQFRN; KKLENTKTRIQFRNG;
KLENTKTRIQFRNGN; LENTKTRIQFRNGNK; ENTKTRIQFRNGNKI;
NTKTRIQFRNGNKID; TKTRIQFRNGNKIDS; KTRIQFRNGNKIDSL;
TRIQFRNGNKIDSLG; RIQFRNGNKIDSLGY; IQFRNGNKIDSLGYQ;
QFRNGNKIDSLGYQG; FRNGNKIDSLGYQGS; RNGNKIDSLGYQGSL;
NGNKIDSLGYQGSLG; GNKIDSLGYQGSLGE; NKIDSLGYQGSLGEP;
KIDSLGYQGSLGEPI; IDSLGYQGSLGEPIL; DSLGYQGSLGEPILL;
SLGYQGSLGEPILLK; LGYQGSLGEPILLKD; GYQGSLGEPILLKDK;
YQGSLGEPILLKDKL; QGSLGEPILLKDKLT; GSLGEPILLKDKLTF;
SLGEPILLKDKLTFS; LGEPILLKDKLTFSI; GEPILLKDKLTFSIC;
EPILLKDKLTFSICD; PILLKDKLTFSICDG; ILLKDKLTFSICDGK;
LLKDKLTFSICDGKN; LKDKLTFSICDGKNI; KDKLTFSICDGKNID;
DKLTFSICDGKNIDN; KLTFSICDGKNIDNR; LTFSICDGKNIDNRK;
TFSICDGKNIDNRKE; FSICDGKNIDNRKEY; SICDGKNIDNRKEYE;
ICDGKNIDNRKEYEI; CDGKNIDNRKEYEIT; DGKNIDNRKEYEITK;

	GKNIDNRKEYEITKN; KNIDNRKEYEITKNA; NIDNRKEYEITKNAP; IDNRKEYEITKNAPS; DNRKEYEITKNAPSL; NRKEYEITKNAPSLD; RKEYEITKNAPSLDS; KEYEITKNAPSLDSL; EYEITKNAPSLDSLI; YEITKNAPSLDSLIE; EITKNAPSLDSLIEY; ITKNAPSLDSLIEYL; TKNAPSLDSLIEYLE; KNAPSLDSLIEYLEH; NAPSLDSLIEYLEHM; APSLDSLIEYLEHMI; PSLDSLIEYLEHMIL; SLDSLIEYLEHMILF; LDSLIEYLEHMILFF; DSLIEYLEHMILFFL; SLIEYLEHMILFFLE; LIEYLEHMILFFLEK; IEYLEHMILFFLEKT; EYLEHMILFFLEKTP; YLEHMILFFLEKTPV; LEHMILFFLEKTPVG; EHMILFFLEKTPVGT; HMILFFLEKTPVGTL; MILFFLEKTPVGTLT; ILFFLEKTPVGTLTA; LFFLEKTPVGTLTAK; FFLEKTPVGTLTAKF; FLEKTPVGTLTAKFA; LEKTPVGTLTAKFAM; EKTPVGTLTAKFAME; KTPVGTLTAKFAMEG; TPVGTLTAKFAMEGS; PVGTLTAKFAMEGSI; VGTLTAKFAMEGSIL; GTLTAKFAMEGSILT; TLTAKFAMEGSILTR; LTAKFAMEGSILTRS; TAKFAMEGSILTRSK; AKFAMEGSILTRSKL; KFAMEGSILTRSKLI; FAMEGSILTRSKLIQ; AMEGSILTRSKLIQA; MEGSILTRSKLIQAF; EGSILTRSKLIQAFT; GSILTRSKLIQAFTN; SILTRSKLIQAFTNT; ILTRSKLIQAFTNTN; LTRSKLIQAFTNTNK; TRSKLIQAFTNTNKF; RSKLIQAFTNTNKFC; SKLIQAFTNTNKFCI; KLIQAFTNTNKFCIP; LIQAFTNTNKFCIPD; IQAFTNTNKFCIPDG; QAFTNTNKFCIPDGR; AFTNTNKFCIPDGRS; FTNTNKFCIPDGRSL; TNTNKFCIPDGRSLP; NTNKFCIPDGRSLPS; TNKFCIPDGRSLPSN; NKFCIPDGRSLPSNC; KFCIPDGRSLPSNCY; FCIPDGRSLPSNCYA; CIPDGRSLPSNCYAY; IPDGRSLPSNCYAYK; PDGRSLPSNCYAYKV; DGRSLPSNCYAYKVL; GRSLPSNCYAYKVLG; RSLPSNCYAYKVLGI; SLPSNCYAYKVLGIS; LPSNCYAYKVLGISS; PSNCYAYKVLGISSA; SNCYAYKVLGISSAP; NCYAYKVLGISSAPK; CYAYKVLGISSAPKL; YAYKVLGISSAPKLS; AYKVLGISSAPKLSG; YKVLGISSAPKLSGR; KVLGISSAPKLSGRF; VLGISSAPKLSGRFL; LGISSAPKLSGRFLR; GISSAPKLSGRFLRH; ISSAPKLSGRFLRHY; SSAPKLSGRFLRHYD; SAPKLSGRFLRHYDS; APKLSGRFLRHYDSG; PKLSGRFLRHYDSGG; KLSGRFLRHYDSGGS; LSGRFLRHYDSGGST; SGRFLRHYDSGGSTD; GRFLRHYDSGGSTDS; RFLRHYDSGGSTDSD; FLRHYDSGGSTDSDG; LRHYDSGGSTDSDGT; RHYDSGGSTDSDGTR; HYDSGGSTDSDGTRS; YDSGGSTDSDGTRSL; DSGGSTDSDGTRSLG; SGGSTDSDGTRSLGH; GGSTDSDGTRSLGHT; GSTDSDGTRSLGHTQ; STDSDGTRSLGHTQE; TDSDGTRSLGHTQED; DSDGTRSLGHTQEDS; SDGTRSLGHTQEDSY; DGTRSLGHTQEDSYK; GTRSLGHTQEDSYKN; TRSLGHTQEDSYKNH; RSLGHTQEDSYKNHD; SLGHTQEDSYKNHDH; LGHTQEDSYKNHDHD; GHTQEDSYKNHDHDL; HTQEDSYKNHDHDLD; TQEDSYKNHDHDLDF; QEDSYKNHDHDLDFS; EDSYKNHDHDLDFSR; DSYKNHDHDLDFSRI; SYKNHDHDLDFSRIN; YKNHDHDLDFSRINF; KNHDHDLDFSRINFK; NHDHDLDFSRINFKG; HDHDLDFSRINFKGK; DHDLDFSRINFKGKL; HDLDFSRINFKGKLV; DLDFSRINFKGKLVK; LDFSRINFKGKLVKR; DFSRINFKGKLVKRM; FSRINFKGKLVKRMT; SRINFKGKLVKRMTM; RINFKGKLVKRMTMI; INFKGKLVKRMTMIY; NFKGKLVKRMTMIYR; FKGKLVKRMTMIYRS; KGKLVKRMTMIYRSA; GKLVKRMTMIYRSAD; KLVKRMTMIYRSADT; LVKRMTMIYRSADTW; VKRMTMIYRSADTWY; KRMTMIYRSADTWYT; RMTMIYRSADTWYTW; MTMIYRSADTWYTWY; TMIYRSADTWYTWYW; MIYRSADTWYTWYWA; IYRSADTWYTWYWAE; YRSADTWYTWYWAEE; RSADTWYTWYWAEEI; SADTWYTWYWAEEIM; ADTWYTWYWAEEIMS;

DTWYTWYWAEEIMSP; TWYTWYWAEEIMSPF; WYTWYWAEEIMSPFI;
YTWYWAEEIMSPFIT; TWYWAEEIMSPFITG; WYWAEEIMSPFITGY;
YWAEEIMSPFITGYS; WAEEIMSPFITGYSY; AEEIMSPFITGYSYE;
EEIMSPFITGYSYEE; EIMSPFITGYSYEEI; IMSPFITGYSYEEID;
MSPFITGYSYEEIDP; SPFITGYSYEEIDPE; PFITGYSYEEIDPEY;
FITGYSYEEIDPEYL; ITGYSYEEIDPEYLL; TGYSYEEIDPEYLLP;
GYSYEEIDPEYLLPP; YSYEEIDPEYLLPPF; SYEEIDPEYLLPPFT;
YEEIDPEYLLPPFTS; EEIDPEYLLPPFTSQ; EIDPEYLLPPFTSQS;
IDPEYLLPPFTSQSG; DPEYLLPPFTSQSGS; PEYLLPPFTSQSGSK;
EYLLPPFTSQSGSKE; YLLPPFTSQSGSKET; LLPPFTSQSGSKETK;
LPPFTSQSGSKETKP; PPFTSQSGSKETKPK; PFTSQSGSKETKPKN;
FTSQSGSKETKPKNT; TSQSGSKETKPKNTC; SQSGSKETKPKNTCY;
QSGSKETKPKNTCYI; SGSKETKPKNTCYIS; GSKETKPKNTCYISF;
SKETKPKNTCYISFY; KETKPKNTCYISFYR; ETKPKNTCYISFYRY;
TKPKNTCYISFYRYD; KPKNTCYISFYRYDL;

16 mers:
MITQQDYTEIKKKLEN; ITQQDYTEIKKKLENT; TQQDYTEIKKKLENTK;
QQDYTEIKKKLENTKT; QDYTEIKKKLENTKTR; DYTEIKKKLENTKTRI;
YTEIKKKLENTKTRIQ; TEIKKKLENTKTRIQF; EIKKKLENTKTRIQFR;
IKKKLENTKTRIQFRN; KKKLENTKTRIQFRNG; KKLENTKTRIQFRNGN;
KLENTKTRIQFRNGNK; LENTKTRIQFRNGNKI; ENTKTRIQFRNGNKID;
NTKTRIQFRNGNKIDS; TKTRIQFRNGNKIDSL; KTRIQFRNGNKIDSLG;
TRIQFRNGNKIDSLGY; RIQFRNGNKIDSLGYQ; IQFRNGNKIDSLGYQG;
QFRNGNKIDSLGYQGS; FRNGNKIDSLGYQGSL; RNGNKIDSLGYQGSLG;
NGNKIDSLGYQGSLGE; GNKIDSLGYQGSLGEP; NKIDSLGYQGSLGEPI;
KIDSLGYQGSLGEPIL; IDSLGYQGSLGEPILL; DSLGYQGSLGEPILLK;
SLGYQGSLGEPILLKD; LGYQGSLGEPILLKDK; GYQGSLGEPILLKDKL;
YQGSLGEPILLKDKLT; QGSLGEPILLKDKLTF; GSLGEPILLKDKLTFS;
SLGEPILLKDKLTFSI; LGEPILLKDKLTFSIC; GEPILLKDKLTFSICD;
EPILLKDKLTFSICDG; PILLKDKLTFSICDGK; ILLKDKLTFSICDGKN;
LLKDKLTFSICDGKNI; LKDKLTFSICDGKNID; KDKLTFSICDGKNIDN;
DKLTFSICDGKNIDNR; KLTFSICDGKNIDNRK; LTFSICDGKNIDNRKE;
TFSICDGKNIDNRKEY; FSICDGKNIDNRKEYE; SICDGKNIDNRKEYEI;
ICDGKNIDNRKEYEIT; CDGKNIDNRKEYEITK; DGKNIDNRKEYEITKN;
GKNIDNRKEYEITKNA; KNIDNRKEYEITKNAP; NIDNRKEYEITKNAPS;
IDNRKEYEITKNAPSL; DNRKEYEITKNAPSLD; NRKEYEITKNAPSLDS;
RKEYEITKNAPSLDSL; KEYEITKNAPSLDSLI; EYEITKNAPSLDSLIE;
YEITKNAPSLDSLIEY; EITKNAPSLDSLIEYL; ITKNAPSLDSLIEYLE;
TKNAPSLDSLIEYLEH; KNAPSLDSLIEYLEHM; NAPSLDSLIEYLEHMI;
APSLDSLIEYLEHMIL; PSLDSLIEYLEHMILF; SLDSLIEYLEHMILFF;
LDSLIEYLEHMILFFL; DSLIEYLEHMILFFLE; SLIEYLEHMILFFLEK;
LIEYLEHMILFFLEKT; IEYLEHMILFFLEKTP; EYLEHMILFFLEKTPV;
YLEHMILFFLEKTPVG; LEHMILFFLEKTPVGT; EHMILFFLEKTPVGTL;
HMILFFLEKTPVGTLT; MILFFLEKTPVGTLTA; ILFFLEKTPVGTLTAK;
LFFLEKTPVGTLTAKF; FFLEKTPVGTLTAKFA; FLEKTPVGTLTAKFAM;
LEKTPVGTLTAKFAME; EKTPVGTLTAKFAMEG; KTPVGTLTAKFAMEGS;
TPVGTLTAKFAMEGSI; PVGTLTAKFAMEGSIL; VGTLTAKFAMEGSILT;
GTLTAKFAMEGSILTR; TLTAKFAMEGSILTRS; LTAKFAMEGSILTRSK;
TAKFAMEGSILTRSKL; AKFAMEGSILTRSKLI; KFAMEGSILTRSKLIQ;
FAMEGSILTRSKLIQA; AMEGSILTRSKLIQAF; MEGSILTRSKLIQAFT;

	EGSILTRSKLIQAFTN; GSILTRSKLIQAFTNT; SILTRSKLIQAFTNTN; ILTRSKLIQAFTNTNK; LTRSKLIQAFTNTNKF; TRSKLIQAFTNTNKFC; RSKLIQAFTNTNKFCI; SKLIQAFTNTNKFCIP; KLIQAFTNTNKFCIPD; LIQAFTNTNKFCIPDG; IQAFTNTNKFCIPDGR; QAFTNTNKFCIPDGRS; AFTNTNKFCIPDGRSL; FTNTNKFCIPDGRSLP; TNTNKFCIPDGRSLPS; NTNKFCIPDGRSLPSN; TNKFCIPDGRSLPSNC; NKFCIPDGRSLPSNCY; KFCIPDGRSLPSNCYA; FCIPDGRSLPSNCYAY; CIPDGRSLPSNCYAYK; IPDGRSLPSNCYAYKV; PDGRSLPSNCYAYKVL; DGRSLPSNCYAYKVLG; GRSLPSNCYAYKVLGI; RSLPSNCYAYKVLGIS; SLPSNCYAYKVLGISS; LPSNCYAYKVLGISSA; PSNCYAYKVLGISSAP; SNCYAYKVLGISSAPK; NCYAYKVLGISSAPKL; CYAYKVLGISSAPKLS; YAYKVLGISSAPKLSG; AYKVLGISSAPKLSGR; YKVLGISSAPKLSGRF; KVLGISSAPKLSGRFL; VLGISSAPKLSGRFLR; LGISSAPKLSGRFLRH; GISSAPKLSGRFLRHY; ISSAPKLSGRFLRHYD; SSAPKLSGRFLRHYDS; SAPKLSGRFLRHYDSG; APKLSGRFLRHYDSGG; PKLSGRFLRHYDSGGS; KLSGRFLRHYDSGGST; LSGRFLRHYDSGGSTD; SGRFLRHYDSGGSTDS; GRFLRHYDSGGSTDSD; RFLRHYDSGGSTDSDG; FLRHYDSGGSTDSDGT; LRHYDSGGSTDSDGTR; RHYDSGGSTDSDGTRS; HYDSGGSTDSDGTRSL; YDSGGSTDSDGTRSLG; DSGGSTDSDGTRSLGH; SGGSTDSDGTRSLGHT; GGSTDSDGTRSLGHTQ; GSTDSDGTRSLGHTQE; STDSDGTRSLGHTQED; TDSDGTRSLGHTQEDS; DSDGTRSLGHTQEDSY; SDGTRSLGHTQEDSYK; DGTRSLGHTQEDSYKN; GTRSLGHTQEDSYKNH; TRSLGHTQEDSYKNHD; RSLGHTQEDSYKNHDH; SLGHTQEDSYKNHDHD; LGHTQEDSYKNHDHDL; GHTQEDSYKNHDHDLD; HTQEDSYKNHDHDLDF; TQEDSYKNHDHDLDFS; QEDSYKNHDHDLDFSR; EDSYKNHDHDLDFSRI; DSYKNHDHDLDFSRIN; SYKNHDHDLDFSRINF; YKNHDHDLDFSRINFK; KNHDHDLDFSRINFKG; NHDHDLDFSRINFKGK; HDHDLDFSRINFKGKL; DHDLDFSRINFKGKLV; HDLDFSRINFKGKLVK; DLDFSRINFKGKLVKR; LDFSRINFKGKLVKRM; DFSRINFKGKLVKRMT; FSRINFKGKLVKRMTM; SRINFKGKLVKRMTMI; RINFKGKLVKRMTMIY; INFKGKLVKRMTMIYR; NFKGKLVKRMTMIYRS; FKGKLVKRMTMIYRSA; KGKLVKRMTMIYRSAD; GKLVKRMTMIYRSADT; KLVKRMTMIYRSADTW; LVKRMTMIYRSADTWY; VKRMTMIYRSADTWYT; KRMTMIYRSADTWYTW; RMTMIYRSADTWYTWY; MTMIYRSADTWYTWYW; TMIYRSADTWYTWYWA; MIYRSADTWYTWYWAE; IYRSADTWYTWYWAEE; YRSADTWYTWYWAEEI; RSADTWYTWYWAEEIM; SADTWYTWYWAEEIMS; ADTWYTWYWAEEIMSP; DTWYTWYWAEEIMSPF; TWYTWYWAEEIMSPFI; WYTWYWAEEIMSPFIT; YTWYWAEEIMSPFITG; TWYWAEEIMSPFITGY; WYWAEEIMSPFITGYS; YWAEEIMSPFITGYSY; WAEEIMSPFITGYSYE; AEEIMSPFITGYSYEE; EEIMSPFITGYSYEEI; EIMSPFITGYSYEEID; IMSPFITGYSYEEIDP; MSPFITGYSYEEIDPE; SPFITGYSYEEIDPEY; PFITGYSYEEIDPEYL; FITGYSYEEIDPEYLL; ITGYSYEEIDPEYLLP; TGYSYEEIDPEYLLPP; GYSYEEIDPEYLLPPF; YSYEEIDPEYLLPPFT; SYEEIDPEYLLPPFTS; YEEIDPEYLLPPFTSQ; EEIDPEYLLPPFTSQS; EIDPEYLLPPFTSQSG; IDPEYLLPPFTSQSGS; DPEYLLPPFTSQSGSK; PEYLLPPFTSQSGSKE; EYLLPPFTSQSGSKET; YLLPPFTSQSGSKETK; LLPPFTSQSGSKETKP; LPPFTSQSGSKETKPK; PPFTSQSGSKETKPKN; PFTSQSGSKETKPKNT; FTSQSGSKETKPKNTC; TSQSGSKETKPKNTCY; SQSGSKETKPKNTCYI; QSGSKETKPKNTCYIS; SGSKETKPKNTCYISF; GSKETKPKNTCYISFY; SKETKPKNTCYISFYR; KETKPKNTCYISFYRY; ETKPKNTCYISFYRYD; TKPKNTCYISFYRYDL;

Seq 30	13 mers: MDLLDLLEKEKQI; DLLDLLEKEKQIN; LLDLLEKEKQINK; LDLLEKEKQINKN; DLLEKEKQINKNK; LLEKEKQINKNKG; LEKEKQINKNKGV; EKEKQINKNKGVF; KEKQINKNKGVFM; EKQINKNKGVFMT; KQINKNKGVFMTK; QINKNKGVFMTKP; INKNKGVFMTKPK; NKNKGVFMTKPKI; KNKGVFMTKPKIF; NKGVFMTKPKIFS; KGVFMTKPKIFSI; GVFMTKPKIFSIN; VFMTKPKIFSINK; FMTKPKIFSINKE; MTKPKIFSINKEK; TKPKIFSINKEKI; KPKIFSINKEKIK; PKIFSINKEKIKI; KIFSINKEKIKIL; IFSINKEKIKILI; FSINKEKIKILII; SINKEKIKILIIV; INKEKIKILIIVV; NKEKIKILIIVVL; KEKIKILIIVVLT; EKIKILIIVVLTS; KIKILIIVVLTST; IKILIIVVLTSTF; KILIIVVLTSTFL; ILIIVVLTSTFLL; LIIVVLTSTFLLG; IIVVLTSTFLLGI; IVVLTSTFLLGII; VVLTSTFLLGIIF; VLTSTFLLGIIFS; LTSTFLLGIIFSN; TSTFLLGIIFSNE; STFLLGIIFSNEN; TFLLGIIFSNENK; FLLGIIFSNENKV; LLGIIFSNENKVA; LGIIFSNENKVAR; GIIFSNENKVARI; IIFSNENKVARIL; IFSNENKVARILE; FSNENKVARILEE; SNENKVARILEEK; NENKVARILEEKF; ENKVARILEEKFF; NKVARILEEKFFD; KVARILEEKFFDF; VARILEEKFFDFD; ARILEEKFFDFDF; RILEEKFFDFDFN; ILEEKFFDFDFNL; LEEKFFDFDFNLI; EEKFFDFDFNLIS; EKFFDFDFNLISK; KFFDFDFNLISKI; FFDFDFNLISKIE; FDFDFNLISKIET; DFDFNLISKIETE; FDFNLISKIETEL; DFNLISKIETELE; FNLISKIETELEG; NLISKIETELEGT; LISKIETELEGTL; ISKIETELEGTLT; SKIETELEGTLTK; KIETELEGTLTKL; IETELEGTLTKLG; ETELEGTLTKLGK; TELEGTLTKLGKD; ELEGTLTKLGKDW; LEGTLTKLGKDWI; EGTLTKLGKDWIL; GTLTKLGKDWILT; TLTKLGKDWILTY; LTKLGKDWILTYN; TKLGKDWILTYNK; KLGKDWILTYNKQ; LGKDWILTYNKQN; GKDWILTYNKQNI; KDWILTYNKQNIP; DWILTYNKQNIPV; WILTYNKQNIPVD; ILTYNKQNIPVDN; LTYNKQNIPVDNK; TYNKQNIPVDNKK; YNKQNIPVDNKKV; NKQNIPVDNKKVN; KQNIPVDNKKVNS; QNIPVDNKKVNSL; NIPVDNKKVNSLI; IPVDNKKVNSLIK; PVDNKKVNSLIKA; VDNKKVNSLIKAL; DNKKVNSLIKALD; NKKVNSLIKALDE; KKVNSLIKALDEL; KVNSLIKALDELQ; VNSLIKALDELQK; NSLIKALDELQKN; SLIKALDELQKNK; LIKALDELQKNKL; IKALDELQKNKLV; KALDELQKNKLVS; ALDELQKNKLVSR; LDELQKNKLVSRD; DELQKNKLVSRDQ; ELQKNKLVSRDQK; LQKNKLVSRDQKK; QKNKLVSRDQKKH; KNKLVSRDQKKHK; NKLVSRDQKKHKE; KLVSRDQKKHKEL; LVSRDQKKHKELG; VSRDQKKHKELGI; SRDQKKHKELGIG; RDQKKHKELGIGE; DQKKHKELGIGEN; QKKHKELGIGENP; KKHKELGIGENPS; KHKELGIGENPSF; HKELGIGENPSFK; KELGIGENPSFKL; ELGIGENPSFKLF; LGIGENPSFKLFD; GIGENPSFKLFDN; IGENPSFKLFDNN; GENPSFKLFDNNN; ENPSFKLFDNNNK; NPSFKLFDNNNKL; PSFKLFDNNNKLL; SFKLFDNNNKLLT; FKLFDNNNKLLTE; KLFDNNNKLLTEI; LFDNNNKLLTEIF; FDNNNKLLTEIFV; DNNNKLLTEIFVG; NNNKLLTEIFVGK;

	NNKLLTEIFVGKS; NKLLTEIFVGKSG; KLLTEIFVGKSGE; LLTEIFVGKSGEG; LTEIFVGKSGEGD; TEIFVGKSGEGDS; EIFVGKSGEGDSR; IFVGKSGEGDSRL; FVGKSGEGDSRLA; VGKSGEGDSRLAY; GKSGEGDSRLAYI; KSGEGDSRLAYIK; SGEGDSRLAYIKG; GEGDSRLAYIKGS; EGDSRLAYIKGSD; GDSRLAYIKGSDE; DSRLAYIKGSDEN; SRLAYIKGSDENV; RLAYIKGSDENVY; LAYIKGSDENVYL; AYIKGSDENVYLT; YIKGSDENVYLTK; IKGSDENVYLTKN; KGSDENVYLTKNI; GSDENVYLTKNIF; SDENVYLTKNIFL; DENVYLTKNIFLS; ENVYLTKNIFLSY; NVYLTKNIFLSYK; VYLTKNIFLSYKG; YLTKNIFLSYKGN; LTKNIFLSYKGNS; TKNIFLSYKGNSY; KNIFLSYKGNSYN; NIFLSYKGNSYNT; IFLSYKGNSYNTF; FLSYKGNSYNTFS; LSYKGNSYNTFSD; SYKGNSYNTFSDT; YKGNSYNTFSDTT; KGNSYNTFSDTTL; GNSYNTFSDTTLF; NSYNTFSDTTLFQ; SYNTFSDTTLFQE; YNTFSDTTLFQEK; NTFSDTTLFQEKN; TFSDTTLFQEKNT; FSDTTLFQEKNTK; SDTTLFQEKNTKL; DTTLFQEKNTKLE; TTLFQEKNTKLEN; TLFQEKNTKLENL; LFQEKNTKLENLS; FQEKNTKLENLSF; QEKNTKLENLSFK; EKNTKLENLSFKI; KNTKLENLSFKII; NTKLENLSFKIIR; TKLENLSFKIIRK; KLENLSFKIIRKL; LENLSFKIIRKLN; ENLSFKIIRKLNK; NLSFKIIRKLNKE; LSFKIIRKLNKEN; SFKIIRKLNKENE; FKIIRKLNKENEN; KIIRKLNKENENN; IIRKLNKENENNI; IRKLNKENENNIN; RKLNKENENNINN; KLNKENENNINNN; LNKENENNINNNY; NKENENNINNNYE; KENENNINNNYEI; ENENNINNNYEII; NENNINNNYEIIS; ENNINNNYEIISK; NNINNNYEIISKD; NINNNYEIISKDG; INNNYEIISKDGL; NNNYEIISKDGLY; NNYEIISKDGLYF; NYEIISKDGLYFL; YEIISKDGLYFLN; EIISKDGLYFLNN; IISKDGLYFLNNQ; ISKDGLYFLNNQK; SKDGLYFLNNQKM; KDGLYFLNNQKMT; DGLYFLNNQKMTK; GLYFLNNQKMTKE; LYFLNNQKMTKER; YFLNNQKMTKERP; FLNNQKMTKERPL; LNNQKMTKERPLN; NNQKMTKERPLNI; NQKMTKERPLNII; QKMTKERPLNIIA; KMTKERPLNIIAE; MTKERPLNIIAEF; TKERPLNIIAEFK; KERPLNIIAEFKA; ERPLNIIAEFKAD; RPLNIIAEFKADG; PLNIIAEFKADGL; LNIIAEFKADGLE; NIIAEFKADGLEI; IIAEFKADGLEID; IAEFKADGLEIDK; AEFKADGLEIDKS; EFKADGLEIDKSK; FKADGLEIDKSKI; KADGLEIDKSKID; ADGLEIDKSKIDD; DGLEIDKSKIDDY; GLEIDKSKIDDYN; LEIDKSKIDDYNL; EIDKSKIDDYNLQ; IDKSKIDDYNLQY; DKSKIDDYNLQYK; KSKIDDYNLQYKI; SKIDDYNLQYKIE; KIDDYNLQYKIEV; IDDYNLQYKIEVK; DDYNLQYKIEVKW; DYNLQYKIEVKWS; YNLQYKIEVKWSN; NLQYKIEVKWSNK; LQYKIEVKWSNKS; QYKIEVKWSNKSV; YKIEVKWSNKSVN; KIEVKWSNKSVNN; IEVKWSNKSVNNI; EVKWSNKSVNNIE; VKWSNKSVNNIEV; KWSNKSVNNIEVY; WSNKSVNNIEVYF; SNKSVNNIEVYFN; NKSVNNIEVYFNK; KSVNNIEVYFNKN; SVNNIEVYFNKNE; VNNIEVYFNKNEE; NNIEVYFNKNEEN; NIEVYFNKNEEND; IEVYFNKNEENDK; EVYFNKNEENDKD; VYFNKNEENDKDI; YFNKNEENDKDIL; FNKNEENDKDILI; NKNEENDKDILIK; KNEENDKDILIKK; NEENDKDILIKKD; EENDKDILIKKDK;

ENDKDILIKKDKD; NDKDILIKKDKDE; DKDILIKKDKDEY;
KDILIKKDKDEYY; DILIKKDKDEYYY; ILIKKDKDEYYYT;
LIKKDKDEYYYTT; IKKDKDEYYYTTS; KKDKDEYYYTTSK;
KDKDEYYYTTSKW; DKDEYYYTTSKWT; KDEYYYTTSKWTF;
DEYYYTTSKWTFF; EYYYTTSKWTFFD; YYYTTSKWTFFDV;
YYTTSKWTFFDVF; YTTSKWTFFDVFD; TTSKWTFFDVFDL;
TSKWTFFDVFDLE; SKWTFFDVFDLEK; KWTFFDVFDLEKK;
WTFFDVFDLEKKL; TFFDVFDLEKKLT; FFDVFDLEKKLTE;
FDVFDLEKKLTEK; DVFDLEKKLTEKD; VFDLEKKLTEKDD;
FDLEKKLTEKDDI; DLEKKLTEKDDIS; LEKKLTEKDDISS;
EKKLTEKDDISSN; KKLTEKDDISSND; KLTEKDDISSNDN;
LTEKDDISSNDNQ; TEKDDISSNDNQE; EKDDISSNDNQED;
KDDISSNDNQEDH; DDISSNDNQEDHH; DISSNDNQEDHHE;
ISSNDNQEDHHEH; SSNDNQEDHHEHH; SNDNQEDHHEHHN;
NDNQEDHHEHHNN; DNQEDHHEHHNNA; NQEDHHEHHNNAD;

14 mers:
MDLLDLLEKEKQIN; DLLDLLEKEKQINK; LLDLLEKEKQINKN;
LDLLEKEKQINKNK; DLLEKEKQINKNKG; LLEKEKQINKNKGV;
LEKEKQINKNKGVF; EKEKQINKNKGVFM; KEKQINKNKGVFMT;
EKQINKNKGVFMTK; KQINKNKGVFMTKP; QINKNKGVFMTKPK;
INKNKGVFMTKPKI; NKNKGVFMTKPKIF; KNKGVFMTKPKIFS;
NKGVFMTKPKIFSI; KGVFMTKPKIFSIN; GVFMTKPKIFSINK;
VFMTKPKIFSINKE; FMTKPKIFSINKEK; MTKPKIFSINKEKI;
TKPKIFSINKEKIK; KPKIFSINKEKIKI; PKIFSINKEKIKIL;
KIFSINKEKIKILI; IFSINKEKIKILII; FSINKEKIKILIIV;
SINKEKIKILIIVV; INKEKIKILIIVVL; NKEKIKILIIVVLT;
KEKIKILIIVVLTS; EKIKILIIVVLTST; KIKILIIVVLTSTF;
IKILIIVVLTSTFL; KILIIVVLTSTFLL; ILIIVVLTSTFLLG;
LIIVVLTSTFLLGI; IIVVLTSTFLLGII; IVVLTSTFLLGIIF;
VVLTSTFLLGIIFS; VLTSTFLLGIIFSN; LTSTFLLGIIFSNE;
TSTFLLGIIFSNEN; STFLLGIIFSNENK; TFLLGIIFSNENKV;
FLLGIIFSNENKVA; LLGIIFSNENKVAR; LGIIFSNENKVARI;
GIIFSNENKVARIL; IIFSNENKVARILE; IFSNENKVARILEE;
FSNENKVARILEEK; SNENKVARILEEKF; NENKVARILEEKFF;
ENKVARILEEKFFD; NKVARILEEKFFDF; KVARILEEKFFDFD;
VARILEEKFFDFDF; ARILEEKFFDFDFN; RILEEKFFDFDFNL;
ILEEKFFDFDFNLI; LEEKFFDFDFNLIS; EEKFFDFDFNLISK;
EKFFDFDFNLISKI; KFFDFDFNLISKIE; FFDFDFNLISKIET;
FDFDFNLISKIETE; DFDFNLISKIETEL; FDFNLISKIETELE;
DFNLISKIETELEG; FNLISKIETELEGT; NLISKIETELEGTL;
LISKIETELEGTLT; ISKIETELEGTLTK; SKIETELEGTLTKL;
KIETELEGTLTKLG; IETELEGTLTKLGK; ETELEGTLTKLGKD;
TELEGTLTKLGKDW; ELEGTLTKLGKDWI; LEGTLTKLGKDWIL;
EGTLTKLGKDWILT; GTLTKLGKDWILTY; TLTKLGKDWILTYN;
LTKLGKDWILTYNK; TKLGKDWILTYNKQ; KLGKDWILTYNKQN;
LGKDWILTYNKQNI; GKDWILTYNKQNIP; KDWILTYNKQNIPV;
DWILTYNKQNIPVD; WILTYNKQNIPVDN; ILTYNKQNIPVDNK;
LTYNKQNIPVDNKK; TYNKQNIPVDNKKV; YNKQNIPVDNKKVN;
NKQNIPVDNKKVNS; KQNIPVDNKKVNSL; QNIPVDNKKVNSLI;
NIPVDNKKVNSLIK; IPVDNKKVNSLIKA; PVDNKKVNSLIKAL;

	VDNKKVNSLIKALD; DNKKVNSLIKALDE; NKKVNSLIKALDEL; KKVNSLIKALDELQ; KVNSLIKALDELQK; VNSLIKALDELQKN; NSLIKALDELQKNK; SLIKALDELQKNKL; LIKALDELQKNKLV; IKALDELQKNKLVS; KALDELQKNKLVSR; ALDELQKNKLVSRD; LDELQKNKLVSRDQ; DELQKNKLVSRDQK; ELQKNKLVSRDQKK; LQKNKLVSRDQKKH; QKNKLVSRDQKKHK; KNKLVSRDQKKHKE; NKLVSRDQKKHKEL; KLVSRDQKKHKELG; LVSRDQKKHKELGI; VSRDQKKHKELGIG; SRDQKKHKELGIGE; RDQKKHKELGIGEN; DQKKHKELGIGENP; QKKHKELGIGENPS; KKHKELGIGENPSF; KHKELGIGENPSFK; HKELGIGENPSFKL; KELGIGENPSFKLF; ELGIGENPSFKLFD; LGIGENPSFKLFDN; GIGENPSFKLFDNN; IGENPSFKLFDNNN; GENPSFKLFDNNNK; ENPSFKLFDNNNKL; NPSFKLFDNNNKLL; PSFKLFDNNNKLLT; SFKLFDNNNKLLTE; FKLFDNNNKLLTEI; KLFDNNNKLLTEIF; LFDNNNKLLTEIFV; FDNNNKLLTEIFVG; DNNNKLLTEIFVGK; NNNKLLTEIFVGKS; NNKLLTEIFVGKSG; NKLLTEIFVGKSGE; KLLTEIFVGKSGEG; LLTEIFVGKSGEGD; LTEIFVGKSGEGDS; TEIFVGKSGEGDSR; EIFVGKSGEGDSRL; IFVGKSGEGDSRLA; FVGKSGEGDSRLAY; VGKSGEGDSRLAYI; GKSGEGDSRLAYIK; KSGEGDSRLAYIKG; SGEGDSRLAYIKGS; GEGDSRLAYIKGSD; EGDSRLAYIKGSDE; GDSRLAYIKGSDEN; DSRLAYIKGSDENV; SRLAYIKGSDENVY; RLAYIKGSDENVYL; LAYIKGSDENVYLT; AYIKGSDENVYLTK; YIKGSDENVYLTKN; IKGSDENVYLTKNI; KGSDENVYLTKNIF; GSDENVYLTKNIFL; SDENVYLTKNIFLS; DENVYLTKNIFLSY; ENVYLTKNIFLSYK; NVYLTKNIFLSYKG; VYLTKNIFLSYKGN; YLTKNIFLSYKGNS; LTKNIFLSYKGNSY; TKNIFLSYKGNSYN; KNIFLSYKGNSYNT; NIFLSYKGNSYNTF; IFLSYKGNSYNTFS; FLSYKGNSYNTFSD; LSYKGNSYNTFSDT; SYKGNSYNTFSDTT; YKGNSYNTFSDTTL; KGNSYNTFSDTTLF; GNSYNTFSDTTLFQ; NSYNTFSDTTLFQE; SYNTFSDTTLFQEK; YNTFSDTTLFQEKN; NTFSDTTLFQEKNT; TFSDTTLFQEKNTK; FSDTTLFQEKNTKL; SDTTLFQEKNTKLE; DTTLFQEKNTKLEN; TTLFQEKNTKLENL; TLFQEKNTKLENLS; LFQEKNTKLENLSF; FQEKNTKLENLSFK; QEKNTKLENLSFKI; EKNTKLENLSFKII; KNTKLENLSFKIIR; NTKLENLSFKIIRK; TKLENLSFKIIRKL; KLENLSFKIIRKLN; LENLSFKIIRKLNK; ENLSFKIIRKLNKE; NLSFKIIRKLNKEN; LSFKIIRKLNKENE; SFKIIRKLNKENEN; FKIIRKLNKENENN; KIIRKLNKENENNI; IIRKLNKENENNIN; IRKLNKENENNINN; RKLNKENENNINNN; KLNKENENNINNNY; LNKENENNINNNYE; NKENENNINNNYEI; KENENNINNNYEII; ENENNINNNYEIIS; NENNINNNYEIISK; ENNINNNYEIISKD; NNINNNYEIISKDG; NINNNYEIISKDGL; INNNYEIISKDGLY; NNNYEIISKDGLYF; NNYEIISKDGLYFL; NYEIISKDGLYFLN; YEIISKDGLYFLNN; EIISKDGLYFLNNQ; IISKDGLYFLNNQK; ISKDGLYFLNNQKM; SKDGLYFLNNQKMT; KDGLYFLNNQKMTK; DGLYFLNNQKMTKE; GLYFLNNQKMTKER; LYFLNNQKMTKERP; YFLNNQKMTKERPL; FLNNQKMTKERPLN; LNNQKMTKERPLNI; NNQKMTKERPLNII; NQKMTKERPLNIIA; QKMTKERPLNIIAE; KMTKERPLNIIAEF; MTKERPLNIIAEFK; TKERPLNIIAEFKA; KERPLNIIAEFKAD; ERPLNIIAEFKADG; RPLNIIAEFKADGL; PLNIIAEFKADGLE; LNIIAEFKADGLEI; NIIAEFKADGLEID; IIAEFKADGLEIDK;

IAEFKADGLEIDKS; AEFKADGLEIDKSK; EFKADGLEIDKSKI;
FKADGLEIDKSKID; KADGLEIDKSKIDD; ADGLEIDKSKIDDY;
DGLEIDKSKIDDYN; GLEIDKSKIDDYNL; LEIDKSKIDDYNLQ;
EIDKSKIDDYNLQY; IDKSKIDDYNLQYK; DKSKIDDYNLQYKI;
KSKIDDYNLQYKIE; SKIDDYNLQYKIEV; KIDDYNLQYKIEVK;
IDDYNLQYKIEVKW; DDYNLQYKIEVKWS; DYNLQYKIEVKWSN;
YNLQYKIEVKWSNK; NLQYKIEVKWSNKS; LQYKIEVKWSNKSV;
QYKIEVKWSNKSVN; YKIEVKWSNKSVNN; KIEVKWSNKSVNNI;
IEVKWSNKSVNNIE; EVKWSNKSVNNIEV; VKWSNKSVNNIEVY;
KWSNKSVNNIEVYF; WSNKSVNNIEVYFN; SNKSVNNIEVYFNK;
NKSVNNIEVYFNKN; KSVNNIEVYFNKNE; SVNNIEVYFNKNEE;
VNNIEVYFNKNEEN; NNIEVYFNKNEEND; NIEVYFNKNEENDK;
IEVYFNKNEENDKD; EVYFNKNEENDKDI; VYFNKNEENDKDIL;
YFNKNEENDKDILI; FNKNEENDKDILIK; NKNEENDKDILIKK;
KNEENDKDILIKKD; NEENDKDILIKKDK; EENDKDILIKKDKD;
ENDKDILIKKDKDE; NDKDILIKKDKDEY; DKDILIKKDKDEYY;
KDILIKKDKDEYYY; DILIKKDKDEYYYT; ILIKKDKDEYYYTT;
LIKKDKDEYYYTTS; IKKDKDEYYYTTSK; KKDKDEYYYTTSKW;
KDKDEYYYTTSKWT; DKDEYYYTTSKWTF; KDEYYYTTSKWTFF;
DEYYYTTSKWTFFD; EYYYTTSKWTFFDV; YYYTTSKWTFFDVF;
YYTTSKWTFFDVFD; YTTSKWTFFDVFDL; TTSKWTFFDVFDLE;
TSKWTFFDVFDLEK; SKWTFFDVFDLEKK; KWTFFDVFDLEKKL;
WTFFDVFDLEKKLT; TFFDVFDLEKKLTE; FFDVFDLEKKLTEK;
FDVFDLEKKLTEKD; DVFDLEKKLTEKDD; VFDLEKKLTEKDDI;
FDLEKKLTEKDDIS; DLEKKLTEKDDISS; LEKKLTEKDDISSN;
EKKLTEKDDISSND; KKLTEKDDISSNDN; KLTEKDDISSNDNQ;
LTEKDDISSNDNQE; TEKDDISSNDNQED; EKDDISSNDNQEDH;
KDDISSNDNQEDHH; DDISSNDNQEDHHE; DISSNDNQEDHHEH;
ISSNDNQEDHHEHH; SSNDNQEDHHEHHN; SNDNQEDHHEHHNN;
NDNQEDHHEHHNNA; DNQEDHHEHHNNAD;

15 mers:
MDLLDLLEKEKQINK; DLLDLLEKEKQINKN; LLDLLEKEKQINKNK;
LDLLEKEKQINKNKG; DLLEKEKQINKNKGV; LLEKEKQINKNKGVF;
LEKEKQINKNKGVFM; EKEKQINKNKGVFMT; KEKQINKNKGVFMTK;
EKQINKNKGVFMTKP; KQINKNKGVFMTKPK; QINKNKGVFMTKPKI;
INKNKGVFMTKPKIF; NKNKGVFMTKPKIFS; KNKGVFMTKPKIFSI;
NKGVFMTKPKIFSIN; KGVFMTKPKIFSINK; GVFMTKPKIFSINKE;
VFMTKPKIFSINKEK; FMTKPKIFSINKEKI; MTKPKIFSINKEKIK;
TKPKIFSINKEKIKI; KPKIFSINKEKIKIL; PKIFSINKEKIKILI;
KIFSINKEKIKILII; IFSINKEKIKILIIV; FSINKEKIKILIIVV;
SINKEKIKILIIVVL; INKEKIKILIIVVLT; NKEKIKILIIVVLTS;
KEKIKILIIVVLTST; EKIKILIIVVLTSTF; KIKILIIVVLTSTFL;
IKILIIVVLTSTFLL; KILIIVVLTSTFLLG; ILIIVVLTSTFLLGI;
LIIVVLTSTFLLGII; IIVVLTSTFLLGIIF; IVVLTSTFLLGIIFS;
VVLTSTFLLGIIFSN; VLTSTFLLGIIFSNE; LTSTFLLGIIFSNEN;
TSTFLLGIIFSNENK; STFLLGIIFSNENKV; TFLLGIIFSNENKVA;
FLLGIIFSNENKVAR; LLGIIFSNENKVARI; LGIIFSNENKVARIL;
GIIFSNENKVARILE; IIFSNENKVARILEE; IFSNENKVARILEEK;
FSNENKVARILEEKF; SNENKVARILEEKFF; NENKVARILEEKFFD;
ENKVARILEEKFFDF; NKVARILEEKFFDFD; KVARILEEKFFDFDF;

	VARILEEKFFDFDFN; ARILEEKFFDFDFNL; RILEEKFFDFDFNLI; ILEEKFFDFDFNLIS; LEEKFFDFDFNLISK; EEKFFDFDFNLISKI; EKFFDFDFNLISKIE; KFFDFDFNLISKIET; FFDFDFNLISKIETE; FDFDFNLISKIETEL; DFDFNLISKIETELE; FDFNLISKIETELEG; DFNLISKIETELEGT; FNLISKIETELEGTL; NLISKIETELEGTLT; LISKIETELEGTLTK; ISKIETELEGTLTKL; SKIETELEGTLTKLG; KIETELEGTLTKLGK; IETELEGTLTKLGKD; ETELEGTLTKLGKDW; TELEGTLTKLGKDWI; ELEGTLTKLGKDWIL; LEGTLTKLGKDWILT; EGTLTKLGKDWILTY; GTLTKLGKDWILTYN; TLTKLGKDWILTYNK; LTKLGKDWILTYNKQ; TKLGKDWILTYNKQN; KLGKDWILTYNKQNI; LGKDWILTYNKQNIP; GKDWILTYNKQNIPV; KDWILTYNKQNIPVD; DWILTYNKQNIPVDN; WILTYNKQNIPVDNK; ILTYNKQNIPVDNKK; LTYNKQNIPVDNKKV; TYNKQNIPVDNKKVN; YNKQNIPVDNKKVNS; NKQNIPVDNKKVNSL; KQNIPVDNKKVNSLI; QNIPVDNKKVNSLIK; NIPVDNKKVNSLIKA; IPVDNKKVNSLIKAL; PVDNKKVNSLIKALD; VDNKKVNSLIKALDE; DNKKVNSLIKALDEL; NKKVNSLIKALDELQ; KKVNSLIKALDELQK; KVNSLIKALDELQKN; VNSLIKALDELQKNK; NSLIKALDELQKNKL; SLIKALDELQKNKLV; LIKALDELQKNKLVS; IKALDELQKNKLVSR; KALDELQKNKLVSRD; ALDELQKNKLVSRDQ; LDELQKNKLVSRDQK; DELQKNKLVSRDQKK; ELQKNKLVSRDQKKH; LQKNKLVSRDQKKHK; QKNKLVSRDQKKHKE; KNKLVSRDQKKHKEL; NKLVSRDQKKHKELG; KLVSRDQKKHKELGI; LVSRDQKKHKELGIG; VSRDQKKHKELGIGE; SRDQKKHKELGIGEN; RDQKKHKELGIGENP; DQKKHKELGIGENPS; QKKHKELGIGENPSF; KKHKELGIGENPSFK; KHKELGIGENPSFKL; HKELGIGENPSFKLF; KELGIGENPSFKLFD; ELGIGENPSFKLFDN; LGIGENPSFKLFDNN; GIGENPSFKLFDNNN; IGENPSFKLFDNNNK; GENPSFKLFDNNNKL; ENPSFKLFDNNNKLL; NPSFKLFDNNNKLLT; PSFKLFDNNNKLLTE; SFKLFDNNNKLLTEI; FKLFDNNNKLLTEIF; KLFDNNNKLLTEIFV; LFDNNNKLLTEIFVG; FDNNNKLLTEIFVGK; DNNNKLLTEIFVGKS; NNNKLLTEIFVGKSG; NNKLLTEIFVGKSGE; NKLLTEIFVGKSGEG; KLLTEIFVGKSGEGD; LLTEIFVGKSGEGDS; LTEIFVGKSGEGDSR; TEIFVGKSGEGDSRL; EIFVGKSGEGDSRLA; IFVGKSGEGDSRLAY; FVGKSGEGDSRLAYI; VGKSGEGDSRLAYIK; GKSGEGDSRLAYIKG; KSGEGDSRLAYIKGS; SGEGDSRLAYIKGSD; GEGDSRLAYIKGSDE; EGDSRLAYIKGSDEN; GDSRLAYIKGSDENV; DSRLAYIKGSDENVY; SRLAYIKGSDENVYL; RLAYIKGSDENVYLT; LAYIKGSDENVYLTK; AYIKGSDENVYLTKN; YIKGSDENVYLTKNI; IKGSDENVYLTKNIF; KGSDENVYLTKNIFL; GSDENVYLTKNIFLS; SDENVYLTKNIFLSY; DENVYLTKNIFLSYK; ENVYLTKNIFLSYKG; NVYLTKNIFLSYKGN; VYLTKNIFLSYKGNS; YLTKNIFLSYKGNSY; LTKNIFLSYKGNSYN; TKNIFLSYKGNSYNT; KNIFLSYKGNSYNTF; NIFLSYKGNSYNTFS; IFLSYKGNSYNTFSD; FLSYKGNSYNTFSDT; LSYKGNSYNTFSDTT; SYKGNSYNTFSDTTL; YKGNSYNTFSDTTLF; KGNSYNTFSDTTLFQ; GNSYNTFSDTTLFQE; NSYNTFSDTTLFQEK; SYNTFSDTTLFQEKN; YNTFSDTTLFQEKNT; NTFSDTTLFQEKNTK; TFSDTTLFQEKNTKL; FSDTTLFQEKNTKLE; SDTTLFQEKNTKLEN; DTTLFQEKNTKLENL; TTLFQEKNTKLENLS; TLFQEKNTKLENLSF; LFQEKNTKLENLSFK; FQEKNTKLENLSFKI; QEKNTKLENLSFKII; EKNTKLENLSFKIIR; KNTKLENLSFKIIRK; NTKLENLSFKIIRKL; TKLENLSFKIIRKLN; KLENLSFKIIRKLNK; LENLSFKIIRKLNKE; ENLSFKIIRKLNKEN; NLSFKIIRKLNKENE;

	LSFKIIRKLNKENEN; SFKIIRKLNKENENN; FKIIRKLNKENENNI; KIIRKLNKENENNIN; IIRKLNKENENNINN; IRKLNKENENNINNN; RKLNKENENNINNNY; KLNKENENNINNNYE; LNKENENNINNNYEI; NKENENNINNNYEII; KENENNINNNYEIIS; ENENNINNNYEIISK; NENNINNNYEIISKD; ENNINNNYEIISKDG; NNINNNYEIISKDGL; NINNNYEIISKDGLY; INNNYEIISKDGLYF; NNNYEIISKDGLYFL; NNYEIISKDGLYFLN; NYEIISKDGLYFLNN; YEIISKDGLYFLNNQ; EIISKDGLYFLNNQK; IISKDGLYFLNNQKM; ISKDGLYFLNNQKMT; SKDGLYFLNNQKMTK; KDGLYFLNNQKMTKE; DGLYFLNNQKMTKER; GLYFLNNQKMTKERP; LYFLNNQKMTKERPL; YFLNNQKMTKERPLN; FLNNQKMTKERPLNI; LNNQKMTKERPLNII; NNQKMTKERPLNIIA; NQKMTKERPLNIIAE; QKMTKERPLNIIAEF; KMTKERPLNIIAEFK; MTKERPLNIIAEFKA; TKERPLNIIAEFKAD; KERPLNIIAEFKADG; ERPLNIIAEFKADGL; RPLNIIAEFKADGLE; PLNIIAEFKADGLEI; LNIIAEFKADGLEID; NIIAEFKADGLEIDK; IIAEFKADGLEIDKS; IAEFKADGLEIDKSK; AEFKADGLEIDKSKI; EFKADGLEIDKSKID; FKADGLEIDKSKIDD; KADGLEIDKSKIDDY; ADGLEIDKSKIDDYN; DGLEIDKSKIDDYNL; GLEIDKSKIDDYNLQ; LEIDKSKIDDYNLQY; EIDKSKIDDYNLQYK; IDKSKIDDYNLQYKI; DKSKIDDYNLQYKIE; KSKIDDYNLQYKIEV; SKIDDYNLQYKIEVK; KIDDYNLQYKIEVKW; IDDYNLQYKIEVKWS; DDYNLQYKIEVKWSN; DYNLQYKIEVKWSNK; YNLQYKIEVKWSNKS; NLQYKIEVKWSNKSV; LQYKIEVKWSNKSVN; QYKIEVKWSNKSVNN; YKIEVKWSNKSVNNI; KIEVKWSNKSVNNIE; IEVKWSNKSVNNIEV; EVKWSNKSVNNIEVY; VKWSNKSVNNIEVYF; KWSNKSVNNIEVYFN; WSNKSVNNIEVYFNK; SNKSVNNIEVYFNKN; NKSVNNIEVYFNKNE; KSVNNIEVYFNKNEE; SVNNIEVYFNKNEEN; VNNIEVYFNKNEEND; NNIEVYFNKNEENDK; NIEVYFNKNEENDKD; IEVYFNKNEENDKDI; EVYFNKNEENDKDIL; VYFNKNEENDKDILI; YFNKNEENDKDILIK; FNKNEENDKDILIKK; NKNEENDKDILIKKD; KNEENDKDILIKKDK; NEENDKDILIKKDKD; EENDKDILIKKDKDE; ENDKDILIKKDKDEY; NDKDILIKKDKDEYY; DKDILIKKDKDEYYY; KDILIKKDKDEYYYT; DILIKKDKDEYYYTT; ILIKKDKDEYYYTTS; LIKKDKDEYYYTTSK; IKKDKDEYYYTTSKW; KKDKDEYYYTTSKWT; KDKDEYYYTTSKWTF; DKDEYYYTTSKWTFF; KDEYYYTTSKWTFFD; DEYYYTTSKWTFFDV; EYYYTTSKWTFFDVF; YYYTTSKWTFFDVFD; YYTTSKWTFFDVFDL; YTTSKWTFFDVFDLE; TTSKWTFFDVFDLEK; TSKWTFFDVFDLEKK; SKWTFFDVFDLEKKL; KWTFFDVFDLEKKLT; WTFFDVFDLEKKLTE; TFFDVFDLEKKLTEK; FFDVFDLEKKLTEKD; FDVFDLEKKLTEKDD; DVFDLEKKLTEKDDI; VFDLEKKLTEKDDIS; FDLEKKLTEKDDISS; DLEKKLTEKDDISSN; LEKKLTEKDDISSND; EKKLTEKDDISSNDN; KKLTEKDDISSNDNQ; KLTEKDDISSNDNQE; LTEKDDISSNDNQED; TEKDDISSNDNQEDH; EKDDISSNDNQEDHH; KDDISSNDNQEDHHE; DDISSNDNQEDHHEH; DISSNDNQEDHHEHH; ISSNDNQEDHHEHHN; SSNDNQEDHHEHHNN; SNDNQEDHHEHHNNA; NDNQEDHHEHHNNAD; 16 mers: MDLLDLLEKEKQINKN; DLLDLLEKEKQINKNK; LLDLLEKEKQINKNKG; LDLLEKEKQINKNKGV; DLLEKEKQINKNKGVF; LLEKEKQINKNKGVFM; LEKEKQINKNKGVFMT; EKEKQINKNKGVFMTK; KEKQINKNKGVFMTKP; EKQINKNKGVFMTKPK; KQINKNKGVFMTKPKI; QINKNKGVFMTKPKIF;

	INKNKGVFMTKPKIFS; NKNKGVFMTKPKIFSI; KNKGVFMTKPKIFSIN; NKGVFMTKPKIFSINK; KGVFMTKPKIFSINKE; GVFMTKPKIFSINKEK; VFMTKPKIFSINKEKI; FMTKPKIFSINKEKIK; MTKPKIFSINKEKIKI; TKPKIFSINKEKIKIL; KPKIFSINKEKIKILI; PKIFSINKEKIKILII; KIFSINKEKIKILIIV; IFSINKEKIKILIIVV; FSINKEKIKILIIVVL; SINKEKIKILIIVVLT; INKEKIKILIIVVLTS; NKEKIKILIIVVLTST; KEKIKILIIVVLTSTF; EKIKILIIVVLTSTFL; KIKILIIVVLTSTFLL; IKILIIVVLTSTFLLG; KILIIVVLTSTFLLGI; ILIIVVLTSTFLLGII; LIIVVLTSTFLLGIIF; IIVVLTSTFLLGIIFS; IVVLTSTFLLGIIFSN; VVLTSTFLLGIIFSNE; VLTSTFLLGIIFSNEN; LTSTFLLGIIFSNENK; TSTFLLGIIFSNENKV; STFLLGIIFSNENKVA; TFLLGIIFSNENKVAR; FLLGIIFSNENKVARI; LLGIIFSNENKVARIL; LGIIFSNENKVARILE; GIIFSNENKVARILEE; IIFSNENKVARILEEK; IFSNENKVARILEEKF; FSNENKVARILEEKFF; SNENKVARILEEKFFD; NENKVARILEEKFFDF; ENKVARILEEKFFDFD; NKVARILEEKFFDFDF; KVARILEEKFFDFDFN; VARILEEKFFDFDFNL; ARILEEKFFDFDFNLI; RILEEKFFDFDFNLIS; ILEEKFFDFDFNLISK; LEEKFFDFDFNLISKI; EEKFFDFDFNLISKIE; EKFFDFDFNLISKIET; KFFDFDFNLISKIETE; FFDFDFNLISKIETEL; FDFDFNLISKIETELE; DFDFNLISKIETELEG; FDFNLISKIETELEGT; DFNLISKIETELEGTL; FNLISKIETELEGTLT; NLISKIETELEGTLTK; LISKIETELEGTLTKL; ISKIETELEGTLTKLG; SKIETELEGTLTKLGK; KIETELEGTLTKLGKD; IETELEGTLTKLGKDW; ETELEGTLTKLGKDWI; TELEGTLTKLGKDWIL; ELEGTLTKLGKDWILT; LEGTLTKLGKDWILTY; EGTLTKLGKDWILTYN; GTLTKLGKDWILTYNK; TLTKLGKDWILTYNKQ; LTKLGKDWILTYNKQN; TKLGKDWILTYNKQNI; KLGKDWILTYNKQNIP; LGKDWILTYNKQNIPV; GKDWILTYNKQNIPVD; KDWILTYNKQNIPVDN; DWILTYNKQNIPVDNK; WILTYNKQNIPVDNKK; ILTYNKQNIPVDNKKV; LTYNKQNIPVDNKKVN; TYNKQNIPVDNKKVNS; YNKQNIPVDNKKVNSL; NKQNIPVDNKKVNSLI; KQNIPVDNKKVNSLIK; QNIPVDNKKVNSLIKA; NIPVDNKKVNSLIKAL; IPVDNKKVNSLIKALD; PVDNKKVNSLIKALDE; VDNKKVNSLIKALDEL; DNKKVNSLIKALDELQ; NKKVNSLIKALDELQK; KKVNSLIKALDELQKN; KVNSLIKALDELQKNK; VNSLIKALDELQKNKL; NSLIKALDELQKNKLV; SLIKALDELQKNKLVS; LIKALDELQKNKLVSR; IKALDELQKNKLVSRD; KALDELQKNKLVSRDQ; ALDELQKNKLVSRDQK; LDELQKNKLVSRDQKK; DELQKNKLVSRDQKKH; ELQKNKLVSRDQKKHK; LQKNKLVSRDQKKHKE; QKNKLVSRDQKKHKEL; KNKLVSRDQKKHKELG; NKLVSRDQKKHKELGI; KLVSRDQKKHKELGIG; LVSRDQKKHKELGIGE; VSRDQKKHKELGIGEN; SRDQKKHKELGIGENP; RDQKKHKELGIGENPS; DQKKHKELGIGENPSF; QKKHKELGIGENPSFK; KKHKELGIGENPSFKL; KHKELGIGENPSFKLF; HKELGIGENPSFKLFD; KELGIGENPSFKLFDN; ELGIGENPSFKLFDNN; LGIGENPSFKLFDNNN; GIGENPSFKLFDNNNK; IGENPSFKLFDNNNKL; GENPSFKLFDNNNKLL; ENPSFKLFDNNNKLLT; NPSFKLFDNNNKLLTE; PSFKLFDNNNKLLTEI; SFKLFDNNNKLLTEIF; FKLFDNNNKLLTEIFV; KLFDNNNKLLTEIFVG; LFDNNNKLLTEIFVGK; FDNNNKLLTEIFVGKS; DNNNKLLTEIFVGKSG; NNNKLLTEIFVGKSGE; NNKLLTEIFVGKSGEG; NKLLTEIFVGKSGEGD; KLLTEIFVGKSGEGDS; LLTEIFVGKSGEGDSR; LTEIFVGKSGEGDSRL; TEIFVGKSGEGDSRLA; EIFVGKSGEGDSRLAY; IFVGKSGEGDSRLAYI; FVGKSGEGDSRLAYIK; VGKSGEGDSRLAYIKG; GKSGEGDSRLAYIKGS; KSGEGDSRLAYIKGSD; SGEGDSRLAYIKGSDE; GEGDSRLAYIKGSDEN; EGDSRLAYIKGSDENV; GDSRLAYIKGSDENVY; DSRLAYIKGSDENVYL; SRLAYIKGSDENVYLT;

	RLAYIKGSDENVYLTK; LAYIKGSDENVYLTKN; AYIKGSDENVYLTKNI; YIKGSDENVYLTKNIF; IKGSDENVYLTKNIFL; KGSDENVYLTKNIFLS; GSDENVYLTKNIFLSY; SDENVYLTKNIFLSYK; DENVYLTKNIFLSYKG; ENVYLTKNIFLSYKGN; NVYLTKNIFLSYKGNS; VYLTKNIFLSYKGNSY; YLTKNIFLSYKGNSYN; LTKNIFLSYKGNSYNT; TKNIFLSYKGNSYNTF; KNIFLSYKGNSYNTFS; NIFLSYKGNSYNTFSD; IFLSYKGNSYNTFSDT; FLSYKGNSYNTFSDTT; LSYKGNSYNTFSDTTL; SYKGNSYNTFSDTTLF; YKGNSYNTFSDTTLFQ; KGNSYNTFSDTTLFQE; GNSYNTFSDTTLFQEK; NSYNTFSDTTLFQEKN; SYNTFSDTTLFQEKNT; YNTFSDTTLFQEKNTK; NTFSDTTLFQEKNTKL; TFSDTTLFQEKNTKLE; FSDTTLFQEKNTKLEN; SDTTLFQEKNTKLENL; DTTLFQEKNTKLENLS; TTLFQEKNTKLENLSF; TLFQEKNTKLENLSFK; LFQEKNTKLENLSFKI; FQEKNTKLENLSFKII; QEKNTKLENLSFKIIR; EKNTKLENLSFKIIRK; KNTKLENLSFKIIRKL; NTKLENLSFKIIRKLN; TKLENLSFKIIRKLNK; KLENLSFKIIRKLNKE; LENLSFKIIRKLNKEN; ENLSFKIIRKLNKENE; NLSFKIIRKLNKENEN; LSFKIIRKLNKENENN; SFKIIRKLNKENENNI; FKIIRKLNKENENNIN; KIIRKLNKENENNINN; IIRKLNKENENNINNN; IRKLNKENENNINNNY; RKLNKENENNINNNYE; KLNKENENNINNNYEI; LNKENENNINNNYEII; NKENENNINNNYEIIS; KENENNINNNYEIISK; ENENNINNNYEIISKD; NENNINNNYEIISKDG; ENNINNNYEIISKDGL; NNINNNYEIISKDGLY; NINNNYEIISKDGLYF; INNNYEIISKDGLYFL; NNNYEIISKDGLYFLN; NNYEIISKDGLYFLNN; NYEIISKDGLYFLNNQ; YEIISKDGLYFLNNQK; EIISKDGLYFLNNQKM; IISKDGLYFLNNQKMT; ISKDGLYFLNNQKMTK; SKDGLYFLNNQKMTKE; KDGLYFLNNQKMTKER; DGLYFLNNQKMTKERP; GLYFLNNQKMTKERPL; LYFLNNQKMTKERPLN; YFLNNQKMTKERPLNI; FLNNQKMTKERPLNII; LNNQKMTKERPLNIIA; NNQKMTKERPLNIIAE; NQKMTKERPLNIIAEF; QKMTKERPLNIIAEFK; KMTKERPLNIIAEFKA; MTKERPLNIIAEFKAD; TKERPLNIIAEFKADG; KERPLNIIAEFKADGL; ERPLNIIAEFKADGLE; RPLNIIAEFKADGLEI; PLNIIAEFKADGLEID; LNIIAEFKADGLEIDK; NIIAEFKADGLEIDKS; IIAEFKADGLEIDKSK; IAEFKADGLEIDKSKI; AEFKADGLEIDKSKID; EFKADGLEIDKSKIDD; FKADGLEIDKSKIDDY; KADGLEIDKSKIDDYN; ADGLEIDKSKIDDYNL; DGLEIDKSKIDDYNLQ; GLEIDKSKIDDYNLQY; LEIDKSKIDDYNLQYK; EIDKSKIDDYNLQYKI; IDKSKIDDYNLQYKIE; DKSKIDDYNLQYKIEV; KSKIDDYNLQYKIEVK; SKIDDYNLQYKIEVKW; KIDDYNLQYKIEVKWS; IDDYNLQYKIEVKWSN; DDYNLQYKIEVKWSNK; DYNLQYKIEVKWSNKS; YNLQYKIEVKWSNKSV; NLQYKIEVKWSNKSVN; LQYKIEVKWSNKSVNN; QYKIEVKWSNKSVNNI; YKIEVKWSNKSVNNIE; KIEVKWSNKSVNNIEV; IEVKWSNKSVNNIEVY; EVKWSNKSVNNIEVYF; VKWSNKSVNNIEVYFN; KWSNKSVNNIEVYFNK; WSNKSVNNIEVYFNKN; SNKSVNNIEVYFNKNE; NKSVNNIEVYFNKNEE; KSVNNIEVYFNKNEEN; SVNNIEVYFNKNEEND; VNNIEVYFNKNEENDK; NNIEVYFNKNEENDKD; NIEVYFNKNEENDKDI; IEVYFNKNEENDKDIL; EVYFNKNEENDKDILI; VYFNKNEENDKDILIK; YFNKNEENDKDILIKK; FNKNEENDKDILIKKD; NKNEENDKDILIKKDK; KNEENDKDILIKKDKD; NEENDKDILIKKDKDE; EENDKDILIKKDKDEY; ENDKDILIKKDKDEYY; NDKDILIKKDKDEYYY; DKDILIKKDKDEYYYT; KDILIKKDKDEYYYTT; DILIKKDKDEYYYTTS; ILIKKDKDEYYYTTSK; LIKKDKDEYYYTTSKW; IKKDKDEYYYTTSKWT; KKDKDEYYYTTSKWTF; KDKDEYYYTTSKWTFF; DKDEYYYTTSKWTFFD; KDEYYYTTSKWTFFDV; DEYYYTTSKWTFFDVF; EYYYTTSKWTFFDVFD; YYYTTSKWTFFDVFDL; YYTTSKWTFFDVFDLE; YTTSKWTFFDVFDLEK; TTSKWTFFDVFDLEKK;

	TSKWTFFDVFDLEKKL; SKWTFFDVFDLEKKLT; KWTFFDVFDLEKKLTE; WTFFDVFDLEKKLTEK; TFFDVFDLEKKLTEKD; FFDVFDLEKKLTEKDD; FDVFDLEKKLTEKDDI; DVFDLEKKLTEKDDIS; VFDLEKKLTEKDDISS; FDLEKKLTEKDDISSN; DLEKKLTEKDDISSND; LEKKLTEKDDISSNDN; EKKLTEKDDISSNDNQ; KKLTEKDDISSNDNQE; KLTEKDDISSNDNQED; LTEKDDISSNDNQEDH; TEKDDISSNDNQEDHH; EKDDISSNDNQEDHHE; KDDISSNDNQEDHHEH; DDISSNDNQEDHHEHH; DISSNDNQEDHHEHHN; ISSNDNQEDHHEHHNN; SSNDNQEDHHEHHNNA; SNDNQEDHHEHHNNAD;
Seq 31	13 mers: MKKLIIIFTLFLS; KKLIIIFTLFLSQ; KLIIIFTLFLSQA; LIIIFTLFLSQAC; IIIFTLFLSQACN; IIFTLFLSQACNL; IFTLFLSQACNLS; FTLFLSQACNLST; TLFLSQACNLSTM; LFLSQACNLSTMH; FLSQACNLSTMHK; LSQACNLSTMHKI; SQACNLSTMHKID; QACNLSTMHKIDT; ACNLSTMHKIDTK; CNLSTMHKIDTKE; NLSTMHKIDTKED; LSTMHKIDTKEDM; STMHKIDTKEDMK; TMHKIDTKEDMKI; MHKIDTKEDMKIL; HKIDTKEDMKILY; KIDTKEDMKILYS; IDTKEDMKILYSE; DTKEDMKILYSEI; TKEDMKILYSEIA; KEDMKILYSEIAE; EDMKILYSEIAEL; DMKILYSEIAELR; MKILYSEIAELRK; KILYSEIAELRKK; ILYSEIAELRKKL; LYSEIAELRKKLN; YSEIAELRKKLNL; SEIAELRKKLNLN; EIAELRKKLNLNH; IAELRKKLNLNHL; AELRKKLNLNHLE; ELRKKLNLNHLEI; LRKKLNLNHLEID; RKKLNLNHLEIDD; KKLNLNHLEIDDT; KLNLNHLEIDDTL; LNLNHLEIDDTLE; NLNHLEIDDTLEK; LNHLEIDDTLEKV; NHLEIDDTLEKVA; HLEIDDTLEKVAK; LEIDDTLEKVAKE; EIDDTLEKVAKEY; IDDTLEKVAKEYA; DDTLEKVAKEYAI; DTLEKVAKEYAIK; TLEKVAKEYAIKL; LEKVAKEYAIKLG; EKVAKEYAIKLGE; KVAKEYAIKLGEN; VAKEYAIKLGENR; AKEYAIKLGENRT; KEYAIKLGENRTI; EYAIKLGENRTIT; YAIKLGENRTITH; AIKLGENRTITHT; IKLGENRTITHTL; KLGENRTITHTLF; LGENRTITHTLFG; GENRTITHTLFGT; ENRTITHTLFGTT; NRTITHTLFGTTP; RTITHTLFGTTPM; TITHTLFGTTPMQ; ITHTLFGTTPMQR; THTLFGTTPMQRI; HTLFGTTPMQRIH; TLFGTTPMQRIHK; LFGTTPMQRIHKY; FGTTPMQRIHKYD; GTTPMQRIHKYDQ; TTPMQRIHKYDQS; TPMQRIHKYDQSF; PMQRIHKYDQSFN; MQRIHKYDQSFNL; QRIHKYDQSFNLT; RIHKYDQSFNLTR; IHKYDQSFNLTRE; HKYDQSFNLTREI; KYDQSFNLTREIL; YDQSFNLTREILA; DQSFNLTREILAS; QSFNLTREILASG; SFNLTREILASGI; FNLTREILASGIE; NLTREILASGIEL; LTREILASGIELN; TREILASGIELNR; REILASGIELNRV; EILASGIELNRVV; ILASGIELNRVVN; LASGIELNRVVNA; ASGIELNRVVNAW; SGIELNRVVNAWL; GIELNRVVNAWLN; IELNRVVNAWLNS; ELNRVVNAWLNSP; LNRVVNAWLNSPS; NRVVNAWLNSPSH; RVVNAWLNSPSHK; VVNAWLNSPSHKE; VNAWLNSPSHKEA; NAWLNSPSHKEAL; AWLNSPSHKEALI; WLNSPSHKEALIN; LNSPSHKEALINT; NSPSHKEALINTD; SPSHKEALINTDT; PSHKEALINTDTD; SHKEALINTDTDK; HKEALINTDTDKI; KEALINTDTDKIG; EALINTDTDKIGG;

	ALINTDTDKIGGY; LINTDTDKIGGYR; INTDTDKIGGYRL; NTDTDKIGGYRLK; TDTDKIGGYRLKT; DTDKIGGYRLKTT; TDKIGGYRLKTTD; DKIGGYRLKTTDN; KIGGYRLKTTDNI; IGGYRLKTTDNID; GGYRLKTTDNIDI; GYRLKTTDNIDIF; YRLKTTDNIDIFV; RLKTTDNIDIFVV; LKTTDNIDIFVVL; KTTDNIDIFVVLF; TTDNIDIFVVLFG; TDNIDIFVVLFGK; DNIDIFVVLFGKR; NIDIFVVLFGKRK; IDIFVVLFGKRKY; DIFVVLFGKRKYK; IFVVLFGKRKYKN; 14 mers: MKKLIIIFTLFLSQ; KKLIIIFTLFLSQA; KLIIIFTLFLSQAC; LIIIFTLFLSQACN; IIIFTLFLSQACNL; IIFTLFLSQACNLS; IFTLFLSQACNLST; FTLFLSQACNLSTM; TLFLSQACNLSTMH; LFLSQACNLSTMHK; FLSQACNLSTMHKI; LSQACNLSTMHKID; SQACNLSTMHKIDT; QACNLSTMHKIDTK; ACNLSTMHKIDTKE; CNLSTMHKIDTKED; NLSTMHKIDTKEDM; LSTMHKIDTKEDMK; STMHKIDTKEDMKI; TMHKIDTKEDMKIL; MHKIDTKEDMKILY; HKIDTKEDMKILYS; KIDTKEDMKILYSE; IDTKEDMKILYSEI; DTKEDMKILYSEIA; TKEDMKILYSEIAE; KEDMKILYSEIAEL; EDMKILYSEIAELR; DMKILYSEIAELRK; MKILYSEIAELRKK; KILYSEIAELRKKL; ILYSEIAELRKKLN; LYSEIAELRKKLNL; YSEIAELRKKLNLN; SEIAELRKKLNLNH; EIAELRKKLNLNHL; IAELRKKLNLNHLE; AELRKKLNLNHLEI; ELRKKLNLNHLEID; LRKKLNLNHLEIDD; RKKLNLNHLEIDDT; KKLNLNHLEIDDTL; KLNLNHLEIDDTLE; LNLNHLEIDDTLEK; NLNHLEIDDTLEKV; LNHLEIDDTLEKVA; NHLEIDDTLEKVAK; HLEIDDTLEKVAKE; LEIDDTLEKVAKEY; EIDDTLEKVAKEYA; IDDTLEKVAKEYAI; DDTLEKVAKEYAIK; DTLEKVAKEYAIKL; TLEKVAKEYAIKLG; LEKVAKEYAIKLGE; EKVAKEYAIKLGEN; KVAKEYAIKLGENR; VAKEYAIKLGENRT; AKEYAIKLGENRTI; KEYAIKLGENRTIT; EYAIKLGENRTITH; YAIKLGENRTITHT; AIKLGENRTITHTL; IKLGENRTITHTLF; KLGENRTITHTLFG; LGENRTITHTLFGT; GENRTITHTLFGTT; ENRTITHTLFGTTP; NRTITHTLFGTTPM; RTITHTLFGTTPMQ; TITHTLFGTTPMQR; ITHTLFGTTPMQRI; THTLFGTTPMQRIH; HTLFGTTPMQRIHK; TLFGTTPMQRIHKY; LFGTTPMQRIHKYD; FGTTPMQRIHKYDQ; GTTPMQRIHKYDQS; TTPMQRIHKYDQSF; TPMQRIHKYDQSFN; PMQRIHKYDQSFNL; MQRIHKYDQSFNLT; QRIHKYDQSFNLTR; RIHKYDQSFNLTRE; IHKYDQSFNLTREI; HKYDQSFNLTREIL; KYDQSFNLTREILA; YDQSFNLTREILAS; DQSFNLTREILASG; QSFNLTREILASGI; SFNLTREILASGIE; FNLTREILASGIEL; NLTREILASGIELN; LTREILASGIELNR; TREILASGIELNRV; REILASGIELNRVV; EILASGIELNRVVN; ILASGIELNRVVNA; LASGIELNRVVNAW; ASGIELNRVVNAWL; SGIELNRVVNAWLN; GIELNRVVNAWLNS; IELNRVVNAWLNSP; ELNRVVNAWLNSPS; LNRVVNAWLNSPSH; NRVVNAWLNSPSHK; RVVNAWLNSPSHKE; VVNAWLNSPSHKEA; VNAWLNSPSHKEAL; NAWLNSPSHKEALI; AWLNSPSHKEALIN; WLNSPSHKEALINT; LNSPSHKEALINTD; NSPSHKEALINTDT; SPSHKEALINTDTD; PSHKEALINTDTDK; SHKEALINTDTDKI; HKEALINTDTDKIG; KEALINTDTDKIGG; EALINTDTDKIGGY; ALINTDTDKIGGYR; LINTDTDKIGGYRL; INTDTDKIGGYRLK;

NTDTDKIGGYRLKT; TDTDKIGGYRLKTT; DTDKIGGYRLKTTD;
TDKIGGYRLKTTDN; DKIGGYRLKTTDNI; KIGGYRLKTTDNID;
IGGYRLKTTDNIDI; GGYRLKTTDNIDIF; GYRLKTTDNIDIFV;
YRLKTTDNIDIFVV; RLKTTDNIDIFVVL; LKTTDNIDIFVVLF;
KTTDNIDIFVVLFG; TTDNIDIFVVLFGK; TDNIDIFVVLFGKR;
DNIDIFVVLFGKRK; NIDIFVVLFGKRKY; IDIFVVLFGKRKYK;
DIFVVLFGKRKYKN;

15 mers:
MKKLIIIFTLFLSQA; KKLIIIFTLFLSQAC; KLIIIFTLFLSQACN;
LIIIFTLFLSQACNL; IIIFTLFLSQACNLS; IIFTLFLSQACNLST;
IFTLFLSQACNLSTM; FTLFLSQACNLSTMH; TLFLSQACNLSTMHK;
LFLSQACNLSTMHKI; FLSQACNLSTMHKID; LSQACNLSTMHKIDT;
SQACNLSTMHKIDTK; QACNLSTMHKIDTKE; ACNLSTMHKIDTKED;
CNLSTMHKIDTKEDM; NLSTMHKIDTKEDMK; LSTMHKIDTKEDMKI;
STMHKIDTKEDMKIL; TMHKIDTKEDMKILY; MHKIDTKEDMKILYS;
HKIDTKEDMKILYSE; KIDTKEDMKILYSEI; IDTKEDMKILYSEIA;
DTKEDMKILYSEIAE; TKEDMKILYSEIAEL; KEDMKILYSEIAELR;
EDMKILYSEIAELRK; DMKILYSEIAELRKK; MKILYSEIAELRKKL;
KILYSEIAELRKKLN; ILYSEIAELRKKLNL; LYSEIAELRKKLNLN;
YSEIAELRKKLNLNH; SEIAELRKKLNLNHL; EIAELRKKLNLNHLE;
IAELRKKLNLNHLEI; AELRKKLNLNHLEID; ELRKKLNLNHLEIDD;
LRKKLNLNHLEIDDT; RKKLNLNHLEIDDTL; KKLNLNHLEIDDTLE;
KLNLNHLEIDDTLEK; LNLNHLEIDDTLEKV; NLNHLEIDDTLEKVA;
LNHLEIDDTLEKVAK; NHLEIDDTLEKVAKE; HLEIDDTLEKVAKEY;
LEIDDTLEKVAKEYA; EIDDTLEKVAKEYAI; IDDTLEKVAKEYAIK;
DDTLEKVAKEYAIKL; DTLEKVAKEYAIKLG; TLEKVAKEYAIKLGE;
LEKVAKEYAIKLGEN; EKVAKEYAIKLGENR; KVAKEYAIKLGENRT;
VAKEYAIKLGENRTI; AKEYAIKLGENRTIT; KEYAIKLGENRTITH;
EYAIKLGENRTITHT; YAIKLGENRTITHTL; AIKLGENRTITHTLF;
IKLGENRTITHTLFG; KLGENRTITHTLFGT; LGENRTITHTLFGTT;
GENRTITHTLFGTTP; ENRTITHTLFGTTPM; NRTITHTLFGTTPMQ;
RTITHTLFGTTPMQR; TITHTLFGTTPMQRI; ITHTLFGTTPMQRIH;
THTLFGTTPMQRIHK; HTLFGTTPMQRIHKY; TLFGTTPMQRIHKYD;
LFGTTPMQRIHKYDQ; FGTTPMQRIHKYDQS; GTTPMQRIHKYDQSF;
TTPMQRIHKYDQSFN; TPMQRIHKYDQSFNL; PMQRIHKYDQSFNLT;
MQRIHKYDQSFNLTR; QRIHKYDQSFNLTRE; RIHKYDQSFNLTREI;
IHKYDQSFNLTREIL; HKYDQSFNLTREILA; KYDQSFNLTREILAS;
YDQSFNLTREILASG; DQSFNLTREILASGI; QSFNLTREILASGIE;
SFNLTREILASGIEL; FNLTREILASGIELN; NLTREILASGIELNR;
LTREILASGIELNRV; TREILASGIELNRVV; REILASGIELNRVVN;
EILASGIELNRVVNA; ILASGIELNRVVNAW; LASGIELNRVVNAWL;
ASGIELNRVVNAWLN; SGIELNRVVNAWLNS; GIELNRVVNAWLNSP;
IELNRVVNAWLNSPS; ELNRVVNAWLNSPSH; LNRVVNAWLNSPSHK;
NRVVNAWLNSPSHKE; RVVNAWLNSPSHKEA; VVNAWLNSPSHKEAL;
VNAWLNSPSHKEALI; NAWLNSPSHKEALIN; AWLNSPSHKEALINT;
WLNSPSHKEALINTD; LNSPSHKEALINTDT; NSPSHKEALINTDTD;
SPSHKEALINTDTDK; PSHKEALINTDTDKI; SHKEALINTDTDKIG;
HKEALINTDTDKIGG; KEALINTDTDKIGGY; EALINTDTDKIGGYR;
ALINTDTDKIGGYRL; LINTDTDKIGGYRLK; INTDTDKIGGYRLKT;
NTDTDKIGGYRLKTT; TDTDKIGGYRLKTTD; DTDKIGGYRLKTTDN;

	TDKIGGYRLKTTDNI; DKIGGYRLKTTDNID; KIGGYRLKTTDNIDI; IGGYRLKTTDNIDIF; GGYRLKTTDNIDIFV; GYRLKTTDNIDIFVV; YRLKTTDNIDIFVVL; RLKTTDNIDIFVVLF; LKTTDNIDIFVVLFG; KTTDNIDIFVVLFGK; TTDNIDIFVVLFGKR; TDNIDIFVVLFGKRK; DNIDIFVVLFGKRKY; NIDIFVVLFGKRKYK; IDIFVVLFGKRKYKN; 16 mers: MKKLIIIFTLFLSQAC; KKLIIIFTLFLSQACN; KLIIIFTLFLSQACNL; LIIIFTLFLSQACNLS; IIIFTLFLSQACNLST; IIFTLFLSQACNLSTM; IFTLFLSQACNLSTMH; FTLFLSQACNLSTMHK; TLFLSQACNLSTMHKI; LFLSQACNLSTMHKID; FLSQACNLSTMHKIDT; LSQACNLSTMHKIDTK; SQACNLSTMHKIDTKE; QACNLSTMHKIDTKED; ACNLSTMHKIDTKEDM; CNLSTMHKIDTKEDMK; NLSTMHKIDTKEDMKI; LSTMHKIDTKEDMKIL; STMHKIDTKEDMKILY; TMHKIDTKEDMKILYS; MHKIDTKEDMKILYSE; HKIDTKEDMKILYSEI; KIDTKEDMKILYSEIA; IDTKEDMKILYSEIAE; DTKEDMKILYSEIAEL; TKEDMKILYSEIAELR; KEDMKILYSEIAELRK; EDMKILYSEIAELRKK; DMKILYSEIAELRKKL; MKILYSEIAELRKKLN; KILYSEIAELRKKLNL; ILYSEIAELRKKLNLN; LYSEIAELRKKLNLNH; YSEIAELRKKLNLNHL; SEIAELRKKLNLNHLE; EIAELRKKLNLNHLEI; IAELRKKLNLNHLEID; AELRKKLNLNHLEIDD; ELRKKLNLNHLEIDDT; LRKKLNLNHLEIDDTL; RKKLNLNHLEIDDTLE; KKLNLNHLEIDDTLEK; KLNLNHLEIDDTLEKV; LNLNHLEIDDTLEKVA; NLNHLEIDDTLEKVAK; LNHLEIDDTLEKVAKE; NHLEIDDTLEKVAKEY; HLEIDDTLEKVAKEYA; LEIDDTLEKVAKEYAI; EIDDTLEKVAKEYAIK; IDDTLEKVAKEYAIKL; DDTLEKVAKEYAIKLG; DTLEKVAKEYAIKLGE; TLEKVAKEYAIKLGEN; LEKVAKEYAIKLGENR; EKVAKEYAIKLGENRT; KVAKEYAIKLGENRTI; VAKEYAIKLGENRTIT; AKEYAIKLGENRTITH; KEYAIKLGENRTITHT; EYAIKLGENRTITHTL; YAIKLGENRTITHTLF; AIKLGENRTITHTLFG; IKLGENRTITHTLFGT; KLGENRTITHTLFGTT; LGENRTITHTLFGTTP; GENRTITHTLFGTTPM; ENRTITHTLFGTTPMQ; NRTITHTLFGTTPMQR; RTITHTLFGTTPMQRI; TITHTLFGTTPMQRIH; ITHTLFGTTPMQRIHK; THTLFGTTPMQRIHKY; HTLFGTTPMQRIHKYD; TLFGTTPMQRIHKYDQ; LFGTTPMQRIHKYDQS; FGTTPMQRIHKYDQSF; GTTPMQRIHKYDQSFN; TTPMQRIHKYDQSFNL; TPMQRIHKYDQSFNLT; PMQRIHKYDQSFNLTR; MQRIHKYDQSFNLTRE; QRIHKYDQSFNLTREI; RIHKYDQSFNLTREIL; IHKYDQSFNLTREILA; HKYDQSFNLTREILAS; KYDQSFNLTREILASG; YDQSFNLTREILASGI; DQSFNLTREILASGIE; QSFNLTREILASGIEL; SFNLTREILASGIELN; FNLTREILASGIELNR; NLTREILASGIELNRV; LTREILASGIELNRVV; TREILASGIELNRVVN; REILASGIELNRVVNA; EILASGIELNRVVNAW; ILASGIELNRVVNAWL; LASGIELNRVVNAWLN; ASGIELNRVVNAWLNS; SGIELNRVVNAWLNSP; GIELNRVVNAWLNSPS; IELNRVVNAWLNSPSH; ELNRVVNAWLNSPSHK; LNRVVNAWLNSPSHKE; NRVVNAWLNSPSHKEA; RVVNAWLNSPSHKEAL; VVNAWLNSPSHKEALI; VNAWLNSPSHKEALIN; NAWLNSPSHKEALINT; AWLNSPSHKEALINTD; WLNSPSHKEALINTDT; LNSPSHKEALINTDTD; NSPSHKEALINTDTDK; SPSHKEALINTDTDKI; PSHKEALINTDTDKIG; SHKEALINTDTDKIGG; HKEALINTDTDKIGGY; KEALINTDTDKIGGYR; EALINTDTDKIGGYRL; ALINTDTDKIGGYRLK; LINTDTDKIGGYRLKT; INTDTDKIGGYRLKTT; NTDTDKIGGYRLKTTD; TDTDKIGGYRLKTTDN; DTDKIGGYRLKTTDNI; TDKIGGYRLKTTDNID; DKIGGYRLKTTDNIDI; KIGGYRLKTTDNIDIF; IGGYRLKTTDNIDIFV; GGYRLKTTDNIDIFVV; GYRLKTTDNIDIFVVL;

	YRLKTTDNIDIFVVLF; RLKTTDNIDIFVVLFG; LKTTDNIDIFVVLFGK; KTTDNIDIFVVLFGKR; TTDNIDIFVVLFGKRK; TDNIDIFVVLFGKRKY; DNIDIFVVLFGKRKYK; NIDIFVVLFGKRKYKN;
Seq 32	13 mers: MMQRISILLMLLA; MQRISILLMLLAV; QRISILLMLLAVF; RISILLMLLAVFS; ISILLMLLAVFSC; SILLMLLAVFSCK; ILLMLLAVFSCKQ; LLMLLAVFSCKQF; LMLLAVFSCKQFG; MLLAVFSCKQFGD; LLAVFSCKQFGDV; LAVFSCKQFGDVK; AVFSCKQFGDVKS; VFSCKQFGDVKSL; FSCKQFGDVKSLT; SCKQFGDVKSLTE; CKQFGDVKSLTEI; KQFGDVKSLTEID; QFGDVKSLTEIDS; FGDVKSLTEIDSG; GDVKSLTEIDSGN; DVKSLTEIDSGNG; VKSLTEIDSGNGI; KSLTEIDSGNGIP; SLTEIDSGNGIPL; LTEIDSGNGIPLV; TEIDSGNGIPLVV; EIDSGNGIPLVVS; IDSGNGIPLVVSD; DSGNGIPLVVSDV; SGNGIPLVVSDVV; GNGIPLVVSDVVK; NGIPLVVSDVVKD; GIPLVVSDVVKDL; IPLVVSDVVKDLI; PLVVSDVVKDLIP; LVVSDVVKDLIPK; VVSDVVKDLIPKE; VSDVVKDLIPKEI; SDVVKDLIPKEIS; DVVKDLIPKEISL; VVKDLIPKEISLT; VKDLIPKEISLTP; KDLIPKEISLTPE; DLIPKEISLTPEE; LIPKEISLTPEEA; IPKEISLTPEEAE; PKEISLTPEEAEK; KEISLTPEEAEKL; EISLTPEEAEKLE; ISLTPEEAEKLES; SLTPEEAEKLESL; LTPEEAEKLESLK; TPEEAEKLESLKV; PEEAEKLESLKVF; EEAEKLESLKVFL; EAEKLESLKVFLK; AEKLESLKVFLKD; EKLESLKVFLKDA; KLESLKVFLKDAM; LESLKVFLKDAMS; ESLKVFLKDAMSV; SLKVFLKDAMSVN; LKVFLKDAMSVNG; KVFLKDAMSVNGR; VFLKDAMSVNGRE; FLKDAMSVNGREE; LKDAMSVNGREEA; KDAMSVNGREEAL; DAMSVNGREEALK; AMSVNGREEALKA; MSVNGREEALKAE; SVNGREEALKAEY; VNGREEALKAEYE; NGREEALKAEYEK; GREEALKAEYEKS; REEALKAEYEKSY; EEALKAEYEKSYK; EALKAEYEKSYKE; ALKAEYEKSYKEF; LKAEYEKSYKEFF; KAEYEKSYKEFFD; AEYEKSYKEFFDW; EYEKSYKEFFDWL; YEKSYKEFFDWLS; EKSYKEFFDWLSK; KSYKEFFDWLSKD; SYKEFFDWLSKDV; YKEFFDWLSKDVN; KEFFDWLSKDVNR; EFFDWLSKDVNRQ; FFDWLSKDVNRQK; FDWLSKDVNRQKE; DWLSKDVNRQKEF; WLSKDVNRQKEFI; LSKDVNRQKEFIS; SKDVNRQKEFISS; KDVNRQKEFISSF; DVNRQKEFISSFD; VNRQKEFISSFDN; NRQKEFISSFDNI; RQKEFISSFDNIS; QKEFISSFDNISS; KEFISSFDNISSI; EFISSFDNISSIV; FISSFDNISSIVS; ISSFDNISSIVSK; SSFDNISSIVSKA; SFDNISSIVSKAV; FDNISSIVSKAVD; DNISSIVSKAVDA; NISSIVSKAVDAS; ISSIVSKAVDASK; SSIVSKAVDASKK; SIVSKAVDASKKR; IVSKAVDASKKRR; VSKAVDASKKRRP; SKAVDASKKRRPT; KAVDASKKRRPTE; AVDASKKRRPTEQ; VDASKKRRPTEQQ; DASKKRRPTEQQS; ASKKRRPTEQQSL; SKKRRPTEQQSLG; KKRRPTEQQSLGF; KRRPTEQQSLGFK; RRPTEQQSLGFKE; RPTEQQSLGFKEY; PTEQQSLGFKEYV; TEQQSLGFKEYVC; EQQSLGFKEYVCY; QQSLGFKEYVCYK; QSLGFKEYVCYKI; SLGFKEYVCYKIK; LGFKEYVCYKIKN;

GFKEYVCYKIKNS; FKEYVCYKIKNSK; KEYVCYKIKNSKG;
EYVCYKIKNSKGE; YVCYKIKNSKGEA; VCYKIKNSKGEAL;
CYKIKNSKGEALS; YKIKNSKGEALSL; KIKNSKGEALSLF;
IKNSKGEALSLFF; KNSKGEALSLFFQ; NSKGEALSLFFQK;
SKGEALSLFFQKV; KGEALSLFFQKVV; GEALSLFFQKVVD;
EALSLFFQKVVDA; ALSLFFQKVVDAF; LSLFFQKVVDAFG;
SLFFQKVVDAFGA; LFFQKVVDAFGAD; FFQKVVDAFGADP;
FQKVVDAFGADPY; QKVVDAFGADPYK; KVVDAFGADPYKK;
VVDAFGADPYKKD; VDAFGADPYKKDN; DAFGADPYKKDND;
AFGADPYKKDNDE; FGADPYKKDNDES; GADPYKKDNDESV;
ADPYKKDNDESVQ; DPYKKDNDESVQK; PYKKDNDESVQKP;
YKKDNDESVQKPV; KKDNDESVQKPVK; KDNDESVQKPVKC;
DNDESVQKPVKCN; NDESVQKPVKCNE; DESVQKPVKCNEE;
ESVQKPVKCNEEI; SVQKPVKCNEEIF; VQKPVKCNEEIFK;
QKPVKCNEEIFKV; KPVKCNEEIFKVI; PVKCNEEIFKVIK;
VKCNEEIFKVIKK; KCNEEIFKVIKKV; CNEEIFKVIKKVL;
NEEIFKVIKKVLT; EEIFKVIKKVLTE; EIFKVIKKVLTES;
IFKVIKKVLTESE; FKVIKKVLTESES; KVIKKVLTESESN;
VIKKVLTESESNN; IKKVLTESESNNE; KKVLTESESNNEL;
KVLTESESNNELK; VLTESESNNELKN; LTESESNNELKNL;
TESESNNELKNLK; ESESNNELKNLKN; SESNNELKNLKNY;
ESNNELKNLKNYG; SNNELKNLKNYGN; NNELKNLKNYGNV;

14 mers:
MMQRISILLMLLAV; MQRISILLMLLAVF; QRISILLMLLAVFS;
RISILLMLLAVFSC; ISILLMLLAVFSCK; SILLMLLAVFSCKQ;
ILLMLLAVFSCKQF; LLMLLAVFSCKQFG; LMLLAVFSCKQFGD;
MLLAVFSCKQFGDV; LLAVFSCKQFGDVK; LAVFSCKQFGDVKS;
AVFSCKQFGDVKSL; VFSCKQFGDVKSLT; FSCKQFGDVKSLTE;
SCKQFGDVKSLTEI; CKQFGDVKSLTEID; KQFGDVKSLTEIDS;
QFGDVKSLTEIDSG; FGDVKSLTEIDSGN; GDVKSLTEIDSGNG;
DVKSLTEIDSGNGI; VKSLTEIDSGNGIP; KSLTEIDSGNGIPL;
SLTEIDSGNGIPLV; LTEIDSGNGIPLVV; TEIDSGNGIPLVVS;
EIDSGNGIPLVVSD; IDSGNGIPLVVSDV; DSGNGIPLVVSDVV;
SGNGIPLVVSDVVK; GNGIPLVVSDVVKD; NGIPLVVSDVVKDL;
GIPLVVSDVVKDLI; IPLVVSDVVKDLIP; PLVVSDVVKDLIPK;
LVVSDVVKDLIPKE; VVSDVVKDLIPKEI; VSDVVKDLIPKEIS;
SDVVKDLIPKEISL; DVVKDLIPKEISLT; VVKDLIPKEISLTP;
VKDLIPKEISLTPE; KDLIPKEISLTPEE; DLIPKEISLTPEEA;
LIPKEISLTPEEAE; IPKEISLTPEEAEK; PKEISLTPEEAEKL;
KEISLTPEEAEKLE; EISLTPEEAEKLES; ISLTPEEAEKLESL;
SLTPEEAEKLESLK; LTPEEAEKLESLKV; TPEEAEKLESLKVF;
PEEAEKLESLKVFL; EEAEKLESLKVFLK; EAEKLESLKVFLKD;
AEKLESLKVFLKDA; EKLESLKVFLKDAM; KLESLKVFLKDAMS;
LESLKVFLKDAMSV; ESLKVFLKDAMSVN; SLKVFLKDAMSVNG;
LKVFLKDAMSVNGR; KVFLKDAMSVNGRE; VFLKDAMSVNGREE;
FLKDAMSVNGREEA; LKDAMSVNGREEAL; KDAMSVNGREEALK;
DAMSVNGREEALKA; AMSVNGREEALKAE; MSVNGREEALKAEY;
SVNGREEALKAEYE; VNGREEALKAEYEK; NGREEALKAEYEKS;
GREEALKAEYEKSY; REEALKAEYEKSYK; EEALKAEYEKSYKE;
EALKAEYEKSYKEF; ALKAEYEKSYKEFF; LKAEYEKSYKEFFD;

	KAEYEKSYKEFFDW; AEYEKSYKEFFDWL; EYEKSYKEFFDWLS; YEKSYKEFFDWLSK; EKSYKEFFDWLSKD; KSYKEFFDWLSKDV; SYKEFFDWLSKDVN; YKEFFDWLSKDVNR; KEFFDWLSKDVNRQ; EFFDWLSKDVNRQK; FFDWLSKDVNRQKE; FDWLSKDVNRQKEF; DWLSKDVNRQKEFI; WLSKDVNRQKEFIS; LSKDVNRQKEFISS; SKDVNRQKEFISSF; KDVNRQKEFISSFD; DVNRQKEFISSFDN; VNRQKEFISSFDNI; NRQKEFISSFDNIS; RQKEFISSFDNISS; QKEFISSFDNISSI; KEFISSFDNISSIV; EFISSFDNISSIVS; FISSFDNISSIVSK; ISSFDNISSIVSKA; SSFDNISSIVSKAV; SFDNISSIVSKAVD; FDNISSIVSKAVDA; DNISSIVSKAVDAS; NISSIVSKAVDASK; ISSIVSKAVDASKK; SSIVSKAVDASKKR; SIVSKAVDASKKRR; IVSKAVDASKKRRP; VSKAVDASKKRRPT; SKAVDASKKRRPTE; KAVDASKKRRPTEQ; AVDASKKRRPTEQQ; VDASKKRRPTEQQS; DASKKRRPTEQQSL; ASKKRRPTEQQSLG; SKKRRPTEQQSLGF; KKRRPTEQQSLGFK; KRRPTEQQSLGFKE; RRPTEQQSLGFKEY; RPTEQQSLGFKEYV; PTEQQSLGFKEYVC; TEQQSLGFKEYVCY; EQQSLGFKEYVCYK; QQSLGFKEYVCYKI; QSLGFKEYVCYKIK; SLGFKEYVCYKIKN; LGFKEYVCYKIKNS; GFKEYVCYKIKNSK; FKEYVCYKIKNSKG; KEYVCYKIKNSKGE; EYVCYKIKNSKGEA; YVCYKIKNSKGEAL; VCYKIKNSKGEALS; CYKIKNSKGEALSL; YKIKNSKGEALSLF; KIKNSKGEALSLFF; IKNSKGEALSLFFQ; KNSKGEALSLFFQK; NSKGEALSLFFQKV; SKGEALSLFFQKVV; KGEALSLFFQKVVD; GEALSLFFQKVVDA; EALSLFFQKVVDAF; ALSLFFQKVVDAFG; LSLFFQKVVDAFGA; SLFFQKVVDAFGAD; LFFQKVVDAFGADP; FFQKVVDAFGADPY; FQKVVDAFGADPYK; QKVVDAFGADPYKK; KVVDAFGADPYKKD; VVDAFGADPYKKDN; VDAFGADPYKKDND; DAFGADPYKKDNDE; AFGADPYKKDNDES; FGADPYKKDNDESV; GADPYKKDNDESVQ; ADPYKKDNDESVQK; DPYKKDNDESVQKP; PYKKDNDESVQKPV; YKKDNDESVQKPVK; KKDNDESVQKPVKC; KDNDESVQKPVKCN; DNDESVQKPVKCNE; NDESVQKPVKCNEE; DESVQKPVKCNEEI; ESVQKPVKCNEEIF; SVQKPVKCNEEIFK; VQKPVKCNEEIFKV; QKPVKCNEEIFKVI; KPVKCNEEIFKVIK; PVKCNEEIFKVIKK; VKCNEEIFKVIKKV; KCNEEIFKVIKKVL; CNEEIFKVIKKVLT; NEEIFKVIKKVLTE; EEIFKVIKKVLTES; EIFKVIKKVLTESE; IFKVIKKVLTESES; FKVIKKVLTESESN; KVIKKVLTESESNN; VIKKVLTESESNNE; IKKVLTESESNNEL; KKVLTESESNNELK; KVLTESESNNELKN; VLTESESNNELKNL; LTESESNNELKNLK; TESESNNELKNLKN; ESESNNELKNLKNY; SESNNELKNLKNYG; ESNNELKNLKNYGN; SNNELKNLKNYGNV; 15 mers: MMQRISILLMLLAVF; MQRISILLMLLAVFS; QRISILLMLLAVFSC; RISILLMLLAVFSCK; ISILLMLLAVFSCKQ; SILLMLLAVFSCKQF; ILLMLLAVFSCKQFG; LLMLLAVFSCKQFGD; LMLLAVFSCKQFGDV; MLLAVFSCKQFGDVK; LLAVFSCKQFGDVKS; LAVFSCKQFGDVKSL; AVFSCKQFGDVKSLT; VFSCKQFGDVKSLTE; FSCKQFGDVKSLTEI; SCKQFGDVKSLTEID; CKQFGDVKSLTEIDS; KQFGDVKSLTEIDSG; QFGDVKSLTEIDSGN; FGDVKSLTEIDSGNG; GDVKSLTEIDSGNGI; DVKSLTEIDSGNGIP; VKSLTEIDSGNGIPL; KSLTEIDSGNGIPLV; SLTEIDSGNGIPLVV; LTEIDSGNGIPLVVS; TEIDSGNGIPLVVSD;

	EIDSGNGIPLVVSDV; IDSGNGIPLVVSDVV; DSGNGIPLVVSDVVK; SGNGIPLVVSDVVKD; GNGIPLVVSDVVKDL; NGIPLVVSDVVKDLI; GIPLVVSDVVKDLIP; IPLVVSDVVKDLIPK; PLVVSDVVKDLIPKE; LVVSDVVKDLIPKEI; VVSDVVKDLIPKEIS; VSDVVKDLIPKEISL; SDVVKDLIPKEISLT; DVVKDLIPKEISLTP; VVKDLIPKEISLTPE; VKDLIPKEISLTPEE; KDLIPKEISLTPEEA; DLIPKEISLTPEEAE; LIPKEISLTPEEAEK; IPKEISLTPEEAEKL; PKEISLTPEEAEKLE; KEISLTPEEAEKLES; EISLTPEEAEKLESL; ISLTPEEAEKLESLK; SLTPEEAEKLESLKV; LTPEEAEKLESLKVF; TPEEAEKLESLKVFL; PEEAEKLESLKVFLK; EEAEKLESLKVFLKD; EAEKLESLKVFLKDA; AEKLESLKVFLKDAM; EKLESLKVFLKDAMS; KLESLKVFLKDAMSV; LESLKVFLKDAMSVN; ESLKVFLKDAMSVNG; SLKVFLKDAMSVNGR; LKVFLKDAMSVNGRE; KVFLKDAMSVNGREE; VFLKDAMSVNGREEA; FLKDAMSVNGREEAL; LKDAMSVNGREEALK; KDAMSVNGREEALKA; DAMSVNGREEALKAE; AMSVNGREEALKAEY; MSVNGREEALKAEYE; SVNGREEALKAEYEK; VNGREEALKAEYEKS; NGREEALKAEYEKSY; GREEALKAEYEKSYK; REEALKAEYEKSYKE; EEALKAEYEKSYKEF; EALKAEYEKSYKEFF; ALKAEYEKSYKEFFD; LKAEYEKSYKEFFDW; KAEYEKSYKEFFDWL; AEYEKSYKEFFDWLS; EYEKSYKEFFDWLSK; YEKSYKEFFDWLSKD; EKSYKEFFDWLSKDV; KSYKEFFDWLSKDVN; SYKEFFDWLSKDVNR; YKEFFDWLSKDVNRQ; KEFFDWLSKDVNRQK; EFFDWLSKDVNRQKE; FFDWLSKDVNRQKEF; FDWLSKDVNRQKEFI; DWLSKDVNRQKEFIS; WLSKDVNRQKEFISS; LSKDVNRQKEFISSF; SKDVNRQKEFISSFD; KDVNRQKEFISSFDN; DVNRQKEFISSFDNI; VNRQKEFISSFDNIS; NRQKEFISSFDNISS; RQKEFISSFDNISSI; QKEFISSFDNISSIV; KEFISSFDNISSIVS; EFISSFDNISSIVSK; FISSFDNISSIVSKA; ISSFDNISSIVSKAV; SSFDNISSIVSKAVD; SFDNISSIVSKAVDA; FDNISSIVSKAVDAS; DNISSIVSKAVDASK; NISSIVSKAVDASKK; ISSIVSKAVDASKKR; SSIVSKAVDASKKRR; SIVSKAVDASKKRRP; IVSKAVDASKKRRPT; VSKAVDASKKRRPTE; SKAVDASKKRRPTEQ; KAVDASKKRRPTEQQ; AVDASKKRRPTEQQS; VDASKKRRPTEQQSL; DASKKRRPTEQQSLG; ASKKRRPTEQQSLGF; SKKRRPTEQQSLGFK; KKRRPTEQQSLGFKE; KRRPTEQQSLGFKEY; RRPTEQQSLGFKEYV; RPTEQQSLGFKEYVC; PTEQQSLGFKEYVCY; TEQQSLGFKEYVCYK; EQQSLGFKEYVCYKI; QQSLGFKEYVCYKIK; QSLGFKEYVCYKIKN; SLGFKEYVCYKIKNS; LGFKEYVCYKIKNSK; GFKEYVCYKIKNSKG; FKEYVCYKIKNSKGE; KEYVCYKIKNSKGEA; EYVCYKIKNSKGEAL; YVCYKIKNSKGEALS; VCYKIKNSKGEALSL; CYKIKNSKGEALSLF; YKIKNSKGEALSLFF; KIKNSKGEALSLFFQ; IKNSKGEALSLFFQK; KNSKGEALSLFFQKV; NSKGEALSLFFQKVV; SKGEALSLFFQKVVD; KGEALSLFFQKVVDA; GEALSLFFQKVVDAF; EALSLFFQKVVDAFG; ALSLFFQKVVDAFGA; LSLFFQKVVDAFGAD; SLFFQKVVDAFGADP; LFFQKVVDAFGADPY; FFQKVVDAFGADPYK; FQKVVDAFGADPYKK; QKVVDAFGADPYKKD; KVVDAFGADPYKKDN; VVDAFGADPYKKDND; VDAFGADPYKKDNDE; DAFGADPYKKDNDES; AFGADPYKKDNDESV; FGADPYKKDNDESVQ; GADPYKKDNDESVQK; ADPYKKDNDESVQKP; DPYKKDNDESVQKPV; PYKKDNDESVQKPVK; YKKDNDESVQKPVKC; KKDNDESVQKPVKCN; KDNDESVQKPVKCNE; DNDESVQKPVKCNEE; NDESVQKPVKCNEEI; DESVQKPVKCNEEIF; ESVQKPVKCNEEIFK; SVQKPVKCNEEIFKV; VQKPVKCNEEIFKVI; QKPVKCNEEIFKVIK; KPVKCNEEIFKVIKK; PVKCNEEIFKVIKKV;

	VKCNEEIFKVIKKVL; KCNEEIFKVIKKVLT; CNEEIFKVIKKVLTE; NEEIFKVIKKVLTES; EEIFKVIKKVLTESE; EIFKVIKKVLTESES; IFKVIKKVLTESESN; FKVIKKVLTESESNN; KVIKKVLTESESNNE; VIKKVLTESESNNEL; IKKVLTESESNNELK; KKVLTESESNNELKN; KVLTESESNNELKNL; VLTESESNNELKNLK; LTESESNNELKNLKN; TESESNNELKNLKNY; ESESNNELKNLKNYG; SESNNELKNLKNYGN; ESNNELKNLKNYGNV; 16 mers: MMQRISILLMLLAVFS; MQRISILLMLLAVFSC; QRISILLMLLAVFSCK; RISILLMLLAVFSCKQ; ISILLMLLAVFSCKQF; SILLMLLAVFSCKQFG; ILLMLLAVFSCKQFGD; LLMLLAVFSCKQFGDV; LMLLAVFSCKQFGDVK; MLLAVFSCKQFGDVKS; LLAVFSCKQFGDVKSL; LAVFSCKQFGDVKSLT; AVFSCKQFGDVKSLTE; VFSCKQFGDVKSLTEI; FSCKQFGDVKSLTEID; SCKQFGDVKSLTEIDS; CKQFGDVKSLTEIDSG; KQFGDVKSLTEIDSGN; QFGDVKSLTEIDSGNG; FGDVKSLTEIDSGNGI; GDVKSLTEIDSGNGIP; DVKSLTEIDSGNGIPL; VKSLTEIDSGNGIPLV; KSLTEIDSGNGIPLVV; SLTEIDSGNGIPLVVS; LTEIDSGNGIPLVVSD; TEIDSGNGIPLVVSDV; EIDSGNGIPLVVSDVV; IDSGNGIPLVVSDVVK; DSGNGIPLVVSDVVKD; SGNGIPLVVSDVVKDL; GNGIPLVVSDVVKDLI; NGIPLVVSDVVKDLIP; GIPLVVSDVVKDLIPK; IPLVVSDVVKDLIPKE; PLVVSDVVKDLIPKEI; LVVSDVVKDLIPKEIS; VVSDVVKDLIPKEISL; VSDVVKDLIPKEISLT; SDVVKDLIPKEISLTP; DVVKDLIPKEISLTPE; VVKDLIPKEISLTPEE; VKDLIPKEISLTPEEA; KDLIPKEISLTPEEAE; DLIPKEISLTPEEAEK; LIPKEISLTPEEAEKL; IPKEISLTPEEAEKLE; PKEISLTPEEAEKLES; KEISLTPEEAEKLESL; EISLTPEEAEKLESLK; ISLTPEEAEKLESLKV; SLTPEEAEKLESLKVF; LTPEEAEKLESLKVFL; TPEEAEKLESLKVFLK; PEEAEKLESLKVFLKD; EEAEKLESLKVFLKDA; EAEKLESLKVFLKDAM; AEKLESLKVFLKDAMS; EKLESLKVFLKDAMSV; KLESLKVFLKDAMSVN; LESLKVFLKDAMSVNG; ESLKVFLKDAMSVNGR; SLKVFLKDAMSVNGRE; LKVFLKDAMSVNGREE; KVFLKDAMSVNGREEA; VFLKDAMSVNGREEAL; FLKDAMSVNGREEALK; LKDAMSVNGREEALKA; KDAMSVNGREEALKAE; DAMSVNGREEALKAEY; AMSVNGREEALKAEYE; MSVNGREEALKAEYEK; SVNGREEALKAEYEKS; VNGREEALKAEYEKSY; NGREEALKAEYEKSYK; GREEALKAEYEKSYKE; REEALKAEYEKSYKEF; EEALKAEYEKSYKEFF; EALKAEYEKSYKEFFD; ALKAEYEKSYKEFFDW; LKAEYEKSYKEFFDWL; KAEYEKSYKEFFDWLS; AEYEKSYKEFFDWLSK; EYEKSYKEFFDWLSKD; YEKSYKEFFDWLSKDV; EKSYKEFFDWLSKDVN; KSYKEFFDWLSKDVNR; SYKEFFDWLSKDVNRQ; YKEFFDWLSKDVNRQK; KEFFDWLSKDVNRQKE; EFFDWLSKDVNRQKEF; FFDWLSKDVNRQKEFI; FDWLSKDVNRQKEFIS; DWLSKDVNRQKEFISS; WLSKDVNRQKEFISSF; LSKDVNRQKEFISSFD; SKDVNRQKEFISSFDN; KDVNRQKEFISSFDNI; DVNRQKEFISSFDNIS; VNRQKEFISSFDNISS; NRQKEFISSFDNISSI; RQKEFISSFDNISSIV; QKEFISSFDNISSIVS; KEFISSFDNISSIVSK; EFISSFDNISSIVSKA; FISSFDNISSIVSKAV; ISSFDNISSIVSKAVD; SSFDNISSIVSKAVDA; SFDNISSIVSKAVDAS; FDNISSIVSKAVDASK; DNISSIVSKAVDASKK; NISSIVSKAVDASKKR; ISSIVSKAVDASKKRR; SSIVSKAVDASKKRRP; SIVSKAVDASKKRRPT; IVSKAVDASKKRRPTE; VSKAVDASKKRRPTEQ; SKAVDASKKRRPTEQQ; KAVDASKKRRPTEQQS; AVDASKKRRPTEQQSL; VDASKKRRPTEQQSLG; DASKKRRPTEQQSLGF; ASKKRRPTEQQSLGFK; SKKRRPTEQQSLGFKE; KKRRPTEQQSLGFKEY; KRRPTEQQSLGFKEYV;

	RRPTEQQSLGFKEYVC; RPTEQQSLGFKEYVCY; PTEQQSLGFKEYVCYK; TEQQSLGFKEYVCYKI; EQQSLGFKEYVCYKIK; QQSLGFKEYVCYKIKN; QSLGFKEYVCYKIKNS; SLGFKEYVCYKIKNSK; LGFKEYVCYKIKNSKG; GFKEYVCYKIKNSKGE; FKEYVCYKIKNSKGEA; KEYVCYKIKNSKGEAL; EYVCYKIKNSKGEALS; YVCYKIKNSKGEALSL; VCYKIKNSKGEALSLF; CYKIKNSKGEALSLFF; YKIKNSKGEALSLFFQ; KIKNSKGEALSLFFQK; IKNSKGEALSLFFQKV; KNSKGEALSLFFQKVV; NSKGEALSLFFQKVVD; SKGEALSLFFQKVVDA; KGEALSLFFQKVVDAF; GEALSLFFQKVVDAFG; EALSLFFQKVVDAFGA; ALSLFFQKVVDAFGAD; LSLFFQKVVDAFGADP; SLFFQKVVDAFGADPY; LFFQKVVDAFGADPYK; FFQKVVDAFGADPYKK; FQKVVDAFGADPYKKD; QKVVDAFGADPYKKDN; KVVDAFGADPYKKDND; VVDAFGADPYKKDNDE; VDAFGADPYKKDNDES; DAFGADPYKKDNDESV; AFGADPYKKDNDESVQ; FGADPYKKDNDESVQK; GADPYKKDNDESVQKP; ADPYKKDNDESVQKPV; DPYKKDNDESVQKPVK; PYKKDNDESVQKPVKC; YKKDNDESVQKPVKCN; KKDNDESVQKPVKCNE; KDNDESVQKPVKCNEE; DNDESVQKPVKCNEEI; NDESVQKPVKCNEEIF; DESVQKPVKCNEEIFK; ESVQKPVKCNEEIFKV; SVQKPVKCNEEIFKVI; VQKPVKCNEEIFKVIK; QKPVKCNEEIFKVIKK; KPVKCNEEIFKVIKKV; PVKCNEEIFKVIKKVL; VKCNEEIFKVIKKVLT; KCNEEIFKVIKKVLTE; CNEEIFKVIKKVLTES; NEEIFKVIKKVLTESE; EEIFKVIKKVLTESES; EIFKVIKKVLTESESN; IFKVIKKVLTESESNN; FKVIKKVLTESESNNE; KVIKKVLTESESNNEL; VIKKVLTESESNNELK; IKKVLTESESNNELKN; KKVLTESESNNELKNL; KVLTESESNNELKNLK; VLTESESNNELKNLKN; LTESESNNELKNLKNY; TESESNNELKNLKNYG; ESESNNELKNLKNYGN; SESNNELKNLKNYGNV;
Seq 33	13 mers: MKRISILSILLLL; KRISILSILLLLL; RISILSILLLLLL; ISILSILLLLLLF; SILSILLLLLLFS; ILSILLLLLLFSC; LSILLLLLLFSCK; SILLLLLLFSCKQ; ILLLLLLFSCKQY; LLLLLLFSCKQYG; LLLLLFSCKQYGD; LLLLFSCKQYGDV; LLLFSCKQYGDVK; LLFSCKQYGDVKS; LFSCKQYGDVKSL; FSCKQYGDVKSLT; SCKQYGDVKSLTE; CKQYGDVKSLTEV; KQYGDVKSLTEVA; QYGDVKSLTEVAT; YGDVKSLTEVATD; GDVKSLTEVATDL; DVKSLTEVATDLE; VKSLTEVATDLED; KSLTEVATDLEDD; SLTEVATDLEDDN; LTEVATDLEDDNS; TEVATDLEDDNSF; EVATDLEDDNSFA; VATDLEDDNSFAS; ATDLEDDNSFASG; TDLEDDNSFASGS; DLEDDNSFASGSV; LEDDNSFASGSVE; EDDNSFASGSVES; DDNSFASGSVESK; DNSFASGSVESKD; NSFASGSVESKDQ; SFASGSVESKDQI; FASGSVESKDQII; ASGSVESKDQIIE; SGSVESKDQIIEK; GSVESKDQIIEKG; SVESKDQIIEKGP; VESKDQIIEKGPV; ESKDQIIEKGPVL; SKDQIIEKGPVLT; KDQIIEKGPVLTS; DQIIEKGPVLTSE; QIIEKGPVLTSEE; IIEKGPVLTSEEF; IEKGPVLTSEEFE; EKGPVLTSEEFER; KGPVLTSEEFERL; GPVLTSEEFERLE; PVLTSEEFERLEA; VLTSEEFERLEAL; LTSEEFERLEALK; TSEEFERLEALKT; SEEFERLEALKTF; EEFERLEALKTFL; EFERLEALKTFLK; FERLEALKTFLKD; ERLEALKTFLKDA; RLEALKTFLKDAM; LEALKTFLKDAMG; EALKTFLKDAMGV; ALKTFLKDAMGVN; LKTFLKDAMGVNG; KTFLKDAMGVNGR; TFLKDAMGVNGRE; FLKDAMGVNGREG;

	LKDAMGVNGREGD; KDAMGVNGREGDT; DAMGVNGREGDTK; AMGVNGREGDTKA; MGVNGREGDTKAE; GVNGREGDTKAEY; VNGREGDTKAEYE; NGREGDTKAEYEK; GREGDTKAEYEKS; REGDTKAEYEKSY; EGDTKAEYEKSYK; GDTKAEYEKSYKE; DTKAEYEKSYKEF; TKAEYEKSYKEFF; KAEYEKSYKEFFD; AEYEKSYKEFFDW; EYEKSYKEFFDWL; YEKSYKEFFDWLS; EKSYKEFFDWLSK; KSYKEFFDWLSKD; SYKEFFDWLSKDV; YKEFFDWLSKDVN; KEFFDWLSKDVNR; EFFDWLSKDVNRQ; FFDWLSKDVNRQK; FDWLSKDVNRQKE; DWLSKDVNRQKEF; WLSKDVNRQKEFV; LSKDVNRQKEFVS; SKDVNRQKEFVSF; KDVNRQKEFVSFF; DVNRQKEFVSFFN; VNRQKEFVSFFNN; NRQKEFVSFFNNI; RQKEFVSFFNNIC; QKEFVSFFNNICG; KEFVSFFNNICGI; EFVSFFNNICGII; FVSFFNNICGIIT; VSFFNNICGIITK; SFFNNICGIITKA; FFNNICGIITKAV; FNNICGIITKAVD; NNICGIITKAVDA; NICGIITKAVDAS; ICGIITKAVDASK; CGIITKAVDASKK; GIITKAVDASKKR; IITKAVDASKKRY; ITKAVDASKKRYN; TKAVDASKKRYNS; KAVDASKKRYNSN; AVDASKKRYNSNP; VDASKKRYNSNPK; DASKKRYNSNPKS; ASKKRYNSNPKSL; SKKRYNSNPKSLG; KKRYNSNPKSLGF; KRYNSNPKSLGFN; RYNSNPKSLGFNE; YNSNPKSLGFNEY; NSNPKSLGFNEYV; SNPKSLGFNEYVC; NPKSLGFNEYVCY; PKSLGFNEYVCYD; KSLGFNEYVCYDI; SLGFNEYVCYDIK; LGFNEYVCYDIKT; GFNEYVCYDIKTR; FNEYVCYDIKTRT; NEYVCYDIKTRTG; EYVCYDIKTRTGD; YVCYDIKTRTGDD; VCYDIKTRTGDDL; CYDIKTRTGDDLS; YDIKTRTGDDLSL; DIKTRTGDDLSLF; IKTRTGDDLSLFF; KTRTGDDLSLFFQ; TRTGDDLSLFFQK; RTGDDLSLFFQKV; TGDDLSLFFQKVA; GDDLSLFFQKVAD; DDLSLFFQKVADA; DLSLFFQKVADAF; LSLFFQKVADAFG; SLFFQKVADAFGT; LFFQKVADAFGTQ; FFQKVADAFGTQE; FQKVADAFGTQEY; QKVADAFGTQEYK; KVADAFGTQEYKN; VADAFGTQEYKNK; ADAFGTQEYKNKD; DAFGTQEYKNKDE; AFGTQEYKNKDED; FGTQEYKNKDEDD; GTQEYKNKDEDDE; TQEYKNKDEDDEN; QEYKNKDEDDENN; EYKNKDEDDENNQ; YKNKDEDDENNQK; KNKDEDDENNQKP; NKDEDDENNQKPE; KDEDDENNQKPEK; DEDDENNQKPEKC; EDDENNQKPEKCN; DDENNQKPEKCNE; DENNQKPEKCNEE; ENNQKPEKCNEEI; NNQKPEKCNEEIF; NQKPEKCNEEIFK; QKPEKCNEEIFKV; KPEKCNEEIFKVI; PEKCNEEIFKVIK; EKCNEEIFKVIKR; KCNEEIFKVIKRV; CNEEIFKVIKRVF; NEEIFKVIKRVFT; EEIFKVIKRVFTE; EIFKVIKRVFTES; IFKVIKRVFTESE; FKVIKRVFTESEN; KVIKRVFTESENN; VIKRVFTESENNN; IKRVFTESENNNE; KRVFTESENNNEL; RVFTESENNNELA; VFTESENNNELAN; FTESENNNELANL; TESENNNELANLK; ESENNNELANLKN; SENNNELANLKNL; ENNNELANLKNLN; NNNELANLKNLNS; NNELANLKNLNSY; NELANLKNLNSYN; ELANLKNLNSYNL; LANLKNLNSYNLN; ANLKNLNSYNLNS; NLKNLNSYNLNSN; LKNLNSYNLNSNN; KNLNSYNLNSNNK; 14 mers: MKRISILSILLLLL; KRISILSILLLLLL; RISILSILLLLLLF;

	ISILSILLLLLLFS; SILSILLLLLLFSC; ILSILLLLLLFSCK; LSILLLLLLFSCKQ; SILLLLLLFSCKQY; ILLLLLLFSCKQYG; LLLLLLFSCKQYGD; LLLLLFSCKQYGDV; LLLLFSCKQYGDVK; LLLFSCKQYGDVKS; LLFSCKQYGDVKSL; LFSCKQYGDVKSLT; FSCKQYGDVKSLTE; SCKQYGDVKSLTEV; CKQYGDVKSLTEVA; KQYGDVKSLTEVAT; QYGDVKSLTEVATD; YGDVKSLTEVATDL; GDVKSLTEVATDLE; DVKSLTEVATDLED; VKSLTEVATDLEDD; KSLTEVATDLEDDN; SLTEVATDLEDDNS; LTEVATDLEDDNSF; TEVATDLEDDNSFA; EVATDLEDDNSFAS; VATDLEDDNSFASG; ATDLEDDNSFASGS; TDLEDDNSFASGSV; DLEDDNSFASGSVE; LEDDNSFASGSVES; EDDNSFASGSVESK; DDNSFASGSVESKD; DNSFASGSVESKDQ; NSFASGSVESKDQI; SFASGSVESKDQII; FASGSVESKDQIIE; ASGSVESKDQIIEK; SGSVESKDQIIEKG; GSVESKDQIIEKGP; SVESKDQIIEKGPV; VESKDQIIEKGPVL; ESKDQIIEKGPVLT; SKDQIIEKGPVLTS; KDQIIEKGPVLTSE; DQIIEKGPVLTSEE; QIIEKGPVLTSEEF; IIEKGPVLTSEEFE; IEKGPVLTSEEFER; EKGPVLTSEEFERL; KGPVLTSEEFERLE; GPVLTSEEFERLEA; PVLTSEEFERLEAL; VLTSEEFERLEALK; LTSEEFERLEALKT; TSEEFERLEALKTF; SEEFERLEALKTFL; EEFERLEALKTFLK; EFERLEALKTFLKD; FERLEALKTFLKDA; ERLEALKTFLKDAM; RLEALKTFLKDAMG; LEALKTFLKDAMGV; EALKTFLKDAMGVN; ALKTFLKDAMGVNG; LKTFLKDAMGVNGR; KTFLKDAMGVNGRE; TFLKDAMGVNGREG; FLKDAMGVNGREGD; LKDAMGVNGREGDT; KDAMGVNGREGDTK; DAMGVNGREGDTKA; AMGVNGREGDTKAE; MGVNGREGDTKAEY; GVNGREGDTKAEYE; VNGREGDTKAEYEK; NGREGDTKAEYEKS; GREGDTKAEYEKSY; REGDTKAEYEKSYK; EGDTKAEYEKSYKE; GDTKAEYEKSYKEF; DTKAEYEKSYKEFF; TKAEYEKSYKEFFD; KAEYEKSYKEFFDW; AEYEKSYKEFFDWL; EYEKSYKEFFDWLS; YEKSYKEFFDWLSK; EKSYKEFFDWLSKD; KSYKEFFDWLSKDV; SYKEFFDWLSKDVN; YKEFFDWLSKDVNR; KEFFDWLSKDVNRQ; EFFDWLSKDVNRQK; FFDWLSKDVNRQKE; FDWLSKDVNRQKEF; DWLSKDVNRQKEFV; WLSKDVNRQKEFVS; LSKDVNRQKEFVSF; SKDVNRQKEFVSFF; KDVNRQKEFVSFFN; DVNRQKEFVSFFNN; VNRQKEFVSFFNNI; NRQKEFVSFFNNIC; RQKEFVSFFNNICG; QKEFVSFFNNICGI; KEFVSFFNNICGII; EFVSFFNNICGIIT; FVSFFNNICGIITK; VSFFNNICGIITKA; SFFNNICGIITKAV; FFNNICGIITKAVD; FNNICGIITKAVDA; NNICGIITKAVDAS; NICGIITKAVDASK; ICGIITKAVDASKK; CGIITKAVDASKKR; GIITKAVDASKKRY; IITKAVDASKKRYN; ITKAVDASKKRYNS; TKAVDASKKRYNSN; KAVDASKKRYNSNP; AVDASKKRYNSNPK; VDASKKRYNSNPKS; DASKKRYNSNPKSL; ASKKRYNSNPKSLG; SKKRYNSNPKSLGF; KKRYNSNPKSLGFN; KRYNSNPKSLGFNE; RYNSNPKSLGFNEY; YNSNPKSLGFNEYV; NSNPKSLGFNEYVC; SNPKSLGFNEYVCY; NPKSLGFNEYVCYD; PKSLGFNEYVCYDI; KSLGFNEYVCYDIK; SLGFNEYVCYDIKT; LGFNEYVCYDIKTR; GFNEYVCYDIKTRT; FNEYVCYDIKTRTG; NEYVCYDIKTRTGD; EYVCYDIKTRTGDD; YVCYDIKTRTGDDL; VCYDIKTRTGDDLS; CYDIKTRTGDDLSL; YDIKTRTGDDLSLF; DIKTRTGDDLSLFF; IKTRTGDDLSLFFQ; KTRTGDDLSLFFQK; TRTGDDLSLFFQKV; RTGDDLSLFFQKVA; TGDDLSLFFQKVAD; GDDLSLFFQKVADA; DDLSLFFQKVADAF;

DLSLFFQKVADAFG; LSLFFQKVADAFGT; SLFFQKVADAFGTQ;
LFFQKVADAFGTQE; FFQKVADAFGTQEY; FQKVADAFGTQEYK;
QKVADAFGTQEYKN; KVADAFGTQEYKNK; VADAFGTQEYKNKD;
ADAFGTQEYKNKDE; DAFGTQEYKNKDED; AFGTQEYKNKDEDD;
FGTQEYKNKDEDDE; GTQEYKNKDEDDEN; TQEYKNKDEDDENN;
QEYKNKDEDDENNQ; EYKNKDEDDENNQK; YKNKDEDDENNQKP;
KNKDEDDENNQKPE; NKDEDDENNQKPEK; KDEDDENNQKPEKC;
DEDDENNQKPEKCN; EDDENNQKPEKCNE; DDENNQKPEKCNEE;
DENNQKPEKCNEEI; ENNQKPEKCNEEIF; NNQKPEKCNEEIFK;
NQKPEKCNEEIFKV; QKPEKCNEEIFKVI; KPEKCNEEIFKVIK;
PEKCNEEIFKVIKR; EKCNEEIFKVIKRV; KCNEEIFKVIKRVF;
CNEEIFKVIKRVFT; NEEIFKVIKRVFTE; EEIFKVIKRVFTES;
EIFKVIKRVFTESE; IFKVIKRVFTESEN; FKVIKRVFTESENN;
KVIKRVFTESENNN; VIKRVFTESENNNE; IKRVFTESENNNEL;
KRVFTESENNNELA; RVFTESENNNELAN; VFTESENNNELANL;
FTESENNNELANLK; TESENNNELANLKN; ESENNNELANLKNL;
SENNNELANLKNLN; ENNNELANLKNLNS; NNNELANLKNLNSY;
NNELANLKNLNSYN; NELANLKNLNSYNL; ELANLKNLNSYNLN;
LANLKNLNSYNLNS; ANLKNLNSYNLNSN; NLKNLNSYNLNSNN;
LKNLNSYNLNSNNK;

15 mers:
MKRISILSILLLLLL; KRISILSILLLLLLF; RISILSILLLLLLFS;
ISILSILLLLLLFSC; SILSILLLLLLFSCK; ILSILLLLLLFSCKQ;
LSILLLLLLFSCKQY; SILLLLLLFSCKQYG; ILLLLLLFSCKQYGD;
LLLLLLFSCKQYGDV; LLLLLFSCKQYGDVK; LLLLFSCKQYGDVKS;
LLLFSCKQYGDVKSL; LLFSCKQYGDVKSLT; LFSCKQYGDVKSLTE;
FSCKQYGDVKSLTEV; SCKQYGDVKSLTEVA; CKQYGDVKSLTEVAT;
KQYGDVKSLTEVATD; QYGDVKSLTEVATDL; YGDVKSLTEVATDLE;
GDVKSLTEVATDLED; DVKSLTEVATDLEDD; VKSLTEVATDLEDDN;
KSLTEVATDLEDDNS; SLTEVATDLEDDNSF; LTEVATDLEDDNSFA;
TEVATDLEDDNSFAS; EVATDLEDDNSFASG; VATDLEDDNSFASGS;
ATDLEDDNSFASGSV; TDLEDDNSFASGSVE; DLEDDNSFASGSVES;
LEDDNSFASGSVESK; EDDNSFASGSVESKD; DDNSFASGSVESKDQ;
DNSFASGSVESKDQI; NSFASGSVESKDQII; SFASGSVESKDQIIE;
FASGSVESKDQIIEK; ASGSVESKDQIIEKG; SGSVESKDQIIEKGP;
GSVESKDQIIEKGPV; SVESKDQIIEKGPVL; VESKDQIIEKGPVLT;
ESKDQIIEKGPVLTS; SKDQIIEKGPVLTSE; KDQIIEKGPVLTSEE;
DQIIEKGPVLTSEEF; QIIEKGPVLTSEEFE; IIEKGPVLTSEEFER;
IEKGPVLTSEEFERL; EKGPVLTSEEFERLE; KGPVLTSEEFERLEA;
GPVLTSEEFERLEAL; PVLTSEEFERLEALK; VLTSEEFERLEALKT;
LTSEEFERLEALKTF; TSEEFERLEALKTFL; SEEFERLEALKTFLK;
EEFERLEALKTFLKD; EFERLEALKTFLKDA; FERLEALKTFLKDAM;
ERLEALKTFLKDAMG; RLEALKTFLKDAMGV; LEALKTFLKDAMGVN;
EALKTFLKDAMGVNG; ALKTFLKDAMGVNGR; LKTFLKDAMGVNGRE;
KTFLKDAMGVNGREG; TFLKDAMGVNGREGD; FLKDAMGVNGREGDT;
LKDAMGVNGREGDTK; KDAMGVNGREGDTKA; DAMGVNGREGDTKAE;
AMGVNGREGDTKAEY; MGVNGREGDTKAEYE; GVNGREGDTKAEYEK;
VNGREGDTKAEYEKS; NGREGDTKAEYEKSY; GREGDTKAEYEKSYK;
REGDTKAEYEKSYKE; EGDTKAEYEKSYKEF; GDTKAEYEKSYKEFF;
DTKAEYEKSYKEFFD; TKAEYEKSYKEFFDW; KAEYEKSYKEFFDWL;

	AEYEKSYKEFFDWLS; EYEKSYKEFFDWLSK; YEKSYKEFFDWLSKD; EKSYKEFFDWLSKDV; KSYKEFFDWLSKDVN; SYKEFFDWLSKDVNR; YKEFFDWLSKDVNRQ; KEFFDWLSKDVNRQK; EFFDWLSKDVNRQKE; FFDWLSKDVNRQKEF; FDWLSKDVNRQKEFV; DWLSKDVNRQKEFVS; WLSKDVNRQKEFVSF; LSKDVNRQKEFVSFF; SKDVNRQKEFVSFFN; KDVNRQKEFVSFFNN; DVNRQKEFVSFFNNI; VNRQKEFVSFFNNIC; NRQKEFVSFFNNICG; RQKEFVSFFNNICGI; QKEFVSFFNNICGII; KEFVSFFNNICGIIT; EFVSFFNNICGIITK; FVSFFNNICGIITKA; VSFFNNICGIITKAV; SFFNNICGIITKAVD; FFNNICGIITKAVDA; FNNICGIITKAVDAS; NNICGIITKAVDASK; NICGIITKAVDASKK; ICGIITKAVDASKKR; CGIITKAVDASKKRY; GIITKAVDASKKRYN; IITKAVDASKKRYNS; ITKAVDASKKRYNSN; TKAVDASKKRYNSNP; KAVDASKKRYNSNPK; AVDASKKRYNSNPKS; VDASKKRYNSNPKSL; DASKKRYNSNPKSLG; ASKKRYNSNPKSLGF; SKKRYNSNPKSLGFN; KKRYNSNPKSLGFNE; KRYNSNPKSLGFNEY; RYNSNPKSLGFNEYV; YNSNPKSLGFNEYVC; NSNPKSLGFNEYVCY; SNPKSLGFNEYVCYD; NPKSLGFNEYVCYDI; PKSLGFNEYVCYDIK; KSLGFNEYVCYDIKT; SLGFNEYVCYDIKTR; LGFNEYVCYDIKTRT; GFNEYVCYDIKTRTG; FNEYVCYDIKTRTGD; NEYVCYDIKTRTGDD; EYVCYDIKTRTGDDL; YVCYDIKTRTGDDLS; VCYDIKTRTGDDLSL; CYDIKTRTGDDLSLF; YDIKTRTGDDLSLFF; DIKTRTGDDLSLFFQ; IKTRTGDDLSLFFQK; KTRTGDDLSLFFQKV; TRTGDDLSLFFQKVA; RTGDDLSLFFQKVAD; TGDDLSLFFQKVADA; GDDLSLFFQKVADAF; DDLSLFFQKVADAFG; DLSLFFQKVADAFGT; LSLFFQKVADAFGTQ; SLFFQKVADAFGTQE; LFFQKVADAFGTQEY; FFQKVADAFGTQEYK; FQKVADAFGTQEYKN; QKVADAFGTQEYKNK; KVADAFGTQEYKNKD; VADAFGTQEYKNKDE; ADAFGTQEYKNKDED; DAFGTQEYKNKDEDD; AFGTQEYKNKDEDDE; FGTQEYKNKDEDDEN; GTQEYKNKDEDDENN; TQEYKNKDEDDENNQ; QEYKNKDEDDENNQK; EYKNKDEDDENNQKP; YKNKDEDDENNQKPE; KNKDEDDENNQKPEK; NKDEDDENNQKPEKC; KDEDDENNQKPEKCN; DEDDENNQKPEKCNE; EDDENNQKPEKCNEE; DDENNQKPEKCNEEI; DENNQKPEKCNEEIF; ENNQKPEKCNEEIFK; NNQKPEKCNEEIFKV; NQKPEKCNEEIFKVI; QKPEKCNEEIFKVIK; KPEKCNEEIFKVIKR; PEKCNEEIFKVIKRV; EKCNEEIFKVIKRVF; KCNEEIFKVIKRVFT; CNEEIFKVIKRVFTE; NEEIFKVIKRVFTES; EEIFKVIKRVFTESE; EIFKVIKRVFTESEN; IFKVIKRVFTESENN; FKVIKRVFTESENNN; KVIKRVFTESENNNE; VIKRVFTESENNNEL; IKRVFTESENNNELA; KRVFTESENNNELAN; RVFTESENNNELANL; VFTESENNNELANLK; FTESENNNELANLKN; TESENNNELANLKNL; ESENNNELANLKNLN; SENNNELANLKNLNS; ENNNELANLKNLNSY; NNNELANLKNLNSYN; NNELANLKNLNSYNL; NELANLKNLNSYNLN; ELANLKNLNSYNLNS; LANLKNLNSYNLNSN; ANLKNLNSYNLNSNN; NLKNLNSYNLNSNNK; 16 mers: MKRISILSILLLLLLF; KRISILSILLLLLLFS; RISILSILLLLLLFSC; ISILSILLLLLLFSCK; SILSILLLLLLFSCKQ; ILSILLLLLLFSCKQY; LSILLLLLLFSCKQYG; SILLLLLLFSCKQYGD; ILLLLLLFSCKQYGDV; LLLLLLFSCKQYGDVK; LLLLLFSCKQYGDVKS; LLLLFSCKQYGDVKSL; LLLFSCKQYGDVKSLT; LLFSCKQYGDVKSLTE; LFSCKQYGDVKSLTEV; FSCKQYGDVKSLTEVA; SCKQYGDVKSLTEVAT; CKQYGDVKSLTEVATD; KQYGDVKSLTEVATDL; QYGDVKSLTEVATDLE; YGDVKSLTEVATDLED;

	GDVKSLTEVATDLEDD; DVKSLTEVATDLEDDN; VKSLTEVATDLEDDNS; KSLTEVATDLEDDNSF; SLTEVATDLEDDNSFA; LTEVATDLEDDNSFAS; TEVATDLEDDNSFASG; EVATDLEDDNSFASGS; VATDLEDDNSFASGSV; ATDLEDDNSFASGSVE; TDLEDDNSFASGSVES; DLEDDNSFASGSVESK; LEDDNSFASGSVESKD; EDDNSFASGSVESKDQ; DDNSFASGSVESKDQI; DNSFASGSVESKDQII; NSFASGSVESKDQIIE; SFASGSVESKDQIIEK; FASGSVESKDQIIEKG; ASGSVESKDQIIEKGP; SGSVESKDQIIEKGPV; GSVESKDQIIEKGPVL; SVESKDQIIEKGPVLT; VESKDQIIEKGPVLTS; ESKDQIIEKGPVLTSE; SKDQIIEKGPVLTSEE; KDQIIEKGPVLTSEEF; DQIIEKGPVLTSEEFE; QIIEKGPVLTSEEFER; IIEKGPVLTSEEFERL; IEKGPVLTSEEFERLE; EKGPVLTSEEFERLEA; KGPVLTSEEFERLEAL; GPVLTSEEFERLEALK; PVLTSEEFERLEALKT; VLTSEEFERLEALKTF; LTSEEFERLEALKTFL; TSEEFERLEALKTFLK; SEEFERLEALKTFLKD; EEFERLEALKTFLKDA; EFERLEALKTFLKDAM; FERLEALKTFLKDAMG; ERLEALKTFLKDAMGV; RLEALKTFLKDAMGVN; LEALKTFLKDAMGVNG; EALKTFLKDAMGVNGR; ALKTFLKDAMGVNGRE; LKTFLKDAMGVNGREG; KTFLKDAMGVNGREGD; TFLKDAMGVNGREGDT; FLKDAMGVNGREGDTK; LKDAMGVNGREGDTKA; KDAMGVNGREGDTKAE; DAMGVNGREGDTKAEY; AMGVNGREGDTKAEYE; MGVNGREGDTKAEYEK; GVNGREGDTKAEYEKS; VNGREGDTKAEYEKSY; NGREGDTKAEYEKSYK; GREGDTKAEYEKSYKE; REGDTKAEYEKSYKEF; EGDTKAEYEKSYKEFF; GDTKAEYEKSYKEFFD; DTKAEYEKSYKEFFDW; TKAEYEKSYKEFFDWL; KAEYEKSYKEFFDWLS; AEYEKSYKEFFDWLSK; EYEKSYKEFFDWLSKD; YEKSYKEFFDWLSKDV; EKSYKEFFDWLSKDVN; KSYKEFFDWLSKDVNR; SYKEFFDWLSKDVNRQ; YKEFFDWLSKDVNRQK; KEFFDWLSKDVNRQKE; EFFDWLSKDVNRQKEF; FFDWLSKDVNRQKEFV; FDWLSKDVNRQKEFVS; DWLSKDVNRQKEFVSF; WLSKDVNRQKEFVSFF; LSKDVNRQKEFVSFFN; SKDVNRQKEFVSFFNN; KDVNRQKEFVSFFNNI; DVNRQKEFVSFFNNIC; VNRQKEFVSFFNNICG; NRQKEFVSFFNNICGI; RQKEFVSFFNNICGII; QKEFVSFFNNICGIIT; KEFVSFFNNICGIITK; EFVSFFNNICGIITKA; FVSFFNNICGIITKAV; VSFFNNICGIITKAVD; SFFNNICGIITKAVDA; FFNNICGIITKAVDAS; FNNICGIITKAVDASK; NNICGIITKAVDASKK; NICGIITKAVDASKKR; ICGIITKAVDASKKRY; CGIITKAVDASKKRYN; GIITKAVDASKKRYNS; IITKAVDASKKRYNSN; ITKAVDASKKRYNSNP; TKAVDASKKRYNSNPK; KAVDASKKRYNSNPKS; AVDASKKRYNSNPKSL; VDASKKRYNSNPKSLG; DASKKRYNSNPKSLGF; ASKKRYNSNPKSLGFN; SKKRYNSNPKSLGFNE; KKRYNSNPKSLGFNEY; KRYNSNPKSLGFNEYV; RYNSNPKSLGFNEYVC; YNSNPKSLGFNEYVCY; NSNPKSLGFNEYVCYD; SNPKSLGFNEYVCYDI; NPKSLGFNEYVCYDIK; PKSLGFNEYVCYDIKT; KSLGFNEYVCYDIKTR; SLGFNEYVCYDIKTRT; LGFNEYVCYDIKTRTG; GFNEYVCYDIKTRTGD; FNEYVCYDIKTRTGDD; NEYVCYDIKTRTGDDL; EYVCYDIKTRTGDDLS; YVCYDIKTRTGDDLSL; VCYDIKTRTGDDLSLF; CYDIKTRTGDDLSLFF; YDIKTRTGDDLSLFFQ; DIKTRTGDDLSLFFQK; IKTRTGDDLSLFFQKV; KTRTGDDLSLFFQKVA; TRTGDDLSLFFQKVAD; RTGDDLSLFFQKVADA; TGDDLSLFFQKVADAF; GDDLSLFFQKVADAFG; DDLSLFFQKVADAFGT; DLSLFFQKVADAFGTQ; LSLFFQKVADAFGTQE; SLFFQKVADAFGTQEY; LFFQKVADAFGTQEYK; FFQKVADAFGTQEYKN; FQKVADAFGTQEYKNK; QKVADAFGTQEYKNKD; KVADAFGTQEYKNKDE; VADAFGTQEYKNKDED; ADAFGTQEYKNKDEDD; DAFGTQEYKNKDEDDE; AFGTQEYKNKDEDDEN; FGTQEYKNKDEDDENN; GTQEYKNKDEDDENNQ; TQEYKNKDEDDENNQK; QEYKNKDEDDENNQKP; EYKNKDEDDENNQKPE; YKNKDEDDENNQKPEK;

	KNKDEDDENNQKPEKC; NKDEDDENNQKPEKCN; KDEDDENNQKPEKCNE; DEDDENNQKPEKCNEE; EDDENNQKPEKCNEEI; DDENNQKPEKCNEEIF; DENNQKPEKCNEEIFK; ENNQKPEKCNEEIFKV; NNQKPEKCNEEIFKVI; NQKPEKCNEEIFKVIK; QKPEKCNEEIFKVIKR; KPEKCNEEIFKVIKRV; PEKCNEEIFKVIKRVF; EKCNEEIFKVIKRVFT; KCNEEIFKVIKRVFTE; CNEEIFKVIKRVFTES; NEEIFKVIKRVFTESE; EEIFKVIKRVFTESEN; EIFKVIKRVFTESENN; IFKVIKRVFTESENNN; FKVIKRVFTESENNNE; KVIKRVFTESENNNEL; VIKRVFTESENNNELA; IKRVFTESENNNELAN; KRVFTESENNNELANL; RVFTESENNNELANLK; VFTESENNNELANLKN; FTESENNNELANLKNL; TESENNNELANLKNLN; ESENNNELANLKNLNS; SENNNELANLKNLNSY; ENNNELANLKNLNSYN; NNNELANLKNLNSYNL; NNELANLKNLNSYNLN; NELANLKNLNSYNLNS; ELANLKNLNSYNLNSN; LANLKNLNSYNLNSNN; ANLKNLNSYNLNSNNK;
Seq 34	13 mers: MKIKPLIQLKLLG; KIKPLIQLKLLGL; IKPLIQLKLLGLF; KPLIQLKLLGLFL; PLIQLKLLGLFLF; LIQLKLLGLFLFS; IQLKLLGLFLFSC; QLKLLGLFLFSCT; LKLLGLFLFSCTI; KLLGLFLFSCTID; LLGLFLFSCTIDA; LGLFLFSCTIDAN; GLFLFSCTIDANL; LFLFSCTIDANLN; FLFSCTIDANLNE; LFSCTIDANLNED; FSCTIDANLNEDY; SCTIDANLNEDYK; CTIDANLNEDYKN; TIDANLNEDYKNK; IDANLNEDYKNKV; DANLNEDYKNKVK; ANLNEDYKNKVKG; NLNEDYKNKVKGI; LNEDYKNKVKGIL; NEDYKNKVKGILN; EDYKNKVKGILNK; DYKNKVKGILNKA; YKNKVKGILNKAA; KNKVKGILNKAAD; NKVKGILNKAADD; KVKGILNKAADDQ; VKGILNKAADDQE; KGILNKAADDQET; GILNKAADDQETT; ILNKAADDQETTS; LNKAADDQETTSA; NKAADDQETTSAD; KAADDQETTSADT; AADDQETTSADTN; ADDQETTSADTNS; DDQETTSADTNSN; DQETTSADTNSNA; QETTSADTNSNAA; ETTSADTNSNAAK; TTSADTNSNAAKN; TSADTNSNAAKNI; SADTNSNAAKNIP; ADTNSNAAKNIPI; DTNSNAAKNIPIA; TNSNAAKNIPIAD; NSNAAKNIPIADN; SNAAKNIPIADND; NAAKNIPIADNDK; AAKNIPIADNDKV; AKNIPIADNDKVA; KNIPIADNDKVAA; NIPIADNDKVAAE; IPIADNDKVAAEL; PIADNDKVAAELK; IADNDKVAAELKK; ADNDKVAAELKKQ; DNDKVAAELKKQS; NDKVAAELKKQSQ; DKVAAELKKQSQA; KVAAELKKQSQAA; VAAELKKQSQAAK; AAELKKQSQAAKT; AELKKQSQAAKTV; ELKKQSQAAKTVA; LKKQSQAAKTVAA; KKQSQAAKTVAAA; KQSQAAKTVAAAP; QSQAAKTVAAAPN; SQAAKTVAAAPNK; QAAKTVAAAPNKG; AAKTVAAAPNKGS; AKTVAAAPNKGSQ; KTVAAAPNKGSQN; TVAAAPNKGSQNQ; VAAAPNKGSQNQP; AAAPNKGSQNQPQ; AAPNKGSQNQPQT; APNKGSQNQPQTT; PNKGSQNQPQTTP; NKGSQNQPQTTPN; KGSQNQPQTTPNK; GSQNQPQTTPNKG; SQNQPQTTPNKGS; QNQPQTTPNKGSQ; NQPQTTPNKGSQN; QPQTTPNKGSQNQ; PQTTPNKGSQNQQ; QTTPNKGSQNQQA; TTPNKGSQNQQAA; TPNKGSQNQQAAP; PNKGSQNQQAAPS; NKGSQNQQAAPSP; KGSQNQQAAPSPQ; GSQNQQAAPSPQL; SQNQQAAPSPQLQ; QNQQAAPSPQLQS; NQQAAPSPQLQSL; QQAAPSPQLQSLS; QAAPSPQLQSLSF;

	AAPSPQLQSLSFS; APSPQLQSLSFSA; PSPQLQSLSFSAD; SPQLQSLSFSADL; PQLQSLSFSADLS; QLQSLSFSADLSN; LQSLSFSADLSNL; QSLSFSADLSNLP; SLSFSADLSNLPK; LSFSADLSNLPKT; SFSADLSNLPKTT; FSADLSNLPKTTA; SADLSNLPKTTAA; ADLSNLPKTTAAR; DLSNLPKTTAARA; LSNLPKTTAARAA; SNLPKTTAARAAS; NLPKTTAARAASL; LPKTTAARAASLT; PKTTAARAASLTK; KTTAARAASLTKQ; TTAARAASLTKQR; TAARAASLTKQRI; AARAASLTKQRIP; ARAASLTKQRIPI; RAASLTKQRIPIQ; AASLTKQRIPIQA; ASLTKQRIPIQAV; SLTKQRIPIQAVT; LTKQRIPIQAVTT; TKQRIPIQAVTTV; KQRIPIQAVTTVP; QRIPIQAVTTVPG; RIPIQAVTTVPGN; IPIQAVTTVPGNT; PIQAVTTVPGNTR; IQAVTTVPGNTRT; QAVTTVPGNTRTF; AVTTVPGNTRTFN; VTTVPGNTRTFNS; TTVPGNTRTFNSR; TVPGNTRTFNSRN; VPGNTRTFNSRNS; PGNTRTFNSRNSG; GNTRTFNSRNSGL; NTRTFNSRNSGLP; TRTFNSRNSGLPT; RTFNSRNSGLPTF; TFNSRNSGLPTFA; FNSRNSGLPTFAL; NSRNSGLPTFALN; SRNSGLPTFALNY; RNSGLPTFALNYS; NSGLPTFALNYSF; SGLPTFALNYSFS; GLPTFALNYSFSQ; LPTFALNYSFSQP; PTFALNYSFSQPT; TFALNYSFSQPTR; FALNYSFSQPTRQ; ALNYSFSQPTRQQ; LNYSFSQPTRQQT; NYSFSQPTRQQTN; YSFSQPTRQQTNS; SFSQPTRQQTNSS; FSQPTRQQTNSSS; SQPTRQQTNSSSA; QPTRQQTNSSSAV; PTRQQTNSSSAVQ; TRQQTNSSSAVQT; RQQTNSSSAVQTT; QQTNSSSAVQTTT; QTNSSSAVQTTTS; TNSSSAVQTTTSS; NSSSAVQTTTSSG; SSSAVQTTTSSGS; SSAVQTTTSSGSK; SAVQTTTSSGSKL; AVQTTTSSGSKLQ; VQTTTSSGSKLQT; QTTTSSGSKLQTL; TTTSSGSKLQTLK; TTSSGSKLQTLKN; TSSGSKLQTLKNE; SSGSKLQTLKNEL; SGSKLQTLKNELI; GSKLQTLKNELIR; SKLQTLKNELIRA; KLQTLKNELIRAI; LQTLKNELIRAIS; QTLKNELIRAISE; TLKNELIRAISEE; LKNELIRAISEEK; KNELIRAISEEKN; NELIRAISEEKNK; ELIRAISEEKNKT; LIRAISEEKNKTQ; IRAISEEKNKTQN; RAISEEKNKTQNN; AISEEKNKTQNNF; ISEEKNKTQNNFG; SEEKNKTQNNFGF; EEKNKTQNNFGFR; EKNKTQNNFGFRE; KNKTQNNFGFRET; NKTQNNFGFRETY; KTQNNFGFRETYD; TQNNFGFRETYDQ; QNNFGFRETYDQF; NNFGFRETYDQFK; NFGFRETYDQFKM; FGFRETYDQFKMK; GFRETYDQFKMKD; FRETYDQFKMKDS; RETYDQFKMKDSA; ETYDQFKMKDSAF; TYDQFKMKDSAFE; YDQFKMKDSAFEL; DQFKMKDSAFELL; QFKMKDSAFELLD; FKMKDSAFELLDV; KMKDSAFELLDVI; MKDSAFELLDVIS; KDSAFELLDVISS; DSAFELLDVISSA; SAFELLDVISSAK; AFELLDVISSAKV; FELLDVISSAKVY; ELLDVISSAKVYD; LLDVISSAKVYDR; LDVISSAKVYDRS; DVISSAKVYDRSY; VISSAKVYDRSYA; ISSAKVYDRSYAP; SSAKVYDRSYAPQ; SAKVYDRSYAPQL; AKVYDRSYAPQLN; KVYDRSYAPQLNS; VYDRSYAPQLNSN; YDRSYAPQLNSNT; DRSYAPQLNSNTP; RSYAPQLNSNTPE; SYAPQLNSNTPEA; YAPQLNSNTPEAE; APQLNSNTPEAEN; PQLNSNTPEAENE; QLNSNTPEAENER; LNSNTPEAENERN; NSNTPEAENERNK; SNTPEAENERNKF; NTPEAENERNKFY; TPEAENERNKFYA; PEAENERNKFYAL;

	EAENERNKFYALM; AENERNKFYALMD; ENERNKFYALMDF; NERNKFYALMDFD; ERNKFYALMDFDQ; RNKFYALMDFDQY; NKFYALMDFDQYK; KFYALMDFDQYKI; FYALMDFDQYKIE; YALMDFDQYKIEQ; ALMDFDQYKIEQF; LMDFDQYKIEQFG; MDFDQYKIEQFGS; DFDQYKIEQFGSI; FDQYKIEQFGSIM; DQYKIEQFGSIME; QYKIEQFGSIMEA; YKIEQFGSIMEAL; KIEQFGSIMEALY; IEQFGSIMEALYN; EQFGSIMEALYNE; QFGSIMEALYNEN; FGSIMEALYNENQ; GSIMEALYNENQN; SIMEALYNENQNH; IMEALYNENQNHS; MEALYNENQNHSL; EALYNENQNHSLI; ALYNENQNHSLIR; LYNENQNHSLIRE; YNENQNHSLIREL; NENQNHSLIRELM; ENQNHSLIRELMI; NQNHSLIRELMIS; QNHSLIRELMISG; NHSLIRELMISGL; HSLIRELMISGLG; SLIRELMISGLGT; LIRELMISGLGTQ; IRELMISGLGTQI; RELMISGLGTQIS; ELMISGLGTQISF; LMISGLGTQISFE; MISGLGTQISFEL; ISGLGTQISFELA; SGLGTQISFELAL; GLGTQISFELALE; LGTQISFELALEE; GTQISFELALEEI; TQISFELALEEIN; QISFELALEEINK; ISFELALEEINKK; SFELALEEINKKI; FELALEEINKKIE; ELALEEINKKIEI; LALEEINKKIEIF; ALEEINKKIEIFN; LEEINKKIEIFNQ; EEINKKIEIFNQD; EINKKIEIFNQDY; INKKIEIFNQDYL; NKKIEIFNQDYLN; KKIEIFNQDYLNA; KIEIFNQDYLNAK; IEIFNQDYLNAKI; EIFNQDYLNAKIN; IFNQDYLNAKINS; FNQDYLNAKINSF; NQDYLNAKINSFD; QDYLNAKINSFDF; DYLNAKINSFDFT; YLNAKINSFDFTM; LNAKINSFDFTMK; NAKINSFDFTMKL; AKINSFDFTMKLK; KINSFDFTMKLKE; INSFDFTMKLKEL; NSFDFTMKLKELK; SFDFTMKLKELKS; FDFTMKLKELKSK; DFTMKLKELKSKL; FTMKLKELKSKLN; TMKLKELKSKLNQ; MKLKELKSKLNQI; KLKELKSKLNQIL; LKELKSKLNQILD; KELKSKLNQILDK; ELKSKLNQILDKR; LKSKLNQILDKRK; KSKLNQILDKRKE; SKLNQILDKRKEW; KLNQILDKRKEWS; LNQILDKRKEWSR; NQILDKRKEWSRQ; QILDKRKEWSRQA; ILDKRKEWSRQAD; LDKRKEWSRQADG; DKRKEWSRQADGL; KRKEWSRQADGLI; RKEWSRQADGLIA; KEWSRQADGLIAN; EWSRQADGLIANA; WSRQADGLIANAS; SRQADGLIANASS; RQADGLIANASSN; QADGLIANASSNS; ADGLIANASSNSS; DGLIANASSNSSL; GLIANASSNSSLS; LIANASSNSSLSD; IANASSNSSLSDS; ANASSNSSLSDSK; NASSNSSLSDSKS; ASSNSSLSDSKSL; SSNSSLSDSKSLA; SNSSLSDSKSLAE; NSSLSDSKSLAEY; SSLSDSKSLAEYI; SLSDSKSLAEYIK; LSDSKSLAEYIKK; SDSKSLAEYIKKR; DSKSLAEYIKKRY; SKSLAEYIKKRYL; KSLAEYIKKRYLD; SLAEYIKKRYLDN; LAEYIKKRYLDNM; AEYIKKRYLDNMQ; EYIKKRYLDNMQN; YIKKRYLDNMQNA; IKKRYLDNMQNAR; KKRYLDNMQNARQ; KRYLDNMQNARQS; RYLDNMQNARQSV; YLDNMQNARQSVL; LDNMQNARQSVLE; DNMQNARQSVLEA; NMQNARQSVLEAY; MQNARQSVLEAYI; QNARQSVLEAYIS; NARQSVLEAYISI; ARQSVLEAYISIM; 14 mers: MKIKPLIQLKLLGL; KIKPLIQLKLLGLF; IKPLIQLKLLGLFL; KPLIQLKLLGLFLF; PLIQLKLLGLFLFS; LIQLKLLGLFLFSC;

	IQLKLLGLFLFSCT; QLKLLGLFLFSCTI; LKLLGLFLFSCTID; KLLGLFLFSCTIDA; LLGLFLFSCTIDAN; LGLFLFSCTIDANL; GLFLFSCTIDANLN; LFLFSCTIDANLNE; FLFSCTIDANLNED; LFSCTIDANLNEDY; FSCTIDANLNEDYK; SCTIDANLNEDYKN; CTIDANLNEDYKNK; TIDANLNEDYKNKV; IDANLNEDYKNKVK; DANLNEDYKNKVKG; ANLNEDYKNKVKGI; NLNEDYKNKVKGIL; LNEDYKNKVKGILN; NEDYKNKVKGILNK; EDYKNKVKGILNKA; DYKNKVKGILNKAA; YKNKVKGILNKAAD; KNKVKGILNKAADD; NKVKGILNKAADDQ; KVKGILNKAADDQE; VKGILNKAADDQET; KGILNKAADDQETT; GILNKAADDQETTS; ILNKAADDQETTSA; LNKAADDQETTSAD; NKAADDQETTSADT; KAADDQETTSADTN; AADDQETTSADTNS; ADDQETTSADTNSN; DDQETTSADTNSNA; DQETTSADTNSNAA; QETTSADTNSNAAK; ETTSADTNSNAAKN; TTSADTNSNAAKNI; TSADTNSNAAKNIP; SADTNSNAAKNIPI; ADTNSNAAKNIPIA; DTNSNAAKNIPIAD; TNSNAAKNIPIADN; NSNAAKNIPIADND; SNAAKNIPIADNDK; NAAKNIPIADNDKV; AAKNIPIADNDKVA; AKNIPIADNDKVAA; KNIPIADNDKVAAE; NIPIADNDKVAAEL; IPIADNDKVAAELK; PIADNDKVAAELKK; IADNDKVAAELKKQ; ADNDKVAAELKKQS; DNDKVAAELKKQSQ; NDKVAAELKKQSQA; DKVAAELKKQSQAA; KVAAELKKQSQAAK; VAAELKKQSQAAKT; AAELKKQSQAAKTV; AELKKQSQAAKTVA; ELKKQSQAAKTVAA; LKKQSQAAKTVAAA; KKQSQAAKTVAAAP; KQSQAAKTVAAAPN; QSQAAKTVAAAPNK; SQAAKTVAAAPNKG; QAAKTVAAAPNKGS; AAKTVAAAPNKGSQ; AKTVAAAPNKGSQN; KTVAAAPNKGSQNQ; TVAAAPNKGSQNQP; VAAAPNKGSQNQPQ; AAAPNKGSQNQPQT; AAPNKGSQNQPQTT; APNKGSQNQPQTTP; PNKGSQNQPQTTPN; NKGSQNQPQTTPNK; KGSQNQPQTTPNKG; GSQNQPQTTPNKGS; SQNQPQTTPNKGSQ; QNQPQTTPNKGSQN; NQPQTTPNKGSQNQ; QPQTTPNKGSQNQQ; PQTTPNKGSQNQQA; QTTPNKGSQNQQAA; TTPNKGSQNQQAAP; TPNKGSQNQQAAPS; PNKGSQNQQAAPSP; NKGSQNQQAAPSPQ; KGSQNQQAAPSPQL; GSQNQQAAPSPQLQ; SQNQQAAPSPQLQS; QNQQAAPSPQLQSL; NQQAAPSPQLQSLS; QQAAPSPQLQSLSF; QAAPSPQLQSLSFS; AAPSPQLQSLSFSA; APSPQLQSLSFSAD; PSPQLQSLSFSADL; SPQLQSLSFSADLS; PQLQSLSFSADLSN; QLQSLSFSADLSNL; LQSLSFSADLSNLP; QSLSFSADLSNLPK; SLSFSADLSNLPKT; LSFSADLSNLPKTT; SFSADLSNLPKTTA; FSADLSNLPKTTAA; SADLSNLPKTTAAR; ADLSNLPKTTAARA; DLSNLPKTTAARAA; LSNLPKTTAARAAS; SNLPKTTAARAASL; NLPKTTAARAASLT; LPKTTAARAASLTK; PKTTAARAASLTKQ; KTTAARAASLTKQR; TTAARAASLTKQRI; TAARAASLTKQRIP; AARAASLTKQRIPI; ARAASLTKQRIPIQ; RAASLTKQRIPIQA; AASLTKQRIPIQAV; ASLTKQRIPIQAVT; SLTKQRIPIQAVTT; LTKQRIPIQAVTTV; TKQRIPIQAVTTVP; KQRIPIQAVTTVPG; QRIPIQAVTTVPGN; RIPIQAVTTVPGNT; IPIQAVTTVPGNTR; PIQAVTTVPGNTRT; IQAVTTVPGNTRTF; QAVTTVPGNTRTFN; AVTTVPGNTRTFNS; VTTVPGNTRTFNSR; TTVPGNTRTFNSRN; TVPGNTRTFNSRNS; VPGNTRTFNSRNSG; PGNTRTFNSRNSGL; GNTRTFNSRNSGLP; NTRTFNSRNSGLPT; TRTFNSRNSGLPTF; RTFNSRNSGLPTFA; TFNSRNSGLPTFAL; FNSRNSGLPTFALN; NSRNSGLPTFALNY; SRNSGLPTFALNYS; RNSGLPTFALNYSF; NSGLPTFALNYSFS;

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GLIANASSNSSLSDS; LIANASSNSSLSDSK; IANASSNSSLSDSKS;
ANASSNSSLSDSKSL; NASSNSSLSDSKSLA; ASSNSSLSDSKSLAE;
SSNSSLSDSKSLAEY; SNSSLSDSKSLAEYI; NSSLSDSKSLAEYIK;
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QNARQSVLEAYISIM;

16 mers:
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IQLKLLGLFLFSCTID; QLKLLGLFLFSCTIDA; LKLLGLFLFSCTIDAN;
KLLGLFLFSCTIDANL; LLGLFLFSCTIDANLN; LGLFLFSCTIDANLNE;
GLFLFSCTIDANLNED; LFLFSCTIDANLNEDY; FLFSCTIDANLNEDYK;
LFSCTIDANLNEDYKN; FSCTIDANLNEDYKNK; SCTIDANLNEDYKNKV;
CTIDANLNEDYKNKVK; TIDANLNEDYKNKVKG; IDANLNEDYKNKVKGI;
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DQETTSADTNSNAAKN; QETTSADTNSNAAKNI; ETTSADTNSNAAKNIP;
TTSADTNSNAAKNIPI; TSADTNSNAAKNIPIA; SADTNSNAAKNIPIAD;
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GSQNQQAAPSPQLQSL; SQNQQAAPSPQLQSLS; QNQQAAPSPQLQSLSF;
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AAPSPQLQSLSFSADL; APSPQLQSLSFSADLS; PSPQLQSLSFSADLSN;
SPQLQSLSFSADLSNL; PQLQSLSFSADLSNLP; QLQSLSFSADLSNLPK;
LQSLSFSADLSNLPKT; QSLSFSADLSNLPKTT; SLSFSADLSNLPKTTA;

	LSFSADLSNLPKTTAA; SFSADLSNLPKTTAAR; FSADLSNLPKTTAARA; SADLSNLPKTTAARAA; ADLSNLPKTTAARAAS; DLSNLPKTTAARAASL; LSNLPKTTAARAASLT; SNLPKTTAARAASLTK; NLPKTTAARAASLTKQ; LPKTTAARAASLTKQR; PKTTAARAASLTKQRI; KTTAARAASLTKQRIP; TTAARAASLTKQRIPI; TAARAASLTKQRIPIQ; AARAASLTKQRIPIQA; ARAASLTKQRIPIQAV; RAASLTKQRIPIQAVT; AASLTKQRIPIQAVTT; ASLTKQRIPIQAVTTV; SLTKQRIPIQAVTTVP; LTKQRIPIQAVTTVPG; TKQRIPIQAVTTVPGN; KQRIPIQAVTTVPGNT; QRIPIQAVTTVPGNTR; RIPIQAVTTVPGNTRT; IPIQAVTTVPGNTRTF; PIQAVTTVPGNTRTFN; IQAVTTVPGNTRTFNS; QAVTTVPGNTRTFNSR; AVTTVPGNTRTFNSRN; VTTVPGNTRTFNSRNS; TTVPGNTRTFNSRNSG; TVPGNTRTFNSRNSGL; VPGNTRTFNSRNSGLP; PGNTRTFNSRNSGLPT; GNTRTFNSRNSGLPTF; NTRTFNSRNSGLPTFA; TRTFNSRNSGLPTFAL; RTFNSRNSGLPTFALN; TFNSRNSGLPTFALNY; FNSRNSGLPTFALNYS; NSRNSGLPTFALNYSF; SRNSGLPTFALNYSFS; RNSGLPTFALNYSFSQ; NSGLPTFALNYSFSQP; SGLPTFALNYSFSQPT; GLPTFALNYSFSQPTR; LPTFALNYSFSQPTRQ; PTFALNYSFSQPTRQQ; TFALNYSFSQPTRQQT; FALNYSFSQPTRQQTN; ALNYSFSQPTRQQTNS; LNYSFSQPTRQQTNSS; NYSFSQPTRQQTNSSS; YSFSQPTRQQTNSSSA; SFSQPTRQQTNSSSAV; FSQPTRQQTNSSSAVQ; SQPTRQQTNSSSAVQT; QPTRQQTNSSSAVQTT; PTRQQTNSSSAVQTTT; TRQQTNSSSAVQTTTS; RQQTNSSSAVQTTTSS; QQTNSSSAVQTTTSSG; QTNSSSAVQTTTSSGS; TNSSSAVQTTTSSGSK; NSSSAVQTTTSSGSKL; SSSAVQTTTSSGSKLQ; SSAVQTTTSSGSKLQT; SAVQTTTSSGSKLQTL; AVQTTTSSGSKLQTLK; VQTTTSSGSKLQTLKN; QTTTSSGSKLQTLKNE; TTTSSGSKLQTLKNEL; TTSSGSKLQTLKNELI; TSSGSKLQTLKNELIR; SSGSKLQTLKNELIRA; SGSKLQTLKNELIRAI; GSKLQTLKNELIRAIS; SKLQTLKNELIRAISE; KLQTLKNELIRAISEE; LQTLKNELIRAISEEK; QTLKNELIRAISEEKN; TLKNELIRAISEEKNK; LKNELIRAISEEKNKT; KNELIRAISEEKNKTQ; NELIRAISEEKNKTQN; ELIRAISEEKNKTQNN; LIRAISEEKNKTQNNF; IRAISEEKNKTQNNFG; RAISEEKNKTQNNFGF; AISEEKNKTQNNFGFR; ISEEKNKTQNNFGFRE; SEEKNKTQNNFGFRET; EEKNKTQNNFGFRETY; EKNKTQNNFGFRETYD; KNKTQNNFGFRETYDQ; NKTQNNFGFRETYDQF; KTQNNFGFRETYDQFK; TQNNFGFRETYDQFKM; QNNFGFRETYDQFKMK; NNFGFRETYDQFKMKD; NFGFRETYDQFKMKDS; FGFRETYDQFKMKDSA; GFRETYDQFKMKDSAF; FRETYDQFKMKDSAFE; RETYDQFKMKDSAFEL; ETYDQFKMKDSAFELL; TYDQFKMKDSAFELLD; YDQFKMKDSAFELLDV; DQFKMKDSAFELLDVI; QFKMKDSAFELLDVIS; FKMKDSAFELLDVISS; KMKDSAFELLDVISSA; MKDSAFELLDVISSAK; KDSAFELLDVISSAKV; DSAFELLDVISSAKVY; SAFELLDVISSAKVYD; AFELLDVISSAKVYDR; FELLDVISSAKVYDRS; ELLDVISSAKVYDRSY; LLDVISSAKVYDRSYA; LDVISSAKVYDRSYAP; DVISSAKVYDRSYAPQ; VISSAKVYDRSYAPQL; ISSAKVYDRSYAPQLN; SSAKVYDRSYAPQLNS; SAKVYDRSYAPQLNSN; AKVYDRSYAPQLNSNT; KVYDRSYAPQLNSNTP; VYDRSYAPQLNSNTPE; YDRSYAPQLNSNTPEA; DRSYAPQLNSNTPEAE; RSYAPQLNSNTPEAEN; SYAPQLNSNTPEAENE; YAPQLNSNTPEAENER; APQLNSNTPEAENERN; PQLNSNTPEAENERNK; QLNSNTPEAENERNKF; LNSNTPEAENERNKFY; NSNTPEAENERNKFYA; SNTPEAENERNKFYAL; NTPEAENERNKFYALM; TPEAENERNKFYALMD; PEAENERNKFYALMDF; EAENERNKFYALMDFD; AENERNKFYALMDFDQ; ENERNKFYALMDFDQY; NERNKFYALMDFDQYK; ERNKFYALMDFDQYKI; RNKFYALMDFDQYKIE; NKFYALMDFDQYKIEQ; KFYALMDFDQYKIEQF; FYALMDFDQYKIEQFG;

	YALMDFDQYKIEQFGS; ALMDFDQYKIEQFGSI; LMDFDQYKIEQFGSIM; MDFDQYKIEQFGSIME; DFDQYKIEQFGSIMEA; FDQYKIEQFGSIMEAL; DQYKIEQFGSIMEALY; QYKIEQFGSIMEALYN; YKIEQFGSIMEALYNE; KIEQFGSIMEALYNEN; IEQFGSIMEALYNENQ; EQFGSIMEALYNENQN; QFGSIMEALYNENQNH; FGSIMEALYNENQNHS; GSIMEALYNENQNHSL; SIMEALYNENQNHSLI; IMEALYNENQNHSLIR; MEALYNENQNHSLIRE; EALYNENQNHSLIREL; ALYNENQNHSLIRELM; LYNENQNHSLIRELMI; YNENQNHSLIRELMIS; NENQNHSLIRELMISG; ENQNHSLIRELMISGL; NQNHSLIRELMISGLG; QNHSLIRELMISGLGT; NHSLIRELMISGLGTQ; HSLIRELMISGLGTQI; SLIRELMISGLGTQIS; LIRELMISGLGTQISF; IRELMISGLGTQISFE; RELMISGLGTQISFEL; ELMISGLGTQISFELA; LMISGLGTQISFELAL; MISGLGTQISFELALE; ISGLGTQISFELALEE; SGLGTQISFELALEEI; GLGTQISFELALEEIN; LGTQISFELALEEINK; GTQISFELALEEINKK; TQISFELALEEINKKI; QISFELALEEINKKIE; ISFELALEEINKKIEI; SFELALEEINKKIEIF; FELALEEINKKIEIFN; ELALEEINKKIEIFNQ; LALEEINKKIEIFNQD; ALEEINKKIEIFNQDY; LEEINKKIEIFNQDYL; EEINKKIEIFNQDYLN; EINKKIEIFNQDYLNA; INKKIEIFNQDYLNAK; NKKIEIFNQDYLNAKI; KKIEIFNQDYLNAKIN; KIEIFNQDYLNAKINS; IEIFNQDYLNAKINSF; EIFNQDYLNAKINSFD; IFNQDYLNAKINSFDF; FNQDYLNAKINSFDFT; NQDYLNAKINSFDFTM; QDYLNAKINSFDFTMK; DYLNAKINSFDFTMKL; YLNAKINSFDFTMKLK; LNAKINSFDFTMKLKE; NAKINSFDFTMKLKEL; AKINSFDFTMKLKELK; KINSFDFTMKLKELKS; INSFDFTMKLKELKSK; NSFDFTMKLKELKSKL; SFDFTMKLKELKSKLN; FDFTMKLKELKSKLNQ; DFTMKLKELKSKLNQI; FTMKLKELKSKLNQIL; TMKLKELKSKLNQILD; MKLKELKSKLNQILDK; KLKELKSKLNQILDKR; LKELKSKLNQILDKRK; KELKSKLNQILDKRKE; ELKSKLNQILDKRKEW; LKSKLNQILDKRKEWS; KSKLNQILDKRKEWSR; SKLNQILDKRKEWSRQ; KLNQILDKRKEWSRQA; LNQILDKRKEWSRQAD; NQILDKRKEWSRQADG; QILDKRKEWSRQADGL; ILDKRKEWSRQADGLI; LDKRKEWSRQADGLIA; DKRKEWSRQADGLIAN; KRKEWSRQADGLIANA; RKEWSRQADGLIANAS; KEWSRQADGLIANASS; EWSRQADGLIANASSN; WSRQADGLIANASSNS; SRQADGLIANASSNSS; RQADGLIANASSNSSL; QADGLIANASSNSSLS; ADGLIANASSNSSLSD; DGLIANASSNSSLSDS; GLIANASSNSSLSDSK; LIANASSNSSLSDSKS; IANASSNSSLSDSKSL; ANASSNSSLSDSKSLA; NASSNSSLSDSKSLAE; ASSNSSLSDSKSLAEY; SSNSSLSDSKSLAEYI; SNSSLSDSKSLAEYIK; NSSLSDSKSLAEYIKK; SSLSDSKSLAEYIKKR; SLSDSKSLAEYIKKRY; LSDSKSLAEYIKKRYL; SDSKSLAEYIKKRYLD; DSKSLAEYIKKRYLDN; SKSLAEYIKKRYLDNM; KSLAEYIKKRYLDNMQ; SLAEYIKKRYLDNMQN; LAEYIKKRYLDNMQNA; AEYIKKRYLDNMQNAR; EYIKKRYLDNMQNARQ; YIKKRYLDNMQNARQS; IKKRYLDNMQNARQSV; KKRYLDNMQNARQSVL; KRYLDNMQNARQSVLE; RYLDNMQNARQSVLEA; YLDNMQNARQSVLEAY; LDNMQNARQSVLEAYI; DNMQNARQSVLEAYIS; NMQNARQSVLEAYISI; MQNARQSVLEAYISIM;
Seq 35	13 mers: MSSCTIDANLNKD; SSCTIDANLNKDY; SCTIDANLNKDYK; CTIDANLNKDYKN; TIDANLNKDYKNK; IDANLNKDYKNKV; DANLNKDYKNKVE; ANLNKDYKNKVEE; NLNKDYKNKVEEL; LNKDYKNKVEELL; NKDYKNKVEELLN; KDYKNKVEELLNS; DYKNKVEELLNSS; YKNKVEELLNSST; KNKVEELLNSSTD;

	NKVEELLNSSTDD; KVEELLNSSTDDQ; VEELLNSSTDDQA; EELLNSSTDDQAK; ELLNSSTDDQAKI; LLNSSTDDQAKIS; LNSSTDDQAKISI; NSSTDDQAKISIN; SSTDDQAKISINT; STDDQAKISINTG; TDDQAKISINTGS; DDQAKISINTGSN; DQAKISINTGSNA; QAKISINTGSNAT; AKISINTGSNATK; KISINTGSNATKN; ISINTGSNATKNK; SINTGSNATKNKT; INTGSNATKNKTN; NTGSNATKNKTNI; TGSNATKNKTNIK; GSNATKNKTNIKV; SNATKNKTNIKVA; NATKNKTNIKVAG; ATKNKTNIKVAGL; TKNKTNIKVAGLQ; KNKTNIKVAGLQK; NKTNIKVAGLQKN; KTNIKVAGLQKNT; TNIKVAGLQKNTQ; NIKVAGLQKNTQS; IKVAGLQKNTQSK; KVAGLQKNTQSKK; VAGLQKNTQSKKN; AGLQKNTQSKKNN; GLQKNTQSKKNNN; LQKNTQSKKNNNL; QKNTQSKKNNNLQ; KNTQSKKNNNLQG; NTQSKKNNNLQGL; TQSKKNNNLQGLN; QSKKNNNLQGLNP; SKKNNNLQGLNPA; KKNNNLQGLNPAN; KNNNLQGLNPANQ; NNNLQGLNPANQV; NNLQGLNPANQVN; NLQGLNPANQVNP; LQGLNPANQVNPG; QGLNPANQVNPGN; GLNPANQVNPGNP; LNPANQVNPGNPM; NPANQVNPGNPMQ; PANQVNPGNPMQI; ANQVNPGNPMQIA; NQVNPGNPMQIAN; QVNPGNPMQIANQ; VNPGNPMQIANQA; NPGNPMQIANQAN; PGNPMQIANQANQ; GNPMQIANQANQA; NPMQIANQANQAN; PMQIANQANQANQ; MQIANQANQANQA; QIANQANQANQAN; IANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAN; QANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAN; QANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAS; QANQANQANQASQ; ANQANQANQASQA; NQANQANQASQAS; QANQANQASQASQ; ANQANQASQASQA; NQANQASQASQAS; QANQASQASQASQ; ANQASQASQASQV; NQASQASQASQVA; QASQASQASQVAS; ASQASQASQVASS; SQASQASQVASSA; QASQASQVASSAS; ASQASQVASSASQ; SQASQVASSASQA; QASQVASSASQAS; ASQVASSASQASP; SQVASSASQASPV; QVASSASQASPVA; VASSASQASPVAS; ASSASQASPVASP; SSASQASPVASPA; SASQASPVASPAT; ASQASPVASPATN; SQASPVASPATNV; QASPVASPATNVQ; ASPVASPATNVQA; SPVASPATNVQAT; PVASPATNVQATP; VASPATNVQATPP; ASPATNVQATPPK; SPATNVQATPPKQ; PATNVQATPPKQI; ATNVQATPPKQIA; TNVQATPPKQIAS; NVQATPPKQIASA; VQATPPKQIASAQ; QATPPKQIASAQA; ATPPKQIASAQAI; TPPKQIASAQAIQ; PPKQIASAQAIQT; PKQIASAQAIQTV; KQIASAQAIQTVP; QIASAQAIQTVPN; IASAQAIQTVPNN; ASAQAIQTVPNNT; SAQAIQTVPNNTS; AQAIQTVPNNTST; QAIQTVPNNTSTP; AIQTVPNNTSTPN; IQTVPNNTSTPNQ; QTVPNNTSTPNQS; TVPNNTSTPNQSI; VPNNTSTPNQSII; PNNTSTPNQSIIK; NNTSTPNQSIIKP; NTSTPNQSIIKPQ; TSTPNQSIIKPQQ; STPNQSIIKPQQY; TPNQSIIKPQQYT; PNQSIIKPQQYTF; NQSIIKPQQYTFS; QSIIKPQQYTFSS; SIIKPQQYTFSSS; IIKPQQYTFSSSF; IKPQQYTFSSSFS; KPQQYTFSSSFSQ; PQQYTFSSSFSQP; QQYTFSSSFSQPT; QYTFSSSFSQPTS; YTFSSSFSQPTSQ; TFSSSFSQPTSQT; FSSSFSQPTSQTN; SSSFSQPTSQTNF; SSFSQPTSQTNFN; SFSQPTSQTNFNN; FSQPTSQTNFNNS; SQPTSQTNFNNSQ; QPTSQTNFNNSQS;

	PTSQTNFNNSQSN; TSQTNFNNSQSNN; SQTNFNNSQSNNV; QTNFNNSQSNNVL; TNFNNSQSNNVLT; NFNNSQSNNVLTN; FNNSQSNNVLTNY; NNSQSNNVLTNYR; NSQSNNVLTNYRH; SQSNNVLTNYRHQ; QSNNVLTNYRHQT; SNNVLTNYRHQTQ; NNVLTNYRHQTQP; NVLTNYRHQTQPS; VLTNYRHQTQPSF; LTNYRHQTQPSFV; TNYRHQTQPSFVV; NYRHQTQPSFVVP; YRHQTQPSFVVPV; RHQTQPSFVVPVY; HQTQPSFVVPVYS; QTQPSFVVPVYSG; TQPSFVVPVYSGN; QPSFVVPVYSGNS; PSFVVPVYSGNSP; SFVVPVYSGNSPL; FVVPVYSGNSPLQ; VVPVYSGNSPLQK; VPVYSGNSPLQKL; PVYSGNSPLQKLK; VYSGNSPLQKLKN; YSGNSPLQKLKNN; SGNSPLQKLKNNL; GNSPLQKLKNNLL; NSPLQKLKNNLLR; SPLQKLKNNLLRR; PLQKLKNNLLRRI; LQKLKNNLLRRIA; QKLKNNLLRRIAE; KLKNNLLRRIAEE; LKNNLLRRIAEEK; KNNLLRRIAEEKN; NNLLRRIAEEKNK; NLLRRIAEEKNKT; LLRRIAEEKNKTH; LRRIAEEKNKTHN; RRIAEEKNKTHNH; RIAEEKNKTHNHG; IAEEKNKTHNHGF; AEEKNKTHNHGFR; EEKNKTHNHGFRE; EKNKTHNHGFRET; KNKTHNHGFRETY; NKTHNHGFRETYD; KTHNHGFRETYDQ; THNHGFRETYDQF; HNHGFRETYDQFK; NHGFRETYDQFKM; HGFRETYDQFKMK; GFRETYDQFKMKD; FRETYDQFKMKDS; RETYDQFKMKDSA; ETYDQFKMKDSAF; TYDQFKMKDSAFT; YDQFKMKDSAFTL; DQFKMKDSAFTLL; QFKMKDSAFTLLD; FKMKDSAFTLLDV; KMKDSAFTLLDVI; MKDSAFTLLDVIS; KDSAFTLLDVISN; DSAFTLLDVISNI; SAFTLLDVISNIS; AFTLLDVISNISV; FTLLDVISNISVF; TLLDVISNISVFD; LLDVISNISVFDR; LDVISNISVFDRG; DVISNISVFDRGS; VISNISVFDRGSA; ISNISVFDRGSAP; SNISVFDRGSAPQ; NISVFDRGSAPQL; ISVFDRGSAPQLS; SVFDRGSAPQLSS; VFDRGSAPQLSSN; FDRGSAPQLSSNT; DRGSAPQLSSNTP; RGSAPQLSSNTPE; GSAPQLSSNTPEA; SAPQLSSNTPEAE; APQLSSNTPEAES; PQLSSNTPEAESE; QLSSNTPEAESER; LSSNTPEAESERN; SSNTPEAESERNR; SNTPEAESERNRL; NTPEAESERNRLY; TPEAESERNRLYA; PEAESERNRLYAM; EAESERNRLYAMM; AESERNRLYAMMD; ESERNRLYAMMDF; SERNRLYAMMDFD; ERNRLYAMMDFDQ; RNRLYAMMDFDQA; NRLYAMMDFDQAK; RLYAMMDFDQAKT; LYAMMDFDQAKTT; YAMMDFDQAKTTE; AMMDFDQAKTTEF; MMDFDQAKTTEFG; MDFDQAKTTEFGS; DFDQAKTTEFGSI; FDQAKTTEFGSIM; DQAKTTEFGSIMN; QAKTTEFGSIMNI; AKTTEFGSIMNIL; KTTEFGSIMNILY; TTEFGSIMNILYQ; TEFGSIMNILYQE; EFGSIMNILYQEN; FGSIMNILYQENQ; GSIMNILYQENQN; SIMNILYQENQNH; IMNILYQENQNHS; MNILYQENQNHSL; NILYQENQNHSLI; ILYQENQNHSLIR; LYQENQNHSLIRS; YQENQNHSLIRSL; QENQNHSLIRSLI; ENQNHSLIRSLII; NQNHSLIRSLIIS; QNHSLIRSLIISG; NHSLIRSLIISGL; HSLIRSLIISGLG; SLIRSLIISGLGI; LIRSLIISGLGIQ; IRSLIISGLGIQI; RSLIISGLGIQIS; SLIISGLGIQISL; LIISGLGIQISLE; IISGLGIQISLES; ISGLGIQISLEST; SGLGIQISLESTL; GLGIQISLESTLE; LGIQISLESTLEE; GIQISLESTLEEI; IQISLESTLEEIE; QISLESTLEEIEK; ISLESTLEEIEKK; SLESTLEEIEKKI;

LESTLEEIEKKIE; ESTLEEIEKKIES; STLEEIEKKIESF;
TLEEIEKKIESFN; LEEIEKKIESFNT; EEIEKKIESFNTQ;
EIEKKIESFNTQY; IEKKIESFNTQYL; EKKIESFNTQYLN;
KKIESFNTQYLNT; KIESFNTQYLNTI; IESFNTQYLNTII;
ESFNTQYLNTIIN; SFNTQYLNTIINS; FNTQYLNTIINSY;
NTQYLNTIINSYT; TQYLNTIINSYTF; QYLNTIINSYTFK;
YLNTIINSYTFKD; LNTIINSYTFKDK; NTIINSYTFKDKL;
TIINSYTFKDKLK; IINSYTFKDKLKE; INSYTFKDKLKEL;
NSYTFKDKLKELE; SYTFKDKLKELES; YTFKDKLKELESK;
TFKDKLKELESKL; FKDKLKELESKLN; KDKLKELESKLNS;
DKLKELESKLNSI; KLKELESKLNSIL; LKELESKLNSILA;
KELESKLNSILAE; ELESKLNSILAEK; LESKLNSILAEKK;
ESKLNSILAEKKE; SKLNSILAEKKEW; KLNSILAEKKEWL;
LNSILAEKKEWLN; NSILAEKKEWLNY; SILAEKKEWLNYA;
ILAEKKEWLNYAD; LAEKKEWLNYADA; AEKKEWLNYADAI;
EKKEWLNYADAII; KKEWLNYADAIIT; KEWLNYADAIITN;
EWLNYADAIITNT; WLNYADAIITNTS; LNYADAIITNTSS;
NYADAIITNTSSN; YADAIITNTSSNS; ADAIITNTSSNSK;
DAIITNTSSNSKR; AIITNTSSNSKRN; IITNTSSNSKRND;
ITNTSSNSKRNDP; TNTSSNSKRNDPQ; NTSSNSKRNDPQS;
TSSNSKRNDPQSL; SSNSKRNDPQSLG; SNSKRNDPQSLGQ;
NSKRNDPQSLGQY; SKRNDPQSLGQYI; KRNDPQSLGQYIK;
RNDPQSLGQYIKN; NDPQSLGQYIKNK; DPQSLGQYIKNKY;
PQSLGQYIKNKYL; QSLGQYIKNKYLD; SLGQYIKNKYLDK;
LGQYIKNKYLDKM; GQYIKNKYLDKMQ; QYIKNKYLDKMQD;
YIKNKYLDKMQDA; IKNKYLDKMQDAR; KNKYLDKMQDARQ;
NKYLDKMQDARQS; KYLDKMQDARQSA; YLDKMQDARQSAL;
LDKMQDARQSALD; DKMQDARQSALDL; KMQDARQSALDLY;
MQDARQSALDLYL; QDARQSALDLYLN; DARQSALDLYLNI;
ARQSALDLYLNIT; RQSALDLYLNITE; QSALDLYLNITEI;
SALDLYLNITEIR;

14 mers:
MSSCTIDANLNKDY; SSCTIDANLNKDYK; SCTIDANLNKDYKN;
CTIDANLNKDYKNK; TIDANLNKDYKNKV; IDANLNKDYKNKVE;
DANLNKDYKNKVEE; ANLNKDYKNKVEEL; NLNKDYKNKVEELL;
LNKDYKNKVEELLN; NKDYKNKVEELLNS; KDYKNKVEELLNSS;
DYKNKVEELLNSST; YKNKVEELLNSSTD; KNKVEELLNSSTDD;
NKVEELLNSSTDDQ; KVEELLNSSTDDQA; VEELLNSSTDDQAK;
EELLNSSTDDQAKI; ELLNSSTDDQAKIS; LLNSSTDDQAKISI;
LNSSTDDQAKISIN; NSSTDDQAKISINT; SSTDDQAKISINTG;
STDDQAKISINTGS; TDDQAKISINTGSN; DDQAKISINTGSNA;
DQAKISINTGSNAT; QAKISINTGSNATK; AKISINTGSNATKN;
KISINTGSNATKNK; ISINTGSNATKNKT; SINTGSNATKNKTN;
INTGSNATKNKTNI; NTGSNATKNKTNIK; TGSNATKNKTNIKV;
GSNATKNKTNIKVA; SNATKNKTNIKVAG; NATKNKTNIKVAGL;
ATKNKTNIKVAGLQ; TKNKTNIKVAGLQK; KNKTNIKVAGLQKN;
NKTNIKVAGLQKNT; KTNIKVAGLQKNTQ; TNIKVAGLQKNTQS;
NIKVAGLQKNTQSK; IKVAGLQKNTQSKK; KVAGLQKNTQSKKN;
VAGLQKNTQSKKNN; AGLQKNTQSKKNNN; GLQKNTQSKKNNNL;
LQKNTQSKKNNNLQ; QKNTQSKKNNNLQG; KNTQSKKNNNLQGL;

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15 mers:
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	GSIMNILYQENQNHSL; SIMNILYQENQNHSLI; IMNILYQENQNHSLIR; MNILYQENQNHSLIRS; NILYQENQNHSLIRSL; ILYQENQNHSLIRSLI; LYQENQNHSLIRSLII; YQENQNHSLIRSLIIS; QENQNHSLIRSLIISG; ENQNHSLIRSLIISGL; NQNHSLIRSLIISGLG; QNHSLIRSLIISGLGI; NHSLIRSLIISGLGIQ; HSLIRSLIISGLGIQI; SLIRSLIISGLGIQIS; LIRSLIISGLGIQISL; IRSLIISGLGIQISLE; RSLIISGLGIQISLES; SLIISGLGIQISLEST; LIISGLGIQISLESTL; IISGLGIQISLESTLE; ISGLGIQISLESTLEE; SGLGIQISLESTLEEI; GLGIQISLESTLEEIE; LGIQISLESTLEEIEK; GIQISLESTLEEIEKK; IQISLESTLEEIEKKI; QISLESTLEEIEKKIE; ISLESTLEEIEKKIES; SLESTLEEIEKKIESF; LESTLEEIEKKIESFN; ESTLEEIEKKIESFNT; STLEEIEKKIESFNTQ; TLEEIEKKIESFNTQY; LEEIEKKIESFNTQYL; EEIEKKIESFNTQYLN; EIEKKIESFNTQYLNT; IEKKIESFNTQYLNTI; EKKIESFNTQYLNTII; KKIESFNTQYLNTIIN; KIESFNTQYLNTIINS; IESFNTQYLNTIINSY; ESFNTQYLNTIINSYT; SFNTQYLNTIINSYTF; FNTQYLNTIINSYTFK; NTQYLNTIINSYTFKD; TQYLNTIINSYTFKDK; QYLNTIINSYTFKDKL; YLNTIINSYTFKDKLK; LNTIINSYTFKDKLKE; NTIINSYTFKDKLKEL; TIINSYTFKDKLKELE; IINSYTFKDKLKELES; INSYTFKDKLKELESK; NSYTFKDKLKELESKL; SYTFKDKLKELESKLN; YTFKDKLKELESKLNS; TFKDKLKELESKLNSI; FKDKLKELESKLNSIL; KDKLKELESKLNSILA; DKLKELESKLNSILAE; KLKELESKLNSILAEK; LKELESKLNSILAEKK; KELESKLNSILAEKKE; ELESKLNSILAEKKEW; LESKLNSILAEKKEWL; ESKLNSILAEKKEWLN; SKLNSILAEKKEWLNY; KLNSILAEKKEWLNYA; LNSILAEKKEWLNYAD; NSILAEKKEWLNYADA; SILAEKKEWLNYADAI; ILAEKKEWLNYADAII; LAEKKEWLNYADAIIT; AEKKEWLNYADAIITN; EKKEWLNYADAIITNT; KKEWLNYADAIITNTS; KEWLNYADAIITNTSS; EWLNYADAIITNTSSN; WLNYADAIITNTSSNS; LNYADAIITNTSSNSK; NYADAIITNTSSNSKR; YADAIITNTSSNSKRN; ADAIITNTSSNSKRND; DAIITNTSSNSKRNDP; AIITNTSSNSKRNDPQ; IITNTSSNSKRNDPQS; ITNTSSNSKRNDPQSL; TNTSSNSKRNDPQSLG; NTSSNSKRNDPQSLGQ; TSSNSKRNDPQSLGQY; SSNSKRNDPQSLGQYI; SNSKRNDPQSLGQYIK; NSKRNDPQSLGQYIKN; SKRNDPQSLGQYIKNK; KRNDPQSLGQYIKNKY; RNDPQSLGQYIKNKYL; NDPQSLGQYIKNKYLD; DPQSLGQYIKNKYLDK; PQSLGQYIKNKYLDKM; QSLGQYIKNKYLDKMQ; SLGQYIKNKYLDKMQD; LGQYIKNKYLDKMQDA; GQYIKNKYLDKMQDAR; QYIKNKYLDKMQDARQ; YIKNKYLDKMQDARQS; IKNKYLDKMQDARQSA; KNKYLDKMQDARQSAL; NKYLDKMQDARQSALD; KYLDKMQDARQSALDL; YLDKMQDARQSALDLY; LDKMQDARQSALDLYL; DKMQDARQSALDLYLN; KMQDARQSALDLYLNI; MQDARQSALDLYLNIT; QDARQSALDLYLNITE; DARQSALDLYLNITEI; ARQSALDLYLNITEIR;
Seq 36	13 mers: MSSCTIDANLNKD; SSCTIDANLNKDY; SCTIDANLNKDYK; CTIDANLNKDYKN; TIDANLNKDYKNK; IDANLNKDYKNKV; DANLNKDYKNKVE; ANLNKDYKNKVEE; NLNKDYKNKVEEL; LNKDYKNKVEELL; NKDYKNKVEELLN; KDYKNKVEELLNS; DYKNKVEELLNSS; YKNKVEELLNSST; KNKVEELLNSSTD; NKVEELLNSSTDD; KVEELLNSSTDDQ; VEELLNSSTDDQA; EELLNSSTDDQAK; ELLNSSTDDQAKI; LLNSSTDDQAKIS; LNSSTDDQAKISI; NSSTDDQAKISIN; SSTDDQAKISINT;

	STDDQAKISINTG; TDDQAKISINTGS; DDQAKISINTGSN; DQAKISINTGSNA; QAKISINTGSNAT; AKISINTGSNATK; KISINTGSNATKN; ISINTGSNATKNK; SINTGSNATKNKT; INTGSNATKNKTN; NTGSNATKNKTNI; TGSNATKNKTNIK; GSNATKNKTNIKV; SNATKNKTNIKVA; NATKNKTNIKVAG; ATKNKTNIKVAGL; TKNKTNIKVAGLQ; KNKTNIKVAGLQK; NKTNIKVAGLQKN; KTNIKVAGLQKNT; TNIKVAGLQKNTQ; NIKVAGLQKNTQS; IKVAGLQKNTQSK; KVAGLQKNTQSKK; VAGLQKNTQSKKN; AGLQKNTQSKKNN; GLQKNTQSKKNNN; LQKNTQSKKNNNL; QKNTQSKKNNNLQ; KNTQSKKNNNLQG; NTQSKKNNNLQGL; TQSKKNNNLQGLN; QSKKNNNLQGLNP; SKKNNNLQGLNPA; KKNNNLQGLNPAN; KNNNLQGLNPANQ; NNNLQGLNPANQV; NNLQGLNPANQVN; NLQGLNPANQVNP; LQGLNPANQVNPG; QGLNPANQVNPGN; GLNPANQVNPGNP; LNPANQVNPGNPM; NPANQVNPGNPMQ; PANQVNPGNPMQI; ANQVNPGNPMQIA; NQVNPGNPMQIAN; QVNPGNPMQIANQ; VNPGNPMQIANQA; NPGNPMQIANQAN; PGNPMQIANQANQ; GNPMQIANQANQA; NPMQIANQANQAN; PMQIANQANQANQ; MQIANQANQANQA; QIANQANQANQAN; IANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAN; QANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAN; QANQANQANQANQ; ANQANQANQANQA; NQANQANQANQAS; QANQANQANQASQ; ANQANQANQASQA; NQANQANQASQAS; QANQANQASQASQ; ANQANQASQASQA; NQANQASQASQAS; QANQASQASQASQ; ANQASQASQASQV; NQASQASQASQVA; QASQASQASQVAS; ASQASQASQVASS; SQASQASQVASSA; QASQASQVASSAS; ASQASQVASSASQ; SQASQVASSASQA; QASQVASSASQAS; ASQVASSASQASP; SQVASSASQASPV; QVASSASQASPVA; VASSASQASPVAS; ASSASQASPVASP; SSASQASPVASPA; SASQASPVASPAT; ASQASPVASPATN; SQASPVASPATNV; QASPVASPATNVQ; ASPVASPATNVQA; SPVASPATNVQAT; PVASPATNVQATP; VASPATNVQATPP; ASPATNVQATPPK; SPATNVQATPPKQ; PATNVQATPPKQI; ATNVQATPPKQIA; TNVQATPPKQIAS; NVQATPPKQIASA; VQATPPKQIASAQ; QATPPKQIASAQA; ATPPKQIASAQAI; TPPKQIASAQAIQ; PPKQIASAQAIQT; PKQIASAQAIQTV; KQIASAQAIQTVP; QIASAQAIQTVPN; IASAQAIQTVPNN; ASAQAIQTVPNNT; SAQAIQTVPNNTS; AQAIQTVPNNTST; QAIQTVPNNTSTP; AIQTVPNNTSTPN; IQTVPNNTSTPNQ; QTVPNNTSTPNQS; TVPNNTSTPNQSI; VPNNTSTPNQSII; PNNTSTPNQSIIK; NNTSTPNQSIIKP; NTSTPNQSIIKPQ; TSTPNQSIIKPQQ; STPNQSIIKPQQY; TPNQSIIKPQQYT; PNQSIIKPQQYTF; NQSIIKPQQYTFS; QSIIKPQQYTFSS; SIIKPQQYTFSSS; IIKPQQYTFSSSF; IKPQQYTFSSSFS; KPQQYTFSSSFSQ; PQQYTFSSSFSQP; QQYTFSSSFSQPT; QYTFSSSFSQPTS; YTFSSSFSQPTSQ; TFSSSFSQPTSQT; FSSSFSQPTSQTN; SSSFSQPTSQTNF; SSFSQPTSQTNFN; SFSQPTSQTNFNN; FSQPTSQTNFNNS; SQPTSQTNFNNSQ; QPTSQTNFNNSQS; PTSQTNFNNSQSN; TSQTNFNNSQSNN; SQTNFNNSQSNNV; QTNFNNSQSNNVL; TNFNNSQSNNVLT; NFNNSQSNNVLTN; FNNSQSNNVLTNY; NNSQSNNVLTNYR; NSQSNNVLTNYRH;

	SQSNNVLTNYRHQ; QSNNVLTNYRHQT; SNNVLTNYRHQTQ; NNVLTNYRHQTQP; NVLTNYRHQTQPS; VLTNYRHQTQPSF; LTNYRHQTQPSFV; TNYRHQTQPSFVV; NYRHQTQPSFVVP; YRHQTQPSFVVPV; RHQTQPSFVVPVY; HQTQPSFVVPVYS; QTQPSFVVPVYSG; TQPSFVVPVYSGN; QPSFVVPVYSGNS; PSFVVPVYSGNSP; SFVVPVYSGNSPL; FVVPVYSGNSPLQ; VVPVYSGNSPLQK; VPVYSGNSPLQKL; PVYSGNSPLQKLK; VYSGNSPLQKLKN; YSGNSPLQKLKNN; SGNSPLQKLKNNL; GNSPLQKLKNNLL; NSPLQKLKNNLLR; SPLQKLKNNLLRR; PLQKLKNNLLRRI; LQKLKNNLLRRIA; QKLKNNLLRRIAE; KLKNNLLRRIAEE; LKNNLLRRIAEEK; KNNLLRRIAEEKN; NNLLRRIAEEKNK; NLLRRIAEEKNKT; LLRRIAEEKNKTH; LRRIAEEKNKTHN; RRIAEEKNKTHNH; RIAEEKNKTHNHG; IAEEKNKTHNHGF; AEEKNKTHNHGFR; EEKNKTHNHGFRE; EKNKTHNHGFRET; KNKTHNHGFRETY; NKTHNHGFRETYD; KTHNHGFRETYDQ; THNHGFRETYDQF; HNHGFRETYDQFK; NHGFRETYDQFKM; HGFRETYDQFKMK; GFRETYDQFKMKD; FRETYDQFKMKDS; RETYDQFKMKDSA; ETYDQFKMKDSAF; TYDQFKMKDSAFT; YDQFKMKDSAFTL; DQFKMKDSAFTLL; QFKMKDSAFTLLD; FKMKDSAFTLLDV; KMKDSAFTLLDVI; MKDSAFTLLDVIS; KDSAFTLLDVISN; DSAFTLLDVISNI; SAFTLLDVISNIS; AFTLLDVISNISV; FTLLDVISNISVF; TLLDVISNISVFD; LLDVISNISVFDR; LDVISNISVFDRG; DVISNISVFDRGS; VISNISVFDRGSA; ISNISVFDRGSAP; SNISVFDRGSAPQ; NISVFDRGSAPQL; ISVFDRGSAPQLS; SVFDRGSAPQLSS; VFDRGSAPQLSSN; FDRGSAPQLSSNT; DRGSAPQLSSNTP; RGSAPQLSSNTPE; GSAPQLSSNTPEA; SAPQLSSNTPEAE; APQLSSNTPEAES; PQLSSNTPEAESE; QLSSNTPEAESER; LSSNTPEAESERN; SSNTPEAESERNR; SNTPEAESERNRL; NTPEAESERNRLY; TPEAESERNRLYA; PEAESERNRLYAM; EAESERNRLYAMM; AESERNRLYAMMD; ESERNRLYAMMDF; SERNRLYAMMDFD; ERNRLYAMMDFDQ; RNRLYAMMDFDQA; NRLYAMMDFDQAK; RLYAMMDFDQAKT; LYAMMDFDQAKTT; YAMMDFDQAKTTE; AMMDFDQAKTTEF; MMDFDQAKTTEFG; MDFDQAKTTEFGS; DFDQAKTTEFGSI; FDQAKTTEFGSIM; DQAKTTEFGSIMN; QAKTTEFGSIMNI; AKTTEFGSIMNIL; KTTEFGSIMNILY; TTEFGSIMNILYQ; TEFGSIMNILYQE; EFGSIMNILYQEN; FGSIMNILYQENQ; GSIMNILYQENQN; SIMNILYQENQNH; IMNILYQENQNHS; MNILYQENQNHSL; NILYQENQNHSLI; ILYQENQNHSLIR; LYQENQNHSLIRS; YQENQNHSLIRSL; QENQNHSLIRSLI; ENQNHSLIRSLII; NQNHSLIRSLIIS; QNHSLIRSLIISG; NHSLIRSLIISGL; HSLIRSLIISGLG; SLIRSLIISGLGI; LIRSLIISGLGIQ; IRSLIISGLGIQI; RSLIISGLGIQIS; SLIISGLGIQISL; LIISGLGIQISLE; IISGLGIQISLES; ISGLGIQISLEST; SGLGIQISLESTL; GLGIQISLESTLE; LGIQISLESTLEE; GIQISLESTLEEI; IQISLESTLEEIE; QISLESTLEEIEK; ISLESTLEEIEKK; SLESTLEEIEKKI; LESTLEEIEKKIE; ESTLEEIEKKIES; STLEEIEKKIESF; TLEEIEKKIESFN; LEEIEKKIESFNT; EEIEKKIESFNTQ; EIEKKIESFNTQY; IEKKIESFNTQYL; EKKIESFNTQYLN;

KKIESFNTQYLNT; KIESFNTQYLNTI; IESFNTQYLNTII;
ESFNTQYLNTIIN; SFNTQYLNTIINS; FNTQYLNTIINSY;
NTQYLNTIINSYT; TQYLNTIINSYTF; QYLNTIINSYTFK;
YLNTIINSYTFKD; LNTIINSYTFKDK; NTIINSYTFKDKL;
TIINSYTFKDKLK; IINSYTFKDKLKE; INSYTFKDKLKEL;
NSYTFKDKLKELE; SYTFKDKLKELES; YTFKDKLKELESK;
TFKDKLKELESKL; FKDKLKELESKLN; KDKLKELESKLNS;
DKLKELESKLNSI; KLKELESKLNSIL; LKELESKLNSILA;
KELESKLNSILAE; ELESKLNSILAEK; LESKLNSILAEKK;
ESKLNSILAEKKE; SKLNSILAEKKEW; KLNSILAEKKEWL;
LNSILAEKKEWLN; NSILAEKKEWLNY; SILAEKKEWLNYA;
ILAEKKEWLNYAD; LAEKKEWLNYADA; AEKKEWLNYADAI;
EKKEWLNYADAII; KKEWLNYADAIIT; KEWLNYADAIITN;
EWLNYADAIITNT; WLNYADAIITNTS; LNYADAIITNTSS;
NYADAIITNTSSN; YADAIITNTSSNS; ADAIITNTSSNSK;
DAIITNTSSNSKR; AIITNTSSNSKRN; IITNTSSNSKRND;
ITNTSSNSKRNDP; TNTSSNSKRNDPQ; NTSSNSKRNDPQS;
TSSNSKRNDPQSL; SSNSKRNDPQSLG; SNSKRNDPQSLGQ;
NSKRNDPQSLGQY; SKRNDPQSLGQYI; KRNDPQSLGQYIK;
RNDPQSLGQYIKN; NDPQSLGQYIKNK; DPQSLGQYIKNKY;
PQSLGQYIKNKYL; QSLGQYIKNKYLD; SLGQYIKNKYLDK;
LGQYIKNKYLDKM; GQYIKNKYLDKMQ; QYIKNKYLDKMQD;
YIKNKYLDKMQDA; IKNKYLDKMQDAR; KNKYLDKMQDARQ;
NKYLDKMQDARQS; KYLDKMQDARQSA; YLDKMQDARQSAL;
LDKMQDARQSALD; DKMQDARQSALDL; KMQDARQSALDLY;
MQDARQSALDLYL; QDARQSALDLYLN; DARQSALDLYLNI;
ARQSALDLYLNIT; RQSALDLYLNITE; QSALDLYLNITEI;
SALDLYLNITEIR;

14 mers:
MSSCTIDANLNKDY; SSCTIDANLNKDYK; SCTIDANLNKDYKN;
CTIDANLNKDYKNK; TIDANLNKDYKNKV; IDANLNKDYKNKVE;
DANLNKDYKNKVEE; ANLNKDYKNKVEEL; NLNKDYKNKVEELL;
LNKDYKNKVEELLN; NKDYKNKVEELLNS; KDYKNKVEELLNSS;
DYKNKVEELLNSST; YKNKVEELLNSSTD; KNKVEELLNSSTDD;
NKVEELLNSSTDDQ; KVEELLNSSTDDQA; VEELLNSSTDDQAK;
EELLNSSTDDQAKI; ELLNSSTDDQAKIS; LLNSSTDDQAKISI;
LNSSTDDQAKISIN; NSSTDDQAKISINT; SSTDDQAKISINTG;
STDDQAKISINTGS; TDDQAKISINTGSN; DDQAKISINTGSNA;
DQAKISINTGSNAT; QAKISINTGSNATK; AKISINTGSNATKN;
KISINTGSNATKNK; ISINTGSNATKNKT; SINTGSNATKNKTN;
INTGSNATKNKTNI; NTGSNATKNKTNIK; TGSNATKNKTNIKV;
GSNATKNKTNIKVA; SNATKNKTNIKVAG; NATKNKTNIKVAGL;
ATKNKTNIKVAGLQ; TKNKTNIKVAGLQK; KNKTNIKVAGLQKN;
NKTNIKVAGLQKNT; KTNIKVAGLQKNTQ; TNIKVAGLQKNTQS;
NIKVAGLQKNTQSK; IKVAGLQKNTQSKK; KVAGLQKNTQSKKN;
VAGLQKNTQSKKNN; AGLQKNTQSKKNNN; GLQKNTQSKKNNNL;
LQKNTQSKKNNNLQ; QKNTQSKKNNNLQG; KNTQSKKNNNLQGL;
NTQSKKNNNLQGLN; TQSKKNNNLQGLNP; QSKKNNNLQGLNPA;
SKKNNNLQGLNPAN; KKNNNLQGLNPANQ; KNNNLQGLNPANQV;
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16 mers:
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LNKDYKNKVEELLNSS; NKDYKNKVEELLNSST; KDYKNKVEELLNSSTD;
DYKNKVEELLNSSTDD; YKNKVEELLNSSTDDQ; KNKVEELLNSSTDDQA;
NKVEELLNSSTDDQAK; KVEELLNSSTDDQAKI; VEELLNSSTDDQAKIS;
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LNPANQVNPGNPMQIA; NPANQVNPGNPMQIAN; PANQVNPGNPMQIANQ;
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VNPGNPMQIANQANQA; NPGNPMQIANQANQAN; PGNPMQIANQANQANQ;
GNPMQIANQANQANQA; NPMQIANQANQANQAN; PMQIANQANQANQANQ;
MQIANQANQANQANQA; QIANQANQANQANQAN; IANQANQANQANQANQ;
ANQANQANQANQANQA; NQANQANQANQANQAN; QANQANQANQANQANQ;
ANQANQANQANQANQA; NQANQANQANQANQAS; QANQANQANQANQASQ;
ANQANQANQANQASQA; NQANQANQANQASQAS; QANQANQANQASQASQ;
ANQANQANQASQASQA; NQANQANQASQASQAS; QANQANQASQASQASQ;
ANQANQASQASQASQV; NQANQASQASQASQVA; QANQASQASQASQVAS;
ANQASQASQASQVASS; NQASQASQASQVASSA; QASQASQASQVASSAS;
ASQASQASQVASSASQ; SQASQASQVASSASQA; QASQASQVASSASQAS;
ASQASQVASSASQASP; SQASQVASSASQASPV; QASQVASSASQASPVA;
ASQVASSASQASPVAS; SQVASSASQASPVASP; QVASSASQASPVASPA;
VASSASQASPVASPAT; ASSASQASPVASPATN; SSASQASPVASPATNV;
SASQASPVASPATNVQ; ASQASPVASPATNVQA; SQASPVASPATNVQAT;
QASPVASPATNVQATP; ASPVASPATNVQATPP; SPVASPATNVQATPPK;
PVASPATNVQATPPKQ; VASPATNVQATPPKQI; ASPATNVQATPPKQIA;
SPATNVQATPPKQIAS; PATNVQATPPKQIASA; ATNVQATPPKQIASAQ;
TNVQATPPKQIASAQA; NVQATPPKQIASAQAI; VQATPPKQIASAQAIQ;
QATPPKQIASAQAIQT; ATPPKQIASAQAIQTV; TPPKQIASAQAIQTVP;
PPKQIASAQAIQTVPN; PKQIASAQAIQTVPNN; KQIASAQAIQTVPNNT;
QIASAQAIQTVPNNTS; IASAQAIQTVPNNTST; ASAQAIQTVPNNTSTP;
SAQAIQTVPNNTSTPN; AQAIQTVPNNTSTPNQ; QAIQTVPNNTSTPNQS;
AIQTVPNNTSTPNQSI; IQTVPNNTSTPNQSII; QTVPNNTSTPNQSIIK;
TVPNNTSTPNQSIIKP; VPNNTSTPNQSIIKPQ; PNNTSTPNQSIIKPQQ;
NNTSTPNQSIIKPQQY; NTSTPNQSIIKPQQYT; TSTPNQSIIKPQQYTF;

	STPNQSIIKPQQYTFS; TPNQSIIKPQQYTFSS; PNQSIIKPQQYTFSSS; NQSIIKPQQYTFSSSF; QSIIKPQQYTFSSSFS; SIIKPQQYTFSSSFSQ; IIKPQQYTFSSSFSQP; IKPQQYTFSSSFSQPT; KPQQYTFSSSFSQPTS; PQQYTFSSSFSQPTSQ; QQYTFSSSFSQPTSQT; QYTFSSSFSQPTSQTN; YTFSSSFSQPTSQTNF; TFSSSFSQPTSQTNFN; FSSSFSQPTSQTNFNN; SSSFSQPTSQTNFNNS; SSFSQPTSQTNFNNSQ; SFSQPTSQTNFNNSQS; FSQPTSQTNFNNSQSN; SQPTSQTNFNNSQSNN; QPTSQTNFNNSQSNNV; PTSQTNFNNSQSNNVL; TSQTNFNNSQSNNVLT; SQTNFNNSQSNNVLTN; QTNFNNSQSNNVLTNY; TNFNNSQSNNVLTNYR; NFNNSQSNNVLTNYRH; FNNSQSNNVLTNYRHQ; NNSQSNNVLTNYRHQT; NSQSNNVLTNYRHQTQ; SQSNNVLTNYRHQTQP; QSNNVLTNYRHQTQPS; SNNVLTNYRHQTQPSF; NNVLTNYRHQTQPSFV; NVLTNYRHQTQPSFVV; VLTNYRHQTQPSFVVP; LTNYRHQTQPSFVVPV; TNYRHQTQPSFVVPVY; NYRHQTQPSFVVPVYS; YRHQTQPSFVVPVYSG; RHQTQPSFVVPVYSGN; HQTQPSFVVPVYSGNS; QTQPSFVVPVYSGNSP; TQPSFVVPVYSGNSPL; QPSFVVPVYSGNSPLQ; PSFVVPVYSGNSPLQK; SFVVPVYSGNSPLQKL; FVVPVYSGNSPLQKLK; VVPVYSGNSPLQKLKN; VPVYSGNSPLQKLKNN; PVYSGNSPLQKLKNNL; VYSGNSPLQKLKNNLL; YSGNSPLQKLKNNLLR; SGNSPLQKLKNNLLRR; GNSPLQKLKNNLLRRI; NSPLQKLKNNLLRRIA; SPLQKLKNNLLRRIAE; PLQKLKNNLLRRIAEE; LQKLKNNLLRRIAEEK; QKLKNNLLRRIAEEKN; KLKNNLLRRIAEEKNK; LKNNLLRRIAEEKNKT; KNNLLRRIAEEKNKTH; NNLLRRIAEEKNKTHN; NLLRRIAEEKNKTHNH; LLRRIAEEKNKTHNHG; LRRIAEEKNKTHNHGF; RRIAEEKNKTHNHGFR; RIAEEKNKTHNHGFRE; IAEEKNKTHNHGFRET; AEEKNKTHNHGFRETY; EEKNKTHNHGFRETYD; EKNKTHNHGFRETYDQ; KNKTHNHGFRETYDQF; NKTHNHGFRETYDQFK; KTHNHGFRETYDQFKM; THNHGFRETYDQFKMK; HNHGFRETYDQFKMKD; NHGFRETYDQFKMKDS; HGFRETYDQFKMKDSA; GFRETYDQFKMKDSAF; FRETYDQFKMKDSAFT; RETYDQFKMKDSAFTL; ETYDQFKMKDSAFTLL; TYDQFKMKDSAFTLLD; YDQFKMKDSAFTLLDV; DQFKMKDSAFTLLDVI; QFKMKDSAFTLLDVIS; FKMKDSAFTLLDVISN; KMKDSAFTLLDVISNI; MKDSAFTLLDVISNIS; KDSAFTLLDVISNISV; DSAFTLLDVISNISVF; SAFTLLDVISNISVFD; AFTLLDVISNISVFDR; FTLLDVISNISVFDRG; TLLDVISNISVFDRGS; LLDVISNISVFDRGSA; LDVISNISVFDRGSAP; DVISNISVFDRGSAPQ; VISNISVFDRGSAPQL; ISNISVFDRGSAPQLS; SNISVFDRGSAPQLSS; NISVFDRGSAPQLSSN; ISVFDRGSAPQLSSNT; SVFDRGSAPQLSSNTP; VFDRGSAPQLSSNTPE; FDRGSAPQLSSNTPEA; DRGSAPQLSSNTPEAE; RGSAPQLSSNTPEAES; GSAPQLSSNTPEAESE; SAPQLSSNTPEAESER; APQLSSNTPEAESERN; PQLSSNTPEAESERNR; QLSSNTPEAESERNRL; LSSNTPEAESERNRLY; SSNTPEAESERNRLYA; SNTPEAESERNRLYAM; NTPEAESERNRLYAMM; TPEAESERNRLYAMMD; PEAESERNRLYAMMDF; EAESERNRLYAMMDFD; AESERNRLYAMMDFDQ; ESERNRLYAMMDFDQA; SERNRLYAMMDFDQAK; ERNRLYAMMDFDQAKT; RNRLYAMMDFDQAKTT; NRLYAMMDFDQAKTTE; RLYAMMDFDQAKTTEF; LYAMMDFDQAKTTEFG; YAMMDFDQAKTTEFGS; AMMDFDQAKTTEFGSI; MMDFDQAKTTEFGSIM; MDFDQAKTTEFGSIMN; DFDQAKTTEFGSIMNI; FDQAKTTEFGSIMNIL; DQAKTTEFGSIMNILY; QAKTTEFGSIMNILYQ; AKTTEFGSIMNILYQE; KTTEFGSIMNILYQEN; TTEFGSIMNILYQENQ; TEFGSIMNILYQENQN; EFGSIMNILYQENQNH; FGSIMNILYQENQNHS; GSIMNILYQENQNHSL; SIMNILYQENQNHSLI; IMNILYQENQNHSLIR; MNILYQENQNHSLIRS; NILYQENQNHSLIRSL; ILYQENQNHSLIRSLI; LYQENQNHSLIRSLII; YQENQNHSLIRSLIIS; QENQNHSLIRSLIISG;

	ENQNHSLIRSLIISGL; NQNHSLIRSLIISGLG; QNHSLIRSLIISGLGI; NHSLIRSLIISGLGIQ; HSLIRSLIISGLGIQI; SLIRSLIISGLGIQIS; LIRSLIISGLGIQISL; IRSLIISGLGIQISLE; RSLIISGLGIQISLES; SLIISGLGIQISLEST; LIISGLGIQISLESTL; IISGLGIQISLESTLE; ISGLGIQISLESTLEE; SGLGIQISLESTLEEI; GLGIQISLESTLEEIE; LGIQISLESTLEEIEK; GIQISLESTLEEIEKK; IQISLESTLEEIEKKI; QISLESTLEEIEKKIE; ISLESTLEEIEKKIES; SLESTLEEIEKKIESF; LESTLEEIEKKIESFN; ESTLEEIEKKIESFNT; STLEEIEKKIESFNTQ; TLEEIEKKIESFNTQY; LEEIEKKIESFNTQYL; EEIEKKIESFNTQYLN; EIEKKIESFNTQYLNT; IEKKIESFNTQYLNTI; EKKIESFNTQYLNTII; KKIESFNTQYLNTIIN; KIESFNTQYLNTIINS; IESFNTQYLNTIINSY; ESFNTQYLNTIINSYT; SFNTQYLNTIINSYTF; FNTQYLNTIINSYTFK; NTQYLNTIINSYTFKD; TQYLNTIINSYTFKDK; QYLNTIINSYTFKDKL; YLNTIINSYTFKDKLK; LNTIINSYTFKDKLKE; NTIINSYTFKDKLKEL; TIINSYTFKDKLKELE; IINSYTFKDKLKELES; INSYTFKDKLKELESK; NSYTFKDKLKELESKL; SYTFKDKLKELESKLN; YTFKDKLKELESKLNS; TFKDKLKELESKLNSI; FKDKLKELESKLNSIL; KDKLKELESKLNSILA; DKLKELESKLNSILAE; KLKELESKLNSILAEK; LKELESKLNSILAEKK; KELESKLNSILAEKKE; ELESKLNSILAEKKEW; LESKLNSILAEKKEWL; ESKLNSILAEKKEWLN; SKLNSILAEKKEWLNY; KLNSILAEKKEWLNYA; LNSILAEKKEWLNYAD; NSILAEKKEWLNYADA; SILAEKKEWLNYADAI; ILAEKKEWLNYADAII; LAEKKEWLNYADAIIT; AEKKEWLNYADAIITN; EKKEWLNYADAIITNT; KKEWLNYADAIITNTS; KEWLNYADAIITNTSS; EWLNYADAIITNTSSN; WLNYADAIITNTSSNS; LNYADAIITNTSSNSK; NYADAIITNTSSNSKR; YADAIITNTSSNSKRN; ADAIITNTSSNSKRND; DAIITNTSSNSKRNDP; AIITNTSSNSKRNDPQ; IITNTSSNSKRNDPQS; ITNTSSNSKRNDPQSL; TNTSSNSKRNDPQSLG; NTSSNSKRNDPQSLGQ; TSSNSKRNDPQSLGQY; SSNSKRNDPQSLGQYI; SNSKRNDPQSLGQYIK; NSKRNDPQSLGQYIKN; SKRNDPQSLGQYIKNK; KRNDPQSLGQYIKNKY; RNDPQSLGQYIKNKYL; NDPQSLGQYIKNKYLD; DPQSLGQYIKNKYLDK; PQSLGQYIKNKYLDKM; QSLGQYIKNKYLDKMQ; SLGQYIKNKYLDKMQD; LGQYIKNKYLDKMQDA; GQYIKNKYLDKMQDAR; QYIKNKYLDKMQDARQ; YIKNKYLDKMQDARQS; IKNKYLDKMQDARQSA; KNKYLDKMQDARQSAL; NKYLDKMQDARQSALD; KYLDKMQDARQSALDL; YLDKMQDARQSALDLY; LDKMQDARQSALDLYL; DKMQDARQSALDLYLN; KMQDARQSALDLYLNI; MQDARQSALDLYLNIT; QDARQSALDLYLNITE; DARQSALDLYLNITEI; ARQSALDLYLNITEIR;
Seq 37	13 mers: MKKTKLNIIKLNI; KKTKLNIIKLNIL; KTKLNIIKLNILT; TKLNIIKLNILTT; KLNIIKLNILTTT; LNIIKLNILTTTL; NIIKLNILTTTLT; IIKLNILTTTLTL; IKLNILTTTLTLI; KLNILTTTLTLIC; LNILTTTLTLICI; NILTTTLTLICIS; ILTTTLTLICISC; LTTTLTLICISCA; TTTLTLICISCAV; TTLTLICISCAVN; TLTLICISCAVNK; LTLICISCAVNKI; TLICISCAVNKID; LICISCAVNKIDP; ICISCAVNKIDPE; CISCAVNKIDPEP; ISCAVNKIDPEPK; SCAVNKIDPEPKS; CAVNKIDPEPKSK; AVNKIDPEPKSKT; VNKIDPEPKSKTN; NKIDPEPKSKTNK; KIDPEPKSKTNKK; IDPEPKSKTNKKE; DPEPKSKTNKKEN; PEPKSKTNKKENI; EPKSKTNKKENIK;

	PKSKTNKKENIKN; KSKTNKKENIKNF; SKTNKKENIKNFV; KTNKKENIKNFVN; TNKKENIKNFVNK; NKKENIKNFVNKF; KKENIKNFVNKFQ; KENIKNFVNKFQD; ENIKNFVNKFQDL; NIKNFVNKFQDLE; IKNFVNKFQDLEP; KNFVNKFQDLEPS; NFVNKFQDLEPSK; FVNKFQDLEPSKK; VNKFQDLEPSKKQ; NKFQDLEPSKKQN; KFQDLEPSKKQNK; FQDLEPSKKQNKD; QDLEPSKKQNKDL; DLEPSKKQNKDLE; LEPSKKQNKDLEP; EPSKKQNKDLEPL; PSKKQNKDLEPLR; SKKQNKDLEPLRE; KKQNKDLEPLREK; KQNKDLEPLREKY; QNKDLEPLREKYP; NKDLEPLREKYPE; KDLEPLREKYPEA; DLEPLREKYPEAT; LEPLREKYPEATA; EPLREKYPEATAS; PLREKYPEATASK; LREKYPEATASKL; REKYPEATASKLE; EKYPEATASKLET; KYPEATASKLETT; YPEATASKLETTL; PEATASKLETTLK; EATASKLETTLKI; ATASKLETTLKIL; TASKLETTLKILE; ASKLETTLKILEA; SKLETTLKILEAQ; KLETTLKILEAQK; LETTLKILEAQKE; ETTLKILEAQKEK; TTLKILEAQKEKE; TLKILEAQKEKEN; LKILEAQKEKENI; KILEAQKEKENIE; ILEAQKEKENIEI; LEAQKEKENIEIA; EAQKEKENIEIAK; AQKEKENIEIAKI; QKEKENIEIAKID; KEKENIEIAKIDN; EKENIEIAKIDNT; KENIEIAKIDNTQ; ENIEIAKIDNTQI; NIEIAKIDNTQID; IEIAKIDNTQIDF; EIAKIDNTQIDFL; IAKIDNTQIDFLK; AKIDNTQIDFLKT; KIDNTQIDFLKTF; IDNTQIDFLKTFK; DNTQIDFLKTFKT; NTQIDFLKTFKTD; TQIDFLKTFKTDP; QIDFLKTFKTDPH; IDFLKTFKTDPHD; DFLKTFKTDPHDS; FLKTFKTDPHDSL; LKTFKTDPHDSLP; KTFKTDPHDSLPE; TFKTDPHDSLPED; FKTDPHDSLPEDE; KTDPHDSLPEDEK; TDPHDSLPEDEKM; DPHDSLPEDEKMQ; PHDSLPEDEKMQM; HDSLPEDEKMQMK; DSLPEDEKMQMKK; SLPEDEKMQMKKI; LPEDEKMQMKKII; PEDEKMQMKKIIY; EDEKMQMKKIIYS; DEKMQMKKIIYSS; EKMQMKKIIYSSL; KMQMKKIIYSSLN; MQMKKIIYSSLNY; QMKKIIYSSLNYE; MKKIIYSSLNYET; KKIIYSSLNYETE; KIIYSSLNYETEK; IIYSSLNYETEKI; IYSSLNYETEKIK; YSSLNYETEKIKI; SSLNYETEKIKIL; SLNYETEKIKILQ; LNYETEKIKILQE; NYETEKIKILQEI; YETEKIKILQEIL; ETEKIKILQEILE; TEKIKILQEILEK; EKIKILQEILEKL; KIKILQEILEKLD; IKILQEILEKLDK; KILQEILEKLDKN; ILQEILEKLDKNL; LQEILEKLDKNLQ; QEILEKLDKNLQH; EILEKLDKNLQHK; ILEKLDKNLQHKK; LEKLDKNLQHKKI; EKLDKNLQHKKIA; KLDKNLQHKKIAK; LDKNLQHKKIAKN; DKNLQHKKIAKNF; KNLQHKKIAKNFI; NLQHKKIAKNFIY; LQHKKIAKNFIYD; QHKKIAKNFIYDI; HKKIAKNFIYDIP; KKIAKNFIYDIPI; KIAKNFIYDIPII; IAKNFIYDIPIII; AKNFIYDIPIIIQ; KNFIYDIPIIIQS; NFIYDIPIIIQSR; FIYDIPIIIQSRL; IYDIPIIIQSRLD; YDIPIIIQSRLDI; DIPIIIQSRLDII; IPIIIQSRLDIIS; PIIIQSRLDIISK; IIIQSRLDIISKV; IIQSRLDIISKVI; IQSRLDIISKVIK; QSRLDIISKVIKN; SRLDIISKVIKNP; RLDIISKVIKNPI; LDIISKVIKNPIK; DIISKVIKNPIKD; IISKVIKNPIKDE; ISKVIKNPIKDEL; SKVIKNPIKDELQ; KVIKNPIKDELQI; VIKNPIKDELQIL; IKNPIKDELQILN; KNPIKDELQILNQ; NPIKDELQILNQK;

PIKDELQILNQKE; IKDELQILNQKEI; KDELQILNQKEIE;
DELQILNQKEIEE; ELQILNQKEIEEL; LQILNQKEIEELL;
QILNQKEIEELLM; ILNQKEIEELLMR; LNQKEIEELLMRI;
NQKEIEELLMRIE; QKEIEELLMRIES; KEIEELLMRIESE;
EIEELLMRIESEL; IEELLMRIESELK; EELLMRIESELKI;
ELLMRIESELKIK; LLMRIESELKIKE; LMRIESELKIKEN;
MRIESELKIKENF; RIESELKIKENFK; IESELKIKENFKK;
ESELKIKENFKKA; SELKIKENFKKAL; ELKIKENFKKALN;
LKIKENFKKALNK; KIKENFKKALNKT; IKENFKKALNKTI;
KENFKKALNKTID; ENFKKALNKTIDA; NFKKALNKTIDAY;
FKKALNKTIDAYN; KKALNKTIDAYNQ; KALNKTIDAYNQD;
ALNKTIDAYNQDS; LNKTIDAYNQDSE; NKTIDAYNQDSEN;
KTIDAYNQDSENI; TIDAYNQDSENIK; IDAYNQDSENIKT;
DAYNQDSENIKTS; AYNQDSENIKTSA; YNQDSENIKTSAE;
NQDSENIKTSAEQ; QDSENIKTSAEQL; DSENIKTSAEQLE;
SENIKTSAEQLEK; ENIKTSAEQLEKH; NIKTSAEQLEKHI;
IKTSAEQLEKHIN; KTSAEQLEKHINE; TSAEQLEKHINEN;
SAEQLEKHINENY; AEQLEKHINENYK; EQLEKHINENYKE;
QLEKHINENYKEF; LEKHINENYKEFN; EKHINENYKEFNS;
KHINENYKEFNSL; HINENYKEFNSLK; INENYKEFNSLKP;
NENYKEFNSLKPI; ENYKEFNSLKPIY;

14 mers:
MKKTKLNIIKLNIL; KKTKLNIIKLNILT; KTKLNIIKLNILTT;
TKLNIIKLNILTTT; KLNIIKLNILTTTL; LNIIKLNILTTTLT;
NIIKLNILTTTLTL; IIKLNILTTTLTLI; IKLNILTTTLTLIC;
KLNILTTTLTLICI; LNILTTTLTLICIS; NILTTTLTLICISC;
ILTTTLTLICISCA; LTTTLTLICISCAV; TTTLTLICISCAVN;
TTLTLICISCAVNK; TLTLICISCAVNKI; LTLICISCAVNKID;
TLICISCAVNKIDP; LICISCAVNKIDPE; ICISCAVNKIDPEP;
CISCAVNKIDPEPK; ISCAVNKIDPEPKS; SCAVNKIDPEPKSK;
CAVNKIDPEPKSKT; AVNKIDPEPKSKTN; VNKIDPEPKSKTNK;
NKIDPEPKSKTNKK; KIDPEPKSKTNKKE; IDPEPKSKTNKKEN;
DPEPKSKTNKKENI; PEPKSKTNKKENIK; EPKSKTNKKENIKN;
PKSKTNKKENIKNF; KSKTNKKENIKNFV; SKTNKKENIKNFVN;
KTNKKENIKNFVNK; TNKKENIKNFVNKF; NKKENIKNFVNKFQ;
KKENIKNFVNKFQD; KENIKNFVNKFQDL; ENIKNFVNKFQDLE;
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NFVNKFQDLEPSKK; FVNKFQDLEPSKKQ; VNKFQDLEPSKKQN;
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KYPEATASKLETTL; YPEATASKLETTLK; PEATASKLETTLKI;
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ASKLETTLKILEAQ; SKLETTLKILEAQK; KLETTLKILEAQKE;
LETTLKILEAQKEK; ETTLKILEAQKEKE; TTLKILEAQKEKEN;
TLKILEAQKEKENI; LKILEAQKEKENIE; KILEAQKEKENIEI;

	ILEAQKEKENIEIA; LEAQKEKENIEIAK; EAQKEKENIEIAKI; AQKEKENIEIAKID; QKEKENIEIAKIDN; KEKENIEIAKIDNT; EKENIEIAKIDNTQ; KENIEIAKIDNTQI; ENIEIAKIDNTQID; NIEIAKIDNTQIDF; IEIAKIDNTQIDFL; EIAKIDNTQIDFLK; IAKIDNTQIDFLKT; AKIDNTQIDFLKTF; KIDNTQIDFLKTFK; IDNTQIDFLKTFKT; DNTQIDFLKTFKTD; NTQIDFLKTFKTDP; TQIDFLKTFKTDPH; QIDFLKTFKTDPHD; IDFLKTFKTDPHDS; DFLKTFKTDPHDSL; FLKTFKTDPHDSLP; LKTFKTDPHDSLPE; KTFKTDPHDSLPED; TFKTDPHDSLPEDE; FKTDPHDSLPEDEK; KTDPHDSLPEDEKM; TDPHDSLPEDEKMQ; DPHDSLPEDEKMQM; PHDSLPEDEKMQMK; HDSLPEDEKMQMKK; DSLPEDEKMQMKKI; SLPEDEKMQMKKII; LPEDEKMQMKKIIY; PEDEKMQMKKIIYS; EDEKMQMKKIIYSS; DEKMQMKKIIYSSL; EKMQMKKIIYSSLN; KMQMKKIIYSSLNY; MQMKKIIYSSLNYE; QMKKIIYSSLNYET; MKKIIYSSLNYETE; KKIIYSSLNYETEK; KIIYSSLNYETEKI; IIYSSLNYETEKIK; IYSSLNYETEKIKI; YSSLNYETEKIKIL; SSLNYETEKIKILQ; SLNYETEKIKILQE; LNYETEKIKILQEI; NYETEKIKILQEIL; YETEKIKILQEILE; ETEKIKILQEILEK; TEKIKILQEILEKL; EKIKILQEILEKLD; KIKILQEILEKLDK; IKILQEILEKLDKN; KILQEILEKLDKNL; ILQEILEKLDKNLQ; LQEILEKLDKNLQH; QEILEKLDKNLQHK; EILEKLDKNLQHKK; ILEKLDKNLQHKKI; LEKLDKNLQHKKIA; EKLDKNLQHKKIAK; KLDKNLQHKKIAKN; LDKNLQHKKIAKNF; DKNLQHKKIAKNFI; KNLQHKKIAKNFIY; NLQHKKIAKNFIYD; LQHKKIAKNFIYDI; QHKKIAKNFIYDIP; HKKIAKNFIYDIPI; KKIAKNFIYDIPII; KIAKNFIYDIPIII; IAKNFIYDIPIIIQ; AKNFIYDIPIIIQS; KNFIYDIPIIIQSR; NFIYDIPIIIQSRL; FIYDIPIIIQSRLD; IYDIPIIIQSRLDI; YDIPIIIQSRLDII; DIPIIIQSRLDIIS; IPIIIQSRLDIISK; PIIIQSRLDIISKV; IIIQSRLDIISKVI; IIQSRLDIISKVIK; IQSRLDIISKVIKN; QSRLDIISKVIKNP; SRLDIISKVIKNPI; RLDIISKVIKNPIK; LDIISKVIKNPIKD; DIISKVIKNPIKDE; IISKVIKNPIKDEL; ISKVIKNPIKDELQ; SKVIKNPIKDELQI; KVIKNPIKDELQIL; VIKNPIKDELQILN; IKNPIKDELQILNQ; KNPIKDELQILNQK; NPIKDELQILNQKE; PIKDELQILNQKEI; IKDELQILNQKEIE; KDELQILNQKEIEE; DELQILNQKEIEEL; ELQILNQKEIEELL; LQILNQKEIEELLM; QILNQKEIEELLMR; ILNQKEIEELLMRI; LNQKEIEELLMRIE; NQKEIEELLMRIES; QKEIEELLMRIESE; KEIEELLMRIESEL; EIEELLMRIESELK; IEELLMRIESELKI; EELLMRIESELKIK; ELLMRIESELKIKE; LLMRIESELKIKEN; LMRIESELKIKENF; MRIESELKIKENFK; RIESELKIKENFKK; IESELKIKENFKKA; ESELKIKENFKKAL; SELKIKENFKKALN; ELKIKENFKKALNK; LKIKENFKKALNKT; KIKENFKKALNKTI; IKENFKKALNKTID; KENFKKALNKTIDA; ENFKKALNKTIDAY; NFKKALNKTIDAYN; FKKALNKTIDAYNQ; KKALNKTIDAYNQD; KALNKTIDAYNQDS; ALNKTIDAYNQDSE; LNKTIDAYNQDSEN; NKTIDAYNQDSENI; KTIDAYNQDSENIK; TIDAYNQDSENIKT; IDAYNQDSENIKTS; DAYNQDSENIKTSA; AYNQDSENIKTSAE; YNQDSENIKTSAEQ; NQDSENIKTSAEQL; QDSENIKTSAEQLE; DSENIKTSAEQLEK; SENIKTSAEQLEKH; ENIKTSAEQLEKHI; NIKTSAEQLEKHIN; IKTSAEQLEKHINE; KTSAEQLEKHINEN; TSAEQLEKHINENY;

	SAEQLEKHINENYK; AEQLEKHINENYKE; EQLEKHINENYKEF; QLEKHINENYKEFN; LEKHINENYKEFNS; EKHINENYKEFNSL; KHINENYKEFNSLK; HINENYKEFNSLKP; INENYKEFNSLKPI; NENYKEFNSLKPIY; 15 mers: MKKTKLNIIKLNILT; KKTKLNIIKLNILTT; KTKLNIIKLNILTTT; TKLNIIKLNILTTTL; KLNIIKLNILTTTLT; LNIIKLNILTTTLTL; NIIKLNILTTTLTLI; IIKLNILTTTLTLIC; IKLNILTTTLTLICI; KLNILTTTLTLICIS; LNILTTTLTLICISC; NILTTTLTLICISCA; ILTTTLTLICISCAV; LTTTLTLICISCAVN; TTTLTLICISCAVNK; TTLTLICISCAVNKI; TLTLICISCAVNKID; LTLICISCAVNKIDP; TLICISCAVNKIDPE; LICISCAVNKIDPEP; ICISCAVNKIDPEPK; CISCAVNKIDPEPKS; ISCAVNKIDPEPKSK; SCAVNKIDPEPKSKT; CAVNKIDPEPKSKTN; AVNKIDPEPKSKTNK; VNKIDPEPKSKTNKK; NKIDPEPKSKTNKKE; KIDPEPKSKTNKKEN; IDPEPKSKTNKKENI; DPEPKSKTNKKENIK; PEPKSKTNKKENIKN; EPKSKTNKKENIKNF; PKSKTNKKENIKNFV; KSKTNKKENIKNFVN; SKTNKKENIKNFVNK; KTNKKENIKNFVNKF; TNKKENIKNFVNKFQ; NKKENIKNFVNKFQD; KKENIKNFVNKFQDL; KENIKNFVNKFQDLE; ENIKNFVNKFQDLEP; NIKNFVNKFQDLEPS; IKNFVNKFQDLEPSK; KNFVNKFQDLEPSKK; NFVNKFQDLEPSKKQ; FVNKFQDLEPSKKQN; VNKFQDLEPSKKQNK; NKFQDLEPSKKQNKD; KFQDLEPSKKQNKDL; FQDLEPSKKQNKDLE; QDLEPSKKQNKDLEP; DLEPSKKQNKDLEPL; LEPSKKQNKDLEPLR; EPSKKQNKDLEPLRE; PSKKQNKDLEPLREK; SKKQNKDLEPLREKY; KKQNKDLEPLREKYP; KQNKDLEPLREKYPE; QNKDLEPLREKYPEA; NKDLEPLREKYPEAT; KDLEPLREKYPEATA; DLEPLREKYPEATAS; LEPLREKYPEATASK; EPLREKYPEATASKL; PLREKYPEATASKLE; LREKYPEATASKLET; REKYPEATASKLETT; EKYPEATASKLETTL; KYPEATASKLETTLK; YPEATASKLETTLKI; PEATASKLETTLKIL; EATASKLETTLKILE; ATASKLETTLKILEA; TASKLETTLKILEAQ; ASKLETTLKILEAQK; SKLETTLKILEAQKE; KLETTLKILEAQKEK; LETTLKILEAQKEKE; ETTLKILEAQKEKEN; TTLKILEAQKEKENI; TLKILEAQKEKENIE; LKILEAQKEKENIEI; KILEAQKEKENIEIA; ILEAQKEKENIEIAK; LEAQKEKENIEIAKI; EAQKEKENIEIAKID; AQKEKENIEIAKIDN; QKEKENIEIAKIDNT; KEKENIEIAKIDNTQ; EKENIEIAKIDNTQI; KENIEIAKIDNTQID; ENIEIAKIDNTQIDF; NIEIAKIDNTQIDFL; IEIAKIDNTQIDFLK; EIAKIDNTQIDFLKT; IAKIDNTQIDFLKTF; AKIDNTQIDFLKTFK; KIDNTQIDFLKTFKT; IDNTQIDFLKTFKTD; DNTQIDFLKTFKTDP; NTQIDFLKTFKTDPH; TQIDFLKTFKTDPHD; QIDFLKTFKTDPHDS; IDFLKTFKTDPHDSL; DFLKTFKTDPHDSLP; FLKTFKTDPHDSLPE; LKTFKTDPHDSLPED; KTFKTDPHDSLPEDE; TFKTDPHDSLPEDEK; FKTDPHDSLPEDEKM; KTDPHDSLPEDEKMQ; TDPHDSLPEDEKMQM; DPHDSLPEDEKMQMK; PHDSLPEDEKMQMKK; HDSLPEDEKMQMKKI; DSLPEDEKMQMKKII; SLPEDEKMQMKKIIY; LPEDEKMQMKKIIYS; PEDEKMQMKKIIYSS; EDEKMQMKKIIYSSL; DEKMQMKKIIYSSLN; EKMQMKKIIYSSLNY; KMQMKKIIYSSLNYE; MQMKKIIYSSLNYET; QMKKIIYSSLNYETE; MKKIIYSSLNYETEK; KKIIYSSLNYETEKI; KIIYSSLNYETEKIK; IIYSSLNYETEKIKI; IYSSLNYETEKIKIL; YSSLNYETEKIKILQ; SSLNYETEKIKILQE; SLNYETEKIKILQEI; LNYETEKIKILQEIL;

	NYETEKIKILQEILE; YETEKIKILQEILEK; ETEKIKILQEILEKL; TEKIKILQEILEKLD; EKIKILQEILEKLDK; KIKILQEILEKLDKN; IKILQEILEKLDKNL; KILQEILEKLDKNLQ; ILQEILEKLDKNLQH; LQEILEKLDKNLQHK; QEILEKLDKNLQHKK; EILEKLDKNLQHKKI; ILEKLDKNLQHKKIA; LEKLDKNLQHKKIAK; EKLDKNLQHKKIAKN; KLDKNLQHKKIAKNF; LDKNLQHKKIAKNFI; DKNLQHKKIAKNFIY; KNLQHKKIAKNFIYD; NLQHKKIAKNFIYDI; LQHKKIAKNFIYDIP; QHKKIAKNFIYDIPI; HKKIAKNFIYDIPII; KKIAKNFIYDIPIII; KIAKNFIYDIPIIIQ; IAKNFIYDIPIIIQS; AKNFIYDIPIIIQSR; KNFIYDIPIIIQSRL; NFIYDIPIIIQSRLD; FIYDIPIIIQSRLDI; IYDIPIIIQSRLDII; YDIPIIIQSRLDIIS; DIPIIIQSRLDIISK; IPIIIQSRLDIISKV; PIIIQSRLDIISKVI; IIIQSRLDIISKVIK; IIQSRLDIISKVIKN; IQSRLDIISKVIKNP; QSRLDIISKVIKNPI; SRLDIISKVIKNPIK; RLDIISKVIKNPIKD; LDIISKVIKNPIKDE; DIISKVIKNPIKDEL; IISKVIKNPIKDELQ; ISKVIKNPIKDELQI; SKVIKNPIKDELQIL; KVIKNPIKDELQILN; VIKNPIKDELQILNQ; IKNPIKDELQILNQK; KNPIKDELQILNQKE; NPIKDELQILNQKEI; PIKDELQILNQKEIE; IKDELQILNQKEIEE; KDELQILNQKEIEEL; DELQILNQKEIEELL; ELQILNQKEIEELLM; LQILNQKEIEELLMR; QILNQKEIEELLMRI; ILNQKEIEELLMRIE; LNQKEIEELLMRIES; NQKEIEELLMRIESE; QKEIEELLMRIESEL; KEIEELLMRIESELK; EIEELLMRIESELKI; IEELLMRIESELKIK; EELLMRIESELKIKE; ELLMRIESELKIKEN; LLMRIESELKIKENF; LMRIESELKIKENFK; MRIESELKIKENFKK; RIESELKIKENFKKA; IESELKIKENFKKAL; ESELKIKENFKKALN; SELKIKENFKKALNK; ELKIKENFKKALNKT; LKIKENFKKALNKTI; KIKENFKKALNKTID; IKENFKKALNKTIDA; KENFKKALNKTIDAY; ENFKKALNKTIDAYN; NFKKALNKTIDAYNQ; FKKALNKTIDAYNQD; KKALNKTIDAYNQDS; KALNKTIDAYNQDSE; ALNKTIDAYNQDSEN; LNKTIDAYNQDSENI; NKTIDAYNQDSENIK; KTIDAYNQDSENIKT; TIDAYNQDSENIKTS; IDAYNQDSENIKTSA; DAYNQDSENIKTSAE; AYNQDSENIKTSAEQ; YNQDSENIKTSAEQL; NQDSENIKTSAEQLE; QDSENIKTSAEQLEK; DSENIKTSAEQLEKH; SENIKTSAEQLEKHI; ENIKTSAEQLEKHIN; NIKTSAEQLEKHINE; IKTSAEQLEKHINEN; KTSAEQLEKHINENY; TSAEQLEKHINENYK; SAEQLEKHINENYKE; AEQLEKHINENYKEF; EQLEKHINENYKEFN; QLEKHINENYKEFNS; LEKHINENYKEFNSL; EKHINENYKEFNSLK; KHINENYKEFNSLKP; HINENYKEFNSLKPI; INENYKEFNSLKPIY; 16 mers: MKKTKLNIIKLNILTT; KKTKLNIIKLNILTTT; KTKLNIIKLNILTTTL; TKLNIIKLNILTTTLT; KLNIIKLNILTTTLTL; LNIIKLNILTTTLTLI; NIIKLNILTTTLTLIC; IIKLNILTTTLTLICI; IKLNILTTTLTLICIS; KLNILTTTLTLICISC; LNILTTTLTLICISCA; NILTTTLTLICISCAV; ILTTTLTLICISCAVN; LTTTLTLICISCAVNK; TTTLTLICISCAVNKI; TTLTLICISCAVNKID; TLTLICISCAVNKIDP; LTLICISCAVNKIDPE; TLICISCAVNKIDPEP; LICISCAVNKIDPEPK; ICISCAVNKIDPEPKS; CISCAVNKIDPEPKSK; ISCAVNKIDPEPKSKT; SCAVNKIDPEPKSKTN; CAVNKIDPEPKSKTNK; AVNKIDPEPKSKTNKK; VNKIDPEPKSKTNKKE; NKIDPEPKSKTNKKEN; KIDPEPKSKTNKKENI; IDPEPKSKTNKKENIK; DPEPKSKTNKKENIKN; PEPKSKTNKKENIKNF; EPKSKTNKKENIKNFV; PKSKTNKKENIKNFVN; KSKTNKKENIKNFVNK; SKTNKKENIKNFVNKF;

	KTNKKENIKNFVNKFQ; TNKKENIKNFVNKFQD; NKKENIKNFVNKFQDL; KKENIKNFVNKFQDLE; KENIKNFVNKFQDLEP; ENIKNFVNKFQDLEPS; NIKNFVNKFQDLEPSK; IKNFVNKFQDLEPSKK; KNFVNKFQDLEPSKKQ; NFVNKFQDLEPSKKQN; FVNKFQDLEPSKKQNK; VNKFQDLEPSKKQNKD; NKFQDLEPSKKQNKDL; KFQDLEPSKKQNKDLE; FQDLEPSKKQNKDLEP; QDLEPSKKQNKDLEPL; DLEPSKKQNKDLEPLR; LEPSKKQNKDLEPLRE; EPSKKQNKDLEPLREK; PSKKQNKDLEPLREKY; SKKQNKDLEPLREKYP; KKQNKDLEPLREKYPE; KQNKDLEPLREKYPEA; QNKDLEPLREKYPEAT; NKDLEPLREKYPEATA; KDLEPLREKYPEATAS; DLEPLREKYPEATASK; LEPLREKYPEATASKL; EPLREKYPEATASKLE; PLREKYPEATASKLET; LREKYPEATASKLETT; REKYPEATASKLETTL; EKYPEATASKLETTLK; KYPEATASKLETTLKI; YPEATASKLETTLKIL; PEATASKLETTLKILE; EATASKLETTLKILEA; ATASKLETTLKILEAQ; TASKLETTLKILEAQK; ASKLETTLKILEAQKE; SKLETTLKILEAQKEK; KLETTLKILEAQKEKE; LETTLKILEAQKEKEN; ETTLKILEAQKEKENI; TTLKILEAQKEKENIE; TLKILEAQKEKENIEI; LKILEAQKEKENIEIA; KILEAQKEKENIEIAK; ILEAQKEKENIEIAKI; LEAQKEKENIEIAKID; EAQKEKENIEIAKIDN; AQKEKENIEIAKIDNT; QKEKENIEIAKIDNTQ; KEKENIEIAKIDNTQI; EKENIEIAKIDNTQID; KENIEIAKIDNTQIDF; ENIEIAKIDNTQIDFL; NIEIAKIDNTQIDFLK; IEIAKIDNTQIDFLKT; EIAKIDNTQIDFLKTF; IAKIDNTQIDFLKTFK; AKIDNTQIDFLKTFKT; KIDNTQIDFLKTFKTD; IDNTQIDFLKTFKTDP; DNTQIDFLKTFKTDPH; NTQIDFLKTFKTDPHD; TQIDFLKTFKTDPHDS; QIDFLKTFKTDPHDSL; IDFLKTFKTDPHDSLP; DFLKTFKTDPHDSLPE; FLKTFKTDPHDSLPED; LKTFKTDPHDSLPEDE; KTFKTDPHDSLPEDEK; TFKTDPHDSLPEDEKM; FKTDPHDSLPEDEKMQ; KTDPHDSLPEDEKMQM; TDPHDSLPEDEKMQMK; DPHDSLPEDEKMQMKK; PHDSLPEDEKMQMKKI; HDSLPEDEKMQMKKII; DSLPEDEKMQMKKIIY; SLPEDEKMQMKKIIYS; LPEDEKMQMKKIIYSS; PEDEKMQMKKIIYSSL; EDEKMQMKKIIYSSLN; DEKMQMKKIIYSSLNY; EKMQMKKIIYSSLNYE; KMQMKKIIYSSLNYET; MQMKKIIYSSLNYETE; QMKKIIYSSLNYETEK; MKKIIYSSLNYETEKI; KKIIYSSLNYETEKIK; KIIYSSLNYETEKIKI; IIYSSLNYETEKIKIL; IYSSLNYETEKIKILQ; YSSLNYETEKIKILQE; SSLNYETEKIKILQEI; SLNYETEKIKILQEIL; LNYETEKIKILQEILE; NYETEKIKILQEILEK; YETEKIKILQEILEKL; ETEKIKILQEILEKLD; TEKIKILQEILEKLDK; EKIKILQEILEKLDKN; KIKILQEILEKLDKNL; IKILQEILEKLDKNLQ; KILQEILEKLDKNLQH; ILQEILEKLDKNLQHK; LQEILEKLDKNLQHKK; QEILEKLDKNLQHKKI; EILEKLDKNLQHKKIA; ILEKLDKNLQHKKIAK; LEKLDKNLQHKKIAKN; EKLDKNLQHKKIAKNF; KLDKNLQHKKIAKNFI; LDKNLQHKKIAKNFIY; DKNLQHKKIAKNFIYD; KNLQHKKIAKNFIYDI; NLQHKKIAKNFIYDIP; LQHKKIAKNFIYDIPI; QHKKIAKNFIYDIPII; HKKIAKNFIYDIPIII; KKIAKNFIYDIPIIIQ; KIAKNFIYDIPIIIQS; IAKNFIYDIPIIIQSR; AKNFIYDIPIIIQSRL; KNFIYDIPIIIQSRLD; NFIYDIPIIIQSRLDI; FIYDIPIIIQSRLDII; IYDIPIIIQSRLDIIS; YDIPIIIQSRLDIISK; DIPIIIQSRLDIISKV; IPIIIQSRLDIISKVI; PIIIQSRLDIISKVIK; IIIQSRLDIISKVIKN; IIQSRLDIISKVIKNP; IQSRLDIISKVIKNPI; QSRLDIISKVIKNPIK; SRLDIISKVIKNPIKD; RLDIISKVIKNPIKDE; LDIISKVIKNPIKDEL; DIISKVIKNPIKDELQ; IISKVIKNPIKDELQI; ISKVIKNPIKDELQIL; SKVIKNPIKDELQILN; KVIKNPIKDELQILNQ; VIKNPIKDELQILNQK; IKNPIKDELQILNQKE; KNPIKDELQILNQKEI; NPIKDELQILNQKEIE; PIKDELQILNQKEIEE; IKDELQILNQKEIEEL; KDELQILNQKEIEELL;

	DELQILNQKEIEELLM; ELQILNQKEIEELLMR; LQILNQKEIEELLMRI; QILNQKEIEELLMRIE; ILNQKEIEELLMRIES; LNQKEIEELLMRIESE; NQKEIEELLMRIESEL; QKEIEELLMRIESELK; KEIEELLMRIESELKI; EIEELLMRIESELKIK; IEELLMRIESELKIKE; EELLMRIESELKIKEN; ELLMRIESELKIKENF; LLMRIESELKIKENFK; LMRIESELKIKENFKK; MRIESELKIKENFKKA; RIESELKIKENFKKAL; IESELKIKENFKKALN; ESELKIKENFKKALNK; SELKIKENFKKALNKT; ELKIKENFKKALNKTI; LKIKENFKKALNKTID; KIKENFKKALNKTIDA; IKENFKKALNKTIDAY; KENFKKALNKTIDAYN; ENFKKALNKTIDAYNQ; NFKKALNKTIDAYNQD; FKKALNKTIDAYNQDS; KKALNKTIDAYNQDSE; KALNKTIDAYNQDSEN; ALNKTIDAYNQDSENI; LNKTIDAYNQDSENIK; NKTIDAYNQDSENIKT; KTIDAYNQDSENIKTS; TIDAYNQDSENIKTSA; IDAYNQDSENIKTSAE; DAYNQDSENIKTSAEQ; AYNQDSENIKTSAEQL; YNQDSENIKTSAEQLE; NQDSENIKTSAEQLEK; QDSENIKTSAEQLEKH; DSENIKTSAEQLEKHI; SENIKTSAEQLEKHIN; ENIKTSAEQLEKHINE; NIKTSAEQLEKHINEN; IKTSAEQLEKHINENY; KTSAEQLEKHINENYK; TSAEQLEKHINENYKE; SAEQLEKHINENYKEF; AEQLEKHINENYKEFN; EQLEKHINENYKEFNS; QLEKHINENYKEFNSL; LEKHINENYKEFNSLK; EKHINENYKEFNSLKP; KHINENYKEFNSLKPI; HINENYKEFNSLKPIY;
Seq 38	13 mers: MRILVGVCIIALA; RILVGVCIIALAL; ILVGVCIIALALL; LVGVCIIALALLG; VGVCIIALALLGC; GVCIIALALLGCY; VCIIALALLGCYL; CIIALALLGCYLP; IIALALLGCYLPD; IALALLGCYLPDN; ALALLGCYLPDNQ; LALLGCYLPDNQE; ALLGCYLPDNQEQ; LLGCYLPDNQEQA; LGCYLPDNQEQAV; GCYLPDNQEQAVQ; CYLPDNQEQAVQT; YLPDNQEQAVQTF; LPDNQEQAVQTFF; PDNQEQAVQTFFE; DNQEQAVQTFFEN; NQEQAVQTFFENS; QEQAVQTFFENSE; EQAVQTFFENSES; QAVQTFFENSESS; AVQTFFENSESSD; VQTFFENSESSDM; QTFFENSESSDMG; TFFENSESSDMGS; FFENSESSDMGSD; FENSESSDMGSDE; ENSESSDMGSDEI; NSESSDMGSDEIV; SESSDMGSDEIVT; ESSDMGSDEIVTE; SSDMGSDEIVTEG; SDMGSDEIVTEGI; DMGSDEIVTEGIF; MGSDEIVTEGIFS; GSDEIVTEGIFSS; SDEIVTEGIFSSL; DEIVTEGIFSSLK; EIVTEGIFSSLKL; IVTEGIFSSLKLY; VTEGIFSSLKLYA; TEGIFSSLKLYAS; EGIFSSLKLYASE; GIFSSLKLYASEH; IFSSLKLYASEHR; FSSLKLYASEHRL; SSLKLYASEHRLL; SLKLYASEHRLLV; LKLYASEHRLLVE; KLYASEHRLLVEI; LYASEHRLLVEIK; YASEHRLLVEIKK; ASEHRLLVEIKKT; SEHRLLVEIKKTL; EHRLLVEIKKTLI; HRLLVEIKKTLIS; RLLVEIKKTLISL; LLVEIKKTLISLK; LVEIKKTLISLKD; VEIKKTLISLKDP; EIKKTLISLKDPN; IKKTLISLKDPNY; KKTLISLKDPNYR; KTLISLKDPNYRG; TLISLKDPNYRGV; LISLKDPNYRGVV; ISLKDPNYRGVVL; SLKDPNYRGVVLP; LKDPNYRGVVLPV; KDPNYRGVVLPVS; DPNYRGVVLPVSD; PNYRGVVLPVSDY; NYRGVVLPVSDYN; YRGVVLPVSDYNE; RGVVLPVSDYNEE; GVVLPVSDYNEEY; VVLPVSDYNEEYF; VLPVSDYNEEYFN; LPVSDYNEEYFNK; PVSDYNEEYFNKF; VSDYNEEYFNKFF; SDYNEEYFNKFFL; DYNEEYFNKFFLD;

	YNEEYFNKFFLDL; NEEYFNKFFLDLG; EEYFNKFFLDLGS; EYFNKFFLDLGSE; YFNKFFLDLGSEQ; FNKFFLDLGSEQS; NKFFLDLGSEQSK; KFFLDLGSEQSKD; FFLDLGSEQSKDL; FLDLGSEQSKDLI; LDLGSEQSKDLIK; DLGSEQSKDLIKL; LGSEQSKDLIKLF; GSEQSKDLIKLFI; SEQSKDLIKLFIM; EQSKDLIKLFIMV; QSKDLIKLFIMVK; SKDLIKLFIMVKN; KDLIKLFIMVKNE; DLIKLFIMVKNEQ; LIKLFIMVKNEQN; IKLFIMVKNEQNN; KLFIMVKNEQNNN; LFIMVKNEQNNNK; FIMVKNEQNNNKF; IMVKNEQNNNKFM; MVKNEQNNNKFMR; VKNEQNNNKFMRI; KNEQNNNKFMRIV; NEQNNNKFMRIVR; EQNNNKFMRIVRW; QNNNKFMRIVRWL; NNNKFMRIVRWLY; NNKFMRIVRWLYS; NKFMRIVRWLYSC; KFMRIVRWLYSCI; FMRIVRWLYSCIE; MRIVRWLYSCIEE; RIVRWLYSCIEEL; IVRWLYSCIEELY; VRWLYSCIEELYS; RWLYSCIEELYSP; WLYSCIEELYSPD; LYSCIEELYSPDI; YSCIEELYSPDIK; SCIEELYSPDIKY; CIEELYSPDIKYS; IEELYSPDIKYSG; EELYSPDIKYSGE; ELYSPDIKYSGEE; LYSPDIKYSGEEG; YSPDIKYSGEEGS; SPDIKYSGEEGSP; PDIKYSGEEGSPE; DIKYSGEEGSPEY; IKYSGEEGSPEYY; KYSGEEGSPEYYR; YSGEEGSPEYYRN; SGEEGSPEYYRNM; GEEGSPEYYRNMP; EEGSPEYYRNMPR; EGSPEYYRNMPRP; GSPEYYRNMPRPT; SPEYYRNMPRPTA; PEYYRNMPRPTAY; EYYRNMPRPTAYQ; YYRNMPRPTAYQQ; YRNMPRPTAYQQY; RNMPRPTAYQQYL; NMPRPTAYQQYLK; MPRPTAYQQYLKV; PRPTAYQQYLKVK; RPTAYQQYLKVKR; PTAYQQYLKVKRY; TAYQQYLKVKRYD; AYQQYLKVKRYDY; YQQYLKVKRYDYN; QQYLKVKRYDYNR; QYLKVKRYDYNRP; YLKVKRYDYNRPV; LKVKRYDYNRPVP; KVKRYDYNRPVPI; VKRYDYNRPVPIL; KRYDYNRPVPILP; RYDYNRPVPILPT; 14 mers: MRILVGVCIIALAL; RILVGVCIIALALL; ILVGVCIIALALLG; LVGVCIIALALLGC; VGVCIIALALLGCY; GVCIIALALLGCYL; VCIIALALLGCYLP; CIIALALLGCYLPD; IIALALLGCYLPDN; IALALLGCYLPDNQ; ALALLGCYLPDNQE; LALLGCYLPDNQEQ; ALLGCYLPDNQEQA; LLGCYLPDNQEQAV; LGCYLPDNQEQAVQ; GCYLPDNQEQAVQT; CYLPDNQEQAVQTF; YLPDNQEQAVQTFF; LPDNQEQAVQTFFE; PDNQEQAVQTFFEN; DNQEQAVQTFFENS; NQEQAVQTFFENSE; QEQAVQTFFENSES; EQAVQTFFENSESS; QAVQTFFENSESSD; AVQTFFENSESSDM; VQTFFENSESSDMG; QTFFENSESSDMGS; TFFENSESSDMGSD; FFENSESSDMGSDE; FENSESSDMGSDEI; ENSESSDMGSDEIV; NSESSDMGSDEIVT; SESSDMGSDEIVTE; ESSDMGSDEIVTEG; SSDMGSDEIVTEGI; SDMGSDEIVTEGIF; DMGSDEIVTEGIFS; MGSDEIVTEGIFSS; GSDEIVTEGIFSSL; SDEIVTEGIFSSLK; DEIVTEGIFSSLKL; EIVTEGIFSSLKLY; IVTEGIFSSLKLYA; VTEGIFSSLKLYAS; TEGIFSSLKLYASE; EGIFSSLKLYASEH; GIFSSLKLYASEHR; IFSSLKLYASEHRL; FSSLKLYASEHRLL; SSLKLYASEHRLLV; SLKLYASEHRLLVE; LKLYASEHRLLVEI; KLYASEHRLLVEIK; LYASEHRLLVEIKK; YASEHRLLVEIKKT; ASEHRLLVEIKKTL; SEHRLLVEIKKTLI; EHRLLVEIKKTLIS; HRLLVEIKKTLISL;

	RLLVEIKKTLISLK; LLVEIKKTLISLKD; LVEIKKTLISLKDP; VEIKKTLISLKDPN; EIKKTLISLKDPNY; IKKTLISLKDPNYR; KKTLISLKDPNYRG; KTLISLKDPNYRGV; TLISLKDPNYRGVV; LISLKDPNYRGVVL; ISLKDPNYRGVVLP; SLKDPNYRGVVLPV; LKDPNYRGVVLPVS; KDPNYRGVVLPVSD; DPNYRGVVLPVSDY; PNYRGVVLPVSDYN; NYRGVVLPVSDYNE; YRGVVLPVSDYNEE; RGVVLPVSDYNEEY; GVVLPVSDYNEEYF; VVLPVSDYNEEYFN; VLPVSDYNEEYFNK; LPVSDYNEEYFNKF; PVSDYNEEYFNKFF; VSDYNEEYFNKFFL; SDYNEEYFNKFFLD; DYNEEYFNKFFLDL; YNEEYFNKFFLDLG; NEEYFNKFFLDLGS; EEYFNKFFLDLGSE; EYFNKFFLDLGSEQ; YFNKFFLDLGSEQS; FNKFFLDLGSEQSK; NKFFLDLGSEQSKD; KFFLDLGSEQSKDL; FFLDLGSEQSKDLI; FLDLGSEQSKDLIK; LDLGSEQSKDLIKL; DLGSEQSKDLIKLF; LGSEQSKDLIKLFI; GSEQSKDLIKLFIM; SEQSKDLIKLFIMV; EQSKDLIKLFIMVK; QSKDLIKLFIMVKN; SKDLIKLFIMVKNE; KDLIKLFIMVKNEQ; DLIKLFIMVKNEQN; LIKLFIMVKNEQNN; IKLFIMVKNEQNNN; KLFIMVKNEQNNNK; LFIMVKNEQNNNKF; FIMVKNEQNNNKFM; IMVKNEQNNNKFMR; MVKNEQNNNKFMRI; VKNEQNNNKFMRIV; KNEQNNNKFMRIVR; NEQNNNKFMRIVRW; EQNNNKFMRIVRWL; QNNNKFMRIVRWLY; NNNKFMRIVRWLYS; NNKFMRIVRWLYSC; NKFMRIVRWLYSCI; KFMRIVRWLYSCIE; FMRIVRWLYSCIEE; MRIVRWLYSCIEEL; RIVRWLYSCIEELY; IVRWLYSCIEELYS; VRWLYSCIEELYSP; RWLYSCIEELYSPD; WLYSCIEELYSPDI; LYSCIEELYSPDIK; YSCIEELYSPDIKY; SCIEELYSPDIKYS; CIEELYSPDIKYSG; IEELYSPDIKYSGE; EELYSPDIKYSGEE; ELYSPDIKYSGEEG; LYSPDIKYSGEEGS; YSPDIKYSGEEGSP; SPDIKYSGEEGSPE; PDIKYSGEEGSPEY; DIKYSGEEGSPEYY; IKYSGEEGSPEYYR; KYSGEEGSPEYYRN; YSGEEGSPEYYRNM; SGEEGSPEYYRNMP; GEEGSPEYYRNMPR; EEGSPEYYRNMPRP; EGSPEYYRNMPRPT; GSPEYYRNMPRPTA; SPEYYRNMPRPTAY; PEYYRNMPRPTAYQ; EYYRNMPRPTAYQQ; YYRNMPRPTAYQQY; YRNMPRPTAYQQYL; RNMPRPTAYQQYLK; NMPRPTAYQQYLKV; MPRPTAYQQYLKVK; PRPTAYQQYLKVKR; RPTAYQQYLKVKRY; PTAYQQYLKVKRYD; TAYQQYLKVKRYDY; AYQQYLKVKRYDYN; YQQYLKVKRYDYNR; QQYLKVKRYDYNRP; QYLKVKRYDYNRPV; YLKVKRYDYNRPVP; LKVKRYDYNRPVPI; KVKRYDYNRPVPIL; VKRYDYNRPVPILP; KRYDYNRPVPILPT; 15 mers: MRILVGVCIIALALL; RILVGVCIIALALLG; ILVGVCIIALALLGC; LVGVCIIALALLGCY; VGVCIIALALLGCYL; GVCIIALALLGCYLP; VCIIALALLGCYLPD; CIIALALLGCYLPDN; IIALALLGCYLPDNQ; IALALLGCYLPDNQE; ALALLGCYLPDNQEQ; LALLGCYLPDNQEQA; ALLGCYLPDNQEQAV; LLGCYLPDNQEQAVQ; LGCYLPDNQEQAVQT; GCYLPDNQEQAVQTF; CYLPDNQEQAVQTFF; YLPDNQEQAVQTFFE; LPDNQEQAVQTFFEN; PDNQEQAVQTFFENS; DNQEQAVQTFFENSE; NQEQAVQTFFENSES; QEQAVQTFFENSESS; EQAVQTFFENSESSD; QAVQTFFENSESSDM; AVQTFFENSESSDMG; VQTFFENSESSDMGS; QTFFENSESSDMGSD; TFFENSESSDMGSDE; FFENSESSDMGSDEI; FENSESSDMGSDEIV; ENSESSDMGSDEIVT; NSESSDMGSDEIVTE; SESSDMGSDEIVTEG; ESSDMGSDEIVTEGI; SSDMGSDEIVTEGIF;

	SDMGSDEIVTEGIFS; DMGSDEIVTEGIFSS; MGSDEIVTEGIFSSL; GSDEIVTEGIFSSLK; SDEIVTEGIFSSLKL; DEIVTEGIFSSLKLY; EIVTEGIFSSLKLYA; IVTEGIFSSLKLYAS; VTEGIFSSLKLYASE; TEGIFSSLKLYASEH; EGIFSSLKLYASEHR; GIFSSLKLYASEHRL; IFSSLKLYASEHRLL; FSSLKLYASEHRLLV; SSLKLYASEHRLLVE; SLKLYASEHRLLVEI; LKLYASEHRLLVEIK; KLYASEHRLLVEIKK; LYASEHRLLVEIKKT; YASEHRLLVEIKKTL; ASEHRLLVEIKKTLI; SEHRLLVEIKKTLIS; EHRLLVEIKKTLISL; HRLLVEIKKTLISLK; RLLVEIKKTLISLKD; LLVEIKKTLISLKDP; LVEIKKTLISLKDPN; VEIKKTLISLKDPNY; EIKKTLISLKDPNYR; IKKTLISLKDPNYRG; KKTLISLKDPNYRGV; KTLISLKDPNYRGVV; TLISLKDPNYRGVVL; LISLKDPNYRGVVLP; ISLKDPNYRGVVLPV; SLKDPNYRGVVLPVS; LKDPNYRGVVLPVSD; KDPNYRGVVLPVSDY; DPNYRGVVLPVSDYN; PNYRGVVLPVSDYNE; NYRGVVLPVSDYNEE; YRGVVLPVSDYNEEY; RGVVLPVSDYNEEYF; GVVLPVSDYNEEYFN; VVLPVSDYNEEYFNK; VLPVSDYNEEYFNKF; LPVSDYNEEYFNKFF; PVSDYNEEYFNKFFL; VSDYNEEYFNKFFLD; SDYNEEYFNKFFLDL; DYNEEYFNKFFLDLG; YNEEYFNKFFLDLGS; NEEYFNKFFLDLGSE; EEYFNKFFLDLGSEQ; EYFNKFFLDLGSEQS; YFNKFFLDLGSEQSK; FNKFFLDLGSEQSKD; NKFFLDLGSEQSKDL; KFFLDLGSEQSKDLI; FFLDLGSEQSKDLIK; FLDLGSEQSKDLIKL; LDLGSEQSKDLIKLF; DLGSEQSKDLIKLFI; LGSEQSKDLIKLFIM; GSEQSKDLIKLFIMV; SEQSKDLIKLFIMVK; EQSKDLIKLFIMVKN; QSKDLIKLFIMVKNE; SKDLIKLFIMVKNEQ; KDLIKLFIMVKNEQN; DLIKLFIMVKNEQNN; LIKLFIMVKNEQNNN; IKLFIMVKNEQNNNK; KLFIMVKNEQNNNKF; LFIMVKNEQNNNKFM; FIMVKNEQNNNKFMR; IMVKNEQNNNKFMRI; MVKNEQNNNKFMRIV; VKNEQNNNKFMRIVR; KNEQNNNKFMRIVRW; NEQNNNKFMRIVRWL; EQNNNKFMRIVRWLY; QNNNKFMRIVRWLYS; NNNKFMRIVRWLYSC; NNKFMRIVRWLYSCI; NKFMRIVRWLYSCIE; KFMRIVRWLYSCIEE; FMRIVRWLYSCIEEL; MRIVRWLYSCIEELY; RIVRWLYSCIEELYS; IVRWLYSCIEELYSP; VRWLYSCIEELYSPD; RWLYSCIEELYSPDI; WLYSCIEELYSPDIK; LYSCIEELYSPDIKY; YSCIEELYSPDIKYS; SCIEELYSPDIKYSG; CIEELYSPDIKYSGE; IEELYSPDIKYSGEE; EELYSPDIKYSGEEG; ELYSPDIKYSGEEGS; LYSPDIKYSGEEGSP; YSPDIKYSGEEGSPE; SPDIKYSGEEGSPEY; PDIKYSGEEGSPEYY; DIKYSGEEGSPEYYR; IKYSGEEGSPEYYRN; KYSGEEGSPEYYRNM; YSGEEGSPEYYRNMP; SGEEGSPEYYRNMPR; GEEGSPEYYRNMPRP; EEGSPEYYRNMPRPT; EGSPEYYRNMPRPTA; GSPEYYRNMPRPTAY; SPEYYRNMPRPTAYQ; PEYYRNMPRPTAYQQ; EYYRNMPRPTAYQQY; YYRNMPRPTAYQQYL; YRNMPRPTAYQQYLK; RNMPRPTAYQQYLKV; NMPRPTAYQQYLKVK; MPRPTAYQQYLKVKR; PRPTAYQQYLKVKRY; RPTAYQQYLKVKRYD; PTAYQQYLKVKRYDY; TAYQQYLKVKRYDYN; AYQQYLKVKRYDYNR; YQQYLKVKRYDYNRP; QQYLKVKRYDYNRPV; QYLKVKRYDYNRPVP; YLKVKRYDYNRPVPI; LKVKRYDYNRPVPIL; KVKRYDYNRPVPILP; VKRYDYNRPVPILPT; 16 mers: MRILVGVCIIALALLG; RILVGVCIIALALLGC; ILVGVCIIALALLGCY; LVGVCIIALALLGCYL; VGVCIIALALLGCYLP; GVCIIALALLGCYLPD; VCIIALALLGCYLPDN; CIIALALLGCYLPDNQ; IIALALLGCYLPDNQE; IALALLGCYLPDNQEQ; ALALLGCYLPDNQEQA; LALLGCYLPDNQEQAV;

	ALLGCYLPDNQEQAVQ; LLGCYLPDNQEQAVQT; LGCYLPDNQEQAVQTF; GCYLPDNQEQAVQTFF; CYLPDNQEQAVQTFFE; YLPDNQEQAVQTFFEN; LPDNQEQAVQTFFENS; PDNQEQAVQTFFENSE; DNQEQAVQTFFENSES; NQEQAVQTFFENSESS; QEQAVQTFFENSESSD; EQAVQTFFENSESSDM; QAVQTFFENSESSDMG; AVQTFFENSESSDMGS; VQTFFENSESSDMGSD; QTFFENSESSDMGSDE; TFFENSESSDMGSDEI; FFENSESSDMGSDEIV; FENSESSDMGSDEIVT; ENSESSDMGSDEIVTE; NSESSDMGSDEIVTEG; SESSDMGSDEIVTEGI; ESSDMGSDEIVTEGIF; SSDMGSDEIVTEGIFS; SDMGSDEIVTEGIFSS; DMGSDEIVTEGIFSSL; MGSDEIVTEGIFSSLK; GSDEIVTEGIFSSLKL; SDEIVTEGIFSSLKLY; DEIVTEGIFSSLKLYA; EIVTEGIFSSLKLYAS; IVTEGIFSSLKLYASE; VTEGIFSSLKLYASEH; TEGIFSSLKLYASEHR; EGIFSSLKLYASEHRL; GIFSSLKLYASEHRLL; IFSSLKLYASEHRLLV; FSSLKLYASEHRLLVE; SSLKLYASEHRLLVEI; SLKLYASEHRLLVEIK; LKLYASEHRLLVEIKK; KLYASEHRLLVEIKKT; LYASEHRLLVEIKKTL; YASEHRLLVEIKKTLI; ASEHRLLVEIKKTLIS; SEHRLLVEIKKTLISL; EHRLLVEIKKTLISLK; HRLLVEIKKTLISLKD; RLLVEIKKTLISLKDP; LLVEIKKTLISLKDPN; LVEIKKTLISLKDPNY; VEIKKTLISLKDPNYR; EIKKTLISLKDPNYRG; IKKTLISLKDPNYRGV; KKTLISLKDPNYRGVV; KTLISLKDPNYRGVVL; TLISLKDPNYRGVVLP; LISLKDPNYRGVVLPV; ISLKDPNYRGVVLPVS; SLKDPNYRGVVLPVSD; LKDPNYRGVVLPVSDY; KDPNYRGVVLPVSDYN; DPNYRGVVLPVSDYNE; PNYRGVVLPVSDYNEE; NYRGVVLPVSDYNEEY; YRGVVLPVSDYNEEYF; RGVVLPVSDYNEEYFN; GVVLPVSDYNEEYFNK; VVLPVSDYNEEYFNKF; VLPVSDYNEEYFNKFF; LPVSDYNEEYFNKFFL; PVSDYNEEYFNKFFLD; VSDYNEEYFNKFFLDL; SDYNEEYFNKFFLDLG; DYNEEYFNKFFLDLGS; YNEEYFNKFFLDLGSE; NEEYFNKFFLDLGSEQ; EEYFNKFFLDLGSEQS; EYFNKFFLDLGSEQSK; YFNKFFLDLGSEQSKD; FNKFFLDLGSEQSKDL; NKFFLDLGSEQSKDLI; KFFLDLGSEQSKDLIK; FFLDLGSEQSKDLIKL; FLDLGSEQSKDLIKLF; LDLGSEQSKDLIKLFI; DLGSEQSKDLIKLFIM; LGSEQSKDLIKLFIMV; GSEQSKDLIKLFIMVK; SEQSKDLIKLFIMVKN; EQSKDLIKLFIMVKNE; QSKDLIKLFIMVKNEQ; SKDLIKLFIMVKNEQN; KDLIKLFIMVKNEQNN; DLIKLFIMVKNEQNNN; LIKLFIMVKNEQNNNK; IKLFIMVKNEQNNNKF; KLFIMVKNEQNNNKFM; LFIMVKNEQNNNKFMR; FIMVKNEQNNNKFMRI; IMVKNEQNNNKFMRIV; MVKNEQNNNKFMRIVR; VKNEQNNNKFMRIVRW; KNEQNNNKFMRIVRWL; NEQNNNKFMRIVRWLY; EQNNNKFMRIVRWLYS; QNNNKFMRIVRWLYSC; NNNKFMRIVRWLYSCI; NNKFMRIVRWLYSCIE; NKFMRIVRWLYSCIEE; KFMRIVRWLYSCIEEL; FMRIVRWLYSCIEELY; MRIVRWLYSCIEELYS; RIVRWLYSCIEELYSP; IVRWLYSCIEELYSPD; VRWLYSCIEELYSPDI; RWLYSCIEELYSPDIK; WLYSCIEELYSPDIKY; LYSCIEELYSPDIKYS; YSCIEELYSPDIKYSG; SCIEELYSPDIKYSGE; CIEELYSPDIKYSGEE; IEELYSPDIKYSGEEG; EELYSPDIKYSGEEGS; ELYSPDIKYSGEEGSP; LYSPDIKYSGEEGSPE; YSPDIKYSGEEGSPEY; SPDIKYSGEEGSPEYY; PDIKYSGEEGSPEYYR; DIKYSGEEGSPEYYRN; IKYSGEEGSPEYYRNM; KYSGEEGSPEYYRNMP; YSGEEGSPEYYRNMPR; SGEEGSPEYYRNMPRP; GEEGSPEYYRNMPRPT; EEGSPEYYRNMPRPTA; EGSPEYYRNMPRPTAY; GSPEYYRNMPRPTAYQ; SPEYYRNMPRPTAYQQ; PEYYRNMPRPTAYQQY; EYYRNMPRPTAYQQYL; YYRNMPRPTAYQQYLK; YRNMPRPTAYQQYLKV; RNMPRPTAYQQYLKVK; NMPRPTAYQQYLKVKR; MPRPTAYQQYLKVKRY; PRPTAYQQYLKVKRYD; RPTAYQQYLKVKRYDY; PTAYQQYLKVKRYDYN; TAYQQYLKVKRYDYNR; AYQQYLKVKRYDYNRP; YQQYLKVKRYDYNRPV; QQYLKVKRYDYNRPVP;

	QYLKVKRYDYNRPVPI; YLKVKRYDYNRPVPIL; LKVKRYDYNRPVPILP; KVKRYDYNRPVPILPT;
Seq 39	13 mers: MRNKNIFKLFFAS; RNKNIFKLFFASM; NKNIFKLFFASML; KNIFKLFFASMLF; NIFKLFFASMLFV; IFKLFFASMLFVM; FKLFFASMLFVMA; KLFFASMLFVMAC; LFFASMLFVMACK; FFASMLFVMACKA; FASMLFVMACKAY; ASMLFVMACKAYV; SMLFVMACKAYVE; MLFVMACKAYVEE; LFVMACKAYVEEK; FVMACKAYVEEKK; VMACKAYVEEKKE; MACKAYVEEKKEI; ACKAYVEEKKEID; CKAYVEEKKEIDS; KAYVEEKKEIDSL; AYVEEKKEIDSLM; YVEEKKEIDSLME; VEEKKEIDSLMED; EEKKEIDSLMEDV; EKKEIDSLMEDVL; KKEIDSLMEDVLA; KEIDSLMEDVLAL; EIDSLMEDVLALV; IDSLMEDVLALVN; DSLMEDVLALVND; SLMEDVLALVNDS; LMEDVLALVNDSS; MEDVLALVNDSSG; EDVLALVNDSSGG; DVLALVNDSSGGK; VLALVNDSSGGKF; LALVNDSSGGKFK; ALVNDSSGGKFKD; LVNDSSGGKFKDY; VNDSSGGKFKDYK; NDSSGGKFKDYKD; DSSGGKFKDYKDK; SSGGKFKDYKDKI; SGGKFKDYKDKIN; GGKFKDYKDKINE; GKFKDYKDKINEL; KFKDYKDKINELK; FKDYKDKINELKE; KDYKDKINELKEN; DYKDKINELKENL; YKDKINELKENLK; KDKINELKENLKD; DKINELKENLKDI; KINELKENLKDIG; INELKENLKDIGN; NELKENLKDIGNA; ELKENLKDIGNAE; LKENLKDIGNAEL; KENLKDIGNAELK; ENLKDIGNAELKE; NLKDIGNAELKEK; LKDIGNAELKEKL; KDIGNAELKEKLL; DIGNAELKEKLLN; IGNAELKEKLLNL; GNAELKEKLLNLQ; NAELKEKLLNLQN; AELKEKLLNLQNS; ELKEKLLNLQNSF; LKEKLLNLQNSFQ; KEKLLNLQNSFQD; EKLLNLQNSFQDK; KLLNLQNSFQDKL; LLNLQNSFQDKLA; LNLQNSFQDKLAA; NLQNSFQDKLAAK; LQNSFQDKLAAKL; QNSFQDKLAAKLA; NSFQDKLAAKLAA; SFQDKLAAKLAAL; FQDKLAAKLAALK; QDKLAAKLAALKA; DKLAAKLAALKAA; KLAAKLAALKAAK; LAAKLAALKAAKN; AAKLAALKAAKNT; AKLAALKAAKNTI; KLAALKAAKNTIE; LAALKAAKNTIEN; AALKAAKNTIENI; ALKAAKNTIENIT; LKAAKNTIENITD; KAAKNTIENITDK; AAKNTIENITDKD; AKNTIENITDKDQ; KNTIENITDKDQD; NTIENITDKDQDI; TIENITDKDQDIS; IENITDKDQDISK; ENITDKDQDISKR; NITDKDQDISKRK; ITDKDQDISKRKI; TDKDQDISKRKIW; DKDQDISKRKIWS; KDQDISKRKIWSE; DQDISKRKIWSEA; QDISKRKIWSEAK; DISKRKIWSEAKL; ISKRKIWSEAKLV; SKRKIWSEAKLVG; KRKIWSEAKLVGV; RKIWSEAKLVGVT; KIWSEAKLVGVTV; IWSEAKLVGVTVP; WSEAKLVGVTVPL; SEAKLVGVTVPLL; EAKLVGVTVPLLG; AKLVGVTVPLLGS; KLVGVTVPLLGSN; LVGVTVPLLGSNT; VGVTVPLLGSNTS; GVTVPLLGSNTSG; VTVPLLGSNTSGN; TVPLLGSNTSGNG; VPLLGSNTSGNGD; PLLGSNTSGNGDK; LLGSNTSGNGDKM; LGSNTSGNGDKMS; GSNTSGNGDKMSK; SNTSGNGDKMSKN; NTSGNGDKMSKNA; TSGNGDKMSKNAV; SGNGDKMSKNAVE; GNGDKMSKNAVEQ; NGDKMSKNAVEQI; GDKMSKNAVEQID; DKMSKNAVEQIDK;

	KMSKNAVEQIDKV; MSKNAVEQIDKVI; SKNAVEQIDKVIK; KNAVEQIDKVIKF; NAVEQIDKVIKFL; AVEQIDKVIKFLE; VEQIDKVIKFLEE; EQIDKVIKFLEEG; QIDKVIKFLEEGT; IDKVIKFLEEGTN; 14 mers: MRNKNIFKLFFASM; RNKNIFKLFFASML; NKNIFKLFFASMLF; KNIFKLFFASMLFV; NIFKLFFASMLFVM; IFKLFFASMLFVMA; FKLFFASMLFVMAC; KLFFASMLFVMACK; LFFASMLFVMACKA; FFASMLFVMACKAY; FASMLFVMACKAYV; ASMLFVMACKAYVE; SMLFVMACKAYVEE; MLFVMACKAYVEEK; LFVMACKAYVEEKK; FVMACKAYVEEKKE; VMACKAYVEEKKEI; MACKAYVEEKKEID; ACKAYVEEKKEIDS; CKAYVEEKKEIDSL; KAYVEEKKEIDSLM; AYVEEKKEIDSLME; YVEEKKEIDSLMED; VEEKKEIDSLMEDV; EEKKEIDSLMEDVL; EKKEIDSLMEDVLA; KKEIDSLMEDVLAL; KEIDSLMEDVLALV; EIDSLMEDVLALVN; IDSLMEDVLALVND; DSLMEDVLALVNDS; SLMEDVLALVNDSS; LMEDVLALVNDSSG; MEDVLALVNDSSGG; EDVLALVNDSSGGK; DVLALVNDSSGGKF; VLALVNDSSGGKFK; LALVNDSSGGKFKD; ALVNDSSGGKFKDY; LVNDSSGGKFKDYK; VNDSSGGKFKDYKD; NDSSGGKFKDYKDK; DSSGGKFKDYKDKI; SSGGKFKDYKDKIN; SGGKFKDYKDKINE; GGKFKDYKDKINEL; GKFKDYKDKINELK; KFKDYKDKINELKE; FKDYKDKINELKEN; KDYKDKINELKENL; DYKDKINELKENLK; YKDKINELKENLKD; KDKINELKENLKDI; DKINELKENLKDIG; KINELKENLKDIGN; INELKENLKDIGNA; NELKENLKDIGNAE; ELKENLKDIGNAEL; LKENLKDIGNAELK; KENLKDIGNAELKE; ENLKDIGNAELKEK; NLKDIGNAELKEKL; LKDIGNAELKEKLL; KDIGNAELKEKLLN; DIGNAELKEKLLNL; IGNAELKEKLLNLQ; GNAELKEKLLNLQN; NAELKEKLLNLQNS; AELKEKLLNLQNSF; ELKEKLLNLQNSFQ; LKEKLLNLQNSFQD; KEKLLNLQNSFQDK; EKLLNLQNSFQDKL; KLLNLQNSFQDKLA; LLNLQNSFQDKLAA; LNLQNSFQDKLAAK; NLQNSFQDKLAAKL; LQNSFQDKLAAKLA; QNSFQDKLAAKLAA; NSFQDKLAAKLAAL; SFQDKLAAKLAALK; FQDKLAAKLAALKA; QDKLAAKLAALKAA; DKLAAKLAALKAAK; KLAAKLAALKAAKN; LAAKLAALKAAKNT; AAKLAALKAAKNTI; AKLAALKAAKNTIE; KLAALKAAKNTIEN; LAALKAAKNTIENI; AALKAAKNTIENIT; ALKAAKNTIENITD; LKAAKNTIENITDK; KAAKNTIENITDKD; AAKNTIENITDKDQ; AKNTIENITDKDQD; KNTIENITDKDQDI; NTIENITDKDQDIS; TIENITDKDQDISK; IENITDKDQDISKR; ENITDKDQDISKRK; NITDKDQDISKRKI; ITDKDQDISKRKIW; TDKDQDISKRKIWS; DKDQDISKRKIWSE; KDQDISKRKIWSEA; DQDISKRKIWSEAK; QDISKRKIWSEAKL; DISKRKIWSEAKLV; ISKRKIWSEAKLVG; SKRKIWSEAKLVGV; KRKIWSEAKLVGVT; RKIWSEAKLVGVTV; KIWSEAKLVGVTVP; IWSEAKLVGVTVPL; WSEAKLVGVTVPLL; SEAKLVGVTVPLLG; EAKLVGVTVPLLGS; AKLVGVTVPLLGSN; KLVGVTVPLLGSNT; LVGVTVPLLGSNTS; VGVTVPLLGSNTSG; GVTVPLLGSNTSGN; VTVPLLGSNTSGNG; TVPLLGSNTSGNGD; VPLLGSNTSGNGDK; PLLGSNTSGNGDKM; LLGSNTSGNGDKMS; LGSNTSGNGDKMSK; GSNTSGNGDKMSKN; SNTSGNGDKMSKNA; NTSGNGDKMSKNAV; TSGNGDKMSKNAVE; SGNGDKMSKNAVEQ; GNGDKMSKNAVEQI;

	NGDKMSKNAVEQID; GDKMSKNAVEQIDK; DKMSKNAVEQIDKV; KMSKNAVEQIDKVI; MSKNAVEQIDKVIK; SKNAVEQIDKVIKF; KNAVEQIDKVIKFL; NAVEQIDKVIKFLE; AVEQIDKVIKFLEE; VEQIDKVIKFLEEG; EQIDKVIKFLEEGT; QIDKVIKFLEEGTN; 15 mers: MRNKNIFKLFFASML; RNKNIFKLFFASMLF; NKNIFKLFFASMLFV; KNIFKLFFASMLFVM; NIFKLFFASMLFVMA; IFKLFFASMLFVMAC; FKLFFASMLFVMACK; KLFFASMLFVMACKA; LFFASMLFVMACKAY; FFASMLFVMACKAYV; FASMLFVMACKAYVE; ASMLFVMACKAYVEE; SMLFVMACKAYVEEK; MLFVMACKAYVEEKK; LFVMACKAYVEEKKE; FVMACKAYVEEKKEI; VMACKAYVEEKKEID; MACKAYVEEKKEIDS; ACKAYVEEKKEIDSL; CKAYVEEKKEIDSLM; KAYVEEKKEIDSLME; AYVEEKKEIDSLMED; YVEEKKEIDSLMEDV; VEEKKEIDSLMEDVL; EEKKEIDSLMEDVLA; EKKEIDSLMEDVLAL; KKEIDSLMEDVLALV; KEIDSLMEDVLALVN; EIDSLMEDVLALVND; IDSLMEDVLALVNDS; DSLMEDVLALVNDSS; SLMEDVLALVNDSSG; LMEDVLALVNDSSGG; MEDVLALVNDSSGGK; EDVLALVNDSSGGKF; DVLALVNDSSGGKFK; VLALVNDSSGGKFKD; LALVNDSSGGKFKDY; ALVNDSSGGKFKDYK; LVNDSSGGKFKDYKD; VNDSSGGKFKDYKDK; NDSSGGKFKDYKDKI; DSSGGKFKDYKDKIN; SSGGKFKDYKDKINE; SGGKFKDYKDKINEL; GGKFKDYKDKINELK; GKFKDYKDKINELKE; KFKDYKDKINELKEN; FKDYKDKINELKENL; KDYKDKINELKENLK; DYKDKINELKENLKD; YKDKINELKENLKDI; KDKINELKENLKDIG; DKINELKENLKDIGN; KINELKENLKDIGNA; INELKENLKDIGNAE; NELKENLKDIGNAEL; ELKENLKDIGNAELK; LKENLKDIGNAELKE; KENLKDIGNAELKEK; ENLKDIGNAELKEKL; NLKDIGNAELKEKLL; LKDIGNAELKEKLLN; KDIGNAELKEKLLNL; DIGNAELKEKLLNLQ; IGNAELKEKLLNLQN; GNAELKEKLLNLQNS; NAELKEKLLNLQNSF; AELKEKLLNLQNSFQ; ELKEKLLNLQNSFQD; LKEKLLNLQNSFQDK; KEKLLNLQNSFQDKL; EKLLNLQNSFQDKLA; KLLNLQNSFQDKLAA; LLNLQNSFQDKLAAK; LNLQNSFQDKLAAKL; NLQNSFQDKLAAKLA; LQNSFQDKLAAKLAA; QNSFQDKLAAKLAAL; NSFQDKLAAKLAALK; SFQDKLAAKLAALKA; FQDKLAAKLAALKAA; QDKLAAKLAALKAAK; DKLAAKLAALKAAKN; KLAAKLAALKAAKNT; LAAKLAALKAAKNTI; AAKLAALKAAKNTIE; AKLAALKAAKNTIEN; KLAALKAAKNTIENI; LAALKAAKNTIENIT; AALKAAKNTIENITD; ALKAAKNTIENITDK; LKAAKNTIENITDKD; KAAKNTIENITDKDQ; AAKNTIENITDKDQD; AKNTIENITDKDQDI; KNTIENITDKDQDIS; NTIENITDKDQDISK; TIENITDKDQDISKR; IENITDKDQDISKRK; ENITDKDQDISKRKI; NITDKDQDISKRKIW; ITDKDQDISKRKIWS; TDKDQDISKRKIWSE; DKDQDISKRKIWSEA; KDQDISKRKIWSEAK; DQDISKRKIWSEAKL; QDISKRKIWSEAKLV; DISKRKIWSEAKLVG; ISKRKIWSEAKLVGV; SKRKIWSEAKLVGVT; KRKIWSEAKLVGVTV; RKIWSEAKLVGVTVP; KIWSEAKLVGVTVPL; IWSEAKLVGVTVPLL; WSEAKLVGVTVPLLG; SEAKLVGVTVPLLGS; EAKLVGVTVPLLGSN; AKLVGVTVPLLGSNT; KLVGVTVPLLGSNTS; LVGVTVPLLGSNTSG; VGVTVPLLGSNTSGN; GVTVPLLGSNTSGNG; VTVPLLGSNTSGNGD; TVPLLGSNTSGNGDK; VPLLGSNTSGNGDKM; PLLGSNTSGNGDKMS; LLGSNTSGNGDKMSK; LGSNTSGNGDKMSKN; GSNTSGNGDKMSKNA; SNTSGNGDKMSKNAV; NTSGNGDKMSKNAVE; TSGNGDKMSKNAVEQ; SGNGDKMSKNAVEQI; GNGDKMSKNAVEQID;

	NGDKMSKNAVEQIDK; GDKMSKNAVEQIDKV; DKMSKNAVEQIDKVI; KMSKNAVEQIDKVIK; MSKNAVEQIDKVIKF; SKNAVEQIDKVIKFL; KNAVEQIDKVIKFLE; NAVEQIDKVIKFLEE; AVEQIDKVIKFLEEG; VEQIDKVIKFLEEGT; EQIDKVIKFLEEGTN; 16 mers: MRNKNIFKLFFASMLF; RNKNIFKLFFASMLFV; NKNIFKLFFASMLFVM; KNIFKLFFASMLFVMA; NIFKLFFASMLFVMAC; IFKLFFASMLFVMACK; FKLFFASMLFVMACKA; KLFFASMLFVMACKAY; LFFASMLFVMACKAYV; FFASMLFVMACKAYVE; FASMLFVMACKAYVEE; ASMLFVMACKAYVEEK; SMLFVMACKAYVEEKK; MLFVMACKAYVEEKKE; LFVMACKAYVEEKKEI; FVMACKAYVEEKKEID; VMACKAYVEEKKEIDS; MACKAYVEEKKEIDSL; ACKAYVEEKKEIDSLM; CKAYVEEKKEIDSLME; KAYVEEKKEIDSLMED; AYVEEKKEIDSLMEDV; YVEEKKEIDSLMEDVL; VEEKKEIDSLMEDVLA; EEKKEIDSLMEDVLAL; EKKEIDSLMEDVLALV; KKEIDSLMEDVLALVN; KEIDSLMEDVLALVND; EIDSLMEDVLALVNDS; IDSLMEDVLALVNDSS; DSLMEDVLALVNDSSG; SLMEDVLALVNDSSGG; LMEDVLALVNDSSGGK; MEDVLALVNDSSGGKF; EDVLALVNDSSGGKFK; DVLALVNDSSGGKFKD; VLALVNDSSGGKFKDY; LALVNDSSGGKFKDYK; ALVNDSSGGKFKDYKD; LVNDSSGGKFKDYKDK; VNDSSGGKFKDYKDKI; NDSSGGKFKDYKDKIN; DSSGGKFKDYKDKINE; SSGGKFKDYKDKINEL; SGGKFKDYKDKINELK; GGKFKDYKDKINELKE; GKFKDYKDKINELKEN; KFKDYKDKINELKENL; FKDYKDKINELKENLK; KDYKDKINELKENLKD; DYKDKINELKENLKDI; YKDKINELKENLKDIG; KDKINELKENLKDIGN; DKINELKENLKDIGNA; KINELKENLKDIGNAE; INELKENLKDIGNAEL; NELKENLKDIGNAELK; ELKENLKDIGNAELKE; LKENLKDIGNAELKEK; KENLKDIGNAELKEKL; ENLKDIGNAELKEKLL; NLKDIGNAELKEKLLN; LKDIGNAELKEKLLNL; KDIGNAELKEKLLNLQ; DIGNAELKEKLLNLQN; IGNAELKEKLLNLQNS; GNAELKEKLLNLQNSF; NAELKEKLLNLQNSFQ; AELKEKLLNLQNSFQD; ELKEKLLNLQNSFQDK; LKEKLLNLQNSFQDKL; KEKLLNLQNSFQDKLA; EKLLNLQNSFQDKLAA; KLLNLQNSFQDKLAAK; LLNLQNSFQDKLAAKL; LNLQNSFQDKLAAKLA; NLQNSFQDKLAAKLAA; LQNSFQDKLAAKLAAL; QNSFQDKLAAKLAALK; NSFQDKLAAKLAALKA; SFQDKLAAKLAALKAA; FQDKLAAKLAALKAAK; QDKLAAKLAALKAAKN; DKLAAKLAALKAAKNT; KLAAKLAALKAAKNTI; LAAKLAALKAAKNTIE; AAKLAALKAAKNTIEN; AKLAALKAAKNTIENI; KLAALKAAKNTIENIT; LAALKAAKNTIENITD; AALKAAKNTIENITDK; ALKAAKNTIENITDKD; LKAAKNTIENITDKDQ; KAAKNTIENITDKDQD; AAKNTIENITDKDQDI; AKNTIENITDKDQDIS; KNTIENITDKDQDISK; NTIENITDKDQDISKR; TIENITDKDQDISKRK; IENITDKDQDISKRKI; ENITDKDQDISKRKIW; NITDKDQDISKRKIWS; ITDKDQDISKRKIWSE; TDKDQDISKRKIWSEA; DKDQDISKRKIWSEAK; KDQDISKRKIWSEAKL; DQDISKRKIWSEAKLV; QDISKRKIWSEAKLVG; DISKRKIWSEAKLVGV; ISKRKIWSEAKLVGVT; SKRKIWSEAKLVGVTV; KRKIWSEAKLVGVTVP; RKIWSEAKLVGVTVPL; KIWSEAKLVGVTVPLL; IWSEAKLVGVTVPLLG; WSEAKLVGVTVPLLGS; SEAKLVGVTVPLLGSN; EAKLVGVTVPLLGSNT; AKLVGVTVPLLGSNTS; KLVGVTVPLLGSNTSG; LVGVTVPLLGSNTSGN; VGVTVPLLGSNTSGNG; GVTVPLLGSNTSGNGD; VTVPLLGSNTSGNGDK; TVPLLGSNTSGNGDKM; VPLLGSNTSGNGDKMS; PLLGSNTSGNGDKMSK; LLGSNTSGNGDKMSKN; LGSNTSGNGDKMSKNA; GSNTSGNGDKMSKNAV; SNTSGNGDKMSKNAVE; NTSGNGDKMSKNAVEQ; TSGNGDKMSKNAVEQI; SGNGDKMSKNAVEQID; GNGDKMSKNAVEQIDK;

	NGDKMSKNAVEQIDKV; GDKMSKNAVEQIDKVI; DKMSKNAVEQIDKVIK; KMSKNAVEQIDKVIKF; MSKNAVEQIDKVIKFL; SKNAVEQIDKVIKFLE; KNAVEQIDKVIKFLEE; NAVEQIDKVIKFLEEG; AVEQIDKVIKFLEEGT; VEQIDKVIKFLEEGTN;
Seq 40	13 mers: MKDNILKNNKLIA; KDNILKNNKLIAI; DNILKNNKLIAIF; NILKNNKLIAIFL; ILKNNKLIAIFLL; LKNNKLIAIFLLH; KNNKLIAIFLLHV; NNKLIAIFLLHVL; NKLIAIFLLHVLT; KLIAIFLLHVLTV; LIAIFLLHVLTVL; IAIFLLHVLTVLI; AIFLLHVLTVLIL; IFLLHVLTVLILI; FLLHVLTVLILIS; LLHVLTVLILISC; LHVLTVLILISCS; HVLTVLILISCSL; VLTVLILISCSLE; LTVLILISCSLEV; TVLILISCSLEVK; VLILISCSLEVKD; LILISCSLEVKDS; ILISCSLEVKDSN; LISCSLEVKDSNE; ISCSLEVKDSNES; SCSLEVKDSNESK; CSLEVKDSNESKK; SLEVKDSNESKKH; LEVKDSNESKKHK; EVKDSNESKKHKK; VKDSNESKKHKKE; KDSNESKKHKKEK; DSNESKKHKKEKR; SNESKKHKKEKRK; NESKKHKKEKRKG; ESKKHKKEKRKGK; SKKHKKEKRKGKV; KKHKKEKRKGKVE; KHKKEKRKGKVEN; HKKEKRKGKVENL; KKEKRKGKVENLL; KEKRKGKVENLLV; EKRKGKVENLLVA; KRKGKVENLLVAI; RKGKVENLLVAIN; KGKVENLLVAINN; GKVENLLVAINNL; KVENLLVAINNLK; VENLLVAINNLKN; ENLLVAINNLKNP; NLLVAINNLKNPT; LLVAINNLKNPTK; LVAINNLKNPTKP; VAINNLKNPTKPA; AINNLKNPTKPAA; INNLKNPTKPAAG; NNLKNPTKPAAGK; NLKNPTKPAAGKN; LKNPTKPAAGKNK; KNPTKPAAGKNKA; NPTKPAAGKNKAN; PTKPAAGKNKANS; TKPAAGKNKANSK; KPAAGKNKANSKA; PAAGKNKANSKAS; AAGKNKANSKASK; AGKNKANSKASKQ; GKNKANSKASKQK; KNKANSKASKQKN; NKANSKASKQKNN; KANSKASKQKNNP; ANSKASKQKNNPN; NSKASKQKNNPNA; SKASKQKNNPNAN; KASKQKNNPNANA; ASKQKNNPNANAN; SKQKNNPNANANN; KQKNNPNANANNA; QKNNPNANANNAP; KNNPNANANNAPK; NNPNANANNAPKK; NPNANANNAPKKI; PNANANNAPKKIL; NANANNAPKKILD; ANANNAPKKILDP; NANNAPKKILDPE; ANNAPKKILDPEV; NNAPKKILDPEVA; NAPKKILDPEVAK; APKKILDPEVAKL; PKKILDPEVAKLI; KKILDPEVAKLIQ; KILDPEVAKLIQK; ILDPEVAKLIQKI; LDPEVAKLIQKIL; DPEVAKLIQKILD; PEVAKLIQKILDR; EVAKLIQKILDRS; VAKLIQKILDRSE; AKLIQKILDRSEN; KLIQKILDRSENI; LIQKILDRSENII; IQKILDRSENIIQ; QKILDRSENIIQI; KILDRSENIIQIS; ILDRSENIIQISE; LDRSENIIQISEM; DRSENIIQISEMD; RSENIIQISEMDS; SENIIQISEMDSS; ENIIQISEMDSSR; NIIQISEMDSSRG; IIQISEMDSSRGE; IQISEMDSSRGEP; QISEMDSSRGEPN; ISEMDSSRGEPND; SEMDSSRGEPNDQ; EMDSSRGEPNDQF; MDSSRGEPNDQFG; DSSRGEPNDQFGM; SSRGEPNDQFGMR; SRGEPNDQFGMRA; RGEPNDQFGMRAE; GEPNDQFGMRAEI; EPNDQFGMRAEIF; PNDQFGMRAEIFS; NDQFGMRAEIFSK; DQFGMRAEIFSKI; QFGMRAEIFSKIF; FGMRAEIFSKIFF; GMRAEIFSKIFFN;

	MRAEIFSKIFFNA; RAEIFSKIFFNAN; AEIFSKIFFNANS; EIFSKIFFNANST; IFSKIFFNANSTV; FSKIFFNANSTVH; SKIFFNANSTVHF; KIFFNANSTVHFD; IFFNANSTVHFDS; FFNANSTVHFDSH; FNANSTVHFDSHE; NANSTVHFDSHEY; ANSTVHFDSHEYT; NSTVHFDSHEYTE; STVHFDSHEYTEE; TVHFDSHEYTEER; VHFDSHEYTEERR; HFDSHEYTEERRM; FDSHEYTEERRML; DSHEYTEERRMLY; SHEYTEERRMLYT; HEYTEERRMLYTS; EYTEERRMLYTSL; YTEERRMLYTSLN; TEERRMLYTSLNF; EERRMLYTSLNFN; ERRMLYTSLNFNE; RRMLYTSLNFNEG; RMLYTSLNFNEGK; MLYTSLNFNEGKI; LYTSLNFNEGKIF; YTSLNFNEGKIFN; TSLNFNEGKIFNL; SLNFNEGKIFNLG; LNFNEGKIFNLGQ; NFNEGKIFNLGQI; FNEGKIFNLGQIL; NEGKIFNLGQILS; EGKIFNLGQILSK; GKIFNLGQILSKL; KIFNLGQILSKLS; IFNLGQILSKLSQ; FNLGQILSKLSQD; NLGQILSKLSQDS; LGQILSKLSQDSN; GQILSKLSQDSNY; QILSKLSQDSNYR; ILSKLSQDSNYRG; LSKLSQDSNYRGL; SKLSQDSNYRGLV; KLSQDSNYRGLVK; LSQDSNYRGLVKE; SQDSNYRGLVKET; QDSNYRGLVKETL; DSNYRGLVKETLI; SNYRGLVKETLIN; NYRGLVKETLINR; YRGLVKETLINRG; RGLVKETLINRGF; GLVKETLINRGFS; LVKETLINRGFSI; VKETLINRGFSIQ; KETLINRGFSIQL; ETLINRGFSIQLA; TLINRGFSIQLAM; LINRGFSIQLAME; INRGFSIQLAMEE; NRGFSIQLAMEEI; RGFSIQLAMEEIS; GFSIQLAMEEISA; FSIQLAMEEISAK; SIQLAMEEISAKI; IQLAMEEISAKIL; QLAMEEISAKILN; LAMEEISAKILNV; AMEEISAKILNVK; MEEISAKILNVKD; EEISAKILNVKDK; EISAKILNVKDKL; ISAKILNVKDKLQ; SAKILNVKDKLQQ; AKILNVKDKLQQL; KILNVKDKLQQLN; ILNVKDKLQQLNK; LNVKDKLQQLNKP; NVKDKLQQLNKPN; VKDKLQQLNKPNL; KDKLQQLNKPNLE; DKLQQLNKPNLET; KLQQLNKPNLETL; LQQLNKPNLETLY; QQLNKPNLETLYN; QLNKPNLETLYND; LNKPNLETLYNDF; NKPNLETLYNDFE; KPNLETLYNDFEK; PNLETLYNDFEKL; NLETLYNDFEKLT; LETLYNDFEKLTS; ETLYNDFEKLTSL; TLYNDFEKLTSLK; LYNDFEKLTSLKE; YNDFEKLTSLKEK; NDFEKLTSLKEKW; DFEKLTSLKEKWL; FEKLTSLKEKWLK; EKLTSLKEKWLKD; KLTSLKEKWLKDT; LTSLKEKWLKDTD; TSLKEKWLKDTDD; SLKEKWLKDTDDL; LKEKWLKDTDDLI; KEKWLKDTDDLID; EKWLKDTDDLIDE; KWLKDTDDLIDEY; WLKDTDDLIDEYN; LKDTDDLIDEYNT; KDTDDLIDEYNTN; DTDDLIDEYNTNP; TDDLIDEYNTNPD; DDLIDEYNTNPDL; DLIDEYNTNPDLQ; LIDEYNTNPDLQT; IDEYNTNPDLQTD; DEYNTNPDLQTDV; EYNTNPDLQTDVS; YNTNPDLQTDVSK; NTNPDLQTDVSKL; TNPDLQTDVSKLN; NPDLQTDVSKLND; PDLQTDVSKLNDT; DLQTDVSKLNDTL; LQTDVSKLNDTLR; QTDVSKLNDTLRS; TDVSKLNDTLRSK; DVSKLNDTLRSKN; VSKLNDTLRSKNS; SKLNDTLRSKNSR; KLNDTLRSKNSRA; LNDTLRSKNSRAQ; NDTLRSKNSRAQF; DTLRSKNSRAQFA; TLRSKNSRAQFAN; LRSKNSRAQFANI; RSKNSRAQFANIH; SKNSRAQFANIHD; KNSRAQFANIHDI; NSRAQFANIHDII; SRAQFANIHDIIL; RAQFANIHDIILD; AQFANIHDIILDL; QFANIHDIILDLV; FANIHDIILDLVN;

ANIHDIILDLVNT; NIHDIILDLVNTT; IHDIILDLVNTTT;
HDIILDLVNTTTN; DIILDLVNTTTNI; IILDLVNTTTNIL;
ILDLVNTTTNILA; LDLVNTTTNILAP; DLVNTTTNILAPI;
LVNTTTNILAPIQ;

14 mers:
MKDNILKNNKLIAI; KDNILKNNKLIAIF; DNILKNNKLIAIFL;
NILKNNKLIAIFLL; ILKNNKLIAIFLLH; LKNNKLIAIFLLHV;
KNNKLIAIFLLHVL; NNKLIAIFLLHVLT; NKLIAIFLLHVLTV;
KLIAIFLLHVLTVL; LIAIFLLHVLTVLI; IAIFLLHVLTVLIL;
AIFLLHVLTVLILI; IFLLHVLTVLILIS; FLLHVLTVLILISC;
LLHVLTVLILISCS; LHVLTVLILISCSL; HVLTVLILISCSLE;
VLTVLILISCSLEV; LTVLILISCSLEVK; TVLILISCSLEVKD;
VLILISCSLEVKDS; LILISCSLEVKDSN; ILISCSLEVKDSNE;
LISCSLEVKDSNES; ISCSLEVKDSNESK; SCSLEVKDSNESKK;
CSLEVKDSNESKKH; SLEVKDSNESKKHK; LEVKDSNESKKHKK;
EVKDSNESKKHKKE; VKDSNESKKHKKEK; KDSNESKKHKKEKR;
DSNESKKHKKEKRK; SNESKKHKKEKRKG; NESKKHKKEKRKGK;
ESKKHKKEKRKGKV; SKKHKKEKRKGKVE; KKHKKEKRKGKVEN;
KHKKEKRKGKVENL; HKKEKRKGKVENLL; KKEKRKGKVENLLV;
KEKRKGKVENLLVA; EKRKGKVENLLVAI; KRKGKVENLLVAIN;
RKGKVENLLVAINN; KGKVENLLVAINNL; GKVENLLVAINNLK;
KVENLLVAINNLKN; VENLLVAINNLKNP; ENLLVAINNLKNPT;
NLLVAINNLKNPTK; LLVAINNLKNPTKP; LVAINNLKNPTKPA;
VAINNLKNPTKPAA; AINNLKNPTKPAAG; INNLKNPTKPAAGK;
NNLKNPTKPAAGKN; NLKNPTKPAAGKNK; LKNPTKPAAGKNKA;
KNPTKPAAGKNKAN; NPTKPAAGKNKANS; PTKPAAGKNKANSK;
TKPAAGKNKANSKA; KPAAGKNKANSKAS; PAAGKNKANSKASK;
AAGKNKANSKASKQ; AGKNKANSKASKQK; GKNKANSKASKQKN;
KNKANSKASKQKNN; NKANSKASKQKNNP; KANSKASKQKNNPN;
ANSKASKQKNNPNA; NSKASKQKNNPNAN; SKASKQKNNPNANA;
KASKQKNNPNANAN; ASKQKNNPNANANN; SKQKNNPNANANNA;
KQKNNPNANANNAP; QKNNPNANANNAPK; KNNPNANANNAPKK;
NNPNANANNAPKKI; NPNANANNAPKKIL; PNANANNAPKKILD;
NANANNAPKKILDP; ANANNAPKKILDPE; NANNAPKKILDPEV;
ANNAPKKILDPEVA; NNAPKKILDPEVAK; NAPKKILDPEVAKL;
APKKILDPEVAKLI; PKKILDPEVAKLIQ; KKILDPEVAKLIQK;
KILDPEVAKLIQKI; ILDPEVAKLIQKIL; LDPEVAKLIQKILD;
DPEVAKLIQKILDR; PEVAKLIQKILDRS; EVAKLIQKILDRSE;
VAKLIQKILDRSEN; AKLIQKILDRSENI; KLIQKILDRSENII;
LIQKILDRSENIIQ; IQKILDRSENIIQI; QKILDRSENIIQIS;
KILDRSENIIQISE; ILDRSENIIQISEM; LDRSENIIQISEMD;
DRSENIIQISEMDS; RSENIIQISEMDSS; SENIIQISEMDSSR;
ENIIQISEMDSSRG; NIIQISEMDSSRGE; IIQISEMDSSRGEP;
IQISEMDSSRGEPN; QISEMDSSRGEPND; ISEMDSSRGEPNDQ;
SEMDSSRGEPNDQF; EMDSSRGEPNDQFG; MDSSRGEPNDQFGM;
DSSRGEPNDQFGMR; SSRGEPNDQFGMRA; SRGEPNDQFGMRAE;
RGEPNDQFGMRAEI; GEPNDQFGMRAEIF; EPNDQFGMRAEIFS;
PNDQFGMRAEIFSK; NDQFGMRAEIFSKI; DQFGMRAEIFSKIF;
QFGMRAEIFSKIFF; FGMRAEIFSKIFFN; GMRAEIFSKIFFNA;
MRAEIFSKIFFNAN; RAEIFSKIFFNANS; AEIFSKIFFNANST;

	EIFSKIFFNANSTV; IFSKIFFNANSTVH; FSKIFFNANSTVHF; SKIFFNANSTVHFD; KIFFNANSTVHFDS; IFFNANSTVHFDSH; FFNANSTVHFDSHE; FNANSTVHFDSHEY; NANSTVHFDSHEYT; ANSTVHFDSHEYTE; NSTVHFDSHEYTEE; STVHFDSHEYTEER; TVHFDSHEYTEERR; VHFDSHEYTEERRM; HFDSHEYTEERRML; FDSHEYTEERRMLY; DSHEYTEERRMLYT; SHEYTEERRMLYTS; HEYTEERRMLYTSL; EYTEERRMLYTSLN; YTEERRMLYTSLNF; TEERRMLYTSLNFN; EERRMLYTSLNFNE; ERRMLYTSLNFNEG; RRMLYTSLNFNEGK; RMLYTSLNFNEGKI; MLYTSLNFNEGKIF; LYTSLNFNEGKIFN; YTSLNFNEGKIFNL; TSLNFNEGKIFNLG; SLNFNEGKIFNLGQ; LNFNEGKIFNLGQI; NFNEGKIFNLGQIL; FNEGKIFNLGQILS; NEGKIFNLGQILSK; EGKIFNLGQILSKL; GKIFNLGQILSKLS; KIFNLGQILSKLSQ; IFNLGQILSKLSQD; FNLGQILSKLSQDS; NLGQILSKLSQDSN; LGQILSKLSQDSNY; GQILSKLSQDSNYR; QILSKLSQDSNYRG; ILSKLSQDSNYRGL; LSKLSQDSNYRGLV; SKLSQDSNYRGLVK; KLSQDSNYRGLVKE; LSQDSNYRGLVKET; SQDSNYRGLVKETL; QDSNYRGLVKETLI; DSNYRGLVKETLIN; SNYRGLVKETLINR; NYRGLVKETLINRG; YRGLVKETLINRGF; RGLVKETLINRGFS; GLVKETLINRGFSI; LVKETLINRGFSIQ; VKETLINRGFSIQL; KETLINRGFSIQLA; ETLINRGFSIQLAM; TLINRGFSIQLAME; LINRGFSIQLAMEE; INRGFSIQLAMEEI; NRGFSIQLAMEEIS; RGFSIQLAMEEISA; GFSIQLAMEEISAK; FSIQLAMEEISAKI; SIQLAMEEISAKIL; IQLAMEEISAKILN; QLAMEEISAKILNV; LAMEEISAKILNVK; AMEEISAKILNVKD; MEEISAKILNVKDK; EEISAKILNVKDKL; EISAKILNVKDKLQ; ISAKILNVKDKLQQ; SAKILNVKDKLQQL; AKILNVKDKLQQLN; KILNVKDKLQQLNK; ILNVKDKLQQLNKP; LNVKDKLQQLNKPN; NVKDKLQQLNKPNL; VKDKLQQLNKPNLE; KDKLQQLNKPNLET; DKLQQLNKPNLETL; KLQQLNKPNLETLY; LQQLNKPNLETLYN; QQLNKPNLETLYND; QLNKPNLETLYNDF; LNKPNLETLYNDFE; NKPNLETLYNDFEK; KPNLETLYNDFEKL; PNLETLYNDFEKLT; NLETLYNDFEKLTS; LETLYNDFEKLTSL; ETLYNDFEKLTSLK; TLYNDFEKLTSLKE; LYNDFEKLTSLKEK; YNDFEKLTSLKEKW; NDFEKLTSLKEKWL; DFEKLTSLKEKWLK; FEKLTSLKEKWLKD; EKLTSLKEKWLKDT; KLTSLKEKWLKDTD; LTSLKEKWLKDTDD; TSLKEKWLKDTDDL; SLKEKWLKDTDDLI; LKEKWLKDTDDLID; KEKWLKDTDDLIDE; EKWLKDTDDLIDEY; KWLKDTDDLIDEYN; WLKDTDDLIDEYNT; LKDTDDLIDEYNTN; KDTDDLIDEYNTNP; DTDDLIDEYNTNPD; TDDLIDEYNTNPDL; DDLIDEYNTNPDLQ; DLIDEYNTNPDLQT; LIDEYNTNPDLQTD; IDEYNTNPDLQTDV; DEYNTNPDLQTDVS; EYNTNPDLQTDVSK; YNTNPDLQTDVSKL; NTNPDLQTDVSKLN; TNPDLQTDVSKLND; NPDLQTDVSKLNDT; PDLQTDVSKLNDTL; DLQTDVSKLNDTLR; LQTDVSKLNDTLRS; QTDVSKLNDTLRSK; TDVSKLNDTLRSKN; DVSKLNDTLRSKNS; VSKLNDTLRSKNSR; SKLNDTLRSKNSRA; KLNDTLRSKNSRAQ; LNDTLRSKNSRAQF; NDTLRSKNSRAQFA; DTLRSKNSRAQFAN; TLRSKNSRAQFANI; LRSKNSRAQFANIH; RSKNSRAQFANIHD; SKNSRAQFANIHDI; KNSRAQFANIHDII; NSRAQFANIHDIIL; SRAQFANIHDIILD; RAQFANIHDIILDL; AQFANIHDIILDLV; QFANIHDIILDLVN; FANIHDIILDLVNT; ANIHDIILDLVNTT; NIHDIILDLVNTTT; IHDIILDLVNTTTN;

	HDIILDLVNTTTNI; DIILDLVNTTTNIL; IILDLVNTTTNILA; ILDLVNTTTNILAP; LDLVNTTTNILAPI; DLVNTTTNILAPIQ; 15 mers: MKDNILKNNKLIAIF; KDNILKNNKLIAIFL; DNILKNNKLIAIFLL; NILKNNKLIAIFLLH; ILKNNKLIAIFLLHV; LKNNKLIAIFLLHVL; KNNKLIAIFLLHVLT; NNKLIAIFLLHVLTV; NKLIAIFLLHVLTVL; KLIAIFLLHVLTVLI; LIAIFLLHVLTVLIL; IAIFLLHVLTVLILI; AIFLLHVLTVLILIS; IFLLHVLTVLILISC; FLLHVLTVLILISCS; LLHVLTVLILISCSL; LHVLTVLILISCSLE; HVLTVLILISCSLEV; VLTVLILISCSLEVK; LTVLILISCSLEVKD; TVLILISCSLEVKDS; VLILISCSLEVKDSN; LILISCSLEVKDSNE; ILISCSLEVKDSNES; LISCSLEVKDSNESK; ISCSLEVKDSNESKK; SCSLEVKDSNESKKH; CSLEVKDSNESKKHK; SLEVKDSNESKKHKK; LEVKDSNESKKHKKE; EVKDSNESKKHKKEK; VKDSNESKKHKKEKR; KDSNESKKHKKEKRK; DSNESKKHKKEKRKG; SNESKKHKKEKRKGK; NESKKHKKEKRKGKV; ESKKHKKEKRKGKVE; SKKHKKEKRKGKVEN; KKHKKEKRKGKVENL; KHKKEKRKGKVENLL; HKKEKRKGKVENLLV; KKEKRKGKVENLLVA; KEKRKGKVENLLVAI; EKRKGKVENLLVAIN; KRKGKVENLLVAINN; RKGKVENLLVAINNL; KGKVENLLVAINNLK; GKVENLLVAINNLKN; KVENLLVAINNLKNP; VENLLVAINNLKNPT; ENLLVAINNLKNPTK; NLLVAINNLKNPTKP; LLVAINNLKNPTKPA; LVAINNLKNPTKPAA; VAINNLKNPTKPAAG; AINNLKNPTKPAAGK; INNLKNPTKPAAGKN; NNLKNPTKPAAGKNK; NLKNPTKPAAGKNKA; LKNPTKPAAGKNKAN; KNPTKPAAGKNKANS; NPTKPAAGKNKANSK; PTKPAAGKNKANSKA; TKPAAGKNKANSKAS; KPAAGKNKANSKASK; PAAGKNKANSKASKQ; AAGKNKANSKASKQK; AGKNKANSKASKQKN; GKNKANSKASKQKNN; KNKANSKASKQKNNP; NKANSKASKQKNNPN; KANSKASKQKNNPNA; ANSKASKQKNNPNAN; NSKASKQKNNPNANA; SKASKQKNNPNANAN; KASKQKNNPNANANN; ASKQKNNPNANANNA; SKQKNNPNANANNAP; KQKNNPNANANNAPK; QKNNPNANANNAPKK; KNNPNANANNAPKKI; NNPNANANNAPKKIL; NPNANANNAPKKILD; PNANANNAPKKILDP; NANANNAPKKILDPE; ANANNAPKKILDPEV; NANNAPKKILDPEVA; ANNAPKKILDPEVAK; NNAPKKILDPEVAKL; NAPKKILDPEVAKLI; APKKILDPEVAKLIQ; PKKILDPEVAKLIQK; KKILDPEVAKLIQKI; KILDPEVAKLIQKIL; ILDPEVAKLIQKILD; LDPEVAKLIQKILDR; DPEVAKLIQKILDRS; PEVAKLIQKILDRSE; EVAKLIQKILDRSEN; VAKLIQKILDRSENI; AKLIQKILDRSENII; KLIQKILDRSENIIQ; LIQKILDRSENIIQI; IQKILDRSENIIQIS; QKILDRSENIIQISE; KILDRSENIIQISEM; ILDRSENIIQISEMD; LDRSENIIQISEMDS; DRSENIIQISEMDSS; RSENIIQISEMDSSR; SENIIQISEMDSSRG; ENIIQISEMDSSRGE; NIIQISEMDSSRGEP; IIQISEMDSSRGEPN; IQISEMDSSRGEPND; QISEMDSSRGEPNDQ; ISEMDSSRGEPNDQF; SEMDSSRGEPNDQFG; EMDSSRGEPNDQFGM; MDSSRGEPNDQFGMR; DSSRGEPNDQFGMRA; SSRGEPNDQFGMRAE; SRGEPNDQFGMRAEI; RGEPNDQFGMRAEIF; GEPNDQFGMRAEIFS; EPNDQFGMRAEIFSK; PNDQFGMRAEIFSKI; NDQFGMRAEIFSKIF; DQFGMRAEIFSKIFF; QFGMRAEIFSKIFFN; FGMRAEIFSKIFFNA; GMRAEIFSKIFFNAN; MRAEIFSKIFFNANS; RAEIFSKIFFNANST; AEIFSKIFFNANSTV; EIFSKIFFNANSTVH; IFSKIFFNANSTVHF; FSKIFFNANSTVHFD; SKIFFNANSTVHFDS; KIFFNANSTVHFDSH; IFFNANSTVHFDSHE;

	FFNANSTVHFDSHEY; FNANSTVHFDSHEYT; NANSTVHFDSHEYTE; ANSTVHFDSHEYTEE; NSTVHFDSHEYTEER; STVHFDSHEYTEERR; TVHFDSHEYTEERRM; VHFDSHEYTEERRML; HFDSHEYTEERRMLY; FDSHEYTEERRMLYT; DSHEYTEERRMLYTS; SHEYTEERRMLYTSL; HEYTEERRMLYTSLN; EYTEERRMLYTSLNF; YTEERRMLYTSLNFN; TEERRMLYTSLNFNE; EERRMLYTSLNFNEG; ERRMLYTSLNFNEGK; RRMLYTSLNFNEGKI; RMLYTSLNFNEGKIF; MLYTSLNFNEGKIFN; LYTSLNFNEGKIFNL; YTSLNFNEGKIFNLG; TSLNFNEGKIFNLGQ; SLNFNEGKIFNLGQI; LNFNEGKIFNLGQIL; NFNEGKIFNLGQILS; FNEGKIFNLGQILSK; NEGKIFNLGQILSKL; EGKIFNLGQILSKLS; GKIFNLGQILSKLSQ; KIFNLGQILSKLSQD; IFNLGQILSKLSQDS; FNLGQILSKLSQDSN; NLGQILSKLSQDSNY; LGQILSKLSQDSNYR; GQILSKLSQDSNYRG; QILSKLSQDSNYRGL; ILSKLSQDSNYRGLV; LSKLSQDSNYRGLVK; SKLSQDSNYRGLVKE; KLSQDSNYRGLVKET; LSQDSNYRGLVKETL; SQDSNYRGLVKETLI; QDSNYRGLVKETLIN; DSNYRGLVKETLINR; SNYRGLVKETLINRG; NYRGLVKETLINRGF; YRGLVKETLINRGFS; RGLVKETLINRGFSI; GLVKETLINRGFSIQ; LVKETLINRGFSIQL; VKETLINRGFSIQLA; KETLINRGFSIQLAM; ETLINRGFSIQLAME; TLINRGFSIQLAMEE; LINRGFSIQLAMEEI; INRGFSIQLAMEEIS; NRGFSIQLAMEEISA; RGFSIQLAMEEISAK; GFSIQLAMEEISAKI; FSIQLAMEEISAKIL; SIQLAMEEISAKILN; IQLAMEEISAKILNV; QLAMEEISAKILNVK; LAMEEISAKILNVKD; AMEEISAKILNVKDK; MEEISAKILNVKDKL; EEISAKILNVKDKLQ; EISAKILNVKDKLQQ; ISAKILNVKDKLQQL; SAKILNVKDKLQQLN; AKILNVKDKLQQLNK; KILNVKDKLQQLNKP; ILNVKDKLQQLNKPN; LNVKDKLQQLNKPNL; NVKDKLQQLNKPNLE; VKDKLQQLNKPNLET; KDKLQQLNKPNLETL; DKLQQLNKPNLETLY; KLQQLNKPNLETLYN; LQQLNKPNLETLYND; QQLNKPNLETLYNDF; QLNKPNLETLYNDFE; LNKPNLETLYNDFEK; NKPNLETLYNDFEKL; KPNLETLYNDFEKLT; PNLETLYNDFEKLTS; NLETLYNDFEKLTSL; LETLYNDFEKLTSLK; ETLYNDFEKLTSLKE; TLYNDFEKLTSLKEK; LYNDFEKLTSLKEKW; YNDFEKLTSLKEKWL; NDFEKLTSLKEKWLK; DFEKLTSLKEKWLKD; FEKLTSLKEKWLKDT; EKLTSLKEKWLKDTD; KLTSLKEKWLKDTDD; LTSLKEKWLKDTDDL; TSLKEKWLKDTDDLI; SLKEKWLKDTDDLID; LKEKWLKDTDDLIDE; KEKWLKDTDDLIDEY; EKWLKDTDDLIDEYN; KWLKDTDDLIDEYNT; WLKDTDDLIDEYNTN; LKDTDDLIDEYNTNP; KDTDDLIDEYNTNPD; DTDDLIDEYNTNPDL; TDDLIDEYNTNPDLQ; DDLIDEYNTNPDLQT; DLIDEYNTNPDLQTD; LIDEYNTNPDLQTDV; IDEYNTNPDLQTDVS; DEYNTNPDLQTDVSK; EYNTNPDLQTDVSKL; YNTNPDLQTDVSKLN; NTNPDLQTDVSKLND; TNPDLQTDVSKLNDT; NPDLQTDVSKLNDTL; PDLQTDVSKLNDTLR; DLQTDVSKLNDTLRS; LQTDVSKLNDTLRSK; QTDVSKLNDTLRSKN; TDVSKLNDTLRSKNS; DVSKLNDTLRSKNSR; VSKLNDTLRSKNSRA; SKLNDTLRSKNSRAQ; KLNDTLRSKNSRAQF; LNDTLRSKNSRAQFA; NDTLRSKNSRAQFAN; DTLRSKNSRAQFANI; TLRSKNSRAQFANIH; LRSKNSRAQFANIHD; RSKNSRAQFANIHDI; SKNSRAQFANIHDII; KNSRAQFANIHDIIL; NSRAQFANIHDIILD; SRAQFANIHDIILDL; RAQFANIHDIILDLV; AQFANIHDIILDLVN; QFANIHDIILDLVNT; FANIHDIILDLVNTT; ANIHDIILDLVNTTT; NIHDIILDLVNTTTN; IHDIILDLVNTTTNI; HDIILDLVNTTTNIL; DIILDLVNTTTNILA; IILDLVNTTTNILAP; ILDLVNTTTNILAPI; LDLVNTTTNILAPIQ;

16 mers:
MKDNILKNNKLIAIFL; KDNILKNNKLIAIFLL; DNILKNNKLIAIFLLH;
NILKNNKLIAIFLLHV; ILKNNKLIAIFLLHVL; LKNNKLIAIFLLHVLT;
KNNKLIAIFLLHVLTV; NNKLIAIFLLHVLTVL; NKLIAIFLLHVLTVLI;
KLIAIFLLHVLTVLIL; LIAIFLLHVLTVLILI; IAIFLLHVLTVLILIS;
AIFLLHVLTVLILISC; IFLLHVLTVLILISCS; FLLHVLTVLILISCSL;
LLHVLTVLILISCSLE; LHVLTVLILISCSLEV; HVLTVLILISCSLEVK;
VLTVLILISCSLEVKD; LTVLILISCSLEVKDS; TVLILISCSLEVKDSN;
VLILISCSLEVKDSNE; LILISCSLEVKDSNES; ILISCSLEVKDSNESK;
LISCSLEVKDSNESKK; ISCSLEVKDSNESKKH; SCSLEVKDSNESKKHK;
CSLEVKDSNESKKHKK; SLEVKDSNESKKHKKE; LEVKDSNESKKHKKEK;
EVKDSNESKKHKKEKR; VKDSNESKKHKKEKRK; KDSNESKKHKKEKRKG;
DSNESKKHKKEKRKGK; SNESKKHKKEKRKGKV; NESKKHKKEKRKGKVE;
ESKKHKKEKRKGKVEN; SKKHKKEKRKGKVENL; KKHKKEKRKGKVENLL;
KHKKEKRKGKVENLLV; HKKEKRKGKVENLLVA; KKEKRKGKVENLLVAI;
KEKRKGKVENLLVAIN; EKRKGKVENLLVAINN; KRKGKVENLLVAINNL;
RKGKVENLLVAINNLK; KGKVENLLVAINNLKN; GKVENLLVAINNLKNP;
KVENLLVAINNLKNPT; VENLLVAINNLKNPTK; ENLLVAINNLKNPTKP;
NLLVAINNLKNPTKPA; LLVAINNLKNPTKPAA; LVAINNLKNPTKPAAG;
VAINNLKNPTKPAAGK; AINNLKNPTKPAAGKN; INNLKNPTKPAAGKNK;
NNLKNPTKPAAGKNKA; NLKNPTKPAAGKNKAN; LKNPTKPAAGKNKANS;
KNPTKPAAGKNKANSK; NPTKPAAGKNKANSKA; PTKPAAGKNKANSKAS;
TKPAAGKNKANSKASK; KPAAGKNKANSKASKQ; PAAGKNKANSKASKQK;
AAGKNKANSKASKQKN; AGKNKANSKASKQKNN; GKNKANSKASKQKNNP;
KNKANSKASKQKNNPN; NKANSKASKQKNNPNA; KANSKASKQKNNPNAN;
ANSKASKQKNNPNANA; NSKASKQKNNPNANAN; SKASKQKNNPNANANN;
KASKQKNNPNANANNA; ASKQKNNPNANANNAP; SKQKNNPNANANNAPK;
KQKNNPNANANNAPKK; QKNNPNANANNAPKKI; KNNPNANANNAPKKIL;
NNPNANANNAPKKILD; NPNANANNAPKKILDP; PNANANNAPKKILDPE;
NANANNAPKKILDPEV; ANANNAPKKILDPEVA; NANNAPKKILDPEVAK;
ANNAPKKILDPEVAKL; NNAPKKILDPEVAKLI; NAPKKILDPEVAKLIQ;
APKKILDPEVAKLIQK; PKKILDPEVAKLIQKI; KKILDPEVAKLIQKIL;
KILDPEVAKLIQKILD; ILDPEVAKLIQKILDR; LDPEVAKLIQKILDRS;
DPEVAKLIQKILDRSE; PEVAKLIQKILDRSEN; EVAKLIQKILDRSENI;
VAKLIQKILDRSENII; AKLIQKILDRSENIIQ; KLIQKILDRSENIIQI;
LIQKILDRSENIIQIS; IQKILDRSENIIQISE; QKILDRSENIIQISEM;
KILDRSENIIQISEMD; ILDRSENIIQISEMDS; LDRSENIIQISEMDSS;
DRSENIIQISEMDSSR; RSENIIQISEMDSSRG; SENIIQISEMDSSRGE;
ENIIQISEMDSSRGEP; NIIQISEMDSSRGEPN; IIQISEMDSSRGEPND;
IQISEMDSSRGEPNDQ; QISEMDSSRGEPNDQF; ISEMDSSRGEPNDQFG;
SEMDSSRGEPNDQFGM; EMDSSRGEPNDQFGMR; MDSSRGEPNDQFGMRA;
DSSRGEPNDQFGMRAE; SSRGEPNDQFGMRAEI; SRGEPNDQFGMRAEIF;
RGEPNDQFGMRAEIFS; GEPNDQFGMRAEIFSK; EPNDQFGMRAEIFSKI;
PNDQFGMRAEIFSKIF; NDQFGMRAEIFSKIFF; DQFGMRAEIFSKIFFN;
QFGMRAEIFSKIFFNA; FGMRAEIFSKIFFNAN; GMRAEIFSKIFFNANS;
MRAEIFSKIFFNANST; RAEIFSKIFFNANSTV; AEIFSKIFFNANSTVH;
EIFSKIFFNANSTVHF; IFSKIFFNANSTVHFD; FSKIFFNANSTVHFDS;
SKIFFNANSTVHFDSH; KIFFNANSTVHFDSHE; IFFNANSTVHFDSHEY;
FFNANSTVHFDSHEYT; FNANSTVHFDSHEYTE; NANSTVHFDSHEYTEE;
ANSTVHFDSHEYTEER; NSTVHFDSHEYTEERR; STVHFDSHEYTEERRM;

	TVHFDSHEYTEERRML; VHFDSHEYTEERRMLY; HFDSHEYTEERRMLYT; FDSHEYTEERRMLYTS; DSHEYTEERRMLYTSL; SHEYTEERRMLYTSLN; HEYTEERRMLYTSLNF; EYTEERRMLYTSLNFN; YTEERRMLYTSLNFNE; TEERRMLYTSLNFNEG; EERRMLYTSLNFNEGK; ERRMLYTSLNFNEGKI; RRMLYTSLNFNEGKIF; RMLYTSLNFNEGKIFN; MLYTSLNFNEGKIFNL; LYTSLNFNEGKIFNLG; YTSLNFNEGKIFNLGQ; TSLNFNEGKIFNLGQI; SLNFNEGKIFNLGQIL; LNFNEGKIFNLGQILS; NFNEGKIFNLGQILSK; FNEGKIFNLGQILSKL; NEGKIFNLGQILSKLS; EGKIFNLGQILSKLSQ; GKIFNLGQILSKLSQD; KIFNLGQILSKLSQDS; IFNLGQILSKLSQDSN; FNLGQILSKLSQDSNY; NLGQILSKLSQDSNYR; LGQILSKLSQDSNYRG; GQILSKLSQDSNYRGL; QILSKLSQDSNYRGLV; ILSKLSQDSNYRGLVK; LSKLSQDSNYRGLVKE; SKLSQDSNYRGLVKET; KLSQDSNYRGLVKETL; LSQDSNYRGLVKETLI; SQDSNYRGLVKETLIN; QDSNYRGLVKETLINR; DSNYRGLVKETLINRG; SNYRGLVKETLINRGF; NYRGLVKETLINRGFS; YRGLVKETLINRGFSI; RGLVKETLINRGFSIQ; GLVKETLINRGFSIQL; LVKETLINRGFSIQLA; VKETLINRGFSIQLAM; KETLINRGFSIQLAME; ETLINRGFSIQLAMEE; TLINRGFSIQLAMEEI; LINRGFSIQLAMEEIS; INRGFSIQLAMEEISA; NRGFSIQLAMEEISAK; RGFSIQLAMEEISAKI; GFSIQLAMEEISAKIL; FSIQLAMEEISAKILN; SIQLAMEEISAKILNV; IQLAMEEISAKILNVK; QLAMEEISAKILNVKD; LAMEEISAKILNVKDK; AMEEISAKILNVKDKL; MEEISAKILNVKDKLQ; EEISAKILNVKDKLQQ; EISAKILNVKDKLQQL; ISAKILNVKDKLQQLN; SAKILNVKDKLQQLNK; AKILNVKDKLQQLNKP; KILNVKDKLQQLNKPN; ILNVKDKLQQLNKPNL; LNVKDKLQQLNKPNLE; NVKDKLQQLNKPNLET; VKDKLQQLNKPNLETL; KDKLQQLNKPNLETLY; DKLQQLNKPNLETLYN; KLQQLNKPNLETLYND; LQQLNKPNLETLYNDF; QQLNKPNLETLYNDFE; QLNKPNLETLYNDFEK; LNKPNLETLYNDFEKL; NKPNLETLYNDFEKLT; KPNLETLYNDFEKLTS; PNLETLYNDFEKLTSL; NLETLYNDFEKLTSLK; LETLYNDFEKLTSLKE; ETLYNDFEKLTSLKEK; TLYNDFEKLTSLKEKW; LYNDFEKLTSLKEKWL; YNDFEKLTSLKEKWLK; NDFEKLTSLKEKWLKD; DFEKLTSLKEKWLKDT; FEKLTSLKEKWLKDTD; EKLTSLKEKWLKDTDD; KLTSLKEKWLKDTDDL; LTSLKEKWLKDTDDLI; TSLKEKWLKDTDDLID; SLKEKWLKDTDDLIDE; LKEKWLKDTDDLIDEY; KEKWLKDTDDLIDEYN; EKWLKDTDDLIDEYNT; KWLKDTDDLIDEYNTN; WLKDTDDLIDEYNTNP; LKDTDDLIDEYNTNPD; KDTDDLIDEYNTNPDL; DTDDLIDEYNTNPDLQ; TDDLIDEYNTNPDLQT; DDLIDEYNTNPDLQTD; DLIDEYNTNPDLQTDV; LIDEYNTNPDLQTDVS; IDEYNTNPDLQTDVSK; DEYNTNPDLQTDVSKL; EYNTNPDLQTDVSKLN; YNTNPDLQTDVSKLND; NTNPDLQTDVSKLNDT; TNPDLQTDVSKLNDTL; NPDLQTDVSKLNDTLR; PDLQTDVSKLNDTLRS; DLQTDVSKLNDTLRSK; LQTDVSKLNDTLRSKN; QTDVSKLNDTLRSKNS; TDVSKLNDTLRSKNSR; DVSKLNDTLRSKNSRA; VSKLNDTLRSKNSRAQ; SKLNDTLRSKNSRAQF; KLNDTLRSKNSRAQFA; LNDTLRSKNSRAQFAN; NDTLRSKNSRAQFANI; DTLRSKNSRAQFANIH; TLRSKNSRAQFANIHD; LRSKNSRAQFANIHDI; RSKNSRAQFANIHDII; SKNSRAQFANIHDIIL; KNSRAQFANIHDIILD; NSRAQFANIHDIILDL; SRAQFANIHDIILDLV; RAQFANIHDIILDLVN; AQFANIHDIILDLVNT; QFANIHDIILDLVNTT; FANIHDIILDLVNTTT; ANIHDIILDLVNTTTN; NIHDIILDLVNTTTNI; IHDIILDLVNTTTNIL; HDIILDLVNTTTNILA; DIILDLVNTTTNILAP; IILDLVNTTTNILAPI; ILDLVNTTTNILAPIQ;
Seq 41	

	13 mers: MKNNKLIAIFLLH; KNNKLIAIFLLHI; NNKLIAIFLLHIL; NKLIAIFLLHILT; KLIAIFLLHILTG; LIAIFLLHILTGL; IAIFLLHILTGLI; AIFLLHILTGLIL; IFLLHILTGLILL; FLLHILTGLILLS; LLHILTGLILLSC; LHILTGLILLSCS; HILTGLILLSCSL; ILTGLILLSCSLE; LTGLILLSCSLEV; TGLILLSCSLEVN; GLILLSCSLEVNQ; LILLSCSLEVNQD; ILLSCSLEVNQDD; LLSCSLEVNQDDN; LSCSLEVNQDDNQ; SCSLEVNQDDNQE; CSLEVNQDDNQEK; SLEVNQDDNQEKQ; LEVNQDDNQEKQK; EVNQDDNQEKQKK; VNQDDNQEKQKKA; NQDDNQEKQKKAK; QDDNQEKQKKAKT; DDNQEKQKKAKTK; DNQEKQKKAKTKT; NQEKQKKAKTKTS; QEKQKKAKTKTSK; EKQKKAKTKTSKS; KQKKAKTKTSKSE; QKKAKTKTSKSEN; KKAKTKTSKSENN; KAKTKTSKSENNS; AKTKTSKSENNSS; KTKTSKSENNSSK; TKTSKSENNSSKM; KTSKSENNSSKMK; TSKSENNSSKMKK; SKSENNSSKMKKL; KSENNSSKMKKLS; SENNSSKMKKLSK; ENNSSKMKKLSKN; NNSSKMKKLSKNA; NSSKMKKLSKNAK; SSKMKKLSKNAKN; SKMKKLSKNAKNK; KMKKLSKNAKNKK; MKKLSKNAKNKKP; KKLSKNAKNKKPT; KLSKNAKNKKPTV; LSKNAKNKKPTVD; SKNAKNKKPTVDN; KNAKNKKPTVDNL; NAKNKKPTVDNLL; AKNKKPTVDNLLV; KNKKPTVDNLLVA; NKKPTVDNLLVAI; KKPTVDNLLVAIN; KPTVDNLLVAINT; PTVDNLLVAINTL; TVDNLLVAINTLK; VDNLLVAINTLKN; DNLLVAINTLKNP; NLLVAINTLKNPP; LLVAINTLKNPPK; LVAINTLKNPPKT; VAINTLKNPPKTA; AINTLKNPPKTAG; INTLKNPPKTAGK; NTLKNPPKTAGKN; TLKNPPKTAGKNK; LKNPPKTAGKNKS; KNPPKTAGKNKSN; NPPKTAGKNKSNS; PPKTAGKNKSNSA; PKTAGKNKSNSAA; KTAGKNKSNSAAA; TAGKNKSNSAAAL; AGKNKSNSAAALK; GKNKSNSAAALKQ; KNKSNSAAALKQP; NKSNSAAALKQPN; KSNSAAALKQPNN; SNSAAALKQPNNA; NSAAALKQPNNAN; SAAALKQPNNANA; AAALKQPNNANAL; AALKQPNNANALK; ALKQPNNANALKQ; LKQPNNANALKQI; KQPNNANALKQID; QPNNANALKQIDP; PNNANALKQIDPE; NNANALKQIDPEA; NANALKQIDPEAK; ANALKQIDPEAKE; NALKQIDPEAKEL; ALKQIDPEAKELI; LKQIDPEAKELIQ; KQIDPEAKELIQK; QIDPEAKELIQKI; IDPEAKELIQKIL; DPEAKELIQKILE; PEAKELIQKILER; EAKELIQKILERS; AKELIQKILERSE; KELIQKILERSED; ELIQKILERSEDI; LIQKILERSEDIV; IQKILERSEDIVQ; QKILERSEDIVQI; KILERSEDIVQIS; ILERSEDIVQISE; LERSEDIVQISEI; ERSEDIVQISEID; RSEDIVQISEIDA; SEDIVQISEIDAN; EDIVQISEIDANK; DIVQISEIDANKG; IVQISEIDANKGE; VQISEIDANKGEP; QISEIDANKGEPD; ISEIDANKGEPDD; SEIDANKGEPDDQ; EIDANKGEPDDQF; IDANKGEPDDQFE; DANKGEPDDQFEM; ANKGEPDDQFEMK; NKGEPDDQFEMKA; KGEPDDQFEMKAE; GEPDDQFEMKAEI; EPDDQFEMKAEIF; PDDQFEMKAEIFS; DDQFEMKAEIFSK; DQFEMKAEIFSKI; QFEMKAEIFSKIF; FEMKAEIFSKIFF; EMKAEIFSKIFFN; MKAEIFSKIFFNA; KAEIFSKIFFNAG; AEIFSKIFFNAGS; EIFSKIFFNAGST; IFSKIFFNAGSTV; FSKIFFNAGSTVT; SKIFFNAGSTVTF;

	KIFFNAGSTVTFD; IFFNAGSTVTFDD; FFNAGSTVTFDDN; FNAGSTVTFDDNE; NAGSTVTFDDNEY; AGSTVTFDDNEYV; GSTVTFDDNEYVN; STVTFDDNEYVNE; TVTFDDNEYVNER; VTFDDNEYVNERR; TFDDNEYVNERRI; FDDNEYVNERRIL; DDNEYVNERRILY; DNEYVNERRILYT; NEYVNERRILYTS; EYVNERRILYTSL; YVNERRILYTSLN; VNERRILYTSLNF; NERRILYTSLNFN; ERRILYTSLNFNE; RRILYTSLNFNEN; RILYTSLNFNENK; ILYTSLNFNENKI; LYTSLNFNENKIL; YTSLNFNENKILN; TSLNFNENKILNL; SLNFNENKILNLG; LNFNENKILNLGK; NFNENKILNLGKI; FNENKILNLGKIL; NENKILNLGKILS; ENKILNLGKILSK; NKILNLGKILSKL; KILNLGKILSKLS; ILNLGKILSKLSQ; LNLGKILSKLSQD; NLGKILSKLSQDS; LGKILSKLSQDSN; GKILSKLSQDSNY; KILSKLSQDSNYR; ILSKLSQDSNYRS; LSKLSQDSNYRSL; SKLSQDSNYRSLV; KLSQDSNYRSLVK; LSQDSNYRSLVKE; SQDSNYRSLVKEI; QDSNYRSLVKEIL; DSNYRSLVKEILI; SNYRSLVKEILIN; NYRSLVKEILINR; YRSLVKEILINRG; RSLVKEILINRGF; SLVKEILINRGFS; LVKEILINRGFSI; VKEILINRGFSIQ; KEILINRGFSIQL; EILINRGFSIQLA; ILINRGFSIQLAI; LINRGFSIQLAIE; INRGFSIQLAIEE; NRGFSIQLAIEEI; RGFSIQLAIEEIS; GFSIQLAIEEISL; FSIQLAIEEISLR; SIQLAIEEISLRT; IQLAIEEISLRTL; QLAIEEISLRTLN; LAIEEISLRTLNV; AIEEISLRTLNVK; IEEISLRTLNVKD; EEISLRTLNVKDK; EISLRTLNVKDKI; ISLRTLNVKDKIQ; SLRTLNVKDKIQH; LRTLNVKDKIQHL; RTLNVKDKIQHLN; TLNVKDKIQHLNK; LNVKDKIQHLNKP; NVKDKIQHLNKPN; VKDKIQHLNKPNL; KDKIQHLNKPNLK; DKIQHLNKPNLKT; KIQHLNKPNLKTL; IQHLNKPNLKTLY; QHLNKPNLKTLYH; HLNKPNLKTLYHD; LNKPNLKTLYHDF; NKPNLKTLYHDFN; KPNLKTLYHDFNK; PNLKTLYHDFNKL; NLKTLYHDFNKLI; LKTLYHDFNKLIP; KTLYHDFNKLIPL; TLYHDFNKLIPLK; LYHDFNKLIPLKE; YHDFNKLIPLKEK; HDFNKLIPLKEKW; DFNKLIPLKEKWL; FNKLIPLKEKWLK; NKLIPLKEKWLKD; KLIPLKEKWLKDV; LIPLKEKWLKDVD; IPLKEKWLKDVDD; PLKEKWLKDVDDI; LKEKWLKDVDDII; KEKWLKDVDDIIK; EKWLKDVDDIIKD; KWLKDVDDIIKDY; WLKDVDDIIKDYN; LKDVDDIIKDYNA; KDVDDIIKDYNAN; DVDDIIKDYNANP; VDDIIKDYNANPE; DDIIKDYNANPEL; DIIKDYNANPELR; IIKDYNANPELRT; IKDYNANPELRTD; KDYNANPELRTDI; DYNANPELRTDIS; YNANPELRTDISK; NANPELRTDISKL; ANPELRTDISKLN; NPELRTDISKLND; PELRTDISKLNDY; ELRTDISKLNDYI; LRTDISKLNDYII; RTDISKLNDYIIS; TDISKLNDYIISK; DISKLNDYIISKN; ISKLNDYIISKNS; SKLNDYIISKNSK; KLNDYIISKNSKA; LNDYIISKNSKAQ; NDYIISKNSKAQF; DYIISKNSKAQFT; YIISKNSKAQFTD; IISKNSKAQFTDI; ISKNSKAQFTDIH; SKNSKAQFTDIHN; KNSKAQFTDIHNI; NSKAQFTDIHNII; SKAQFTDIHNIIL; KAQFTDIHNIILN; AQFTDIHNIILNL; QFTDIHNIILNLI; FTDIHNIILNLIN; TDIHNIILNLINT; DIHNIILNLINTT; IHNIILNLINTTT; HNIILNLINTTTN; NIILNLINTTTNI; IILNLINTTTNIL; ILNLINTTTNILA;

	LNLINTTTNILAP; NLINTTTNILAPI; LINTTTNILAPIQ; 14 mers: MKNNKLIAIFLLHI; KNNKLIAIFLLHIL; NNKLIAIFLLHILT; NKLIAIFLLHILTG; KLIAIFLLHILTGL; LIAIFLLHILTGLI; IAIFLLHILTGLIL; AIFLLHILTGLILL; IFLLHILTGLILLS; FLLHILTGLILLSC; LLHILTGLILLSCS; LHILTGLILLSCSL; HILTGLILLSCSLE; ILTGLILLSCSLEV; LTGLILLSCSLEVN; TGLILLSCSLEVNQ; GLILLSCSLEVNQD; LILLSCSLEVNQDD; ILLSCSLEVNQDDN; LLSCSLEVNQDDNQ; LSCSLEVNQDDNQE; SCSLEVNQDDNQEK; CSLEVNQDDNQEKQ; SLEVNQDDNQEKQK; LEVNQDDNQEKQKK; EVNQDDNQEKQKKA; VNQDDNQEKQKKAK; NQDDNQEKQKKAKT; QDDNQEKQKKAKTK; DDNQEKQKKAKTKT; DNQEKQKKAKTKTS; NQEKQKKAKTKTSK; QEKQKKAKTKTSKS; EKQKKAKTKTSKSE; KQKKAKTKTSKSEN; QKKAKTKTSKSENN; KKAKTKTSKSENNS; KAKTKTSKSENNSS; AKTKTSKSENNSSK; KTKTSKSENNSSKM; TKTSKSENNSSKMK; KTSKSENNSSKMKK; TSKSENNSSKMKKL; SKSENNSSKMKKLS; KSENNSSKMKKLSK; SENNSSKMKKLSKN; ENNSSKMKKLSKNA; NNSSKMKKLSKNAK; NSSKMKKLSKNAKN; SSKMKKLSKNAKNK; SKMKKLSKNAKNKK; KMKKLSKNAKNKKP; MKKLSKNAKNKKPT; KKLSKNAKNKKPTV; KLSKNAKNKKPTVD; LSKNAKNKKPTVDN; SKNAKNKKPTVDNL; KNAKNKKPTVDNLL; NAKNKKPTVDNLLV; AKNKKPTVDNLLVA; KNKKPTVDNLLVAI; NKKPTVDNLLVAIN; KKPTVDNLLVAINT; KPTVDNLLVAINTL; PTVDNLLVAINTLK; TVDNLLVAINTLKN; VDNLLVAINTLKNP; DNLLVAINTLKNPP; NLLVAINTLKNPPK; LLVAINTLKNPPKT; LVAINTLKNPPKTA; VAINTLKNPPKTAG; AINTLKNPPKTAGK; INTLKNPPKTAGKN; NTLKNPPKTAGKNK; TLKNPPKTAGKNKS; LKNPPKTAGKNKSN; KNPPKTAGKNKSNS; NPPKTAGKNKSNSA; PPKTAGKNKSNSAA; PKTAGKNKSNSAAA; KTAGKNKSNSAAAL; TAGKNKSNSAAALK; AGKNKSNSAAALKQ; GKNKSNSAAALKQP; KNKSNSAAALKQPN; NKSNSAAALKQPNN; KSNSAAALKQPNNA; SNSAAALKQPNNAN; NSAAALKQPNNANA; SAAALKQPNNANAL; AAALKQPNNANALK; AALKQPNNANALKQ; ALKQPNNANALKQI; LKQPNNANALKQID; KQPNNANALKQIDP; QPNNANALKQIDPE; PNNANALKQIDPEA; NNANALKQIDPEAK; NANALKQIDPEAKE; ANALKQIDPEAKEL; NALKQIDPEAKELI; ALKQIDPEAKELIQ; LKQIDPEAKELIQK; KQIDPEAKELIQKI; QIDPEAKELIQKIL; IDPEAKELIQKILE; DPEAKELIQKILER; PEAKELIQKILERS; EAKELIQKILERSE; AKELIQKILERSED; KELIQKILERSEDI; ELIQKILERSEDIV; LIQKILERSEDIVQ; IQKILERSEDIVQI; QKILERSEDIVQIS; KILERSEDIVQISE; ILERSEDIVQISEI; LERSEDIVQISEID; ERSEDIVQISEIDA; RSEDIVQISEIDAN; SEDIVQISEIDANK; EDIVQISEIDANKG; DIVQISEIDANKGE; IVQISEIDANKGEP; VQISEIDANKGEPD; QISEIDANKGEPDD; ISEIDANKGEPDDQ; SEIDANKGEPDDQF; EIDANKGEPDDQFE; IDANKGEPDDQFEM; DANKGEPDDQFEMK; ANKGEPDDQFEMKA; NKGEPDDQFEMKAE; KGEPDDQFEMKAEI; GEPDDQFEMKAEIF; EPDDQFEMKAEIFS; PDDQFEMKAEIFSK; DDQFEMKAEIFSKI; DQFEMKAEIFSKIF; QFEMKAEIFSKIFF; FEMKAEIFSKIFFN; EMKAEIFSKIFFNA; MKAEIFSKIFFNAG;

	KAEIFSKIFFNAGS; AEIFSKIFFNAGST; EIFSKIFFNAGSTV; IFSKIFFNAGSTVT; FSKIFFNAGSTVTF; SKIFFNAGSTVTFD; KIFFNAGSTVTFDD; IFFNAGSTVTFDDN; FFNAGSTVTFDDNE; FNAGSTVTFDDNEY; NAGSTVTFDDNEYV; AGSTVTFDDNEYVN; GSTVTFDDNEYVNE; STVTFDDNEYVNER; TVTFDDNEYVNERR; VTFDDNEYVNERRI; TFDDNEYVNERRIL; FDDNEYVNERRILY; DDNEYVNERRILYT; DNEYVNERRILYTS; NEYVNERRILYTSL; EYVNERRILYTSLN; YVNERRILYTSLNF; VNERRILYTSLNFN; NERRILYTSLNFNE; ERRILYTSLNFNEN; RRILYTSLNFNENK; RILYTSLNFNENKI; ILYTSLNFNENKIL; LYTSLNFNENKILN; YTSLNFNENKILNL; TSLNFNENKILNLG; SLNFNENKILNLGK; LNFNENKILNLGKI; NFNENKILNLGKIL; FNENKILNLGKILS; NENKILNLGKILSK; ENKILNLGKILSKL; NKILNLGKILSKLS; KILNLGKILSKLSQ; ILNLGKILSKLSQD; LNLGKILSKLSQDS; NLGKILSKLSQDSN; LGKILSKLSQDSNY; GKILSKLSQDSNYR; KILSKLSQDSNYRS; ILSKLSQDSNYRSL; LSKLSQDSNYRSLV; SKLSQDSNYRSLVK; KLSQDSNYRSLVKE; LSQDSNYRSLVKEI; SQDSNYRSLVKEIL; QDSNYRSLVKEILI; DSNYRSLVKEILIN; SNYRSLVKEILINR; NYRSLVKEILINRG; YRSLVKEILINRGF; RSLVKEILINRGFS; SLVKEILINRGFSI; LVKEILINRGFSIQ; VKEILINRGFSIQL; KEILINRGFSIQLA; EILINRGFSIQLAI; ILINRGFSIQLAIE; LINRGFSIQLAIEE; INRGFSIQLAIEEI; NRGFSIQLAIEEIS; RGFSIQLAIEEISL; GFSIQLAIEEISLR; FSIQLAIEEISLRT; SIQLAIEEISLRTL; IQLAIEEISLRTLN; QLAIEEISLRTLNV; LAIEEISLRTLNVK; AIEEISLRTLNVKD; IEEISLRTLNVKDK; EEISLRTLNVKDKI; EISLRTLNVKDKIQ; ISLRTLNVKDKIQH; SLRTLNVKDKIQHL; LRTLNVKDKIQHLN; RTLNVKDKIQHLNK; TLNVKDKIQHLNKP; LNVKDKIQHLNKPN; NVKDKIQHLNKPNL; VKDKIQHLNKPNLK; KDKIQHLNKPNLKT; DKIQHLNKPNLKTL; KIQHLNKPNLKTLY; IQHLNKPNLKTLYH; QHLNKPNLKTLYHD; HLNKPNLKTLYHDF; LNKPNLKTLYHDFN; NKPNLKTLYHDFNK; KPNLKTLYHDFNKL; PNLKTLYHDFNKLI; NLKTLYHDFNKLIP; LKTLYHDFNKLIPL; KTLYHDFNKLIPLK; TLYHDFNKLIPLKE; LYHDFNKLIPLKEK; YHDFNKLIPLKEKW; HDFNKLIPLKEKWL; DFNKLIPLKEKWLK; FNKLIPLKEKWLKD; NKLIPLKEKWLKDV; KLIPLKEKWLKDVD; LIPLKEKWLKDVDD; IPLKEKWLKDVDDI; PLKEKWLKDVDDII; LKEKWLKDVDDIIK; KEKWLKDVDDIIKD; EKWLKDVDDIIKDY; KWLKDVDDIIKDYN; WLKDVDDIIKDYNA; LKDVDDIIKDYNAN; KDVDDIIKDYNANP; DVDDIIKDYNANPE; VDDIIKDYNANPEL; DDIIKDYNANPELR; DIIKDYNANPELRT; IIKDYNANPELRTD; IKDYNANPELRTDI; KDYNANPELRTDIS; DYNANPELRTDISK; YNANPELRTDISKL; NANPELRTDISKLN; ANPELRTDISKLND; NPELRTDISKLNDY; PELRTDISKLNDYI; ELRTDISKLNDYII; LRTDISKLNDYIIS; RTDISKLNDYIISK; TDISKLNDYIISKN; DISKLNDYIISKNS; ISKLNDYIISKNSK; SKLNDYIISKNSKA; KLNDYIISKNSKAQ; LNDYIISKNSKAQF; NDYIISKNSKAQFT; DYIISKNSKAQFTD; YIISKNSKAQFTDI; IISKNSKAQFTDIH; ISKNSKAQFTDIHN; SKNSKAQFTDIHNI; KNSKAQFTDIHNII; NSKAQFTDIHNIIL; SKAQFTDIHNIILN; KAQFTDIHNIILNL; AQFTDIHNIILNLI; QFTDIHNIILNLIN; FTDIHNIILNLINT; TDIHNIILNLINTT;

	DIHNIILNLINTTT; IHNIILNLINTTTN; HNIILNLINTTTNI; NIILNLINTTTNIL; IILNLINTTTNILA; ILNLINTTTNILAP; LNLINTTTNILAPI; NLINTTTNILAPIQ; 15 mers: MKNNKLIAIFLLHIL; KNNKLIAIFLLHILT; NNKLIAIFLLHILTG; NKLIAIFLLHILTGL; KLIAIFLLHILTGLI; LIAIFLLHILTGLIL; IAIFLLHILTGLILL; AIFLLHILTGLILLS; IFLLHILTGLILLSC; FLLHILTGLILLSCS; LLHILTGLILLSCSL; LHILTGLILLSCSLE; HILTGLILLSCSLEV; ILTGLILLSCSLEVN; LTGLILLSCSLEVNQ; TGLILLSCSLEVNQD; GLILLSCSLEVNQDD; LILLSCSLEVNQDDN; ILLSCSLEVNQDDNQ; LLSCSLEVNQDDNQE; LSCSLEVNQDDNQEK; SCSLEVNQDDNQEKQ; CSLEVNQDDNQEKQK; SLEVNQDDNQEKQKK; LEVNQDDNQEKQKKA; EVNQDDNQEKQKKAK; VNQDDNQEKQKKAKT; NQDDNQEKQKKAKTK; QDDNQEKQKKAKTKT; DDNQEKQKKAKTKTS; DNQEKQKKAKTKTSK; NQEKQKKAKTKTSKS; QEKQKKAKTKTSKSE; EKQKKAKTKTSKSEN; KQKKAKTKTSKSENN; QKKAKTKTSKSENNS; KKAKTKTSKSENNSS; KAKTKTSKSENNSSK; AKTKTSKSENNSSKM; KTKTSKSENNSSKMK; TKTSKSENNSSKMKK; KTSKSENNSSKMKKL; TSKSENNSSKMKKLS; SKSENNSSKMKKLSK; KSENNSSKMKKLSKN; SENNSSKMKKLSKNA; ENNSSKMKKLSKNAK; NNSSKMKKLSKNAKN; NSSKMKKLSKNAKNK; SSKMKKLSKNAKNKK; SKMKKLSKNAKNKKP; KMKKLSKNAKNKKPT; MKKLSKNAKNKKPTV; KKLSKNAKNKKPTVD; KLSKNAKNKKPTVDN; LSKNAKNKKPTVDNL; SKNAKNKKPTVDNLL; KNAKNKKPTVDNLLV; NAKNKKPTVDNLLVA; AKNKKPTVDNLLVAI; KNKKPTVDNLLVAIN; NKKPTVDNLLVAINT; KKPTVDNLLVAINTL; KPTVDNLLVAINTLK; PTVDNLLVAINTLKN; TVDNLLVAINTLKNP; VDNLLVAINTLKNPP; DNLLVAINTLKNPPK; NLLVAINTLKNPPKT; LLVAINTLKNPPKTA; LVAINTLKNPPKTAG; VAINTLKNPPKTAGK; AINTLKNPPKTAGKN; INTLKNPPKTAGKNK; NTLKNPPKTAGKNKS; TLKNPPKTAGKNKSN; LKNPPKTAGKNKSNS; KNPPKTAGKNKSNSA; NPPKTAGKNKSNSAA; PPKTAGKNKSNSAAA; PKTAGKNKSNSAAAL; KTAGKNKSNSAAALK; TAGKNKSNSAAALKQ; AGKNKSNSAAALKQP; GKNKSNSAAALKQPN; KNKSNSAAALKQPNN; NKSNSAAALKQPNNA; KSNSAAALKQPNNAN; SNSAAALKQPNNANA; NSAAALKQPNNANAL; SAAALKQPNNANALK; AAALKQPNNANALKQ; AALKQPNNANALKQI; ALKQPNNANALKQID; LKQPNNANALKQIDP; KQPNNANALKQIDPE; QPNNANALKQIDPEA; PNNANALKQIDPEAK; NNANALKQIDPEAKE; NANALKQIDPEAKEL; ANALKQIDPEAKELI; NALKQIDPEAKELIQ; ALKQIDPEAKELIQK; LKQIDPEAKELIQKI; KQIDPEAKELIQKIL; QIDPEAKELIQKILE; IDPEAKELIQKILER; DPEAKELIQKILERS; PEAKELIQKILERSE; EAKELIQKILERSED; AKELIQKILERSEDI; KELIQKILERSEDIV; ELIQKILERSEDIVQ; LIQKILERSEDIVQI; IQKILERSEDIVQIS; QKILERSEDIVQISE; KILERSEDIVQISEI; ILERSEDIVQISEID; LERSEDIVQISEIDA; ERSEDIVQISEIDAN; RSEDIVQISEIDANK; SEDIVQISEIDANKG; EDIVQISEIDANKGE; DIVQISEIDANKGEP; IVQISEIDANKGEPD; VQISEIDANKGEPDD; QISEIDANKGEPDDQ; ISEIDANKGEPDDQF; SEIDANKGEPDDQFE; EIDANKGEPDDQFEM; IDANKGEPDDQFEMK; DANKGEPDDQFEMKA; ANKGEPDDQFEMKAE; NKGEPDDQFEMKAEI; KGEPDDQFEMKAEIF; GEPDDQFEMKAEIFS; EPDDQFEMKAEIFSK; PDDQFEMKAEIFSKI;

	DDQFEMKAEIFSKIF; DQFEMKAEIFSKIFF; QFEMKAEIFSKIFFN; FEMKAEIFSKIFFNA; EMKAEIFSKIFFNAG; MKAEIFSKIFFNAGS; KAEIFSKIFFNAGST; AEIFSKIFFNAGSTV; EIFSKIFFNAGSTVT; IFSKIFFNAGSTVTF; FSKIFFNAGSTVTFD; SKIFFNAGSTVTFDD; KIFFNAGSTVTFDDN; IFFNAGSTVTFDDNE; FFNAGSTVTFDDNEY; FNAGSTVTFDDNEYV; NAGSTVTFDDNEYVN; AGSTVTFDDNEYVNE; GSTVTFDDNEYVNER; STVTFDDNEYVNERR; TVTFDDNEYVNERRI; VTFDDNEYVNERRIL; TFDDNEYVNERRILY; FDDNEYVNERRILYT; DDNEYVNERRILYTS; DNEYVNERRILYTSL; NEYVNERRILYTSLN; EYVNERRILYTSLNF; YVNERRILYTSLNFN; VNERRILYTSLNFNE; NERRILYTSLNFNEN; ERRILYTSLNFNENK; RRILYTSLNFNENKI; RILYTSLNFNENKIL; ILYTSLNFNENKILN; LYTSLNFNENKILNL; YTSLNFNENKILNLG; TSLNFNENKILNLGK; SLNFNENKILNLGKI; LNFNENKILNLGKIL; NFNENKILNLGKILS; FNENKILNLGKILSK; NENKILNLGKILSKL; ENKILNLGKILSKLS; NKILNLGKILSKLSQ; KILNLGKILSKLSQD; ILNLGKILSKLSQDS; LNLGKILSKLSQDSN; NLGKILSKLSQDSNY; LGKILSKLSQDSNYR; GKILSKLSQDSNYRS; KILSKLSQDSNYRSL; ILSKLSQDSNYRSLV; LSKLSQDSNYRSLVK; SKLSQDSNYRSLVKE; KLSQDSNYRSLVKEI; LSQDSNYRSLVKEIL; SQDSNYRSLVKEILI; QDSNYRSLVKEILIN; DSNYRSLVKEILINR; SNYRSLVKEILINRG; NYRSLVKEILINRGF; YRSLVKEILINRGFS; RSLVKEILINRGFSI; SLVKEILINRGFSIQ; LVKEILINRGFSIQL; VKEILINRGFSIQLA; KEILINRGFSIQLAI; EILINRGFSIQLAIE; ILINRGFSIQLAIEE; LINRGFSIQLAIEEI; INRGFSIQLAIEEIS; NRGFSIQLAIEEISL; RGFSIQLAIEEISLR; GFSIQLAIEEISLRT; FSIQLAIEEISLRTL; SIQLAIEEISLRTLN; IQLAIEEISLRTLNV; QLAIEEISLRTLNVK; LAIEEISLRTLNVKD; AIEEISLRTLNVKDK; IEEISLRTLNVKDKI; EEISLRTLNVKDKIQ; EISLRTLNVKDKIQH; ISLRTLNVKDKIQHL; SLRTLNVKDKIQHLN; LRTLNVKDKIQHLNK; RTLNVKDKIQHLNKP; TLNVKDKIQHLNKPN; LNVKDKIQHLNKPNL; NVKDKIQHLNKPNLK; VKDKIQHLNKPNLKT; KDKIQHLNKPNLKTL; DKIQHLNKPNLKTLY; KIQHLNKPNLKTLYH; IQHLNKPNLKTLYHD; QHLNKPNLKTLYHDF; HLNKPNLKTLYHDFN; LNKPNLKTLYHDFNK; NKPNLKTLYHDFNKL; KPNLKTLYHDFNKLI; PNLKTLYHDFNKLIP; NLKTLYHDFNKLIPL; LKTLYHDFNKLIPLK; KTLYHDFNKLIPLKE; TLYHDFNKLIPLKEK; LYHDFNKLIPLKEKW; YHDFNKLIPLKEKWL; HDFNKLIPLKEKWLK; DFNKLIPLKEKWLKD; FNKLIPLKEKWLKDV; NKLIPLKEKWLKDVD; KLIPLKEKWLKDVDD; LIPLKEKWLKDVDDI; IPLKEKWLKDVDDII; PLKEKWLKDVDDIIK; LKEKWLKDVDDIIKD; KEKWLKDVDDIIKDY; EKWLKDVDDIIKDYN; KWLKDVDDIIKDYNA; WLKDVDDIIKDYNAN; LKDVDDIIKDYNANP; KDVDDIIKDYNANPE; DVDDIIKDYNANPEL; VDDIIKDYNANPELR; DDIIKDYNANPELRT; DIIKDYNANPELRTD; IIKDYNANPELRTDI; IKDYNANPELRTDIS; KDYNANPELRTDISK; DYNANPELRTDISKL; YNANPELRTDISKLN; NANPELRTDISKLND; ANPELRTDISKLNDY; NPELRTDISKLNDYI; PELRTDISKLNDYII; ELRTDISKLNDYIIS; LRTDISKLNDYIISK; RTDISKLNDYIISKN; TDISKLNDYIISKNS; DISKLNDYIISKNSK; ISKLNDYIISKNSKA; SKLNDYIISKNSKAQ; KLNDYIISKNSKAQF; LNDYIISKNSKAQFT; NDYIISKNSKAQFTD; DYIISKNSKAQFTDI; YIISKNSKAQFTDIH; IISKNSKAQFTDIHN; ISKNSKAQFTDIHNI; SKNSKAQFTDIHNII; KNSKAQFTDIHNIIL; NSKAQFTDIHNIILN;

	SKAQFTDIHNIILNL; KAQFTDIHNIILNLI; AQFTDIHNIILNLIN; QFTDIHNIILNLINT; FTDIHNIILNLINTT; TDIHNIILNLINTTT; DIHNIILNLINTTTN; IHNIILNLINTTTNI; HNIILNLINTTTNIL; NIILNLINTTTNILA; IILNLINTTTNILAP; ILNLINTTTNILAPI; LNLINTTTNILAPIQ; 16 mers: MKNNKLIAIFLLHILT; KNNKLIAIFLLHILTG; NNKLIAIFLLHILTGL; NKLIAIFLLHILTGLI; KLIAIFLLHILTGLIL; LIAIFLLHILTGLILL; IAIFLLHILTGLILLS; AIFLLHILTGLILLSC; IFLLHILTGLILLSCS; FLLHILTGLILLSCSL; LLHILTGLILLSCSLE; LHILTGLILLSCSLEV; HILTGLILLSCSLEVN; ILTGLILLSCSLEVNQ; LTGLILLSCSLEVNQD; TGLILLSCSLEVNQDD; GLILLSCSLEVNQDDN; LILLSCSLEVNQDDNQ; ILLSCSLEVNQDDNQE; LLSCSLEVNQDDNQEK; LSCSLEVNQDDNQEKQ; SCSLEVNQDDNQEKQK; CSLEVNQDDNQEKQKK; SLEVNQDDNQEKQKKA; LEVNQDDNQEKQKKAK; EVNQDDNQEKQKKAKT; VNQDDNQEKQKKAKTK; NQDDNQEKQKKAKTKT; QDDNQEKQKKAKTKTS; DDNQEKQKKAKTKTSK; DNQEKQKKAKTKTSKS; NQEKQKKAKTKTSKSE; QEKQKKAKTKTSKSEN; EKQKKAKTKTSKSENN; KQKKAKTKTSKSENNS; QKKAKTKTSKSENNSS; KKAKTKTSKSENNSSK; KAKTKTSKSENNSSKM; AKTKTSKSENNSSKMK; KTKTSKSENNSSKMKK; TKTSKSENNSSKMKKL; KTSKSENNSSKMKKLS; TSKSENNSSKMKKLSK; SKSENNSSKMKKLSKN; KSENNSSKMKKLSKNA; SENNSSKMKKLSKNAK; ENNSSKMKKLSKNAKN; NNSSKMKKLSKNAKNK; NSSKMKKLSKNAKNKK; SSKMKKLSKNAKNKKP; SKMKKLSKNAKNKKPT; KMKKLSKNAKNKKPTV; MKKLSKNAKNKKPTVD; KKLSKNAKNKKPTVDN; KLSKNAKNKKPTVDNL; LSKNAKNKKPTVDNLL; SKNAKNKKPTVDNLLV; KNAKNKKPTVDNLLVA; NAKNKKPTVDNLLVAI; AKNKKPTVDNLLVAIN; KNKKPTVDNLLVAINT; NKKPTVDNLLVAINTL; KKPTVDNLLVAINTLK; KPTVDNLLVAINTLKN; PTVDNLLVAINTLKNP; TVDNLLVAINTLKNPP; VDNLLVAINTLKNPPK; DNLLVAINTLKNPPKT; NLLVAINTLKNPPKTA; LLVAINTLKNPPKTAG; LVAINTLKNPPKTAGK; VAINTLKNPPKTAGKN; AINTLKNPPKTAGKNK; INTLKNPPKTAGKNKS; NTLKNPPKTAGKNKSN; TLKNPPKTAGKNKSNS; LKNPPKTAGKNKSNSA; KNPPKTAGKNKSNSAA; NPPKTAGKNKSNSAAA; PPKTAGKNKSNSAAAL; PKTAGKNKSNSAAALK; KTAGKNKSNSAAALKQ; TAGKNKSNSAAALKQP; AGKNKSNSAAALKQPN; GKNKSNSAAALKQPNN; KNKSNSAAALKQPNNA; NKSNSAAALKQPNNAN; KSNSAAALKQPNNANA; SNSAAALKQPNNANAL; NSAAALKQPNNANALK; SAAALKQPNNANALKQ; AAALKQPNNANALKQI; AALKQPNNANALKQID; ALKQPNNANALKQIDP; LKQPNNANALKQIDPE; KQPNNANALKQIDPEA; QPNNANALKQIDPEAK; PNNANALKQIDPEAKE; NNANALKQIDPEAKEL; NANALKQIDPEAKELI; ANALKQIDPEAKELIQ; NALKQIDPEAKELIQK; ALKQIDPEAKELIQKI; LKQIDPEAKELIQKIL; KQIDPEAKELIQKILE; QIDPEAKELIQKILER; IDPEAKELIQKILERS; DPEAKELIQKILERSE; PEAKELIQKILERSED; EAKELIQKILERSEDI; AKELIQKILERSEDIV; KELIQKILERSEDIVQ; ELIQKILERSEDIVQI; LIQKILERSEDIVQIS; IQKILERSEDIVQISE; QKILERSEDIVQISEI; KILERSEDIVQISEID; ILERSEDIVQISEIDA; LERSEDIVQISEIDAN; ERSEDIVQISEIDANK; RSEDIVQISEIDANKG; SEDIVQISEIDANKGE; EDIVQISEIDANKGEP; DIVQISEIDANKGEPD; IVQISEIDANKGEPDD; VQISEIDANKGEPDDQ; QISEIDANKGEPDDQF; ISEIDANKGEPDDQFE; SEIDANKGEPDDQFEM; EIDANKGEPDDQFEMK; IDANKGEPDDQFEMKA; DANKGEPDDQFEMKAE;

	ANKGEPDDQFEMKAEI; NKGEPDDQFEMKAEIF; KGEPDDQFEMKAEIFS; GEPDDQFEMKAEIFSK; EPDDQFEMKAEIFSKI; PDDQFEMKAEIFSKIF; DDQFEMKAEIFSKIFF; DQFEMKAEIFSKIFFN; QFEMKAEIFSKIFFNA; FEMKAEIFSKIFFNAG; EMKAEIFSKIFFNAGS; MKAEIFSKIFFNAGST; KAEIFSKIFFNAGSTV; AEIFSKIFFNAGSTVT; EIFSKIFFNAGSTVTF; IFSKIFFNAGSTVTFD; FSKIFFNAGSTVTFDD; SKIFFNAGSTVTFDDN; KIFFNAGSTVTFDDNE; IFFNAGSTVTFDDNEY; FFNAGSTVTFDDNEYV; FNAGSTVTFDDNEYVN; NAGSTVTFDDNEYVNE; AGSTVTFDDNEYVNER; GSTVTFDDNEYVNERR; STVTFDDNEYVNERRI; TVTFDDNEYVNERRIL; VTFDDNEYVNERRILY; TFDDNEYVNERRILYT; FDDNEYVNERRILYTS; DDNEYVNERRILYTSL; DNEYVNERRILYTSLN; NEYVNERRILYTSLNF; EYVNERRILYTSLNFN; YVNERRILYTSLNFNE; VNERRILYTSLNFNEN; NERRILYTSLNFNENK; ERRILYTSLNFNENKI; RRILYTSLNFNENKIL; RILYTSLNFNENKILN; ILYTSLNFNENKILNL; LYTSLNFNENKILNLG; YTSLNFNENKILNLGK; TSLNFNENKILNLGKI; SLNFNENKILNLGKIL; LNFNENKILNLGKILS; NFNENKILNLGKILSK; FNENKILNLGKILSKL; NENKILNLGKILSKLS; ENKILNLGKILSKLSQ; NKILNLGKILSKLSQD; KILNLGKILSKLSQDS; ILNLGKILSKLSQDSN; LNLGKILSKLSQDSNY; NLGKILSKLSQDSNYR; LGKILSKLSQDSNYRS; GKILSKLSQDSNYRSL; KILSKLSQDSNYRSLV; ILSKLSQDSNYRSLVK; LSKLSQDSNYRSLVKE; SKLSQDSNYRSLVKEI; KLSQDSNYRSLVKEIL; LSQDSNYRSLVKEILI; SQDSNYRSLVKEILIN; QDSNYRSLVKEILINR; DSNYRSLVKEILINRG; SNYRSLVKEILINRGF; NYRSLVKEILINRGFS; YRSLVKEILINRGFSI; RSLVKEILINRGFSIQ; SLVKEILINRGFSIQL; LVKEILINRGFSIQLA; VKEILINRGFSIQLAI; KEILINRGFSIQLAIE; EILINRGFSIQLAIEE; ILINRGFSIQLAIEEI; LINRGFSIQLAIEEIS; INRGFSIQLAIEEISL; NRGFSIQLAIEEISLR; RGFSIQLAIEEISLRT; GFSIQLAIEEISLRTL; FSIQLAIEEISLRTLN; SIQLAIEEISLRTLNV; IQLAIEEISLRTLNVK; QLAIEEISLRTLNVKD; LAIEEISLRTLNVKDK; AIEEISLRTLNVKDKI; IEEISLRTLNVKDKIQ; EEISLRTLNVKDKIQH; EISLRTLNVKDKIQHL; ISLRTLNVKDKIQHLN; SLRTLNVKDKIQHLNK; LRTLNVKDKIQHLNKP; RTLNVKDKIQHLNKPN; TLNVKDKIQHLNKPNL; LNVKDKIQHLNKPNLK; NVKDKIQHLNKPNLKT; VKDKIQHLNKPNLKTL; KDKIQHLNKPNLKTLY; DKIQHLNKPNLKTLYH; KIQHLNKPNLKTLYHD; IQHLNKPNLKTLYHDF; QHLNKPNLKTLYHDFN; HLNKPNLKTLYHDFNK; LNKPNLKTLYHDFNKL; NKPNLKTLYHDFNKLI; KPNLKTLYHDFNKLIP; PNLKTLYHDFNKLIPL; NLKTLYHDFNKLIPLK; LKTLYHDFNKLIPLKE; KTLYHDFNKLIPLKEK; TLYHDFNKLIPLKEKW; LYHDFNKLIPLKEKWL; YHDFNKLIPLKEKWLK; HDFNKLIPLKEKWLKD; DFNKLIPLKEKWLKDV; FNKLIPLKEKWLKDVD; NKLIPLKEKWLKDVDD; KLIPLKEKWLKDVDDI; LIPLKEKWLKDVDDII; IPLKEKWLKDVDDIIK; PLKEKWLKDVDDIIKD; LKEKWLKDVDDIIKDY; KEKWLKDVDDIIKDYN; EKWLKDVDDIIKDYNA; KWLKDVDDIIKDYNAN; WLKDVDDIIKDYNANP; LKDVDDIIKDYNANPE; KDVDDIIKDYNANPEL; DVDDIIKDYNANPELR; VDDIIKDYNANPELRT; DDIIKDYNANPELRTD; DIIKDYNANPELRTDI; IIKDYNANPELRTDIS; IKDYNANPELRTDISK; KDYNANPELRTDISKL; DYNANPELRTDISKLN; YNANPELRTDISKLND; NANPELRTDISKLNDY; ANPELRTDISKLNDYI; NPELRTDISKLNDYII; PELRTDISKLNDYIIS; ELRTDISKLNDYIISK; LRTDISKLNDYIISKN; RTDISKLNDYIISKNS; TDISKLNDYIISKNSK; DISKLNDYIISKNSKA; ISKLNDYIISKNSKAQ; SKLNDYIISKNSKAQF; KLNDYIISKNSKAQFT; LNDYIISKNSKAQFTD; NDYIISKNSKAQFTDI; DYIISKNSKAQFTDIH;

	YIISKNSKAQFTDIHN; IISKNSKAQFTDIHNI; ISKNSKAQFTDIHNII; SKNSKAQFTDIHNIIL; KNSKAQFTDIHNIILN; NSKAQFTDIHNIILNL; SKAQFTDIHNIILNLI; KAQFTDIHNIILNLIN; AQFTDIHNIILNLINT; QFTDIHNIILNLINTT; FTDIHNIILNLINTTT; TDIHNIILNLINTTTN; DIHNIILNLINTTTNI; IHNIILNLINTTTNIL; HNIILNLINTTTNILA; NIILNLINTTTNILAP; IILNLINTTTNILAPI; ILNLINTTTNILAPIQ;
Seq 42	13 mers: MKKVKSKYLALGL; KKVKSKYLALGLL; KVKSKYLALGLLF; VKSKYLALGLLFG; KSKYLALGLLFGF; SKYLALGLLFGFI; KYLALGLLFGFIS; YLALGLLFGFISC; LALGLLFGFISCD; ALGLLFGFISCDL; LGLLFGFISCDLF; GLLFGFISCDLFI; LLFGFISCDLFIR; LFGFISCDLFIRY; FGFISCDLFIRYE; GFISCDLFIRYEM; FISCDLFIRYEMK; ISCDLFIRYEMKE; SCDLFIRYEMKEE; CDLFIRYEMKEES; DLFIRYEMKEESP; LFIRYEMKEESPG; FIRYEMKEESPGL; IRYEMKEESPGLF; RYEMKEESPGLFD; YEMKEESPGLFDK; EMKEESPGLFDKG; MKEESPGLFDKGN; KEESPGLFDKGNS; EESPGLFDKGNSI; ESPGLFDKGNSIL; SPGLFDKGNSILE; PGLFDKGNSILET; GLFDKGNSILETS; LFDKGNSILETSE; FDKGNSILETSEE; DKGNSILETSEES; KGNSILETSEESI; GNSILETSEESIK; NSILETSEESIKK; SILETSEESIKKP; ILETSEESIKKPM; LETSEESIKKPMN; ETSEESIKKPMNK; TSEESIKKPMNKK; SEESIKKPMNKKG; EESIKKPMNKKGK; ESIKKPMNKKGKG; SIKKPMNKKGKGK; IKKPMNKKGKGKI; KKPMNKKGKGKIA; KPMNKKGKGKIAR; PMNKKGKGKIARK; MNKKGKGKIARKK; NKKGKGKIARKKG; KKGKGKIARKKGK; KGKGKIARKKGKS; GKGKIARKKGKSK; KGKIARKKGKSKV; GKIARKKGKSKVS; KIARKKGKSKVSR; IARKKGKSKVSRK; ARKKGKSKVSRKE; RKKGKSKVSRKEP; KKGKSKVSRKEPY; KGKSKVSRKEPYI; GKSKVSRKEPYIH; KSKVSRKEPYIHS; SKVSRKEPYIHSL; KVSRKEPYIHSLK; VSRKEPYIHSLKR; SRKEPYIHSLKRD; RKEPYIHSLKRDS; KEPYIHSLKRDSA; EPYIHSLKRDSAN; PYIHSLKRDSANK; YIHSLKRDSANKS; IHSLKRDSANKSN; HSLKRDSANKSNF; SLKRDSANKSNFL; LKRDSANKSNFLQ; KRDSANKSNFLQK; RDSANKSNFLQKN; DSANKSNFLQKNV; SANKSNFLQKNVI; ANKSNFLQKNVIL; NKSNFLQKNVILE; KSNFLQKNVILEE; SNFLQKNVILEEE; NFLQKNVILEEES; FLQKNVILEEESL; LQKNVILEEESLK; QKNVILEEESLKT; KNVILEEESLKTE; NVILEEESLKTEL; VILEEESLKTELL; ILEEESLKTELLK; LEEESLKTELLKE; EEESLKTELLKEQ; EESLKTELLKEQS; ESLKTELLKEQSE; SLKTELLKEQSET; LKTELLKEQSETR; KTELLKEQSETRK; TELLKEQSETRKE; ELLKEQSETRKEK; LLKEQSETRKEKI; LKEQSETRKEKIQ; KEQSETRKEKIQK; EQSETRKEKIQKQ; QSETRKEKIQKQQ; SETRKEKIQKQQD; ETRKEKIQKQQDE; TRKEKIQKQQDEY; RKEKIQKQQDEYK; KEKIQKQQDEYKG; EKIQKQQDEYKGM; KIQKQQDEYKGMT; IQKQQDEYKGMTQ; QKQQDEYKGMTQG; KQQDEYKGMTQGS; QQDEYKGMTQGSL; QDEYKGMTQGSLN; DEYKGMTQGSLNS; EYKGMTQGSLNSL; YKGMTQGSLNSLS;

	KGMTQGSLNSLSG; GMTQGSLNSLSGE; MTQGSLNSLSGES; TQGSLNSLSGESG; QGSLNSLSGESGE; GSLNSLSGESGEL; SLNSLSGESGELK; LNSLSGESGELKE; NSLSGESGELKET; SLSGESGELKETI; LSGESGELKETIE; SGESGELKETIES; GESGELKETIESN; ESGELKETIESNE; SGELKETIESNEI; GELKETIESNEID; ELKETIESNEIDI; LKETIESNEIDIT; KETIESNEIDITI; ETIESNEIDITID; TIESNEIDITIDS; IESNEIDITIDSD; ESNEIDITIDSDL; SNEIDITIDSDLR; NEIDITIDSDLRP; EIDITIDSDLRPK; IDITIDSDLRPKS; DITIDSDLRPKSS; ITIDSDLRPKSSL; TIDSDLRPKSSLQ; IDSDLRPKSSLQD; DSDLRPKSSLQDI; SDLRPKSSLQDIA; DLRPKSSLQDIAG; LRPKSSLQDIAGS; RPKSSLQDIAGSN; PKSSLQDIAGSNS; KSSLQDIAGSNSI; SSLQDIAGSNSIS; SLQDIAGSNSISY; LQDIAGSNSISYT; QDIAGSNSISYTD; DIAGSNSISYTDE; IAGSNSISYTDEI; AGSNSISYTDEIE; GSNSISYTDEIEE; SNSISYTDEIEEE; NSISYTDEIEEED; SISYTDEIEEEDY; ISYTDEIEEEDYA; SYTDEIEEEDYAR; YTDEIEEEDYARY; TDEIEEEDYARYY; DEIEEEDYARYYL; EIEEEDYARYYLD; IEEEDYARYYLDE; EEEDYARYYLDED; EEDYARYYLDEDD; EDYARYYLDEDDE; DYARYYLDEDDED; YARYYLDEDDEDD; ARYYLDEDDEDDE; RYYLDEDDEDDEY; YYLDEDDEDDEYY; YLDEDDEDDEYYE; LDEDDEDDEYYED; DEDDEDDEYYEDD; EDDEDDEYYEDDY; DDEDDEYYEDDYE; DEDDEYYEDDYEE; EDDEYYEDDYEEI; DDEYYEDDYEEIR; DEYYEDDYEEIRL; EYYEDDYEEIRLS; YYEDDYEEIRLSN; YEDDYEEIRLSNR; EDDYEEIRLSNRY; DDYEEIRLSNRYQ; DYEEIRLSNRYQS; YEEIRLSNRYQSY; EEIRLSNRYQSYL; EIRLSNRYQSYLE; IRLSNRYQSYLEG; RLSNRYQSYLEGV; LSNRYQSYLEGVK; SNRYQSYLEGVKY; NRYQSYLEGVKYN; RYQSYLEGVKYNV; YQSYLEGVKYNVD; QSYLEGVKYNVDS; SYLEGVKYNVDSA; YLEGVKYNVDSAI; LEGVKYNVDSAIN; EGVKYNVDSAINT; GVKYNVDSAINTI; VKYNVDSAINTIN; KYNVDSAINTINK; YNVDSAINTINKI; NVDSAINTINKIY; VDSAINTINKIYD; DSAINTINKIYDT; SAINTINKIYDTY; AINTINKIYDTYT; INTINKIYDTYTL; NTINKIYDTYTLF; TINKIYDTYTLFS; INKIYDTYTLFST; NKIYDTYTLFSTK; KIYDTYTLFSTKL; IYDTYTLFSTKLT; YDTYTLFSTKLTQ; DTYTLFSTKLTQM; TYTLFSTKLTQMY; YTLFSTKLTQMYS; TLFSTKLTQMYST; LFSTKLTQMYSTR; FSTKLTQMYSTRL; STKLTQMYSTRLD; TKLTQMYSTRLDN; KLTQMYSTRLDNL; LTQMYSTRLDNLA; TQMYSTRLDNLAK; QMYSTRLDNLAKA; MYSTRLDNLAKAK; YSTRLDNLAKAKA; STRLDNLAKAKAK; TRLDNLAKAKAKE; RLDNLAKAKAKEE; LDNLAKAKAKEEA; DNLAKAKAKEEAA; NLAKAKAKEEAAK; LAKAKAKEEAAKF; AKAKAKEEAAKFT; KAKAKEEAAKFTK; AKAKEEAAKFTKE; KAKEEAAKFTKED; AKEEAAKFTKEDL; KEEAAKFTKEDLE; EEAAKFTKEDLEK; EAAKFTKEDLEKN; AAKFTKEDLEKNF; AKFTKEDLEKNFK; KFTKEDLEKNFKT; FTKEDLEKNFKTL; TKEDLEKNFKTLL; KEDLEKNFKTLLN; EDLEKNFKTLLNY; DLEKNFKTLLNYI; LEKNFKTLLNYIQ; EKNFKTLLNYIQV; KNFKTLLNYIQVS; NFKTLLNYIQVSV; FKTLLNYIQVSVK;

KTLLNYIQVSVKT; TLLNYIQVSVKTA; LLNYIQVSVKTAA;
LNYIQVSVKTAAN; NYIQVSVKTAANF; YIQVSVKTAANFV;
IQVSVKTAANFVY; QVSVKTAANFVYI; VSVKTAANFVYIN;
SVKTAANFVYIND; VKTAANFVYINDT; KTAANFVYINDTH;
TAANFVYINDTHA; AANFVYINDTHAK; ANFVYINDTHAKR;
NFVYINDTHAKRK; FVYINDTHAKRKL; VYINDTHAKRKLE;
YINDTHAKRKLEN; INDTHAKRKLENI; NDTHAKRKLENIE;
DTHAKRKLENIEA; THAKRKLENIEAE; HAKRKLENIEAEI;
AKRKLENIEAEIK; KRKLENIEAEIKT; RKLENIEAEIKTL;
KLENIEAEIKTLI; LENIEAEIKTLIA; ENIEAEIKTLIAK;
NIEAEIKTLIAKI; IEAEIKTLIAKIK; EAEIKTLIAKIKE;
AEIKTLIAKIKEQ; EIKTLIAKIKEQS; IKTLIAKIKEQSN;
KTLIAKIKEQSNL; TLIAKIKEQSNLY; LIAKIKEQSNLYE;
IAKIKEQSNLYEA; AKIKEQSNLYEAY; KIKEQSNLYEAYK;
IKEQSNLYEAYKA; KEQSNLYEAYKAI; EQSNLYEAYKAIV;
QSNLYEAYKAIVT; SNLYEAYKAIVTS; NLYEAYKAIVTSI;
LYEAYKAIVTSIL; YEAYKAIVTSILL; EAYKAIVTSILLM;
AYKAIVTSILLMR; YKAIVTSILLMRD; KAIVTSILLMRDS;
AIVTSILLMRDSL; IVTSILLMRDSLK; VTSILLMRDSLKE;
TSILLMRDSLKEV; SILLMRDSLKEVQ; ILLMRDSLKEVQG;
LLMRDSLKEVQGI; LMRDSLKEVQGII; MRDSLKEVQGIID;
RDSLKEVQGIIDK; DSLKEVQGIIDKN; SLKEVQGIIDKNG;
LKEVQGIIDKNGV; KEVQGIIDKNGVW; EVQGIIDKNGVWY;

14 mers:
MKKVKSKYLALGLL; KKVKSKYLALGLLF; KVKSKYLALGLLFG;
VKSKYLALGLLFGF; KSKYLALGLLFGFI; SKYLALGLLFGFIS;
KYLALGLLFGFISC; YLALGLLFGFISCD; LALGLLFGFISCDL;
ALGLLFGFISCDLF; LGLLFGFISCDLFI; GLLFGFISCDLFIR;
LLFGFISCDLFIRY; LFGFISCDLFIRYE; FGFISCDLFIRYEM;
GFISCDLFIRYEMK; FISCDLFIRYEMKE; ISCDLFIRYEMKEE;
SCDLFIRYEMKEES; CDLFIRYEMKEESP; DLFIRYEMKEESPG;
LFIRYEMKEESPGL; FIRYEMKEESPGLF; IRYEMKEESPGLFD;
RYEMKEESPGLFDK; YEMKEESPGLFDKG; EMKEESPGLFDKGN;
MKEESPGLFDKGNS; KEESPGLFDKGNSI; EESPGLFDKGNSIL;
ESPGLFDKGNSILE; SPGLFDKGNSILET; PGLFDKGNSILETS;
GLFDKGNSILETSE; LFDKGNSILETSEE; FDKGNSILETSEES;
DKGNSILETSEESI; KGNSILETSEESIK; GNSILETSEESIKK;
NSILETSEESIKKP; SILETSEESIKKPM; ILETSEESIKKPMN;
LETSEESIKKPMNK; ETSEESIKKPMNKK; TSEESIKKPMNKKG;
SEESIKKPMNKKGK; EESIKKPMNKKGKG; ESIKKPMNKKGKGK;
SIKKPMNKKGKGKI; IKKPMNKKGKGKIA; KKPMNKKGKGKIAR;
KPMNKKGKGKIARK; PMNKKGKGKIARKK; MNKKGKGKIARKKG;
NKKGKGKIARKKGK; KKGKGKIARKKGKS; KGKGKIARKKGKSK;
GKGKIARKKGKSKV; KGKIARKKGKSKVS; GKIARKKGKSKVSR;
KIARKKGKSKVSRK; IARKKGKSKVSRKE; ARKKGKSKVSRKEP;
RKKGKSKVSRKEPY; KKGKSKVSRKEPYI; KGKSKVSRKEPYIH;
GKSKVSRKEPYIHS; KSKVSRKEPYIHSL; SKVSRKEPYIHSLK;
KVSRKEPYIHSLKR; VSRKEPYIHSLKRD; SRKEPYIHSLKRDS;
RKEPYIHSLKRDSA; KEPYIHSLKRDSAN; EPYIHSLKRDSANK;
PYIHSLKRDSANKS; YIHSLKRDSANKSN; IHSLKRDSANKSNF;

	HSLKRDSANKSNFL; SLKRDSANKSNFLQ; LKRDSANKSNFLQK; KRDSANKSNFLQKN; RDSANKSNFLQKNV; DSANKSNFLQKNVI; SANKSNFLQKNVIL; ANKSNFLQKNVILE; NKSNFLQKNVILEE; KSNFLQKNVILEEE; SNFLQKNVILEEES; NFLQKNVILEEESL; FLQKNVILEEESLK; LQKNVILEEESLKT; QKNVILEEESLKTE; KNVILEEESLKTEL; NVILEEESLKTELL; VILEEESLKTELLK; ILEEESLKTELLKE; LEEESLKTELLKEQ; EEESLKTELLKEQS; EESLKTELLKEQSE; ESLKTELLKEQSET; SLKTELLKEQSETR; LKTELLKEQSETRK; KTELLKEQSETRKE; TELLKEQSETRKEK; ELLKEQSETRKEKI; LLKEQSETRKEKIQ; LKEQSETRKEKIQK; KEQSETRKEKIQKQ; EQSETRKEKIQKQQ; QSETRKEKIQKQQD; SETRKEKIQKQQDE; ETRKEKIQKQQDEY; TRKEKIQKQQDEYK; RKEKIQKQQDEYKG; KEKIQKQQDEYKGM; EKIQKQQDEYKGMT; KIQKQQDEYKGMTQ; IQKQQDEYKGMTQG; QKQQDEYKGMTQGS; KQQDEYKGMTQGSL; QQDEYKGMTQGSLN; QDEYKGMTQGSLNS; DEYKGMTQGSLNSL; EYKGMTQGSLNSLS; YKGMTQGSLNSLSG; KGMTQGSLNSLSGE; GMTQGSLNSLSGES; MTQGSLNSLSGESG; TQGSLNSLSGESGE; QGSLNSLSGESGEL; GSLNSLSGESGELK; SLNSLSGESGELKE; LNSLSGESGELKET; NSLSGESGELKETI; SLSGESGELKETIE; LSGESGELKETIES; SGESGELKETIESN; GESGELKETIESNE; ESGELKETIESNEI; SGELKETIESNEID; GELKETIESNEIDI; ELKETIESNEIDIT; LKETIESNEIDITI; KETIESNEIDITID; ETIESNEIDITIDS; TIESNEIDITIDSD; IESNEIDITIDSDL; ESNEIDITIDSDLR; SNEIDITIDSDLRP; NEIDITIDSDLRPK; EIDITIDSDLRPKS; IDITIDSDLRPKSS; DITIDSDLRPKSSL; ITIDSDLRPKSSLQ; TIDSDLRPKSSLQD; IDSDLRPKSSLQDI; DSDLRPKSSLQDIA; SDLRPKSSLQDIAG; DLRPKSSLQDIAGS; LRPKSSLQDIAGSN; RPKSSLQDIAGSNS; PKSSLQDIAGSNSI; KSSLQDIAGSNSIS; SSLQDIAGSNSISY; SLQDIAGSNSISYT; LQDIAGSNSISYTD; QDIAGSNSISYTDE; DIAGSNSISYTDEI; IAGSNSISYTDEIE; AGSNSISYTDEIEE; GSNSISYTDEIEEE; SNSISYTDEIEEED; NSISYTDEIEEEDY; SISYTDEIEEEDYA; ISYTDEIEEEDYAR; SYTDEIEEEDYARY; YTDEIEEEDYARYY; TDEIEEEDYARYYL; DEIEEEDYARYYLD; EIEEEDYARYYLDE; IEEEDYARYYLDED; EEEDYARYYLDEDD; EEDYARYYLDEDDE; EDYARYYLDEDDED; DYARYYLDEDDEDD; YARYYLDEDDEDDE; ARYYLDEDDEDDEY; RYYLDEDDEDDEYY; YYLDEDDEDDEYYE; YLDEDDEDDEYYED; LDEDDEDDEYYEDD; DEDDEDDEYYEDDY; EDDEDDEYYEDDYE; DDEDDEYYEDDYEE; DEDDEYYEDDYEEI; EDDEYYEDDYEEIR; DDEYYEDDYEEIRL; DEYYEDDYEEIRLS; EYYEDDYEEIRLSN; YYEDDYEEIRLSNR; YEDDYEEIRLSNRY; EDDYEEIRLSNRYQ; DDYEEIRLSNRYQS; DYEEIRLSNRYQSY; YEEIRLSNRYQSYL; EEIRLSNRYQSYLE; EIRLSNRYQSYLEG; IRLSNRYQSYLEGV; RLSNRYQSYLEGVK; LSNRYQSYLEGVKY; SNRYQSYLEGVKYN; NRYQSYLEGVKYNV; RYQSYLEGVKYNVD; YQSYLEGVKYNVDS; QSYLEGVKYNVDSA; SYLEGVKYNVDSAI; YLEGVKYNVDSAIN; LEGVKYNVDSAINT; EGVKYNVDSAINTI; GVKYNVDSAINTIN; VKYNVDSAINTINK; KYNVDSAINTINKI; YNVDSAINTINKIY; NVDSAINTINKIYD; VDSAINTINKIYDT; DSAINTINKIYDTY; SAINTINKIYDTYT; AINTINKIYDTYTL; INTINKIYDTYTLF; NTINKIYDTYTLFS;

	TINKIYDTYTLFST; INKIYDTYTLFSTK; NKIYDTYTLFSTKL; KIYDTYTLFSTKLT; IYDTYTLFSTKLTQ; YDTYTLFSTKLTQM; DTYTLFSTKLTQMY; TYTLFSTKLTQMYS; YTLFSTKLTQMYST; TLFSTKLTQMYSTR; LFSTKLTQMYSTRL; FSTKLTQMYSTRLD; STKLTQMYSTRLDN; TKLTQMYSTRLDNL; KLTQMYSTRLDNLA; LTQMYSTRLDNLAK; TQMYSTRLDNLAKA; QMYSTRLDNLAKAK; MYSTRLDNLAKAKA; YSTRLDNLAKAKAK; STRLDNLAKAKAKE; TRLDNLAKAKAKEE; RLDNLAKAKAKEEA; LDNLAKAKAKEEAA; DNLAKAKAKEEAAK; NLAKAKAKEEAAKF; LAKAKAKEEAAKFT; AKAKAKEEAAKFTK; KAKAKEEAAKFTKE; AKAKEEAAKFTKED; KAKEEAAKFTKEDL; AKEEAAKFTKEDLE; KEEAAKFTKEDLEK; EEAAKFTKEDLEKN; EAAKFTKEDLEKNF; AAKFTKEDLEKNFK; AKFTKEDLEKNFKT; KFTKEDLEKNFKTL; FTKEDLEKNFKTLL; TKEDLEKNFKTLLN; KEDLEKNFKTLLNY; EDLEKNFKTLLNYI; DLEKNFKTLLNYIQ; LEKNFKTLLNYIQV; EKNFKTLLNYIQVS; KNFKTLLNYIQVSV; NFKTLLNYIQVSVK; FKTLLNYIQVSVKT; KTLLNYIQVSVKTA; TLLNYIQVSVKTAA; LLNYIQVSVKTAAN; LNYIQVSVKTAANF; NYIQVSVKTAANFV; YIQVSVKTAANFVY; IQVSVKTAANFVYI; QVSVKTAANFVYIN; VSVKTAANFVYIND; SVKTAANFVYINDT; VKTAANFVYINDTH; KTAANFVYINDTHA; TAANFVYINDTHAK; AANFVYINDTHAKR; ANFVYINDTHAKRK; NFVYINDTHAKRKL; FVYINDTHAKRKLE; VYINDTHAKRKLEN; YINDTHAKRKLENI; INDTHAKRKLENIE; NDTHAKRKLENIEA; DTHAKRKLENIEAE; THAKRKLENIEAEI; HAKRKLENIEAEIK; AKRKLENIEAEIKT; KRKLENIEAEIKTL; RKLENIEAEIKTLI; KLENIEAEIKTLIA; LENIEAEIKTLIAK; ENIEAEIKTLIAKI; NIEAEIKTLIAKIK; IEAEIKTLIAKIKE; EAEIKTLIAKIKEQ; AEIKTLIAKIKEQS; EIKTLIAKIKEQSN; IKTLIAKIKEQSNL; KTLIAKIKEQSNLY; TLIAKIKEQSNLYE; LIAKIKEQSNLYEA; IAKIKEQSNLYEAY; AKIKEQSNLYEAYK; KIKEQSNLYEAYKA; IKEQSNLYEAYKAI; KEQSNLYEAYKAIV; EQSNLYEAYKAIVT; QSNLYEAYKAIVTS; SNLYEAYKAIVTSI; NLYEAYKAIVTSIL; LYEAYKAIVTSILL; YEAYKAIVTSILLM; EAYKAIVTSILLMR; AYKAIVTSILLMRD; YKAIVTSILLMRDS; KAIVTSILLMRDSL; AIVTSILLMRDSLK; IVTSILLMRDSLKE; VTSILLMRDSLKEV; TSILLMRDSLKEVQ; SILLMRDSLKEVQG; ILLMRDSLKEVQGI; LLMRDSLKEVQGII; LMRDSLKEVQGIID; MRDSLKEVQGIIDK; RDSLKEVQGIIDKN; DSLKEVQGIIDKNG; SLKEVQGIIDKNGV; LKEVQGIIDKNGVW; KEVQGIIDKNGVWY; 15 mers: MKKVKSKYLALGLLF; KKVKSKYLALGLLFG; KVKSKYLALGLLFGF; VKSKYLALGLLFGFI; KSKYLALGLLFGFIS; SKYLALGLLFGFISC; KYLALGLLFGFISCD; YLALGLLFGFISCDL; LALGLLFGFISCDLF; ALGLLFGFISCDLFI; LGLLFGFISCDLFIR; GLLFGFISCDLFIRY; LLFGFISCDLFIRYE; LFGFISCDLFIRYEM; FGFISCDLFIRYEMK; GFISCDLFIRYEMKE; FISCDLFIRYEMKEE; ISCDLFIRYEMKEES; SCDLFIRYEMKEESP; CDLFIRYEMKEESPG; DLFIRYEMKEESPGL; LFIRYEMKEESPGLF; FIRYEMKEESPGLFD; IRYEMKEESPGLFDK; RYEMKEESPGLFDKG; YEMKEESPGLFDKGN; EMKEESPGLFDKGNS; MKEESPGLFDKGNSI; KEESPGLFDKGNSIL; EESPGLFDKGNSILE;

	ESPGLFDKGNSILET; SPGLFDKGNSILETS; PGLFDKGNSILETSE; GLFDKGNSILETSEE; LFDKGNSILETSEES; FDKGNSILETSEESI; DKGNSILETSEESIK; KGNSILETSEESIKK; GNSILETSEESIKKP; NSILETSEESIKKPM; SILETSEESIKKPMN; ILETSEESIKKPMNK; LETSEESIKKPMNKK; ETSEESIKKPMNKKG; TSEESIKKPMNKKGK; SEESIKKPMNKKGKG; EESIKKPMNKKGKGK; ESIKKPMNKKGKGKI; SIKKPMNKKGKGKIA; IKKPMNKKGKGKIAR; KKPMNKKGKGKIARK; KPMNKKGKGKIARKK; PMNKKGKGKIARKKG; MNKKGKGKIARKKGK; NKKGKGKIARKKGKS; KKGKGKIARKKGKSK; KGKGKIARKKGKSKV; GKGKIARKKGKSKVS; KGKIARKKGKSKVSR; GKIARKKGKSKVSRK; KIARKKGKSKVSRKE; IARKKGKSKVSRKEP; ARKKGKSKVSRKEPY; RKKGKSKVSRKEPYI; KKGKSKVSRKEPYIH; KGKSKVSRKEPYIHS; GKSKVSRKEPYIHSL; KSKVSRKEPYIHSLK; SKVSRKEPYIHSLKR; KVSRKEPYIHSLKRD; VSRKEPYIHSLKRDS; SRKEPYIHSLKRDSA; RKEPYIHSLKRDSAN; KEPYIHSLKRDSANK; EPYIHSLKRDSANKS; PYIHSLKRDSANKSN; YIHSLKRDSANKSNF; IHSLKRDSANKSNFL; HSLKRDSANKSNFLQ; SLKRDSANKSNFLQK; LKRDSANKSNFLQKN; KRDSANKSNFLQKNV; RDSANKSNFLQKNVI; DSANKSNFLQKNVIL; SANKSNFLQKNVILE; ANKSNFLQKNVILEE; NKSNFLQKNVILEEE; KSNFLQKNVILEEES; SNFLQKNVILEEESL; NFLQKNVILEEESLK; FLQKNVILEEESLKT; LQKNVILEEESLKTE; QKNVILEEESLKTEL; KNVILEEESLKTELL; NVILEEESLKTELLK; VILEEESLKTELLKE; ILEEESLKTELLKEQ; LEEESLKTELLKEQS; EEESLKTELLKEQSE; EESLKTELLKEQSET; ESLKTELLKEQSETR; SLKTELLKEQSETRK; LKTELLKEQSETRKE; KTELLKEQSETRKEK; TELLKEQSETRKEKI; ELLKEQSETRKEKIQ; LLKEQSETRKEKIQK; LKEQSETRKEKIQKQ; KEQSETRKEKIQKQQ; EQSETRKEKIQKQQD; QSETRKEKIQKQQDE; SETRKEKIQKQQDEY; ETRKEKIQKQQDEYK; TRKEKIQKQQDEYKG; RKEKIQKQQDEYKGM; KEKIQKQQDEYKGMT; EKIQKQQDEYKGMTQ; KIQKQQDEYKGMTQG; IQKQQDEYKGMTQGS; QKQQDEYKGMTQGSL; KQQDEYKGMTQGSLN; QQDEYKGMTQGSLNS; QDEYKGMTQGSLNSL; DEYKGMTQGSLNSLS; EYKGMTQGSLNSLSG; YKGMTQGSLNSLSGE; KGMTQGSLNSLSGES; GMTQGSLNSLSGESG; MTQGSLNSLSGESGE; TQGSLNSLSGESGEL; QGSLNSLSGESGELK; GSLNSLSGESGELKE; SLNSLSGESGELKET; LNSLSGESGELKETI; NSLSGESGELKETIE; SLSGESGELKETIES; LSGESGELKETIESN; SGESGELKETIESNE; GESGELKETIESNEI; ESGELKETIESNEID; SGELKETIESNEIDI; GELKETIESNEIDIT; ELKETIESNEIDITI; LKETIESNEIDITID; KETIESNEIDITIDS; ETIESNEIDITIDSD; TIESNEIDITIDSDL; IESNEIDITIDSDLR; ESNEIDITIDSDLRP; SNEIDITIDSDLRPK; NEIDITIDSDLRPKS; EIDITIDSDLRPKSS; IDITIDSDLRPKSSL; DITIDSDLRPKSSLQ; ITIDSDLRPKSSLQD; TIDSDLRPKSSLQDI; IDSDLRPKSSLQDIA; DSDLRPKSSLQDIAG; SDLRPKSSLQDIAGS; DLRPKSSLQDIAGSN; LRPKSSLQDIAGSNS; RPKSSLQDIAGSNSI; PKSSLQDIAGSNSIS; KSSLQDIAGSNSISY; SSLQDIAGSNSISYT; SLQDIAGSNSISYTD; LQDIAGSNSISYTDE; QDIAGSNSISYTDEI; DIAGSNSISYTDEIE; IAGSNSISYTDEIEE; AGSNSISYTDEIEEE; GSNSISYTDEIEEED; SNSISYTDEIEEEDY; NSISYTDEIEEEDYA; SISYTDEIEEEDYAR; ISYTDEIEEEDYARY; SYTDEIEEEDYARYY; YTDEIEEEDYARYYL; TDEIEEEDYARYYLD; DEIEEEDYARYYLDE; EIEEEDYARYYLDED; IEEEDYARYYLDEDD; EEEDYARYYLDEDDE;

	EEDYARYYLDEDDED; EDYARYYLDEDDEDD; DYARYYLDEDDEDDE; YARYYLDEDDEDDEY; ARYYLDEDDEDDEYY; RYYLDEDDEDDEYYE; YYLDEDDEDDEYYED; YLDEDDEDDEYYEDD; LDEDDEDDEYYEDDY; DEDDEDDEYYEDDYE; EDDEDDEYYEDDYEE; DDEDDEYYEDDYEEI; DEDDEYYEDDYEEIR; EDDEYYEDDYEEIRL; DDEYYEDDYEEIRLS; DEYYEDDYEEIRLSN; EYYEDDYEEIRLSNR; YYEDDYEEIRLSNRY; YEDDYEEIRLSNRYQ; EDDYEEIRLSNRYQS; DDYEEIRLSNRYQSY; DYEEIRLSNRYQSYL; YEEIRLSNRYQSYLE; EEIRLSNRYQSYLEG; EIRLSNRYQSYLEGV; IRLSNRYQSYLEGVK; RLSNRYQSYLEGVKY; LSNRYQSYLEGVKYN; SNRYQSYLEGVKYNV; NRYQSYLEGVKYNVD; RYQSYLEGVKYNVDS; YQSYLEGVKYNVDSA; QSYLEGVKYNVDSAI; SYLEGVKYNVDSAIN; YLEGVKYNVDSAINT; LEGVKYNVDSAINTI; EGVKYNVDSAINTIN; GVKYNVDSAINTINK; VKYNVDSAINTINKI; KYNVDSAINTINKIY; YNVDSAINTINKIYD; NVDSAINTINKIYDT; VDSAINTINKIYDTY; DSAINTINKIYDTYT; SAINTINKIYDTYTL; AINTINKIYDTYTLF; INTINKIYDTYTLFS; NTINKIYDTYTLFST; TINKIYDTYTLFSTK; INKIYDTYTLFSTKL; NKIYDTYTLFSTKLT; KIYDTYTLFSTKLTQ; IYDTYTLFSTKLTQM; YDTYTLFSTKLTQMY; DTYTLFSTKLTQMYS; TYTLFSTKLTQMYST; YTLFSTKLTQMYSTR; TLFSTKLTQMYSTRL; LFSTKLTQMYSTRLD; FSTKLTQMYSTRLDN; STKLTQMYSTRLDNL; TKLTQMYSTRLDNLA; KLTQMYSTRLDNLAK; LTQMYSTRLDNLAKA; TQMYSTRLDNLAKAK; QMYSTRLDNLAKAKA; MYSTRLDNLAKAKAK; YSTRLDNLAKAKAKE; STRLDNLAKAKAKEE; TRLDNLAKAKAKEEA; RLDNLAKAKAKEEAA; LDNLAKAKAKEEAAK; DNLAKAKAKEEAAKF; NLAKAKAKEEAAKFT; LAKAKAKEEAAKFTK; AKAKAKEEAAKFTKE; KAKAKEEAAKFTKED; AKAKEEAAKFTKEDL; KAKEEAAKFTKEDLE; AKEEAAKFTKEDLEK; KEEAAKFTKEDLEKN; EEAAKFTKEDLEKNF; EAAKFTKEDLEKNFK; AAKFTKEDLEKNFKT; AKFTKEDLEKNFKTL; KFTKEDLEKNFKTLL; FTKEDLEKNFKTLLN; TKEDLEKNFKTLLNY; KEDLEKNFKTLLNYI; EDLEKNFKTLLNYIQ; DLEKNFKTLLNYIQV; LEKNFKTLLNYIQVS; EKNFKTLLNYIQVSV; KNFKTLLNYIQVSVK; NFKTLLNYIQVSVKT; FKTLLNYIQVSVKTA; KTLLNYIQVSVKTAA; TLLNYIQVSVKTAAN; LLNYIQVSVKTAANF; LNYIQVSVKTAANFV; NYIQVSVKTAANFVY; YIQVSVKTAANFVYI; IQVSVKTAANFVYIN; QVSVKTAANFVYIND; VSVKTAANFVYINDT; SVKTAANFVYINDTH; VKTAANFVYINDTHA; KTAANFVYINDTHAK; TAANFVYINDTHAKR; AANFVYINDTHAKRK; ANFVYINDTHAKRKL; NFVYINDTHAKRKLE; FVYINDTHAKRKLEN; VYINDTHAKRKLENI; YINDTHAKRKLENIE; INDTHAKRKLENIEA; NDTHAKRKLENIEAE; DTHAKRKLENIEAEI; THAKRKLENIEAEIK; HAKRKLENIEAEIKT; AKRKLENIEAEIKTL; KRKLENIEAEIKTLI; RKLENIEAEIKTLIA; KLENIEAEIKTLIAK; LENIEAEIKTLIAKI; ENIEAEIKTLIAKIK; NIEAEIKTLIAKIKE; IEAEIKTLIAKIKEQ; EAEIKTLIAKIKEQS; AEIKTLIAKIKEQSN; EIKTLIAKIKEQSNL; IKTLIAKIKEQSNLY; KTLIAKIKEQSNLYE; TLIAKIKEQSNLYEA; LIAKIKEQSNLYEAY; IAKIKEQSNLYEAYK; AKIKEQSNLYEAYKA; KIKEQSNLYEAYKAI; IKEQSNLYEAYKAIV; KEQSNLYEAYKAIVT; EQSNLYEAYKAIVTS; QSNLYEAYKAIVTSI; SNLYEAYKAIVTSIL; NLYEAYKAIVTSILL; LYEAYKAIVTSILLM; YEAYKAIVTSILLMR; EAYKAIVTSILLMRD; AYKAIVTSILLMRDS; YKAIVTSILLMRDSL; KAIVTSILLMRDSLK; AIVTSILLMRDSLKE; IVTSILLMRDSLKEV; VTSILLMRDSLKEVQ;

	TSILLMRDSLKEVQG; SILLMRDSLKEVQGI; ILLMRDSLKEVQGII; LLMRDSLKEVQGIID; LMRDSLKEVQGIIDK; MRDSLKEVQGIIDKN; RDSLKEVQGIIDKNG; DSLKEVQGIIDKNGV; SLKEVQGIIDKNGVW; LKEVQGIIDKNGVWY; 16 mers: MKKVKSKYLALGLLFG; KKVKSKYLALGLLFGF; KVKSKYLALGLLFGFI; VKSKYLALGLLFGFIS; KSKYLALGLLFGFISC; SKYLALGLLFGFISCD; KYLALGLLFGFISCDL; YLALGLLFGFISCDLF; LALGLLFGFISCDLFI; ALGLLFGFISCDLFIR; LGLLFGFISCDLFIRY; GLLFGFISCDLFIRYE; LLFGFISCDLFIRYEM; LFGFISCDLFIRYEMK; FGFISCDLFIRYEMKE; GFISCDLFIRYEMKEE; FISCDLFIRYEMKEES; ISCDLFIRYEMKEESP; SCDLFIRYEMKEESPG; CDLFIRYEMKEESPGL; DLFIRYEMKEESPGLF; LFIRYEMKEESPGLFD; FIRYEMKEESPGLFDK; IRYEMKEESPGLFDKG; RYEMKEESPGLFDKGN; YEMKEESPGLFDKGNS; EMKEESPGLFDKGNSI; MKEESPGLFDKGNSIL; KEESPGLFDKGNSILE; EESPGLFDKGNSILET; ESPGLFDKGNSILETS; SPGLFDKGNSILETSE; PGLFDKGNSILETSEE; GLFDKGNSILETSEES; LFDKGNSILETSEESI; FDKGNSILETSEESIK; DKGNSILETSEESIKK; KGNSILETSEESIKKP; GNSILETSEESIKKPM; NSILETSEESIKKPMN; SILETSEESIKKPMNK; ILETSEESIKKPMNKK; LETSEESIKKPMNKKG; ETSEESIKKPMNKKGK; TSEESIKKPMNKKGKG; SEESIKKPMNKKGKGK; EESIKKPMNKKGKGKI; ESIKKPMNKKGKGKIA; SIKKPMNKKGKGKIAR; IKKPMNKKGKGKIARK; KKPMNKKGKGKIARKK; KPMNKKGKGKIARKKG; PMNKKGKGKIARKKGK; MNKKGKGKIARKKGKS; NKKGKGKIARKKGKSK; KKGKGKIARKKGKSKV; KGKGKIARKKGKSKVS; GKGKIARKKGKSKVSR; KGKIARKKGKSKVSRK; GKIARKKGKSKVSRKE; KIARKKGKSKVSRKEP; IARKKGKSKVSRKEPY; ARKKGKSKVSRKEPYI; RKKGKSKVSRKEPYIH; KKGKSKVSRKEPYIHS; KGKSKVSRKEPYIHSL; GKSKVSRKEPYIHSLK; KSKVSRKEPYIHSLKR; SKVSRKEPYIHSLKRD; KVSRKEPYIHSLKRDS; VSRKEPYIHSLKRDSA; SRKEPYIHSLKRDSAN; RKEPYIHSLKRDSANK; KEPYIHSLKRDSANKS; EPYIHSLKRDSANKSN; PYIHSLKRDSANKSNF; YIHSLKRDSANKSNFL; IHSLKRDSANKSNFLQ; HSLKRDSANKSNFLQK; SLKRDSANKSNFLQKN; LKRDSANKSNFLQKNV; KRDSANKSNFLQKNVI; RDSANKSNFLQKNVIL; DSANKSNFLQKNVILE; SANKSNFLQKNVILEE; ANKSNFLQKNVILEEE; NKSNFLQKNVILEEES; KSNFLQKNVILEEESL; SNFLQKNVILEEESLK; NFLQKNVILEEESLKT; FLQKNVILEEESLKTE; LQKNVILEEESLKTEL; QKNVILEEESLKTELL; KNVILEEESLKTELLK; NVILEEESLKTELLKE; VILEEESLKTELLKEQ; ILEEESLKTELLKEQS; LEEESLKTELLKEQSE; EEESLKTELLKEQSET; EESLKTELLKEQSETR; ESLKTELLKEQSETRK; SLKTELLKEQSETRKE; LKTELLKEQSETRKEK; KTELLKEQSETRKEKI; TELLKEQSETRKEKIQ; ELLKEQSETRKEKIQK; LLKEQSETRKEKIQKQ; LKEQSETRKEKIQKQQ; KEQSETRKEKIQKQQD; EQSETRKEKIQKQQDE; QSETRKEKIQKQQDEY; SETRKEKIQKQQDEYK; ETRKEKIQKQQDEYKG; TRKEKIQKQQDEYKGM; RKEKIQKQQDEYKGMT; KEKIQKQQDEYKGMTQ; EKIQKQQDEYKGMTQG; KIQKQQDEYKGMTQGS; IQKQQDEYKGMTQGSL; QKQQDEYKGMTQGSLN; KQQDEYKGMTQGSLNS; QQDEYKGMTQGSLNSL; QDEYKGMTQGSLNSLS; DEYKGMTQGSLNSLSG; EYKGMTQGSLNSLSGE; YKGMTQGSLNSLSGES; KGMTQGSLNSLSGESG; GMTQGSLNSLSGESGE; MTQGSLNSLSGESGEL; TQGSLNSLSGESGELK; QGSLNSLSGESGELKE; GSLNSLSGESGELKET; SLNSLSGESGELKETI; LNSLSGESGELKETIE; NSLSGESGELKETIES;

	SLSGESGELKETIESN; LSGESGELKETIESNE; SGESGELKETIESNEI; GESGELKETIESNEID; ESGELKETIESNEIDI; SGELKETIESNEIDIT; GELKETIESNEIDITI; ELKETIESNEIDITID; LKETIESNEIDITIDS; KETIESNEIDITIDSD; ETIESNEIDITIDSDL; TIESNEIDITIDSDLR; IESNEIDITIDSDLRP; ESNEIDITIDSDLRPK; SNEIDITIDSDLRPKS; NEIDITIDSDLRPKSS; EIDITIDSDLRPKSSL; IDITIDSDLRPKSSLQ; DITIDSDLRPKSSLQD; ITIDSDLRPKSSLQDI; TIDSDLRPKSSLQDIA; IDSDLRPKSSLQDIAG; DSDLRPKSSLQDIAGS; SDLRPKSSLQDIAGSN; DLRPKSSLQDIAGSNS; LRPKSSLQDIAGSNSI; RPKSSLQDIAGSNSIS; PKSSLQDIAGSNSISY; KSSLQDIAGSNSISYT; SSLQDIAGSNSISYTD; SLQDIAGSNSISYTDE; LQDIAGSNSISYTDEI; QDIAGSNSISYTDEIE; DIAGSNSISYTDEIEE; IAGSNSISYTDEIEEE; AGSNSISYTDEIEEED; GSNSISYTDEIEEEDY; SNSISYTDEIEEEDYA; NSISYTDEIEEEDYAR; SISYTDEIEEEDYARY; ISYTDEIEEEDYARYY; SYTDEIEEEDYARYYL; YTDEIEEEDYARYYLD; TDEIEEEDYARYYLDE; DEIEEEDYARYYLDED; EIEEEDYARYYLDEDD; IEEEDYARYYLDEDDE; EEEDYARYYLDEDDED; EEDYARYYLDEDDEDD; EDYARYYLDEDDEDDE; DYARYYLDEDDEDDEY; YARYYLDEDDEDDEYY; ARYYLDEDDEDDEYYE; RYYLDEDDEDDEYYED; YYLDEDDEDDEYYEDD; YLDEDDEDDEYYEDDY; LDEDDEDDEYYEDDYE; DEDDEDDEYYEDDYEE; EDDEDDEYYEDDYEEI; DDEDDEYYEDDYEEIR; DEDDEYYEDDYEEIRL; EDDEYYEDDYEEIRLS; DDEYYEDDYEEIRLSN; DEYYEDDYEEIRLSNR; EYYEDDYEEIRLSNRY; YYEDDYEEIRLSNRYQ; YEDDYEEIRLSNRYQS; EDDYEEIRLSNRYQSY; DDYEEIRLSNRYQSYL; DYEEIRLSNRYQSYLE; YEEIRLSNRYQSYLEG; EEIRLSNRYQSYLEGV; EIRLSNRYQSYLEGVK; IRLSNRYQSYLEGVKY; RLSNRYQSYLEGVKYN; LSNRYQSYLEGVKYNV; SNRYQSYLEGVKYNVD; NRYQSYLEGVKYNVDS; RYQSYLEGVKYNVDSA; YQSYLEGVKYNVDSAI; QSYLEGVKYNVDSAIN; SYLEGVKYNVDSAINT; YLEGVKYNVDSAINTI; LEGVKYNVDSAINTIN; EGVKYNVDSAINTINK; GVKYNVDSAINTINKI; VKYNVDSAINTINKIY; KYNVDSAINTINKIYD; YNVDSAINTINKIYDT; NVDSAINTINKIYDTY; VDSAINTINKIYDTYT; DSAINTINKIYDTYTL; SAINTINKIYDTYTLF; AINTINKIYDTYTLFS; INTINKIYDTYTLFST; NTINKIYDTYTLFSTK; TINKIYDTYTLFSTKL; INKIYDTYTLFSTKLT; NKIYDTYTLFSTKLTQ; KIYDTYTLFSTKLTQM; IYDTYTLFSTKLTQMY; YDTYTLFSTKLTQMYS; DTYTLFSTKLTQMYST; TYTLFSTKLTQMYSTR; YTLFSTKLTQMYSTRL; TLFSTKLTQMYSTRLD; LFSTKLTQMYSTRLDN; FSTKLTQMYSTRLDNL; STKLTQMYSTRLDNLA; TKLTQMYSTRLDNLAK; KLTQMYSTRLDNLAKA; LTQMYSTRLDNLAKAK; TQMYSTRLDNLAKAKA; QMYSTRLDNLAKAKAK; MYSTRLDNLAKAKAKE; YSTRLDNLAKAKAKEE; STRLDNLAKAKAKEEA; TRLDNLAKAKAKEEAA; RLDNLAKAKAKEEAAK; LDNLAKAKAKEEAAKF; DNLAKAKAKEEAAKFT; NLAKAKAKEEAAKFTK; LAKAKAKEEAAKFTKE; AKAKAKEEAAKFTKED; KAKAKEEAAKFTKEDL; AKAKEEAAKFTKEDLE; KAKEEAAKFTKEDLEK; AKEEAAKFTKEDLEKN; KEEAAKFTKEDLEKNF; EEAAKFTKEDLEKNFK; EAAKFTKEDLEKNFKT; AAKFTKEDLEKNFKTL; AKFTKEDLEKNFKTLL; KFTKEDLEKNFKTLLN; FTKEDLEKNFKTLLNY; TKEDLEKNFKTLLNYI; KEDLEKNFKTLLNYIQ; EDLEKNFKTLLNYIQV; DLEKNFKTLLNYIQVS; LEKNFKTLLNYIQVSV; EKNFKTLLNYIQVSVK; KNFKTLLNYIQVSVKT; NFKTLLNYIQVSVKTA; FKTLLNYIQVSVKTAA; KTLLNYIQVSVKTAAN; TLLNYIQVSVKTAANF; LLNYIQVSVKTAANFV; LNYIQVSVKTAANFVY; NYIQVSVKTAANFVYI; YIQVSVKTAANFVYIN; IQVSVKTAANFVYIND; QVSVKTAANFVYINDT; VSVKTAANFVYINDTH;

	SVKTAANFVYINDTHA; VKTAANFVYINDTHAK; KTAANFVYINDTHAKR; TAANFVYINDTHAKRK; AANFVYINDTHAKRKL; ANFVYINDTHAKRKLE; NFVYINDTHAKRKLEN; FVYINDTHAKRKLENI; VYINDTHAKRKLENIE; YINDTHAKRKLENIEA; INDTHAKRKLENIEAE; NDTHAKRKLENIEAEI; DTHAKRKLENIEAEIK; THAKRKLENIEAEIKT; HAKRKLENIEAEIKTL; AKRKLENIEAEIKTLI; KRKLENIEAEIKTLIA; RKLENIEAEIKTLIAK; KLENIEAEIKTLIAKI; LENIEAEIKTLIAKIK; ENIEAEIKTLIAKIKE; NIEAEIKTLIAKIKEQ; IEAEIKTLIAKIKEQS; EAEIKTLIAKIKEQSN; AEIKTLIAKIKEQSNL; EIKTLIAKIKEQSNLY; IKTLIAKIKEQSNLYE; KTLIAKIKEQSNLYEA; TLIAKIKEQSNLYEAY; LIAKIKEQSNLYEAYK; IAKIKEQSNLYEAYKA; AKIKEQSNLYEAYKAI; KIKEQSNLYEAYKAIV; IKEQSNLYEAYKAIVT; KEQSNLYEAYKAIVTS; EQSNLYEAYKAIVTSI; QSNLYEAYKAIVTSIL; SNLYEAYKAIVTSILL; NLYEAYKAIVTSILLM; LYEAYKAIVTSILLMR; YEAYKAIVTSILLMRD; EAYKAIVTSILLMRDS; AYKAIVTSILLMRDSL; YKAIVTSILLMRDSLK; KAIVTSILLMRDSLKE; AIVTSILLMRDSLKEV; IVTSILLMRDSLKEVQ; VTSILLMRDSLKEVQG; TSILLMRDSLKEVQGI; SILLMRDSLKEVQGII; ILLMRDSLKEVQGIID; LLMRDSLKEVQGIIDK; LMRDSLKEVQGIIDKN; MRDSLKEVQGIIDKNG; RDSLKEVQGIIDKNGV; DSLKEVQGIIDKNGVW; SLKEVQGIIDKNGVWY;
Seq 43	13 mers: MKIKSKCLALGLL; KIKSKCLALGLLF; IKSKCLALGLLFG; KSKCLALGLLFGF; SKCLALGLLFGFI; KCLALGLLFGFIS; CLALGLLFGFISC; LALGLLFGFISCD; ALGLLFGFISCDL; LGLLFGFISCDLF; GLLFGFISCDLFI; LLFGFISCDLFIR; LFGFISCDLFIRD; FGFISCDLFIRDE; GFISCDLFIRDEI; FISCDLFIRDEIK; ISCDLFIRDEIKE; SCDLFIRDEIKEK; CDLFIRDEIKEKS; DLFIRDEIKEKSL; LFIRDEIKEKSLG; FIRDEIKEKSLGL; IRDEIKEKSLGLC; RDEIKEKSLGLCD; DEIKEKSLGLCDE; EIKEKSLGLCDEE; IKEKSLGLCDEES; KEKSLGLCDEESS; EKSLGLCDEESSI; KSLGLCDEESSIL; SLGLCDEESSILE; LGLCDEESSILET; GLCDEESSILETG; LCDEESSILETGD; CDEESSILETGDK; DEESSILETGDKS; EESSILETGDKSV; ESSILETGDKSVK; SSILETGDKSVKK; SILETGDKSVKKS; ILETGDKSVKKSL; LETGDKSVKKSLN; ETGDKSVKKSLNK; TGDKSVKKSLNKK; GDKSVKKSLNKKG; DKSVKKSLNKKGK; KSVKKSLNKKGKD; SVKKSLNKKGKDK; VKKSLNKKGKDKV; KKSLNKKGKDKVA; KSLNKKGKDKVAR; SLNKKGKDKVARK; LNKKGKDKVARKK; NKKGKDKVARKKV; KKGKDKVARKKVE; KGKDKVARKKVEG; GKDKVARKKVEGN; KDKVARKKVEGNA; DKVARKKVEGNAV; KVARKKVEGNAVK; VARKKVEGNAVKK; ARKKVEGNAVKKD; RKKVEGNAVKKDP; KKVEGNAVKKDPF; KVEGNAVKKDPFN; VEGNAVKKDPFNH; EGNAVKKDPFNHH; GNAVKKDPFNHHV; NAVKKDPFNHHVK; AVKKDPFNHHVKR; VKKDPFNHHVKRE; KKDPFNHHVKRES; KDPFNHHVKRESV; DPFNHHVKRESVN; PFNHHVKRESVNN; FNHHVKRESVNNS; NHHVKRESVNNSN; HHVKRESVNNSNL; HVKRESVNNSNLS; VKRESVNNSNLSQ; KRESVNNSNLSQK; RESVNNSNLSQKN; ESVNNSNLSQKNV; SVNNSNLSQKNVI; VNNSNLSQKNVIS; NNSNLSQKNVISE; NSNLSQKNVISEE;

	SNLSQKNVISEEE; NLSQKNVISEEEI; LSQKNVISEEEIL; SQKNVISEEEILK; QKNVISEEEILKT; KNVISEEEILKTK; NVISEEEILKTKL; VISEEEILKTKLL; ISEEEILKTKLLR; SEEEILKTKLLRE; EEEILKTKLLRER; EEILKTKLLRERP; EILKTKLLRERPE; ILKTKLLRERPET; LKTKLLRERPETR; KTKLLRERPETRK; TKLLRERPETRKE; KLLRERPETRKEE; LLRERPETRKEEI; LRERPETRKEEIQ; RERPETRKEEIQK; ERPETRKEEIQKQ; RPETRKEEIQKQQ; PETRKEEIQKQQD; ETRKEEIQKQQDE; TRKEEIQKQQDEH; RKEEIQKQQDEHK; KEEIQKQQDEHKR; EEIQKQQDEHKRM; EIQKQQDEHKRML; IQKQQDEHKRMLQ; QKQQDEHKRMLQG; KQQDEHKRMLQGS; QQDEHKRMLQGSL; QDEHKRMLQGSLS; DEHKRMLQGSLSF; EHKRMLQGSLSFL; HKRMLQGSLSFLS; KRMLQGSLSFLSG; RMLQGSLSFLSGE; MLQGSLSFLSGES; LQGSLSFLSGESG; QGSLSFLSGESGE; GSLSFLSGESGEL; SLSFLSGESGELK; LSFLSGESGELKD; SFLSGESGELKDT; FLSGESGELKDTI; LSGESGELKDTIE; SGESGELKDTIES; GESGELKDTIESN; ESGELKDTIESNE; SGELKDTIESNEI; GELKDTIESNEID; ELKDTIESNEIDF; LKDTIESNEIDFT; KDTIESNEIDFTI; DTIESNEIDFTID; TIESNEIDFTIDS; IESNEIDFTIDSD; ESNEIDFTIDSDL; SNEIDFTIDSDLR; NEIDFTIDSDLRL; EIDFTIDSDLRLK; IDFTIDSDLRLKS; DFTIDSDLRLKSD; FTIDSDLRLKSDL; TIDSDLRLKSDLQ; IDSDLRLKSDLQA; DSDLRLKSDLQAI; SDLRLKSDLQAIS; DLRLKSDLQAISG; LRLKSDLQAISGS; RLKSDLQAISGSN; LKSDLQAISGSNS; KSDLQAISGSNSI; SDLQAISGSNSIS; DLQAISGSNSISY; LQAISGSNSISYT; QAISGSNSISYTD; AISGSNSISYTDE; ISGSNSISYTDEI; SGSNSISYTDEIE; GSNSISYTDEIEE; SNSISYTDEIEEE; NSISYTDEIEEED; SISYTDEIEEEDY; ISYTDEIEEEDYD; SYTDEIEEEDYDQ; YTDEIEEEDYDQY; TDEIEEEDYDQYS; DEIEEEDYDQYSL; EIEEEDYDQYSLE; IEEEDYDQYSLEE; EEEDYDQYSLEED; EEDYDQYSLEEDY; EDYDQYSLEEDYY; DYDQYSLEEDYYY; YDQYSLEEDYYYD; DQYSLEEDYYYDG; QYSLEEDYYYDGE; YSLEEDYYYDGET; SLEEDYYYDGETR; LEEDYYYDGETRL; EEDYYYDGETRLS; EDYYYDGETRLSN; DYYYDGETRLSNR; YYYDGETRLSNRY; YYDGETRLSNRYE; YDGETRLSNRYES; DGETRLSNRYESY; GETRLSNRYESYL; ETRLSNRYESYLE; TRLSNRYESYLEG; RLSNRYESYLEGV; LSNRYESYLEGVK; SNRYESYLEGVKY; NRYESYLEGVKYN; RYESYLEGVKYNV; YESYLEGVKYNVS; ESYLEGVKYNVSS; SYLEGVKYNVSSA; YLEGVKYNVSSAI; LEGVKYNVSSAIK; EGVKYNVSSAIKT; GVKYNVSSAIKTI; VKYNVSSAIKTIV; KYNVSSAIKTIVK; YNVSSAIKTIVKI; NVSSAIKTIVKIY; VSSAIKTIVKIYD; SSAIKTIVKIYDN; SAIKTIVKIYDNY; AIKTIVKIYDNYT; IKTIVKIYDNYTL; KTIVKIYDNYTLL; TIVKIYDNYTLLS; IVKIYDNYTLLST; VKIYDNYTLLSTK; KIYDNYTLLSTKQ; IYDNYTLLSTKQT; YDNYTLLSTKQTQ; DNYTLLSTKQTQM; NYTLLSTKQTQMY; YTLLSTKQTQMYS; TLLSTKQTQMYST; LLSTKQTQMYSTR; LSTKQTQMYSTRL; STKQTQMYSTRLD; TKQTQMYSTRLDN; KQTQMYSTRLDNL; QTQMYSTRLDNLA; TQMYSTRLDNLAK;

	QMYSTRLDNLAKA; MYSTRLDNLAKAK; YSTRLDNLAKAKA; STRLDNLAKAKAR; TRLDNLAKAKARE; RLDNLAKAKAREE; LDNLAKAKAREEA; DNLAKAKAREEAK; NLAKAKAREEAKK; LAKAKAREEAKKF; AKAKAREEAKKFT; KAKAREEAKKFTK; AKAREEAKKFTKE; KAREEAKKFTKEE; AREEAKKFTKEEL; REEAKKFTKEELE; EEAKKFTKEELEK; EAKKFTKEELEKD; AKKFTKEELEKDL; KKFTKEELEKDLK; KFTKEELEKDLKT; FTKEELEKDLKTL; TKEELEKDLKTLL; KEELEKDLKTLLN; EELEKDLKTLLNY; ELEKDLKTLLNYI; LEKDLKTLLNYIQ; EKDLKTLLNYIQV; KDLKTLLNYIQVS; DLKTLLNYIQVSA; LKTLLNYIQVSAR; KTLLNYIQVSART; TLLNYIQVSARTA; LLNYIQVSARTAT; LNYIQVSARTATN; NYIQVSARTATNF; YIQVSARTATNFV; IQVSARTATNFVY; QVSARTATNFVYA; VSARTATNFVYAR; SARTATNFVYARE; ARTATNFVYAREI; RTATNFVYAREIY; TATNFVYAREIYS; ATNFVYAREIYSK; TNFVYAREIYSKR; NFVYAREIYSKRK; FVYAREIYSKRKL; VYAREIYSKRKLD; YAREIYSKRKLDA; AREIYSKRKLDAI; REIYSKRKLDAIE; EIYSKRKLDAIET; IYSKRKLDAIETE; YSKRKLDAIETEI; SKRKLDAIETEIK; KRKLDAIETEIKN; RKLDAIETEIKNL; KLDAIETEIKNLI; LDAIETEIKNLIL; DAIETEIKNLILK; AIETEIKNLILKI; IETEIKNLILKIK; ETEIKNLILKIKG; TEIKNLILKIKGQ; EIKNLILKIKGQS; IKNLILKIKGQSD; KNLILKIKGQSDL; NLILKIKGQSDLY; LILKIKGQSDLYE; ILKIKGQSDLYEA; LKIKGQSDLYEAY; KIKGQSDLYEAYK; IKGQSDLYEAYKA; KGQSDLYEAYKAI; GQSDLYEAYKAIV; QSDLYEAYKAIVR; SDLYEAYKAIVRS; DLYEAYKAIVRSI; LYEAYKAIVRSIL; YEAYKAIVRSILL; EAYKAIVRSILLM; AYKAIVRSILLMK; YKAIVRSILLMKD; KAIVRSILLMKDS; AIVRSILLMKDSL; IVRSILLMKDSLK; VRSILLMKDSLKI; RSILLMKDSLKII; SILLMKDSLKIIE; ILLMKDSLKIIEI; LLMKDSLKIIEIV; LMKDSLKIIEIVI; MKDSLKIIEIVID; KDSLKIIEIVIDK; DSLKIIEIVIDKN; SLKIIEIVIDKNG; LKIIEIVIDKNGV; KIIEIVIDKNGVW; IIEIVIDKNGVWY; 14 mers: MKIKSKCLALGLLF; KIKSKCLALGLLFG; IKSKCLALGLLFGF; KSKCLALGLLFGFI; SKCLALGLLFGFIS; KCLALGLLFGFISC; CLALGLLFGFISCD; LALGLLFGFISCDL; ALGLLFGFISCDLF; LGLLFGFISCDLFI; GLLFGFISCDLFIR; LLFGFISCDLFIRD; LFGFISCDLFIRDE; FGFISCDLFIRDEI; GFISCDLFIRDEIK; FISCDLFIRDEIKE; ISCDLFIRDEIKEK; SCDLFIRDEIKEKS; CDLFIRDEIKEKSL; DLFIRDEIKEKSLG; LFIRDEIKEKSLGL; FIRDEIKEKSLGLC; IRDEIKEKSLGLCD; RDEIKEKSLGLCDE; DEIKEKSLGLCDEE; EIKEKSLGLCDEES; IKEKSLGLCDEESS; KEKSLGLCDEESSI; EKSLGLCDEESSIL; KSLGLCDEESSILE; SLGLCDEESSILET; LGLCDEESSILETG; GLCDEESSILETGD; LCDEESSILETGDK; CDEESSILETGDKS; DEESSILETGDKSV; EESSILETGDKSVK; ESSILETGDKSVKK; SSILETGDKSVKKS; SILETGDKSVKKSL; ILETGDKSVKKSLN; LETGDKSVKKSLNK; ETGDKSVKKSLNKK; TGDKSVKKSLNKKG; GDKSVKKSLNKKGK;

	DKSVKKSLNKKGKD; KSVKKSLNKKGKDK; SVKKSLNKKGKDKV; VKKSLNKKGKDKVA; KKSLNKKGKDKVAR; KSLNKKGKDKVARK; SLNKKGKDKVARKK; LNKKGKDKVARKKV; NKKGKDKVARKKVE; KKGKDKVARKKVEG; KGKDKVARKKVEGN; GKDKVARKKVEGNA; KDKVARKKVEGNAV; DKVARKKVEGNAVK; KVARKKVEGNAVKK; VARKKVEGNAVKKD; ARKKVEGNAVKKDP; RKKVEGNAVKKDPF; KKVEGNAVKKDPFN; KVEGNAVKKDPFNH; VEGNAVKKDPFNHH; EGNAVKKDPFNHHV; GNAVKKDPFNHHVK; NAVKKDPFNHHVKR; AVKKDPFNHHVKRE; VKKDPFNHHVKRES; KKDPFNHHVKRESV; KDPFNHHVKRESVN; DPFNHHVKRESVNN; PFNHHVKRESVNNS; FNHHVKRESVNNSN; NHHVKRESVNNSNL; HHVKRESVNNSNLS; HVKRESVNNSNLSQ; VKRESVNNSNLSQK; KRESVNNSNLSQKN; RESVNNSNLSQKNV; ESVNNSNLSQKNVI; SVNNSNLSQKNVIS; VNNSNLSQKNVISE; NNSNLSQKNVISEE; NSNLSQKNVISEEE; SNLSQKNVISEEEI; NLSQKNVISEEEIL; LSQKNVISEEEILK; SQKNVISEEEILKT; QKNVISEEEILKTK; KNVISEEEILKTKL; NVISEEEILKTKLL; VISEEEILKTKLLR; ISEEEILKTKLLRE; SEEEILKTKLLRER; EEEILKTKLLRERP; EEILKTKLLRERPE; EILKTKLLRERPET; ILKTKLLRERPETR; LKTKLLRERPETRK; KTKLLRERPETRKE; TKLLRERPETRKEE; KLLRERPETRKEEI; LLRERPETRKEEIQ; LRERPETRKEEIQK; RERPETRKEEIQKQ; ERPETRKEEIQKQQ; RPETRKEEIQKQQD; PETRKEEIQKQQDE; ETRKEEIQKQQDEH; TRKEEIQKQQDEHK; RKEEIQKQQDEHKR; KEEIQKQQDEHKRM; EEIQKQQDEHKRML; EIQKQQDEHKRMLQ; IQKQQDEHKRMLQG; QKQQDEHKRMLQGS; KQQDEHKRMLQGSL; QQDEHKRMLQGSLS; QDEHKRMLQGSLSF; DEHKRMLQGSLSFL; EHKRMLQGSLSFLS; HKRMLQGSLSFLSG; KRMLQGSLSFLSGE; RMLQGSLSFLSGES; MLQGSLSFLSGESG; LQGSLSFLSGESGE; QGSLSFLSGESGEL; GSLSFLSGESGELK; SLSFLSGESGELKD; LSFLSGESGELKDT; SFLSGESGELKDTI; FLSGESGELKDTIE; LSGESGELKDTIES; SGESGELKDTIESN; GESGELKDTIESNE; ESGELKDTIESNEI; SGELKDTIESNEID; GELKDTIESNEIDF; ELKDTIESNEIDFT; LKDTIESNEIDFTI; KDTIESNEIDFTID; DTIESNEIDFTIDS; TIESNEIDFTIDSD; IESNEIDFTIDSDL; ESNEIDFTIDSDLR; SNEIDFTIDSDLRL; NEIDFTIDSDLRLK; EIDFTIDSDLRLKS; IDFTIDSDLRLKSD; DFTIDSDLRLKSDL; FTIDSDLRLKSDLQ; TIDSDLRLKSDLQA; IDSDLRLKSDLQAI; DSDLRLKSDLQAIS; SDLRLKSDLQAISG; DLRLKSDLQAISGS; LRLKSDLQAISGSN; RLKSDLQAISGSNS; LKSDLQAISGSNSI; KSDLQAISGSNSIS; SDLQAISGSNSISY; DLQAISGSNSISYT; LQAISGSNSISYTD; QAISGSNSISYTDE; AISGSNSISYTDEI; ISGSNSISYTDEIE; SGSNSISYTDEIEE; GSNSISYTDEIEEE; SNSISYTDEIEEED; NSISYTDEIEEEDY; SISYTDEIEEEDYD; ISYTDEIEEEDYDQ; SYTDEIEEEDYDQY; YTDEIEEEDYDQYS; TDEIEEEDYDQYSL; DEIEEEDYDQYSLE; EIEEEDYDQYSLEE; IEEEDYDQYSLEED; EEEDYDQYSLEEDY; EEDYDQYSLEEDYY; EDYDQYSLEEDYYY; DYDQYSLEEDYYYD; YDQYSLEEDYYYDG; DQYSLEEDYYYDGE; QYSLEEDYYYDGET; YSLEEDYYYDGETR; SLEEDYYYDGETRL; LEEDYYYDGETRLS; EEDYYYDGETRLSN; EDYYYDGETRLSNR; DYYYDGETRLSNRY; YYYDGETRLSNRYE; YYDGETRLSNRYES; YDGETRLSNRYESY; DGETRLSNRYESYL;

	GETRLSNRYESYLE; ETRLSNRYESYLEG; TRLSNRYESYLEGV; RLSNRYESYLEGVK; LSNRYESYLEGVKY; SNRYESYLEGVKYN; NRYESYLEGVKYNV; RYESYLEGVKYNVS; YESYLEGVKYNVSS; ESYLEGVKYNVSSA; SYLEGVKYNVSSAI; YLEGVKYNVSSAIK; LEGVKYNVSSAIKT; EGVKYNVSSAIKTI; GVKYNVSSAIKTIV; VKYNVSSAIKTIVK; KYNVSSAIKTIVKI; YNVSSAIKTIVKIY; NVSSAIKTIVKIYD; VSSAIKTIVKIYDN; SSAIKTIVKIYDNY; SAIKTIVKIYDNYT; AIKTIVKIYDNYTL; IKTIVKIYDNYTLL; KTIVKIYDNYTLLS; TIVKIYDNYTLLST; IVKIYDNYTLLSTK; VKIYDNYTLLSTKQ; KIYDNYTLLSTKQT; IYDNYTLLSTKQTQ; YDNYTLLSTKQTQM; DNYTLLSTKQTQMY; NYTLLSTKQTQMYS; YTLLSTKQTQMYST; TLLSTKQTQMYSTR; LLSTKQTQMYSTRL; LSTKQTQMYSTRLD; STKQTQMYSTRLDN; TKQTQMYSTRLDNL; KQTQMYSTRLDNLA; QTQMYSTRLDNLAK; TQMYSTRLDNLAKA; QMYSTRLDNLAKAK; MYSTRLDNLAKAKA; YSTRLDNLAKAKAR; STRLDNLAKAKARE; TRLDNLAKAKAREE; RLDNLAKAKAREEA; LDNLAKAKAREEAK; DNLAKAKAREEAKK; NLAKAKAREEAKKF; LAKAKAREEAKKFT; AKAKAREEAKKFTK; KAKAREEAKKFTKE; AKAREEAKKFTKEE; KAREEAKKFTKEEL; AREEAKKFTKEELE; REEAKKFTKEELEK; EEAKKFTKEELEKD; EAKKFTKEELEKDL; AKKFTKEELEKDLK; KKFTKEELEKDLKT; KFTKEELEKDLKTL; FTKEELEKDLKTLL; TKEELEKDLKTLLN; KEELEKDLKTLLNY; EELEKDLKTLLNYI; ELEKDLKTLLNYIQ; LEKDLKTLLNYIQV; EKDLKTLLNYIQVS; KDLKTLLNYIQVSA; DLKTLLNYIQVSAR; LKTLLNYIQVSART; KTLLNYIQVSARTA; TLLNYIQVSARTAT; LLNYIQVSARTATN; LNYIQVSARTATNF; NYIQVSARTATNFV; YIQVSARTATNFVY; IQVSARTATNFVYA; QVSARTATNFVYAR; VSARTATNFVYARE; SARTATNFVYAREI; ARTATNFVYAREIY; RTATNFVYAREIYS; TATNFVYAREIYSK; ATNFVYAREIYSKR; TNFVYAREIYSKRK; NFVYAREIYSKRKL; FVYAREIYSKRKLD; VYAREIYSKRKLDA; YAREIYSKRKLDAI; AREIYSKRKLDAIE; REIYSKRKLDAIET; EIYSKRKLDAIETE; IYSKRKLDAIETEI; YSKRKLDAIETEIK; SKRKLDAIETEIKN; KRKLDAIETEIKNL; RKLDAIETEIKNLI; KLDAIETEIKNLIL; LDAIETEIKNLILK; DAIETEIKNLILKI; AIETEIKNLILKIK; IETEIKNLILKIKG; ETEIKNLILKIKGQ; TEIKNLILKIKGQS; EIKNLILKIKGQSD; IKNLILKIKGQSDL; KNLILKIKGQSDLY; NLILKIKGQSDLYE; LILKIKGQSDLYEA; ILKIKGQSDLYEAY; LKIKGQSDLYEAYK; KIKGQSDLYEAYKA; IKGQSDLYEAYKAI; KGQSDLYEAYKAIV; GQSDLYEAYKAIVR; QSDLYEAYKAIVRS; SDLYEAYKAIVRSI; DLYEAYKAIVRSIL; LYEAYKAIVRSILL; YEAYKAIVRSILLM; EAYKAIVRSILLMK; AYKAIVRSILLMKD; YKAIVRSILLMKDS; KAIVRSILLMKDSL; AIVRSILLMKDSLK; IVRSILLMKDSLKI; VRSILLMKDSLKII; RSILLMKDSLKIIE; SILLMKDSLKIIEI; ILLMKDSLKIIEIV; LLMKDSLKIIEIVI; LMKDSLKIIEIVID; MKDSLKIIEIVIDK; KDSLKIIEIVIDKN; DSLKIIEIVIDKNG; SLKIIEIVIDKNGV; LKIIEIVIDKNGVW; KIIEIVIDKNGVWY; 15 mers: MKIKSKCLALGLLFG; KIKSKCLALGLLFGF; IKSKCLALGLLFGFI; KSKCLALGLLFGFIS; SKCLALGLLFGFISC; KCLALGLLFGFISCD;

	CLALGLLFGFISCDL; LALGLLFGFISCDLF; ALGLLFGFISCDLFI; LGLLFGFISCDLFIR; GLLFGFISCDLFIRD; LLFGFISCDLFIRDE; LFGFISCDLFIRDEI; FGFISCDLFIRDEIK; GFISCDLFIRDEIKE; FISCDLFIRDEIKEK; ISCDLFIRDEIKEKS; SCDLFIRDEIKEKSL; CDLFIRDEIKEKSLG; DLFIRDEIKEKSLGL; LFIRDEIKEKSLGLC; FIRDEIKEKSLGLCD; IRDEIKEKSLGLCDE; RDEIKEKSLGLCDEE; DEIKEKSLGLCDEES; EIKEKSLGLCDEESS; IKEKSLGLCDEESSI; KEKSLGLCDEESSIL; EKSLGLCDEESSILE; KSLGLCDEESSILET; SLGLCDEESSILETG; LGLCDEESSILETGD; GLCDEESSILETGDK; LCDEESSILETGDKS; CDEESSILETGDKSV; DEESSILETGDKSVK; EESSILETGDKSVKK; ESSILETGDKSVKKS; SSILETGDKSVKKSL; SILETGDKSVKKSLN; ILETGDKSVKKSLNK; LETGDKSVKKSLNKK; ETGDKSVKKSLNKKG; TGDKSVKKSLNKKGK; GDKSVKKSLNKKGKD; DKSVKKSLNKKGKDK; KSVKKSLNKKGKDKV; SVKKSLNKKGKDKVA; VKKSLNKKGKDKVAR; KKSLNKKGKDKVARK; KSLNKKGKDKVARKK; SLNKKGKDKVARKKV; LNKKGKDKVARKKVE; NKKGKDKVARKKVEG; KKGKDKVARKKVEGN; KGKDKVARKKVEGNA; GKDKVARKKVEGNAV; KDKVARKKVEGNAVK; DKVARKKVEGNAVKK; KVARKKVEGNAVKKD; VARKKVEGNAVKKDP; ARKKVEGNAVKKDPF; RKKVEGNAVKKDPFN; KKVEGNAVKKDPFNH; KVEGNAVKKDPFNHH; VEGNAVKKDPFNHHV; EGNAVKKDPFNHHVK; GNAVKKDPFNHHVKR; NAVKKDPFNHHVKRE; AVKKDPFNHHVKRES; VKKDPFNHHVKRESV; KKDPFNHHVKRESVN; KDPFNHHVKRESVNN; DPFNHHVKRESVNNS; PFNHHVKRESVNNSN; FNHHVKRESVNNSNL; NHHVKRESVNNSNLS; HHVKRESVNNSNLSQ; HVKRESVNNSNLSQK; VKRESVNNSNLSQKN; KRESVNNSNLSQKNV; RESVNNSNLSQKNVI; ESVNNSNLSQKNVIS; SVNNSNLSQKNVISE; VNNSNLSQKNVISEE; NNSNLSQKNVISEEE; NSNLSQKNVISEEEI; SNLSQKNVISEEEIL; NLSQKNVISEEEILK; LSQKNVISEEEILKT; SQKNVISEEEILKTK; QKNVISEEEILKTKL; KNVISEEEILKTKLL; NVISEEEILKTKLLR; VISEEEILKTKLLRE; ISEEEILKTKLLRER; SEEEILKTKLLRERP; EEEILKTKLLRERPE; EEILKTKLLRERPET; EILKTKLLRERPETR; ILKTKLLRERPETRK; LKTKLLRERPETRKE; KTKLLRERPETRKEE; TKLLRERPETRKEEI; KLLRERPETRKEEIQ; LLRERPETRKEEIQK; LRERPETRKEEIQKQ; RERPETRKEEIQKQQ; ERPETRKEEIQKQQD; RPETRKEEIQKQQDE; PETRKEEIQKQQDEH; ETRKEEIQKQQDEHK; TRKEEIQKQQDEHKR; RKEEIQKQQDEHKRM; KEEIQKQQDEHKRML; EEIQKQQDEHKRMLQ; EIQKQQDEHKRMLQG; IQKQQDEHKRMLQGS; QKQQDEHKRMLQGSL; KQQDEHKRMLQGSLS; QQDEHKRMLQGSLSF; QDEHKRMLQGSLSFL; DEHKRMLQGSLSFLS; EHKRMLQGSLSFLSG; HKRMLQGSLSFLSGE; KRMLQGSLSFLSGES; RMLQGSLSFLSGESG; MLQGSLSFLSGESGE; LQGSLSFLSGESGEL; QGSLSFLSGESGELK; GSLSFLSGESGELKD; SLSFLSGESGELKDT; LSFLSGESGELKDTI; SFLSGESGELKDTIE; FLSGESGELKDTIES; LSGESGELKDTIESN; SGESGELKDTIESNE; GESGELKDTIESNEI; ESGELKDTIESNEID; SGELKDTIESNEIDF; GELKDTIESNEIDFT; ELKDTIESNEIDFTI; LKDTIESNEIDFTID; KDTIESNEIDFTIDS; DTIESNEIDFTIDSD; TIESNEIDFTIDSDL; IESNEIDFTIDSDLR; ESNEIDFTIDSDLRL; SNEIDFTIDSDLRLK; NEIDFTIDSDLRLKS; EIDFTIDSDLRLKSD; IDFTIDSDLRLKSDL; DFTIDSDLRLKSDLQ; FTIDSDLRLKSDLQA; TIDSDLRLKSDLQAI; IDSDLRLKSDLQAIS; DSDLRLKSDLQAISG; SDLRLKSDLQAISGS; DLRLKSDLQAISGSN;

	LRLKSDLQAISGSNS; RLKSDLQAISGSNSI; LKSDLQAISGSNSIS; KSDLQAISGSNSISY; SDLQAISGSNSISYT; DLQAISGSNSISYTD; LQAISGSNSISYTDE; QAISGSNSISYTDEI; AISGSNSISYTDEIE; ISGSNSISYTDEIEE; SGSNSISYTDEIEEE; GSNSISYTDEIEEED; SNSISYTDEIEEEDY; NSISYTDEIEEEDYD; SISYTDEIEEEDYDQ; ISYTDEIEEEDYDQY; SYTDEIEEEDYDQYS; YTDEIEEEDYDQYSL; TDEIEEEDYDQYSLE; DEIEEEDYDQYSLEE; EIEEEDYDQYSLEED; IEEEDYDQYSLEEDY; EEEDYDQYSLEEDYY; EEDYDQYSLEEDYYY; EDYDQYSLEEDYYYD; DYDQYSLEEDYYYDG; YDQYSLEEDYYYDGE; DQYSLEEDYYYDGET; QYSLEEDYYYDGETR; YSLEEDYYYDGETRL; SLEEDYYYDGETRLS; LEEDYYYDGETRLSN; EEDYYYDGETRLSNR; EDYYYDGETRLSNRY; DYYYDGETRLSNRYE; YYYDGETRLSNRYES; YYDGETRLSNRYESY; YDGETRLSNRYESYL; DGETRLSNRYESYLE; GETRLSNRYESYLEG; ETRLSNRYESYLEGV; TRLSNRYESYLEGVK; RLSNRYESYLEGVKY; LSNRYESYLEGVKYN; SNRYESYLEGVKYNV; NRYESYLEGVKYNVS; RYESYLEGVKYNVSS; YESYLEGVKYNVSSA; ESYLEGVKYNVSSAI; SYLEGVKYNVSSAIK; YLEGVKYNVSSAIKT; LEGVKYNVSSAIKTI; EGVKYNVSSAIKTIV; GVKYNVSSAIKTIVK; VKYNVSSAIKTIVKI; KYNVSSAIKTIVKIY; YNVSSAIKTIVKIYD; NVSSAIKTIVKIYDN; VSSAIKTIVKIYDNY; SSAIKTIVKIYDNYT; SAIKTIVKIYDNYTL; AIKTIVKIYDNYTLL; IKTIVKIYDNYTLLS; KTIVKIYDNYTLLST; TIVKIYDNYTLLSTK; IVKIYDNYTLLSTKQ; VKIYDNYTLLSTKQT; KIYDNYTLLSTKQTQ; IYDNYTLLSTKQTQM; YDNYTLLSTKQTQMY; DNYTLLSTKQTQMYS; NYTLLSTKQTQMYST; YTLLSTKQTQMYSTR; TLLSTKQTQMYSTRL; LLSTKQTQMYSTRLD; LSTKQTQMYSTRLDN; STKQTQMYSTRLDNL; TKQTQMYSTRLDNLA; KQTQMYSTRLDNLAK; QTQMYSTRLDNLAKA; TQMYSTRLDNLAKAK; QMYSTRLDNLAKAKA; MYSTRLDNLAKAKAR; YSTRLDNLAKAKARE; STRLDNLAKAKAREE; TRLDNLAKAKAREEA; RLDNLAKAKAREEAK; LDNLAKAKAREEAKK; DNLAKAKAREEAKKF; NLAKAKAREEAKKFT; LAKAKAREEAKKFTK; AKAKAREEAKKFTKE; KAKAREEAKKFTKEE; AKAREEAKKFTKEEL; KAREEAKKFTKEELE; AREEAKKFTKEELEK; REEAKKFTKEELEKD; EEAKKFTKEELEKDL; EAKKFTKEELEKDLK; AKKFTKEELEKDLKT; KKFTKEELEKDLKTL; KFTKEELEKDLKTLL; FTKEELEKDLKTLLN; TKEELEKDLKTLLNY; KEELEKDLKTLLNYI; EELEKDLKTLLNYIQ; ELEKDLKTLLNYIQV; LEKDLKTLLNYIQVS; EKDLKTLLNYIQVSA; KDLKTLLNYIQVSAR; DLKTLLNYIQVSART; LKTLLNYIQVSARTA; KTLLNYIQVSARTAT; TLLNYIQVSARTATN; LLNYIQVSARTATNF; LNYIQVSARTATNFV; NYIQVSARTATNFVY; YIQVSARTATNFVYA; IQVSARTATNFVYAR; QVSARTATNFVYARE; VSARTATNFVYAREI; SARTATNFVYAREIY; ARTATNFVYAREIYS; RTATNFVYAREIYSK; TATNFVYAREIYSKR; ATNFVYAREIYSKRK; TNFVYAREIYSKRKL; NFVYAREIYSKRKLD; FVYAREIYSKRKLDA; VYAREIYSKRKLDAI; YAREIYSKRKLDAIE; AREIYSKRKLDAIET; REIYSKRKLDAIETE; EIYSKRKLDAIETEI; IYSKRKLDAIETEIK; YSKRKLDAIETEIKN; SKRKLDAIETEIKNL; KRKLDAIETEIKNLI; RKLDAIETEIKNLIL; KLDAIETEIKNLILK; LDAIETEIKNLILKI; DAIETEIKNLILKIK; AIETEIKNLILKIKG; IETEIKNLILKIKGQ; ETEIKNLILKIKGQS; TEIKNLILKIKGQSD; EIKNLILKIKGQSDL; IKNLILKIKGQSDLY; KNLILKIKGQSDLYE; NLILKIKGQSDLYEA; LILKIKGQSDLYEAY; ILKIKGQSDLYEAYK; LKIKGQSDLYEAYKA;

	KIKGQSDLYEAYKAI; IKGQSDLYEAYKAIV; KGQSDLYEAYKAIVR; GQSDLYEAYKAIVRS; QSDLYEAYKAIVRSI; SDLYEAYKAIVRSIL; DLYEAYKAIVRSILL; LYEAYKAIVRSILLM; YEAYKAIVRSILLMK; EAYKAIVRSILLMKD; AYKAIVRSILLMKDS; YKAIVRSILLMKDSL; KAIVRSILLMKDSLK; AIVRSILLMKDSLKI; IVRSILLMKDSLKII; VRSILLMKDSLKIIE; RSILLMKDSLKIIEI; SILLMKDSLKIIEIV; ILLMKDSLKIIEIVI; LLMKDSLKIIEIVID; LMKDSLKIIEIVIDK; MKDSLKIIEIVIDKN; KDSLKIIEIVIDKNG; DSLKIIEIVIDKNGV; SLKIIEIVIDKNGVW; LKIIEIVIDKNGVWY; 16 mers: MKIKSKCLALGLLFGF; KIKSKCLALGLLFGFI; IKSKCLALGLLFGFIS; KSKCLALGLLFGFISC; SKCLALGLLFGFISCD; KCLALGLLFGFISCDL; CLALGLLFGFISCDLF; LALGLLFGFISCDLFI; ALGLLFGFISCDLFIR; LGLLFGFISCDLFIRD; GLLFGFISCDLFIRDE; LLFGFISCDLFIRDEI; LFGFISCDLFIRDEIK; FGFISCDLFIRDEIKE; GFISCDLFIRDEIKEK; FISCDLFIRDEIKEKS; ISCDLFIRDEIKEKSL; SCDLFIRDEIKEKSLG; CDLFIRDEIKEKSLGL; DLFIRDEIKEKSLGLC; LFIRDEIKEKSLGLCD; FIRDEIKEKSLGLCDE; IRDEIKEKSLGLCDEE; RDEIKEKSLGLCDEES; DEIKEKSLGLCDEESS; EIKEKSLGLCDEESSI; IKEKSLGLCDEESSIL; KEKSLGLCDEESSILE; EKSLGLCDEESSILET; KSLGLCDEESSILETG; SLGLCDEESSILETGD; LGLCDEESSILETGDK; GLCDEESSILETGDKS; LCDEESSILETGDKSV; CDEESSILETGDKSVK; DEESSILETGDKSVKK; EESSILETGDKSVKKS; ESSILETGDKSVKKSL; SSILETGDKSVKKSLN; SILETGDKSVKKSLNK; ILETGDKSVKKSLNKK; LETGDKSVKKSLNKKG; ETGDKSVKKSLNKKGK; TGDKSVKKSLNKKGKD; GDKSVKKSLNKKGKDK; DKSVKKSLNKKGKDKV; KSVKKSLNKKGKDKVA; SVKKSLNKKGKDKVAR; VKKSLNKKGKDKVARK; KKSLNKKGKDKVARKK; KSLNKKGKDKVARKKV; SLNKKGKDKVARKKVE; LNKKGKDKVARKKVEG; NKKGKDKVARKKVEGN; KKGKDKVARKKVEGNA; KGKDKVARKKVEGNAV; GKDKVARKKVEGNAVK; KDKVARKKVEGNAVKK; DKVARKKVEGNAVKKD; KVARKKVEGNAVKKDP; VARKKVEGNAVKKDPF; ARKKVEGNAVKKDPFN; RKKVEGNAVKKDPFNH; KKVEGNAVKKDPFNHH; KVEGNAVKKDPFNHHV; VEGNAVKKDPFNHHVK; EGNAVKKDPFNHHVKR; GNAVKKDPFNHHVKRE; NAVKKDPFNHHVKRES; AVKKDPFNHHVKRESV; VKKDPFNHHVKRESVN; KKDPFNHHVKRESVNN; KDPFNHHVKRESVNNS; DPFNHHVKRESVNNSN; PFNHHVKRESVNNSNL; FNHHVKRESVNNSNLS; NHHVKRESVNNSNLSQ; HHVKRESVNNSNLSQK; HVKRESVNNSNLSQKN; VKRESVNNSNLSQKNV; KRESVNNSNLSQKNVI; RESVNNSNLSQKNVIS; ESVNNSNLSQKNVISE; SVNNSNLSQKNVISEE; VNNSNLSQKNVISEEE; NNSNLSQKNVISEEEI; NSNLSQKNVISEEEIL; SNLSQKNVISEEEILK; NLSQKNVISEEEILKT; LSQKNVISEEEILKTK; SQKNVISEEEILKTKL; QKNVISEEEILKTKLL; KNVISEEEILKTKLLR; NVISEEEILKTKLLRE; VISEEEILKTKLLRER; ISEEEILKTKLLRERP; SEEEILKTKLLRERPE; EEEILKTKLLRERPET; EEILKTKLLRERPETR; EILKTKLLRERPETRK; ILKTKLLRERPETRKE; LKTKLLRERPETRKEE; KTKLLRERPETRKEEI; TKLLRERPETRKEEIQ; KLLRERPETRKEEIQK; LLRERPETRKEEIQKQ; LRERPETRKEEIQKQQ; RERPETRKEEIQKQQD; ERPETRKEEIQKQQDE; RPETRKEEIQKQQDEH; PETRKEEIQKQQDEHK; ETRKEEIQKQQDEHKR; TRKEEIQKQQDEHKRM; RKEEIQKQQDEHKRML; KEEIQKQQDEHKRMLQ; EEIQKQQDEHKRMLQG; EIQKQQDEHKRMLQGS; IQKQQDEHKRMLQGSL; QKQQDEHKRMLQGSLS; KQQDEHKRMLQGSLSF;

	QQDEHKRMLQGSLSFL; QDEHKRMLQGSLSFLS; DEHKRMLQGSLSFLSG; EHKRMLQGSLSFLSGE; HKRMLQGSLSFLSGES; KRMLQGSLSFLSGESG; RMLQGSLSFLSGESGE; MLQGSLSFLSGESGEL; LQGSLSFLSGESGELK; QGSLSFLSGESGELKD; GSLSFLSGESGELKDT; SLSFLSGESGELKDTI; LSFLSGESGELKDTIE; SFLSGESGELKDTIES; FLSGESGELKDTIESN; LSGESGELKDTIESNE; SGESGELKDTIESNEI; GESGELKDTIESNEID; ESGELKDTIESNEIDF; SGELKDTIESNEIDFT; GELKDTIESNEIDFTI; ELKDTIESNEIDFTID; LKDTIESNEIDFTIDS; KDTIESNEIDFTIDSD; DTIESNEIDFTIDSDL; TIESNEIDFTIDSDLR; IESNEIDFTIDSDLRL; ESNEIDFTIDSDLRLK; SNEIDFTIDSDLRLKS; NEIDFTIDSDLRLKSD; EIDFTIDSDLRLKSDL; IDFTIDSDLRLKSDLQ; DFTIDSDLRLKSDLQA; FTIDSDLRLKSDLQAI; TIDSDLRLKSDLQAIS; IDSDLRLKSDLQAISG; DSDLRLKSDLQAISGS; SDLRLKSDLQAISGSN; DLRLKSDLQAISGSNS; LRLKSDLQAISGSNSI; RLKSDLQAISGSNSIS; LKSDLQAISGSNSISY; KSDLQAISGSNSISYT; SDLQAISGSNSISYTD; DLQAISGSNSISYTDE; LQAISGSNSISYTDEI; QAISGSNSISYTDEIE; AISGSNSISYTDEIEE; ISGSNSISYTDEIEEE; SGSNSISYTDEIEEED; GSNSISYTDEIEEEDY; SNSISYTDEIEEEDYD; NSISYTDEIEEEDYDQ; SISYTDEIEEEDYDQY; ISYTDEIEEEDYDQYS; SYTDEIEEEDYDQYSL; YTDEIEEEDYDQYSLE; TDEIEEEDYDQYSLEE; DEIEEEDYDQYSLEED; EIEEEDYDQYSLEEDY; IEEEDYDQYSLEEDYY; EEEDYDQYSLEEDYYY; EEDYDQYSLEEDYYYD; EDYDQYSLEEDYYYDG; DYDQYSLEEDYYYDGE; YDQYSLEEDYYYDGET; DQYSLEEDYYYDGETR; QYSLEEDYYYDGETRL; YSLEEDYYYDGETRLS; SLEEDYYYDGETRLSN; LEEDYYYDGETRLSNR; EEDYYYDGETRLSNRY; EDYYYDGETRLSNRYE; DYYYDGETRLSNRYES; YYYDGETRLSNRYESY; YYDGETRLSNRYESYL; YDGETRLSNRYESYLE; DGETRLSNRYESYLEG; GETRLSNRYESYLEGV; ETRLSNRYESYLEGVK; TRLSNRYESYLEGVKY; RLSNRYESYLEGVKYN; LSNRYESYLEGVKYNV; SNRYESYLEGVKYNVS; NRYESYLEGVKYNVSS; RYESYLEGVKYNVSSA; YESYLEGVKYNVSSAI; ESYLEGVKYNVSSAIK; SYLEGVKYNVSSAIKT; YLEGVKYNVSSAIKTI; LEGVKYNVSSAIKTIV; EGVKYNVSSAIKTIVK; GVKYNVSSAIKTIVKI; VKYNVSSAIKTIVKIY; KYNVSSAIKTIVKIYD; YNVSSAIKTIVKIYDN; NVSSAIKTIVKIYDNY; VSSAIKTIVKIYDNYT; SSAIKTIVKIYDNYTL; SAIKTIVKIYDNYTLL; AIKTIVKIYDNYTLLS; IKTIVKIYDNYTLLST; KTIVKIYDNYTLLSTK; TIVKIYDNYTLLSTKQ; IVKIYDNYTLLSTKQT; VKIYDNYTLLSTKQTQ; KIYDNYTLLSTKQTQM; IYDNYTLLSTKQTQMY; YDNYTLLSTKQTQMYS; DNYTLLSTKQTQMYST; NYTLLSTKQTQMYSTR; YTLLSTKQTQMYSTRL; TLLSTKQTQMYSTRLD; LLSTKQTQMYSTRLDN; LSTKQTQMYSTRLDNL; STKQTQMYSTRLDNLA; TKQTQMYSTRLDNLAK; KQTQMYSTRLDNLAKA; QTQMYSTRLDNLAKAK; TQMYSTRLDNLAKAKA; QMYSTRLDNLAKAKAR; MYSTRLDNLAKAKARE; YSTRLDNLAKAKAREE; STRLDNLAKAKAREEA; TRLDNLAKAKAREEAK; RLDNLAKAKAREEAKK; LDNLAKAKAREEAKKF; DNLAKAKAREEAKKFT; NLAKAKAREEAKKFTK; LAKAKAREEAKKFTKE; AKAKAREEAKKFTKEE; KAKAREEAKKFTKEEL; AKAREEAKKFTKEELE; KAREEAKKFTKEELEK; AREEAKKFTKEELEKD; REEAKKFTKEELEKDL; EEAKKFTKEELEKDLK; EAKKFTKEELEKDLKT; AKKFTKEELEKDLKTL; KKFTKEELEKDLKTLL; KFTKEELEKDLKTLLN; FTKEELEKDLKTLLNY; TKEELEKDLKTLLNYI; KEELEKDLKTLLNYIQ; EELEKDLKTLLNYIQV; ELEKDLKTLLNYIQVS; LEKDLKTLLNYIQVSA; EKDLKTLLNYIQVSAR; KDLKTLLNYIQVSART; DLKTLLNYIQVSARTA; LKTLLNYIQVSARTAT; KTLLNYIQVSARTATN; TLLNYIQVSARTATNF;

	LLNYIQVSARTATNFV; LNYIQVSARTATNFVY; NYIQVSARTATNFVYA; YIQVSARTATNFVYAR; IQVSARTATNFVYARE; QVSARTATNFVYAREI; VSARTATNFVYAREIY; SARTATNFVYAREIYS; ARTATNFVYAREIYSK; RTATNFVYAREIYSKR; TATNFVYAREIYSKRK; ATNFVYAREIYSKRKL; TNFVYAREIYSKRKLD; NFVYAREIYSKRKLDA; FVYAREIYSKRKLDAI; VYAREIYSKRKLDAIE; YAREIYSKRKLDAIET; AREIYSKRKLDAIETE; REIYSKRKLDAIETEI; EIYSKRKLDAIETEIK; IYSKRKLDAIETEIKN; YSKRKLDAIETEIKNL; SKRKLDAIETEIKNLI; KRKLDAIETEIKNLIL; RKLDAIETEIKNLILK; KLDAIETEIKNLILKI; LDAIETEIKNLILKIK; DAIETEIKNLILKIKG; AIETEIKNLILKIKGQ; IETEIKNLILKIKGQS; ETEIKNLILKIKGQSD; TEIKNLILKIKGQSDL; EIKNLILKIKGQSDLY; IKNLILKIKGQSDLYE; KNLILKIKGQSDLYEA; NLILKIKGQSDLYEAY; LILKIKGQSDLYEAYK; ILKIKGQSDLYEAYKA; LKIKGQSDLYEAYKAI; KIKGQSDLYEAYKAIV; IKGQSDLYEAYKAIVR; KGQSDLYEAYKAIVRS; GQSDLYEAYKAIVRSI; QSDLYEAYKAIVRSIL; SDLYEAYKAIVRSILL; DLYEAYKAIVRSILLM; LYEAYKAIVRSILLMK; YEAYKAIVRSILLMKD; EAYKAIVRSILLMKDS; AYKAIVRSILLMKDSL; YKAIVRSILLMKDSLK; KAIVRSILLMKDSLKI; AIVRSILLMKDSLKII; IVRSILLMKDSLKIIE; VRSILLMKDSLKIIEI; RSILLMKDSLKIIEIV; SILLMKDSLKIIEIVI; ILLMKDSLKIIEIVID; LLMKDSLKIIEIVIDK; LMKDSLKIIEIVIDKN; MKDSLKIIEIVIDKNG; KDSLKIIEIVIDKNGV; DSLKIIEIVIDKNGVW; SLKIIEIVIDKNGVWY;
Seq 44	13 mers: MKKVKSKYLALGL; KKVKSKYLALGLL; KVKSKYLALGLLF; VKSKYLALGLLFG; KSKYLALGLLFGF; SKYLALGLLFGFI; KYLALGLLFGFIS; YLALGLLFGFISC; LALGLLFGFISCD; ALGLLFGFISCDL; LGLLFGFISCDLF; GLLFGFISCDLFI; LLFGFISCDLFIR; LFGFISCDLFIRY; FGFISCDLFIRYE; GFISCDLFIRYEM; FISCDLFIRYEMK; ISCDLFIRYEMKE; SCDLFIRYEMKEE; CDLFIRYEMKEES; DLFIRYEMKEESP; LFIRYEMKEESPG; FIRYEMKEESPGL; IRYEMKEESPGLF; RYEMKEESPGLFD; YEMKEESPGLFDK; EMKEESPGLFDKG; MKEESPGLFDKGN; KEESPGLFDKGNS; EESPGLFDKGNSI; ESPGLFDKGNSIL; SPGLFDKGNSILE; PGLFDKGNSILET; GLFDKGNSILETS; LFDKGNSILETSE; FDKGNSILETSEE; DKGNSILETSEES; KGNSILETSEESI; GNSILETSEESIK; NSILETSEESIKK; SILETSEESIKKP; ILETSEESIKKPM; LETSEESIKKPMN; ETSEESIKKPMNK; TSEESIKKPMNKK; SEESIKKPMNKKG; EESIKKPMNKKGK; ESIKKPMNKKGKG; SIKKPMNKKGKGK; IKKPMNKKGKGKI; KKPMNKKGKGKIA; KPMNKKGKGKIAR; PMNKKGKGKIARK; MNKKGKGKIARKN; NKKGKGKIARKNG; KKGKGKIARKNGK; KGKGKIARKNGKS; GKGKIARKNGKSK; KGKIARKNGKSKV; GKIARKNGKSKVS; KIARKNGKSKVSG; IARKNGKSKVSGK; ARKNGKSKVSGKE; RKNGKSKVSGKEP; KNGKSKVSGKEPF; NGKSKVSGKEPFI; GKSKVSGKEPFIH; KSKVSGKEPFIHS; SKVSGKEPFIHSF; KVSGKEPFIHSFK; VSGKEPFIHSFKR; SGKEPFIHSFKRD; GKEPFIHSFKRDA; KEPFIHSFKRDAA; EPFIHSFKRDAAN; PFIHSFKRDAANK; FIHSFKRDAANKS; IHSFKRDAANKSN;

	HSFKRDAANKSNF; SFKRDAANKSNFL; FKRDAANKSNFLQ; KRDAANKSNFLQK; RDAANKSNFLQKN; DAANKSNFLQKNV; AANKSNFLQKNVM; ANKSNFLQKNVML; NKSNFLQKNVMLE; KSNFLQKNVMLEE; SNFLQKNVMLEEE; NFLQKNVMLEEES; FLQKNVMLEEESL; LQKNVMLEEESLK; QKNVMLEEESLKT; KNVMLEEESLKTE; NVMLEEESLKTEL; VMLEEESLKTELL; MLEEESLKTELLK; LEEESLKTELLKE; EEESLKTELLKEQ; EESLKTELLKEQS; ESLKTELLKEQSE; SLKTELLKEQSET; LKTELLKEQSETR; KTELLKEQSETRK; TELLKEQSETRKE; ELLKEQSETRKEK; LLKEQSETRKEKI; LKEQSETRKEKIQ; KEQSETRKEKIQK; EQSETRKEKIQKQ; QSETRKEKIQKQQ; SETRKEKIQKQQD; ETRKEKIQKQQDE; TRKEKIQKQQDEY; RKEKIQKQQDEYK; KEKIQKQQDEYKG; EKIQKQQDEYKGM; KIQKQQDEYKGMT; IQKQQDEYKGMTK; QKQQDEYKGMTKG; KQQDEYKGMTKGS; QQDEYKGMTKGSL; QDEYKGMTKGSLN; DEYKGMTKGSLNS; EYKGMTKGSLNSL; YKGMTKGSLNSLS; KGMTKGSLNSLSG; GMTKGSLNSLSGE; MTKGSLNSLSGES; TKGSLNSLSGESG; KGSLNSLSGESGE; GSLNSLSGESGEL; SLNSLSGESGELK; LNSLSGESGELKE; NSLSGESGELKET; SLSGESGELKETI; LSGESGELKETIE; SGESGELKETIES; GESGELKETIESN; ESGELKETIESNE; SGELKETIESNEI; GELKETIESNEID; ELKETIESNEIDI; LKETIESNEIDIT; KETIESNEIDITI; ETIESNEIDITID; TIESNEIDITIDS; IESNEIDITIDSD; ESNEIDITIDSDL; SNEIDITIDSDLR; NEIDITIDSDLRP; EIDITIDSDLRPK; IDITIDSDLRPKS; DITIDSDLRPKSS; ITIDSDLRPKSSL; TIDSDLRPKSSLQ; IDSDLRPKSSLQD; DSDLRPKSSLQDI; SDLRPKSSLQDIA; DLRPKSSLQDIAG; LRPKSSLQDIAGS; RPKSSLQDIAGSN; PKSSLQDIAGSNS; KSSLQDIAGSNSI; SSLQDIAGSNSIS; SLQDIAGSNSISY; LQDIAGSNSISYT; QDIAGSNSISYTD; DIAGSNSISYTDE; IAGSNSISYTDEI; AGSNSISYTDEIE; GSNSISYTDEIEE; SNSISYTDEIEEE; NSISYTDEIEEED; SISYTDEIEEEDY; ISYTDEIEEEDYA; SYTDEIEEEDYAR; YTDEIEEEDYARY; TDEIEEEDYARYY; DEIEEEDYARYYL; EIEEEDYARYYLD; IEEEDYARYYLDE; EEEDYARYYLDED; EEDYARYYLDEDD; EDYARYYLDEDDE; DYARYYLDEDDED; YARYYLDEDDEDD; ARYYLDEDDEDDE; RYYLDEDDEDDEY; YYLDEDDEDDEYY; YLDEDDEDDEYYE; LDEDDEDDEYYED; DEDDEDDEYYEDD; EDDEDDEYYEDDY; DDEDDEYYEDDYE; DEDDEYYEDDYEE; EDDEYYEDDYEEI; DDEYYEDDYEEIR; DEYYEDDYEEIRL; EYYEDDYEEIRLS; YYEDDYEEIRLSN; YEDDYEEIRLSNR; EDDYEEIRLSNRY; DDYEEIRLSNRYQ; DYEEIRLSNRYQS; YEEIRLSNRYQSY; EEIRLSNRYQSYL; EIRLSNRYQSYLE; IRLSNRYQSYLEG; RLSNRYQSYLEGV; LSNRYQSYLEGVK; SNRYQSYLEGVKY; NRYQSYLEGVKYN; RYQSYLEGVKYNV; YQSYLEGVKYNVD; QSYLEGVKYNVDS; SYLEGVKYNVDSA; YLEGVKYNVDSAI; LEGVKYNVDSAIN; EGVKYNVDSAINT; GVKYNVDSAINTI; VKYNVDSAINTIN; KYNVDSAINTINK; YNVDSAINTINKI; NVDSAINTINKIY; VDSAINTINKIYD; DSAINTINKIYDT; SAINTINKIYDTY; AINTINKIYDTYT; INTINKIYDTYTL; NTINKIYDTYTLF;

	TINKIYDTYTLFS; INKIYDTYTLFST; NKIYDTYTLFSTK; KIYDTYTLFSTKL; IYDTYTLFSTKLT; YDTYTLFSTKLTQ; DTYTLFSTKLTQM; TYTLFSTKLTQMY; YTLFSTKLTQMYS; TLFSTKLTQMYST; LFSTKLTQMYSTR; FSTKLTQMYSTRL; STKLTQMYSTRLD; TKLTQMYSTRLDN; KLTQMYSTRLDNL; LTQMYSTRLDNLA; TQMYSTRLDNLAK; QMYSTRLDNLAKA; MYSTRLDNLAKAK; YSTRLDNLAKAKA; STRLDNLAKAKAK; TRLDNLAKAKAKE; RLDNLAKAKAKEE; LDNLAKAKAKEEA; DNLAKAKAKEEAA; NLAKAKAKEEAAK; LAKAKAKEEAAKF; AKAKAKEEAAKFT; KAKAKEEAAKFTK; AKAKEEAAKFTKE; KAKEEAAKFTKED; AKEEAAKFTKEDL; KEEAAKFTKEDLE; EEAAKFTKEDLEK; EAAKFTKEDLEKN; AAKFTKEDLEKNF; AKFTKEDLEKNFK; KFTKEDLEKNFKT; FTKEDLEKNFKTL; TKEDLEKNFKTLL; KEDLEKNFKTLLN; EDLEKNFKTLLNY; DLEKNFKTLLNYI; LEKNFKTLLNYIQ; EKNFKTLLNYIQV; KNFKTLLNYIQVS; NFKTLLNYIQVSV; FKTLLNYIQVSVK; KTLLNYIQVSVKT; TLLNYIQVSVKTA; LLNYIQVSVKTAT; LNYIQVSVKTATN; NYIQVSVKTATNF; YIQVSVKTATNFV; IQVSVKTATNFVY; QVSVKTATNFVYI; VSVKTATNFVYIN; SVKTATNFVYINE; VKTATNFVYINEM; KTATNFVYINEMH; TATNFVYINEMHA; ATNFVYINEMHAK; TNFVYINEMHAKR; NFVYINEMHAKRK; FVYINEMHAKRKL; VYINEMHAKRKLE; YINEMHAKRKLEN; INEMHAKRKLENI; NEMHAKRKLENIE; EMHAKRKLENIEA; MHAKRKLENIEAK; HAKRKLENIEAKI; AKRKLENIEAKIK; KRKLENIEAKIKT; RKLENIEAKIKTL; KLENIEAKIKTLI; LENIEAKIKTLIA; ENIEAKIKTLIAK; NIEAKIKTLIAKI; IEAKIKTLIAKIK; EAKIKTLIAKIKE; AKIKTLIAKIKEK; KIKTLIAKIKEKS; IKTLIAKIKEKSN; KTLIAKIKEKSNL; TLIAKIKEKSNLY; LIAKIKEKSNLYS; IAKIKEKSNLYSA; AKIKEKSNLYSAY; KIKEKSNLYSAYK; IKEKSNLYSAYKA; KEKSNLYSAYKAI; EKSNLYSAYKAIV; KSNLYSAYKAIVS; SNLYSAYKAIVSS; NLYSAYKAIVSSI; LYSAYKAIVSSIL; YSAYKAIVSSILL; SAYKAIVSSILLM; AYKAIVSSILLMR; YKAIVSSILLMRD; KAIVSSILLMRDS; AIVSSILLMRDSL; IVSSILLMRDSLK; VSSILLMRDSLKE; SSILLMRDSLKEV; SILLMRDSLKEVQ; ILLMRDSLKEVQY; LLMRDSLKEVQYA; LMRDSLKEVQYAI; MRDSLKEVQYAID; RDSLKEVQYAIDK; DSLKEVQYAIDKN; SLKEVQYAIDKNG; LKEVQYAIDKNGI; KEVQYAIDKNGIW; EVQYAIDKNGIWY; VQYAIDKNGIWYR; QYAIDKNGIWYRK; YAIDKNGIWYRKL; AIDKNGIWYRKLD; IDKNGIWYRKLDA; DKNGIWYRKLDAI; KNGIWYRKLDAIE; NGIWYRKLDAIET; GIWYRKLDAIETE; IWYRKLDAIETEI; WYRKLDAIETEIK; YRKLDAIETEIKN; RKLDAIETEIKNL; KLDAIETEIKNLI; LDAIETEIKNLIL; DAIETEIKNLILK; AIETEIKNLILKI; IETEIKNLILKIK; ETEIKNLILKIKG; TEIKNLILKIKGQ; EIKNLILKIKGQS; IKNLILKIKGQSD; KNLILKIKGQSDL; NLILKIKGQSDLY; LILKIKGQSDLYE; ILKIKGQSDLYEA; LKIKGQSDLYEAY; KIKGQSDLYEAYK; IKGQSDLYEAYKA; KGQSDLYEAYKAI; GQSDLYEAYKAIV; QSDLYEAYKAIVR; SDLYEAYKAIVRS; DLYEAYKAIVRSI; LYEAYKAIVRSIL; YEAYKAIVRSILL;

EAYKAIVRSILLM; AYKAIVRSILLMK; YKAIVRSILLMKD;
KAIVRSILLMKDS; AIVRSILLMKDSL; IVRSILLMKDSLK;
VRSILLMKDSLKI; RSILLMKDSLKII; SILLMKDSLKIIE;
ILLMKDSLKIIEI; LLMKDSLKIIEIV; LMKDSLKIIEIVI;
MKDSLKIIEIVID; KDSLKIIEIVIDK; DSLKIIEIVIDKN;
SLKIIEIVIDKNG; LKIIEIVIDKNGV; KIIEIVIDKNGVW;
IIEIVIDKNGVWY;

14 mers:
MKKVKSKYLALGLL; KKVKSKYLALGLLF; KVKSKYLALGLLFG;
VKSKYLALGLLFGF; KSKYLALGLLFGFI; SKYLALGLLFGFIS;
KYLALGLLFGFISC; YLALGLLFGFISCD; LALGLLFGFISCDL;
ALGLLFGFISCDLF; LGLLFGFISCDLFI; GLLFGFISCDLFIR;
LLFGFISCDLFIRY; LFGFISCDLFIRYE; FGFISCDLFIRYEM;
GFISCDLFIRYEMK; FISCDLFIRYEMKE; ISCDLFIRYEMKEE;
SCDLFIRYEMKEES; CDLFIRYEMKEESP; DLFIRYEMKEESPG;
LFIRYEMKEESPGL; FIRYEMKEESPGLF; IRYEMKEESPGLFD;
RYEMKEESPGLFDK; YEMKEESPGLFDKG; EMKEESPGLFDKGN;
MKEESPGLFDKGNS; KEESPGLFDKGNSI; EESPGLFDKGNSIL;
ESPGLFDKGNSILE; SPGLFDKGNSILET; PGLFDKGNSILETS;
GLFDKGNSILETSE; LFDKGNSILETSEE; FDKGNSILETSEES;
DKGNSILETSEESI; KGNSILETSEESIK; GNSILETSEESIKK;
NSILETSEESIKKP; SILETSEESIKKPM; ILETSEESIKKPMN;
LETSEESIKKPMNK; ETSEESIKKPMNKK; TSEESIKKPMNKKG;
SEESIKKPMNKKGK; EESIKKPMNKKGKG; ESIKKPMNKKGKGK;
SIKKPMNKKGKGKI; IKKPMNKKGKGKIA; KKPMNKKGKGKIAR;
KPMNKKGKGKIARK; PMNKKGKGKIARKN; MNKKGKGKIARKNG;
NKKGKGKIARKNGK; KKGKGKIARKNGKS; KGKGKIARKNGKSK;
GKGKIARKNGKSKV; KGKIARKNGKSKVS; GKIARKNGKSKVSG;
KIARKNGKSKVSGK; IARKNGKSKVSGKE; ARKNGKSKVSGKEP;
RKNGKSKVSGKEPF; KNGKSKVSGKEPFI; NGKSKVSGKEPFIH;
GKSKVSGKEPFIHS; KSKVSGKEPFIHSF; SKVSGKEPFIHSFK;
KVSGKEPFIHSFKR; VSGKEPFIHSFKRD; SGKEPFIHSFKRDA;
GKEPFIHSFKRDAA; KEPFIHSFKRDAAN; EPFIHSFKRDAANK;
PFIHSFKRDAANKS; FIHSFKRDAANKSN; IHSFKRDAANKSNF;
HSFKRDAANKSNFL; SFKRDAANKSNFLQ; FKRDAANKSNFLQK;
KRDAANKSNFLQKN; RDAANKSNFLQKNV; DAANKSNFLQKNVM;
AANKSNFLQKNVML; ANKSNFLQKNVMLE; NKSNFLQKNVMLEE;
KSNFLQKNVMLEEE; SNFLQKNVMLEEES; NFLQKNVMLEEESL;
FLQKNVMLEEESLK; LQKNVMLEEESLKT; QKNVMLEEESLKTE;
KNVMLEEESLKTEL; NVMLEEESLKTELL; VMLEEESLKTELLK;
MLEEESLKTELLKE; LEEESLKTELLKEQ; EEESLKTELLKEQS;
EESLKTELLKEQSE; ESLKTELLKEQSET; SLKTELLKEQSETR;
LKTELLKEQSETRK; KTELLKEQSETRKE; TELLKEQSETRKEK;
ELLKEQSETRKEKI; LLKEQSETRKEKIQ; LKEQSETRKEKIQK;
KEQSETRKEKIQKQ; EQSETRKEKIQKQQ; QSETRKEKIQKQQD;
SETRKEKIQKQQDE; ETRKEKIQKQQDEY; TRKEKIQKQQDEYK;
RKEKIQKQQDEYKG; KEKIQKQQDEYKGM; EKIQKQQDEYKGMT;
KIQKQQDEYKGMTK; IQKQQDEYKGMTKG; QKQQDEYKGMTKGS;
KQQDEYKGMTKGSL; QQDEYKGMTKGSLN; QDEYKGMTKGSLNS;
DEYKGMTKGSLNSL; EYKGMTKGSLNSLS; YKGMTKGSLNSLSG;

	KGMTKGSLNSLSGE; GMTKGSLNSLSGES; MTKGSLNSLSGESG; TKGSLNSLSGESGE; KGSLNSLSGESGEL; GSLNSLSGESGELK; SLNSLSGESGELKE; LNSLSGESGELKET; NSLSGESGELKETI; SLSGESGELKETIE; LSGESGELKETIES; SGESGELKETIESN; GESGELKETIESNE; ESGELKETIESNEI; SGELKETIESNEID; GELKETIESNEIDI; ELKETIESNEIDIT; LKETIESNEIDITI; KETIESNEIDITID; ETIESNEIDITIDS; TIESNEIDITIDSD; IESNEIDITIDSDL; ESNEIDITIDSDLR; SNEIDITIDSDLRP; NEIDITIDSDLRPK; EIDITIDSDLRPKS; IDITIDSDLRPKSS; DITIDSDLRPKSSL; ITIDSDLRPKSSLQ; TIDSDLRPKSSLQD; IDSDLRPKSSLQDI; DSDLRPKSSLQDIA; SDLRPKSSLQDIAG; DLRPKSSLQDIAGS; LRPKSSLQDIAGSN; RPKSSLQDIAGSNS; PKSSLQDIAGSNSI; KSSLQDIAGSNSIS; SSLQDIAGSNSISY; SLQDIAGSNSISYT; LQDIAGSNSISYTD; QDIAGSNSISYTDE; DIAGSNSISYTDEI; IAGSNSISYTDEIE; AGSNSISYTDEIEE; GSNSISYTDEIEEE; SNSISYTDEIEEED; NSISYTDEIEEEDY; SISYTDEIEEEDYA; ISYTDEIEEEDYAR; SYTDEIEEEDYARY; YTDEIEEEDYARYY; TDEIEEEDYARYYL; DEIEEEDYARYYLD; EIEEEDYARYYLDE; IEEEDYARYYLDED; EEEDYARYYLDEDD; EEDYARYYLDEDDE; EDYARYYLDEDDED; DYARYYLDEDDEDD; YARYYLDEDDEDDE; ARYYLDEDDEDDEY; RYYLDEDDEDDEYY; YYLDEDDEDDEYYE; YLDEDDEDDEYYED; LDEDDEDDEYYEDD; DEDDEDDEYYEDDY; EDDEDDEYYEDDYE; DDEDDEYYEDDYEE; DEDDEYYEDDYEEI; EDDEYYEDDYEEIR; DDEYYEDDYEEIRL; DEYYEDDYEEIRLS; EYYEDDYEEIRLSN; YYEDDYEEIRLSNR; YEDDYEEIRLSNRY; EDDYEEIRLSNRYQ; DDYEEIRLSNRYQS; DYEEIRLSNRYQSY; YEEIRLSNRYQSYL; EEIRLSNRYQSYLE; EIRLSNRYQSYLEG; IRLSNRYQSYLEGV; RLSNRYQSYLEGVK; LSNRYQSYLEGVKY; SNRYQSYLEGVKYN; NRYQSYLEGVKYNV; RYQSYLEGVKYNVD; YQSYLEGVKYNVDS; QSYLEGVKYNVDSA; SYLEGVKYNVDSAI; YLEGVKYNVDSAIN; LEGVKYNVDSAINT; EGVKYNVDSAINTI; GVKYNVDSAINTIN; VKYNVDSAINTINK; KYNVDSAINTINKI; YNVDSAINTINKIY; NVDSAINTINKIYD; VDSAINTINKIYDT; DSAINTINKIYDTY; SAINTINKIYDTYT; AINTINKIYDTYTL; INTINKIYDTYTLF; NTINKIYDTYTLFS; TINKIYDTYTLFST; INKIYDTYTLFSTK; NKIYDTYTLFSTKL; KIYDTYTLFSTKLT; IYDTYTLFSTKLTQ; YDTYTLFSTKLTQM; DTYTLFSTKLTQMY; TYTLFSTKLTQMYS; YTLFSTKLTQMYST; TLFSTKLTQMYSTR; LFSTKLTQMYSTRL; FSTKLTQMYSTRLD; STKLTQMYSTRLDN; TKLTQMYSTRLDNL; KLTQMYSTRLDNLA; LTQMYSTRLDNLAK; TQMYSTRLDNLAKA; QMYSTRLDNLAKAK; MYSTRLDNLAKAKA; YSTRLDNLAKAKAK; STRLDNLAKAKAKE; TRLDNLAKAKAKEE; RLDNLAKAKAKEEA; LDNLAKAKAKEEAA; DNLAKAKAKEEAAK; NLAKAKAKEEAAKF; LAKAKAKEEAAKFT; AKAKAKEEAAKFTK; KAKAKEEAAKFTKE; AKAKEEAAKFTKED; KAKEEAAKFTKEDL; AKEEAAKFTKEDLE; KEEAAKFTKEDLEK; EEAAKFTKEDLEKN; EAAKFTKEDLEKNF; AAKFTKEDLEKNFK; AKFTKEDLEKNFKT; KFTKEDLEKNFKTL; FTKEDLEKNFKTLL; TKEDLEKNFKTLLN; KEDLEKNFKTLLNY; EDLEKNFKTLLNYI; DLEKNFKTLLNYIQ; LEKNFKTLLNYIQV; EKNFKTLLNYIQVS; KNFKTLLNYIQVSV; NFKTLLNYIQVSVK; FKTLLNYIQVSVKT;

	KTLLNYIQVSVKTA; TLLNYIQVSVKTAT; LLNYIQVSVKTATN; LNYIQVSVKTATNF; NYIQVSVKTATNFV; YIQVSVKTATNFVY; IQVSVKTATNFVYI; QVSVKTATNFVYIN; VSVKTATNFVYINE; SVKTATNFVYINEM; VKTATNFVYINEMH; KTATNFVYINEMHA; TATNFVYINEMHAK; ATNFVYINEMHAKR; TNFVYINEMHAKRK; NFVYINEMHAKRKL; FVYINEMHAKRKLE; VYINEMHAKRKLEN; YINEMHAKRKLENI; INEMHAKRKLENIE; NEMHAKRKLENIEA; EMHAKRKLENIEAK; MHAKRKLENIEAKI; HAKRKLENIEAKIK; AKRKLENIEAKIKT; KRKLENIEAKIKTL; RKLENIEAKIKTLI; KLENIEAKIKTLIA; LENIEAKIKTLIAK; ENIEAKIKTLIAKI; NIEAKIKTLIAKIK; IEAKIKTLIAKIKE; EAKIKTLIAKIKEK; AKIKTLIAKIKEKS; KIKTLIAKIKEKSN; IKTLIAKIKEKSNL; KTLIAKIKEKSNLY; TLIAKIKEKSNLYS; LIAKIKEKSNLYSA; IAKIKEKSNLYSAY; AKIKEKSNLYSAYK; KIKEKSNLYSAYKA; IKEKSNLYSAYKAI; KEKSNLYSAYKAIV; EKSNLYSAYKAIVS; KSNLYSAYKAIVSS; SNLYSAYKAIVSSI; NLYSAYKAIVSSIL; LYSAYKAIVSSILL; YSAYKAIVSSILLM; SAYKAIVSSILLMR; AYKAIVSSILLMRD; YKAIVSSILLMRDS; KAIVSSILLMRDSL; AIVSSILLMRDSLK; IVSSILLMRDSLKE; VSSILLMRDSLKEV; SSILLMRDSLKEVQ; SILLMRDSLKEVQY; ILLMRDSLKEVQYA; LLMRDSLKEVQYAI; LMRDSLKEVQYAID; MRDSLKEVQYAIDK; RDSLKEVQYAIDKN; DSLKEVQYAIDKNG; SLKEVQYAIDKNGI; LKEVQYAIDKNGIW; KEVQYAIDKNGIWY; EVQYAIDKNGIWYR; VQYAIDKNGIWYRK; QYAIDKNGIWYRKL; YAIDKNGIWYRKLD; AIDKNGIWYRKLDA; IDKNGIWYRKLDAI; DKNGIWYRKLDAIE; KNGIWYRKLDAIET; NGIWYRKLDAIETE; GIWYRKLDAIETEI; IWYRKLDAIETEIK; WYRKLDAIETEIKN; YRKLDAIETEIKNL; RKLDAIETEIKNLI; KLDAIETEIKNLIL; LDAIETEIKNLILK; DAIETEIKNLILKI; AIETEIKNLILKIK; IETEIKNLILKIKG; ETEIKNLILKIKGQ; TEIKNLILKIKGQS; EIKNLILKIKGQSD; IKNLILKIKGQSDL; KNLILKIKGQSDLY; NLILKIKGQSDLYE; LILKIKGQSDLYEA; ILKIKGQSDLYEAY; LKIKGQSDLYEAYK; KIKGQSDLYEAYKA; IKGQSDLYEAYKAI; KGQSDLYEAYKAIV; GQSDLYEAYKAIVR; QSDLYEAYKAIVRS; SDLYEAYKAIVRSI; DLYEAYKAIVRSIL; LYEAYKAIVRSILL; YEAYKAIVRSILLM; EAYKAIVRSILLMK; AYKAIVRSILLMKD; YKAIVRSILLMKDS; KAIVRSILLMKDSL; AIVRSILLMKDSLK; IVRSILLMKDSLKI; VRSILLMKDSLKII; RSILLMKDSLKIIE; SILLMKDSLKIIEI; ILLMKDSLKIIEIV; LLMKDSLKIIEIVI; LMKDSLKIIEIVID; MKDSLKIIEIVIDK; KDSLKIIEIVIDKN; DSLKIIEIVIDKNG; SLKIIEIVIDKNGV; LKIIEIVIDKNGVW; KIIEIVIDKNGVWY; 15 mers: MKKVKSKYLALGLLF; KKVKSKYLALGLLFG; KVKSKYLALGLLFGF; VKSKYLALGLLFGFI; KSKYLALGLLFGFIS; SKYLALGLLFGFISC; KYLALGLLFGFISCD; YLALGLLFGFISCDL; LALGLLFGFISCDLF; ALGLLFGFISCDLFI; LGLLFGFISCDLFIR; GLLFGFISCDLFIRY; LLFGFISCDLFIRYE; LFGFISCDLFIRYEM; FGFISCDLFIRYEMK; GFISCDLFIRYEMKE; FISCDLFIRYEMKEE; ISCDLFIRYEMKEES; SCDLFIRYEMKEESP; CDLFIRYEMKEESPG; DLFIRYEMKEESPGL; LFIRYEMKEESPGLF; FIRYEMKEESPGLFD; IRYEMKEESPGLFDK;

	RYEMKEESPGLFDKG; YEMKEESPGLFDKGN; EMKEESPGLFDKGNS; MKEESPGLFDKGNSI; KEESPGLFDKGNSIL; EESPGLFDKGNSILE; ESPGLFDKGNSILET; SPGLFDKGNSILETS; PGLFDKGNSILETSE; GLFDKGNSILETSEE; LFDKGNSILETSEES; FDKGNSILETSEESI; DKGNSILETSEESIK; KGNSILETSEESIKK; GNSILETSEESIKKP; NSILETSEESIKKPM; SILETSEESIKKPMN; ILETSEESIKKPMNK; LETSEESIKKPMNKK; ETSEESIKKPMNKKG; TSEESIKKPMNKKGK; SEESIKKPMNKKGKG; EESIKKPMNKKGKGK; ESIKKPMNKKGKGKI; SIKKPMNKKGKGKIA; IKKPMNKKGKGKIAR; KKPMNKKGKGKIARK; KPMNKKGKGKIARKN; PMNKKGKGKIARKNG; MNKKGKGKIARKNGK; NKKGKGKIARKNGKS; KKGKGKIARKNGKSK; KGKGKIARKNGKSKV; GKGKIARKNGKSKVS; KGKIARKNGKSKVSG; GKIARKNGKSKVSGK; KIARKNGKSKVSGKE; IARKNGKSKVSGKEP; ARKNGKSKVSGKEPF; RKNGKSKVSGKEPFI; KNGKSKVSGKEPFIH; NGKSKVSGKEPFIHS; GKSKVSGKEPFIHSF; KSKVSGKEPFIHSFK; SKVSGKEPFIHSFKR; KVSGKEPFIHSFKRD; VSGKEPFIHSFKRDA; SGKEPFIHSFKRDAA; GKEPFIHSFKRDAAN; KEPFIHSFKRDAANK; EPFIHSFKRDAANKS; PFIHSFKRDAANKSN; FIHSFKRDAANKSNF; IHSFKRDAANKSNFL; HSFKRDAANKSNFLQ; SFKRDAANKSNFLQK; FKRDAANKSNFLQKN; KRDAANKSNFLQKNV; RDAANKSNFLQKNVM; DAANKSNFLQKNVML; AANKSNFLQKNVMLE; ANKSNFLQKNVMLEE; NKSNFLQKNVMLEEE; KSNFLQKNVMLEEES; SNFLQKNVMLEEESL; NFLQKNVMLEEESLK; FLQKNVMLEEESLKT; LQKNVMLEEESLKTE; QKNVMLEEESLKTEL; KNVMLEEESLKTELL; NVMLEEESLKTELLK; VMLEEESLKTELLKE; MLEEESLKTELLKEQ; LEEESLKTELLKEQS; EEESLKTELLKEQSE; EESLKTELLKEQSET; ESLKTELLKEQSETR; SLKTELLKEQSETRK; LKTELLKEQSETRKE; KTELLKEQSETRKEK; TELLKEQSETRKEKI; ELLKEQSETRKEKIQ; LLKEQSETRKEKIQK; LKEQSETRKEKIQKQ; KEQSETRKEKIQKQQ; EQSETRKEKIQKQQD; QSETRKEKIQKQQDE; SETRKEKIQKQQDEY; ETRKEKIQKQQDEYK; TRKEKIQKQQDEYKG; RKEKIQKQQDEYKGM; KEKIQKQQDEYKGMT; EKIQKQQDEYKGMTK; KIQKQQDEYKGMTKG; IQKQQDEYKGMTKGS; QKQQDEYKGMTKGSL; KQQDEYKGMTKGSLN; QQDEYKGMTKGSLNS; QDEYKGMTKGSLNSL; DEYKGMTKGSLNSLS; EYKGMTKGSLNSLSG; YKGMTKGSLNSLSGE; KGMTKGSLNSLSGES; GMTKGSLNSLSGESG; MTKGSLNSLSGESGE; TKGSLNSLSGESGEL; KGSLNSLSGESGELK; GSLNSLSGESGELKE; SLNSLSGESGELKET; LNSLSGESGELKETI; NSLSGESGELKETIE; SLSGESGELKETIES; LSGESGELKETIESN; SGESGELKETIESNE; GESGELKETIESNEI; ESGELKETIESNEID; SGELKETIESNEIDI; GELKETIESNEIDIT; ELKETIESNEIDITI; LKETIESNEIDITID; KETIESNEIDITIDS; ETIESNEIDITIDSD; TIESNEIDITIDSDL; IESNEIDITIDSDLR; ESNEIDITIDSDLRP; SNEIDITIDSDLRPK; NEIDITIDSDLRPKS; EIDITIDSDLRPKSS; IDITIDSDLRPKSSL; DITIDSDLRPKSSLQ; ITIDSDLRPKSSLQD; TIDSDLRPKSSLQDI; IDSDLRPKSSLQDIA; DSDLRPKSSLQDIAG; SDLRPKSSLQDIAGS; DLRPKSSLQDIAGSN; LRPKSSLQDIAGSNS; RPKSSLQDIAGSNSI; PKSSLQDIAGSNSIS; KSSLQDIAGSNSISY; SSLQDIAGSNSISYT; SLQDIAGSNSISYTD; LQDIAGSNSISYTDE; QDIAGSNSISYTDEI; DIAGSNSISYTDEIE; IAGSNSISYTDEIEE; AGSNSISYTDEIEEE; GSNSISYTDEIEEED; SNSISYTDEIEEEDY; NSISYTDEIEEEDYA; SISYTDEIEEEDYAR; ISYTDEIEEEDYARY; SYTDEIEEEDYARYY;

	YTDEIEEEDYARYYL; TDEIEEEDYARYYLD; DEIEEEDYARYYLDE; EIEEEDYARYYLDED; IEEEDYARYYLDEDD; EEEDYARYYLDEDDE; EEDYARYYLDEDDED; EDYARYYLDEDDEDD; DYARYYLDEDDEDDE; YARYYLDEDDEDDEY; ARYYLDEDDEDDEYY; RYYLDEDDEDDEYYE; YYLDEDDEDDEYYED; YLDEDDEDDEYYEDD; LDEDDEDDEYYEDDY; DEDDEDDEYYEDDYE; EDDEDDEYYEDDYEE; DDEDDEYYEDDYEEI; DEDDEYYEDDYEEIR; EDDEYYEDDYEEIRL; DDEYYEDDYEEIRLS; DEYYEDDYEEIRLSN; EYYEDDYEEIRLSNR; YYEDDYEEIRLSNRY; YEDDYEEIRLSNRYQ; EDDYEEIRLSNRYQS; DDYEEIRLSNRYQSY; DYEEIRLSNRYQSYL; YEEIRLSNRYQSYLE; EEIRLSNRYQSYLEG; EIRLSNRYQSYLEGV; IRLSNRYQSYLEGVK; RLSNRYQSYLEGVKY; LSNRYQSYLEGVKYN; SNRYQSYLEGVKYNV; NRYQSYLEGVKYNVD; RYQSYLEGVKYNVDS; YQSYLEGVKYNVDSA; QSYLEGVKYNVDSAI; SYLEGVKYNVDSAIN; YLEGVKYNVDSAINT; LEGVKYNVDSAINTI; EGVKYNVDSAINTIN; GVKYNVDSAINTINK; VKYNVDSAINTINKI; KYNVDSAINTINKIY; YNVDSAINTINKIYD; NVDSAINTINKIYDT; VDSAINTINKIYDTY; DSAINTINKIYDTYT; SAINTINKIYDTYTL; AINTINKIYDTYTLF; INTINKIYDTYTLFS; NTINKIYDTYTLFST; TINKIYDTYTLFSTK; INKIYDTYTLFSTKL; NKIYDTYTLFSTKLT; KIYDTYTLFSTKLTQ; IYDTYTLFSTKLTQM; YDTYTLFSTKLTQMY; DTYTLFSTKLTQMYS; TYTLFSTKLTQMYST; YTLFSTKLTQMYSTR; TLFSTKLTQMYSTRL; LFSTKLTQMYSTRLD; FSTKLTQMYSTRLDN; STKLTQMYSTRLDNL; TKLTQMYSTRLDNLA; KLTQMYSTRLDNLAK; LTQMYSTRLDNLAKA; TQMYSTRLDNLAKAK; QMYSTRLDNLAKAKA; MYSTRLDNLAKAKAK; YSTRLDNLAKAKAKE; STRLDNLAKAKAKEE; TRLDNLAKAKAKEEA; RLDNLAKAKAKEEAA; LDNLAKAKAKEEAAK; DNLAKAKAKEEAAKF; NLAKAKAKEEAAKFT; LAKAKAKEEAAKFTK; AKAKAKEEAAKFTKE; KAKAKEEAAKFTKED; AKAKEEAAKFTKEDL; KAKEEAAKFTKEDLE; AKEEAAKFTKEDLEK; KEEAAKFTKEDLEKN; EEAAKFTKEDLEKNF; EAAKFTKEDLEKNFK; AAKFTKEDLEKNFKT; AKFTKEDLEKNFKTL; KFTKEDLEKNFKTLL; FTKEDLEKNFKTLLN; TKEDLEKNFKTLLNY; KEDLEKNFKTLLNYI; EDLEKNFKTLLNYIQ; DLEKNFKTLLNYIQV; LEKNFKTLLNYIQVS; EKNFKTLLNYIQVSV; KNFKTLLNYIQVSVK; NFKTLLNYIQVSVKT; FKTLLNYIQVSVKTA; KTLLNYIQVSVKTAT; TLLNYIQVSVKTATN; LLNYIQVSVKTATNF; LNYIQVSVKTATNFV; NYIQVSVKTATNFVY; YIQVSVKTATNFVYI; IQVSVKTATNFVYIN; QVSVKTATNFVYINE; VSVKTATNFVYINEM; SVKTATNFVYINEMH; VKTATNFVYINEMHA; KTATNFVYINEMHAK; TATNFVYINEMHAKR; ATNFVYINEMHAKRK; TNFVYINEMHAKRKL; NFVYINEMHAKRKLE; FVYINEMHAKRKLEN; VYINEMHAKRKLENI; YINEMHAKRKLENIE; INEMHAKRKLENIEA; NEMHAKRKLENIEAK; EMHAKRKLENIEAKI; MHAKRKLENIEAKIK; HAKRKLENIEAKIKT; AKRKLENIEAKIKTL; KRKLENIEAKIKTLI; RKLENIEAKIKTLIA; KLENIEAKIKTLIAK; LENIEAKIKTLIAKI; ENIEAKIKTLIAKIK; NIEAKIKTLIAKIKE; IEAKIKTLIAKIKEK; EAKIKTLIAKIKEKS; AKIKTLIAKIKEKSN; KIKTLIAKIKEKSNL; IKTLIAKIKEKSNLY; KTLIAKIKEKSNLYS; TLIAKIKEKSNLYSA; LIAKIKEKSNLYSAY; IAKIKEKSNLYSAYK; AKIKEKSNLYSAYKA; KIKEKSNLYSAYKAI; IKEKSNLYSAYKAIV; KEKSNLYSAYKAIVS; EKSNLYSAYKAIVSS; KSNLYSAYKAIVSSI; SNLYSAYKAIVSSIL; NLYSAYKAIVSSILL; LYSAYKAIVSSILLM; YSAYKAIVSSILLMR; SAYKAIVSSILLMRD;

	AYKAIVSSILLMRDS; YKAIVSSILLMRDSL; KAIVSSILLMRDSLK; AIVSSILLMRDSLKE; IVSSILLMRDSLKEV; VSSILLMRDSLKEVQ; SSILLMRDSLKEVQY; SILLMRDSLKEVQYA; ILLMRDSLKEVQYAI; LLMRDSLKEVQYAID; LMRDSLKEVQYAIDK; MRDSLKEVQYAIDKN; RDSLKEVQYAIDKNG; DSLKEVQYAIDKNGI; SLKEVQYAIDKNGIW; LKEVQYAIDKNGIWY; KEVQYAIDKNGIWYR; EVQYAIDKNGIWYRK; VQYAIDKNGIWYRKL; QYAIDKNGIWYRKLD; YAIDKNGIWYRKLDA; AIDKNGIWYRKLDAI; IDKNGIWYRKLDAIE; DKNGIWYRKLDAIET; KNGIWYRKLDAIETE; NGIWYRKLDAIETEI; GIWYRKLDAIETEIK; IWYRKLDAIETEIKN; WYRKLDAIETEIKNL; YRKLDAIETEIKNLI; RKLDAIETEIKNLIL; KLDAIETEIKNLILK; LDAIETEIKNLILKI; DAIETEIKNLILKIK; AIETEIKNLILKIKG; IETEIKNLILKIKGQ; ETEIKNLILKIKGQS; TEIKNLILKIKGQSD; EIKNLILKIKGQSDL; IKNLILKIKGQSDLY; KNLILKIKGQSDLYE; NLILKIKGQSDLYEA; LILKIKGQSDLYEAY; ILKIKGQSDLYEAYK; LKIKGQSDLYEAYKA; KIKGQSDLYEAYKAI; IKGQSDLYEAYKAIV; KGQSDLYEAYKAIVR; GQSDLYEAYKAIVRS; QSDLYEAYKAIVRSI; SDLYEAYKAIVRSIL; DLYEAYKAIVRSILL; LYEAYKAIVRSILLM; YEAYKAIVRSILLMK; EAYKAIVRSILLMKD; AYKAIVRSILLMKDS; YKAIVRSILLMKDSL; KAIVRSILLMKDSLK; AIVRSILLMKDSLKI; IVRSILLMKDSLKII; VRSILLMKDSLKIIE; RSILLMKDSLKIIEI; SILLMKDSLKIIEIV; ILLMKDSLKIIEIVI; LLMKDSLKIIEIVID; LMKDSLKIIEIVIDK; MKDSLKIIEIVIDKN; KDSLKIIEIVIDKNG; DSLKIIEIVIDKNGV; SLKIIEIVIDKNGVW; LKIIEIVIDKNGVWY; 16 mers: MKKVKSKYLALGLLFG; KKVKSKYLALGLLFGF; KVKSKYLALGLLFGFI; VKSKYLALGLLFGFIS; KSKYLALGLLFGFISC; SKYLALGLLFGFISCD; KYLALGLLFGFISCDL; YLALGLLFGFISCDLF; LALGLLFGFISCDLFI; ALGLLFGFISCDLFIR; LGLLFGFISCDLFIRY; GLLFGFISCDLFIRYE; LLFGFISCDLFIRYEM; LFGFISCDLFIRYEMK; FGFISCDLFIRYEMKE; GFISCDLFIRYEMKEE; FISCDLFIRYEMKEES; ISCDLFIRYEMKEESP; SCDLFIRYEMKEESPG; CDLFIRYEMKEESPGL; DLFIRYEMKEESPGLF; LFIRYEMKEESPGLFD; FIRYEMKEESPGLFDK; IRYEMKEESPGLFDKG; RYEMKEESPGLFDKGN; YEMKEESPGLFDKGNS; EMKEESPGLFDKGNSI; MKEESPGLFDKGNSIL; KEESPGLFDKGNSILE; EESPGLFDKGNSILET; ESPGLFDKGNSILETS; SPGLFDKGNSILETSE; PGLFDKGNSILETSEE; GLFDKGNSILETSEES; LFDKGNSILETSEESI; FDKGNSILETSEESIK; DKGNSILETSEESIKK; KGNSILETSEESIKKP; GNSILETSEESIKKPM; NSILETSEESIKKPMN; SILETSEESIKKPMNK; ILETSEESIKKPMNKK; LETSEESIKKPMNKKG; ETSEESIKKPMNKKGK; TSEESIKKPMNKKGKG; SEESIKKPMNKKGKGK; EESIKKPMNKKGKGKI; ESIKKPMNKKGKGKIA; SIKKPMNKKGKGKIAR; IKKPMNKKGKGKIARK; KKPMNKKGKGKIARKN; KPMNKKGKGKIARKNG; PMNKKGKGKIARKNGK; MNKKGKGKIARKNGKS; NKKGKGKIARKNGKSK; KKGKGKIARKNGKSKV; KGKGKIARKNGKSKVS; GKGKIARKNGKSKVSG; KGKIARKNGKSKVSGK; GKIARKNGKSKVSGKE; KIARKNGKSKVSGKEP; IARKNGKSKVSGKEPF; ARKNGKSKVSGKEPFI; RKNGKSKVSGKEPFIH; KNGKSKVSGKEPFIHS; NGKSKVSGKEPFIHSF; GKSKVSGKEPFIHSFK; KSKVSGKEPFIHSFKR; SKVSGKEPFIHSFKRD; KVSGKEPFIHSFKRDA; VSGKEPFIHSFKRDAA; SGKEPFIHSFKRDAAN; GKEPFIHSFKRDAANK; KEPFIHSFKRDAANKS; EPFIHSFKRDAANKSN;

	PFIHSFKRDAANKSNF; FIHSFKRDAANKSNFL; IHSFKRDAANKSNFLQ; HSFKRDAANKSNFLQK; SFKRDAANKSNFLQKN; FKRDAANKSNFLQKNV; KRDAANKSNFLQKNVM; RDAANKSNFLQKNVML; DAANKSNFLQKNVMLE; AANKSNFLQKNVMLEE; ANKSNFLQKNVMLEEE; NKSNFLQKNVMLEEES; KSNFLQKNVMLEEESL; SNFLQKNVMLEEESLK; NFLQKNVMLEEESLKT; FLQKNVMLEEESLKTE; LQKNVMLEEESLKTEL; QKNVMLEEESLKTELL; KNVMLEEESLKTELLK; NVMLEEESLKTELLKE; VMLEEESLKTELLKEQ; MLEEESLKTELLKEQS; LEEESLKTELLKEQSE; EEESLKTELLKEQSET; EESLKTELLKEQSETR; ESLKTELLKEQSETRK; SLKTELLKEQSETRKE; LKTELLKEQSETRKEK; KTELLKEQSETRKEKI; TELLKEQSETRKEKIQ; ELLKEQSETRKEKIQK; LLKEQSETRKEKIQKQ; LKEQSETRKEKIQKQQ; KEQSETRKEKIQKQQD; EQSETRKEKIQKQQDE; QSETRKEKIQKQQDEY; SETRKEKIQKQQDEYK; ETRKEKIQKQQDEYKG; TRKEKIQKQQDEYKGM; RKEKIQKQQDEYKGMT; KEKIQKQQDEYKGMTK; EKIQKQQDEYKGMTKG; KIQKQQDEYKGMTKGS; IQKQQDEYKGMTKGSL; QKQQDEYKGMTKGSLN; KQQDEYKGMTKGSLNS; QQDEYKGMTKGSLNSL; QDEYKGMTKGSLNSLS; DEYKGMTKGSLNSLSG; EYKGMTKGSLNSLSGE; YKGMTKGSLNSLSGES; KGMTKGSLNSLSGESG; GMTKGSLNSLSGESGE; MTKGSLNSLSGESGEL; TKGSLNSLSGESGELK; KGSLNSLSGESGELKE; GSLNSLSGESGELKET; SLNSLSGESGELKETI; LNSLSGESGELKETIE; NSLSGESGELKETIES; SLSGESGELKETIESN; LSGESGELKETIESNE; SGESGELKETIESNEI; GESGELKETIESNEID; ESGELKETIESNEIDI; SGELKETIESNEIDIT; GELKETIESNEIDITI; ELKETIESNEIDITID; LKETIESNEIDITIDS; KETIESNEIDITIDSD; ETIESNEIDITIDSDL; TIESNEIDITIDSDLR; IESNEIDITIDSDLRP; ESNEIDITIDSDLRPK; SNEIDITIDSDLRPKS; NEIDITIDSDLRPKSS; EIDITIDSDLRPKSSL; IDITIDSDLRPKSSLQ; DITIDSDLRPKSSLQD; ITIDSDLRPKSSLQDI; TIDSDLRPKSSLQDIA; IDSDLRPKSSLQDIAG; DSDLRPKSSLQDIAGS; SDLRPKSSLQDIAGSN; DLRPKSSLQDIAGSNS; LRPKSSLQDIAGSNSI; RPKSSLQDIAGSNSIS; PKSSLQDIAGSNSISY; KSSLQDIAGSNSISYT; SSLQDIAGSNSISYTD; SLQDIAGSNSISYTDE; LQDIAGSNSISYTDEI; QDIAGSNSISYTDEIE; DIAGSNSISYTDEIEE; IAGSNSISYTDEIEEE; AGSNSISYTDEIEEED; GSNSISYTDEIEEEDY; SNSISYTDEIEEEDYA; NSISYTDEIEEEDYAR; SISYTDEIEEEDYARY; ISYTDEIEEEDYARYY; SYTDEIEEEDYARYYL; YTDEIEEEDYARYYLD; TDEIEEEDYARYYLDE; DEIEEEDYARYYLDED; EIEEEDYARYYLDEDD; IEEEDYARYYLDEDDE; EEEDYARYYLDEDDED; EEDYARYYLDEDDEDD; EDYARYYLDEDDEDDE; DYARYYLDEDDEDDEY; YARYYLDEDDEDDEYY; ARYYLDEDDEDDEYYE; RYYLDEDDEDDEYYED; YYLDEDDEDDEYYEDD; YLDEDDEDDEYYEDDY; LDEDDEDDEYYEDDYE; DEDDEDDEYYEDDYEE; EDDEDDEYYEDDYEEI; DDEDDEYYEDDYEEIR; DEDDEYYEDDYEEIRL; EDDEYYEDDYEEIRLS; DDEYYEDDYEEIRLSN; DEYYEDDYEEIRLSNR; EYYEDDYEEIRLSNRY; YYEDDYEEIRLSNRYQ; YEDDYEEIRLSNRYQS; EDDYEEIRLSNRYQSY; DDYEEIRLSNRYQSYL; DYEEIRLSNRYQSYLE; YEEIRLSNRYQSYLEG; EEIRLSNRYQSYLEGV; EIRLSNRYQSYLEGVK; IRLSNRYQSYLEGVKY; RLSNRYQSYLEGVKYN; LSNRYQSYLEGVKYNV; SNRYQSYLEGVKYNVD; NRYQSYLEGVKYNVDS; RYQSYLEGVKYNVDSA; YQSYLEGVKYNVDSAI; QSYLEGVKYNVDSAIN; SYLEGVKYNVDSAINT; YLEGVKYNVDSAINTI; LEGVKYNVDSAINTIN; EGVKYNVDSAINTINK; GVKYNVDSAINTINKI; VKYNVDSAINTINKIY; KYNVDSAINTINKIYD; YNVDSAINTINKIYDT; NVDSAINTINKIYDTY; VDSAINTINKIYDTYT; DSAINTINKIYDTYTL; SAINTINKIYDTYTLF;

	AINTINKIYDTYTLFS; INTINKIYDTYTLFST; NTINKIYDTYTLFSTK; TINKIYDTYTLFSTKL; INKIYDTYTLFSTKLT; NKIYDTYTLFSTKLTQ; KIYDTYTLFSTKLTQM; IYDTYTLFSTKLTQMY; YDTYTLFSTKLTQMYS; DTYTLFSTKLTQMYST; TYTLFSTKLTQMYSTR; YTLFSTKLTQMYSTRL; TLFSTKLTQMYSTRLD; LFSTKLTQMYSTRLDN; FSTKLTQMYSTRLDNL; STKLTQMYSTRLDNLA; TKLTQMYSTRLDNLAK; KLTQMYSTRLDNLAKA; LTQMYSTRLDNLAKAK; TQMYSTRLDNLAKAKA; QMYSTRLDNLAKAKAK; MYSTRLDNLAKAKAKE; YSTRLDNLAKAKAKEE; STRLDNLAKAKAKEEA; TRLDNLAKAKAKEEAA; RLDNLAKAKAKEEAAK; LDNLAKAKAKEEAAKF; DNLAKAKAKEEAAKFT; NLAKAKAKEEAAKFTK; LAKAKAKEEAAKFTKE; AKAKAKEEAAKFTKED; KAKAKEEAAKFTKEDL; AKAKEEAAKFTKEDLE; KAKEEAAKFTKEDLEK; AKEEAAKFTKEDLEKN; KEEAAKFTKEDLEKNF; EEAAKFTKEDLEKNFK; EAAKFTKEDLEKNFKT; AAKFTKEDLEKNFKTL; AKFTKEDLEKNFKTLL; KFTKEDLEKNFKTLLN; FTKEDLEKNFKTLLNY; TKEDLEKNFKTLLNYI; KEDLEKNFKTLLNYIQ; EDLEKNFKTLLNYIQV; DLEKNFKTLLNYIQVS; LEKNFKTLLNYIQVSV; EKNFKTLLNYIQVSVK; KNFKTLLNYIQVSVKT; NFKTLLNYIQVSVKTA; FKTLLNYIQVSVKTAT; KTLLNYIQVSVKTATN; TLLNYIQVSVKTATNF; LLNYIQVSVKTATNFV; LNYIQVSVKTATNFVY; NYIQVSVKTATNFVYI; YIQVSVKTATNFVYIN; IQVSVKTATNFVYINE; QVSVKTATNFVYINEM; VSVKTATNFVYINEMH; SVKTATNFVYINEMHA; VKTATNFVYINEMHAK; KTATNFVYINEMHAKR; TATNFVYINEMHAKRK; ATNFVYINEMHAKRKL; TNFVYINEMHAKRKLE; NFVYINEMHAKRKLEN; FVYINEMHAKRKLENI; VYINEMHAKRKLENIE; YINEMHAKRKLENIEA; INEMHAKRKLENIEAK; NEMHAKRKLENIEAKI; EMHAKRKLENIEAKIK; MHAKRKLENIEAKIKT; HAKRKLENIEAKIKTL; AKRKLENIEAKIKTLI; KRKLENIEAKIKTLIA; RKLENIEAKIKTLIAK; KLENIEAKIKTLIAKI; LENIEAKIKTLIAKIK; ENIEAKIKTLIAKIKE; NIEAKIKTLIAKIKEK; IEAKIKTLIAKIKEKS; EAKIKTLIAKIKEKSN; AKIKTLIAKIKEKSNL; KIKTLIAKIKEKSNLY; IKTLIAKIKEKSNLYS; KTLIAKIKEKSNLYSA; TLIAKIKEKSNLYSAY; LIAKIKEKSNLYSAYK; IAKIKEKSNLYSAYKA; AKIKEKSNLYSAYKAI; KIKEKSNLYSAYKAIV; IKEKSNLYSAYKAIVS; KEKSNLYSAYKAIVSS; EKSNLYSAYKAIVSSI; KSNLYSAYKAIVSSIL; SNLYSAYKAIVSSILL; NLYSAYKAIVSSILLM; LYSAYKAIVSSILLMR; YSAYKAIVSSILLMRD; SAYKAIVSSILLMRDS; AYKAIVSSILLMRDSL; YKAIVSSILLMRDSLK; KAIVSSILLMRDSLKE; AIVSSILLMRDSLKEV; IVSSILLMRDSLKEVQ; VSSILLMRDSLKEVQY; SSILLMRDSLKEVQYA; SILLMRDSLKEVQYAI; ILLMRDSLKEVQYAID; LLMRDSLKEVQYAIDK; LMRDSLKEVQYAIDKN; MRDSLKEVQYAIDKNG; RDSLKEVQYAIDKNGI; DSLKEVQYAIDKNGIW; SLKEVQYAIDKNGIWY; LKEVQYAIDKNGIWYR; KEVQYAIDKNGIWYRK; EVQYAIDKNGIWYRKL; VQYAIDKNGIWYRKLD; QYAIDKNGIWYRKLDA; YAIDKNGIWYRKLDAI; AIDKNGIWYRKLDAIE; IDKNGIWYRKLDAIET; DKNGIWYRKLDAIETE; KNGIWYRKLDAIETEI; NGIWYRKLDAIETEIK; GIWYRKLDAIETEIKN; IWYRKLDAIETEIKNL; WYRKLDAIETEIKNLI; YRKLDAIETEIKNLIL; RKLDAIETEIKNLILK; KLDAIETEIKNLILKI; LDAIETEIKNLILKIK; DAIETEIKNLILKIKG; AIETEIKNLILKIKGQ; IETEIKNLILKIKGQS; ETEIKNLILKIKGQSD; TEIKNLILKIKGQSDL; EIKNLILKIKGQSDLY; IKNLILKIKGQSDLYE; KNLILKIKGQSDLYEA; NLILKIKGQSDLYEAY; LILKIKGQSDLYEAYK; ILKIKGQSDLYEAYKA; LKIKGQSDLYEAYKAI; KIKGQSDLYEAYKAIV; IKGQSDLYEAYKAIVR; KGQSDLYEAYKAIVRS; GQSDLYEAYKAIVRSI; QSDLYEAYKAIVRSIL; SDLYEAYKAIVRSILL;

	DLYEAYKAIVRSILLM; LYEAYKAIVRSILLMK; YEAYKAIVRSILLMKD; EAYKAIVRSILLMKDS; AYKAIVRSILLMKDSL; YKAIVRSILLMKDSLK; KAIVRSILLMKDSLKI; AIVRSILLMKDSLKII; IVRSILLMKDSLKIIE; VRSILLMKDSLKIIEI; RSILLMKDSLKIIEIV; SILLMKDSLKIIEIVI; ILLMKDSLKIIEIVID; LLMKDSLKIIEIVIDK; LMKDSLKIIEIVIDKN; MKDSLKIIEIVIDKNG; KDSLKIIEIVIDKNGV; DSLKIIEIVIDKNGVW; SLKIIEIVIDKNGVWY;

Fig. 34.

Antigen designation	HLA-chain Class 2	Amino acid sequence 15 mer peptide	9mer core peptide
NP_212517.1 Basic membrane protein A (bmpA) [Borrelia burgdorferi B31 Seq1	HLA-DRB1*0101	GSFADLEAGRSVATR	LEAGRSVAT
		IGSFADLEAGRSVAT	FADLEAGRS
		FADLEAGRSVATRMY	LEAGRSVAT
		SFADLEAGRSVATRM	LEAGRSVAT
		ADLEAGRSVATRMYS	LEAGRSVAT
		AFLTGYIAAKLSKTG	YIAAKLSKT
		FLTGYIAAKLSKTGK	IAAKLSKTG
		LTGYIAAKLSKTGKI	IAAKLSKTG
		TGYIAAKLSKTGKIG	IAAKLSKTG
		DLEAGRSVATRMYSD	LEAGRSVAT
		LEAGRSVATRMYSDE	LEAGRSVAT
		GAFLTGYIAAKLSKT	LTGYIAAKL
		GYIAAKLSKTGKIGF	IAAKLSKTG
		IHHAAGLGGIGAIEV	IHHAAGLGG
		LVGMTFRAQEGAFLT	FRAQEGAFL
		NLVGMTFRAQEGAFL	LVGMTFRAQ
		HHAAGLGGIGAIEVA	LGGIGAIEV
		HAAGLGGIGAIEVAK	LGGIGAIEV
		AAGLGGIGAIEVAKE	LGGIGAIEV
		AGLGGIGAIEVAKEL	LGGIGAIEV
		EGAFLTGYIAAKLSK	LTGYIAAKL
		YIAAKLSKTGKIGFL	IAAKLSKTG
		GMTFRAQEGAFLTGY	FRAQEGAFL
		QEGAFLTGYIAAKLS	LTGYIAAKL
		EKEIDNLSSKIINKE	IDNLSSKII
		LEKEIDNLSSKIINK	IDNLSSKII
		KEIDNLSSKIINKEI	IDNLSSKII
		MTFRAQEGAFLTGYI	FRAQEGAFL
		ELEKEIDNLSSKIIN	IDNLSSKII
		VGMTFRAQEGAFLTG	FRAQEGAFL
		FELEKEIDNLSSKII	FELEKEIDN
		DMKYAIIDPIYSNDP	YAIIDPIYS
		MKYAIIDPIYSNDPI	YAIIDPIYS
		DPIPANLVGMTFRAQ	IPANLVGMT
		TQYIGSFADLEAGRS	IGSFADLEA
		QYIGSFADLEAGRSV	FADLEAGRS
		YIGSFADLEAGRSVA	FADLEAGRS
		IPANLVGMTFRAQEG	LVGMTFRAQ
		PANLVGMTFRAQEGA	LVGMTFRAQ
		PIPANLVGMTFRAQE	LVGMTFRAQ
		AQEGAFLTGYIAAKL	FLTGYIAAK
		SDLIWLIGYRFSDVA	LIWLIGYRF
		ANLVGMTFRAQEGAF	LVGMTFRAQ
		GSDLIWLIGYRFSDV	LIWLIGYRF
		VAKVAALQNPDMKYA	VAALQNPDM
		DAGSDLIWLIGYRFS	LIWLIGYRF
		AGSDLIWLIGYRFSD	LIWLIGYRF
		IDIIHHAAGLGGIGA	IHHAAGLGG
		PDMKYAIIDPIYSND	YAIIDPIYS
		NPDMKYAIIDPIYSN	YAIIDPIYS
		AKVAALQNPDMKYAI	LQNPDMKYA
		QNPDMKYAIIDPIYS	MKYAIIDPI

		FSDVAKVAALQNPDM VAKVAALQN
		EIDIIHHAAGLGGIG IHHAAGLGG
		DEIDIIHHAAGLGGI IHHAAGLGG
		SDVAKVAALQNPDMK VAKVAALQN
		SDEIDIIHHAAGLGG IIHHAAGLG
		YLAPDNVITSTTKDV YLAPDNVIT
		DPIYSNDPIPANLVG NDPIPANLV
		IDPIYSNDPIPANLV IYSNDPIPA
		LIWLIGYRFSDVAKV LIWLIGYRF
		VAALQNPDMKYAIID LQNPDMKYA
		KVAALQNPDMKYAII LQNPDMKYA
		DIIHHAAGLGGIGAI IHHAAGLGG
		GYRFSDVAKVAALQN YRFSDVAKV
		YRFSDVAKVAALQNP VAKVAALQN
		YAIIDPIYSNDPIPA YAIIDPIYS
		TFRAQEGAFLTGYIA FRAQEGAFL
		KDAGSDLIWLIGYRF GSDLIWLIG
		GLGGIGAIEVAKELG LGGIGAIEV
		IYSNDPIPANLVGMT NDPIPANLV
		LGGIGAIEVAKELGS LGGIGAIEV
		IAAKLSKTGKIGFLG IAAKLSKTG
		CSGKGSLGSEIPKVS KGSLGSEIP
		FRAQEGAFLTGYIAA FRAQEGAFL
		PIYSNDPIPANLVGM YSNDPIPAN
		DQAYLAPDNVITSTT YLAPDNVIT
		LAPDNVITSTTKDVG VITSTTKDV
		QAYLAPDNVITSTTK YLAPDNVIT
		AALQNPDMKYAIIDP LQNPDMKYA
		DLIWLIGYRFSDVAK LIWLIGYRF
		PDNVITSTTKDVGRA VITSTTKDV
		SGKGSLGSEIPKVSL LGSEIPKVS
		LSDLEGLKDAGSDLI LEGLKDAGS
		RFSDVAKVAALQNPD VAKVAALQN
		KYAIIDPIYSNDPIP YAIIDPIYS
		APDNVITSTTKDVGR VITSTTKDV
		AIIDPIYSNDPIPAN IYSNDPIPA
		SDLEGLKDAGSDLIW LKDAGSDLI
		KGSLGSEIPKVSLII LGSEIPKVS
		EDQAYLAPDNVITST YLAPDNVIT
		YEAGAKYANKDIKIS YEAGAKYAN
		DEDQAYLAPDNVITS YLAPDNVIT
		VGFVRNPKMISFELE FVRNPKMIS
		VVGFVRNPKMISFEL FVRNPKMIS
		YSNDPIPANLVGMTF IPANLVGMT
		DVAKVAALQNPDMKY VAALQNPDM
		EIDNLSSKIINKEII IDNLSSKII
		VDEDQAYLAPDNVIT VDEDQAYLA
		IDNLSSKIINKEIIV IDNLSSKII
		DNVITSTTKDVGRAL VITSTTKDV
		GVVGFVRNPKMISFE FVRNPKMIS
		AKYANKDIKISTQYI YANKDIKIS
		EGVVGFVRNPKMISF FVRNPKMIS
		GKGSLGSEIPKVSLI LGSEIPKVS
		MNKILLLILLESIVF MNKILLLIL
		KDVGRALNIFTSNHL VGRALNIFT
		GYRFSDVAKVAALQ YRFSDVAKV
		GSLGSEIPKVSLIID LGSEIPKVS

		LEGLKDAGSDLIWLI LKDAGSDLI NKILLLILLESIVFL LILLESIVF IIDPIYSNDPIPANL IYSNDPIPA EGLKDAGSDLIWLIG LKDAGSDLI AGAKYANKDIKISTQ YANKDIKIS IIHHAAGLGGIGAIE IHHAAGLGG EAGAKYANKDIKIST YANKDIKIS GAKYANKDIKISTQY YANKDIKIS IWLIGYRFSDVAKVA YRFSDVAKV LIGYRFSDVAKVAAL YRFSDVAKV WLIGYRFSDVAKVAA YRFSDVAKV GGKLINYGLKEGVVG LINYGLKEG GKLINYGLKEGVVGF YGLKEGVVG KILLLILLESIVFLS LILLESIVF IELVLKESSSNSYLS LKESSSNSY KIELVLKESSSNSYL LKESSSNSY VGRALNIFTSNHLKT LNIFTSNHL FKIELVLKESSSNSY LVLKESSSN KLINYGLKEGVVGFV YGLKEGVVG ILLLILLESIVFLSC LILLESIVF GRALNIFTSNHLKTN LNIFTSNHL LINYGLKEGVVGFVR YGLKEGVVG DVGRALNIFTSNHLK LNIFTSNHL NDPIPANLVGMTFRA IPANLVGMT DKSFNESALNGVKKV FNESALNGV RALNIFTSNHLKTNT LNIFTSNHL GFVRNPKMISFELEK VRNPKMISF ELVLKESSSNSYLSD LKESSSNSY SNDPIPANLVGMTFR IPANLVGMT DDKSFNESALNGVKK FNESALNGV LLLILLESIVFLSCS LILLESIVF AYLAPDNVITSTTKD YLAPDNVIT ALQNPDMKYAIIDPI LQNPDMKYA FDDKSFNESALNGVK FNESALNGV TFDDKSFNESALNGV SFNESALNG LQNPDMKYAIIDPIY LQNPDMKYA TKDVGRALNIFTSNH VGRALNIFT TTKDVGRALNIFTSN VGRALNIFT KEGVVGFVRNPKMIS VGFVRNPKM SIVFLSCSGKGSLGS FLSCSGKGS YSDEIDIIHHAAGLG EIDIIHHAA INYGLKEGVVGFVRN YGLKEGVVG STTKDVGRALNIFTS VGRALNIFT
	HLA-DRB1*0301	None
	HLA-DRB1*0401	FKIELVLKESSSNSY VLKESSSNS IELVLKESSSNSYLS LKESSSNSY ELVLKESSSNSYLSD LKESSSNSY KIELVLKESSSNSYL LKESSSNSY LVLKESSSNSYLSDL LKESSSNSY KIINKEIIVPSNKES INKEIIVPS SKIINKEIIVPSNKE INKEIIVPS SSKIINKEIIVPSNK INKEIIVPS LSSKIINKEIIVPSN INKEIIVPS NLSSKIINKEIIVPS LSSKIINKE EGVVGFVRNPKMISF FVRNPKMIS KEGVVGFVRNPKMIS VVGFVRNPK

		ISFELEKEIDNLSSK LEKEIDNLS MISFELEKEIDNLSS LEKEIDNLS GVVGFVRNPKMISFE FVRNPKMIS FELEKEIDNLSSKII LEKEIDNLS SFELEKEIDNLSSKI LEKEIDNLS AIIDPIYSNDPIPAN IYSNDPIPA VVGFVRNPKMISFEL FVRNPKMIS VGFVRNPKMISFELE FVRNPKMIS IIDPIYSNDPIPANL IYSNDPIPA IDPIYSNDPIPANLV IYSNDPIPA KMISFELEKEIDNLS MISFELEKE DPIYSNDPIPANLVG IYSNDPIPA VLKESSSNSYLSDLE LKESSSNSY LKESSSNSYLSDLEG LKESSSNSY RALNIFTSNHLKTNT LNIFTSNHL GRALNIFTSNHLKTN LNIFTSNHL VGRALNIFTSNHLKT LNIFTSNHL IINKEIIVPSNKESY INKEIIVPS KDVGRALNIFTSNHL VGRALNIFT INKEIIVPSNKESYE INKEIIVPS DVGRALNIFTSNHLK LNIFTSNHL YAIIDPIYSNDPIPA IDPIYSNDP
	HLA-DRB1*0404	VGRALNIFTSNHLKT ALNIFTSNH GRALNIFTSNHLKTN ALNIFTSNH KDVGRALNIFTSNHL ALNIFTSNH DVGRALNIFTSNHLK ALNIFTSNH TKDVGRALNIFTSNH VGRALNIFT RALNIFTSNHLKTNT ALNIFTSNH ALNIFTSNHLKTNTF ALNIFTSNH FKIELVLKESSSNSY VLKESSSNS KIELVLKESSSNSYL VLKESSSNS IELVLKESSSNSYLS VLKESSSNS ELVLKESSSNSYLSD VLKESSSNS
	HLA-DRB1*0405	AIIDPIYSNDPIPAN IYSNDPIPA IIDPIYSNDPIPANL YSNDPIPAN IDPIYSNDPIPANLV YSNDPIPAN DPIYSNDPIPANLVG YSNDPIPAN PIYSNDPIPANLVGM YSNDPIPAN KIINKEIIVPSNKES EIIVPSNKE KEGVVGFVRNPKMIS VVGFVRNPK EGVVGFVRNPKMISF FVRNPKMIS IYSNDPIPANLVGMT YSNDPIPAN INKEIIVPSNKESYE EIIVPSNKE SKIINKEIIVPSNKE INKEIIVPS GVVGFVRNPKMISFE FVRNPKMIS IINKEIIVPSNKESY EIIVPSNKE
	HLA-DRB1*0701	VGRALNIFTSNHLKT LNIFTSNHL GRALNIFTSNHLKTN LNIFTSNHL DVGRALNIFTSNHLK LNIFTSNHL KDVGRALNIFTSNHL ALNIFTSNH RALNIFTSNHLKTNT LNIFTSNHL LAPDNVITSTTKDVG VITSTTKDV APDNVITSTTKDVGR VITSTTKDV PDNVITSTTKDVGRA VITSTTKDV DNVITSTTKDVGRAL VITSTTKDV
	HLA-DRB1*0802	None

	HLA-DRB1*0901	WLIGYRFSDVAKVAA	YRFSDVAKV
		LIGYRFSDVAKVAAL	YRFSDVAKV
		IGYRFSDVAKVAALQ	YRFSDVAKV
		LEGLKDAGSDLIWLI	LKDAGSDLI
		GAFLTGYIAAKLSKT	LTGYIAAKL
		DLEGLKDAGSDLIWL	LKDAGSDLI
		SDLEGLKDAGSDLIW	LKDAGSDLI
		LSDLEGLKDAGSDLI	LEGLKDAGS
		LIWLIGYRFSDVAKV	LIGYRFSDV
		EGLKDAGSDLIWLIG	LKDAGSDLI
		IWLIGYRFSDVAKVA	YRFSDVAKV
		AFLTGYIAAKLSKTG	YIAAKLSKT
	HLA-DRB1*1101	GSDLIWLIGYRFSDV	LIWLIGYRF
		SDLIWLIGYRFSDVA	LIWLIGYRF
		AGSDLIWLIGYRFSD	LIWLIGYRF
		DAGSDLIWLIGYRFS	LIWLIGYRF
		PIPANLVGMTFRAQE	LVGMTFRAQ
		PANLVGMTFRAQEGA	LVGMTFRAQ
		IPANLVGMTFRAQEG	LVGMTFRAQ
		DLIWLIGYRFSDVAK	LIWLIGYRF
		ANLVGMTFRAQEGAF	LVGMTFRAQ
		DPIPANLVGMTFRAQ	PANLVGMTF
	HLA-DRB1*1302	KYANKDIKISTQYIG	YANKDIKIS
		NLSSKIINKEIIVPS	IINKEIIVP
		LSSKIINKEIIVPSN	INKEIIVPS
		YANKDIKISTQYIGS	IKISTQYIG
		SSKIINKEIIVPSNK	IINKEIIVP
		SKIINKEIIVPSNKE	IINKEIIVP
		ANKDIKISTQYIGSF	IKISTQYIG
		NKDIKISTQYIGSFA	IKISTQYIG
		KDIKISTQYIGSFAD	IKISTQYIG
		VGRALNIFTSNHLKT	LNIFTSNHL
		KIINKEIIVPSNKES	INKEIIVPS
		EGVVGFVRNPKMISF	FVRNPKMIS
		MNKILLLILLESIVF	ILLLILLES
		KDVGRALNIFTSNHL	VGRALNIFT
		DNLSSKIINKEIIVP	LSSKIINKE
		RALNIFTSNHLKTNT	LNIFTSNHL
		KEGVVGFVRNPKMIS	VGFVRNPKM
		NKILLLILLESIVFL	ILLLILLES
		GVVGFVRNPKMISFE	FVRNPKMIS
		GRALNIFTSNHLKTN	LNIFTSNHL
		GGKLINYGLKEGVVG	LINYGLKEG
		VVGFVRNPKMISFEL	FVRNPKMIS
		DVGRALNIFTSNHLK	LNIFTSNHL
		ILLLILLESIVFLSC	LILLESIVF
		KILLLILLESIVFLS	ILLLILLES
		ELEKEIDNLSSKIIN	IDNLSSKII
		GKLINYGLKEGVVGF	LINYGLKEG
		LEKEIDNLSSKIINK	IDNLSSKII
		EKEIDNLSSKIINKE	IDNLSSKII
		KEIDNLSSKIINKEI	IDNLSSKII
		FELEKEIDNLSSKII	LEKEIDNLS
		IINKEIIVPSNKESY	IINKEIIVP
		ALNIFTSNHLKTNTF	LNIFTSNHL
		LNIFTSNHLKTNTFE	LNIFTSNHL
		VGFVRNPKMISFELE	FVRNPKMIS

		IDNLSSKIINKEIIV IDNLSSKII DIKISTQYIGSFADL IKISTQYIG KLINYGLKEGVVGFV YGLKEGVVG EIDNLSSKIINKEII IDNLSSKII FEGGKLINYGLKEGV LINYGLKEG DAGSDLIWLIGYRFS LIWLIGYRF AGSDLIWLIGYRFSD LIWLIGYRF SDLIWLIGYRFSDVA LIWLIGYRF LINYGLKEGVVGFVR YGLKEGVVG IFTSNHLKTNTFEGG SNHLKTNTF GSDLIWLIGYRFSDV LIWLIGYRF LLLILLESIVFLSCS LILLESIVF EGGKLINYGLKEGVV LINYGLKEG TFEGGKLINYGLKEG GGKLINYGL AKYANKDIKISTQYI YANKDIKIS IKISTQYIGSFADLE IKISTQYIG GSLGSEIPKVSLIID LGSEIPKVS AGAKYANKDIKISTQ YANKDIKIS GAKYANKDIKISTQY YANKDIKIS EAGAKYANKDIKIST YANKDIKIS PDMKYAIIDPIYSND MKYAIIDPI QNPDMKYAIIDPIYS MKYAIIDPI NPDMKYAIIDPIYSN MKYAIIDPI KDAGSDLIWLIGYRF AGSDLIWLI FTSNHLKTNTFEGGK SNHLKTNTF
	HLA-DRB1*1501	NKILLLILLESIVFL ILLLILLES MNKILLLILLESIVF ILLLILLES KILLLILLESIVFLS LILLESIVF GSDLIWLIGYRFSDV DLIWLIGYR SDLIWLIGYRFSDVA LIGYRFSDV DLIWLIGYRFSDVAK LIGYRFSDV ILLLILLESIVFLSC LILLESIVF LIWLIGYRFSDVAKV LIGYRFSDV IWLIGYRFSDVAKVA LIGYRFSDV EGVVGFVRNPKMISF VVGFVRNPK AGSDLIWLIGYRFSD DLIWLIGYR KEGVVGFVRNPKMIS VVGFVRNPK LLLILLESIVFLSCS LILLESIVF LKEGVVGFVRNPKMI VVGFVRNPK DVGRALNIFTSNHLK LNIFTSNHL KDVGRALNIFTSNHL GRALNIFTS LILLESIVFLSCSGK LILLESIVF GLKEGVVGFVRNPKM VVGFVRNPK DAGSDLIWLIGYRFS DLIWLIGYR AFLTGYIAAKLSKTG FLTGYIAAK FLTGYIAAKLSKTGK IAAKLSKTG
	HLA-DRB3*0101	None
	HLA-DRB4*0101	SDLIWLIGYRFSDVA LIWLIGYRF GSDLIWLIGYRFSDV LIWLIGYRF DAGSDLIWLIGYRFS LIWLIGYRF AGSDLIWLIGYRFSD LIWLIGYRF DLIWLIGYRFSDVAK LIWLIGYRF
	HLA-DRB5*0101	None
NP_212516.1 Basic membrane protein B	HLA-DRB1*0101	WLVGYMLTDASLLVS MLTDASLLV IWLVGYMLTDASLLV YMLTDASLL

(bmpB) [Borrelia burgdorferi B31 Seq2		LVGYMLTDASLLVSS MLTDASLLV VGYMLTDASLLVSSE MLTDASLLV SDLIWLVGYMLTDAS LIWLVGYML GYMLTDASLLVSSEN MLTDASLLV GSDLIWLVGYMLTDA LIWLVGYML LIWLVGYMLTDASLL LIWLVGYML DLIWLVGYMLTDASL LIWLVGYML NGSDLIWLVGYMLTD LIWLVGYML IDVIHFAAGLAGIGV FAAGLAGIG DVIHFAAGLAGIGVI FAAGLAGIG IHFAAGLAGIGVIET FAAGLAGIG RNGSDLIWLVGYMLT LIWLVGYML YMLTDASLLVSSENP LTDASLLVS GIDVIHFAAGLAGIG IHFAAGLAG VIHFAAGLAGIGVIE FAAGLAGIG WEGGKVVQMGLRDGV VVQMGLRDG GGKVVQMGLRDGVIG VVQMGLRDG GKVVQMGLRDGVIGL VVQMGLRDG FIFGILLTSCFSRNG FGILLTSCF HFAAGLAGIGVIETA LAGIGVIET IVIFIFGILLTSCFS FGILLTSCF KRNGSDLIWLVGYML GSDLIWLVG RIVIFIFGILLTSCF IFGILLTSC VWEGGKVVQMGLRDG WEGGKVVQM IFIFGILLTSCFSRN FGILLTSCF EGGKVVQMGLRDGVI VVQMGLRDG VIFIFGILLTSCFSR FGILLTSCF FAAGLAGIGVIETAK LAGIGVIET MLTDASLLVSSENPK MLTDASLLV AAGLAGIGVIETAKN LAGIGVIET IGFIGGMKGNIVDAF IGGMKGNIV GFIGGMKGNIVDAFR IGGMKGNIV AGLAGIGVIETAKNL LAGIGVIET IFGILLTSCFSRNGI FGILLTSCF SGKIGFIGGMKGNIV IGFIGGMKG GKIGFIGGMKGNIVD IGGMKGNIV KIGFIGGMKGNIVDA IGGMKGNIV SDVDIGRTIASKMYS VDIGRTIAS KGIDVIHFAAGLAGI IHFAAGLAG FSDVDIGRTIASKMY VDIGRTIAS AFLAGYIAAKKSFSG AGYIAAKKS KVVQMGLRDGVIGLP VVQMGLRDG FLAGYIAAKKSFSGK IAAKKSFSG DKSFNSSANEALLRL FNSSANEAL FGILLTSCFSRNGIE FGILLTSCF KSFNSSANEALLRLK FNSSANEAL VVFRVEQGAFLAGYI FRVEQGAFL AVVFRVEQGAFLAGY FRVEQGAFL VVQMGLRDGVIGLPN VVQMGLRDG AGYIAAKKSFSGKIG IAAKKSFSG SKGIDVIHFAAGLAG VIHFAAGLA LAGYIAAKKSFSGKI IAAKKSFSG VDIGRTIASKMYSKG IGRTIASKM VFSCAISGVYSSYVS ISGVYSSYV SCAISGVYSSYVSDL ISGVYSSYV EVFSCAISGVYSSYV SCAISGVYS NNNVWEGGKVVQMGL WEGGKVVQM

		FSCAISGVYSSYVSD ISGVYSSYV CAISGVYSSYVSDLD ISGVYSSYV NNVWEGGKVVQMGLR WEGGKVVQM NVWEGGKVVQMGLRD WEGGKVVQM KNNNVWEGGKVVQMG WEGGKVVQM IKNNNVWEGGKVVQM NVWEGGKVV MRIVIFIFGILLTSC FIFGILLTS LDDKSFNSSANEALL FNSSANEAL DDKSFNSSANEALLR FNSSANEAL IAVVFRVEQGAFLAG FRVEQGAFL DVDIGRTIASKMYSK IGRTIASKM VLDDKSFNSSANEAL SFNSSANEA LTDASLLVSSENPKI LTDASLLVS GYIAAKKSFSGKIGF IAAKKSFSG SSKKIKISMLVDGVL IKISMLVDG SFSDVDIGRTIASKM VDIGRTIAS FRVEQGAFLAGYIAA VEQGAFLAG VFRVEQGAFLAGYIA VEQGAFLAG SSSKKIKISMLVDGV IKISMLVDG ESSSKKIKISMLVDG KKIKISMLV GAFLAGYIAAKKSFS LAGYIAAKK FIGGMKGNIVDAFRY IGGMKGNIV IGGMKGNIVDAFRYG IGGMKGNIV GLAGIGVIETAKNLG LAGIGVIET LAGIGVIETAKNLGD LAGIGVIET KISYGIIDPIYGDDV YGIIDPIYG ENPKISYGIIDPIYG ENPKISYGI ISYGIIDPIYGDDVQ YGIIDPIYG SKKIKISMLVDGVLD IKISMLVDG SVIKNIGDALYLITG IKNIGDALY KKIKISMLVDGVLDD IKISMLVDG EQGAFLAGYIAAKKS LAGYIAAKK PKISYGIIDPIYGDD YGIIDPIYG TSVIKNIGDALYLIT IKNIGDALY SFNSSANEALLRLKK FNSSANEAL FNSSANEALLRLKKD FNSSANEAL NPKISYGIIDPIYGD YGIIDPIYG NSFSDVDIGRTIASK VDIGRTIAS DIGRTIASKMYSKGI GRTIASKMY QGAFLAGYIAAKKSF LAGYIAAKK SNSFSDVDIGRTIAS FSDVDIGRT GILLTSCFSRNGIES LTSCFSRNG VEQGAFLAGYIAAKK FLAGYIAAK ILLTSCFSRNGIESS LTSCFSRNG IGRTIASKMYSKGID IGRTIASKM LIAVVFRVEQGAFLA FRVEQGAFL VIKNIGDALYLITGE IGDALYLIT DDVQIPENLIAVVFR VQIPENLIA RVEQGAFLAGYIAAK VEQGAFLAG GDDVQIPENLIAVVF VQIPENLIA
	HLA-DRB1*0301	None
	HLA-DRB1*0401	ANKDIEIISEYSNSF ANKDIEIIS NKDIEIISEYSNSFS IISEYSNSF KDIEIISEYSNSFSD IISEYSNSF DIEIISEYSNSFSDV IISEYSNSF IEIISEYSNSFSDVD IISEYSNSF EIISEYSNSFSDVDI IISEYSNSF

		IISEYSNSFSDVDIG IISEYSNSF WLVGYMLTDASLLVS MLTDASLLV IWLVGYMLTDASLLV VGYMLTDAS VGYMLTDASLLVSSE MLTDASLLV LVGYMLTDASLLVSS MLTDASLLV GYMLTDASLLVSSEN MLTDASLLV
	HLA-DRB1*0404	LAGIGVIETAKNLGD VIETAKNLG GLAGIGVIETAKNLG IGVIETAKN AGIGVIETAKNLGDG VIETAKNLG IGVIETAKNLGDGYY VIETAKNLG LIWLVGYMLTDASLL VGYMLTDAS IWLVGYMLTDASLLV YMLTDASLL GIGVIETAKNLGDGY VIETAKNLG WLVGYMLTDASLLVS YMLTDASLL LVGYMLTDASLLVSS YMLTDASLL VGYMLTDASLLVSSE YMLTDASLL SDLIWLVGYMLTDAS WLVGYMLTD DLIWLVGYMLTDASL VGYMLTDAS
	HLA-DRB1*0405	GVYSSYVSDLDNLKR YSSYVSDLD SGVYSSYVSDLDNLK YSSYVSDLD CAISGVYSSYVSDLD ISGVYSSYV AISGVYSSYVSDLDN YSSYVSDLD ISGVYSSYVSDLDNL YSSYVSDLD VYSSYVSDLDNLKRN YSSYVSDLD YSSYVSDLDNLKRNG YSSYVSDLD LAGIGVIETAKNLGD IGVIETAKN AGIGVIETAKNLGDG IETAKNLGD MGLRDGVIGLPNANE RDGVIGLPN EIISEYSNSFSDVDI YSNSFSDVD GIGVIETAKNLGDGY IETAKNLGD IGVIETAKNLGDGYY IETAKNLGD GLRDGVIGLPNANEF VIGLPNANE IEIISEYSNSFSDVD ISEYSNSFS LRDGVIGLPNANEFE VIGLPNANE RDGVIGLPNANEFEY VIGLPNANE
	HLA-DRB1*0701	EVFSCAISGVYSSYV FSCAISGVY EEVFSCAISGVYSSY FSCAISGVY ENIEEVFSCAISGVY VFSCAISGV NIEEVFSCAISGVYS FSCAISGVY IEEVFSCAISGVYSS FSCAISGVY VFSCAISGVYSSYVS FSCAISGVY FSCAISGVYSSYVSD FSCAISGVY VGYMLTDASLLVSSE YMLTDASLL WLVGYMLTDASLLVS YMLTDASLL IWLVGYMLTDASLLV YMLTDASLL LVGYMLTDASLLVSS YMLTDASLL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	LDDKSFNSSANEALL FNSSANEAL DKSFNSSANEALLRL FNSSANEAL DDKSFNSSANEALLR FNSSANEAL VLDDKSFNSSANEAL SFNSSANEA KSFNSSANEALLRLK FNSSANEAL GIDVIHFAAGLAGIG VIHFAAGLA IDVIHFAAGLAGIGV VIHFAAGLA YLAPKNFITSVIKNI YLAPKNFIT

	HLA-DRB1*1101	None
	HLA-DRB1*1302	VSDLDNLKRNGSDLI LDNLKRNGS
		SDLDNLKRNGSDLIW LKRNGSDLI
		RIVIFIFGILLTSCF IFIFGILLT
		NFITSVIKNIGDALY ITSVIKNIG
		IVIFIFGILLTSCFS FGILLTSCF
		LAPKNFITSVIKNIG PKNFITSVI
		LDNLKRNGSDLIWLV LKRNGSDLI
		KNFITSVIKNIGDAL ITSVIKNIG
		LITGEYIKNNNVWEG YIKNNNVWE
		DLDNLKRNGSDLIWL LKRNGSDLI
		ITGEYIKNNNVWEGG IKNNNVWEG
		GEYIKNNNVWEGGKV IKNNNVWEG
		TGEYIKNNNVWEGGK IKNNNVWEG
		VIFIFGILLTSCFSR FGILLTSCF
		IFIFGILLTSCFSRN FGILLTSCF
		EYIKNNNVWEGGKVV IKNNNVWEG
		FITSVIKNIGDALYL ITSVIKNIG
		ITSVIKNIGDALYLI ITSVIKNIG
		APKNFITSVIKNIGD ITSVIKNIG
		PKNFITSVIKNIGDA ITSVIKNIG
		SSKKIKISMLVDGVL IKISMLVDG
		FIFGILLTSCFSRNG FGILLTSCF
		MRIVIFIFGILLTSC IFIFGILLT
		DNLKRNGSDLIWLVG LKRNGSDLI
		SKKIKISMLVDGVLD IKISMLVDG
		VLERKIINKEIIVPC IINKEIIVP
		LERKIINKEIIVPCN IINKEIIVP
		KVLERKIINKEIIVP LERKIINKE
		KKIKISMLVDGVLDD IKISMLVDG
		SSSKKIKISMLVDGV IKISMLVDG
		TSVIKNIGDALYLIT IKNIGDALY
		ESSSKKIKISMLVDG KKIKISMLV
		FEYIKVLERKIINKE IKVLERKII
		EYIKVLERKIINKEI IKVLERKII
		SDLIWLVGYMLTDAS LIWLVGYML
		YIKNNNVWEGGKVVQ IKNNNVWEG
		IKNNNVWEGGKVVQM IKNNNVWEG
		ERKIINKEIIVPCNQ IINKEIIVP
		IKVLERKIINKEIIV IKVLERKII
		SSYVSDLDNLKRNGS YVSDLDNLK
		RKIINKEIIVPCNQE IINKEIIVP
		YVSDLDNLKRNGSDL LDNLKRNGS
		GKVVQMGLRDGVIGL MGLRDGVIG
		SVIKNIGDALYLITG IKNIGDALY
		YIKVLERKIINKEII IKVLERKII
		GGKVVQMGLRDGVIG VQMGLRDGV
		SYVSDLDNLKRNGSD LDNLKRNGS
		DLIWLVGYMLTDASL VGYMLTDAS
		KVVQMGLRDGVIGLP MGLRDGVIG
		IGFIGGMKGNIVDAF IGGMKGNIV
		SGKIGFIGGMKGNIV IGFIGGMKG
		VDIGRTIASKMYSKG IGRTIASKM
		GKIGFIGGMKGNIVD IGGMKGNIV
		IFGILLTSCFSRNGI FGILLTSCF
		LIWLVGYMLTDASLL VGYMLTDAS
		NGSDLIWLVGYMLTD LIWLVGYML

		RNGSDLIWLVGYMLT LIWLVGYML WLVGYMLTDASLLVS VGYMLTDAS FGILLTSCFSRNGIE FGILLTSCF GSDLIWLVGYMLTDA LIWLVGYML ANEFEYIKVLERKII FEYIKVLER NEFEYIKVLERKIIN IKVLERKII EFEYIKVLERKIINK IKVLERKII IWLVGYMLTDASLLV VGYMLTDAS VVQMGLRDGVIGLPN MGLRDGVIG KIKISMLVDGVLDDK IKISMLVDG NLKRNGSDLIWLVGY LKRNGSDLI IKISMLVDGVLDDKS IKISMLVDG LKRNGSDLIWLVGYM LKRNGSDLI YLAPKNFITSVIKNI PKNFITSVI GFIGGMKGNIVDAFR IGGMKGNIV ENPKISYGIIDPIYG ISYGIIDPI VIKNIGDALYLITGE IKNIGDALY SDVDIGRTIASKMYS IGRTIASKM VQMGLRDGVIGLPNA MGLRDGVIG KIGFIGGMKGNIVDA IGGMKGNIV NPKISYGIIDPIYGD YGIIDPIYG PKISYGIIDPIYGDD YGIIDPIYG DVDIGRTIASKMYSK IGRTIASKM SYLAPKNFITSVIKN PKNFITSV FSDVDIGRTIASKMY IGRTIASKM QSYLAPKNFITSVIK PKNFITSVI SFSDVDIGRTIASKM VDIGRTIAS NQEEYEIFIKQILKL YEIFIKQIL LVGYMLTDASLLVSS VGYMLTDAS IGRTIASKMYSKGID IGRTIASKM VGYMLTDASLLVSSE VGYMLTDAS DQSYLAPKNFITSVI LAPKNFITS KIINKEIIVPCNQEE IINKEIIVP FIGGMKGNIVDAFRY IGGMKGNIV
	HLA-DRB1*1501	MRIVIFIFGILLTSC FIFGILLTS VIFIFGILLTSCFSR FIFGILLTS RIVIFIFGILLTSCF FIFGILLTS IVIFIFGILLTSCFS FIFGILLTS AFLAGYIAAKKSFSG FLAGYIAAK IFIFGILLTSCFSRN ILLTSCFSR FLAGYIAAKKSFSGK IAAKKSFSG SDLIWLVGYMLTDAS LVGYMLTDA DLIWLVGYMLTDASL LVGYMLTDA LIWLVGYMLTDASLL LVGYMLTDA GKVVQMGLRDGVIGL VVQMGLRDG GSDLIWLVGYMLTDA LIWLVGYML GGKVVQMGLRDGVIG VVQMGLRDG IWLVGYMLTDASLLV LVGYMLTDA WEGGKVVQMGLRDGV VVQMGLRDG VWEGGKVVQMGLRDG GKVVQMGLR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	SDLIWLVGYMLTDAS LIWLVGYML GSDLIWLVGYMLTDA LIWLVGYML NGSDLIWLVGYMLTD LIWLVGYML RNGSDLIWLVGYMLT LIWLVGYML DLIWLVGYMLTDASL IWLVGYMLT

	HLA-DRB5*0101	None
NP_212518.1 Basic membrane protein C (bmpC) [Borrelia burgdorferi B31 Seq3	HLA-DRB1*0101	AGIFYANPKLRLVSK YANPKLRLV GIFYANPKLRLVSKK YANPKLRLV FKAGIFYANPKLRLV FYANPKLRL KAGIFYANPKLRLVS YANPKLRLV LAIKFRNEEAAFLAG FRNEEAAFL AIKFRNEEAAFLAGY FRNEEAAFL IFYANPKLRLVSKKA YANPKLRLV SLAIKFRNEEAAFLA FRNEEAAFL IKFRNEEAAFLAGYI FRNEEAAFL NSLAIKFRNEEAAFL NSLAIKFRN FPIAGITGLGVYDAA ITGLGVYDA IFPIAGITGLGVYDA IAGITGLGV EKIGFLTGPMSEHVK LTGPMSEHV KEKIGFLTGPMSEHV FLTGPMSEH KIGFLTGPMSEHVKD LTGPMSEHV IGFLTGPMSEHVKDF LTGPMSEHV IKSDKVVVGVLAHGS VVVGVLAHG IAGITGLGVYDAAKE ITGLGVYDA KSDKVVVGVLAHGSF VVGVLAHGS DKVVVGVLAHGSFYD VVGVLAHGS PIAGITGLGVYDAAK ITGLGVYDA SDKVVVGVLAHGSFY VVGVLAHGS GFLTGPMSEHVKDFK LTGPMSEHV KVVVGVLAHGSFYDK VVGVLAHGS FKRFIFITLSLLVFA IFITLSLLV AGITGLGVYDAAKEL ITGLGVYDA KRFIFITLSLLVFAC IFITLSLLV RFIFITLSLLVFACF IFITLSLLV MFKRFIFITLSLLVF IFITLSLLV FYANPKLRLVSKKAP YANPKLRLV NPKLRLVSKKAPSLF LVSKKAPSL ANPKLRLVSKKAPSL KLRLVSKKA PKLRLVSKKAPSLFD LVSKKAPSL AAFLAGYIAAKMSRK LAGYIAAKM KLRLVSKKAPSLFDK LVSKKAPSL AFLAGYIAAKMSRKE LAGYIAAKM FIFITLSLLVFACFK FITLSLLVF EAAFLAGYIAAKMSR LAGYIAAKM EEAAFLAGYIAAKMS LAGYIAAKM YANPKLRLVSKKAPS YANPKLRLV LRLVSKKAPSLFDKE LVSKKAPSL KFRNEEAAFLAGYIA FRNEEAAFL FRNEEAAFLAGYIAA FRNEEAAFL VGVIFPIAGITGLGV FPIAGITGL GVIFPIAGITGLGVY IAGITGLGV KNPLNLFWLIGYRFS LFWLIGYRF NEEAAFLAGYIAAKM FLAGYIAAK PLNLFWLIGYRFSDL LFWLIGYRF NPLNLFWLIGYRFSD LFWLIGYRF LNLFWLIGYRFSDLS LFWLIGYRF VIFPIAGITGLGVYD IAGITGLGV QSYIAPQNVITSIIK YIAPQNVIT FLTGPMSEHVKDFKF LTGPMSEHV DQSYIAPQNVITSII YIAPQNVIT

		VVVGVLAHGSFYDKG	VVGVLAHGS
		IFITLSLLVFACFKS	IFITLSLLV
		NQDQSYIAPQNVITS	YIAPQNVIT
		VVGVLAHGSFYDKGY	VVGVLAHGS
		QDQSYIAPQNVITSI	YIAPQNVIT
		GITGLGVYDAAKELG	ITGLGVYDA
		FLAGYIAAKMSRKEK	LAGYIAAKM
		ITGLGVYDAAKELGP	ITGLGVYDA
		LNQDQSYIAPQNVIT	LNQDQSYIA
		GYRFSDLSVKLSYER	FSDLSVKLS
		GFKAGIFYANPKLRL	FKAGIFYAN
		LTGPMSEHVKDFKFG	LTGPMSEHV
		YRFSDLSVKLSYERP	FSDLSVKLS
		WLIGYRFSDLSVKLS	RFSDLSVKL
		DKVGVIFPIAGITGL	IFPIAGITG
		IGYRFSDLSVKLSYE	FSDLSVKLS
		LAGYIAAKMSRKEKI	LAGYIAAKM
		LIGYRFSDLSVKLSY	FSDLSVKLS
		GKVIYSISSEYINNR	IYSISSEYI
		KVGVIFPIAGITGLG	FPIAGITGL
		DIGKVIYSISSEYIN	IYSISSEYI
		IGKVIYSISSEYINN	IYSISSEYI
		KDIGKVIYSISSEYI	VIYSISSEY
		KVIYSISSEYINNRV	IYSISSEYI
		LRPYPIEGKRLLTVD	IEGKRLLTV
		SLRPYPIEGKRLLTV	YPIEGKRLL
		DNFGIKLITKSLRPY	FGIKLITKS
		FGIKLITKSLRPYPI	LITKSLRPY
		RLVSKKAPSLFDKEK	LVSKKAPSL
		RPYPIEGKRLLTVDE	IEGKRLLTV
		EDKVGVIFPIAGITG	VGVIFPIAG
		QKNPLNLFWLIGYRF	PLNLFWLIG
		SYIAPQNVITSIIKD	YIAPQNVIT
		NLFWLIGYRFSDLSV	LFWLIGYRF
		PYPIEGKRLLTVDEA	IEGKRLLTV
		KYYVIGLNQDQSYIA	YVIGLNQDQ
		FGFKAGIFYANPKLR	FKAGIFYAN
		YPIEGKRLLTVDEAM	IEGKRLLTV
		LVSKKAPSLFDKEKG	LVSKKAPSL
		RDNFGIKLITKSLRP	FGIKLITKS
		LRDNFGIKLITKSLR	FGIKLITKS
		IKLITKSLRPYPIEG	TKSLRPYPI
		KLITKSLRPYPIEGK	TKSLRPYPI
		KDFKFGFKAGIFYAN	GFKAGIFYA
		GIKLITKSLRPYPIE	TKSLRPYPI
		YYVIGLNQDQSYIAP	LNQDQSYIA
		AGYIAAKMSRKEKIG	IAAKMSRKE
		FKFGFKAGIFYANPK	FKAGIFYAN
		LITKSLRPYPIEGKR	TKSLRPYPI
		DFKFGFKAGIFYANP	FKAGIFYAN
		KLRDNFGIKLITKSL	FGIKLITKS
		KFGFKAGIFYANPKL	FKAGIFYAN
		YVIGLNQDQSYIAPQ	LNQDQSYIA
		LFWLIGYRFSDLSVK	LFWLIGYRF
		IGLNQDQSYIAPQNV	LNQDQSYIA
		FITLSLLVFACFKSN	FITLSLLVF
		YIAPQNVITSIIKDI	YIAPQNVIT

		RFSDLSVKLSYERPD FSDLSVKLS FDYGDIQVPKNSLAI IQVPKNSLA VKLRDNFGIKLITKS LRDNFGIKL VIGLNQDQSYIAPQN LNQDQSYIA FSDLSVKLSYERPDI FSDLSVKLS NFGIKLITKSLRPYP LITKSLRPY RKEKIGFLTGPMSEH IGFLTGPMS SNKKSIKSDKVVVGV IKSDKVVVG KKSIKSDKVVVGVLA IKSDKVVVG KSNKKSIKSDKVVVG KKSIKSDKV YINNRVFKGGIIIDR YINNRVFKG KSIKSDKVVVGVLAH IKSDKVVVG NRVFKGGIIIDRGLK FKGGIIIDR SEYINNRVFKGGIII YINNRVFKG RVFKGGIIIDRGLKE FKGGIIIDR SSEYINNRVFKGGII YINNRVFKG ISSEYINNRVFKGGI YINNRVFKG NNRVFKGGIIIDRGL FKGGIIIDR NKKSIKSDKVVVGVL IKSDKVVVG SISSEYINNRVFKGG YINNRVFKG INNRVFKGGIIIDRG FKGGIIIDR YGDIQVPKNSLAIKF IQVPKNSLA DAYEVQKNPLNLFWL VQKNPLNLF SIKSDKVVVGVLAHG IKSDKVVVG EDAYEVQKNPLNLFW VQKNPLNLF DYGDIQVPKNSLAIK IQVPKNSLA TEDAYEVQKNPLNLF YEVQKNPLN GDIQVPKNSLAIKFR IQVPKNSLA GSFYDKGYNQSVHDG YDKGYNQSV GYIAAKMSRKEKIGF IAAKMSRKE AYEVQKNPLNLFWLI VQKNPLNLF IEGKRLLTVDEAMTE IEGKRLLTV AFDYGDIQVPKNSLA YGDIQVPKN KEDKVGVIFPIAGIT VGVIFPIAG TKSLRPYPIEGKRLL TKSLRPYPI YEVQKNPLNLFWLIG VQKNPLNLF PIEGKRLLTVDEAMT IEGKRLLTV VIYSISSEYINNRVF IYSISSEYI
	HLA-DRB1*0301	None
	HLA-DRB1*0401	FKRFIFITLSLLVFA IFITLSLLV KRFIFITLSLLVFAC IFITLSLLV MFKRFIFITLSLLVF IFITLSLLV RFIFITLSLLVFACF IFITLSLLV KDIGKVIYSISSEYI GKVIYSISS DIGKVIYSISSEYIN GKVIYSISS IKDIGKVIYSISSEY GKVIYSISS GKVIYSISSEYINNR VIYSISSEY FIFITLSLLVFACFK IFITLSLLV IFITLSLLVFACFKS IFITLSLLV IGKVIYSISSEYINN VIYSISSEY
	HLA-DRB1*0404	FKRFIFITLSLLVFA IFITLSLLV MFKRFIFITLSLLVF IFITLSLLV
	HLA-DRB1*0405	EGVIEIVKDPDVLNN IVKDPDVLN KEGVIEIVKDPDVLN VIEIVKDPD GVIEIVKDPDVLNNR IVKDPDVLN IEIVKDPDVLNNRLV IVKDPDVLN

		VIEIVKDPDVLNNRL IVKDPDVLN TEDAYEVQKNPLNLF YEVQKNPLN EDAYEVQKNPLNLFW YEVQKNPLN DAYEVQKNPLNLFWL YEVQKNPLN AMTEDAYEVQKNPLN EDAYEVQKN MTEDAYEVQKNPLNL YEVQKNPLN LRLVSKKAPSLFDKE SKKAPSLFD RLVSKKAPSLFDKEK SKKAPSLFD PKLRLVSKKAPSLFD LRLVSKKAP KLRLVSKKAPSLFDK SKKAPSLFD LVSKKAPSLFDKEKG SKKAPSLFD EIVKDPDVLNNRLVD IVKDPDVLN IVKDPDVLNNRLVDE IVKDPDVLN AYEVQKNPLNLFWLI YEVQKNPLN YEVQKNPLNLFWLIG YEVQKNPLN
	HLA-DRB1*0701	MFKRFIFITLSLLVF IFITLSLLV FKRFIFITLSLLVFA IFITLSLLV KRFIFITLSLLVFAC IFITLSLLV RFIFITLSLLVFACF IFITLSLLV PKLRLVSKKAPSLFD VSKKAPSLF
	HLA-DRB1*0802	FGIKLITKSLRPYPI ITKSLRPYP IKLITKSLRPYPIEG ITKSLRPYP GIKLITKSLRPYPIE ITKSLRPYP KLITKSLRPYPIEGK ITKSLRPYP
	HLA-DRB1*0901	None
	HLA-DRB1*1101	PLNLFWLIGYRFSDL FWLIGYRFS LNLFWLIGYRFSDLS FWLIGYRFS NPLNLFWLIGYRFSD FWLIGYRFS KNPLNLFWLIGYRFS LFWLIGYRF NLFWLIGYRFSDLSV FWLIGYRFS SSEYINNRVFKGGII YINNRVFKG ISSEYINNRVFKGGI YINNRVFKG SISSEYINNRVFKGG YINNRVFKG YSISSEYINNRVFKG EYINNRVFK
	HLA-DRB1*1302	DNFGIKLITKSLRPY IKLITKSLR LRDNFGIKLITKSLR FGIKLITKS RDNFGIKLITKSLRP IKLITKSLR NFGIKLITKSLRPYP IKLITKSLR FGIKLITKSLRPYPI IKLITKSLR GIKLITKSLRPYPIE IKLITKSLR IKLITKSLRPYPIEG IKLITKSLR TSIIKDIGKVIYSIS IKDIGKVIY SIIKDIGKVIYSISS IKDIGKVIY IKDIGKVIYSISSEY IGKVIYSIS NVITSIIKDIGKVIY ITSIIKDIG SSEYINNRVFKGGII YINNRVFKG IIKDIGKVIYSISSE IGKVIYSIS SEYINNRVFKGGIII YINNRVFKG ISSEYINNRVFKGGI YINNRVFKG VITSIIKDIGKVIYS IKDIGKVIY SISSEYINNRVFKGG YINNRVFKG ITSIIKDIGKVIYSI IKDIGKVIY DAYEVQKNPLNLFWL VQKNPLNLF AYEVQKNPLNLFWLI VQKNPLNLF YEVQKNPLNLFWLIG VQKNPLNLF TEDAYEVQKNPLNLF YEVQKNPLN

		EDAYEVQKNPLNLFW	VQKNPLNLF
		FKRFIFITLSLLVFA	FITLSLLVF
		IAPQNVITSIIKDIG	PQNVITSII
		MFKRFIFITLSLLVF	FIFITLSLL
		YSISSEYINNRVFKG	EYINNRVFK
		KDIGKVIYSISSEYI	IGKVIYSIS
		RFIFITLSLLVFACF	FITLSLLVF
		KRFIFITLSLLVFAC	FITLSLLVF
		LVFACFKSNKKSIKS	FKSNKKSIK
		EVQKNPLNLFWLIGY	VQKNPLNLF
		LLVFACFKSNKKSIK	FACFKSNKK
		VFACFKSNKKSIKSD	FKSNKKSIK
		FACFKSNKKSIKSDK	FKSNKKSIK
		VQKNPLNLFWLIGYR	VQKNPLNLF
		ACFKSNKKSIKSDKV	FKSNKKSIK
		EYINNRVFKGGIIID	YINNRVFKG
		VKLRDNFGIKLITKS	LRDNFGIKL
		FIFITLSLLVFACFK	FITLSLLVF
		KNPLNLFWLIGYRFS	LFWLIGYRF
		YIAPQNVITSIIKDI	PQNVITSII
		QSYIAPQNVITSIIK	PQNVITSII
		KLRDNFGIKLITKSL	FGIKLITKS
		NPLNLFWLIGYRFSD	LFWLIGYRF
		FKAGIFYANPKLRLV	AGIFYANPK
		SYIAPQNVITSIIKD	PQNVITSII
		DQSYIAPQNVITSII	IAPQNVITS
		QNVITSIIKDIGKVI	ITSIIKDIG
		APQNVITSIIKDIGK	PQNVITSII
		LNLFWLIGYRFSDLS	LFWLIGYRF
		DIGKVIYSISSEYIN	IGKVIYSIS
		NPKLRLVSKKAPSLF	LRLVSKKAP
		PKLRLVSKKAPSLFD	LRLVSKKAP
		PQNVITSIIKDIGKV	PQNVITSII
		IGKVIYSISSEYINN	IGKVIYSIS
		YINNRVFKGGIIIDR	YINNRVFKG
		QKNPLNLFWLIGYRF	LNLFWLIGY
		KAGIFYANPKLRLVS	YANPKLRLV
		FYANPKLRLVSKKAP	YANPKLRLV
		AGIFYANPKLRLVSK	YANPKLRLV
		PLNLFWLIGYRFSDL	LFWLIGYRF
		YANPKLRLVSKKAPS	LRLVSKKAP
		IFITLSLLVFACFKS	FITLSLLVF
		ANPKLRLVSKKAPSL	LRLVSKKAP
		EVIDLENKIISGEII	LENKIISGE
		GIFYANPKLRLVSKK	FYANPKLRL
		GFKAGIFYANPKLRL	IFYANPKLR
		DKVGVIFPIAGITGL	VGVIFPIAG
		KLRLVSKKAPSLFDK	LRLVSKKAP
		CFKSNKKSIKSDKVV	FKSNKKSIK
	HLA-DRB1*1501	KNPLNLFWLIGYRFS	NLFWLIGYR
		QKNPLNLFWLIGYRF	NLFWLIGYR
		VQKNPLNLFWLIGYR	LNLFWLIGY
		LFWLIGYRFSDLSVK	GYRFSDLSV
		NPLNLFWLIGYRFSD	NLFWLIGYR
		FWLIGYRFSDLSVKL	YRFSDLSVK
		PLNLFWLIGYRFSDL	NLFWLIGYR
		WLIGYRFSDLSVKLS	YRFSDLSVK

		LIGYRFSDLSVKLSY YRFSDLSVK DNFGIKLITKSLRPY IKLITKSLR MFKRFIFITLSLLVF IFITLSLLV NFGIKLITKSLRPYP IKLITKSLR FKRFIFITLSLLVFA IFITLSLLV GYRFSDLSVKLSYER YRFSDLSVK LNLFWLIGYRFSDLS NLFWLIGYR FGIKLITKSLRPYPI IKLITKSLR KRFIFITLSLLVFAC IFITLSLLV IGYRFSDLSVKLSYE YRFSDLSVK YRFSDLSVKLSYERP LSVKLSYER RDNFGIKLITKSLRP IKLITKSLR LRDNFGIKLITKSLR NFGIKLITK NLFWLIGYRFSDLSV NLFWLIGYR SLRPYPIEGKRLLTV LRPYPIEGK LRPYPIEGKRLLTVD IEGKRLLTV YINNRVFKGGIIIDR NRVFKGGII RFIFITLSLLVFACF IFITLSLLV IFITLSLLVFACFKS IFITLSLLV LSLLVFACFKSNKKS LLVFACFKS ANPKLRLVSKKAPSL LRLVSKKAP NPKLRLVSKKAPSLF LVSKKAPSL INNRVFKGGIIIDRG FKGGIIIDR IKLITKSLRPYPIEG LITKSLRPY TLSLLVFACFKSNKK LLVFACFKS PYPIEGKRLLTVDEA IEGKRLLTV RPYPIEGKRLLTVDE IEGKRLLTV GIKLITKSLRPYPIE LITKSLRPY YPIEGKRLLTVDEAM IEGKRLLTV LLVFACFKSNKKSIK FACFKSNKK SLLVFACFKSNKKSI FACFKSNKK PKLRLVSKKAPSLFD LVSKKAPSL KAGIFYANPKLRLVS IFYANPKLR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	RFIFITLSLLVFACF FITLSLLVF FIFITLSLLVFACFK LSLLVFACF FITLSLLVFACFKSN LSLLVFACF IFITLSLLVFACFKS LSLLVFACF ITLSLLVFACFKSNK LSLLVFACF NPKLRLVSKKAPSLF LRLVSKKAP PKLRLVSKKAPSLFD VSKKAPSLF KLRLVSKKAPSLFDK VSKKAPSLF LRLVSKKAPSLFDKE VSKKAPSLF LSVKLSYERPDIYYG LSYERPDIY SDLSVKLSYERPDIY LSVKLSYER VKLSYERPDIYYGII LSYERPDIY SVKLSYERPDIYYGI LSYERPDIY DLSVKLSYERPDIYY LSYERPDIY RLVSKKAPSLFDKEK VSKKAPSLF TLSLLVFACFKSNKK LSLLVFACF LSLLVFACFKSNKKS LSLLVFACF TEDAYEVQKNPLNLF YEVQKNPLN EDAYEVQKNPLNLFW VQKNPLNLF DAYEVQKNPLNLFWL VQKNPLNLF AYEVQKNPLNLFWLI VQKNPLNLF FGIKLITKSLRPYPI IKLITKSLR

	HLA-DRB5*0101	AGYIAAKMSRKEKIG YIAAKMSRK FLAGYIAAKMSRKEK YIAAKMSRK LAGYIAAKMSRKEKI YIAAKMSRK AAFLAGYIAAKMSRK GYIAAKMSR AFLAGYIAAKMSRKE YIAAKMSRK KAGIFYANPKLRLVS IFYANPKLR FKAGIFYANPKLRLV IFYANPKLR AGIFYANPKLRLVSK IFYANPKLR FGFKAGIFYANPKLR FKAGIFYAN GFKAGIFYANPKLRL IFYANPKLR GYIAAKMSRKEKIGF YIAAKMSRK YIAAKMSRKEKIGFL YIAAKMSRK GIFYANPKLRLVSKK IFYANPKLR IFYANPKLRLVSKKA IFYANPKLR SLFDKEKGKAMALFM FDKEKGKAM KKAPSLFDKEKGKAM KKAPSLFDK PSLFDKEKGKAMALF FDKEKGKAM KAPSLFDKEKGKAMA FDKEKGKAM APSLFDKEKGKAMAL FDKEKGKAM
NP_212519.1B Basic membrane protein D (bmpD) [Borrelia burgdorferi B31 Seq4	HLA-DRB1*0101	AFLAGYFASKASKTG YFASKASKT FLAGYFASKASKTGK FASKASKTG LAGYFASKASKTGKI FASKASKTG AGYFASKASKTGKIG FASKASKTG GYFASKASKTGKIGF FASKASKTG FGDFGLGRSTASNMY FGLGRSTAS TFGDFGLGRSTASNM FGLGRSTAS GTFGDFGLGRSTASN FGLGRSTAS GDFGLGRSTASNMYR FGLGRSTAS VGTFGDFGLGRSTAS DFGLGRSTA DGVDIIFAAAGLSGI IFAAAGLSG GVDIIFAAAGLSGIG IFAAAGLSG VDIIFAAAGLSGIGV IFAAAGLSG YFASKASKTGKIGFV FASKASKTG VAFLAGYFASKASKT LAGYFASKA DIIFAAAGLSGIGVI IFAAAGLSG RDGVDIIFAAAGLSG IIFAAAGLS SNLIWGIGFRLSDIL IWGIGFRLS NSNLIWGIGFRLSDI IWGIGFRLS GNSNLIWGIGFRLSD IWGIGFRLS DGNSNLIWGIGFRLS LIWGIGFRL DFGLGRSTASNMYRD FGLGRSTAS IIFAAAGLSGIGVIE FAAAGLSGI FGLGRSTASNMYRDG FGLGRSTAS IYNKSLKIGQSIMNG LKIGQSIMN EIYNKSLKIGQSIMN IYNKSLKIG FASKASKTGKIGFVG FASKASKTG NLIWGIGFRLSDILF IWGIGFRLS NKSLKIGQSIMNGII LKIGQSIMN YNKSLKIGQSIMNGI LKIGQSIMN TGVLDGGKTMFLGLK LDGGKTMFL KSLKIGQSIMNGIIK LKIGQSIMN GVLDGGKTMFLGLKE LDGGKTMFL LETGVLDGGKTMFLG LDGGKTMFL EEVAFLAGYFASKAS VAFLAGYFA YLETGVLDGGKTMFL TGVLDGGKT SEEVAFLAGYFASKA VAFLAGYFA

		ETGVLDGGKTMFLGL	LDGGKTMF
		IFAAAGLSGIGVIEA	IFAAAGLSG
		LSDILFQRASENVSV	LFQRASENV
		EVAFLAGYFASKASK	LAGYFASKA
		YRDGVDIIFAAAGLS	VDIIFAAAG
		SDILFQRASENVSVN	LFQRASENV
		DKGFNESSSKAIRKL	FNESSSKAI
		LIWGIGFRLSDILFQ	IWGIGFRLS
		RLSDILFQRASENVS	LFQRASENV
		DDKGFNESSSKAIRK	FNESSSKAI
		FDDKGFNESSSKAIR	FNESSSKAI
		DILFQRASENVSVNY	LFQRASENV
		AFDDKGFNESSSKAI	GFNESSSKA
		IGFVGGVRGKVLESF	VGGVRGKVL
		KGFNESSSKAIRKLK	FNESSSKAI
		GFVGGVRGKVLESFM	VGGVRGKVL
		FRLSDILFQRASENV	LSDILFQRA
		LKIGQSIMNGIIKVP	LKIGQSIMN
		LLNISFRSEEVAFLA	FRSEEVAFL
		NLLNISFRSEEVAFL	NISFRSEEV
		QDQSYLAPNNVIVSA	LAPNNVIVS
		LNISFRSEEVAFLAG	FRSEEVAFL
		NISFRSEEVAFLAGY	FRSEEVAFL
		DQDQSYLAPNNVIVS	YLAPNNVIv
		AKYANSNIKVVSQYV	YANSNIKVV
		ISFRSEEVAFLAGYF	FRSEEVAFL
		FRSEEVAFLAGYFAS	VAFLAGYFA
		FAAAGLSGIGVIEAA	FAAAGLSGI
		DQSYLAPNNVIVSAV	LAPNNVIVS
		SFRSEEVAFLAGYFA	FRSEEVAFL
		QSYLAPNNVIVSAVK	LAPNNVIVS
		YSEIYNKSLKIGQSI	IYNKSLKIG
		NYSEIYNKSLKIGQS	IYNKSLKIG
		SNYSEIYNKSLKIGQ	IYNKSLKIG
		YEAGAKYANSNIKVV	AGAKYANSN
		SLKIGQSIMNGIIKV	LKIGQSIMN
		VSAVKKVDSLMYSLT	VKKVDSLMY
		SAVKKVDSLMYSLTK	VKKVDSLMY
		ILFQRASENVSVNYA	FQRASENVS
		KSNYSEIYNKSLKIG	YSEIYNKSL
		FVGGVRGKVLESFMY	VRGKVLESF
		RSEEVAFLAGYFASK	VAFLAGYFA
		AGAKYANSNIKVVSQ	YANSNIKVV
		VGGVRGKVLESFMYG	VRGKVLESF
		YLAPNNVIVSAVKKV	LAPNNVIVS
		EAGAKYANSNIKVVS	YANSNIKVV
		VLDGGKTMFLGLKED	LDGGKTMFL
		LDGGKTMFLGLKEDG	LDGGKTMFL
		VDQDQSYLAPNNVIV	VDQDQSYLA
		SEIYNKSLKIGQSIM	IYNKSLKIG
		VIVSAVKKVDSLMYS	VKKVDSLMY
		GAKYANSNIKVVSQY	YANSNIKVV
		NVIVSAVKKVDSLMY	VIVSAVKKV
		KIGFVGGVRGKVLES	VGGVRGKVL
		IWGIGFRLSDILFQR	IWGIGFRLS
		TGKIGFVGGVRGKVL	IGFVGGVRG
		LAPNNVIVSAVKKVD	VIVSAVKKV

		VKKVDSLMYSLTKKY VDSLMYSLT
		GKIGFVGGVRGKVLE VGGVRGKVL
		KKVDSLMYSLTKKYL LMYSLTKKY
		DSLMYSLTKKYLETG LMYSLTKKY
		SYLAPNNVIVSAVKK LAPNNVIVS
		LVLNENLKSNYSEIY NENLKSNYS
		GQSIMNGIIKVPYDK IMNGIIKVP
		LGLVLNENLKSNYSE NENLKSNYS
		KIGQSIMNGIIKVPY IMNGIIKVP
		IGQSIMNGIIKVPYD IMNGIIKVP
		GLGLVLNENLKSNYS LVLNENLKS
		VLNENLKSNYSEIYN LKSNYSEIY
		QSIMNGIIKVPYDKV IMNGIIKVP
		INIIEKASTGNSYLG IIEKASTGN
		YFLIFLFIVACSSSD FLFIVACSS
		FLIFLFIVACSSSDD FLFIVACSS
		SKAIRKLKADLNINI IRKLKADLN
		IVSAVKKVDSLMYSL VKKVDSLMY
		GFNESSSKAIRKLKA FNESSSKAI
		LIFLFIVACSSSDDG FLFIVACSS
		KAIRKLKADLNINII IRKLKADLN
		APNNVIVSAVKKVDS VIVSAVKKV
		PNNVIVSAVKKVDSL VIVSAVKKV
		DLNINIIEKASTGNS IIEKASTGN
		LNINIIEKASTGNSY IIEKASTGN
		IGVDQDQSYLAPNNV VDQDQSYLA
		NNVIVSAVKKVDSLM VIVSAVKKV
		EDGNSNLIWGIGFRL NSNLIWGIG
		LFQRASENVSVNYAI LFQRASENV
		KVDSLMYSLTKKYLE LMYSLTKKY
		NINIIEKASTGNSYL IIEKASTGN
		AVKKVDSLMYSLTKK VDSLMYSLT
		VDSLMYSLTKKYLET LMYSLTKKY
		AAGLSGIGVIEAAKE LSGIGVIEA
		DHYIIGVDQDQSYLA YIIGVDQDQ
		ESFMYGYEAGAKYAN FMYGYEAGA
		SIMNGIIKVPYDKVS IMNGIIKVP
		KYANSNIKVVSQYVG YANSNIKVV
		YANSNIKVVSQYVGT YANSNIKVV
		FNESSSKAIRKLKAD FNESSSKAI
	HLA-DRB1*0301	None
	HLA-DRB1*0401	GDFGLGRSTASNMYR GRSTASNMY
		FGDFGLGRSTASNMY FGLGRSTAS
		LVLNENLKSNYSEIY NENLKSNYS
		VLNENLKSNYSEIYN LKSNYSEIY
	HLA-DRB1*0404	IKVVSQYVGTFGDFG VVSQYVGTF
		VVSQYVGTFGDFGLG YVGTFGDFG
		KVVSQYVGTFGDFGL YVGTFGDFG
		SQYVGTFGDFGLGRS YVGTFGDFG
		VSQYVGTFGDFGLGR YVGTFGDFG
		VAFLAGYFASKASKT LAGYFASKA
		EEVAFLAGYFASKAS LAGYFASKA
		SEEVAFLAGYFASKA FLAGYFASK
		EVAFLAGYFASKASK LAGYFASKA
		YVGTFGDFGLGRSTA YVGTFGDFG
		QYVGTFGDFGLGRST YVGTFGDFG

		AFLAGYFASKASKTG LAGYFASKA
	HLA-DRB1*0405	EGVYDEIQIPKNLLN YDEIQIPKN
		GVYDEIQIPKNLLNI IQIPKNLLN
		VYDEIQIPKNLLNIS IQIPKNLLN
		YDEIQIPKNLLNISF IQIPKNLLN
		DEIQIPKNLLNISFR IQIPKNLLN
	HLA-DRB1*0701	YEAGAKYANSNIKVV KYANSNIKV
		EAGAKYANSNIKVVS YANSNIKVV
		AGAKYANSNIKVVSQ YANSNIKVV
		GAKYANSNIKVVSQY YANSNIKVV
		AKYANSNIKVVSQYV YANSNIKVV
		AGYFASKASKTGKIG YFASKASKT
		LAGYFASKASKTGKI YFASKASKT
		AFLAGYFASKASKTG YFASKASKT
		FLAGYFASKASKTGK YFASKASKT
		AFDDKGFNESSSKAI GFNESSSKA
		DKGFNESSSKAIRKL FNESSSKAI
		FDDKGFNESSSKAIR FNESSSKAI
		DDKGFNESSSKAIRK FNESSSKAI
		VAFLAGYFASKASKT VAFLAGYFA
		KGFNESSSKAIRKLK FNESSSKAI
		GIIKVPYDKVSYFVL PYDKVSYFV
		KEDIFMLKKVYYFLI MLKKVYYFL
		EDIFMLKKVYYFLIF MLKKVYYFL
		IIKVPYDKVSYFVLQ YDKVSYFVL
		IKVPYDKVSYFVLQM YDKVSYFVL
		KVPYDKVSYFVLQME YDKVSYFVL
		DQSYLAPNNVIVSAV YLAPNNVIV
		FGDFGLGRSTASNMY LGRSTASNM
		GDFGLGRSTASNMYR LGRSTASNM
		KYANSNIKVVSQYVG YANSNIKVV
		YANSNIKVVSQYVGT YANSNIKVV
		DIFMLKKVYYFLIFL MLKKVYYFL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	GVDIIFAAAGLSGIG IIFAAAGLS
		DGVDIIFAAAGLSGI IIFAAAGLS
		VDIIFAAAGLSGIGV IIFAAAGLS
		DKGFNESSSKAIRKL FNESSSKAI
		KGFNESSSKAIRKLK FNESSSKAI
		AFDDKGFNESSSKAI GFNESSSKA
		FDDKGFNESSSKAIR FNESSSKAI
		DDKGFNESSSKAIRK FNESSSKAI
		RDGVDIIFAAAGLSG IIFAAAGLS
		YRDGVDIIFAAAGLS YRDGVDIIF
		EAGAKYANSNIKVVS YANSNIKVV
		YEAGAKYANSNIKVV AKYANSNIK
		AGAKYANSNIKVVSQ YANSNIKVV
		DIIFAAAGLSGIGVI IIFAAAGLS
		IIFAAAGLSGIGVIE IIFAAAGLS
		GAKYANSNIKVVSQY YANSNIKVV
		LAGYFASKASKTGKI YFASKASKT
		AKYANSNIKVVSQYV YANSNIKVV
		AGYFASKASKTGKIG YFASKASKT
		AFLAGYFASKASKTG YFASKASKT
		FLAGYFASKASKTGK YFASKASKT

		VAFLAGYFASKASKT LAGYFASKA LSDILFQRASENVSV FQRASENVS SDILFQRASENVSVN FQRASENVS DILFQRASENVSVNY FQRASENVS RLSDILFQRASENVS LFQRASENV LIWGIGFRLSDILFQ IGFRLSDIL IWGIGFRLSDILFQR FRLSDILFQ WGIGFRLSDILFQRA FRLSDILFQ ILFQRASENVSVNYA FQRASENVS GFNESSSKAIRKLKA FNESSSKAI GIGFRLSDILFQRAS FRLSDILFQ FNESSSKAIRKLKAD FNESSSKAI IGFRLSDILFQRASE FRLSDILFQ GYFASKASKTGKIGF YFASKASKT
	HLA-DRB1*1101	None
	HLA-DRB1*1302	KYANSNIKVVSQYVG ANSNIKVVS KIGQSIMNGIIKVPY IGQSIMNGI IGQSIMNGIIKVPYD IGQSIMNGI LKIGQSIMNGIIKVP IGQSIMNGI YANSNIKVVSQYVGT IKVVSQYVG ANSNIKVVSQYVGTF IKVVSQYVG SLKIGQSIMNGIIKV IGQSIMNGI KSLKIGQSIMNGIIK IGQSIMNGI NSNIKVVSQYVGTFG IKVVSQYVG SNIKVVSQYVGTFGD IKVVSQYVG NKSLKIGQSIMNGII IGQSIMNGI YNKSLKIGQSIMNGI LKIGQSIMN KEDIFMLKKVYYFLI IFMLKKVYY EDIFMLKKVYYFLIF IFMLKKVYY AKYANSNIKVVSQYV YANSNIKVV GAKYANSNIKVVSQY YANSNIKVV GQSIMNGIIKVPYDK MNGIIKVPY EAGAKYANSNIKVVS YANSNIKVV AGAKYANSNIKVVSQ YANSNIKVV LKADLNINIIEKAST LNINIIEKA QSIMNGIIKVPYDKV MNGIIKVPY EIQIPKNLLNISFRS IPKNLLNIS IQIPKNLLNISFRSE IPKNLLNIS SKEDIFMLKKVYYFL IFMLKKVYY KADLNINIIEKASTG LNINIIEKA DEIQIPKNLLNISFR IPKNLLNIS KSKEDIFMLKKVYYF IFMLKKVYY ADLNINIIEKASTGN LNINIIEKA YDEIQIPKNLLNISF IPKNLLNIS VYDEIQIPKNLLNIS IQIPKNLLN RKLKADLNINIIEKA KADLNINII DIFMLKKVYYFLIFL IFMLKKVYY KLKADLNINIIEKAS LNINIIEKA QIPKNLLNISFRSEE IPKNLLNIS IPKNLLNISFRSEEV IPKNLLNIS SIMNGIIKVPYDKVS MNGIIKVPY GLGLVLNENLKSNYS LNENLKSNY GKIGFVGGVRGKVLE IGFVGGVRG NYSEIYNKSLKIGQS IYNKSLKIG IFMLKKVYYFLIFLF IFMLKKVYY YSEIYNKSLKIGQSI IYNKSLKIG LGLVLNENLKSNYSE LNENLKSNY

		SNYSEIYNKSLKIGQ IYNKSLKIG LAPNNVIVSAVKKVD PNNVIVSAV LNINIIEKASTGNSY LNINIIEKA SEIYNKSLKIGQSIM IYNKSLKIG NIKVVSQYVGTFGDF IKVVSQYVG YLAPNNVIVSAVKKV PNNVIVSAV DGLGLVLNENLKSNY LVLNENLKS DLNINIIEKASTGNS LNINIIEKA SYLAPNNVIVSAVKK LAPNNVIVS EIYNKSLKIGQSIMN IYNKSLKIG TGKIGFVGGVRGKVL IGFVGGVRG DQSYLAPNNVIVSAV LAPNNVIVS IKSKEDIFMLKKVYY IKSKEDIFM QSYLAPNNVIVSAVK LAPNNVIVS KSNYSEIYNKSLKIG SEIYNKSLK IKVVSQYVGTFGDFG IKVVSQYVG LVLNENLKSNYSEIY LNENLKSNY GLVLNENLKSNYSEI LNENLKSNY IYNKSLKIGQSIMNG IYNKSLKIG VSAVKKVDSLMYSLT VKKVDSLMY NVIVSAVKKVDSLMY IVSAVKKVD YEAGAKYANSNIKVV AKYANSNIK KTGKIGFVGGVRGKV IGFVGGVRG SAVKKVDSLMYSLTK VKKVDSLMY VIVSAVKKVDSLMYS VKKVDSLMY IMNGIIKVPYDKVSY MNGIIKVPY APNNVIVSAVKKVDS VIVSAVKKV ASKTGKIGFVGGVRG KIGFVGGVR QDQSYLAPNNVIVSA LAPNNVIVS SKTGKIGFVGGVRGK IGFVGGVRG PNNVIVSAVKKVDSL VIVSAVKKV KIGFVGGVRGKVLES IGFVGGVRG IGFVGGVRGKVLESF IGFVGGVRG VKKVDSLMYSLTKKY VDSLMYSLT AVKKVDSLMYSLTKK VDSLMYSLT
	HLA-DRB1*1501	KVYYFLIFLFIVACS FLIFLFIVA KKVYYFLIFLFIVAC FLIFLFIVA VYYFLIFLFIVACSS FLIFLFIVA LKKVYYFLIFLFIVA YFLIFLFIV YYFLIFLFIVACSSS FLIFLFIVA YEIYFLYFFIKSKED FLYFFIKSK YYEIYFLYFFIKSKE FLYFFIKSK AFLAGYFASKASKTG LAGYFASKA NYYEIYFLYFFIKSK IYFLYFFIK EIYFLYFFIKSKEDI FLYFFIKSK FLAGYFASKASKTGK FASKASKTG VAFLAGYFASKASKT FLAGYFASK YFLIFLFIVACSSSD FLIFLFIVA
	HLA-DRB3*0101	None
	HLA-DRB4*0101	IQIPKNLLNISFRSE IPKNLLNIS
	HLA-DRB5*0101	None
AAC70056.1 Decorin binding protein A	HLA-DRB1*0101	ILTLTLLASLLAACS LTLLASLLA LTLTLLASLLAACSL LTLLASLLA

DbpA [Borrelia afzelii Seq5		LTLLASLLAACSLTG LASLLAACS TLTLLASLLAACSLT LASLLAACS TLLASLLAACSLTGK LASLLAACS NKIILTLTLLASLLA ILTLTLLAS KIILTLTLLASLLAA LTLLASLLA IILTLTLLASLLAAC LTLLASLLA LASLLAACSLTGKAR LLAACSLTG LLASLLAACSLTGKA LASLLAACS IKYNKIILTLTLLAS YNKIILTLT ASLLAACSLTGKARL LLAACSLTG YNKIILTLTLLASLL ILTLTLLAS KYNKIILTLTLLASL ILTLTLLAS MIKYNKIILTLTLLA YNKIILTLT VGGSQIRAAKIRVAD IRAAKIRVA KVGGSQIRAAKIRVA VGGSQIRAA GSQIRAAKIRVADLT IRAAKIRVA GGSQIRAAKIRVADL IRAAKIRVA SQIRAAKIRVADLTI IRAAKIRVA IYDLILNAAKAVEKI LILNAAKAV GIYDLILNAAKAVEK LILNAAKAV FSGIYDLILNAAKAV IYDLILNAA SGIYDLILNAAKAVE LILNAAKAV YDLILNAAKAVEKIG LILNAAKAV LLAACSLTGKARLES LLAACSLTG SLLAACSLTGKARLE LLAACSLTG TGGKVGGSQIRAAKI VGGSQIRAA DLILNAAKAVEKIGM LILNAAKAV GGKVGGSQIRAAKIR VGGSQIRAA QIRAAKIRVADLTIK IRAAKIRVA GKVGGSQIRAAKIRV VGGSQIRAA LILNAAKAVEKIGMQ LILNAAKAV IRAAKIRVADLTIKF IRAAKIRVA QTGGKVGGSQIRAAK VGGSQIRAA TQTGGKVGGSQIRAA GKVGGSQIR KAVEKIGMQGMKQAV IGMQGMKQA DGIIAIVKVMKAKVE IAIVKVMKA GIIAIVKVMKAKVEN VKVMKAKVE VEKIGMQGMKQAVEE IGMQGMKQA AVEKIGMQGMKQAVE IGMQGMKQA AKAVEKIGMQGMKQA VEKIGMQGM EKIGMQGMKQAVEEA IGMQGMKQA IAIVKVMKAKVENIK VKVMKAKVE IIAIVKVMKAKVENI VKVMKAKVE ADGIIAIVKVMKAKV IAIVKVMKA AIVKVMKAKVENIKE VKVMKAKVE TTADGIIAIVKVMKA DGIIAIVKV KIRVADLTIKFLEAT VADLTIKFL IRVADLTIKFLEATE LTIKFLEAT TADGIIAIVKVMKAK IAIVKVMKA KIGMQGMKQAVEEAA IGMQGMKQA IGMQGMKQAVEEAAK IGMQGMKQA VADLTIKFLEATEEE LTIKFLEAT RVADLTIKFLEATEE LTIKFLEAT ADLTIKFLEATEEET LTIKFLEAT EDFSGIYDLILNAAK IYDLILNAA DAGVKTDAFTETQTG VKTDAFTET AGVKTDAFTETQTGG VKTDAFTET

		EDAGVKTDAFTETQT VKTDAFTET AEDAGVKTDAFTETQ VKTDAFTET RAAKIRVADLTIKFL IRVADLTIK EEDFSGIYDLILNAA FSGIYDLIL EAEDAGVKTDAFTET AGVKTDAFT AAKIRVADLTIKFLE VADLTIKFL AKIRVADLTIKFLEA VADLTIKFL LNAAKAVEKIGMQGM LNAAKAVEK
	HLA-DRB1*0301	None
	HLA-DRB1*0401	NKIILTLTLLASLLA IILTLTLLA IKYNKIILTLTLLAS IILTLTLLA MIKYNKIILTLTLLA YNKIILTLT KYNKIILTLTLLASL IILTLTLLA KIILTLTLLASLLAA LTLLASLLA IILTLTLLASLLAAC LTLLASLLA YNKIILTLTLLASLL IILTLTLLA ILTLTLLASLLAACS LTLLASLLA LTLTLLASLLAACSL LTLLASLLA LTLLASLLAACSLTG LTLLASLLA TLTLLASLLAACSLT LTLLASLLA
	HLA-DRB1*0404	NKIILTLTLLASLLA IILTLTLLA IKYNKIILTLTLLAS IILTLTLLA KYNKIILTLTLLASL IILTLTLLA YNKIILTLTLLASLL IILTLTLLA MIKYNKIILTLTLLA YNKIILTLT KIILTLTLLASLLAA IILTLTLLA IILTLTLLASLLAAC IILTLTLLA LTLLASLLAACSLTG LASLLAACS LLASLLAACSLTGKA LLAACSLTG TLLASLLAACSLTGK LLAACSLTG LASLLAACSLTGKAR LLAACSLTG ASLLAACSLTGKARL LLAACSLTG
	HLA-DRB1*0405	NKIILTLTLLASLLA IILTLTLLA IKYNKIILTLTLLAS IILTLTLLA KYNKIILTLTLLASL IILTLTLLA MIKYNKIILTLTLLA YNKIILTLT YNKIILTLTLLASLL IILTLTLLA
	HLA-DRB1*0701	KVGGSQIRAAKIRVA GSQIRAAKI VGGSQIRAAKIRVAD IRAAKIRVA GGSQIRAAKIRVADL IRAAKIRVA GSQIRAAKIRVADLT IRAAKIRVA SQIRAAKIRVADLTI IRAAKIRVA
	HLA-DRB1*0802	None
	HLA-DRB1*0901	YDLILNAAKAVEKIG LILNAAKAV GIYDLILNAAKAVEK LILNAAKAV IYDLILNAAKAVEKI LILNAAKAV
	HLA-DRB1*1101	None
	HLA-DRB1*1302	IKYNKIILTLTLLAS YNKIILTLT MIKYNKIILTLTLLA YNKIILTLT KYNKIILTLTLLASL YNKIILTLT YNKIILTLTLLASLL YNKIILTLT NKIILTLTLLASLLA ILTLTLLAS KIILTLTLLASLLAA LTLLASLLA DGIIAIVKVMKAKVE IAIVKVMKA ADGIIAIVKVMKAKV IAIVKVMKA DLILNAAKAVEKIGM ILNAAKAVE

		IYDLILNAAKAVEKI ILNAAKAVE GIYDLILNAAKAVEK ILNAAKAVE IILTLTLLASLLAAC LTLLASLLA GIIAIVKVMKAKVEN IAIVKVMKA YDLILNAAKAVEKIG ILNAAKAVE TTADGIIAIVKVMKA IIAIVKVMK ILTLTLLASLLAACS LTLLASLLA TADGIIAIVKVMKAK IAIVKVMKA SGIYDLILNAAKAVE LILNAAKAV AKAVEKIGMQGMKQA VEKIGMQGM LILNAAKAVEKIGMQ ILNAAKAVE KAVEKIGMQGMKQAV IGMQGMKQA IAIVKVMKAKVENIK VKVMKAKVE IIAIVKVMKAKVENI VKVMKAKVE
	HLA-DRB1*1501	KIILTLTLLASLLAA ILTLTLLAS NKIILTLTLLASLLA ILTLTLLAS KYNKIILTLTLLASL ILTLTLLAS IKYNKIILTLTLLAS KYNKIILTL YNKIILTLTLLASLL ILTLTLLAS QIRAAKIRVADLTIK IRAAKIRVA IRAAKIRVADLTIKF IRVADLTIK ILTLTLLASLLAACS ILTLTLLAS IILTLTLLASLLAAC ILTLTLLAS TLLASLLAACSLTGK LLAACSLTG LASLLAACSLTGKAR LLAACSLTG LLASLLAACSLTGKA LLAACSLTG
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	GIYDLILNAAKAVEK YDLILNAAK IYDLILNAAKAVEKI LNAAKAVEK YDLILNAAKAVEKIG LNAAKAVEK
AAC70057.1 Decorin binding protein A DbpA [Borrelia garinii] Seq6	HLA-DRB1*0101	EIGIQKMTGTVTKEA IQKMTGTVT IGIQKMTGTVTKEAE IQKMTGTVT LEEIGIQKMTGTVTK IQKMTGTVT EEIGIQKMTGTVTKE IQKMTGTVT PLEEIGIQKMTGTVT IGIQKMTGT LLKLSLIVSLLVACG LSLIVSLLV LKLSLIVSLLVACGL IVSLLVACG LSLIVSLLVACGLTG IVSLLVACG IQKMTGTVTKEAEKT IQKMTGTVT SLIVSLLVACGLTGE IVSLLVACG KLSLIVSLLVACGLT IVSLLVACG GIQKMTGTVTKEAEK IQKMTGTVT NKILLKLSLIVSLLV LKLSLIVSL IKYNKILLKLSLIVS YNKILLKLS KILLKLSLIVSLLVA LKLSLIVSL YNKILLKLSLIVSLL LKLSLIVSL KYNKILLKLSLIVSL ILLKLSLIV MIKYNKILLKLSLIV YNKILLKLS ILLKLSLIVSLLVAC LKLSLIVSL LIVSLLVACGLTGET IVSLLVACG IVSLLVACGLTGETK IVSLLVACG QKMTGTVTKEAEKTP MTGTVTKEA AEKLKKSGSSGAFSA LKKSGSSGA EAEKLKKSGSSGAFS LKKSGSSGA

		EKLKKSGSSGAFSAM LKKSGSSGA EEAEKLKKSGSSGAF LKKSGSSGA KEEAEKLKKSGSSGA AEKLKKSGS LKNLEEKANTAATTT LEEKANTAA FILKAKIKAIQVAER AKIKAIQVA ILKAKIKAIQVAERF IKAIQVAER VSLLVACGLTGETKI LLVACGLTG SGSSGAFSAMYDLMI SSGAFSAMY LKAKIKAIQVAERFV IKAIQVAER ADGIIAIAQAMEEKL IAIAQAMEE FSAMYDLMIDVSKPL FSAMYDLMI KMTGTVTKEAEKTPP MTGTVTKEA MTGTVTKEAEKTPPT MTGTVTKEA ALKNLEEKANTAATT LEEKANTAA SGAFSAMYDLMIDVS FSAMYDLMI TTADGIIAIAQAMEE GIIAIAQAM GAFSAMYDLMIDVSK FSAMYDLMI TADGIIAIAQAMEEK IAIAQAMEE LLVACGLTGETKIRL LLVACGLTG KLKKSGSSGAFSAMY LKKSGSSGA GSSGAFSAMYDLMID FSAMYDLMI LKKSGSSGAFSAMYD LKKSGSSGA KAKIKAIQVAERFVK IKAIQVAER VKFEAFTNTQTGSKI FEAFTNTQT DGIIAIAQAMEEKLN IAIAQAMEE SSGAFSAMYDLMIDV FSAMYDLMI AKIKAIQVAERFVKA IKAIQVAER GVKFEAFTNTQTGSK FEAFTNTQT GIIAIAQAMEEKLNN IAIAQAMEE PEFILKAKIKAIQVA ILKAKIKAI
	HLA-DRB1*0301	None
	HLA-DRB1*0401	LLKLSLIVSLLVACG LSLIVSLLV LKLSLIVSLLVACGL LSLIVSLLV NKILLKLSLIVSLLV ILLKLSLIV ILLKLSLIVSLLVAC LSLIVSLLV KILLKLSLIVSLLVA LSLIVSLLV
	HLA-DRB1*0404	GVKFEAFTNTQTGSK KFEAFTNTQ VKFEAFTNTQTGSKI KFEAFTNTQ EGVKFEAFTNTQTGS KFEAFTNTQ KEGVKFEAFTNTQTG KFEAFTNTQ KFEAFTNTQTGSKIS KFEAFTNTQ KKEGVKFEAFTNTQT KFEAFTNTQ AKKEGVKFEAFTNTQ VKFEAFTNT LIVSLLVACGLTGET LLVACGLTG IVSLLVACGLTGETK LLVACGLTG LSLIVSLLVACGLTG IVSLLVACG SLIVSLLVACGLTGE LLVACGLTG VSLLVACGLTGETKI LLVACGLTH
	HLA-DRB1*0405	GVKFEAFTNTQTGSK FEAFTNTQT KEGVKFEAFTNTQTG FEAFTNTQT VKFEAFTNTQTGSKI FEAFTNTQT KKEGVKFEAFTNTQT GVKFEAFTN EGVKFEAFTNTQTGS FEAFTNTQT
	HLA-DRB1*0701	NKILLKLSLIVSLLV ILLKLSLIV KILLKLSLIVSLLVA LSLIVSLLV ILLKLSLIVSLLVAC LSLIVSLLV

	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	LEEIGIQKMTGTVTK IGIQKMTGT EEIGIQKMTGTVTKE IGIQKMTGT PLEEIGIQKMTGTVT IGIQKMTGT EIGIQKMTGTVTKEA IGIQKMTGT IGIQKMTGTVTKEAE IGIQKMTGT NKILLKLSLIVSLLV LLKLSLIVS KILLKLSLIVSLLVA LLKLSLIVS IKYNKILLKLSLIVS IKYNKILLK KPLEEIGIQKMTGTV IGIQKMTGT YNKILLKLSLIVSLL LLKLSLIVS SKPLEEIGIQKMTGT LEEIGIQKM KYNKILLKLSLIVSL LLKLSLIVS MIKYNKILLKLSLIV IKYNKILLK ILLKLSLIVSLLVAC LLKLSLIVS LLKLSLIVSLLVACG LLKLSLIVS LKLSLIVSLLVACGL LSLIVSLLV AMEEKLNNVNKKQHD LNNVNKKQH MEEKLNNVNKKQHDA LNNVNKKQH EEKLNNVNKKQHDAL LNNVNKKQH EKLNNVNKKQHDALK LNNVNKKQH KDEINKIKANAKKEG INKIKANAK DEINKIKANAKKEGV IKANAKKEG KLSLIVSLLVACGLT LSLIVSLLV LSLIVSLLVACGLTG LSLIVSLLV EINKIKANAKKEGVK IKANAKKEG PEFILKAKIKAIQVA FILKAKIKA KPEFILKAKIKAIQV FILKAKIKA INKIKANAKKEGVKF IKANAKKEG EKPEFILKAKIKAIQ FILKAKIKA GIQKMTGTVTKEAEK IQKMTGTVT
	HLA-DRB1*1501	IKYNKILLKLSLIVS ILLKLSLIV NKILLKLSLIVSLLV LLKLSLIVS KYNKILLKLSLIVSL LLKLSLIVS YNKILLKLSLIVSLL LLKLSLIVS KILLKLSLIVSLLVA LLKLSLIVS ILLKLSLIVSLLVAC LLKLSLIVS LLKLSLIVSLLVACG LLKLSLIVS MIKYNKILLKLSLIV IKYNKILLK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	GVKFEAFTNTQTGSK FEAFTNTQT KAKIKAIQVAERFVK IKAIQVAER VKFEAFTNTQTGSKI FTNTQTGSK AKIKAIQVAERFVKA IQVAERFVK
AAC70021.1 Decorin binding protein B DbpB [Borrelia burgdorferi] Seq7	HLA-DRB1*0101	LEDVGIIGLKARVLE IIGLKARVL EDVGIIGLKARVLEE IIGLKARVL DVGIIGLKARVLEES IIGLKARVL VGIIGLKARVLEESK IIGLKARVL ALFFKLLVACSIGLV FKLLVACSI IALFFKLLVACSIGL FKLLVACSI GIIGLKARVLEESKN IIGLKARVL

		IIGLKARVLEESKNN IIGLKARVL IVIALFFKLLVACSI FFKLLVACS VIALFFKLLVACSIG FKLLVACSI LFFKLLVACSIGLVE FKLLVACSI SGQFLAMFDLMLEVV FLAMFDLML GQFLAMFDLMLEVVE FLAMFDLML SIVIALFFKLLVACS VIALFFKLL FFKLLVACSIGLVER LLVACSIGL GSKVTSGGLALREAK VTSGGLALR TGSKVTSGGLALREA VTSGGLALR SKVTSGGLALREAKV VTSGGLALR FKLLVACSIGLVERT LLVACSIGL FLAMFDLMLEVVESL FLAMFDLML QFLAMFDLMLEVVES FLAMFDLML FEAFTGLKTGSKVTS FTGLKTGSK TSGGLALREAKVQAI LALREAKVQ SGGLALREAKVQAIV LREAKVQAI EAFTGLKTGSKVTSG LKTGSKVTS LKTGSKVTSGGLALR LKTGSKVTS GNSGQFLAMFDLMLE FLAMFDLML NSGQFLAMFDLMLEV FLAMFDLML KTGSKVTSGGLALRE VTSGGLALR AFTGLKTGSKVTSGG LKTGSKVTS FTGLKTGSKVTSGGL LKTGSKVTS KVTSGGLALREAKVQ VTSGGLALR GGLALREAKVQAIVE LREAKVQAI VTSGGLALREAKVQA VTSGGLALR GLALREAKVQAIVET LREAKVQAI LALREAKVQAIVETG LREAKVQAI VLFEAFTGLKTGSKV FTGLKTGSK GVLFEAFTGLKTGSK FEAFTGLKT TGLKTGSKVTSGGLA LKTGSKVTS TGNSGQFLAMFDLML GQFLAMFDL INTAERLLAAKAQIE AERLLAAKA LFEAFTGLKTGSKVT FTGLKTGSK NTAERLLAAKAQIEN LLAAKAQIE TAERLLAAKAQIENQ LLAAKAQIE ILKIKKEATGKGVLF IKKEATGKG LAMFDLMLEVVESLE MFDLMLEVV AERLLAAKAQIENQL LLAAKAQIE NKILKIKKEATGKGV IKKEATGKG LKIKKEATGKGVLFE IKKEATGKG KILKIKKEATGKGVL IKKEATGKG KNKILKIKKEATGKG ILKIKKEAT KLLVACSIGLVERTN LLVACSIGL NPINTAERLLAAKAQ INTAERLLA IGLVERTNAALESSS RTNAALESS SIGLVERTNAALESS ERTNAALES ERLLAAKAQIENQLK LLAAKAQIE NNPINTAERLLAAKA INTAERLLA ALREAKVQAIVETGK LREAKVQAI GLVERTNAALESSSK RTNAALESS GLKTGSKVTSGGLAL LKTGSKVTS LREAKVQAIVETGKF LREAKVQAI LLVACSIGLVERTNA LLVACSIGL
	HLA-DRB1*0301	None

	HLA-DRB1*0401	IVIALFFKLLVACSI FFKLLVACS SIVIALFFKLLVACS IALFFKLLV VIALFFKLLVACSIG FFKLLVACS IALFFKLLVACSIGL FFKLLVACS ALFFKLLVACSIGLV FFKLLVACS
	HLA-DRB1*0404	GVLFEAFTGLKTGSK LFEAFTGLK ARVLEESKNNPINTA VLEESKNNP KGVLFEAFTGLKTGS LFEAFTGLK GKGVLFEAFTGLKTG LFEAFTGLK IGLKARVLEESKNNP ARVLEESKN LKARVLEESKNNPIN VLEESKNNP KARVLEESKNNPINT VLEESKNNP GLKARVLEESKNNPI VLEESKNNP TGKGVLFEAFTGLKT LFEAFTGLK ATGKGVLFEAFTGLK KGVLFEAFT LFEAFTGLKTGSKVT LFEAFTGLK VLFEAFTGLKTGSKV LFEAFTGLK RVLEESKNNPINTAE VLEESKNNP VLEESKNNPINTAER VLEESKNNP
	HLA-DRB1*0405	IVIALFFKLLVACSI IALFFKLLV SIVIALFFKLLVACS IALFFKLLV AMFDLMLEVVESLED MLEVVESLE
	HLA-DRB1*0701	EDVGIIGLKARVLEE IIGLKARVL DVGIIGLKARVLEES IIGLKARVL SLEDVGIIGLKARVL GIIGLKARV LEDVGIIGLKARVLE IIGLKARVL VGIIGLKARVLEESK IIGLKARVL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	LEDVGIIGLKARVLE VGIIGLKAR EDVGIIGLKARVLEE IGLKARVLE ESSSKDLKNKILKIK SSKDLKNKI SSSKDLKNKILKIKK LKNKILKIK SSKDLKNKILKIKKE LKNKILKIK KDLKNKILKIKKEAT LKNKILKIK SKDLKNKILKIKKEA LKNKILKIK DVGIIGLKARVLEES IGLKARVLE VGIIGLKARVLEESK IGLKARVLE DLKNKILKIKKEATG LKNKILKIK LKNKILKIKKEATGK LKNKILKIK GIIGLKARVLEESKN IGLKARVLE SLEDVGIIGLKARVL VGIIGLKAR ESLEDVGIIGLKARV VGIIGLKAR VESLEDVGIIGLKAR LEDVGIIGL AQIENQLKVVKEKQN IENQLKVVK KAQIENQLKVVKEKQ IENQLKVVK AAKAQIENQLKVVKE IENQLKVVK AKAQIENQLKVVKEK IENQLKVVK IIGLKARVLEESKNN IGLKARVLE AFTGLKTGSKVTSGG LKTGSKVTS FTGLKTGSKVTSGGL LKTGSKVTS

		TGLKTGSKVTSGGLA LKTGSKVTS IGLKARVLEESKNNP IGLKARVLE FEAFTGLKTGSKVTS TGLKTGSKV EAFTGLKTGSKVTSG LKTGSKVTS LAAKAQIENQLKVVK AKAQIENQL
	HLA-DRB1*1501	SLEDVGIIGLKARVL VGIIGLKAR LEDVGIIGLKARVLE VGIIGLKAR EDVGIIGLKARVLEE VGIIGLKAR SIVIALFFKLLVACS ALFFKLLVA IVIALFFKLLVACSI ALFFKLLVA GVLFEAFTGLKTGSK FEAFTGLKT DVGIIGLKARVLEES IIGLKARVL VGIIGLKARVLEESK IIGLKARVL VLFEAFTGLKTGSKV FTGLKTGSK VIALFFKLLVACSIG ALFFKLLVA GKGVLFEAFTGLKTG VLFEAFTGL LFEAFTGLKTGSKVT FTGLKTGSK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	None
NP_212694.1 Heat shock protein 90 [Borrelia burgdorferi B31] Seq8	HLA-DRB1*0101	NDPTYQMQKIMLSMG YQMQKIMLS DPTYQMQKIMLSMGQ YQMQKIMLS PTYQMQKIMLSMGQE YQMQKIMLS DSNDPTYQMQKIMLS DPTYQMQKI SNDPTYQMQKIMLSM YQMQKIMLS TYQMQKIMLSMGQEV YQMQKIMLS YQMQKIMLSMGQEVK YQMQKIMLS IVQNLKNLEPEKLEK LKNLEPEKL VQNLKNLEPEKLEKI LKNLEPEKL NKIVQNLKNLEPEKL VQNLKNLEP KIVQNLKNLEPEKLE LKNLEPEKL QNLKNLEPEKLEKIS LKNLEPEKL YTNLFYVPSKAPYDL YTNLFYVPS NLEYTNLFYVPSKAP YTNLFYVPS LEYTNLFYVPSKAPY YTNLFYVPS EIFLRELISNASDAI LRELISNAS IFLRELISNASDAID LRELISNAS KEIFLRELISNASDA LRELISNAS SILLFEEAMLTSGMP LLFEEAMLT HKEIFLRELISNASD LRELISNAS SHKEIFLRELISNAS SHKEIFLRE NLKNLEPEKLEKISI LKNLEPEKL LKNLEPEKLEKISIL LKNLEPEKL ISILLFEEAMLTSGM LLFEEAMLT TNLFYVPSKAPYDLY VPSKAPYDL EYTNLFYVPSKAPYD YTNLFYVPS LIFYFKQIALFIIFR FKQIALFII MILIFYFKQIALFII YFKQIALFI DLLYLIIHSLYSHKE YLIIHSLYS KDHIKEVNLSATLIK EVNLSATLI DHIKEVNLSATLIKE EVNLSATLI IFYFKQIALFIIFRL FKQIALFII LLYLIIHSLYSHKEI YLIIHSLYS

		ILIFYFKQIALFIIF	FKQIALFII
		NDLLYLIIHSLYSHK	YLIIHSLY
		NLSATLIKEPSAIII	LIKEPSAII
		SATLIKEPSAIIIDS	LIKEPSAII
		KISILLFEEAMLTSG	LLFEEAMLT
		VNDLLYLIIHSLYSH	YLIIHSLYS
		LSATLIKEPSAIIID	LIKEPSAII
		GNLEYTNLFYVPSKA	YTNLFYVPS
		ATLIKEPSAIIIDSN	LIKEPSAII
		IPEYEGLKLKAINKN	YEGLKLKAI
		QDLTNHLGVIAKSGT	LTNHLGVIA
		EGNLEYTNLFYVPSK	YTNLFYVPS
		HIKEVNLSATLIKEP	EVNLSATLI
		IKEVNLSATLIKEPS	EVNLSATLI
		PEYEGLKLKAINKNE	YEGLKLKAI
		NLFYVPSKAPYDLYY	VPSKAPYDL
		EVNDLLYLIIHSLYS	LLYLIIHSL
		AEGNLEYTNLFYVPS	EGNLEYTNL
		NKILSKIKSSSVKKI	LSKIKSSSV
		KILSKIKSSSVKKIL	IKSSSVKKI
		LFYVPSKAPYDLYYP	VPSKAPYDL
		EQDLTNHLGVIAKSG	LTNHLGVIA
		EKISILLFEEAMLTS	LLFEEAMLT
		LLFEEAMLTSGMPSK	LLFEEAMLT
		FEEAMLTSGMPSKNP	LTSGMPSKN
		ILLFEEAMLTSGMPS	LLFEEAMLT
		LEKISILLFEEAMLT	ISILLFEEA
		EEAMLTSGMPSKNPG	LTSGMPSKN
		FYFKQIALFIIFRLC	FKQIALFII
		EAMLTSGMPSKNPGK	LTSGMPSKN
		FLRELISNASDAIDK	LRELISNAS
		LKDHIKEVNLSATLI	IKEVNLSAT
		LRELISNASDAIDKL	LRELISNAS
		LIPEYEGLKLKAINK	YEGLKLKAI
		ILSKIKSSSVKKILS	IKSSSVKKI
		LSKIKSSSVKKILSE	IKSSSVKKI
		AMLTSGMPSKNPGKF	LTSGMPSKN
		NLIPEYEGLKLKAIN	YEGLKLKAI
		LNLIPEYEGLKLKAI	LNLIPEYEG
		DEQDLTNHLGVIAKS	LTNHLGVIA
		LFEEAMLTSGMPSKN	EAMLTSGMP
		MDEQDLTNHLGVIAK	LTNHLGVIA
		GMDEQDLTNHLGVIA	DEQDLTNHL
		ENILKENPIVAAYKE	LKENPIVAA
		QMQKIMLSMGQEVKE	IMLSMGQEV
		KVEVTSKKALESDAY	VTSKKALES
		KENILKENPIVAAYK	LKENPIVAA
		SEKVEVTSKKALESD	VTSKKALES
		VSEKVEVTSKKALES	KVEVTSKKA
		EKVEVTSKKALESDA	VTSKKALES
		TLIKEPSAIIIDSND	IKEPSAIII
		VEVTSKKALESDAYI	VTSKKALES
		VNLSATLIKEPSAII	SATLIKEPS
		NILKENPIVAAYKEK	LKENPIVAA
		GGKENILKENPIVAA	ILKENPIVA
		GKENILKENPIVAAY	LKENPIVAA
		LYLIIHSLYSHKEIF	YLIIHSLYS

		YEGLKLKAINKNETS YEGLKLKAI EYEGLKLKAINKNET YEGLKLKAI LTNHLGVIAKSGTKE LTNHLGVIA KEVNLSATLIKEPSA EVNLSATLI SKIKSSSVKKILSEL IKSSSVKKI DLTNHLGVIAKSGTK LTNHLGVIA YLIIHSLYSHKEIFL YLIIHSLYS MQKIMLSMGQEVKEI IMLSMGQEV FYVPSKAPYDLYYPN VPSKAPYDL IKSSSVKKILSELEK VKKILSELE KIKSSSVKKILSELE IKSSSVKKI MLTSGMPSKNPGKFI LTSGMPSKN EVNLSATLIKEPSAI EVNLSATLI YFKQIALFIIFRLCY FKQIALFII LTNEKFKNIALEPKI FKNIALEPK NEKFKNIALEPKIEI FKNIALEPK LIKEPSAIIIDSNDP LIKEPSAII EKFKNIALEPKIEIS FKNIALEPK TNEKFKNIALEPKIE FKNIALEPK QKIMLSMGQEVKEIK IMLSMGQEV ILKENPIVAAYKEKG LKENPIVAA SLTNEKFKNIALEPK LTNEKFKNI LKENPIVAAYKEKGF LKENPIVAA QQNKILSKIKSSSVK LSKIKSSSV KEEKLNETTALWTKN LNETTALWT FYSAFIVSEKVEVTS IVSEKVEVT GFYSAFIVSEKVEVT SAFIVSEKV LQQNKILSKIKSSSV NKILSKIKS QNKILSKIKSSSVKK LSKIKSSSV EEKLNETTALWTKNK LNETTALWT EKEEKLNETTALWTK LNETTALWT IIDCQDLPLNVSREI CQDLPLNVS IDCQDLPLNVSREIL LPLNVSREI EEKEEKLNETTALWT KLNETTALW SAFIVSEKVEVTSKK IVSEKVEVT LTSGMPSKNPGKFIN LTSGMPSKN YSAFIVSEKVEVTSK IVSEKVEVT TNHLGVIAKSGTKEF HLGVIAKSG AFIVSEKVEVTSKKA IVSEKVEVT EKLNETTALWTKNKS LNETTALWT EVTSKKALESDAYIW VTSKKALES VTSKKALESDAYIWS VTSKKALES
	HLA-DRB1*0301	None
	HLA-DRB1*0401	SHKEIFLRELISNAS FLRELISNA HKEIFLRELISNASD LRELISNAS KEIFLRELISNASDA LRELISNAS EIFLRELISNASDAI LRELISNAS IFLRELISNASDAID LRELISNAS DSNDPTYQMQKIMLS DSNDPTYQM SNDPTYQMQKIMLSM YQMQKIMLS DPTYQMQKIMLSMGQ YQMQKIMLS PTYQMQKIMLSMGQE YQMQKIMLS FLRELISNASDAIDK LRELISNAS NDPTYQMQKIMLSMG YQMQKIMLS WKIQEIIKKYSNHIN IIKKYSNHI KWKIQEIIKKYSNHI WKIQEIIKK

		LRELISNASDAIDKL LRELISNAS QEIIKKYSNHINYPI IIKKYSNHI IQEIIKKYSNHINYP IIKKYSNHI KIQEIIKKYSNHINY IIKKYSNHI YQMQKIMLSMGQEVK YQMQKIMLS NDLLYLIIHSLYSHK YLIIHSLYS TYQMQKIMLSMGQEV YQMQKIMLS DLLYLIIHSLYSHKE YLIIHSLYS VNDLLYLIIHSLYSH YLIIHSLYS EVNDLLYLIIHSLYS LYLIIHSLY EGLKLKAINKNETSN LKLKAINKN YEGLKLKAINKNETS LKLKAINKN EYEGLKLKAINKNET LKLKAINKN LLYLIIHSLYSHKEI YLIIHSLYS LKLKAINKNETSNEL LKAINKNET EIIKKYSNHINYPIY IIKKYSNHI IIKKYSNHINYPIYI IIKKYSNHI EEYNEFYKNTTFDYE FYKNTTFDY
	HLA-DRB1*0404	KEIFLRELISNASDA FLRELISNA EIFLRELISNASDAI FLRELISNA SHKEIFLRELISNAS FLRELISNA HKEIFLRELISNASD FLRELISNA YSHKEIFLRELISNA IFLRELISN KEIKPILELNPNNKI ILELNPNNK VKEIKPILELNPNNK IKPILELNP NDLLYLIIHSLYSHK YLIIHSLYS EIKPILELNPNNKIV ILELNPNNK IKPILELNPNNKIVQ ILELNPNNK DLLYLIIHSLYSHKE YLIIHSLYS LLYLIIHSLYSHKEI YLIIHSLYS IFLRELISNASDAID FLRELISNA VNDLLYLIIHSLYSH YLIIHSLYS KPILELNPNNKIVQN ILELNPNNK EVNDLLYLIIHSLYS LLYLIIHSL FLRELISNASDAIDK FLRELISNA FEEAMLTSGMPSKNP MLTSGMPSK EEAMLTSGMPSKNPG MLTSGMPSK
	HLA-DRB1*0405	DSNDPTYQMQKIMLS DSNDPTYQM NPNNKIVQNLKNLEP NKIVQNLKN PNNKIVQNLKNLEPE VQNLKNLEP PTYQMQKIMLSMGQE YQMQKIMLS DPTYQMQKIMLSMGQ YQMQKIMLS SNDPTYQMQKIMLSM YQMQKIMLS NDPTYQMQKIMLSMG YQMQKIMLS LLYLIIHSLYSHKEI YLIIHSLYS DLLYLIIHSLYSHKE YLIIHSLYS NNKIVQNLKNLEPEK VQNLKNLEP NKIVQNLKNLEPEKL VQNLKNLEP VNDLLYLIIHSLYSH YLIIHSLYS EVNDLLYLIIHSLYS LYLIIHSLY NDLLYLIIHSLYSHK YLIIHSLYS IFLRELISNASDAID LRELISNAS KIVQNLKNLEPEKLE VQNLKNLEP HKEIFLRELISNASD LRELISNAS KEIFLRELISNASDA LRELISNAS EIFLRELISNASDAI LRELISNAS EKLISLIRFKSSSVD LIRFKSSSV

		KLISLIRFKSSSVDG IRFKSSSVD
		LISLIRFKSSSVDGF IRFKSSSVD
		SHKEIFLRELISNAS EIFLRELIS
	HLA-DRB1*0701	NKILSKIKSSSVKKI LSKIKSSSV
		KILSKIKSSSVKKIL LSKIKSSSV
		LQQNKILSKIKSSSV LQQNKILSK
		QQNKILSKIKSSSVK LSKIKSSSV
		QNKILSKIKSSSVKK LSKIKSSSV
		LSKIKSSSVKKILSE LSKIKSSSV
		ILSKIKSSSVKKILS LSKIKSSSV
		DLYYPNTKPGVKLFI YPNTKPGVK
		YDLYYPNTKPGVKLF YPNTKPGVK
		ISLIRFKSSSVDGFV LIRFKSSSV
		PYDLYYPNTKPGVKL YPNTKPGVK
		APYDLYYPNTKPGVK YYPNTKPGV
		LISLIRFKSSSVDGF LIRFKSSSV
		KLISLIRFKSSSVDG LIRFKSSSV
		EKLISLIRFKSSSVD LIRFKSSSV
		EEYNEFYKNTTFDYE FYKNTTFDY
		EYNEFYKNTTFDYEN FYKNTTFDY
		QEIIKKYSNHINYPI IIKKYSNHI
		LYYPNTKPGVKLFIN YPNTKPGVK
		YNEFYKNTTFDYENP FYKNTTFDY
		NEFYKNTTFDYENPL FYKNTTFDY
		IFYFKQIALFIIFRL YFKQIALFI
		ILIFYFKQIALFIIF YFKQIALFI
		MILIFYFKQIALFII YFKQIALFI
		LIFYFKQIALFIIFR YFKQIALFI
		AEEYNEFYKNTTFDY EFYKNTTFD
		REKLISLIRFKSSSV ISLIRFKSS
	HLA-DRB1*0802	CYIIKKVKIKLKRKS IIKKVKIKL
		IIKKVKIKLKRKSCM VKIKLKRKS
		YIIKKVKIKLKRKSC VKIKLKRKS
		KKVKIKLKRKSCMKK VKIKLKRKS
	HLA-DRB1*0901	INYPIYIKYSEPIMK YIKYSEPIM
		YPIYIKYSEPIMKDG YIKYSEPIM
		NYPIYIKYSEPIMKD YIKYSEPIM
		PIYIKYSEPIMKDGK YIKYSEPIM
		HINYPIYIKYSEPIM IYIKYSEPI
		KILSKIKSSSVKKIL IKSSSVKKI
		YTNLFYVPSKAPYDL YVPSKAPYD
		TNLFYVPSKAPYDLY YVPSKAPYD
		ILSKIKSSSVKKILS IKSSSVKKI
		NKILSKIKSSSVKKI LSKIKSSSV
		LSKIKSSSVKKILSE IKSSSVKKI
		NLFYVPSKAPYDLYY YVPSKAPYD
		SKIKSSSVKKILSEL IKSSSVKKI
		EYTNLFYVPSKAPYD FYVPSKAPY
		MILIFYFKQIALFII YFKQIALFI
		ILIFYFKQIALFIIF YFKQIALFI
		LIFYFKQIALFIIFR YFKQIALFI
		IYIKYSEPIMKDGKQ YIKYSEPIM
		IFYFKQIALFIIFRL YFKQIALFI
		LFYVPSKAPYDLYYP YVPSKAPYD
		ISLIRFKSSSVDGFV FKSSSVDGF
		LISLIRFKSSSVDGF RFKSSSVDG

	HLA-DRB1*1101	EGNLEYTNLFYVPSK YTNLFYVPS AEGNLEYTNLFYVPS LEYTNLFYV GNLEYTNLFYVPSKA YTNLFYVPS LEYTNLFYVPSKAPY YTNLFYVPS NLEYTNLFYVPSKAP YTNLFYVPS EKLISLIRFKSSSVD LISLIRFKS NREKLISLIRFKSSS LISLIRFKS ENREKLISLIRFKSS LISLIRFKS REKLISLIRFKSSSV LISLIRFKS FENREKLISLIRFKS EKLISLIRF YTNLFYVPSKAPYDL YTNLFYVPS EYTNLFYVPSKAPYD YTNLFYVPS KKVKIKLKRKSCMKK VKIKLKRKS
	HLA-DRB1*1302	EGLKLKAINKNETSN LKAINKNET YEGLKLKAINKNETS LKAINKNET GLKLKAINKNETSNE LKAINKNET LKLKAINKNETSNEL LKAINKNET EYEGLKLKAINKNET LKLKAINKN IIKKVKIKLKRKSCM VKIKLKRKS QDLTNHLGVIAKSGT LTNHLGVIA IKPILELNPNNKIVQ LELNPNNKI KPILELNPNNKIVQN LNPNNKIVQ IKKVKIKLKRKSCMK IKLKRKSCM KDHIKEVNLSATLIK IKEVNLSAT DHIKEVNLSATLIKE VNLSATLIK PGVKLFINRIFITDS LFINRIFIT PILELNPNNKIVQNL LNPNNKIVQ LTNHLGVIAKSGTKE LGVIAKSGT NKIVQNLKNLEPEKL IVQNLKNLE TNHLGVIAKSGTKEF LGVIAKSGT LNPNNKIVQNLKNLE LNPNNKIVQ KPGVKLFINRIFITD LFINRIFIT REILQQNKILSKIKS ILQQNKILS NHLGVIAKSGTKEFI LGVIAKSGT KKVKIKLKRKSCMKK IKLKRKSCM GVKLFINRIFITDSE LFINRIFIT DLTNHLGVIAKSGTK LGVIAKSGT VKLFINRIFITDSEG LFINRIFIT IKEVNLSATLIKEPS VNLSATLIK HIKEVNLSATLIKEP VNLSATLIK ILELNPNNKIVQNLK LNPNNKIVQ CYIIKKVKIKLKRKS IKKVKIKLK NPNNKIVQNLKNLEP IVQNLKNLE PNNKIVQNLKNLEPE IVQNLKNLE KIVQNLKNLEPEKLE VQNLKNLEP EILQQNKILSKIKSS NKILSKIKS FENREKLISLIRFKS EKLISLIRF NNKIVQNLKNLEPEK IVQNLKNLE YIIKKVKIKLKRKSC VKIKLKRKS TKPGVKLFINRIFIT VKLFINRIF ILQQNKILSKIKSSS NKILSKIKS KVKIKLKRKSCMKKQ IKLKRKSCM FRLCYIIKKVKIKLK YIIKKVKIK PTYQMQKIMLSMGQE YQMQKIMLS RLCYIIKKVKIKLKR IKKVKIKLK VKIKLKRKSCMKKQF IKLKRKSCM

		DPTYQMQKIMLSMGQ YQMQKIMLS
		NDPTYQMQKIMLSMG YQMQKIMLS
		LELNPNNKIVQNLKN LNPNNKIVQ
		VSREILQQNKILSKI ILQQNKILS
		ENREKLISLIRFKSS LISLIRFKS
		LCYIIKKVKIKLKRK IKKVKIKLK
		NREKLISLIRFKSSS LISLIRFKS
		SREILQQNKILSKIK ILQQNKILS
		EKLISLIRFKSSSVD LISLIRFKS
		REKLISLIRFKSSSV LISLIRFKS
		IVQNLKNLEPEKLEK IVQNLKNLE
		KLKAINKNETSNELK LKAINKNET
		NKILSKIKSSSVKKI NKILSKIKS
		NVSREILQQNKILSK ILQQNKILS
		LGVIAKSGTKEFINN LGVIAKSGT
		HLGVIAKSGTKEFIN LGVIAKSGT
		LKAINKNETSNELKD LKAINKNET
		SLLPNYLRFIKGIID LPNYLRFIK
		LQQNKILSKIKSSSV NKILSKIKS
		VNDLLYLIIHSLYSH LYLIIHSLY
		YQMQKIMLSMGQEVK YQMQKIMLS
		KLFINRIFITDSEGS LFINRIFIT
		LNVSREILQQNKILS LNVSREILQ
		IFYFKQIALFIIFRL FKQIALFII
		NDLLYLIIHSLYSHK LYLIIHSLY
		FYFKQIALFIIFRLC FKQIALFII
		KEVNLSATLIKEPSA VNLSATLIK
		GSLLPNYLRFIKGII LPNYLRFIK
		EIKPILELNPNNKIV LELNPNNKI
		QQNKILSKIKSSSVK NKILSKIKS
		LKDHIKEVNLSATLI IKEVNLSAT
		KEIKPILELNPNNKI ILELNPNNK
		TYQMQKIMLSMGQEV YQMQKIMLS
		DLLYLIIHSLYSHKE LYLIIHSLY
		IKKYSNHINYPIYIK YSNHINYPI
		IFRLCYIIKKVKIKL YIIKKVKIK
		SNDPTYQMQKIMLSM YQMQKIMLS
		QEIIKKYSNHINYPI IKKYSNHIN
		IIKKYSNHINYPIYI YSNHINYPI
		KKYSNHINYPIYIKY YSNHINYPI
		LLPNYLRFIKGIIDC YLRFIKGII
		DSNDPTYQMQKIMLS TYQMQKIML
		DDKSILIKDNGIGMD LIKDNGIGM
		EIIKKYSNHINYPIY YSNHINYPI
		LPNYLRFIKGIIDCQ YLRFIKGII
		DEQDLTNHLGVIAKS LTNHLGVIA
		MDEQDLTNHLGVIAK LTNHLGVIA
		PEYEGLKLKAINKNE LKLKAINKN
		IPEYEGLKLKAINKN YEGLKLKAI
		FKQIALFIIFRLCYI IALFIIFRL
		LFINRIFITDSEGSL LFINRIFIT
		YFKQIALFIIFRLCY IALFIIFRL
		EILKDHIKEVNLSAT LKDHIKEVN
		DKSILIKDNGIGMDE IKDNGIGMD
		EQDLTNHLGVIAKSG LTNHLGVIA
		KSILIKDNGIGMDEQ LIKDNGIGM
		EVNDLLYLIIHSLYS LYLIIHSLY

		TEVNDLLYLIIHSLY LLYLIIHSL LLYLIIHSLYSHKEI LIIHSLYSH ILKDHIKEVNLSATL IKEVNLSAT LDEAILNLIPEYEGL ILNLIPEYE KILSKIKSSSVKKIL IKSSSVKKI ELDEAILNLIPEYEG ILNLIPEYE ILSKIKSSSVKKILS IKSSSVKKI IIFRLCYIIKKVKIK CYIIKKVKI LISLIRFKSSSVDGF LISLIRFKS YSNHINYPIYIKYSE YSNHINYPI PGKFINIINEFIEKD INIINEFIE ILIFYFKQIALFIIF FKQIALFII QNKILSKIKSSSVKK NKILSKIKS IFLRELISNASDAID LRELISNAS SEGSLLPNYLRFIKG LPNYLRFIK GMDEQDLTNHLGVIA DLTNHLGVI KNPGKFINIINEFIE KFINIINEF NPGKFINIINEFIEK INIINEFIE NEKFKNIALEPKIEI FKNIALEPK MILIFYFKQIALFII IFYFKQIAL DSEGSLLPNYLRFIK EGSLLPNYL EVNLSATLIKEPSAI VNLSATLIK EKFKNIALEPKIEIS FKNIALEPK KQIALFIIFRLCYII IALFIIFRL SGTKEFINNLKQDEK FINNLKQDE EGSLLPNYLRFIKGI LPNYLRFIK LYLIIHSLYSHKEIF LIIHSLYSH LIFYFKQIALFIIFR FKQIALFII KLISLIRFKSSSVDG LISLIRFKS VQNLKNLEPEKLEKI LKNLEPEKL EIFLRELISNASDAI LRELISNAS EEYNEFYKNTTFDYE YNEFYKNTT LSKIKSSSVKKILSE IKSSSVKKI SKIKSSSVKKILSEL IKSSSVKKI WKIQEIIKKYSNHIN IQEIIKKYS GKFINIINEFIEKDF INIINEFIE KYSNHINYPIYIKYS YSNHINYPI GTKEFINNLKQDEKK INNLKQDEK SILIKDNGIGMDEQD LIKDNGIGM DELDEAILNLIPEYE LDEAILNLI SDFENREKLISLIRF FENREKLIS TKEFINNLKQDEKKS INNLKQDEK
	HLA-DRB1*1501	KLISLIRFKSSSVDG LIRFKSSSV LISLIRFKSSSVDGF LIRFKSSSV ISLIRFKSSSVDGFV LIRFKSSSV REKLISLIRFKSSSV ISLIRFKSS SLIRFKSSSVDGFVS LIRFKSSSV NDLLYLIIHSLYSHK LIIHSLYSH LIRFKSSSVDGFVSF LIRFKSSSV DLLYLIIHSLYSHKE LIIHSLYSH LLYLIIHSLYSHKEI LIIHSLYSH LYLIIHSLYSHKEIF LIIHSLYSH VNDLLYLIIHSLYSH YLIIHSLYS YLIIHSLYSHKEIFL LIIHSLYSH SHKEIFLRELISNAS FLRELISNA KEIFLRELISNASDA LRELISNAS

		HKEIFLRELISNASD LRELISNAS EIFLRELISNASDAI LRELISNAS LIIHSLYSHKEIFLR LIIHSLYSH IALFIIFRLCYIIKK FIIFRLCYI ALFIIFRLCYIIKKV FIIFRLCYI IFLRELISNASDAID LRELISNAS QIALFIIFRLCYIIK FIIFRLCYI LFIIFRLCYIIKKVK IFRLCYIIK CYIIKKVKIKLKRKS IKKVKIKLK FIIFRLCYIIKKVKI IFRLCYIIK LCYIIKKVKIKLKRK IKKVKIKLK YIIKKVKIKLKRKSC IKKVKIKLK RLCYIIKKVKIKLKR IKKVKIKLK KKVKIKLKRKSCMKK IKLKRKSCM IKKVKIKLKRKSCMK VKIKLKRKS IIKKVKIKLKRKSCM KKVKIKLKR IIFRLCYIIKKVKIK FRLCYIIKK FRLCYIIKKVKIKLK YIIKKVKIK FKQIALFIIFRLCYI LFIIFRLCY KVKIKLKRKSCMKKQ IKLKRKSCM KQIALFIIFRLCYII FIIFRLCYI IFRLCYIIKKVKIKL YIIKKVKIK VKIKLKRKSCMKKQF IKLKRKSCM
	HLA-DRB3*0101	None
	HLA-DRB4*0101	KEIKPILELNPNNKI ILELNPNNK EIKPILELNPNNKIV ILELNPNNK IKPILELNPNNKIVQ ILELNPNNK KPILELNPNNKIVQN ILELNPNNK PILELNPNNKIVQNL ILELNPNNK VKEIKPILELNPNNK VKEIKPILE ILELNPNNKIVQNLK ILELNPNNK KKVKIKLKRKSCMKK IKLKRKSCM DLLYLIIHSLYSHKE LIIHSLYSH NKIVQNLKNLEPEKL IVQNLKNLE VNDLLYLIIHSLYSH LYLIIHSLY NDLLYLIIHSLYSHK LIIHSLYSH KVKIKLKRKSCMKKQ IKLKRKSCM EYEGLKLKAINKNET LKLKAINKN YEGLKLKAINKNETS LKLKAINKN EGLKLKAINKNETSN LKLKAINKN LLYLIIHSLYSHKEI LIIHSLYSH VKIKLKRKSCMKKQF IKLKRKSCM LYLIIHSLYSHKEIF LIIHSLYSH LSELEKLSKKNPEKF LSELEKLSK IPEYEGLKLKAINKN YEGLKLKAI KIVQNLKNLEPEKLE LKNLEPEKL PEYEGLKLKAINKNE LKLKAINKN IVQNLKNLEPEKLEK LKNLEPEKL PTYQMQKIMLSMGQE YQMQKIMLS NDPTYQMQKIMLSMG YQMQKIMLS DPTYQMQKIMLSMGQ YQMQKIMLS VPSKAPYDLYYPNTK VPSKAPYDL SNDPTYQMQKIMLSM YQMQKIMLS SELEKLSKKNPEKFS LSKKNPEKF

	HLA-DRB5*0101	APYDLYYPNTKPGVK YDLYYPNTK PYDLYYPNTKPGVKL YPNTKPGVK YDLYYPNTKPGVKLF YPNTKPGVK DLYYPNTKPGVKLFI YPNTKPGVK LYYPNTKPGVKLFIN YPNTKPGVK LEYANKWKIQEIIKK YANKWKIQE YANKWKIQEIIKKYS WKIQEIIKK EYANKWKIQEIIKKY WKIQEIIKK ANKWKIQEIIKKYSN WKIQEIIKK NKWKIQEIIKKYSNH WKIQEIIKK YYPNTKPGVKLFINR YPNTKPGVK YPNTKPGVKLFINRI YPNTKPGVK KKIEEEFKDTLTKVK EEFKDTLTK KIEEEFKDTLTKVKE FKDTLTKVK IEEEFKDTLTKVKEI FKDTLTKVK EEEFKDTLTKVKEIL FKDTLTKVK EEFKDTLTKVKEILK FKDTLTKVK
CAA44492.1| Outer surface protein A [Borrelia burgdorferi] Seq9	HLA-DRB1*0101	KKYLLGIGLILALIA LLGIGLILA KYLLGIGLILALIAC LLGIGLILA MKKYLLGIGLILALI LLGIGLILA KTGKWDSKTSTLTIS WDSKTSTLT TGKWDSKTSTLTISV WDSKTSTLT TKKTGKWDSKTSTLT TGKWDSKTS KKTGKWDSKTSTLTI WDSKTSTLT GKWDSKTSTLTISVN WDSKTSTLT LKDFTLEGTLAADGK FTLEGTLAA VLKDFTLEGTLAADG FTLEGTLAA KDFTLEGTLAADGKT FTLEGTLAA SVSVDLPGGMTELVS LPGGMTELV YLLGIGLILALIACK IGLILALIA NSVSVDLPGGMTELV SVDLPGGMT SVDLPGGMTELVSKE LPGGMTELV VSVDLPGGMTELVSK LPGGMTELV VDLPGGMTELVSKEK LPGGMTELV LLGIGLILALIACKQ IGLILALIA KEVLKDFTLEGTLAA LKDFTLEGT EVLKDFTLEGTLAAD FTLEGTLAA TSEKTIVRANGTRLE IVRANGTRL SEKTIVRANGTRLEY IVRANGTRL TTLKVTEGTVVLSKN VTEGTVVLS KTTLKVTEGTVVLSK VTEGTVVLS EKTIVRANGTRLEYT IVRANGTRL GKTTLKVTEGTVVLS LKVTEGTVV KTIVRANGTRLEYTD IVRANGTRL KNILKSGEITVALDD LKSGEITVA LSKNILKSGEITVAL LKSGEITVA SKNILKSGEITVALD LKSGEITVA NILKSGEITVALDDS LKSGEITVA DFTLEGTLAADGKTT FTLEGTLAA FTLEGTLAADGKTTL FTLEGTLAA TLKVTEGTVVLSKNI VTEGTVVLS LGIGLILALIACKQN IGLILALIA VLSKNILKSGEITVA KNILKSGEI KEDAKTLVSKKVTLK AKTLVSKKV EDAKTLVSKKVTLKD AKTLVSKKV

		LKVTEGTVVLSKNIL VTEGTVVLS
		TIVRANGTRLEYTDI VRANGTRLE
		EIFKEDAKTLVSKKV FKEDAKTLV
		SAGTNLEGKAVEITT LEGKAVEIT
		DSAGTNLEGKAVEIT GTNLEGKAV
		KWDSKTSTLTISVNS WDSKTSTLT
		WDSKTSTLTISVNSQ WDSKTSTLT
		IFKEDAKTLVSKKVT AKTLVSKKV
		GTNLEGKAVEITTLK LEGKAVEIT
		AGTNLEGKAVEITTL LEGKAVEIT
		DLPGGMTELVSKEKD LPGGMTELV
		FKEDAKTLVSKKVTL AKTLVSKKV
		DGKTTLKVTEGTVVL LKVTEGTVV
		LPGGMTELVSKEKDK LPGGMTELV
		ITVQKYDSAGTNLEG VQKYDSAGT
		TITVQKYDSAGTNLE VQKYDSAGT
		TNLEGKAVEITTLKE LEGKAVEIT
		NLVFTKEDTITVQKY FTKEDTITV
		AKTLVSKKVTLKDKS AKTLVSKKV
		DAKTLVSKKVTLKDK AKTLVSKKV
		KNLVFTKEDTITVQK FTKEDTITV
		GIGLILALIACKQNV ILALIACKQ
		ETSEKTIVRANGTRL KTIVRANGT
		TKNLVFTKEDTITVQ FTKEDTITV
		IGLILALIACKQNVS ILALIACKQ
		KTKNLVFTKEDTITV VFTKEDTIT
		IVRANGTRLEYTDIK IVRANGTRL
		ADGKTTLKVTEGTVV ADGKTTLKV
		LVFTKEDTITVQKYD FTKEDTITV
		LKSGEITVALDDSDT LKSGEITVA
		ILKSGEITVALDDSD LKSGEITVA
		DTITVQKYDSAGTNL VQKYDSAGT
		EDTITVQKYDSAGTN VQKYDSAGT
		KEDTITVQKYDSAGT ITVQKYDSA
		GLILALIACKQNVST ILALIACKQ
		LEGTLAADGKTTLKV LEGTLAADG
		TISVNSQKTKNLVFT VNSQKTKNL
		LEYTDIKSDGSGKAK IKSDGSGKA
		RLEYTDIKSDGSGKA YTDIKSDGS
		TLTISVNSQKTKNLV VNSQKTKNL
		STLTISVNSQKTKNL TISVNSQKT
		ISVNSQKTKNLVFTK VNSQKTKNL
		TVQKYDSAGTNLEGK VQKYDSAGT
		VQKYDSAGTNLEGKA VQKYDSAGT
		VTEGTVVLSKNILKS VTEGTVVLS
		VALDDSDTTQATKKT LDDSDTTQA
		YTDIKSDGSGKAKEV IKSDGSGKA
		QKYDSAGTNLEGKAV YDSAGTNLE
		TLEGTLAADGKTTLK LEGTLAADG
		LTISVNSQKTKNLVF VNSQKTKNL
		KVTEGTVVLSKNILK VTEGTVVLS
		EYTDIKSDGSGKAKE IKSDGSGKA
		LILALIACKQNVSTL IACKQNVST
		FEIFKEDAKTLVSKK IFKEDAKTL
		KFEIFKEDAKTLVSK IFKEDAKTL
		VRANGTRLEYTDIKS VRANGTRLE
		NLEGKAVEITTLKEL LEGKAVEIT

	HLA-DRB1*0301	None
	HLA-DRB1*0401	KEVLKDFTLEGTLAA VLKDFTLEG EVLKDFTLEGTLAAD FTLEGTLAA VLKDFTLEGTLAADG FTLEGTLAA LKDFTLEGTLAADGK FTLEGTLAA KDFTLEGTLAADGKT FTLEGTLAA KNLVFTKEDTITVQK FTKEDTITV NLVFTKEDTITVQKY FTKEDTITV LVFTKEDTITVQKYD FTKEDTITV DFTLEGTLAADGKTT FTLEGTLAA LEYTDIKSDGSGKAK IKSDGSGKA TKNLVFTKEDTITVQ FTKEDTITV FTLEGTLAADGKTTL FTLEGTLAA RLEYTDIKSDGSGKA YTDIKSDGS KTKNLVFTKEDTITV KTKNLVFTK AKEVLKDFTLEGTLA VLKDFTLEG
	HLA-DRB1*0404	KEVLKDFTLEGTLAA VLKDFTLEG GKAKEVLKDFTLEGT VLKDFTLEG AKEVLKDFTLEGTLA VLKDFTLEG KAKEVLKDFTLEGTL VLKDFTLEG SGKAKEVLKDFTLEG AKEVLKDFT
	HLA-DRB1*0405	TITVQKYDSAGTNLE VQKYDSAGT ITVQKYDSAGTNLEG YDSAGTNLE TVQKYDSAGTNLEGK YDSAGTNLE VQKYDSAGTNLEGKA YDSAGTNLE QKYDSAGTNLEGKAV YDSAGTNLE
	HLA-DRB1*0701	DGKTTLKVTEGTVVL LKVTEGTVV GKTTLKVTEGTVVLS LKVTEGTVV KTTLKVTEGTVVLSK LKVTEGTVV ADGKTTLKVTEGTVV TLKVTEGTV TTLKVTEGTVVLSKN LKVTEGTVV
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	TEGTVVLSKNILKSG TVVLSKNIL EGTVVLSKNILKSGE TVVLSKNIL GTVVLSKNILKSGEI VVLSKNILK VTEGTVVLSKNILKS TVVLSKNIL TVVLSKNILKSGEIT TVVLSKNIL SEKTIVRANGTRLEY IVRANGTRL TSEKTIVRANGTRLE IVRANGTRL EKTIVRANGTRLEYT IVRANGTRL KTIVRANGTRLEYTD IVRANGTRL TLTISVNSQKTKNLV VNSQKTKNL STLTISVNSQKTKNL ISVNSQKTK LTISVNSQKTKNLVF VNSQKTKNL KVTEGTVVLSKNILK TVVLSKNIL TISVNSQKTKNLVFT VNSQKTKNL LKVTEGTVVLSKNIL LKVTEGTVV TIVRANGTRLEYTDI VRANGTRLE ISVNSQKTKNLVFTK VNSQKTKNL

		VVLSKNILKSGEITV VVLSKNILK ETSEKTIVRANGTRL KTIVRANGT EDAKTLVSKKVTLKD LVSKKVTLK DAKTLVSKKVTLKDK LVSKKVTLK
	HLA-DRB1*1501	TEGTVVLSKNILKSG VLSKNILKS EGTVVLSKNILKSGE VLSKNILKS
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	KDKDGKYSLEATVDK KDKDGKYSL DKDGKYSLEATVDKL YSLEATVDK KDGKYSLEATVDKLE YSLEATVDK DGKYSLEATVDKLEL YSLEATVDK GKYSLEATVDKLELK YSLEATVDK
|BAA22351.1| Outer surface protein B [Borrelia garinii] Seq10	HLA-DRB1*0101	KKYLLGFALVLALIA LLGFALVLA ITVQNYDTAGTKLAG YDTAGTKLA TITVQNYDTAGTKLA VQNYDTAGT QNYDTAGTKLAGTAT YDTAGTKLA KYLLGFALVLALIAC LLGFALVLA MKKYLLGFALVLALI LLGFALVLA TVQNYDTAGTKLAGT YDTAGTKLA VQNYDTAGTKLAGTA YDTAGTKLA ATEIKDLEALKAALK IKDLEALKA TATEIKDLEALKAAL IKDLEALKA YLLGFALVLALIACG FALVLALIA GTATEIKDLEALKAA IKDLEALKA AGTATEIKDLEALKA AGTATEIKD LLGFALVLALIACGQ FALVLALIA LGFALVLALIACGQK FALVLALIA YDTAGTKLAGTATEI YDTAGTKLA NYDTAGTKLAGTATE YDTAGTKLA EGVKSDQSKVTMSIT VKSDQSKVT LEGVKSDQSKVTMSI VKSDQSKVT GKLEGVKSDQSKVTM VKSDQSKVT GGKLEGVKSDQSKVT LEGVKSDQS KLEGVKSDQSKVTMS VKSDQSKVT DGTITVQNYDTAGTK VQNYDTAGT GTITVQNYDTAGTKL VQNYDTAGT SKKDLPLVTEDTVKL DLPLVTEDT GFALVLALIACGQKG LVLALIACG TDGTITVQNYDTAGT TITVQNYDT KKDLPLVTEDTVKLF LVTEDTVKL FALVLALIACGQKGA LVLALIACG MLEGNLVGGKTSVEI LVGGKTSVE KDLPLVTEDTVKLFN LVTEDTVKL DLPLVTEDTVKLFND LVTEDTVKL LEGNLVGGKTSVEIK VGGKTSVEI EGNLVGGKTSVEIKE VGGKTSVEI GNLVGGKTSVEIKEG VGGKTSVEI LPLVTEDTVKLFNDT LVTEDTVKL NLVGGKTSVEIKEGT VGGKTSVEI ETLKNGIMLEGNLVG LKNGIMLEG YKTGKLSTKKITRTN LSTKKITRT

		TYKTGKLSTKKITRT TGKLSTKKI
		TGKLSTKKITRTNGT LSTKKITRT
		VETLKNGIMLEGNLV LKNGIMLEG
		KKEIEKAGTVKLFLD IEKAGTVKL
		LKKEIEKAGTVKLFL IEKAGTVKL
		KEIEKAGTVKLFLDD IEKAGTVKL
		KDFVFLTDGTITVQN FLTDGTITV
		VTLKKEIEKAGTVKL LKKEIEKAG
		TLKKEIEKAGTVKLF IEKAGTVKL
		KTGKLSTKKITRTNG LSTKKITRT
		GKLSTKKITRTNGTT LSTKKITRT
		DTAGTKLAGTATEIK GTKLAGTAT
		GVKSDQSKVTMSITD VKSDQSKVT
		VKSDQSKVTMSITDD VKSDQSKVT
		DFVFLTDGTITVQNY FLTDGTITV
		TAGTKLAGTATEIKD LAGTATEIK
		IKDFVFLTDGTITVQ FLTDGTITV
		DGKYELRATVDTVEL YELRATVDT
		FVFLTDGTITVQNYD FLTDGTITV
		GKYELRATVDTVELK YELRATVDT
		ALVLALIACGQKGAE LVLALIACG
		NKDGKYELRATVDTV YELRATVDT
		KNKDGKYELRATVDT DGKYELRAT
		KDGKYELRATVDTVE YELRATVDT
		KAVETLKNGIMLEGN LKNGIMLEG
		AVETLKNGIMLEGNL LKNGIMLEG
		ASKVFKKQGSLTEET FKKQGSLTE
		TLKNGIMLEGNLVGG LKNGIMLEG
		SKVFKKQGSLTEETE FKKQGSLTE
		KIKDFVFLTDGTITV FVFLTDGTI
		LKNGIMLEGNLVGGK LKNGIMLEG
		AGTKLAGTATEIKDL LAGTATEIK
		GTKLAGTATEIKDLE LAGTATEIK
		TKAVETLKNGIMLEG VETLKNGIM
		KTAVWSDTSNTLTVS WSDTSNTLT
		KVFKKQGSLTEETEE FKKQGSLTE
		VASKVFKKQGSLTEE FKKQGSLTE
		KVASKVFKKQGSLTE VFKKQGSLT
		VGGKTSVEIKEGTVT VGGKTSVEI
		TAVWSDTSNTLTVSA VWSDTSNTL
		LVLALIACGQKGAEP LVLALIACG
		TKKTAVWSDTSNTLT VWSDTSNTL
		KKTAVWSDTSNTLTV WSDTSNTLT
		LVGGKTSVEIKEGTV VGGKTSVEI
		KNGIMLEGNLVGGKT IMLEGNLVG
		ETYKTGKLSTKKITR YKTGKLSTK
		LVTEDTVKLFNDTKI LVTEDTVKL
		EETYKTGKLSTKKIT YKTGKLSTK
		TEETYKTGKLSTKKI YKTGKLSTK
		LSTKKITRTNGTTLE LSTKKITRT
		PLVTEDTVKLFNDTK LVTEDTVKL
		VFLTDGTITVQNYDT FLTDGTITV
		KLSTKKITRTNGTTL LSTKKITRT
		VETYDSSNTKVASKV YDSSNTKVA
		YELRATVDTVELKGV YELRATVDT
		TITVETYDSSNTKVA VETYDSSNT
		ITVETYDSSNTKVAS YDSSNTKVA

		AVWSDTSNTLTVSAD WSDTSNTLT ETYDSSNTKVASKVF YDSSNTKVA IMLEGNLVGGKTSVE IMLEGNLVG EIEKAGTVKLFLDDT IEKAGTVKL NGIMLEGNLVGGKTS IMLEGNLVG IEKAGTVKLFLDDTS IEKAGTVKL FLTDGTITVQNYDTA FLTDGTITV KLFLDDTSSGSTKKT FLDDTSSGS KYELRATVDTVELKG YELRATVDT
	HLA-DRB1*0301	DTVKLFNDTKIFISK LFNDTKIFI EDTVKLFNDTKIFIS LFNDTKIFI TVKLFNDTKIFISKE LFNDTKIFI TEDTVKLFNDTKIFI KLFNDTKIF VKLFNDTKIFISKEK LFNDTKIFI
	HLA-DRB1*0401	SKVFKKQGSLTEETE FKKQGSLTE VASKVFKKQGSLTEE FKKQGSLTE ASKVFKKQGSLTEET FKKQGSLTE KVASKVFKKQGSLTE VFKKQGSLT KVFKKQGSLTEETEE FKKQGSLTE TAVWSDTSNTLTVSA VWSDTSNTL
	HLA-DRB1*0404	TAVWSDTSNTLTVSA WSDTSNTLT AVWSDTSNTLTVSAD TSNTLTVSA
	HLA-DRB1*0405	TLEYSDMTNDENATK YSDMTNDEN GTTLEYSDMTNDENA YSDMTNDEN NGTTLEYSDMTNDEN EYSDMTNDE TTLEYSDMTNDENAT YSDMTNDEN LEYSDMTNDENATKA YSDMTNDEN
	HLA-DRB1*0701	ETYDSSNTKVASKVF YDSSNTKVA TYDSSNTKVASKVFK NTKVASKVF YDSSNTKVASKVFKK NTKVASKVF
	HLA-DRB1*0802	None
	HLA-DRB1*0901	MKKYLLGFALVLALI LGFALVLAL KKYLLGFALVLALIA LGFALVLAL
	HLA-DRB1*1101	None
	HLA-DRB1*1302	TKAVETLKNGIMLEG VETLKNGIM KAVETLKNGIMLEGN LKNGIMLEG VETLKNGIMLEGNLV LKNGIMLEG AVETLKNGIMLEGNL LKNGIMLEG ETLKNGIMLEGNLVG LKNGIMLEG LSTKKITRTNGTTLE KKITRTNGT EDTVKLFNDTKIFIS VKLFNDTKI DTVKLFNDTKIFISK VKLFNDTKI TYKTGKLSTKKITRT GKLSTKKIT YKTGKLSTKKITRTN LSTKKITRT TGKLSTKKITRTNGT LSTKKITRT GKLSTKKITRTNGTT LSTKKITRT STKKITRTNGTTLEY ITRTNGTTL

		KTGKLSTKKITRTNG LSTKKITRT KLSTKKITRTNGTTL KKITRTNGT NGIMLEGNLVGGKTS EGNLVGGKT VKLFNDTKIFISKEK LFNDTKIFI IMLEGNLVGGKTSVE EGNLVGGKT
	HLA-DRB1*1501	MKKYLLGFALVLALI LLGFALVLA KKYLLGFALVLALIA LLGFALVLA KYLLGFALVLALIAC LLGFALVLA
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	None
AAM22469.1| Outer surface protein C [Borrelia afzelii] Seq11	HLA-DRB1*0101	TNSVKELTSPVVAES VKELTSPVV NSVKELTSPVVAESP VKELTSPVV ALTNSVKELTSPVVA VKELTSPVV LTNSVKELTSPVVAE VKELTSPVV EALTNSVKELTSPVV LTNSVKELT EGLVKAAQEALTNSV VKAAQEALT SVKELTSPVVAESPK VKELTSPVV VKELTSPVVAESPKK VKELTSPVV GLVKAAQEALTNSVK VKAAQEALT VEGLVKAAQEALTNS VKAAQEALT LAGVHEISTLITEKL VHEISTLIT AGVHEISTLITEKLS VHEISTLIT SVEGLVKAAQEALTN VKAAQEALT KSVEGLVKAAQEALT LVKAAQEAL HEISTLITEKLSKLK ISTLITEKL VHEISTLITEKLSKL ISTLITEKL MKKNTLSAILMTLFL KNTLSAILM NTLSAILMTLFLFIS LSAILMTLF GVHEISTLITEKLSK ISTLITEKL ESLLAGVHEISTLIT LLAGVHEIS KNTLSAILMTLFLFI LSAILMTLF SLLAGVHEISTLITE VHEISTLIT LLAGVHEISTLITEK VHEISTLIT TLSAILMTLFLFISC LMTLFLFIS KELTSPVVAESPKKP LTSPVVAES LSAILMTLFLFISCN LMTLFLFIS LVKAAQEALTNSVKE VKAAQEALT SAILMTLFLFISCNN LMTLFLFIS ISTLITEKLSKLKNS ISTLITEKL EISTLITEKLSKLKN ISTLITEKL VKAAQEALTNSVKEL VKAAQEALT KKNTLSAILMTLFLF LSAILMTLF VLAVKEVETLVSSID VKEVETLVS LAVKEVETLVSSIDE VKEVETLVS AFVLAVKEVETLVSS VKEVETLVS AILMTLFLFISCNNS LMTLFLFIS NAFVLAVKEVETLVS LAVKEVETL FVLAVKEVETLVSSI VKEVETLVS FKSVEGLVKAAQEAL FKSVEGLVK EEFTNKLRVSHADLG FTNKLRVSH VKEVETLVSSIDELA VKEVETLVS EFTNKLRVSHADLGK LRVSHADLG

		GKLFKSVEGLVKAAQ FKSVEGLVK NNSGKGGDSASTNPA GKGGDSAST KLFKSVEGLVKAAQE FKSVEGLVK NSGKGGDSASTNPAD GKGGDSAST
	HLA-DRB1*0301	None
	HLA-DRB1*0401	None
	HLA-DRB1*0404	MTLFLFISCNNSGKG LFISCNNSG TLFLFISCNNSGKGG LFISCNNSG ILMTLFLFISCNNSG FLFISCNNS KKAILKTNADKTKGA ILKTNADKT LMTLFLFISCNNSGK LFISCNNSG AKKAILKTNADKTKG ILKTNADKT KAILKTNADKTKGAE ILKTNADKT LFLFISCNNSGKGGD LFISCNNSG DAKKAILKTNADKTK ILKTNADKT DDAKKAILKTNADKT AILKTNADK
	HLA-DRB1*0405	LAVKEVETLVSSIDE VKEVETLVS VLAVKEVETLVSSID VKEVETLVS VKEVETLVSSIDELA VKEVETLVS AVKEVETLVSSIDEL VKEVETLVS NAFVLAVKEVETLVS FVLAVKEVE TNSVKELTSPVVAES VKELTSPVV LTNSVKELTSPVVAE VKELTSPVV NSVKELTSPVVAESP VKELTSPVV AFVLAVKEVETLVSS VKEVETLVS FVLAVKEVETLVSSI VKEVETLVS
	HLA-DRB1*0701	ALTNSVKELTSPVVA VKELTSPVV EALTNSVKELTSPVV SVKELTSPV LTNSVKELTSPVVAE VKELTSPVV TNSVKELTSPVVAES VKELTSPVV NSVKELTSPVVAESP VKELTSPVV SVKELTSPVVAESPK VKELTSPVV VKELTSPVVAESPKK VKELTSPVV EISKKITDSNAFVLA ITDSNAFVL TEISKKITDSNAFVL SKKITDSNA ISKKITDSNAFVLAV ITDSNAFVL SKKITDSNAFVLAVK ITDSNAFVL KKITDSNAFVLAVKE ITDSNAFVL KITDSNAFVLAVKEV ITDSNAFVL ITDSNAFVLAVKEVE ITDSNAFVL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	EGLVKAAQEALTNSV LVKAAQEAL KSVEGLVKAAQEALT LVKAAQEAL SVEGLVKAAQEALTN LVKAAQEAL VEGLVKAAQEALTNS LVKAAQEAL FKSVEGLVKAAQEAL VEGLVKAAQ
	HLA-DRB1*1101	KKCSEEFTNKLRVSH EFTNKLRVS KCSEEFTNKLRVSHA FTNKLRVSH CSEEFTNKLRVSHAD FTNKLRVSH SEEFTNKLRVSHADL FTNKLRVSH EEFTNKLRVSHADLG FTNKLRVSH EFTNKLRVSHADLGK FTNKLRVSH

		FTNKLRVSHADLGKQ FTNKLRVSH
	HLA-DRB1*1302	EALTNSVKELTSPVV LTNSVKELT QEALTNSVKELTSPV LTNSVKELT AAQEALTNSVKELTS LTNSVKELT AQEALTNSVKELTSP LTNSVKELT ALTNSVKELTSPVVA LTNSVKELT KAAQEALTNSVKELT ALTNSVKEL LTNSVKELTSPVVAE LTNSVKELT MKKNTLSAILMTLFL MKKNTLSAI LAGVHEISTLITEKL VHEISTLIT AGVHEISTLITEKLS ISTLITEKL
	HLA-DRB1*1501	ALTNSVKELTSPVVA VKELTSPVV EALTNSVKELTSPVV NSVKELTSP LTNSVKELTSPVVAE VKELTSPVV TNSVKELTSPVVAES VKELTSPVV NSVKELTSPVVAESP VKELTSPVV VKELTSPVVAESPKK VKELTSPVV
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	None
AAC62927.1| OspE-related lipoprotein [Borrelia garinii] Seq12	HLA-DRB1*0101	NNFVKAMTNVGSFKT VKAMTNVGS NFVKAMTNVGSFKTS VKAMTNVGS AEVNNFVKAMTNVGS FVKAMTNVG VNNFVKAMTNVGSFK VKAMTNVGS EVNNFVKAMTNVGSF VKAMTNVGS FVKAMTNVGSFKTSL MTNVGSFKT VKAMTNVGSFKTSLY MTNVGSFKT NGDWSNLGTLVIRKE WSNLGTLVI GTINGQLRGHSATFF NGQLRGHSA GDWSNLGTLVIRKEQ WSNLGTLVI NNGDWSNLGTLVIRK WSNLGTLVI TINGQLRGHSATFFC LRGHSATFF DNNGDWSNLGTLVIR WSNLGTLVI KDNNGDWSNLGTLVI DWSNLGTLV INGQLRGHSATFFCI LRGHSATFF NGQLRGHSATFFCIE LRGHSATFF LSDQGGLSGQASSDT QGGLSGQAS SDQGGLSGQASSDTI LSGQASSDT GQLRGHSATFFCIEE LRGHSATFF DQGGLSGQASSDTIK LSGQASSDT QGGLSGQASSDTIKF LSGQASSDT GGLSGQASSDTIKFS LSGQASSDT KAMTNVGSFKTSLYY MTNVGSFKT EAEVNNFVKAMTNVG VNNFVKAMT KMKMFIICAVFVLIS MFIICAVFV MKMFIICAVFVLISS MFIICAVFV KKMKMFIICAVFVLI MFIICAVFV NKKMKMFIICAVFVL MFIICAVFV MNKKMKMFIICAVFV MKMFIICAV MFIICAVFVLISSCG MFIICAVFV DWSNLGTLVIRKEQD WSNLGTLVI WSNLGTLVIRKEQDG WSNLGTLVI

		FIICAVFVLISSCGN VFVLISSCG ICAVFVLISSCGNFR VFVLISSCG MTNVGSFKTSLYYGY MTNVGSFKT CAVFVLISSCGNFRS VFVLISSCG KMFIICAVFVLISSC MFIICAVFV IICAVFVLISSCGNF VFVLISSCG QLRGHSATFFCIEEA LRGHSATFF LRGHSATFFCIEEAE LRGHSATFF AMTNVGSFKTSLYYG MTNVGSFKT SSCGNFRSSLSDQGS FRSSLSDQG GLSGQASSDTIKFSE LSGQASSDT LSGQASSDTIKFSEF LSGQASSDT ISSCGNFRSSLSDQG CGNFRSSLS CGNFRSSLSDQGSLS FRSSLSDQG SCGNFRSSLSDQGSL FRSSLSDQG GNFRSSLSDQGSLSD FRSSLSDQG AVFVLISSCGNFRSS VFVLISSCG DGVETGLNVIGTING VETGLNVIG ETGLNVIGTINGQLR LNVIGTING TGLNVIGTINGQLRG LNVIGTING VFVLISSCGNFRSSL VFVLISSCG GVETGLNVIGTINGQ LNVIGTING VETGLNVIGTINGQL LNVIGTING LNVIGTINGQLRGHS IGTINGQLR NVIGTINGQLRGHSA IGTINGQLR GSLSDQGGLSGQASS LSDQGGLSG QGSLSDQGGLSGQAS LSDQGGLSG QDGVETGLNVIGTIN VETGLNVIG GLNVIGTINGQLRGH IGTINGQLR EQDGVETGLNVIGTI VETGLNVIG KEQDGVETGLNVIGT VETGLNVIG NFRSSLSDQGSLSDQ FRSSLSDQG FVLISSCGNFRSSLS FVLISSCGN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	AEVNNFVKAMTNVGS FVKAMTNVG VNNFVKAMTNVGSFK FVKAMTNVG NNFVKAMTNVGSFKT FVKAMTNVG EVNNFVKAMTNVGSF FVKAMTNVG EAEVNNFVKAMTNVG VNNFVKAMT NFVKAMTNVGSFKTS FVKAMTNVG FVKAMTNVGSFKTSL FVKAMTNVG IKNKKDNNGDWSNLG IKNKKDNNG KNKKDNNGDWSNLGT NNGDWSNLG NKKDNNGDWSNLGTL NNGDWSNLG KKDNNGDWSNLGTLV NNGDWSNLG KDNNGDWSNLGTLVI NNGDWSNLG
	HLA-DRB1*0404	AEVNNFVKAMTNVGS FVKAMTNVG NNFVKAMTNVGSFKT FVKAMTNVG VNNFVKAMTNVGSFK FVKAMTNVG EVNNFVKAMTNVGSF FVKAMTNVG EAEVNNFVKAMTNVG VNNFVKAMT CAVFVLISSCGNFRS VFVLISSCG ICAVFVLISSCGNFR VFVLISSCG NFVKAMTNVGSFKTS FVKAMTNVG

	HLA-DRB1*0405	AEVNNFVKAMTNVGS FVKAMTNVG VNNFVKAMTNVGSFK VKAMTNVGS NNFVKAMTNVGSFKT VKAMTNVGS EVNNFVKAMTNVGSF VKAMTNVGS NFVKAMTNVGSFKTS VKAMTNVGS KDNNGDWSNLGTLVI NNGDWSNLG IKFSEFTVNIKNKKD FSEFTVNIK VKAMTNVGSFKTSLY VKAMTNVGS DNNGDWSNLGTLVIR WSNLGTLVI NNGDWSNLGTLVIRK WSNLGTLVI
	HLA-DRB1*0701	KDNNGDWSNLGTLVI DWSNLGTLV DNNGDWSNLGTLVIR WSNLGTLVI NNGDWSNLGTLVIRK WSNLGTLVI NGDWSNLGTLVIRKE WSNLGTLVI GDWSNLGTLVIRKEQ WSNLGTLVI KKMKMFIICAVFVLI FIICAVFVL KMKMFIICAVFVLIS FIICAVFVL MKMFIICAVFVLISS FIICAVFVL NKKMKMFIICAVFVL MFIICAVFV KMFIICAVFVLISSC FIICAVFVL MFIICAVFVLISSCG FIICAVFVL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	NNFVKAMTNVGSFKT FVKAMTNVG AEVNNFVKAMTNVGS FVKAMTNVG EVNNFVKAMTNVGSF FVKAMTNVG VNNFVKAMTNVGSFK FVKAMTNVG EAEVNNFVKAMTNVG VNNFVKAMT NFVKAMTNVGSFKTS FVKAMTNVG FVKAMTNVGSFKTSL FVKAMTNVG
	HLA-DRB1*1101	NNFVKAMTNVGSFKT VKAMTNVGS NFVKAMTNVGSFKTS MTNVGSFKT
	HLA-DRB1*1302	AEVNNFVKAMTNVGS VNNFVKAMT EAEVNNFVKAMTNVG VNNFVKAMT VKAMTNVGSFKTSLY MTNVGSFKT ETGLNVIGTINGQLR LNVIGTING TGLNVIGTINGQLRG LNVIGTING KAMTNVGSFKTSLYY VGSFKTSLY SEFTVNIKNKKDNNG FTVNIKNKK EVNNFVKAMTNVGSF FVKAMTNVG VNNFVKAMTNVGSFK FVKAMTNVG NGDWSNLGTLVIRKE WSNLGTLVI NNFVKAMTNVGSFKT FVKAMTNVG KFSEFTVNIKNKKDN FTVNIKNKK FSEFTVNIKNKKDNN FTVNIKNKK GDWSNLGTLVIRKEQ WSNLGTLVI MTNVGSFKTSLYYGY VGSFKTSLY DNNGDWSNLGTLVIR WSNLGTLVI NNGDWSNLGTLVIRK WSNLGTLVI LNVIGTINGQLRGHS IGTINGQLR AMTNVGSFKTSLYYG VGSFKTSLY GLNVIGTINGQLRGH IGTINGQLR NFVKAMTNVGSFKTS MTNVGSFKT

		KDNNGDWSNLGTLVI DWSNLGTLV FTVNIKNKKDNNGDW FTVNIKNKK EFTVNIKNKKDNNGD FTVNIKNKK TIKFSEFTVNIKNKK EFTVNIKNK IKFSEFTVNIKNKKD FTVNIKNKK FVKAMTNVGSFKTSL MTNVGSFKT EEAEVNNFVKAMTNV VNNFVKAMT DWSNLGTLVIRKEQD WSNLGTLVI VETGLNVIGTINGQL LNVIGTING DGVETGLNVIGTING TGLNVIGTI CIEEAEVNNFVKAMT EVNNFVKAM GVETGLNVIGTINGQ LNVIGTING IEEAEVNNFVKAMTN VNNFVKAMT WSNLGTLVIRKEQDG WSNLGTLVI NVIGTINGQLRGHSA IGTINGQLR TNVGSFKTSLYYGYK VGSFKTSLY VIGTINGQLRGHSAT IGTINGQLR IGTINGQLRGHSATF IGTINGQLR NVGSFKTSLYYGYKE VGSFKTSLY VGSFKTSLYYGYKEE VGSFKTSLY TVNIKNKKDNNGDWS IKNKKDNNG VNIKNKKDNNGDWSN IKNKKDNNG TTKIETINNSEHITF TINNSEHIT TKIETINNSEHITFS TINNSEHIT CAVFVLISSCGNFRS VFVLISSCG
	HLA-DRB1*1501	ICAVFVLISSCGNFR VFVLISSCG CAVFVLISSCGNFRS VFVLISSCG MFIICAVFVLISSCG CAVFVLISS IICAVFVLISSCGNF VFVLISSCG FIICAVFVLISSCGN VFVLISSCG AVFVLISSCGNFRSS VFVLISSCG SSTNGIKGKEITTKI IKGKEITTK STNGIKGKEITTKIE IKGKEITTK NGIKGKEITTKIETI IKGKEITTK QSSTNGIKGKEITTK STNGIKGKE TNGIKGKEITTKIET IKGKEITTK VFVLISSCGNFRSSL VFVLISSCG EVNNFVKAMTNVGSF VKAMTNVGS VNNFVKAMTNVGSFK VKAMTNVGS NNFVKAMTNVGSFKT VKAMTNVGS AEVNNFVKAMTNVGS FVKAMTNVG NKKMKMFIICAVFVL MKMFIICAV NFVKAMTNVGSFKTS VKAMTNVGS KKMKMFIICAVFVLI MKMFIICAV MNKKMKMFIICAVFV MKMFIICAV
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	TSLYYGYKEEQSSTN YGYKEEQSS SLYYGYKEEQSSTNG YKEEQSSTN YGYKEEQSSTNGIKG YKEEQSSTN YYGYKEEQSSTNGIK YKEEQSSTN LYYGYKEEQSSTNGI YKEEQSSTN

CAA57806.1| Outer surface protein G [Borrelia burgdorferi] Seq13	HLA-DRB1*0101	PNNSLFNPPPVLPAS LFNPPPVLP NNSLFNPPPVLPASS LFNPPPVLP NSLFNPPPVLPASSH LFNPPPVLP DPNNSLFNPPPVLPA LFNPPPVLP SLFNPPPVLPASSHD FNPPPVLPA DDPNNSLFNPPPVLP DDPNNSLFN LFNPPPVLPASSHDN LFNPPPVLP DNTPVLKAVQAKDGG LKAVQAKDG TPVLKAVQAKDGGQQ LKAVQAKDG HDNTPVLKAVQAKDG TPVLKAVQA NTPVLKAVQAKDGGQ LKAVQAKDG PVLKAVQAKDGGQQE LKAVQAKDG FNPPPVLPASSHDNT FNPPPVLPA NKKMKNLIICAVFVL MKNLIICAV MNKKMKNLIICAVFV MKNLIICAV KKMKNLIICAVFVLI MKNLIICAV YAKELGVNGSYSVND LGVNGSYSV AKELGVNGSYSVNDG LGVNGSYSV LKYAKELGVNGSYSV YAKELGVNG KELGVNGSYSVNDGT LGVNGSYSV KYAKELGVNGSYSVN LGVNGSYSV KMKNLIICAVFVLII MKNLIICAV MKNLIICAVFVLIIS MKNLIICAV VKKQGNIGQKALKYA KQGNIGQKA VLKAVQAKDGGQQEG LKAVQAKDG LKAVQAKDGGQQEGK LKAVQAKDG PPPVLPASSHDNTPV VLPASSHDN NPPPVLPASSHDNTP VLPASSHDN KQGNIGQKALKYAKE IGQKALKYA KKQGNIGQKALKYAK IGQKALKYA QGNIGQKALKYAKEL IGQKALKYA PPVLPASSHDNTPVL VLPASSHDN GNIGQKALKYAKELG IGQKALKYA LGVNGSYSVNDGTNT LGVNGSYSV ELGVNGSYSVNDGTN LGVNGSYSV KEQVESATGESTEKV VESATGEST EQVESATGESTEKVK VESATGEST QKALKYAKELGVNGS YAKELGVNG KALKYAKELGVNGSY YAKELGVNG FLDKELMQGDDPNNS FLDKELMQG LIICAVFVLIISCKI ICAVFVLII ALKYAKELGVNGSYS YAKELGVNG NIGQKALKYAKELGV IGQKALKYA KELMQGDDPNNSLFN MQGDDPNNS IGQKALKYAKELGVN IGQKALKYA QEFKEQVESATGEST FKEQVESAT LDKELMQGDDPNNSL MQGDDPNNS DKELMQGDDPNNSLF MQGDDPNNS FKEQVESATGESTEK VESATGEST ELMQGDDPNNSLFNP MQGDDPNNS
	HLA-DRB1*0301	None
	HLA-DRB1*0401	FLDKELMQGDDPNNS FLDKELMQG LDKELMQGDDPNNSL MQGDDPNNS KELMQGDDPNNSLFN MQGDDPNNS DKELMQGDDPNNSLF MQGDDPNNS ELMQGDDPNNSLFNP MQGDDPNNS

	HLA-DRB1*0404	None
	HLA-DRB1*0405	DPNNSLFNPPPVLPA NNSLFNPPP PNNSLFNPPPVLPAS FNPPPVLPA
	HLA-DRB1*0701	KMKNLIICAVFVLII LIICAVFVL MKNLIICAVFVLIIS LIICAVFVL KNLIICAVFVLIISC LIICAVFVL KKMKNLIICAVFVLI LIICAVFVL NKKMKNLIICAVFVL MKNLIICAV
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	MNKKMKNLIICAVFV MNKKMKNLI KKMKNLIICAVFVLI MKNLIICAV NKKMKNLIICAVFVL MKNLIICAV AKELGVNGSYSVNDG LGVNGSYSV LKYAKELGVNGSYSV AKELGVNGS YAKELGVNGSYSVND LGVNGSYSV KYAKELGVNGSYSVN LGVNGSYSV KELGVNGSYSVNDGT LGVNGSYSV MKNLIICAVFVLIIS MKNLIICAV LGVNGSYSVNDGTNT LGVNGSYSV KMKNLIICAVFVLII MKNLIICAV LIICAVFVLIISCKI VFVLIISCK ICAVFVLIISCKIDA VFVLIISCK CAVFVLIISCKIDAS VFVLIISCK IICAVFVLIISCKID VFVLIISCK
	HLA-DRB1*1501	CAVFVLIISCKIDAS VFVLIISCK IICAVFVLIISCKID VFVLIISCK ICAVFVLIISCKIDA VFVLIISCK LIICAVFVLIISCKI VFVLIISCK NLIICAVFVLIISCK CAVFVLIIS KKMKNLIICAVFVLI MKNLIICAV NKKMKNLIICAVFVL MKNLIICAV MNKKMKNLIICAVFV MKNLIICAV
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	None
AAC44770.1| FlaA protein (Borrelia burgdorferi) Seq14	HLA-DRB1*0101	LFPSYSQSSAMIMPP YSQSSAMIM NWSVLLTPSARLQAY LLTPSARLQ WSVLLTPSARLQAYV LLTPSARLQ SNPNYIPNISSRIIK IPNISSRII NPNYIPNISSRIIKD IPNISSRII PNYIPNISSRIIKDD IPNISSRII WSNPNYIPNISSRII YIPNISSRI FPSYSQSSAMIMPPF YSQSSAMIM GINNWSVLLTPSARL WSVLLTPSA PSYSQSSAMIMPPFK YSQSSAMIM TESLRKLKAHETFKR LRKLKAHET AYVKNSVVAPAVVKS VKNSVVAPA ILGVRVLFPSYSQSS VRVLFPSYS LGVRVLFPSYSQSSA LFPSYSQSS

		ESLRKLKAHETFKRV	LRKLKAHET
		AKSILFFLLSTVLFA	FFLLSTVLF
		KSILFFLLSTVLFAQ	FFLLSTVLF
		SILFFLLSTVLFAQE	FFLLSTVLF
		EDMNGMEYAYSMGTL	MEYAYSMGT
		YVKNSVVAPAVVKSE	VVAPAVVKS
		VKNSVVAPAVVKSES	VVAPAVVKS
		KNSVVAPAVVKSESK	VVAPAVVKS
		NSVVAPAVVKSESKR	VVAPAVVKS
		FEDMNGMEYAYSMGT	MNGMEYAYS
		GTESLRKLKAHETFK	LRKLKAHET
		DLGINNWSVLLTPSA	INNWSVLLT
		MRFKAFRVSKSHSSK	FRVSKSHSS
		TSGTESLRKLKAHET	TESLRKLKA
		SGTESLRKLKAHETF	LRKLKAHET
		LGINNWSVLLTPSAR	INNWSVLLT
		NYIPNISSRIIKDDV	IPNISSRII
		KMRFKAFRVSKSHSS	FKAFRVSKS
		KAKSILFFLLSTVLF	LFFLLSTVL
		KDDVPNYPLASSKMR	NYPLASSKM
		DDVPNYPLASSKMRF	YPLASSKMR
		SVLLTPSARLQAYVK	LLTPSARLQ
		VRVLFPSYSQSSAMI	LFPSYSQSS
		GVRVLFPSYSQSSAM	LFPSYSQSS
		MNGMEYAYSMGTLKF	MEYAYSMGT
		FKAFRVSKSHSSKVK	FRVSKSHSS
		ILFFLLSTVLFAQET	FFLLSTVLF
		VPNYPLASSKMRFKA	YPLASSKMR
		RFKAFRVSKSHSSKV	FRVSKSHSS
		DVPNYPLASSKMRFK	YPLASSKMR
		YSQSSAMIMPPFKIP	YSQSSAMIM
		DMNGMEYAYSMGTLK	MEYAYSMGT
		KAFRVSKSHSSKVKN	FRVSKSHSS
		NGMEYAYSMGTLKFK	MEYAYSMGT
		SYSQSSAMIMPPFKI	YSQSSAMIM
		GDTILGVRVLFPSYS	ILGVRVLFP
		DTILGVRVLFPSYSQ	VRVLFPSYS
		PNYPLASSKMRFKAF	YPLASSKMR
		TILGVRVLFPSYSQS	VRVLFPSYS
		VDLGINNWSVLLTPS	INNWSVLLT
		MVVDLGINNWSVLLT	VVDLGINNW
		YIPNISSRIIKDDVP	IPNISSRII
		VVDLGINNWSVLLTP	INNWSVLLT
		LFFLLSTVLFAQETD	FFLLSTVLF
		NYVDYVYSGASGIVK	VYSGASGIV
		VLLTPSARLQAYVKN	LLTPSARLQ
		QAYVKNSVVAPAVVK	VKNSVVAPA
		SLRKLKAHETFKRVL	LRKLKAHET
		LRKLKAHETFKRVLK	LRKLKAHET
		IWSNPNYIPNISSRI	IWSNPNYIP
		YVDYVYSGASGIVKP	VYSGASGIV
		VDYVYSGASGIVKPE	VYSGASGIV
		VVAPAVVKSESKRYA	VVAPAVVKS
		LQAYVKNSVVAPAVV	VKNSVVAPA
		RLQAYVKNSVVAPAV	VKNSVVAPA
		SVVAPAVVKSESKRY	VVAPAVVKS
		RKAKSILFFLLSTVL	RKAKSILFF

		ARLQAYVKNSVVAPA	YVKNSVVAP
		SVFKVYETSGTESLR	YETSGTESL
		ESVFKVYETSGTESL	FKVYETSGT
		SSKMRFKAFRVSKSH	FKAFRVSKS
		SKMRFKAFRVSKSHS	FKAFRVSKS
		ASSKMRFKAFRVSKS	MRFKAFRVS
		TNYVDYVYSGASGIV	YVYSGASGI
		IKDDVPNYPLASSKM	VPNYPLASS
		GMEYAYSMGTLKFKG	MEYAYSMGT
		MEYAYSMGTLKFKGW	MEYAYSMGT
		LFEDMNGMEYAYSMG	MNGMEYAYS
		DYVYSGASGIVKPED	VYSGASGIV
		VLFEDMNGMEYAYSM	MNGMEYAYS
		KDLRVLYDKLSVSID	LYDKLSVSI
		VKDLRVLYDKLSVSI	LRVLYDKLS
		FFLLSTVLFAQETDG	FFLLSTVLF
		EVLFEDMNGMEYAYS	FEDMNGMEY
		FKVYETSGTESLRKL	YETSGTESL
		AFRVSKSHSSKVKNF	FRVSKSHSS
		VFKVYETSGTESLRK	YETSGTESL
		NYPLASSKMRFKAFR	YPLASSKMR
		FRVSKSHSSKVKNFI	FRVSKSHSS
		IFYVKDLRVLYDKLS	VKDLRVLYD
		LRVLYDKLSVSIDSD	LYDKLSVSI
		DLRVLYDKLSVSIDS	LYDKLSVSI
		SKRYAGDTILGVRVL	YAGDTILGV
		FAELARDPSSTRLDL	ARDPSSTRL
		LDFAELARDPSSTRL	LARDPSSTR
		FYVKDLRVLYDKLSV	LRVLYDKLS
		DFAELARDPSSTRLD	ARDPSSTRL
		AELARDPSSTRLDLT	ARDPSSTRL
		LLTPSARLQAYVKNS	LLTPSARLQ
		ESKRYAGDTILGVRV	YAGDTILGV
		RIIKDDVPNYPLASS	IKDDVPNYP
		QSSAMIMPPFKIPFY	MIMPPFKIP
		IPNISSRIIKDDVPN	IPNISSRII
		SQSSAMIMPPFKIPF	MIMPPFKIP
		SSAMIMPPFKIPFYS	MIMPPFKIP
		YVYSGASGIVKPEDM	VYSGASGIV
		IIKDDVPNYPLASSK	VPNYPLASS
		KRYAGDTILGVRVLF	YAGDTILGV
		GLIDNIKTMKEIKVS	IKTMKEIKV
		KVYETSGTESLRKLK	YETSGTESL
		RVLYDKLSVSIDSDI	LYDKLSVSI
		KGLIDNIKTMKEIKV	IDNIKTMKE
		IDNIKTMKEIKVSVY	IKTMKEIKV
		SESVFKVYETSGTES	FKVYETSGT
		ADLIWSNPNYIPNIS	LIWSNPNYI
		SARLQAYVKNSVVAP	AYVKNSVVA
		NFIFYVKDLRVLYDK	FYVKDLRVL
		IDSESVFKVYETSGT	IDSESVFKV
		SESKRYAGDTILGVR	YAGDTILGV
		KNFIFYVKDLRVLYD	FYVKDLRVL
		KSESKRYAGDTILGV	RYAGDTILG
		DSESVFKVYETSGTE	FKVYETSGT
		KGWADLIWSNPNYIP	LIWSNPNYI
		GWADLIWSNPNYIPN	LIWSNPNYI

		LIDNIKTMKEIKVSV IKTMKEIKV RYAGDTILGVRVLFP YAGDTILGV WADLIWSNPNYIPNI LIWSNPNYI DNIKTMKEIKVSVYS IKTMKEIKV YAGDTILGVRVLFPS ILGVRVLFP FIFYVKDLRVLYDKL FYVKDLRVL ELARDPSSTRLDLTN ARDPSSTRL YVKDLRVLYDKLSVS LRVLYDKLS APAVVKSESKRYAGD VVKSESKRY VAPAVVKSESKRYAG VVKSESKRY PAVVKSESKRYAGDT VVKSESKRY LASSKMRFKAFRVSK MRFKAFRVS FKGWADLIWSNPNYI FKGWADLIW EYAYSMGTLKFKGWA AYSMGTLKF SAMIMPPFKIPFYSG MIMPPFKIP PLASSKMRFKAFRVS KMRFKAFRV YPLASSKMRFKAFRV YPLASSKMR LLSTVLFAQETDGLA STVLFAQET FLLSTVLFAQETDGL STVLFAQET LTNYVDYVYSGASGI VDYVYSGAS VKNFIFYVKDLRVLY FYVKDLRVL KVKNFIFYVKDLRVL IFYVKDLRV VYSGASGIVKPEDMV VYSGASGIV DLIWSNPNYIPNISS LIWSNPNYI AGDTILGVRVLFPSY ILGVRVLFP VLDFAELARDPSSTR FAELARDPS
	HLA-DRB1*0301	VKNFIFYVKDLRVLY FIFYVKDLR KNFIFYVKDLRVLYD YVKDLRVLY NFIFYVKDLRVLYDK YVKDLRVLY IFYVKDLRVLYDKLS YVKDLRVLY
	HLA-DRB1*0401	KNFIFYVKDLRVLYD YVKDLRVLY NFIFYVKDLRVLYDK YVKDLRVLY VKNFIFYVKDLRVLY FIFYVKDLR FIFYVKDLRVLYDKL YVKDLRVLY IFYVKDLRVLYDKLS YVKDLRVLY ILFFLLSTVLFAQET FFLLSTVLF KSILFFLLSTVLFAQ FFLLSTVLF SILFFLLSTVLFAQE FFLLSTVLF AKSILFFLLSTVLFA FFLLSTVLF KAKSILFFLLSTVLF LFFLLSTVL VLDFAELARDPSSTR FAELARDPS LFFLLSTVLFAQETD FLLSTVLFA LDFAELARDPSSTRL LARDPSSTR ARLQAYVKNSVVAPA YVKNSVVAP KMRFKAFRVSKSHSS FKAFRVSKS RLQAYVKNSVVAPAV VKNSVVAPA MRFKAFRVSKSHSSK FRVSKSHSS DFAELARDPSSTRLD LARDPSSTR LQAYVKNSVVAPAVV VKNSVVAPA FYVKDLRVLYDKLSV YVKDLRVLY FAELARDPSSTRLDL LARDPSSTR YVKDLRVLYDKLSVS YVKDLRVLY QAYVKNSVVAPAVVK VKNSVVAPA AELARDPSSTRLDLT LARDPSSTR INNWSVLLTPSARLQ WSVLLTPSA GINNWSVLLTPSARL WSVLLTPSA

		NNWSVLLTPSARLQA WSVLLTPSA AYVKNSVVAPAVVKS VKNSVVAPA DLGINNWSVLLTPSA GINNWSVLL FFLLSTVLFAQETDG FFLLSTVLF LGINNWSVLLTPSAR WSVLLTPSA FKAFRVSKSHSSKVK FRVSKSHSS RFKAFRVSKSHSSKV FRVSKSHSS LGVRVLFPSYSQSSA LFPSYSQSS ILGVRVLFPSYSQSS VRVLFPSYS GVRVLFPSYSQSSAM LFPSYSQSS NGMEYAYSMGTLKFK MEYAYSMGT MNGMEYAYSMGTLKF MEYAYSMGT
	HLA-DRB1*0404	INNWSVLLTPSARLQ VLLTPSARL NNWSVLLTPSARLQA VLLTPSARL GINNWSVLLTPSARL WSVLLTPSA NWSVLLTPSARLQAY VLLTPSARL WSVLLTPSARLQAYV VLLTPSARL KGWADLIWSNPNYIP WADLIWSNP FKGWADLIWSNPNYI WADLIWSNP ILGVRVLFPSYSQSS ILGVRVLFP KSILFFLLSTVLFAQ FLLSTVLFA LGINNWSVLLTPSAR WSVLLTPSA DLGINNWSVLLTPSA GINNWSVLL AKSILFFLLSTVLFA ILFFLLSTV GWADLIWSNPNYIPN LIWSNPNYI WADLIWSNPNYIPNI LIWSNPNYI ILFFLLSTVLFAQET FLLSTVLFA SILFFLLSTVLFAQE FLLSTVLFA DTILGVRVLFPSYSQ ILGVRVLFP GDTILGVRVLFPSYS ILGVRVLFP AGDTILGVRVLFPSY ILGVRVLFP RYAGDTILGVRVLFP YAGDTILGV YAGDTILGVRVLFPS ILGVRVLFP LFFLLSTVLFAQETD FLLSTVLFA SVLLTPSARLQAYVK VLLTPSARL
	HLA-DRB1*0405	IFYVKDLRVLYDKLS VKDLRVLYD FYVKDLRVLYDKLSV VKDLRVLYD KNFIFYVKDLRVLYD YVKDLRVLY NFIFYVKDLRVLYDK VKDLRVLYD FIFYVKDLRVLYDKL VKDLRVLYD FKGWADLIWSNPNYI ADLIWSNPN GWADLIWSNPNYIPN LIWSNPNYI DLGINNWSVLLTPSA INNWSVLLT KGWADLIWSNPNYIP ADLIWSNPN LGINNWSVLLTPSAR INNWSVLLT DLIWSNPNYIPNISS LIWSNPNYI KMRFKAFRVSKSHSS FKAFRVSKS VVDLGINNWSVLLTP INNWSVLLT VDLGINNWSVLLTPS INNWSVLLT MRFKAFRVSKSHSSK FKAFRVSKS MVVDLGINNWSVLLT GINNWSVLL ASSKMRFKAFRVSKS SKMRFKAFR SSKMRFKAFRVSKSH FKAFRVSKS SKMRFKAFRVSKSHS FKAFRVSKS WADLIWSNPNYIPNI LIWSNPNYI

		LIWSNPNYIPNISSR PNYIPNISS GINNWSVLLTPSARL INNWSVLLT ADLIWSNPNYIPNIS LIWSNPNYI INNWSVLLTPSARLQ INNWSVLLT LKFKGWADLIWSNPN FKGWADLIW YVKDLRVLYDKLSVS VKDLRVLYD VLDFAELARDPSSTR FAELARDPS VKDLRVLYDKLSVSI VKDLRVLYD LDFAELARDPSSTRL LARDPSSTR KFKGWADLIWSNPNY ADLIWSNPN DFAELARDPSSTRLD LARDPSSTR DTILGVRVLFPSYSQ VRVLFPSYS FAELARDPSSTRLDL LARDPSSTR ILGVRVLFPSYSQSS RVLFPSYSQ TILGVRVLFPSYSQS RVLFPSYSQ AELARDPSSTRLDLT LARDPSSTR LGVRVLFPSYSQSSA RVLFPSYSQ
	HLA-DRB1*0701	WSNPNYIPNISSRII YIPNISSRI SNPNYIPNISSRIIK IPNISSRII NPNYIPNISSRIIKD IPNISSRII PNYIPNISSRIIKDD IPNISSRII NYIPNISSRIIKDDV IPNISSRII YIPNISSRIIKDDVP IPNISSRII NWSVLLTPSARLQAY VLLTPSARL GINNWSVLLTPSARL SVLLTPSAR WSVLLTPSARLQAYV VLLTPSARL INNWSVLLTPSARLQ VLLTPSARL NNWSVLLTPSARLQA VLLTPSARL IWSNPNYIPNISSRI WSNPNYIPN RFKAFRVSKSHSSKV FRVSKSHSS FKAFRVSKSHSSKVK VSKSHSSKV KAFRVSKSHSSKVKN VSKSHSSKV IKTMKEIKVSVYSLG MKEIKVSVY KTMKEIKVSVYSLGY MKEIKVSVY NIKTMKEIKVSVYSL MKEIKVSVY KSILFFLLSTVLFAQ LFFLLSTVL SILFFLLSTVLFAQE LFFLLSTVL AKSILFFLLSTVLFA LFFLLSTVL AFRVSKSHSSKVKNF VSKSHSSKV FRVSKSHSSKVKNFI VSKSHSSKV IDNIKTMKEIKVSVY TMKEIKVSV DNIKTMKEIKVSVYS MKEIKVSVY MVVDLGINNWSVLLT LGINNWSVL KMRFKAFRVSKSHSS FKAFRVSKS VVDLGINNWSVLLTP INNWSVLLT SVLLTPSARLQAYVK VLLTPSARL VLLTPSARLQAYVKN VLLTPSARL KAKSILFFLLSTVLF LFFLLSTVL MRFKAFRVSKSHSSK FRVSKSHSS VDLGINNWSVLLTPS LGINNWSVL RVLFPSYSQSSAMIM LFPSYSQSS VVAPAVVKSESKRYA VVKSESKRY VAPAVVKSESKRYAG VVKSESKRY IPNISSRIIKDDVPN IPNISSRII APAVVKSESKRYAGD VVKSESKRY DMVVDLGINNWSVLL LGINNWSVL

		SVVAPAVVKSESKRY SVVAPAVVK RKAKSILFFLLSTVL AKSILFFLL PAVVKSESKRYAGDT VVKSESKRY VLFPSYSQSSAMIMP YSQSSAMIM ILFFLLSTVLFAQET LFFLLSTVL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	NNFVKAMTNVGSFKT FVKAMTNVG AEVNNFVKAMTNVGS FVKAMTNVG EVNNFVKAMTNVGSF FVKAMTNVG VNNFVKAMTNVGSFK FVKAMTNVG EAEVNNFVKAMTNVG VNNFVKAMT NFVKAMTNVGSFKTS FVKAMTNVG FVKAMTNVGSFKTSL FVKAMTNVG
	HLA-DRB1*1101	ASSKMRFKAFRVSKS MRFKAFRVS LASSKMRFKAFRVSK MRFKAFRVS SSKMRFKAFRVSKSH MRFKAFRVS SKMRFKAFRVSKSHS MRFKAFRVS PLASSKMRFKAFRVS ASSKMRFKA
	HLA-DRB1*1302	MVVDLGINNWSVLLT LGINNWSVL VVDLGINNWSVLLTP INNWSVLLT VDLGINNWSVLLTPS INNWSVLLT DLGINNWSVLLTPSA INNWSVLLT LGINNWSVLLTPSAR INNWSVLLT DMVVDLGINNWSVLL LGINNWSVL EDMVVDLGINNWSVL VVDLGINNW GINNWSVLLTPSARL INNWSVLLT INNWSVLLTPSARLQ INNWSVLLT SNPNYIPNISSRIIK IPNISSRII NPNYIPNISSRIIKD IPNISSRII AKSILFFLLSTVLFA FFLLSTVLF KSILFFLLSTVLFAQ FFLLSTVLF SILFFLLSTVLFAQE FFLLSTVLF KAKSILFFLLSTVLF ILFFLLSTV WSNPNYIPNISSRII YIPNISSRI ILFFLLSTVLFAQET FFLLSTVLF PNYIPNISSRIIKDD IPNISSRII VKNFIFYVKDLRVLY VKNFIFYVK SKVKNFIFYVKDLRV VKNFIFYVK NYIPNISSRIIKDDV IPNISSRII SSKVKNFIFYVKDLR VKNFIFYVK KSHSSKVKNFIFYVK SKVKNFIFY ARLQAYVKNSVVAPA YVKNSVVAP IWSNPNYIPNISSRI NPNYIPNIS HSSKVKNFIFYVKDL VKNFIFYVK SHSSKVKNFIFYVKD VKNFIFYVK LQAYVKNSVVAPAVV VKNSVVAPA RLQAYVKNSVVAPAV VKNSVVAPA QAYVKNSVVAPAVVK VKNSVVAPA GDTILGVRVLFPSYS LGVRVLFPS YIPNISSRIIKDDVP IPNISSRII IKTMKEIKVSVYSLG MKEIKVSVY ADLIWSNPNYIPNIS LIWSNPNYI DTILGVRVLFPSYSQ LGVRVLFPS

		LFFLLSTVLFAQETD FFLLSTVLF AYVKNSVVAPAVVKS VKNSVVAPA KGLIDNIKTMKEIKV LIDNIKTMK TILGVRVLFPSYSQS LGVRVLFPS YAGDTILGVRVLFPS TILGVRVLF AGDTILGVRVLFPSY LGVRVLFPS FFLLSTVLFAQETDG FFLLSTVLF LGKGLIDNIKTMKEI LIDNIKTMK KTMKEIKVSVYSLGY IKVSVYSLG KVKNFIFYVKDLRVL VKNFIFYVK DLIWSNPNYIPNISS NPNYIPNIS FLGKGLIDNIKTMKE LIDNIKTMK GKGLIDNIKTMKEIK LIDNIKTMK TMKEIKVSVYSLGYE IKVSVYSLG MKEIKVSVYSLGYEI IKVSVYSLG LIWSNPNYIPNISSR NPNYIPNIS QFLGKGLIDNIKTMK KGLIDNIKT KNFIFYVKDLRVLYD YVKDLRVLY WADLIWSNPNYIPNI LIWSNPNYI SARLQAYVKNSVVAP LQAYVKNSV KEIKVSVYSLGYEID IKVSVYSLG GWADLIWSNPNYIPN LIWSNPNYI GLIDNIKTMKEIKVS LIDNIKTMK YVKNSVVAPAVVKSE VKNSVVAPA KGWADLIWSNPNYIP LIWSNPNYI LGVRVLFPSYSQSSA LGVRVLFPS NFIFYVKDLRVLYDK YVKDLRVLY IFYVKDLRVLYDKLS YVKDLRVLY ILGVRVLFPSYSQSS LGVRVLFPS LIDNIKTMKEIKVSV LIDNIKTMK FIFYVKDLRVLYDKL YVKDLRVLY SSTRLDLTNYVDYVY TRLDLTNYV STRLDLTNYVDYVYS LTNYVDYVY
	HLA-DRB1*1501	KSILFFLLSTVLFAQ ILFFLLSTV AKSILFFLLSTVLFA ILFFLLSTV SKVKNFIFYVKDLRV VKNFIFYVK RKAKSILFFLLSTVL ILFFLLSTV KAKSILFFLLSTVLF ILFFLLSTV SSKVKNFIFYVKDLR VKNFIFYVK KVKNFIFYVKDLRVL VKNFIFYVK KSHSSKVKNFIFYVK KVKNFIFYV SHSSKVKNFIFYVKD VKNFIFYVK HSSKVKNFIFYVKDL VKNFIFYVK VKNFIFYVKDLRVLY VKNFIFYVK ASSKMRFKAFRVSKS MRFKAFRVS SSKMRFKAFRVSKSH MRFKAFRVS SILFFLLSTVLFAQE LFFLLSTVL KRKAKSILFFLLSTV SILFFLLST SKMRFKAFRVSKSHS MRFKAFRVS LASSKMRFKAFRVSK MRFKAFRVS PLASSKMRFKAFRVS KMRFKAFRV KMRFKAFRVSKSHSS MRFKAFRVS ILGVRVLFPSYSQSS VRVLFPSYS DTILGVRVLFPSYSQ VRVLFPSYS ILFFLLSTVLFAQET ILFFLLSTV TILGVRVLFPSYSQS VRVLFPSYS

		MRFKAFRVSKSHSSK FRVSKSHSS LGVRVLFPSYSQSSA VRVLFPSYS GDTILGVRVLFPSYS LGVRVLFPS VKDLRVLYDKLSVSI VLYDKLSVS KNFIFYVKDLRVLYD FIFYVKDLR YVKDLRVLYDKLSVS LRVLYDKLS KDLRVLYDKLSVSID VLYDKLSVS VLDFAELARDPSSTR VLDFAELAR DLRVLYDKLSVSIDS VLYDKLSVS LDFAELARDPSSTRL LARDPSSTR TFKRVLKLREKISIA KRVLKLREK GVRVLFPSYSQSSAM VRVLFPSYS NFIFYVKDLRVLYDK FYVKDLRVL ETFKRVLKLREKISI KRVLKLREK RFKAFRVSKSHSSKV FRVSKSHSS LRVLYDKLSVSIDSD VLYDKLSVS LGINNWSVLLTPSAR INNWSVLLT AELARDPSSTRLDLT LARDPSSTR DFAELARDPSSTRLD LARDPSSTR GINNWSVLLTPSARL SVLLTPSAR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	ADLIWSNPNYIPNIS LIWSNPNYI KGWADLIWSNPNYIP LIWSNPNYI WADLIWSNPNYIPNI LIWSNPNYI GWADLIWSNPNYIPN LIWSNPNYI FKGWADLIWSNPNYI FKGWADLIW DLIWSNPNYIPNISS LIWSNPNYI LIWSNPNYIPNISSR LIWSNPNYI TILGVRVLFPSYSQS VRVLFPSYS DTILGVRVLFPSYSQ VRVLFPSYS GDTILGVRVLFPSYS LGVRVLFPS ILGVRVLFPSYSQSS VRVLFPSYS RIIKDDVPNYPLASS IKDDVPNYP LGVRVLFPSYSQSSA VRVLFPSYS PLASSKMRFKAFRVS LASSKMRFK LASSKMRFKAFRVSK MRFKAFRVS ASSKMRFKAFRVSKS MRFKAFRVS SSKMRFKAFRVSKSH MRFKAFRVS SKMRFKAFRVSKSHS MRFKAFRVS ISSRIIKDDVPNYPL IKDDVPNYP NISSRIIKDDVPNYP SRIIKDDVP SSRIIKDDVPNYPLA IKDDVPNYP SRIIKDDVPNYPLAS IKDDVPNYP IIKDDVPNYPLASSK IKDDVPNYP IKDDVPNYPLASSKM IKDDVPNYP
	HLA-DRB5*0101	DVPNYPLASSKMRFK YPLASSKMR VPNYPLASSKMRFKA YPLASSKMR PNYPLASSKMRFKAF YPLASSKMR KDDVPNYPLASSKMR NYPLASSKM DDVPNYPLASSKMRF YPLASSKMR ESLRKLKAHETFKRV LKAHETFKR LRKLKAHETFKRVLK LKAHETFKR SLRKLKAHETFKRVL LKAHETFKR RKLKAHETFKRVLKL LKAHETFKR

		TESLRKLKAHETFKR LRKLKAHET NYPLASSKMRFKAFR YPLASSKMR YPLASSKMRFKAFRV YPLASSKMR WSNPNYIPNISSRII YIPNISSRI IWSNPNYIPNISSRI NYIPNISSR SNPNYIPNISSRIIK YIPNISSRI NPNYIPNISSRIIKD YIPNISSRI
BAD18055.1 FlaB protein [Borrelia garinii] Seq15	HLA-DRB1*0101	QPAKINTPASLSGSQ INTPASLSG PAKINTPASLSGSQA INTPASLSG MQPAKINTPASLSGS INTPASLSG AKINTPASLSGSQAS INTPASLSG ANLFSGEGAQAAQTA FSGEGAQAA VANLFSGEGAQAAQT FSGEGAQAA NLFSGEGAQAAQTAP FSGEGAQAA GMQPAKINTPASLSG KINTPASLS ANVANLFSGEGAQAA VANLFSGEG NVANLFSGEGAQAAQ FSGEGAQAA YNQMHMLSNKSASQN MHMLSNKSA EKVLVRMKELAVQSG VRMKELAVQ KVLVRMKELAVQSGN MKELAVQSG QAQYNQMHMLSNKSA YNQMHMLSN AQYNQMHMLSNKSAS MHMLSNKSA LFSGEGAQAAQTAPV FSGEGAQAA VLVRMKELAVQSGNG MKELAVQSG NQMHMLSNKSASQNV MHMLSNKSA AEELGMQPAKINTPA LGMQPAKIN FSGEGAQAAQTAPVQ FSGEGAQAA TAEELGMQPAKINTP LGMQPAKIN LVRMKELAVQSGNGT MKELAVQSG QYNQMHMLSNKSASQ MHMLSNKSA VRMKELAVQSGNGTY MKELAVQSG RTAEELGMQPAKINT LGMQPAKIN EELGMQPAKINTPAS LGMQPAKIN VRTAEELGMQPAKIN ELGMQPAKI INTPASLSGSQASWT INTPASLSG KINTPASLSGSQASW INTPASLSG VQQEGAQQPAPATAP VQQEGAQQP RMKELAVQSGNGTYS MKELAVQSG MKELAVQSGNGTYSD MKELAVQSG EGVQQEGAQQPAPAT VQQEGAQQP QMHMLSNKSASQNVR MHMLSNKSA MHMLSNKSASQNVRT MHMLSNKSA AIAVNIYAANVANLF VNIYAANVA LGMQPAKINTPASLS LGMQPAKIN IAVNIYAANVANLFS YAANVANLF ELGMQPAKINTPASL LGMQPAKIN QEGVQQEGAQQPAPA VQQEGAQQP AVNIYAANVANLFSG YAANVANLF PVQEGVQQEGAQQPA VQQEGAQQP APVQEGVQQEGAQQP QEGVQQEGA VQEGVQQEGAQQPAP VQQEGAQQP NIYAANVANLFSGEG YAANVANLF QEGAQQPAPATAPSQ QQPAPATAP VNIYAANVANLFSGE YAANVANLF QQEGAQQPAPATAPS QQPAPATAP

		GVQQEGAQQPAPATA VQQEGAQQP EGAQQPAPATAPSQG QQPAPATAP EAIAVNIYAANVANL VNIYAANVA VEKVLVRMKELAVQS VRMKELAVQ GAQQPAPATAPSQGG QQPAPATAP EVEKVLVRMKELAVQ LVRMKELAV AANVANLFSGEGAQA VANLFSGEG KELAVQSGNGTYSDA VQSGNGTYS DEAIAVNIYAANVAN VNIYAANVA PSQGGVNSPVNVTTT VNSPVNVTT DQAQYNQMHMLSNKS YNQMHMLSN SQGGVNSPVNVTTTV VNSPVNVTT QGGVNSPVNVTTTVD VNSPVNVTT APSQGGVNSPVNVTT GVNSPVNVT QDEAIAVNIYAANVA AVNIYAANV PASLSGSQASWTLRV LSGSQASWT ASLSGSQASWTLRVH LSGSQASWT IYAANVANLFSGEGA VANLFSGEG GGVNSPVNVTTTVDA VNSPVNVTT ELAVQSGNGTYSDAD VQSGNGTYS NTPASLSGSQASWTL LSGSQASWT GEGAQAAQTAPVQEG AQAAQTAPV LAVQSGNGTYSDADR VQSGNGTYS EGAQAAQTAPVQEGV AQAAQTAPV YAANVANLFSGEGAQ VANLFSGEG TPASLSGSQASWTLR LSGSQASWT AQQPAPATAPSQGGV PATAPSQGG ADQAQYNQMHMLSNK YNQMHMLSN HMLSNKSASQNVRTA LSNKSASQN IADQAQYNQMHMLSN QYNQMHMLS SGEGAQAAQTAPVQE AQAAQTAPV VNVTTTVDANTSLAK VTTTVDANT QQPAPATAPSQGGVN PATAPSQGG GVNSPVNVTTTVDAN VNVTTTVDA AQAAQTAPVQEGVQQ AQTAPVQEG GAQAAQTAPVQEGVQ AQTAPVQEG VNSPVNVTTTVDANT VNVTTTVDA SLSGSQASWTLRVHV LSGSQASWT LSGSQASWTLRVHVG LSGSQASWT SKAINFIQTTEGNLN INFIQTTEG NSPVNVTTTVDANTS VNVTTTVDA SPVNVTTTVDANTSL VNVTTTVDA NVTTTVDANTSLAKI VDANTSLAK KAINFIQTTEGNLNE INFIQTTEG QPAPATAPSQGGVNS PATAPSQGG MLSNKSASQNVRTAE LSNKSASQN PAPATAPSQGGVNSP PATAPSQGG VTTTVDANTSLAKIE VDANTSLAK PVNVTTTVDANTSLA VNVTTTVDA QAAQTAPVQEGVQQE AQTAPVQEG
	HLA-DRB1*0301	None
	HLA-DRB1*0401	QYNQMHMLSNKSASQ QMHMLSNKS YNQMHMLSNKSASQN QMHMLSNKS IAVNIYAANVANLFS YAANVANLF QAQYNQMHMLSNKSA QMHMLSNKS NQMHMLSNKSASQNV MLSNKSASQ

		AIAVNIYAANVANLF NIYAANVAN NIYAANVANLFSGEG YAANVANLF AVNIYAANVANLFSG YAANVANLF AQYNQMHMLSNKSAS QMHMLSNKS VNIYAANVANLFSGE YAANVANLF QMHMLSNKSASQNVR MLSNKSASQ GVNSPVNVTTTVDAN VNVTTTVDA GGVNSPVNVTTTVDA VNSPVNVTT NSPVNVTTTVDANTS VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA
	HLA-DRB1*0404	ANVANLFSGEGAQAA VANLFSGEG AANVANLFSGEGAQA VANLFSGEG NIYAANVANLFSGEG YAANVANLF IYAANVANLFSGEGA VANLFSGEG YAANVANLFSGEGAQ VANLFSGEG YNQMHMLSNKSASQN MLSNKSASQ QYNQMHMLSNKSASQ QMHMLSNKS NVANLFSGEGAQAAQ VANLFSGEG VANLFSGEGAQAAQT VANLFSGEG NQMHMLSNKSASQNV MLSNKSASQ QMHMLSNKSASQNVR MLSNKSASQ VNVTTTVDANTSLAK TVDANTSLA PVNVTTTVDANTSLA VNVTTTVDA AQYNQMHMLSNKSAS QMHMLSNKS QAQYNQMHMLSNKSA QMHMLSNKS DQAQYNQMHMLSNKS YNQMHMLSN
	HLA-DRB1*0405	EELGMQPAKINTPAS LGMQPAKIN LGMQPAKINTPASLS PAKINTPAS GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA ELGMQPAKINTPASL PAKINTPAS NSPVNVTTTVDANTS VNVTTTVDA
	HLA-DRB1*0701	GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA
	HLA-DRB1*0802	None
	HLA-DRB1*0901	IAVNIYAANVANLFS VNIYAANVA AIAVNIYAANVANLF VNIYAANVA EAIAVNIYAANVANL VNIYAANVA AVNIYAANVANLFSG IYAANVANL VNIYAANVANLFSGE IYAANVANL
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD IENAIRMIS SLAKIENAIRMISDQ IENAIRMIS RMKELAVQSGNGTYS LAVQSGNGT AIAVNIYAANVANLF VNIYAANVA IAVNIYAANVANLFS VNIYAANVA MKELAVQSGNGTYSD LAVQSGNGT KELAVQSGNGTYSDA LAVQSGNGT LVRMKELAVQSGNGT MKELAVQSG VRMKELAVQSGNGTY LAVQSGNGT

		AVNIYAANVANLFSG YAANVANLF VNIYAANVANLFSGE YAANVANLF SQGGVNSPVNVTTTV GVNSPVNVT QGGVNSPVNVTTTVD GVNSPVNVT GGVNSPVNVTTTVDA GVNSPVNVT EAIAVNIYAANVANL VNIYAANVA PSQGGVNSPVNVTTT GVNSPVNVT APSQGGVNSPVNVTT GVNSPVNVT QDEAIAVNIYAANVA IAVNIYAAN DEAIAVNIYAANVAN VNIYAANVA GVNSPVNVTTTVDAN GVNSPVNVT ELAVQSGNGTYSDAD LAVQSGNGT LAVQSGNGTYSDADR LAVQSGNGT NIYAANVANLFSGEG YAANVANLF SKAINFIQTTEGNLN INFIQTTEG
	HLA-DRB1*1501	EKVLVRMKELAVQSG LVRMKELAV KVLVRMKELAVQSGN LVRMKELAV VEKVLVRMKELAVQS LVRMKELAV EVEKVLVRMKELAVQ LVRMKELAV VLVRMKELAVQSGNG VRMKELAVQ LVRMKELAVQSGNGT VRMKELAVQ NEVEKVLVRMKELAV VLVRMKELA QYNQMHMLSNKSASQ MHMLSNKSA YNQMHMLSNKSASQN MHMLSNKSA AQYNQMHMLSNKSAS MHMLSNKSA VRMKELAVQSGNGTY VRMKELAVQ QAQYNQMHMLSNKSA QMHMLSNKS NQMHMLSNKSASQNV MHMLSNKSA QASWTLRVHVGANQD LRVHVGANQ SQASWTLRVHVGANQ QASWTLRVH
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EVEKVLVRMKELAVQ VEKVLVRMK VEKVLVRMKELAVQS VRMKELAVQ EKVLVRMKELAVQSG VRMKELAVQ KVLVRMKELAVQSGN VRMKELAVQ VLVRMKELAVQSGNG VRMKELAVQ VRMKELAVQSGNGTY VRMKELAVQ LVRMKELAVQSGNGT VRMKELAVQ
	HLA-DRB5*0101	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD AKIENAIRM DANTSLAKIENAIRM LAKIENAIR ANTSLAKIENAIRMI AKIENAIRM SLAKIENAIRMISDQ AKIENAIRM
AAU07005.1| flagellar filament 41 kDa core protein [Borrelia garinii PBi] Seq16	HLA-DRB1*0101	TTNSILTQSAMAMIA ILTQSAMAM TNSILTQSAMAMIAQ ILTQSAMAM NSILTQSAMAMIAQA ILTQSAMAM STTNSILTQSAMAMI ILTQSAMAM ASTTNSILTQSAMAM TNSILTQSA QPAKINTPASLSGSQ INTPASLSG PAKINTPASLSGSQA INTPASLSG SILTQSAMAMIAQAN ILTQSAMAM

		MQPAKINTPASLSGS	INTPASLSG
		AKINTPASLSGSQAS	INTPASLSG
		ILTQSAMAMIAQANQ	ILTQSAMAM
		GMQPAKINTPASLSG	KINTPASLS
		NAIRMISDQRANLGA	IRMISDQRA
		ANVANLFSGEGSQAA	VANLFSGEG
		ANLFSGEGSQAAQTA	FSGEGSQAA
		ENAIRMISDQRANLG	IRMISDQRA
		VANLFSGEGSQAAQT	FSGEGSQAA
		NLFSGEGSQAAQTAP	FSGEGSQAA
		NVANLFSGEGSQAAQ	FSGEGSQAA
		YNQMHMLSNKSASQN	MHMLSNKSA
		EKVLVRMKELAVQSG	VRMKELAVQ
		KVLVRMKELAVQSGN	MKELAVQSG
		QAQYNQMHMLSNKSA	YNQMHMLSN
		AQYNQMHMLSNKSAS	MHMLSNKSA
		NQMHMLSNKSASQNV	MHMLSNKSA
		AEELGMQPAKINTPA	LGMQPAKIN
		VLVRMKELAVQSGNG	MKELAVQSG
		TAEELGMQPAKINTP	LGMQPAKIN
		QYNQMHMLSNKSASQ	MHMLSNKSA
		AKIENAIRMISDQRA	IENAIRMIS
		LVRMKELAVQSGNGT	MKELAVQSG
		RTAEELGMQPAKINT	LGMQPAKIN
		EELGMQPAKINTPAS	LGMQPAKIN
		VRMKELAVQSGNGTY	MKELAVQSG
		VRTAEELGMQPAKIN	ELGMQPAKI
		IENAIRMISDQRANL	IRMISDQRA
		KIENAIRMISDQRAN	IRMISDQRA
		INTPASLSGSQASWT	INTPASLSG
		EYAIENLKASYAQIK	IENLKASYA
		LFSGEGSQAAQTAPV	FSGEGSQAA
		YAIENLKASYAQIKD	IENLKASYA
		FSGEGSQAAQTAPVQ	FSGEGSQAA
		KINTPASLSGSQASW	INTPASLSG
		AIRMISDQRANLGAF	IRMISDQRA
		IRMISDQRANLGAFQ	IRMISDQRA
		RMKELAVQSGNGTYS	MKELAVQSG
		MKELAVQSGNGTYSD	MKELAVQSG
		STEYAIENLKASYAQ	IENLKASYA
		DSTEYAIENLKASYA	YAIENLKAS
		TEYAIENLKASYAQI	IENLKASYA
		QMHMLSNKSASQNVR	MHMLSNKSA
		MHMLSNKSASQNVRT	MHMLSNKSA
		TQSAMAMIAQANQVP	TQSAMAMIA
		AIAVNIYAANVANLF	VNIYAANVA
		LGMQPAKINTPASLS	LGMQPAKIN
		IAVNIYAANVANLFS	YAANVANLF
		AIENLKASYAQIKDA	LKASYAQIK
		IENLKASYAQIKDAT	LKASYAQIK
		ELGMQPAKINTPASL	LGMQPAKIN
		LTQSAMAMIAQANQV	AMAMIAQAN
		QSAMAMIAQANQVPQ	MIAQANQVP
		AVNIYAANVANLFSG	YAANVANLF
		NIYAANVANLFSGEG	YAANVANLF
		QEGAQQPAPATAPSQ	QQPAPATAP
		ATMTDEVVASTTNSI	MTDEVVAST

		VNIYAANVANLFSGE	YAANVANLF
		QQEGAQQPAPATAPS	QQPAPATAP
		AQQEGAQQPAPATAP	AQQPAPATA
		MTDEVVASTTNSILT	VVASTTNSI
		TMTDEVVASTTNSIL	VVASTTNSI
		TDEVVASTTNSILTQ	VVASTTNSI
		EGAQQPAPATAPSQG	QQPAPATAP
		AMAMIAQANQVPQYV	MIAQANQVP
		EAIAVNIYAANVANL	VNIYAANVA
		DEVVASTTNSILTQS	VVASTTNSI
		ENLKASYAQIKDATM	LKASYAQIK
		VEKVLVRMKELAVQS	VRMKELAVQ
		SAMAMIAQANQVPQY	MIAQANQVP
		GAQQPAPATAPSQGG	QQPAPATAP
		EVEKVLVRMKELAVQ	LVRMKELAV
		NAQIRGLSQASRNTS	IRGLSQASR
		KELAVQSGNGTYSDA	VQSGNGTYS
		NLKASYAQIKDATMT	LKASYAQIK
		LKASYAQIKDATMTD	LKASYAQIK
		INAQIRGLSQASRNT	IRGLSQASR
		AQIRGLSQASRNTSK	IRGLSQASR
		DEAIAVNIYAANVAN	VNIYAANVA
		PSQGGVNSPVNVTTT	VNSPVNVTT
		DQAQYNQMHMLSNKS	YNQMHMLSN
		SQGGVNSPVNVTTTV	VNSPVNVTT
		QGGVNSPVNVTTTVD	VNSPVNVTT
		APSQGGVNSPVNVTT	GVNSPVNVT
		QDEAIAVNIYAANVA	AVNIYAANV
		PASLSGSQASWTLRV	LSGSQASWT
		ASLSGSQASWTLRVH	LSGSQASWT
		AANVANLFSGEGSQA	VANLFSGEG
		MAMIAQANQVPQYVL	MIAQANQVP
		IYAANVANLFSGEGS	VANLFSGEG
		GGVNSPVNVTTTVDA	VNSPVNVTT
		ELAVQSGNGTYSDAD	VQSGNGTYS
		NTPASLSGSQASWTL	LSGSQASWT
		LAVQSGNGTYSDADR	VQSGNGTYS
		NNSINAANLSKTQEK	INAANLSKT
		RNNSINAANLSKTQE	INAANLSKT
		SRNNSINAANLSKTQ	INAANLSKT
		NSINAANLSKTQEKL	INAANLSKT
		YAANVANLFSGEGSQ	VANLFSGEG
		ASRNNSINAANLSKT	NSINAANLS
		TPASLSGSQASWTLR	LSGSQASWT
		EVVASTTNSILTQSA	VVASTTNSI
		KINAQIRGLSQASRN	IRGLSQASR
		GKINAQIRGLSQASR	QIRGLSQAS
		VVASTTNSILTQSAM	VVASTTNSI
		AQQPAPATAPSQGGV	PATAPSQGG
		EGSQAAQTAPVQEGA	AQTAPVQEG
		GEGSQAAQTAPVQEG	SQAAQTAPV
		ADQAQYNQMHMLSNK	YNQMHMLSN
		HMLSNKSASQNVRTA	LSNKSASQN
		IADQAQYNQMHMLSN	QYNQMHMLS
		VNVTTTVDANTSLAK	VTTTVDANT
		KASYAQIKDATMTDE	AQIKDATMT
		QIRGLSQASRNTSKA	IRGLSQASR

		ASYAQIKDATMTDEV AQIKDATMT QQPAPATAPSQGGVN PATAPSQGG AMIAQANQVPQYVLS MIAQANQVP GVNSPVNVTTTVDAN VNVTTTVDA IRGLSQASRNTSKAI IRGLSQASR RMISDQRANLGAFQN ISDQRANLG GAQQEGAQQPAPATA GAQQPAPAT MIAQANQVPQYVLSL QANQVPQYV GSQAAQTAPVQEGAQ AQTAPVQEG SQAAQTAPVQEGAQQ AQTAPVQEG DATMTDEVVASTTNS MTDEVVAST VNSPVNVTTTVDANT VNVTTTVDA SLSGSQASWTLRVHV LSGSQASWT LSGSQASWTLRVHVG LSGSQASWT SKAINFIQTTEGNLN INFIQTTEG MIINHNTSAINASRN INHNTSAIN SYAQIKDATMTDEVV AQIKDATMT NSPVNVTTTVDANTS VNVTTTVDA SPVNVTTTVDANTSL VNVTTTVDA NVTTTVDANTSLAKI VDANTSLAK KAINFIQTTEGNLNE INFIQTTEG SGEGSQAAQTAPVQE SQAAQTAPV QPAPATAPSQGGVNS PATAPSQGG MLSNKSASQNVRTAE LSNKSASQN IKDATMTDEVVASTT MTDEVVAST KDATMTDEVVASTTN MTDEVVAST PAPATAPSQGGVNSP PATAPSQGG VTTTVDANTSLAKIE VDANTSLAK QIKDATMTDEVVAST DATMTDEVV PVNVTTTVDANTSLA VNVTTTVDA QAAQTAPVQEGAQQE AQTAPVQEG EGAQQEGAQQPAPAT AQQEGAQQP
	HLA-DRB1*0301	None
	HLA-DRB1*0401	QYNQMHMLSNKSASQ QMHMLSNKS YNQMHMLSNKSASQN QMHMLSNKS IAVNIYAANVANLFS YAANVANLF QAQYNQMHMLSNKSA QMHMLSNKS NQMHMLSNKSASQNV MLSNKSASQ AIAVNIYAANVANLF NIYAANVAN NIYAANVANLFSGEG YAANVANLF AVNIYAANVANLFSG YAANVANLF AQYNQMHMLSNKSAS QMHMLSNKS VNIYAANVANLFSGE YAANVANLF QMHMLSNKSASQNVR MLSNKSASQ GVNSPVNVTTTVDAN VNVTTTVDA GGVNSPVNVTTTVDA VNSPVNVTT NSPVNVTTTVDANTS VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA
	HLA-DRB1*0404	ANVANLFSGEGSQAA VANLFSGEG AANVANLFSGEGSQA VANLFSGEG YAANVANLFSGEGSQ VANLFSGEG NIYAANVANLFSGEG YAANVANLF IYAANVANLFSGEGS VANLFSGEG YNQMHMLSNKSASQN MLSNKSASQ QYNQMHMLSNKSASQ QMHMLSNKS

		NVANLFSGEGSQAAQ VANLFSGEG VANLFSGEGSQAAQT VANLFSGEG ENAIRMISDQRANLG AIRMISDQR NQMHMLSNKSASQNV MLSNKSASQ NAIRMISDQRANLGA ISDQRANLG QMHMLSNKSASQNVR MLSNKSASQ AIRMISDQRANLGAF ISDQRANLG VNVTTTVDANTSLAK TVDANTSLA PVNVTTTVDANTSLA VNVTTTVDA IRMISDQRANLGAFQ ISDQRANLG AQYNQMHMLSNKSAS QMHMLSNKS QAQYNQMHMLSNKSA QMHMLSNKS DQAQYNQMHMLSNKS YNQMHMLSN RMISDQRANLGAFQN ISDQRANLG
	HLA-DRB1*0405	EELGMQPAKINTPAS LGMQPAKIN LGMQPAKINTPASLS PAKINTPAS GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA ELGMQPAKINTPASL PAKINTPAS NSPVNVTTTVDANTS VNVTTTVDA
	HLA-DRB1*0701	TMTDEVVASTTNSIL VVASTTNSI MTDEVVASTTNSILT VVASTTNSI TDEVVASTTNSILTQ VVASTTNSI DEVVASTTNSILTQS VVASTTNSI ATMTDEVVASTTNSI TDEVVASTT EVVASTTNSILTQSA VASTTNSIL NHNTSAINASRNNSI TSAINASRN HNTSAINASRNNSIN INASRNNSI TSAINASRNNSINAA INASRNNSI NTSAINASRNNSINA INASRNNSI SAINASRNNSINAAN INASRNNSI VVASTTNSILTQSAM VVASTTNSI GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA MIINHNTSAINASRN IINHNTSAI
	HLA-DRB1*0802	None
	HLA-DRB1*0901	IAVNIYAANVANLFS VNIYAANVA AIAVNIYAANVANLF VNIYAANVA TTNSILTQSAMAMIA LTQSAMAMI TNSILTQSAMAMIAQ LTQSAMAMI NSILTQSAMAMIAQA LTQSAMAMI SILTQSAMAMIAQAN LTQSAMAMI STTNSILTQSAMAMI ILTQSAMAM EAIAVNIYAANVANL VNIYAANVA AVNIYAANVANLFSG IYAANVANL VNIYAANVANLFSGE IYAANVANL
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD IENAIRMIS SLAKIENAIRMISDQ IENAIRMIS RMKELAVQSGNGTYS LAVQSGNGT

		AIAVNIYAANVANLF VNIYAANVA IAVNIYAANVANLFS VNIYAANVA MKELAVQSGNGTYSD LAVQSGNGT KELAVQSGNGTYSDA LAVQSGNGT LVRMKELAVQSGNGT MKELAVQSG VRMKELAVQSGNGTY LAVQSGNGT AVNIYAANVANLFSG YAANVANLF VNIYAANVANLFSGE YAANVANLF SQGGVNSPVNVTTTV GVNSPVNVT QGGVNSPVNVTTTVD GVNSPVNVT GGVNSPVNVTTTVDA GVNSPVNVT EAIAVNIYAANVANL VNIYAANVA PSQGGVNSPVNVTTT GVNSPVNVT APSQGGVNSPVNVTT GVNSPVNVT QDEAIAVNIYAANVA IAVNIYAAN DEAIAVNIYAANVAN VNIYAANVA GVNSPVNVTTTVDAN GVNSPVNVT ELAVQSGNGTYSDAD LAVQSGNGT LAVQSGNGTYSDADR LAVQSGNGT NIYAANVANLFSGEG YAANVANLF SKAINFIQTTEGNLN INFIQTTEG
	HLA-DRB1*1501	EKVLVRMKELAVQSG LVRMKELAV KVLVRMKELAVQSGN LVRMKELAV VEKVLVRMKELAVQS LVRMKELAV EVEKVLVRMKELAVQ LVRMKELAV VLVRMKELAVQSGNG VRMKELAVQ LVRMKELAVQSGNGT VRMKELAVQ INAQIRGLSQASRNT IRGLSQASR GKINAQIRGLSQASR QIRGLSQAS NAQIRGLSQASRNTS IRGLSQASR KINAQIRGLSQASRN IRGLSQASR AQIRGLSQASRNTSK IRGLSQASR NEVEKVLVRMKELAV VLVRMKELA KIENAIRMISDQRAN AIRMISDQR IENAIRMISDQRANL AIRMISDQR AKIENAIRMISDQRA AIRMISDQR ENAIRMISDQRANLG AIRMISDQR LAKIENAIRMISDQR LAKIENAIR QYNQMHMLSNKSASQ MHMLSNKSA QIRGLSQASRNTSKA IRGLSQASR YNQMHMLSNKSASQN MHMLSNKSA IRGLSQASRNTSKAI IRGLSQASR AQYNQMHMLSNKSAS MHMLSNKSA VRMKELAVQSGNGTY VRMKELAVQ QAQYNQMHMLSNKSA QMHMLSNKS AIRMISDQRANLGAF AIRMISDQR NQMHMLSNKSASQNV MHMLSNKSA QASWTLRVHVGANQD LRVHVGANQ NAIRMISDQRANLGA AIRMISDQR SQASWTLRVHVGANQ QASWTLRVH
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EVEKVLVRMKELAVQ VEKVLVRMK VEKVLVRMKELAVQS VRMKELAVQ EKVLVRMKELAVQSG VRMKELAVQ KVLVRMKELAVQSGN VRMKELAVQ

		VLVRMKELAVQSGNG VRMKELAVQ ENAIRMISDQRANLG IRMISDQRA NAIRMISDQRANLGA IRMISDQRA VRMKELAVQSGNGTY VRMKELAVQ LVRMKELAVQSGNGT VRMKELAVQ AIRMISDQRANLGAF ISDQRANLG IRMISDQRANLGAFQ ISDQRANLG
	HLA-DRB5*0101	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD AKIENAIRM DANTSLAKIENAIRM LAKIENAIR ANTSLAKIENAIRMI AKIENAIRM SLAKIENAIRMISDQ AKIENAIRM
1L8W|A Chain A, Crystal Structure Of Lyme Disease Variable Surface Antigen VlsE1 Of Borrelia Burgdorferi Seq17	HLA-DRB1*0101	DVFTSFGGLVAEAFG FGGLVAEAF SDVKTYFTTVAAKLE YFTTVAAKL LDVFTSFGGLVAEAF FTSFGGLVA VKTYFTTVAAKLEKT YFTTVAAKL KTYFTTVAAKLEKTK FTTVAAKLE KSDVKTYFTTVAAKL VKTYFTTVA DVKTYFTTVAAKLEK YFTTVAAKL FTSFGGLVAEAFGFK FGGLVAEAF VKAVKTAEGASSGTA VKTAEGASS VFTSFGGLVAEAFGF FGGLVAEAF KAVKTAEGASSGTAA VKTAEGASS KLVKAVKTAEGASSG VKTAEGASS DKLVKAVKTAEGASS VKAVKTAEG LVKAVKTAEGASSGT VKTAEGASS TYFTTVAAKLEKTKT FTTVAAKLE TSFGGLVAEAFGFKS FGGLVAEAF KKSDVKTYFTTVAAK VKTYFTTVA AAKVADKASVKGIAK VADKASVKG ADAAKVADKASVKGI VADKASVKG PKKSDVKTYFTTVAA VKTYFTTVA DADAAKVADKASVKG AAKVADKAS DAAKVADKASVKGIA VADKASVKG AKVADKASVKGIAKG VADKASVKG DPKKSDVKTYFTTVA KSDVKTYFT AVKTAEGASSGTAAI VKTAEGASS VKTAEGASSGTAAIG VKTAEGASS YFTTVAAKLEKTKTD FTTVAAKLE GEVVADADAAKVADK VADADAAKV EVVADADAAKVADKA VADADAAKV IGEVVADADAAKVAD VADADAAKV AIGEVVADADAAKVA VADADAAKV AAIGEVVADADAAKV VVADADAAK LLDKLVKAVKTAEGA VKAVKTAEG ELLDKLVKAVKTAEG DKLVKAVKT LDKLVKAVKTAEGAS VKAVKTAEG FTTVAAKLEKTKTDL FTTVAAKLE SFGGLVAEAFGFKSD FGGLVAEAF FGGLVAEAFGFKSDP FGGLVAEAF PTNKFYQSVIQLGNG FYQSVIQLG NKFYQSVIQLGNGFL FYQSVIQLG DPTNKFYQSVIQLGN FYQSVIQLG TNKFYQSVIQLGNGF FYQSVIQLG NGFLDVFTSFGGLVA FLDVFTSFG

		KVADKASVKGIAKGI VADKASVKG VADKASVKGIAKGIK VADKASVKG DDPTNKFYQSVIQLG NKFYQSVIQ GFLDVFTSFGGLVAE FTSFGGLVA FLDVFTSFGGLVAEA FTSFGGLVA VVADADAAKVADKAS VADADAAKV VADADAAKVADKASV VADADAAKV VSELLDKLVKAVKTA LLDKLVKAV SELLDKLVKAVKTAE LLDKLVKAV EVSELLDKLVKAVKT LLDKLVKAV KTDLNSLPKEKSDIS LNSLPKEKS TDLNSLPKEKSDISS LNSLPKEKS
	HLA-DRB1*0301	None
	HLA-DRB1*0401	None
	HLA-DRB1*0404	NGFLDVFTSFGGLVA FLDVFTSFG QLGNGFLDVFTSFGG FLDVFTSFG GNGFLDVFTSFGGLV FLDVFTSFG IQLGNGFLDVFTSFG QLGNGFLDV LGNGFLDVFTSFGGL FLDVFTSFG GFLDVFTSFGGLVAE FLDVFTSFG FLDVFTSFGGLVAEA FLDVFTSFG
	HLA-DRB1*0405	VAEAFGFKSDPKKSD AFGFKSDPK AEAFGFKSDPKKSDV FKSDPKKSD EAFGFKSDPKKSDVK FKSDPKKSD AFGFKSDPKKSDVKT FKSDPKKSD FGFKSDPKKSDVKTY FKSDPKKSD DPTNKFYQSVIQLGN TNKFYQSVI PTNKFYQSVIQLGNG YQSVIQLGN KFYQSVIQLGNGFLD YQSVIQLGN TNKFYQSVIQLGNGF YQSVIQLGN SDVKTYFTTVAAKLE VKTYFTTVA
	HLA-DRB1*0701	KSDVKTYFTTVAAKL DVKTYFTTV SDVKTYFTTVAAKLE YFTTVAAKL DVKTYFTTVAAKLEK YFTTVAAKL VKTYFTTVAAKLEKT YFTTVAAKL KTYFTTVAAKLEKTK YFTTVAAKL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	VKTYFTTVAAKLEKT YFTTVAAKL SDVKTYFTTVAAKLE YFTTVAAKL DVKTYFTTVAAKLEK YFTTVAAKL KTYFTTVAAKLEKTK YFTTVAAKL NKFYQSVIQLGNGFL FYQSVIQLG PTNKFYQSVIQLGNG FYQSVIQLG DPTNKFYQSVIQLGN FYQSVIQLG DDPTNKFYQSVIQLG NKFYQSVIQ
	HLA-DRB1*1101	None
	HLA-DRB1*1302	None
	HLA-DRB1*1501	GLVAEAFGFKSDPKK AFGFKSDPK LVAEAFGFKSDPKKS AFGFKSDPK VAEAFGFKSDPKKSD AFGFKSDPK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	None
CAA57807.1 Associated protein A	HLA-DRB1*0101	IFLFLFVVSLSANIE FVVSLSANI FLFLFVVSLSANIEE VVSLSANIE

(BapA)[Borrelia burgdorferi] Seq18		LFLFVVSLSANIEEN FVVSLSANI FLFVVSLSANIEENY FVVSLSANI LIFLFLFVVSLSANI FLFVVSLSA EAIEYLIKIKISTDS IEYLIKIKI AIEYLIKIKISTDSI IKIKISTDS IEYLIKIKISTDSIF IKIKISTDS EYLIKIKISTDSIFL IKIKISTDS YLIKIKISTDSIFLS IKIKISTDS LFVVSLSANIEENYT VVSLSANIE LLIFLFLFVVSLSAN FLFVVSLSA SLLIFLFLFVVSLSA FLFLFVVSL NTVKQILKQILADLP VKQILKQIL VKQILKQILADLPKD LKQILADLP TVKQILKQILADLPK LKQILADLP ISLLIFLFLFVVSLS FLFLFVVSL KISLLIFLFLFVVSL LIFLFLFVV LIKIKISTDSIFLSE IKIKISTDS IKIKISTDSIFLSED IKIKISTDS EDMIRLIGSYPDSIF IRLIGSYPD FVVSLSANIEENYTE FVVSLSANI FLSEDMIRLIGSYPD FLSEDMIRL SEDMIRLIGSYPDSI IRLIGSYPD DMIRLIGSYPDSIFN IRLIGSYPD DSIFLSEDMIRLIGS FLSEDMIRL KSHVFSDAPRIRGDL VFSDAPRIR EKSHVFSDAPRIRGD VFSDAPRIR YEKSHVFSDAPRIRG VFSDAPRIR SIFLSEDMIRLIGSY FLSEDMIRL SHVFSDAPRIRGDLR VFSDAPRIR DSIFNYLIQLNSDKI IFNYLIQLN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	LLIFLFLFVVSLSAN FLFVVSLSA SLLIFLFLFVVSLSA LFLFVVSLS LIFLFLFVVSLSANI FLFVVSLSA IFLFLFVVSLSANIE FLFVVSLSA FLFLFVVSLSANIEE FLFVVSLSA LFLFVVSLSANIEEN FLFVVSLSA FLFVVSLSANIEENY FLFVVSLSA DNARNNFKKDYSEDK RNNFKKDYS NNFKKDYSEDKANTV FKKDYSEDK NARNNFKKDYSEDKA FKKDYSEDK RNNFKKDYSEDKANT FKKDYSEDK ARNNFKKDYSEDKAN FKKDYSEDK EAIEYLIKIKISTDS YLIKIKIST AIEYLIKIKISTDSI IKIKISTDS IEYLIKIKISTDSIF IKIKISTDS YLIKIKISTDSIFLS IKIKISTDS EYLIKIKISTDSIFL IKIKISTDS
	HLA-DRB1*0404	LIFLFLFVVSLSANI FLFVVSLSA IFLFLFVVSLSANIE FVVSLSANI FLFLFVVSLSANIEE FVVSLSANI LLIFLFLFVVSLSAN LFLFVVSLS SLLIFLFLFVVSLSA LFLFVVSLS LFLFVVSLSANIEEN FVVSLSANI ISLLIFLFLFVVSLS LLIFLFLFV FLFVVSLSANIEENY FVVSLSANI

	HLA-DRB1*0405	FLSEDMIRLIGSYPD EDMIRLIGS LSEDMIRLIGSYPDS IRLIGSYPD EDMIRLIGSYPDSIF IRLIGSYPD SEDMIRLIGSYPDSI IRLIGSYPD DMIRLIGSYPDSIFN IRLIGSYPD MIRLIGSYPDSIFNY IRLIGSYPD IRLIGSYPDSIFNYL IRLIGSYPD FLFLFVVSLSANIEE VVSLSANIE
	HLA-DRB1*0701	None
	HLA-DRB1*0802	None
	HLA-DRB1*0901	IFLFLFVVSLSANIE FVVSLSANI LIFLFLFVVSLSANI LFVVSLSAN FLFLFVVSLSANIEE FVVSLSANI LFLFVVSLSANIEEN FVVSLSANI FLFVVSLSANIEENY FVVSLSANI LFVVSLSANIEENYT FVVSLSANI
	HLA-DRB1*1101	None
	HLA-DRB1*1302	IEYLIKIKISTDSIF YLIKIKIST EAIEYLIKIKISTDS YLIKIKIST AIEYLIKIKISTDSI IKIKISTDS YLIKIKISTDSIFLS IKIKISTDS EYLIKIKISTDSIFL IKIKISTDS IFLFLFVVSLSANIE LFLFVVSLS LEAIEYLIKIKISTD YLIKIKIST ALEAIEYLIKIKIST IEYLIKIKI FLFLFVVSLSANIEE LFLFVVSLS LIKIKISTDSIFLSE IKISTDSIF LFLFVVSLSANIEEN LFLFVVSLS FLSEDMIRLIGSYPD MIRLIGSYP EDMIRLIGSYPDSIF MIRLIGSYP IKIKISTDSIFLSED IKISTDSIF LSEDMIRLIGSYPDS MIRLIGSYP SEDMIRLIGSYPDSI MIRLIGSYP KEDFNLINKRLDNYD FNLINKRLD IFNYLIQLNSDKIDY LIQLNSDKI SIFNYLIQLNSDKID LIQLNSDKI SKEDFNLINKRLDNY FNLINKRLD EDFNLINKRLDNYDF FNLINKRLD DLRKIGIKEKSVFLD IGIKEKSVF LIFLFLFVVSLSANI LFLFVVSLS DSIFNYLIQLNSDKI IFNYLIQLN RKIGIKEKSVFLDAL IGIKEKSVF LLIFLFLFVVSLSAN LFLFVVSLS LRKIGIKEKSVFLDA IGIKEKSVF ISLLIFLFLFVVSLS ISLLIFLFL GDLRKIGIKEKSVFL IGIKEKSVF RGDLRKIGIKEKSVF LRKIGIKEK FNYLIQLNSDKIDYA LIQLNSDKI SLLIFLFLFVVSLSA LFLFVVSLS EKYGDNARNNFKKDY YGDNARNNF DMIRLIGSYPDSIFN IRLIGSYPD NYLIQLNSDKIDYAE LIQLNSDKI NTVKQILKQILADLP VKQILKQIL YAEKYGDNARNNFKK YGDNARNNF AEKYGDNARNNFKKD YGDNARNNF FSKEDFNLINKRLDN FNLINKRLD

		AFSKEDFNLINKRLD DFNLINKRL DALEAIEYLIKIKIS IEYLIKIKI DFNLINKRLDNYDFK FNLINKRLD DYAEKYGDNARNNFK YGDNARNNF IDYAEKYGDNARNNF KYGDNARNN
	HLA-DRB1*1501	ISLLIFLFLFVVSLS LIFLFLFVV KISLLIFLFLFVVSL LIFLFLFVV KKISLLIFLFLFVVS LIFLFLFVV SLLIFLFLFVVSLSA LIFLFLFVV MKKISLLIFLFLFVV LLIFLFLFV LLIFLFLFVVSLSAN LIFLFLFVV LIFLFLFVVSLSANI LIFLFLFVV IFLFLFVVSLSANIE FLFVVSLSA FLFLFVVSLSANIEE FLFVVSLSA SKEDFNLINKRLDNY DFNLINKRL KEDFNLINKRLDNYD LINKRLDNY EDFNLINKRLDNYDF LINKRLDNY DFNLINKRLDNYDFK LINKRLDNY SEDMIRLIGSYPDSI IRLIGSYPD EDMIRLIGSYPDSIF IRLIGSYPD FNLINKRLDNYDFKN LINKRLDNY LFLFVVSLSANIEEN FVVSLSANI
	HLA-DRB3*0101	None
	HLA-DRB4*0101	IRLIGSYPDSIFNYL LIGSYPDSI
	HLA-DRB5*0101	FNYLIQLNSDKIDYA YLIQLNSDK DSIFNYLIQLNSDKI YLIQLNSDK IFNYLIQLNSDKIDY YLIQLNSDK SIFNYLIQLNSDKID YLIQLNSDK PDSIFNYLIQLNSDK IFNYLIQLN DNYDFKNEYEKSHVF FKNEYEKSH RLDNYDFKNEYEKSH YDFKNEYEK LDNYDFKNEYEKSHV FKNEYEKSH
AAL25643.1, P37-47 [Borrelia burgdorferi] Seq19	HLA-DRB1*0101	SSFLTQGTSPSITST LTQGTSPSI ISSFLTQGTSPSITS LTQGTSPSI RPISSFLTQGTSPSI FLTQGTSPS PISSFLTQGTSPSIT LTQGTSPSI SFLTQGTSPSITSTI LTQGTSPSI PRPISSFLTQGTSPS ISSFLTQGT FLTQGTSPSITSTIK LTQGTSPSI NFFTNLEEVRSSIRT FTNLEEVRS PEITEEVIMPIPQTI EVIMPIPQT EITEEVIMPIPQTID VIMPIPQTI ITEEVIMPIPQTIDF VIMPIPQTI TEEVIMPIPQTIDFY VIMPIPQTI SNFFTNLEEVRSSIR FTNLEEVRS DSNFFTNLEEVRSSI FTNLEEVRS GDSNFFTNLEEVRSS FTNLEEVRS GGDSNFFTNLEEVRS GGDSNFFTN EEVIMPIPQTIDFYI VIMPIPQTI IDFYIEPRPISSFLT YIEPRPISS LTQGTSPSITSTIKS LTQGTSPSI DFYIEPRPISSFLTQ YIEPRPISS YIEPRPISSFLTQGT PRPISSFLT IEPRPISSFLTQGTS ISSFLTQGT FYIEPRPISSFLTQG YIEPRPISS

		FTNLEEVRSSIRTKI FTNLEEVRS EPRPISSFLTQGTSP ISSFLTQGT FFTNLEEVRSSIRTK FTNLEEVRS EVIMPIPQTIDFYIE VIMPIPQTI TIDFYIEPRPISSFL YIEPRPISS INNGLNIVQKITQNI INNGLNIVQ QTIDFYIEPRPISSF YIEPRPISS NNGLNIVQKITQNID IVQKITQNI LNIVQKITQNIDNIT IVQKITQNI NGLNIVQKITQNIDN IVQKITQNI GLNIVQKITQNIDNI IVQKITQNI PQTIDFYIEPRPISS FYIEPRPIS VIMPIPQTIDFYIEP VIMPIPQTI KLSQVAQHAPNSKIE VAQHAPNSK EKLSQVAQHAPNSKI VAQHAPNSK LSQVAQHAPNSKIEK VAQHAPNSK HEKLSQVAQHAPNSK KLSQVAQHA SQVAQHAPNSKIEKV VAQHAPNSK VNCKFDSLNLSTKSV FDSLNLSTK CKFDSLNLSTKSVDD SLNLSTKSV NCKFDSLNLSTKSVD SLNLSTKSV
	HLA-DRB1*0301	None
	HLA-DRB1*0401	EKLKKYLKDTNNLSA YLKDTNNLS KLKKYLKDTNNLSAI YLKDTNNLS LKKYLKDTNNLSAIE YLKDTNNLS KKYLKDTNNLSAIEE YLKDTNNLS LEKLKKYLKDTNNLS LEKLKKYLK KYLKDTNNLSAIEES YLKDTNNLS YLKDTNNLSAIEESV YLKDTNNLS PQTIDFYIEPRPISS FYIEPRPIS QTIDFYIEPRPISSF FYIEPRPIS IDFYIEPRPISSFLT FYIEPRPIS TIDFYIEPRPISSFL FYIEPRPIS IPQTIDFYIEPRPIS TIDFYIEPR ISSFLTQGTSPSITS FLTQGTSPS SSFLTQGTSPSITST FLTQGTSPS RPISSFLTQGTSPSI FLTQGTSPS PISSFLTQGTSPSIT FLTQGTSPS PRPISSFLTQGTSPS PRPISSFLT DFYIEPRPISSFLTQ FYIEPRPIS
	HLA-DRB1*0404	EKLKKYLKDTNNLSA YLKDTNNLS KLKKYLKDTNNLSAI LKDTNNLSA LKKYLKDTNNLSAIE LKDTNNLSA KKYLKDTNNLSAIEE LKDTNNLSA EKITHPIFDHITGSG ITHPIFDHI KYLKDTNNLSAIEES LKDTNNLSA KITHPIFDHITGSGN IFDHITGSG ITHPIFDHITGSGNN IFDHITGSG
	HLA-DRB1*0405	KKYLKDTNNLSAIEE YLKDTNNLS EKLKKYLKDTNNLSA YLKDTNNLS LKKYLKDTNNLSAIE YLKDTNNLS KLKKYLKDTNNLSAI YLKDTNNLS NGLNIVQKITQNIDN VQKITQNID NNGLNIVQKITQNID IVQKITQNI GLNIVQKITQNIDNI VQKITQNID

		NIVQKITQNIDNITE VQKITQNID LNIVQKITQNIDNIT VQKITQNID LEKLKKYLKDTNNLS LKKYLKDTN EITEEVIMPIPQTID EVIMPIPQT ITEEVIMPIPQTIDF IMPIPQTID TEEVIMPIPQTIDFY IMPIPQTID EEVIMPIPQTIDFYI IMPIPQTID EVIMPIPQTIDFYIE IMPIPQTID GGDSNFFTNLEEVRS SNFFTNLEE LEIGGDSNFFTNLEE DSNFFTNLE IGGDSNFFTNLEEVR SNFFTNLEE KYLKDTNNLSAIEES YLKDTNNLS EIGGDSNFFTNLEEV SNFFTNLEE IVQKITQNIDNITEN VQKITQNID YLKDTNNLSAIEESV YLKDTNNLS VQKITQNIDNITENL VQKITQNID GDSNFFTNLEEVRSS SNFFTNLEE IDFYIEPRPISSFLT FYIEPRPIS PQTIDFYIEPRPISS FYIEPRPIS RPISSFLTQGTSPSI FLTQGTSPS PRPISSFLTQGTSPS ISSFLTQGT QTIDFYIEPRPISSF FYIEPRPIS TIDFYIEPRPISSFL FYIEPRPIS ISSFLTQGTSPSITS FLTQGTSPS
	HLA-DRB1*0701	TNLEEVRSSIRTKIK LEEVRSSIR FTNLEEVRSSIRTKI LEEVRSSIR SFLTQGTSPSITSTI LTQGTSPSI
	HLA-DRB1*0802	None
	HLA-DRB1*0901	KDIYNSYIPEVKEEI IYNSYIPEV SSNKDIYNSYIPEVK IYNSYIPEV SNKDIYNSYIPEVKE IYNSYIPEV NKDIYNSYIPEVKEE IYNSYIPEV
	HLA-DRB1*1101	None
	HLA-DRB1*1302	EKINNGLNIVQKITQ KINNGLNIV LNIVQKITQNIDNIT LNIVQKITQ KINNGLNIVQKITQN LNIVQKITQ INNGLNIVQKITQNI LNIVQKITQ NNGLNIVQKITQNID LNIVQKITQ NGLNIVQKITQNIDN LNIVQKITQ AKEKINNGLNIVQKI KINNGLNIV KEKINNGLNIVQKIT KINNGLNIV ELAKEKINNGLNIVQ KINNGLNIV LAKEKINNGLNIVQK KINNGLNIV GLNIVQKITQNIDNI LNIVQKITQ NIVQKITQNIDNITE ITQNIDNIT KELAKEKINNGLNIV EKINNGLNI MCAFLLLNLVNCKFD LLLNLVNCK IVQKITQNIDNITEN ITQNIDNIT CAFLLLNLVNCKFDS LLLNLVNCK VQKITQNIDNITENL ITQNIDNIT AFLLLNLVNCKFDSL LLLNLVNCK QKITQNIDNITENLN ITQNIDNIT NSIAKLLQHLSKSED IAKLLQHLS NCKFDSLNLSTKSVD SLNLSTKSV CKFDSLNLSTKSVDD LNLSTKSVD RPISSFLTQGTSPSI FLTQGTSPS

		KFDSLNLSTKSVDDK LNLSTKSVD FLLLNLVNCKFDSLN LLLNLVNCK PISSFLTQGTSPSIT FLTQGTSPS ISSFLTQGTSPSITS FLTQGTSPS PRPISSFLTQGTSPS ISSFLTQGT FDSLNLSTKSVDDKN LNLSTKSVD FTNLEEVRSSIRTKI LEEVRSSIR SSFLTQGTSPSITST FLTQGTSPS SIAKLLQHLSKSEDQ LQHLSKSED IAKLLQHLSKSEDQA LQHLSKSED KITQNIDNITENLNS ITQNIDNIT ITQNIDNITENLNSK ITQNIDNIT DDKNNSIAKLLQHLS DKNNSIAKL TNLEEVRSSIRTKIK VRSSIRTKI
	HLA-DRB1*1501	FTNLEEVRSSIRTKI LEEVRSSIR TNLEEVRSSIRTKIK LEEVRSSIR FFTNLEEVRSSIRTK LEEVRSSIR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EKLSQVAQHAPNSKI VAQHAPNSK HEKLSQVAQHAPNSK EKLSQVAQH KLSQVAQHAPNSKIE VAQHAPNSK LSQVAQHAPNSKIEK VAQHAPNSK SQVAQHAPNSKIEKV VAQHAPNSK QVAQHAPNSKIEKVK VAQHAPNSK VAQHAPNSKIEKVKS VAQHAPNSK
	HLA-DRB5*0101	None
NP_212481.1| fibronectin/fibrinogen-binding protein, putative [Borrelia burgdorferi B31] Seq20	HLA-DRB1*0101	LDKFNLIQSKITMLK FNLIQSKIT DKFNLIQSKITMLKV FNLIQSKIT LCVFYTKLAKKSGKA FYTKLAKKS CVFYTKLAKKSGKAD FYTKLAKKS NSNFKILDAYYRRPK FKILDAYYR SNFKILDAYYRRPKI FKILDAYYR GNLCVFYTKLAKKSG FYTKLAKKS NLCVFYTKLAKKSGK FYTKLAKKS TNSNFKILDAYYRRP FKILDAYYR IATNSNFKILDAYYR NSNFKILDA ATNSNFKILDAYYRR FKILDAYYR KFNLIQSKITMLKVE IQSKITMLK FNLIQSKITMLKVEN IQSKITMLK NLDKFNLIQSKITML FNLIQSKIT AGNLCVFYTKLAKKS LCVFYTKLA NLIQSKITMLKVENL IQSKITMLK DNLDKFNLIQSKITM FNLIQSKIT KDNLDKFNLIQSKIT LDKFNLIQS VFYTKLAKKSGKADL FYTKLAKKS IKEIPFTNSLITKII FTNSLITKI KEIPFTNSLITKIIQ FTNSLITKI LIQSKITMLKVENLI ITMLKVENL LDVLLGAGNLCVFYT LLGAGNLCV DVLLGAGNLCVFYTK LLGAGNLCV ILFIKLWPSSPNIIA LWPSSPNII IQSKITMLKVENLIP ITMLKVENL LIKEIPFTNSLITKI IPFTNSLIT EIPFTNSLITKIIQP FTNSLITKI IPFTNSLITKIIQPD FTNSLITKI

		FYTKLAKKSGKADLY FYTKLAKKS
		NFKILDAYYRRPKIK FKILDAYYR
		FKILDAYYRRPKIKE FKILDAYYR
		LFIKLWPSSPNIIAT LWPSSPNII
		PSLDVLLGAGNLCVF LLGAGNLCV
		SLDVLLGAGNLCVFY LLGAGNLCV
		TPSLDVLLGAGNLCV DVLLGAGNL
		IIKAFQMKNERIISL FQMKNERII
		IKAFQMKNERIISLE MKNERIISL
		IILFIKLWPSSPNII IKLWPSSPN
		KAFQMKNERIISLEI MKNERIISL
		KKNFKKNALKLRFSD FKKNALKLR
		TKKNFKKNALKLRFS FKKNALKLR
		FIKLWPSSPNIIATN LWPSSPNII
		KNFKKNALKLRFSDF FKKNALKLR
		AFQMKNERIISLEIL MKNERIISL
		FKILICLNPNTTRFH LICLNPNTT
		KILICLNPNTTRFHI LICLNPNTT
		IKLWPSSPNIIATNS LWPSSPNII
		VKNLRRVKNKKLGLV LRRVKNKKL
		EKIKISLNQSLSPKE IKISLNQSL
		FQMKNERIISLEILQ MKNERIISL
		LLGAGNLCVFYTKLA LLGAGNLCV
		EEKIKISLNQSLSPK IKISLNQSL
		KEEKIKISLNQSLSP IKISLNQSL
		KSKIQNGKIIKAFQM IQNGKIIKA
		SKIQNGKIIKAFQMK IQNGKIIKA
		ITKKNFKKNALKLRF FKKNALKLR
		MIKMSLNYTEINTLI MIKMSLNYT
		FLKSKIQNGKIIKAF IQNGKIIKA
		LKSKIQNGKIIKAFQ IQNGKIIKA
		DFLKSKIQNGKIIKA KSKIQNGKI
		KNLRRVKNKKLGLVI VKNKKLGLV
		ILICLNPNTTRFHIT LNPNTTRFH
		VLLGAGNLCVFYTKL LLGAGNLCV
		LRRVKNKKLGLVIPK VKNKKLGLV
		YKEEKIKISLNQSLS IKISLNQSL
		NLRRVKNKKLGLVIP VKNKKLGLV
		KKFKILICLNPNTTR LICLNPNTT
		KFKILICLNPNTTRF LICLNPNTT
		NYKEEKIKISLNQSL KIKISLNQS
		DLYYTQVKNLRRVKN YTQVKNLRR
		HITKKNFKKNALKLR NFKKNALKL
		LYYTQVKNLRRVKNK VKNLRRVKN
		RRVKNKKLGLVIPKA VKNKKLGLV
		LICLNPNTTRFHITK LNPNTTRFH
		KIKISLNQSLSPKEN IKISLNQSL
		QSKITMLKVENLIPE ITMLKVENL
		IKISLNQSLSPKENA IKISLNQSL
		SKITMLKVENLIPEE ITMLKVENL
		MIILFIKLWPSSPNI IKLWPSSPN
		KKGKNSFKTIQNQLK KKGKNSFKT
		PFTNSLITKIIQPDY FTNSLITKI
		NFKKNALKLRFSDFL FKKNALKLR
		YTQVKNLRRVKNKKL VKNLRRVKN
		DMIILFIKLWPSSPN FIKLWPSSP
		FKKNALKLRFSDFLK FKKNALKLR

		KLWPSSPNIIATNSN LWPSSPNII TQVKNLRRVKNKKLG VKNLRRVKN KIIQPDYKSLVLEIY IIQPDYKSL QPDYKSLVLEIYNKI YKSLVLEIY IIQPDYKSLVLEIYN YKSLVLEIY IQPDYKSLVLEIYNK YKSLVLEIY PDYKSLVLEIYNKID YKSLVLEIY FTNSLITKIIQPDYK FTNSLITKI YYTQVKNLRRVKNKK VKNLRRVKN KDMIILFIKLWPSSP MIILFIKLW KNSFKTIQNQLKDNL FKTIQNQLK NSFKTIQNQLKDNLD FKTIQNQLK NTLIKEIPFTNSLIT IKEIPFTNS FTYCGFEILIGRNAK YCGFEILIG KEKTPKIGLHFTYCG TPKIGLHFT HFTYCGFEILIGRNA YCGFEILIG TLIKEIPFTNSLITK IKEIPFTNS GKNSFKTIQNQLKDN FKTIQNQLK EKTPKIGLHFTYCGF IGLHFTYCG KGKNSFKTIQNQLKD FKTIQNQLK ICLNPNTTRFHITKK LNPNTTRFH LWPSSPNIIATNSNF LWPSSPNII EIFLKAKEIHESNKM LKAKEIHES IFLKAKEIHESNKMS LKAKEIHES ADLYYTQVKNLRRVK YTQVKNLRR MKNERIISLEILQKD MKNERIISL YCGFEILIGRNAKEN FEILIGRNA LGAGNLCVFYTKLAK LCVFYTKLA QMKNERIISLEILQK MKNERIISL KADLYYTQVKNLRRV YTQVKNLRR NKKFKILICLNPNTT FKILICLNP RVKNKKLGLVIPKAE VKNKKLGLV TPKIGLHFTYCGFEI IGLHFTYCG KIQNGKIIKAFQMKN IQNGKIIKA GKIIKAFQMKNERII AFQMKNERI KTPKIGLHFTYCGFE IGLHFTYCG VKNKKLGLVIPKAEK VKNKKLGLV IQNGKIIKAFQMKNE IQNGKIIKA TEINTLIKEIPFTNS INTLIKEIP INTLIKEIPFTNSLI IKEIPFTNS EINTLIKEIPFTNSL IKEIPFTNS TGEIFLKAKEIHESN LKAKEIHES TTGEIFLKAKEIHES EIFLKAKEI GEIFLKAKEIHESNK LKAKEIHES MELKEEYNNTSYTSY EYNNTSYTS KIIKAFQMKNERIIS FQMKNERII
	HLA-DRB1*0301	None
	HLA-DRB1*0401	DLYYTQVKNLRRVKN YYTQVKNLR SGKADLYYTQVKNLR SGKADLYYT GKADLYYTQVKNLRR YYTQVKNLR KADLYYTQVKNLRRV YYTQVKNLR ADLYYTQVKNLRRVK YYTQVKNLR LYYTQVKNLRRVKNK YYTQVKNLR YYTQVKNLRRVKNKK YYTQVKNLR MELKEEYNNTSYTSY LKEEYNNTS IMELKEEYNNTSYTS LKEEYNNTS DKKIMELKEEYNNTS KIMELKEEY

		KKIMELKEEYNNTSY LKEEYNNTS KIMELKEEYNNTSYT LKEEYNNTS DMIILFIKLWPSSPN LFIKLWPSS MIILFIKLWPSSPNI LFIKLWPSS IILFIKLWPSSPNII LFIKLWPSS ILFIKLWPSSPNIIA IKLWPSSPN ELKEEYNNTSYTSYS LKEEYNNTS LKEEYNNTSYTSYSE LKEEYNNTS WPSSPNIIATNSNFK PNIIATNSN PSSPNIIATNSNFKI IIATNSNFK LFIKLWPSSPNIIAT IKLWPSSPN SSPNIIATNSNFKIL IIATNSNFK GAYVFIKNQKNKTPS FIKNQKNKT PGAYVFIKNQKNKTP FIKNQKNKT PNIIATNSNFKILDA IIATNSNFK SPNIIATNSNFKILD IIATNSNFK KDMIILFIKLWPSSP LFIKLWPSS YPGAYVFIKNQKNKT YVFIKNQKN YVFIKNQKNKTPSLD FIKNQKNKT AYVFIKNQKNKTPSL FIKNQKNKT LIEKYKKELIVLEKR YKKELIVLE
	HLA-DRB1*0404	WPSSPNIIATNSNFK PNIIATNSN PSSPNIIATNSNFKI IIATNSNFK FKILICLNPNTTRFH ILICLNPNT SSPNIIATNSNFKIL IIATNSNFK KFKILICLNPNTTRF ILICLNPNT PNIIATNSNFKILDA IIATNSNFK SPNIIATNSNFKILD IIATNSNFK KKFKILICLNPNTTR ILICLNPNT NKKFKILICLNPNTT ILICLNPNT MIILFIKLWPSSPNI FIKLWPSSP KILICLNPNTTRFHI LICLNPNTT IILFIKLWPSSPNII KLWPSSPNI ILFIKLWPSSPNIIA KLWPSSPNI SNFKILDAYYRRPKI ILDAYYRRP TNSNFKILDAYYRRP FKILDAYYR NSNFKILDAYYRRPK ILDAYYRRP NFKILDAYYRRPKIK ILDAYYRRP FKILDAYYRRPKIKE ILDAYYRRP KDMIILFIKLWPSSP MIILFIKLW ILICLNPNTTRFHIT ILICLNPNT DNKKFKILICLNPNT FKILICLNP NIIATNSNFKILDAY IIATNSNFK IIATNSNFKILDAYY IIATNSNFK DMIILFIKLWPSSPN FIKLWPSSP
	HLA-DRB1*0405	DMIILFIKLWPSSPN FIKLWPSSP MIILFIKLWPSSPNI IKLWPSSPN IILFIKLWPSSPNII IKLWPSSPN ILFIKLWPSSPNIIA IKLWPSSPN LFIKLWPSSPNIIAT IKLWPSSPN FIKLWPSSPNIIATN IKLWPSSPN IKLWPSSPNIIATNS IKLWPSSPN DLYYTQVKNLRRVKN YTQVKNLRR LYYTQVKNLRRVKNK YTQVKNLRR GKADLYYTQVKNLRR YYTQVKNLR ADLYYTQVKNLRRVK YTQVKNLRR

		KADLYYTQVKNLRRV YTQVKNLRR
		KKGKNSFKTIQNQLK KNSFKTIQN
		KGKNSFKTIQNQLKD KNSFKTIQN
		KDMIILFIKLWPSSP ILFIKLWPS
		KLWPSSPNIIATNSN WPSSPNIIA
		YYTQVKNLRRVKNKK YTQVKNLRR
		GKNSFKTIQNQLKDN FKTIQNQLK
		KNSFKTIQNQLKDNL FKTIQNQLK
		DSLKQQIKLLENIEN LKQQIKLLE
		IKMSLNYTEINTLIK IKMSLNYTE
		SLKQQIKLLENIENE IKLLENIEN
		LKQQIKLLENIENEK IKLLENIEN
		WPSSPNIIATNSNFK WPSSPNIIA
		KQQIKLLENIENEKE IKLLENIEN
		KMSLNYTEINTLIKE YTEINTLIK
		MSLNYTEINTLIKEI YTEINTLIK
		SLNYTEINTLIKEIP YTEINTLIK
		QQIKLLENIENEKEK IKLLENIEN
		KAYKKGKNSFKTIQN YKKGKNSFK
		LNYTEINTLIKEIPF YTEINTLIK
		AYKKGKNSFKTIQNQ KNSFKTIQN
		YTQVKNLRRVKNKKL YTQVKNLRR
		LQKDMIILFIKLWPS IILFIKLWP
		YKKGKNSFKTIQNQL KNSFKTIQN
		LWPSSPNIIATNSNF WPSSPNIIA
		QKDMIILFIKLWPSS ILFIKLWPS
		NSFKTIQNQLKDNLD FKTIQNQLK
	HLA-DRB1*0701	ILICLNPNTTRFHIT LNPNTTRFH
		LICLNPNTTRFHITK LNPNTTRFH
		KILICLNPNTTRFHI LNPNTTRFH
		ICLNPNTTRFHITKK LNPNTTRFH
		MELKEEYNNTSYTSY EEYNNTSYT
		ELKEEYNNTSYTSYS YNNTSYTSY
		KEEYNNTSYTSYSEF YNNTSYTSY
		LKEEYNNTSYTSYSE YNNTSYTSY
		EEYNNTSYTSYSEFL YNNTSYTSY
		CLNPNTTRFHITKKN NPNTTRFHI
		SSPNIIATNSNFKIL IIATNSNFK
		FKILICLNPNTTRFH CLNPNTTRF
		SPNIIATNSNFKILD IIATNSNFK
		IKEIPFTNSLITKII IPFTNSLIT
		LIKEIPFTNSLITKI IPFTNSLIT
		PNIIATNSNFKILDA IIATNSNFK
		KEIPFTNSLITKIIQ IPFTNSLIT
		PSSPNIIATNSNFKI IIATNSNFK
		LNPNTTRFHITKKNF LNPNTTRFH
		WPSSPNIIATNSNFK NIIATNSNF
	HLA-DRB1*0802	DMIILFIKLWPSSPN FIKLWPSSP
		MIILFIKLWPSSPNI FIKLWPSSP
		IILFIKLWPSSPNII FIKLWPSSP
		KDMIILFIKLWPSSP LFIKLWPSS
		GNLCVFYTKLAKKSG FYTKLAKKS
		NLCVFYTKLAKKSGK YTKLAKKSG
		ILFIKLWPSSPNIIA FIKLWPSSP
		LCVFYTKLAKKSGKA YTKLAKKSG
		CVFYTKLAKKSGKAD YTKLAKKSG
		VFYTKLAKKSGKADL YTKLAKKSG

		LFIKLWPSSPNIIAT FIKLWPSSP PGAYVFIKNQKNKTP FIKNQKNKT GAYVFIKNQKNKTPS FIKNQKNKT AYVFIKNQKNKTPSL FIKNQKNKT YVFIKNQKNKTPSLD FIKNQKNKT YPGAYVFIKNQKNKT YVFIKNQKN
	HLA-DRB1*0901	ILFIKLWPSSPNIIA LWPSSPNII LFIKLWPSSPNIIAT LWPSSPNII FIKLWPSSPNIIATN LWPSSPNII IKLWPSSPNIIATNS LWPSSPNII IILFIKLWPSSPNII KLWPSSPNI KLWPSSPNIIATNSN LWPSSPNII LWPSSPNIIATNSNF LWPSSPNII IKEIPFTNSLITKII FTNSLITKI KEIPFTNSLITKIIQ FTNSLITKI LIKEIPFTNSLITKI IPFTNSLIT
	HLA-DRB1*1101	DLYYTQVKNLRRVKN QVKNLRRVK LYYTQVKNLRRVKNK VKNLRRVKN YYTQVKNLRRVKNKK VKNLRRVKN YTQVKNLRRVKNKKL VKNLRRVKN TQVKNLRRVKNKKLG VKNLRRVKN QVKNLRRVKNKKLGL VKNLRRVKN VKNLRRVKNKKLGLV VKNLRRVKN NLCVFYTKLAKKSGK YTKLAKKSG LCVFYTKLAKKSGKA YTKLAKKSG GNLCVFYTKLAKKSG FYTKLAKKS CVFYTKLAKKSGKAD YTKLAKKSG VFYTKLAKKSGKADL YTKLAKKSG FYTKLAKKSGKADLY YTKLAKKSG
	HLA-DRB1*1302	KGELILLNINKIQKG LILLNINKI GELILLNINKIQKGI LILLNINKI ELILLNINKIQKGIK LNINKIQKG LILLNINKIQKGIKE LNINKIQKG EKGELILLNINKIQK LILLNINKI KEKGELILLNINKIQ LILLNINKI DLYYTQVKNLRRVKN YYTQVKNLR VKNLRRVKNKKLGLV VKNLRRVKN AYVFIKNQKNKTPSL FIKNQKNKT YVFIKNQKNKTPSLD FIKNQKNKT GAYVFIKNQKNKTPS FIKNQKNKT LYYTQVKNLRRVKNK VKNLRRVKN ILLNINKIQKGIKEI LNINKIQKG EKEKGELILLNINKI KGELILLNI YYTQVKNLRRVKNKK VKNLRRVKN TQVKNLRRVKNKKLG VKNLRRVKN YTQVKNLRRVKNKKL VKNLRRVKN PGAYVFIKNQKNKTP FIKNQKNKT ITKKNFKKNALKLRF FKKNALKLR HITKKNFKKNALKLR KKNFKKNAL VFIKNQKNKTPSLDV FIKNQKNKT LDKFNLIQSKITMLK FNLIQSKIT DKFNLIQSKITMLKV IQSKITMLK KNLRRVKNKKLGLVI VKNKKLGLV NLRRVKNKKLGLVIP VKNKKLGLV TKKNFKKNALKLRFS FKKNALKLR LRRVKNKKLGLVIPK VKNKKLGLV

		KKNFKKNALKLRFSD FKKNALKLR
		FIKNQKNKTPSLDVL FIKNQKNKT
		KFNLIQSKITMLKVE IQSKITMLK
		QVKNLRRVKNKKLGL VKNLRRVKN
		LLNINKIQKGIKEIN LNINKIQKG
		FNLIQSKITMLKVEN IQSKITMLK
		RRVKNKKLGLVIPKA VKNKKLGLV
		YPGAYVFIKNQKNKT VFIKNQKNK
		ISLEILQKDMIILFI LEILQKDMI
		IISLEILQKDMIILF LEILQKDMI
		RVKNKKLGLVIPKAE VKNKKLGLV
		VKNKKLGLVIPKAEK LGLVIPKAE
		KNFKKNALKLRFSDF FKKNALKLR
		IPFTNSLITKIIQPD FTNSLITKI
		NLDKFNLIQSKITML FNLIQSKIT
		FKILICLNPNTTRFH LICLNPNTT
		KKFKILICLNPNTTR LICLNPNTT
		IKEIPFTNSLITKII FTNSLITKI
		KEIPFTNSLITKIIQ FTNSLITKI
		NLIQSKITMLKVENL IQSKITMLK
		KILICLNPNTTRFHI LICLNPNTT
		KFKILICLNPNTTRF LICLNPNTT
		LEILQKDMIILFIKL LQKDMIILF
		EIPFTNSLITKIIQP FTNSLITKI
		SLEILQKDMIILFIK LQKDMIILF
		LNINKIQKGIKEINL LNINKIQKG
		IKLDENLIKKIKNQT ENLIKKIKN
		LNYTEINTLIKEIPF INTLIKEIP
		KADLYYTQVKNLRRV YYTQVKNLR
		ADLYYTQVKNLRRVK YYTQVKNLR
		SLNYTEINTLIKEIP TEINTLIKE
		PFTNSLITKIIQPDY FTNSLITKI
		DNLDKFNLIQSKITM FNLIQSKIT
		DFLKSKIQNGKIIKA LKSKIQNGK
		QPDYKSLVLEIYNKI YKSLVLEIY
		NYTEINTLIKEIPFT INTLIKEIP
		PDYKSLVLEIYNKID YKSLVLEIY
		YTEINTLIKEIPFTN INTLIKEIP
		RIISLEILQKDMIIL LEILQKDMI
		GKADLYYTQVKNLRR YYTQVKNLR
		TEINTLIKEIPFTNS INTLIKEIP
		NKKFKILICLNPNTT FKILICLNP
		IATNSNFKILDAYYR IATNSNFKI
		YKSLVLEIYNKIDNK YKSLVLEIY
		KDNLDKFNLIQSKIT KFNLIQSKI
		ILICLNPNTTRFHIT LICLNPNTT
		LIKEIPFTNSLITKI IPFTNSLIT
		DYKSLVLEIYNKIDN YKSLVLEIY
		LKSKIQNGKIIKAFQ IQNGKIIKA
		FLKSKIQNGKIIKAF IQNGKIIKA
		IKNQKNKTPSLDVLL IKNQKNKTP
		MIKMSLNYTEINTLI MIKMSLNYT
		NFKKNALKLRFSDFL FKKNALKLR
		FTNSLITKIIQPDYK FTNSLITKI
		LDVLLGAGNLCVFYT VLLGAGNLC
		DSLKQQIKLLENIEN LKQQIKLLE
		LVLEIYNKIDNKKFK IYNKIDNKK

		LIQSKITMLKVENLI IQSKITMLK SLVLEIYNKIDNKKF IYNKIDNKK SGKADLYYTQVKNLR LYYTQVKNL KIIQPDYKSLVLEIY IQPDYKSLV DMIILFIKLWPSSPN IILFIKLWP LICLNPNTTRFHITK LICLNPNTT KITMLKVENLIPEEE LKVENLIPE FKKNALKLRFSDFLK FKKNALKLR EILQKDMIILFIKLW LQKDMIILF NERIISLEILQKDMI IISLEILQK ERIISLEILQKDMII LEILQKDMI IILFIKLWPSSPNII IKLWPSSPN KKLGLVIPKAEKNLH LGLVIPKAE KSLVLEIYNKIDNKK LVLEIYNKI DVLLGAGNLCVFYTK AGNLCVFYT ILFIKLWPSSPNIIA IKLWPSSPN LNDQIKKTNIKELLI DQIKKTNIK ITMLKVENLIPEEEY LKVENLIPE SPNIIATNSNFKILD IATNSNFKI SSPNIIATNSNFKIL IATNSNFKI LEIYNKIDNKKFKIL IYNKIDNKK KNKKLGLVIPKAEKN LGLVIPKAE SLNDQIKKTNIKELL DQIKKTNIK VLLGAGNLCVFYTKL AGNLCVFYT PNIIATNSNFKILDA IATNSNFKI IQSKITMLKVENLIP IQSKITMLK ILQKDMIILFIKLWP LQKDMIILF IQKGIKEINLLNYKE IKEINLLNY MIILFIKLWPSSPNI IKLWPSSPN LFIKLWPSSPNIIAT IKLWPSSPN KIQKGIKEINLLNYK IKEINLLNY NKKLGLVIPKAEKNL LGLVIPKAE NKIQKGIKEINLLNY KGIKEINLL SDFLKSKIQNGKIIK LKSKIQNGK NSFKTIQNQLKDNLD IQNQLKDNL QSKITMLKVENLIPE ITMLKVENL NIIATNSNFKILDAY IATNSNFKI SKITMLKVENLIPEE LKVENLIPE IIQPDYKSLVLEIYN YKSLVLEIY ATNSNFKILDAYYRR FKILDAYYR KNSFKTIQNQLKDNL FKTIQNQLK EKRIDSLKQQIKLLE IDSLKQQIK IDSLKQQIKLLENIE LKQQIKLLE PSSPNIIATNSNFKI PNIIATNSN LQKDMIILFIKLWPS IILFIKLWP RIDSLKQQIKLLENI LKQQIKLLE QKGIKEINLLNYKEE IKEINLLNY IQPDYKSLVLEIYNK YKSLVLEIY
	HLA-DRB1*1501	DMIILFIKLWPSSPN LFIKLWPSS KDMIILFIKLWPSSP LFIKLWPSS MIILFIKLWPSSPNI LFIKLWPSS QKDMIILFIKLWPSS ILFIKLWPS IILFIKLWPSSPNII LFIKLWPSS VKNLRRVKNKKLGLV LRRVKNKKL ILFIKLWPSSPNIIA LFIKLWPSS KNLRRVKNKKLGLVI VKNKKLGLV NLRRVKNKKLGLVIP VKNKKLGLV

		LRRVKNKKLGLVIPK VKNKKLGLV LQKDMIILFIKLWPS IILFIKLWP RRVKNKKLGLVIPKA VKNKKLGLV LFIKLWPSSPNIIAT LFIKLWPSS KENALQYFKAYKKGK LQYFKAYKK DLYYTQVKNLRRVKN YTQVKNLRR ENALQYFKAYKKGKN LQYFKAYKK ADLYYTQVKNLRRVK YTQVKNLRR LYYTQVKNLRRVKNK YTQVKNLRR NALQYFKAYKKGKNS LQYFKAYKK KADLYYTQVKNLRRV YTQVKNLRR YTQVKNLRRVKNKKL YTQVKNLRR ATNSNFKILDAYYRR FKILDAYYR GNLCVFYTKLAKKSG VFYTKLAKK TNSNFKILDAYYRRP FKILDAYYR KGELILLNINKIQKG LLNINKIQK IATNSNFKILDAYYR SNFKILDAY NLCVFYTKLAKKSGK VFYTKLAKK LCVFYTKLAKKSGKA VFYTKLAKK SNFKILDAYYRRPKI FKILDAYYR NSNFKILDAYYRRPK FKILDAYYR AGNLCVFYTKLAKKS VFYTKLAKK EKGELILLNINKIQK LILLNINKI TQVKNLRRVKNKKLG LRRVKNKKL YYTQVKNLRRVKNKK YTQVKNLRR GELILLNINKIQKGI LLNINKIQK PKENALQYFKAYKKG LQYFKAYKK VKNKKLGLVIPKAEK VKNKKLGLV RVKNKKLGLVIPKAE VKNKKLGLV
	HLA-DRB3*0101	None
	HLA-DRB4*0101	ILFIKLWPSSPNIIA LWPSSPNII IILFIKLWPSSPNII FIKLWPSSP LFIKLWPSSPNIIAT LWPSSPNII FIKLWPSSPNIIATN LWPSSPNII IKLWPSSPNIIATNS LWPSSPNII KKFKILICLNPNTTR LICLNPNTT FKILICLNPNTTRFH LICLNPNTT KILICLNPNTTRFHI LICLNPNTT KFKILICLNPNTTRF LICLNPNTT RIISLEILQKDMIIL LEILQKDMI NKKFKILICLNPNTT ILICLNPNT IISLEILQKDMIILF LEILQKDMI ISLEILQKDMIILFI LEILQKDMI MIILFIKLWPSSPNI IKLWPSSPN KKLGLVIPKAEKNLH LGLVIPKAE DMIILFIKLWPSSPN FIKLWPSSP KLGLVIPKAEKNLHI IPKAEKNLH LGLVIPKAEKNLHIK IPKAEKNLH GLVIPKAEKNLHIKL IPKAEKNLH LVIPKAEKNLHIKLD IPKAEKNLH ERIISLEILQKDMII LEILQKDMI NERIISLEILQKDMI ISLEILQKD GKADLYYTQVKNLRR YYTQVKNLR KADLYYTQVKNLRRV YYTQVKNLR ADLYYTQVKNLRRVK YYTQVKNLR KLWPSSPNIIATNSN LWPSSPNII DLYYTQVKNLRRVKN YYTQVKNLR

	HLA-DRB5*0101	DLYYTQVKNLRRVKN YYTQVKNLR KNSFKTIQNQLKDNL FKTIQNQLK GKADLYYTQVKNLRR YYTQVKNLR NSFKTIQNQLKDNLD FKTIQNQLK ADLYYTQVKNLRRVK YYTQVKNLR KADLYYTQVKNLRRV YYTQVKNLR KKGKNSFKTIQNQLK KKGKNSFKT KGKNSFKTIQNQLKD FKTIQNQLK GKNSFKTIQNQLKDN FKTIQNQLK LYYTQVKNLRRVKNK YTQVKNLRR LQYFKAYKKGKNSFK YFKAYKKGK NSNFKILDAYYRRPK FKILDAYYR SNFKILDAYYRRPKI FKILDAYYR TNSNFKILDAYYRRP FKILDAYYR YYTQVKNLRRVKNKK YYTQVKNLR QYFKAYKKGKNSFKT YKKGKNSFK YFKAYKKGKNSFKTI YKKGKNSFK GAYVFIKNQKNKTPS IKNQKNKTP PGAYVFIKNQKNKTP YVFIKNQKN ENALQYFKAYKKGKN YFKAYKKGK NALQYFKAYKKGKNS YFKAYKKGK SGKADLYYTQVKNLR ADLYYTQVK SFKTIQNQLKDNLDK FKTIQNQLK ATNSNFKILDAYYRR FKILDAYYR FKTIQNQLKDNLDKF FKTIQNQLK LIPEEEYNQEKTAIK LIPEEEYNQ FKAYKKGKNSFKTIQ YKKGKNSFK AYVFIKNQKNKTPSL IKNQKNKTP KAYKKGKNSFKTIQN YKKGKNSFK IATNSNFKILDAYYR IATNSNFKI NTTRFHITKKNFKKN FHITKKNFK KENALQYFKAYKKGK LQYFKAYKK PNTTRFHITKKNFKK FHITKKNFK TTRFHITKKNFKKNA FHITKKNFK YVFIKNQKNKTPSLD IKNQKNKTP YTQVKNLRRVKNKKL YTQVKNLRR ALQYFKAYKKGKNSF YFKAYKKGK NFKILDAYYRRPKIK FKILDAYYR TRFHITKKNFKKNAL FHITKKNFK FKILDAYYRRPKIKE FKILDAYYR PEEEYNQEKTAIKEK YNQEKTAIK NPNTTRFHITKKNFK RFHITKKNF IPEEEYNQEKTAIKE YNQEKTAIK EEEYNQEKTAIKEKE YNQEKTAIK EEYNQEKTAIKEKEK YNQEKTAIK VFIKNQKNKTPSLDV IKNQKNKTP YPGAYVFIKNQKNKT YVFIKNQKN
AAC44656.1| P30 Borrelia burgdorferi Seq21	HLA-DRB1*0101	VHQSFIPVPVHVTDK FIPVPVHVT LLVHQSFIPVPVHVT HQSFIPVPV LVHQSFIPVPVHVTD FIPVPVHVT HQSFIPVPVHVTDKY FIPVPVHVT QSFIPVPVHVTDKYG FIPVPVHVT ELGIRAIDSKTLEIT IRAIDSKTL LGIRAIDSKTLEITL IRAIDSKTL DSELGIRAIDSKTLE IRAIDSKTL TDSELGIRAIDSKTL ELGIRAIDS

		SELGIRAIDSKTLEI IRAIDSKTL
		TLYRGIVTGDPNTGG IVTGDPNTG
		DTLYRGIVTGDPNTG YRGIVTGDP
		MKLQRSLSLIIFSLT LQRSLSLII
		YRGIVTGDPNTGGHK IVTGDPNTG
		LYRGIVTGDPNTGGH IVTGDPNTG
		ITFYTTNDSSTAYKM YTTNDSSTA
		EEITFYTTNDSSTAY YTTNDSSTA
		SFIPVPVHVTDKYGQ FIPVPVHVT
		EITFYTTNDSSTAYK YTTNDSSTA
		LEEITFYTTNDSSTA ITFYTTNDS
		TFYTTNDSSTAYKMY YTTNDSSTA
		LRDNLTWSDGVAITA LTWSDGVAI
		FIPVPVHVTDKYGQN FIPVPVHVT
		RDNLTWSDGVAITAE LTWSDGVAI
		RGIVTGDPNTGGHKP IVTGDPNTG
		DNLTWSDGVAITAEG LTWSDGVAI
		TSPENMVTSGPFKLK MVTSGPFKL
		GIRAIDSKTLEITLA IRAIDSKTL
		NLTWSDGVAITAEGI LTWSDGVAI
		IRAIDSKTLEITLAS IRAIDSKTL
		LTWSDGVAITAEGIR LTWSDGVAI
		PENMVTSGPFKLKER MVTSGPFKL
		SPENMVTSGPFKLKE MVTSGPFKL
		WSDGVAITAEGIRKS GVAITAEGI
		GQNWTSPENMVTSGP WTSPENMVT
		SDGVAITAEGIRKSY ITAEGIRKS
		WTSPENMVTSGPFKL WTSPENMVT
		QNWTSPENMVTSGPF WTSPENMVT
		FYLRDNLTWSDGVAI LRDNLTWSD
		YLRDNLTWSDGVAIT LTWSDGVAI
		TLEITLASPKPYFID LASPKPYFI
		KTLEITLASPKPYFI ITLASPKPY
		ENMVTSGPFKLKERI MVTSGPFKL
		DKYGQNWTSPENMVT GQNWTSPEN
		KYGQNWTSPENMVTS WTSPENMVT
		GVAITAEGIRKSYLR ITAEGIRKS
		LEITLASPKPYFIDL LASPKPYFI
		DGVAITAEGIRKSYL ITAEGIRKS
		YGQNWTSPENMVTSG WTSPENMVT
		KSYLRILNKETGSTY ILNKETGST
		PYFIDLLVHQSFIPV FIDLLVHQS
		RKSYLRILNKETGST YLRILNKET
		GIVTGDPNTGGHKPG IVTGDPNTG
		EITLASPKPYFIDLL LASPKPYFI
		KPYFIDLLVHQSFIP FIDLLVHQS
		GAEPRSLDPQLAEDN PRSLDPQLA
		AEPRSLDPQLAEDNV PRSLDPQLA
		SPKPYFIDLLVHQSF FIDLLVHQS
		PKPYFIDLLVHQSFI FIDLLVHQS
		ASPKPYFIDLLVHQS YFIDLLVHQ
		FYTTNDSSTAYKMYV YTTNDSSTA
		EGVSTKISLGAEPRS VSTKISLGA
		VAITAEGIRKSYLRI ITAEGIRKS
		SYLRILNKETGSTYV ILNKETGST
		ITLASPKPYFIDLLV LASPKPYFI
		KLQRSLSLIIFSLTV LQRSLSLII

		LQRSLSLIIFSLTVL LQRSLSLII KERKEGVSTKISLGA RKEGVSTKI YLRILNKETGSTYVD ILNKETGST NMVTSGPFKLKERIP MVTSGPFKL ERKEGVSTKISLGAE VSTKISLGA YTTNDSSTAYKMYVN YTTNDSSTA KEGVSTKISLGAEPR VSTKISLGA AITAEGIRKSYLRIL ITAEGIRKS ITAEGIRKSYLRILN ITAEGIRKS RKEGVSTKISLGAEP VSTKISLGA FIDLLVHQSFIPVPV FIDLLVHQS LRILNKETGSTYVDM ILNKETGST ISLGAEPRSLDPQLA LGAEPRSLD IVTGDPNTGGHKPGL IVTGDPNTG NWTSPENMVTSGPFK WTSPENMVT VSTKISLGAEPRSLD VSTKISLGA EGIRKSYLRILNKET IRKSYLRIL GVSTKISLGAEPRSL VSTKISLGA RSLSLIIFSLTVLCC LIIFSLTVL DSKTLEITLASPKPY EITLASPKP SKTLEITLASPKPYF ITLASPKPY YFIDLLVHQSFIPVP FIDLLVHQS MIDTLYRGIVTGDPN YRGIVTGDP MVTSGPFKLKERIPS MVTSGPFKL KMIDTLYRGIVTGDP MIDTLYRGI SLSLIIFSLTVLCCD IFSLTVLCC PRSLDPQLAEDNVAS PRSLDPQLA LSLIIFSLTVLCCDN IFSLTVLCC IDTLYRGIVTGDPNT YRGIVTGDP EPRSLDPQLAEDNVA PRSLDPQLA SLGAEPRSLDPQLAE PRSLDPQLA IRKSYLRILNKETGS YLRILNKET GIRKSYLRILNKETG IRKSYLRIL DLLVHQSFIPVPVHV LVHQSFIPV LGAEPRSLDPQLAED PRSLDPQLA QRSLSLIIFSLTVLC LIIFSLTVL SLIIFSLTVLCCDNK IFSLTVLCC IDLLVHQSFIPVPVH LVHQSFIPV
	HLA-DRB1*0301	None
	HLA-DRB1*0401	ASPKPYFIDLLVHQS YFIDLLVHQ SPKPYFIDLLVHQSF YFIDLLVHQ KPYFIDLLVHQSFIP YFIDLLVHQ PKPYFIDLLVHQSFI YFIDLLVHQ LASPKPYFIDLLVHQ PYFIDLLVH PYFIDLLVHQSFIPV YFIDLLVHQ YFIDLLVHQSFIPVP YFIDLLVHQ EEITFYTTNDSSTAY YTTNDSSTA EKYVFEKDNKYYDSN YVFEKDNKY SEKYVFEKDNKYYDS YVFEKDNKY PSEKYVFEKDNKYYD YVFEKDNKY RIPSEKYVFEKDNKY RIPSEKYVF IPSEKYVFEKDNKYY YVFEKDNKY LEEITFYTTNDSSTA ITFYTTNDS EITFYTTNDSSTAYK YTTNDSSTA ITFYTTNDSSTAYKM YTTNDSSTA

	HLA-DRB1*0404	RKSYLRILNKETGST YLRILNKET KSYLRILNKETGSTY ILNKETGST SYLRILNKETGSTYV ILNKETGST YLRILNKETGSTYVD ILNKETGST LRILNKETGSTYVDM ILNKETGST
	HLA-DRB1*0405	VTDKYGQNWTSPENM GQNWTSPEN HVTDKYGQNWTSPEN YGQNWTSPE TDKYGQNWTSPENMV GQNWTSPEN DKYGQNWTSPENMVT GQNWTSPEN KYGQNWTSPENMVTS GQNWTSPEN YGQNWTSPENMVTSG GQNWTSPEN GQNWTSPENMVTSGP GQNWTSPEN LVHQSFIPVPVHVTD HQSFIPVPV ELEEITFYTTNDSST ITFYTTNDS LEEITFYTTNDSSTA ITFYTTNDS EVELEEITFYTTNDS EITFYTTND LLVHQSFIPVPVHVT HQSFIPVPV VELEEITFYTTNDSS ITFYTTNDS YPFYLRDNLTWSDGV LRDNLTWSD PFYLRDNLTWSDGVA LRDNLTWSD TAYPFYLRDNLTWSD YLRDNLTWS FYLRDNLTWSDGVAI LRDNLTWSD EEITFYTTNDSSTAY ITFYTTNDS AYPFYLRDNLTWSDG LRDNLTWSD
	HLA-DRB1*0701	LLVHQSFIPVPVHVT SFIPVPVHV LVHQSFIPVPVHVTD FIPVPVHVT LGIRAIDSKTLEITL IRAIDSKTL VHQSFIPVPVHVTDK FIPVPVHVT HQSFIPVPVHVTDKY FIPVPVHVT ELGIRAIDSKTLEIT IRAIDSKTL MKLQRSLSLIIFSLT MKLQRSLSL SELGIRAIDSKTLEI IRAIDSKTL TDSELGIRAIDSKTL ELGIRAIDS DSELGIRAIDSKTLE IRAIDSKTL QSFIPVPVHVTDKYG FIPVPVHVT
	HLA-DRB1*0802	MVTSGPFKLKERIPS MVTSGPFKL VTSGPFKLKERIPSE FKLKERIPS SGPFKLKERIPSEKY FKLKERIPS GPFKLKERIPSEKYV FKLKERIPS TSGPFKLKERIPSEK FKLKERIPS SKTLEITLASPKPYF ITLASPKPY KTLEITLASPKPYFI ITLASPKPY DSKTLEITLASPKPY LEITLASPK TLEITLASPKPYFID ITLASPKPY LEITLASPKPYFIDL ITLASPKPY
	HLA-DRB1*0901	MKLQRSLSLIIFSLT LQRSLSLII KTLEITLASPKPYFI ITLASPKPY
	HLA-DRB1*1101	MVTSGPFKLKERIPS VTSGPFKLK VTSGPFKLKERIPSE FKLKERIPS TSGPFKLKERIPSEK FKLKERIPS SGPFKLKERIPSEKY FKLKERIPS GPFKLKERIPSEKYV FKLKERIPS
	HLA-DRB1*1302	QRSLSLIIFSLTVLC LSLIIFSLT RSLSLIIFSLTVLCC LSLIIFSLT LQRSLSLIIFSLTVL LSLIIFSLT LSLIIFSLTVLCCDN LIIFSLTVL

		SLSLIIFSLTVLCCD LIIFSLTVL STYVDMVKSIIKNGQ YVDMVKSII TYVDMVKSIIKNGQE VKSIIKNGQ YVDMVKSIIKNGQEY VKSIIKNGQ MKLQRSLSLIIFSLT LQRSLSLII VDMVKSIIKNGQEYF VKSIIKNGQ KSYLRILNKETGSTY LRILNKETG KLQRSLSLIIFSLTV LSLIIFSLT SYLRILNKETGSTYV LRILNKETG DMVKSIIKNGQEYFD VKSIIKNGQ SLIIFSLTVLCCDNK LIIFSLTVL KTLEITLASPKPYFI ITLASPKPY GSTYVDMVKSIIKNG YVDMVKSII DSKTLEITLASPKPY KTLEITLAS SKTLEITLASPKPYF ITLASPKPY TLEITLASPKPYFID ITLASPKPY LEITLASPKPYFIDL ITLASPKPY RKSYLRILNKETGST LRILNKETG LIIFSLTVLCCDNKE LIIFSLTVL YLRILNKETGSTYVD LRILNKETG LRILNKETGSTYVDM LRILNKETG IRKSYLRILNKETGS LRILNKETG ETGSTYVDMVKSIIK YVDMVKSII TGSTYVDMVKSIIKN YVDMVKSII GIRKSYLRILNKETG YLRILNKET MVTSGPFKLKERIPS MVTSGPFKL WTSPENMVTSGPFKL ENMVTSGPF TSPENMVTSGPFKLK MVTSGPFKL MVKSIIKNGQEYFDG VKSIIKNGQ SPENMVTSGPFKLKE MVTSGPFKL GPFKLKERIPSEKYV FKLKERIPS VKSIIKNGQEYFDGQ VKSIIKNGQ SGPFKLKERIPSEKY FKLKERIPS TSGPFKLKERIPSEK FKLKERIPS
	HLA-DRB1*1501	RKSYLRILNKETGST LRILNKETG KSYLRILNKETGSTY LRILNKETG GIRKSYLRILNKETG YLRILNKET IRKSYLRILNKETGS LRILNKETG SYLRILNKETGSTYV LRILNKETG LQRSLSLIIFSLTVL SLIIFSLTV QRSLSLIIFSLTVLC LIIFSLTVL RSLSLIIFSLTVLCC LIIFSLTVL SLSLIIFSLTVLCCD LIIFSLTVL YPFYLRDNLTWSDGV YLRDNLTWS LSLIIFSLTVLCCDN LIIFSLTVL PFYLRDNLTWSDGVA YLRDNLTWS YLRILNKETGSTYVD LRILNKETG AYPFYLRDNLTWSDG YLRDNLTWS GTAYPFYLRDNLTWS FYLRDNLTW LRILNKETGSTYVDM LRILNKETG TAYPFYLRDNLTWSD YLRDNLTWS
	HLA-DRB3*0101	None
	HLA-DRB4*0101	YFIDLLVHQSFIPVP IDLLVHQSF FIDLLVHQSFIPVPV LVHQSFIPV IDLLVHQSFIPVPVH LVHQSFIPV PYFIDLLVHQSFIPV IDLLVHQSF

	HLA-DRB5*0101	None
NP_045619.1| immunogenic protein P37, putative [Borrelia burgdorferi B31] Seq22	HLA-DRB1*0101	ASLDKIKSLLSTAKS IKSLLSTAK KASLDKIKSLLSTAK LDKIKSLLS LDKIKSLLSTAKSYL IKSLLSTAK SLDKIKSLLSTAKSY IKSLLSTAK DKIKSLLSTAKSYLE IKSLLSTAK QFMADAKASMSSTKS MADAKASMS NKLFILTILFSSVIS LTILFSSVI KIKSLLSTAKSYLEQ IKSLLSTAK INKLFILTILFSSVI LFILTILFS LFILTILFSSVISCK LTILFSSVI IKSLLSTAKSYLEQT IKSLLSTAK RGVGSSKANLALLPS VGSSKANLA KLFILTILFSSVISC LTILFSSVI YHQFMADAKASMSST MADAKASMS GYHQFMADAKASMSS MADAKASMS QTRRGVGSSKANLAL VGSSKANLA EQTRRGVGSSKANLA RRGVGSSKA HQFMADAKASMSSTK MADAKASMS FILTILFSSVISCKL LTILFSSVI RRGVGSSKANLALLP VGSSKANLA AGYHQFMADAKASMS QFMADAKAS MNLINKLFILTILFS LINKLFILT TRRGVGSSKANLALL VGSSKANLA FMADAKASMSSTKSL MADAKASMS MADAKASMSSTKSLL MADAKASMS LINKLFILTILFSSV LFILTILFS GVGSSKANLALLPSL VGSSKANLA VGSSKANLALLPSLE VGSSKANLA GSSKANLALLPSLEE KANLALLPS NLINKLFILTILFSS LINKLFILT SSKANLALLPSLEEA LALLPSLEE ILTILFSSVISCKLY LTILFSSVI ADAKASMSSTKSLLE KASMSSTKS VKASLDKIKSLLSTA LDKIKSLLS ELNDIYKKLQDMDSR YKKLQDMDS KVKASLDKIKSLLST LDKIKSLLS QELNDIYKKLQDMDS LNDIYKKLQ DAKASMSSTKSLLEV KASMSSTKS SKANLALLPSLEEAI LALLPSLEE KANLALLPSLEEAIA LALLPSLEE LTILFSSVISCKLYK LTILFSSVI EAIAKVKSNHASADT IAKVKSNHA AKVKASLDKIKSLLS VKASLDKIK YAGYHQFMADAKASM QFMADAKAS EEAIAKVKSNHASAD IAKVKSNHA NDFEYAQRKADRALE YAQRKADRA DFEYAQRKADRALEE YAQRKADRA KNDFEYAQRKADRAL YAQRKADRA YYAGYHQFMADAKAS YYAGYHQFM FEYAQRKADRALEEA YAQRKADRA SLEEAIAKVKSNHAS IAKVKSNHA GSFNTLKSNDDSKRS FNTLKSNDD ANLALLPSLEEAIAK LALLPSLEE LEEAIAKVKSNHASA IAKVKSNHA

		AKNDFEYAQRKADRA FEYAQRKAD AIAKVKSNHASADTH VKSNHASAD PSLEEAIAKVKSNHA LEEAIAKVK NGSFNTLKSNDDSKR FNTLKSNDD IAKVKSNHASADTHC VKSNHASAD KSLLSTAKSYLEQTR LSTAKSYLE CKLYKKITYNADQVI LYKKITYNA RALEEALSNSNASRH LEEALSNSN AKASMSSTKSLLEVA KASMSSTKS
	HLA-DRB1*0301	None
	HLA-DRB1*0401	PSLEEAIAKVKSNHA PSLEEAIAK SLEEAIAKVKSNHAS IAKVKSNHA LEEAIAKVKSNHASA IAKVKSNHA EEAIAKVKSNHASAD IAKVKSNHA EAIAKVKSNHASADT IAKVKSNHA IAKVKSNHASADTHC IAKVKSNHA AIAKVKSNHASADTH IAKVKSNHA RALEEALSNSNASRH EALSNSNAS DRALEEALSNSNASR EALSNSNAS ADRALEEALSNSNAS LEEALSNSN KASLDKIKSLLSTAK LDKIKSLLS ASLDKIKSLLSTAKS LDKIKSLLS LEEALSNSNASRHES EALSNSNAS ALEEALSNSNASRHE EALSNSNAS ISCKLYKKITYNADQ LYKKITYNA VISCKLYKKITYNAD LYKKITYNA SCKLYKKITYNADQV LYKKITYNA CKLYKKITYNADQVI LYKKITYNA NLINKLFILTILFSS LFILTILFS ADMQPDMQNDNSSSN MQPDMQNDN LINKLFILTILFSSV LFILTILFS NKLFILTILFSSVIS LFILTILFS INKLFILTILFSSVI LFILTILFS
	HLA-DRB1*0404	RSVDNTYMDQDTGKK VDNTYMDQD SVDNTYMDQDTGKKP YMDQDTGKK VDNTYMDQDTGKKPL YMDQDTGKK NTYMDQDTGKKPLMA YMDQDTGKK DNTYMDQDTGKKPLM YMDQDTGKK NKLFILTILFSSVIS ILTILFSSV INKLFILTILFSSVI ILTILFSSV LINKLFILTILFSSV LFILTILFS LFILTILFSSVISCK ILTILFSSV KLFILTILFSSVISC ILTILFSSV EEAIAKVKSNHASAD IAKVKSNHA EAIAKVKSNHASADT IAKVKSNHA RALEEALSNSNASRH LEEALSNSN
	HLA-DRB1*0405	GSSKANLALLPSLEE KANLALLPS SSKANLALLPSLEEA LALLPSLEE KANLALLPSLEEAIA LALLPSLEE SKANLALLPSLEEAI LALLPSLEE ANLALLPSLEEAIAK LALLPSLEE NLALLPSLEEAIAKV LALLPSLEE LALLPSLEEAIAKVK LALLPSLEE KSNNGSFNTLKSNDD NGSFNTLKS SNNGSFNTLKSNDDS FNTLKSNDD

		NNGSFNTLKSNDDSK FNTLKSNDD NGSFNTLKSNDDSKR FNTLKSNDD GSFNTLKSNDDSKRS FNTLKSNDD ADAKASMSSTKSLLE KASMSSTKS DAKASMSSTKSLLEV MSSTKSLLE KASMSSTKSLLEVAK MSSTKSLLE ASMSSTKSLLEVAKN MSSTKSLLE AKASMSSTKSLLEVA MSSTKSLLE KELNENMTKTNKDFQ ENMTKTNKD KQKELNENMTKTNKD LNENMTKTN QKELNENMTKTNKDF ENMTKTNKD ELNENMTKTNKDFQE ENMTKTNKD LNENMTKTNKDFQEL ENMTKTNKD ASLDKIKSLLSTAKS LDKIKSLLS KASLDKIKSLLSTAK LDKIKSLLS SFNTLKSNDDSKRSG FNTLKSNDD FNTLKSNDDSKRSGR FNTLKSNDD
	HLA-DRB1*0701	RALEEALSNSNASRH RALEEALSN ALEEALSNSNASRHE LSNSNASRH EEALSNSNASRHESY LSNSNASRH EALSNSNASRHESYY LSNSNASRH LEEALSNSNASRHES LSNSNASRH ALSNSNASRHESYYY LSNSNASRH LSNSNASRHESYYYA LSNSNASRH DKIKSLLSTAKSYLE LLSTAKSYL KIKSLLSTAKSYLEQ LLSTAKSYL IKSLLSTAKSYLEQT LLSTAKSYL KSLLSTAKSYLEQTR LLSTAKSYL FILTILFSSVISCKL LTILFSSVI INKLFILTILFSSVI ILTILFSSV NKLFILTILFSSVIS LTILFSSVI LFILTILFSSVISCK LTILFSSVI KLFILTILFSSVISC LTILFSSVI LDKIKSLLSTAKSYL SLLSTAKSY SLLSTAKSYLEQTRR LLSTAKSYL
	HLA-DRB1*0802	RALEEALSNSNASRH RALEEALSN ALEEALSNSNASRHE LSNSNASRH EEALSNSNASRHESY LSNSNASRH EALSNSNASRHESYY LSNSNASRH LEEALSNSNASRHES LSNSNASRH ALSNSNASRHESYYY LSNSNASRH LSNSNASRHESYYYA LSNSNASRH DKIKSLLSTAKSYLE LLSTAKSYL KIKSLLSTAKSYLEQ LLSTAKSYL IKSLLSTAKSYLEQT LLSTAKSYL KSLLSTAKSYLEQTR LLSTAKSYL FILTILFSSVISCKL LTILFSSVI INKLFILTILFSSVI ILTILFSSV NKLFILTILFSSVIS LTILFSSVI LFILTILFSSVISCK LTILFSSVI KLFILTILFSSVISC LTILFSSVI LDKIKSLLSTAKSYL SLLSTAKSY SLLSTAKSYLEQTRR LLSTAKSYL
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	MNLINKLFILTILFS LINKLFILT

		NLINKLFILTILFSS LINKLFILT LINKLFILTILFSSV LINKLFILT INKLFILTILFSSVI LFILTILFS NKLFILTILFSSVIS LFILTILFS QVIDKLKSNNGSFNT LKSNNGSFN VIDKLKSNNGSFNTL LKSNNGSFN KLFILTILFSSVISC LTILFSSVI IDKLKSNNGSFNTLK LKSNNGSFN DKLKSNNGSFNTLKS LKSNNGSFN LFILTILFSSVISCK LTILFSSVI DQVIDKLKSNNGSFN IDKLKSNNG RGVGSSKANLALLPS VGSSKANLA
	HLA-DRB1*1501	NKLFILTILFSSVIS LFILTILFS INKLFILTILFSSVI LFILTILFS LINKLFILTILFSSV LFILTILFS NLINKLFILTILFSS LFILTILFS LFILTILFSSVISCK LTILFSSVI KLFILTILFSSVISC FILTILFSS ASLDKIKSLLSTAKS IKSLLSTAK KASLDKIKSLLSTAK LDKIKSLLS LDKIKSLLSTAKSYL IKSLLSTAK MNLINKLFILTILFS LINKLFILT DKIKSLLSTAKSYLE IKSLLSTAK FILTILFSSVISCKL LTILFSSVI SLDKIKSLLSTAKSY IKSLLSTAK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	GKKPLMADMQPDMQN MADMQPDMQ KKPLMADMQPDMQND MADMQPDMQ KPLMADMQPDMQNDN MADMQPDMQ PLMADMQPDMQNDNS MADMQPDMQ TGKKPLMADMQPDMQ LMADMQPDM LMADMQPDMQNDNSS MADMQPDMQ MADMQPDMQNDNSSS MADMQPDMQ
	HLA-DRB5*0101	None
NP_212281.1| flagellin [Borrelia burgdorferi B31] Seq23	HLA-DRB1*0101	TTNSILTQSAMAMIA ILTQSAMAM TNSILTQSAMAMIAQ ILTQSAMAM NSILTQSAMAMIAQA ILTQSAMAM ATTNSILTQSAMAMI ILTQSAMAM AATTNSILTQSAMAM TNSILTQSA QPAKINTPASLSGSQ INTPASLSG PAKINTPASLSGSQA INTPASLSG SILTQSAMAMIAQAN ILTQSAMAM MQPAKINTPASLSGS INTPASLSG AKINTPASLSGSQAS INTPASLSG ILTQSAMAMIAQANQ ILTQSAMAM GMQPAKINTPASLSG KINTPASLS NAIRMISDQRANLGA IRMISDQRA ENAIRMISDQRANLG IRMISDQRA ANLFSGEGAQTAQAA FSGEGAQTA ANVANLFSGEGAQTA VANLFSGEG VANLFSGEGAQTAQA FSGEGAQTA NLFSGEGAQTAQAAP FSGEGAQTA YNQMHMLSNKSASQN MHMLSNKSA NVANLFSGEGAQTAQ FSGEGAQTA EKVLVRMKELAVQSG VRMKELAVQ

		KVLVRMKELAVQSGN MKELAVQSG
		QAQYNQMHMLSNKSA YNQMHMLSN
		AQYNQMHMLSNKSAS MHMLSNKSA
		NQMHMLSNKSASQNV MHMLSNKSA
		AEELGMQPAKINTPA LGMQPAKIN
		VLVRMKELAVQSGNG MKELAVQSG
		TAEELGMQPAKINTP LGMQPAKIN
		QYNQMHMLSNKSASQ MHMLSNKSA
		AKIENAIRMISDQRA IENAIRMIS
		ATMTDEVVAATTNSI MTDEVVAAT
		LVRMKELAVQSGNGT MKELAVQSG
		MTDEVVAATTNSILT VVAATTNSI
		TDEVVAATTNSILTQ VVAATTNSI
		DEVVAATTNSILTQS VVAATTNSI
		RTAEELGMQPAKINT LGMQPAKIN
		EELGMQPAKINTPAS LGMQPAKIN
		TMTDEVVAATTNSIL VVAATTNSI
		VRMKELAVQSGNGTY MKELAVQSG
		VRTAEELGMQPAKIN ELGMQPAKI
		IENAIRMISDQRANL IRMISDQRA
		KIENAIRMISDQRAN IRMISDQRA
		INTPASLSGSQASWT INTPASLSG
		EYAIENLKASYAQIK IENLKASYA
		YAIENLKASYAQIKD IENLKASYA
		KINTPASLSGSQASW INTPASLSG
		LFSGEGAQTAQAAPV FSGEGAQTA
		FSGEGAQTAQAAPVQ FSGEGAQTA
		AIRMISDQRANLGAF IRMISDQRA
		IRMISDQRANLGAFQ IRMISDQRA
		VQQEGAQQPAPATAP VQQEGAQQP
		RMKELAVQSGNGTYS MKELAVQSG
		MKELAVQSGNGTYSD MKELAVQSG
		EGVQQEGAQQPAPAT VQQEGAQQP
		STEYAIENLKASYAQ IENLKASYA
		NSTEYAIENLKASYA YAIENLKAS
		TEYAIENLKASYAQI IENLKASYA
		QMHMLSNKSASQNVR MHMLSNKSA
		MHMLSNKSASQNVRT MHMLSNKSA
		TQSAMAMIAQANQVP TQSAMAMIA
		AIAVNIYAANVANLF VNIYAANVA
		LGMQPAKINTPASLS LGMQPAKIN
		IAVNIYAANVANLFS YAANVANLF
		AIENLKASYAQIKDA LKASYAQIK
		IENLKASYAQIKDAT LKASYAQIK
		ELGMQPAKINTPASL LGMQPAKIN
		LTQSAMAMIAQANQV AMAMIAQAN
		QEGVQQEGAQQPAPA VQQEGAQQP
		QSAMAMIAQANQVPQ MIAQANQVP
		EVVAATTNSILTQSA VVAATTNSI
		AVNIYAANVANLFSG YAANVANLF
		PVQEGVQQEGAQQPA VQQEGAQQP
		VVAATTNSILTQSAM VVAATTNSI
		APVQEGVQQEGAQQP QEGVQQEGA
		VQEGVQQEGAQQPAP VQQEGAQQP
		NIYAANVANLFSGEG YAANVANLF
		QEGAQQPAPATAPSQ QQPAPATAP
		VNIYAANVANLFSGE YAANVANLF

		QQEGAQQPAPATAPS	QQPAPATAP
		GVQQEGAQQPAPATA	VQQEGAQQP
		AANVANLFSGEGAQT	VANLFSGEG
		EGAQQPAPATAPSQG	QQPAPATAP
		AMAMIAQANQVPQYV	MIAQANQVP
		EAIAVNIYAANVANL	VNIYAANVA
		ENLKASYAQIKDATM	LKASYAQIK
		VEKVLVRMKELAVQS	VRMKELAVQ
		SAMAMIAQANQVPQY	MIAQANQVP
		GAQQPAPATAPSQGG	QQPAPATAP
		EVEKVLVRMKELAVQ	LVRMKELAV
		NAQIRGLSQASRNTS	IRGLSQASR
		KELAVQSGNGTYSDA	VQSGNGTYS
		NLKASYAQIKDATMT	LKASYAQIK
		LKASYAQIKDATMTD	LKASYAQIK
		INAQIRGLSQASRNT	IRGLSQASR
		AQIRGLSQASRNTSK	IRGLSQASR
		DEAIAVNIYAANVAN	VNIYAANVA
		GEGAQTAQAAPVQEG	AQTAQAAPV
		PSQGGVNSPVNVTTT	VNSPVNVTT
		DQAQYNQMHMLSNKS	YNQMHMLSN
		EGAQTAQAAPVQEGV	AQTAQAAPV
		SQGGVNSPVNVTTTV	VNSPVNVTT
		QGGVNSPVNVTTTVD	VNSPVNVTT
		APSQGGVNSPVNVTT	GVNSPVNVT
		QDEAIAVNIYAANVA	AVNIYAANV
		PASLSGSQASWTLRV	LSGSQASWT
		ASLSGSQASWTLRVH	LSGSQASWT
		MAMIAQANQVPQYVL	MIAQANQVP
		IYAANVANLFSGEGA	VANLFSGEG
		GGVNSPVNVTTTVDA	VNSPVNVTT
		SRNNGINAANLSKTQ	INAANLSKT
		RNNGINAANLSKTQE	INAANLSKT
		ASRNNGINAANLSKT	NGINAANLS
		ELAVQSGNGTYSDAD	VQSGNGTYS
		NNGINAANLSKTQEK	INAANLSKT
		NTPASLSGSQASWTL	LSGSQASWT
		LAVQSGNGTYSDADR	VQSGNGTYS
		NGINAANLSKTQEKL	INAANLSKT
		YAANVANLFSGEGAQ	VANLFSGEG
		TPASLSGSQASWTLR	LSGSQASWT
		KINAQIRGLSQASRN	IRGLSQASR
		GKINAQIRGLSQASR	QIRGLSQAS
		SGEGAQTAQAAPVQE	AQTAQAAPV
		AQQPAPATAPSQGGV	PATAPSQGG
		ADQAQYNQMHMLSNK	YNQMHMLSN
		HMLSNKSASQNVRTA	LSNKSASQN
		IADQAQYNQMHMLSN	QYNQMHMLS
		VNVTTTVDANTSLAK	VTTTVDANT
		KASYAQIKDATMTDE	AQIKDATMT
		QIRGLSQASRNTSKA	IRGLSQASR
		ASYAQIKDATMTDEV	AQIKDATMT
		GAQTAQAAPVQEGVQ	AQAAPVQEG
		QQPAPATAPSQGGVN	PATAPSQGG
		AMIAQANQVPQYVLS	MIAQANQVP
		GVNSPVNVTTTVDAN	VNVTTTVDA
		IRGLSQASRNTSKAI	IRGLSQASR

		DATMTDEVVAATTNS MTDEVVAAT AQTAQAAPVQEGVQQ AQAAPVQEG RMISDQRANLGAFQN ISDQRANLG MIAQANQVPQYVLSL QANQVPQYV VNSPVNVTTTVDANT VNVTTTVDA SLSGSQASWTLRVHV LSGSQASWT LSGSQASWTLRVHVG LSGSQASWT SKAINFIQTTEGNLN INFIQTTEG MIINHNTSAINASRN INHNTSAIN SYAQIKDATMTDEVV AQIKDATMT NSPVNVTTTVDANTS VNVTTTVDA SPVNVTTTVDANTSL VNVTTTVDA NVTTTVDANTSLAKI VDANTSLAK KAINFIQTTEGNLNE INFIQTTEG QPAPATAPSQGGVNS PATAPSQGG IKDATMTDEVVAATT MTDEVVAAT MLSNKSASQNVRTAE LSNKSASQN KDATMTDEVVAATTN MTDEVVAAT QIKDATMTDEVVAAT DATMTDEVV PAPATAPSQGGVNSP PATAPSQGG QTAQAAPVQEGVQQE AQAAPVQEG VTTTVDANTSLAKIE VDANTSLAK PVNVTTTVDANTSLA VNVTTTVDA VAATTNSILTQSAMA TNSILTQSA
	HLA-DRB1*0301	None
	HLA-DRB1*0401	QYNQMHMLSNKSASQ QMHMLSNKS YNQMHMLSNKSASQN QMHMLSNKS IAVNIYAANVANLFS YAANVANLF QAQYNQMHMLSNKSA QMHMLSNKS NQMHMLSNKSASQNV MLSNKSASQ AIAVNIYAANVANLF NIYAANVAN NIYAANVANLFSGEG YAANVANLF AVNIYAANVANLFSG YAANVANLF AQYNQMHMLSNKSAS QMHMLSNKS VNIYAANVANLFSGE YAANVANLF QMHMLSNKSASQNVR MLSNKSASQ GVNSPVNVTTTVDAN VNVTTTVDA GGVNSPVNVTTTVDA VNSPVNVTT NSPVNVTTTVDANTS VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA
	HLA-DRB1*0404	ANVANLFSGEGAQTA VANLFSGEG AANVANLFSGEGAQT VANLFSGEG NIYAANVANLFSGEG YAANVANLF IYAANVANLFSGEGA VANLFSGEG YAANVANLFSGEGAQ VANLFSGEG YNQMHMLSNKSASQN MLSNKSASQ QYNQMHMLSNKSASQ QMHMLSNKS NVANLFSGEGAQTAQ VANLFSGEG VANLFSGEGAQTAQA VANLFSGEG ENAIRMISDQRANLG AIRMISDQR NQMHMLSNKSASQNV MLSNKSASQ NAIRMISDQRANLGA ISDQRANLG QMHMLSNKSASQNVR MLSNKSASQ AIRMISDQRANLGAF ISDQRANLG VNVTTTVDANTSLAK TVDANTSLA

		PVNVTTTVDANTSLA VNVTTTVDA IRMISDQRANLGAFQ ISDQRANLG AQYNQMHMLSNKSAS QMHMLSNKS QAQYNQMHMLSNKSA QMHMLSNKS DQAQYNQMHMLSNKS YNQMHMLSN RMISDQRANLGAFQN ISDQRANLG MTDEVVAATTNSILT VVAATTNSI
	HLA-DRB1*0405	EELGMQPAKINTPAS LGMQPAKIN LGMQPAKINTPASLS PAKINTPAS GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA VNSPVNVTTTVDANT VNVTTTVDA ELGMQPAKINTPASL PAKINTPAS NSPVNVTTTVDANTS VNVTTTVDA
	HLA-DRB1*0701	TMTDEVVAATTNSIL VVAATTNSI MTDEVVAATTNSILT VVAATTNSI TDEVVAATTNSILTQ VVAATTNSI DEVVAATTNSILTQS VVAATTNSI EVVAATTNSILTQSA VAATTNSIL ATMTDEVVAATTNSI ATMTDEVVA VVAATTNSILTQSAM VVAATTNSI QNRLESIKNSTEYAI LESIKNSTE NRLESIKNSTEYAIE IKNSTEYAI ESIKNSTEYAIENLK IKNSTEYAI RLESIKNSTEYAIEN IKNSTEYAI LESIKNSTEYAIENL IKNSTEYAI GGVNSPVNVTTTVDA PVNVTTTVD GVNSPVNVTTTVDAN VNVTTTVDA MIINHNTSAINASRN IINHNTSAI
	HLA-DRB1*0802	None
	HLA-DRB1*0901	IAVNIYAANVANLFS VNIYAANVA AIAVNIYAANVANLF VNIYAANVA TTNSILTQSAMAMIA LTQSAMAMI TNSILTQSAMAMIAQ LTQSAMAMI NSILTQSAMAMIAQA LTQSAMAMI SILTQSAMAMIAQAN LTQSAMAMI ATTNSILTQSAMAMI ILTQSAMAM EAIAVNIYAANVANL VNIYAANVA AVNIYAANVANLFSG IYAANVANL VNIYAANVANLFSGE IYAANVANL
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD IENAIRMIS SLAKIENAIRMISDQ IENAIRMIS ASRNNGINAANLSKT NGINAANLS SRNNGINAANLSKTQ INAANLSKT LAKIENAIRMISDQR IENAIRMIS AKIENAIRMISDQRA IENAIRMIS RNNGINAANLSKTQE INAANLSKT MGVSGKINAQIRGLS MGVSGKINA MIINHNTSAINASRN IINHNTSAI NNGINAANLSKTQEK INAANLSKT NGINAANLSKTQEKL INAANLSKT IINHNTSAINASRNN IINHNTSAI GVSGKINAQIRGLSQ INAQIRGLS VSGKINAQIRGLSQA INAQIRGLS

		RMKELAVQSGNGTYS	LAVQSGNGT
		AIAVNIYAANVANLF	VNIYAANVA
		IENAIRMISDQRANL	IENAIRMIS
		IAVNIYAANVANLFS	VNIYAANVA
		MKELAVQSGNGTYSD	LAVQSGNGT
		SGKINAQIRGLSQAS	INAQIRGLS
		GKINAQIRGLSQASR	INAQIRGLS
		KIENAIRMISDQRAN	IENAIRMIS
		KELAVQSGNGTYSDA	LAVQSGNGT
		LVRMKELAVQSGNGT	MKELAVQSG
		VRMKELAVQSGNGTY	LAVQSGNGT
		AGMGVSGKINAQIRG	MGVSGKINA
		AVNIYAANVANLFSG	YAANVANLF
		VNIYAANVANLFSGE	YAANVANLF
		SQGGVNSPVNVTTTV	GVNSPVNVT
		QGGVNSPVNVTTTVD	GVNSPVNVT
		GGVNSPVNVTTTVDA	GVNSPVNVT
		INASRNNGINAANLS	SRNNGINAA
		EAIAVNIYAANVANL	VNIYAANVA
		PSQGGVNSPVNVTTT	GVNSPVNVT
		APSQGGVNSPVNVTT	GVNSPVNVT
		QDEAIAVNIYAANVA	IAVNIYAAN
		DEAIAVNIYAANVAN	VNIYAANVA
		GVNSPVNVTTTVDAN	GVNSPVNVT
		NASRNNGINAANLSK	NGINAANLS
		RGLSQASRNTSKAIN	LSQASRNTS
		ELAVQSGNGTYSDAD	LAVQSGNGT
		IRGLSQASRNTSKAI	LSQASRNTS
		LAVQSGNGTYSDADR	LAVQSGNGT
		TSAINASRNNGINAA	AINASRNNG
		QIRGLSQASRNTSKA	LSQASRNTS
		INHNTSAINASRNNG	INHNTSAIN
		NAQIRGLSQASRNTS	RGLSQASRN
		AQIRGLSQASRNTSK	LSQASRNTS
		QNRLESIKNSTEYAI	LESIKNSTE
		NIYAANVANLFSGEG	YAANVANLF
		NRLESIKNSTEYAIE	IKNSTEYAI
		GMGVSGKINAQIRGL	MGVSGKINA
		SKAINFIQTTEGNLN	INFIQTTEG
	HLA-DRB1*1501	EKVLVRMKELAVQSG	LVRMKELAV
		KVLVRMKELAVQSGN	LVRMKELAV
		VEKVLVRMKELAVQS	LVRMKELAV
		EVEKVLVRMKELAVQ	LVRMKELAV
		VLVRMKELAVQSGNG	VRMKELAVQ
		LVRMKELAVQSGNGT	VRMKELAVQ
		INAQIRGLSQASRNT	IRGLSQASR
		GKINAQIRGLSQASR	QIRGLSQAS
		NAQIRGLSQASRNTS	IRGLSQASR
		KINAQIRGLSQASRN	IRGLSQASR
		AQIRGLSQASRNTSK	IRGLSQASR
		NEVEKVLVRMKELAV	VLVRMKELA
		KIENAIRMISDQRAN	AIRMISDQR
		IENAIRMISDQRANL	AIRMISDQR
		AKIENAIRMISDQRA	AIRMISDQR
		ENAIRMISDQRANLG	AIRMISDQR
		LAKIENAIRMISDQR	LAKIENAIR
		QYNQMHMLSNKSASQ	MHMLSNKSA

		QIRGLSQASRNTSKA IRGLSQASR YNQMHMLSNKSASQN MHMLSNKSA IRGLSQASRNTSKAI IRGLSQASR AQYNQMHMLSNKSAS MHMLSNKSA VRMKELAVQSGNGTY VRMKELAVQ QAQYNQMHMLSNKSA QMHMLSNKS AIRMISDQRANLGAF AIRMISDQR NQMHMLSNKSASQNV MHMLSNKSA QASWTLRVHVGANQD LRVHVGANQ NAIRMISDQRANLGA AIRMISDQR SQASWTLRVHVGANQ QASWTLRVH
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EVEKVLVRMKELAVQ VEKVLVRMK VEKVLVRMKELAVQS VRMKELAVQ EKVLVRMKELAVQSG VRMKELAVQ KVLVRMKELAVQSGN VRMKELAVQ VLVRMKELAVQSGNG VRMKELAVQ ENAIRMISDQRANLG IRMISDQRA NAIRMISDQRANLGA IRMISDQRA VRMKELAVQSGNGTY VRMKELAVQ LVRMKELAVQSGNGT VRMKELAVQ AIRMISDQRANLGAF ISDQRANLG IRMISDQRANLGAFQ ISDQRANLG
	HLA-DRB5*0101	NTSLAKIENAIRMIS AKIENAIRM TSLAKIENAIRMISD AKIENAIRM DANTSLAKIENAIRM LAKIENAIR ANTSLAKIENAIRMI AKIENAIRM SLAKIENAIRMISDQ AKIENAIRM
NP_212463.1| oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA-2) [Borrelia burgdorferi B31] Seq24	HLA-DRB1*0101	LTFLSIFTQGYTQFS FLSIFTQGY TFLSIFTQGYTQFSS FTQGYTQFS FLSIFTQGYTQFSSH FTQGYTQFS LSIFTQGYTQFSSHN FTQGYTQFS SIFTQGYTQFSSHNY FTQGYTQFS DNVKIRKALTLAIDR IRKALTLAI LDNVKIRKALTLAID IRKALTLAI PLDNVKIRKALTLAI VKIRKALTL VHQSFIPVPVHVTEK FIPVPVHVT NVKIRKALTLAIDRE IRKALTLAI VKIRKALTLAIDRET IRKALTLAI MLVHQSFIPVPVHVT HQSFIPVPV LVHQSFIPVPVHVTE FIPVPVHVT HQSFIPVPVHVTEKY FIPVPVHVT QSFIPVPVHVTEKYG FIPVPVHVT IFTQGYTQFSSHNYS FTQGYTQFS TMFRGIVTGDPNTGG IVTGDPNTG FTQGYTQFSSHNYSN FTQGYTQFS DTMFRGIVTGDPNTG FRGIVTGDP FRGIVTGDPNTGGNK IVTGDPNTG MFRGIVTGDPNTGGN IVTGDPNTG SLELFNPEIAKTLLA FNPEIAKTL LELFNPEIAKTLLAE FNPEIAKTL KSLELFNPEIAKTLL FNPEIAKTL AKSLELFNPEIAKTL LFNPEIAKT KIRKALTLAIDRETL IRKALTLAI ITFYTTNDSSTAYKM YTTNDSSTA

		EEITFYTTNDSSTAY YTTNDSSTA
		EITFYTTNDSSTAYK YTTNDSSTA
		IRKALTLAIDRETLT IRKALTLAI
		ELFNPEIAKTLLAEA FNPEIAKTL
		SFIPVPVHVTEKYGQ FIPVPVHVT
		LEEITFYTTNDSSTA ITFYTTNDS
		TFYTTNDSSTAYKMY YTTNDSSTA
		FIPVPVHVTEKYGQN FIPVPVHVT
		RGIVTGDPNTGGNKP IVTGDPNTG
		TSPENMVTSGPFKLK MVTSGPFKL
		REKITWSDGVAITAE ITWSDGVAI
		LREKITWSDGVAITA ITWSDGVAI
		EKITWSDGVAITAEG ITWSDGVAI
		YKVLDNGTTPTRRAT LDNGTTPTR
		DAIFGSIPPDLIKNL FGSIPPDLI
		KITWSDGVAITAEGI ITWSDGVAI
		PYFIDMLVHQSFIPV FIDMLVHQS
		PENMVTSGPFKLKER MVTSGPFKL
		LDAIFGSIPPDLIKN FGSIPPDLI
		TYKVLDNGTTPTRRA LDNGTTPTR
		IKPLDNVKIRKALTL IKPLDNVKI
		KPYFIDMLVHQSFIP FIDMLVHQS
		SPENMVTSGPFKLKE MVTSGPFKL
		ELDAIFGSIPPDLIK FGSIPPDLI
		EELDAIFGSIPPDLI IFGSIPPDL
		ITWSDGVAITAEGIR ITWSDGVAI
		WSDGVAITAEGIRKS GVAITAEGI
		LTYKVLDNGTTPTRR VLDNGTTPT
		GQNWTSPENMVTSGP WTSPENMVT
		TLTYKVLDNGTTPTR YKVLDNGTT
		SDGVAITAEGIRKSY ITAEGIRKS
		PKPYFIDMLVHQSFI FIDMLVHQS
		WTSPENMVTSGPFKL WTSPENMVT
		LFNPEIAKTLLAEAG FNPEIAKTL
		SPKPYFIDMLVHQSF FIDMLVHQS
		QNWTSPENMVTSGPF WTSPENMVT
		NTHIKPLDNVKIRKA IKPLDNVKI
		THIKPLDNVKIRKAL IKPLDNVKI
		ENMVTSGPFKLKERI MVTSGPFKL
		AIFGSIPPDLIKNLK FGSIPPDLI
		FNPEIAKTLLAEAGY FNPEIAKTL
		ESPKPYFIDMLVHQS YFIDMLVHQ
		PDLIKNLKLRSDYYS IKNLKLRSD
		KPLDNVKIRKALTLA VKIRKALTL
		EKYGQNWTSPENMVT GQNWTSPEN
		KYGQNWTSPENMVTS WTSPENMVT
		VSFKISLGAEPSSLD FKISLGAEP
		GVAITAEGIRKSYLR ITAEGIRKS
		DLIKNLKLRSDYYSS IKNLKLRSD
		DGVAITAEGIRKSYL ITAEGIRKS
		PEIAKTLLAEAGYPN AKTLLAEAG
		YGQNWTSPENMVTSG WTSPENMVT
		EIAKTLLAEAGYPNG AKTLLAEAG
		LKLRSDYYSSAVNAI LKLRSDYYS
		FNTHIKPLDNVKIRK IKPLDNVKI
		YAFNTHIKPLDNVKI FNTHIKPLD
		AFNTHIKPLDNVKIR IKPLDNVKI

		KVLDNGTTPTRRATP	LDNGTTPTR
		NLREKITWSDGVAIT	ITWSDGVAI
		MKLQRSLFLIIFFLT	MKLQRSLFL
		GIVTGDPNTGGNKPG	IVTGDPNTG
		SFKISLGAEPSSLDP	LGAEPSSLD
		FNLREKITWSDGVAI	LREKITWSD
		NEEWTTYLNTKANGN	WTTYLNTKA
		EEWTTYLNTKANGNY	YLNTKANGN
		IAPIYIYGNSYLFRN	YIYGNSYLF
		KLRSDYYSSAVNAIY	YYSSAVNAI
		FIDMLVHQSFIPVPV	FIDMLVHQS
		ETLTYKVLDNGTTPT	YKVLDNGTT
		LRSDYYSSAVNAIYF	YYSSAVNAI
		APIYIYGNSYLFRND	YIYGNSYLF
		YFIDMLVHQSFIPVP	FIDMLVHQS
		RSDYYSSAVNAIYFY	YYSSAVNAI
		FKISLGAEPSSLDPQ	LGAEPSSLD
		VAITAEGIRKSYLRI	ITAEGIRKS
		SDYYSSAVNAIYFYA	YYSSAVNAI
		IGDYADPLTFLSIFT	YADPLTFLS
		AGWIGDYADPLTFLS	IGDYADPLT
		PIYIYGNSYLFRNDK	YIYGNSYLF
		FYTTNDSSTAYKMYE	YTTNDSSTA
		GDYADPLTFLSIFTQ	YADPLTFLS
		GWIGDYADPLTFLSI	YADPLTFLS
		SIPPDLIKNLKLRSD	LIKNLKLRS
		YADPLTFLSIFTQGY	YADPLTFLS
		IPPDLIKNLKLRSDY	IKNLKLRSD
		NMVTSGPFKLKERIP	MVTSGPFKL
		NPEIAKTLLAEAGYP	AKTLLAEAG
		LIKNLKLRSDYYSSA	LKLRSDYYS
		PPDLIKNLKLRSDYY	IKNLKLRSD
		VLDNGTTPTRRATPN	NGTTPTRRA
		WIGDYADPLTFLSIF	YADPLTFLS
		ISLGAEPSSLDPQLA	LGAEPSSLD
		AITAEGIRKSYLRIL	ITAEGIRKS
		ITAEGIRKSYLRILN	ITAEGIRKS
		KISLGAEPSSLDPQL	LGAEPSSLD
		YTTNDSSTAYKMYEN	YTTNDSSTA
		GVSFKISLGAEPSSL	FKISLGAEP
		LAKGWDISSDGTVYT	GWDISSDGT
		IKNLKLRSDYYSSAV	LKLRSDYYS
		EKDFPIAPIYIYGNS	FPIAPIYIY
		IVTGDPNTGGNKPGL	IVTGDPNTG
		PLTFLSIFTQGYTQF	FLSIFTQGY
		IEKDFPIAPIYIYGN	FPIAPIYIY
		AKGWDISSDGTVYTF	ISSDGTVYT
		GWDISSDGTVYTFNL	ISSDGTVYT
		EGVSFKISLGAEPSS	FKISLGAEP
		IAKTLLAEAGYPNGN	AKTLLAEAG
		KGWDISSDGTVYTFN	ISSDGTVYT
		EWTTYLNTKANGNYE	YLNTKANGN
		HIKPLDNVKIRKALT	IKPLDNVKI
		NWTSPENMVTSGPFK	WTSPENMVT
		EGIRKSYLRILNKET	IRKSYLRIL
		AKTLLAEAGYPNGNG	AKTLLAEAG
		WDISSDGTVYTFNLR	ISSDGTVYT

		KEGVSFKISLGAEPS FKISLGAEP WTTYLNTKANGNYEI YLNTKANGN LDNGTTPTRRATPNF NGTTPTRRA MIDTMFRGIVTGDPN FRGIVTGDP ADPLTFLSIFTQGYT FLSIFTQGY FPIAPIYIYGNSYLF IAPIYIYGN KMIDTMFRGIVTGDP DTMFRGIVT IIEKDFPIAPIYIYG FPIAPIYIY IIIEKDFPIAPIYIY DFPIAPIYI PNFSSYSYAKSLELF YSYAKSLEL DPLTFLSIFTQGYTQ FLSIFTQGY TPNFSSYSYAKSLEL FSSYSYAKS IFGSIPPDLIKNLKL FGSIPPDLI PIAPIYIYGNSYLFR YIYGNSYLF KDFPIAPIYIYGNSY FPIAPIYIY IYIYGNSYLFRNDKW YGNSYLFRN IDTMFRGIVTGDPNT FRGIVTGDP FSSYSYAKSLELFNP YSYAKSLEL NFSSYSYAKSLELFN YSYAKSLEL YAKSLELFNPEIAKT YAKSLELFN MVTSGPFKLKERIPN MVTSGPFKL NDKWTGWNTNILERF WTGWNTNIL DKWTGWNTNILERFD WTGWNTNIL DYYSSAVNAIYFYAF YYSSAVNAI SSYSYAKSLELFNPE YSYAKSLEL TTYLNTKANGNYEIA YLNTKANGN YIYGNSYLFRNDKWT YGNSYLFRN FGSIPPDLIKNLKLR FGSIPPDLI SKYVEMVKSVIKNGQ VEMVKSVIK IRKSYLRILNKETGS YLRILNKET TLEITLESPKPYFID LESPKPYFI GSKYVEMVKSVIKNG VEMVKSVIK KTLEITLESPKPYFI ITLESPKPY GIRKSYLRILNKETG IRKSYLRIL NEELDAIFGSIPPDL LDAIFGSIP IDMLVHQSFIPVPVH LVHQSFIPV DMLVHQSFIPVPVHV LVHQSFIPV YYSSAVNAIYFYAFN YYSSAVNAI ILKLKYNTNEANKKI YNTNEANKK SLGAEPSSLDPQLAE LGAEPSSLD DFPIAPIYIYGNSYL IAPIYIYGN LKLKYNTNEANKKIC YNTNEANKK
	HLA-DRB1*0301	None
	HLA-DRB1*0401	RIPNEKYVFEKNNKY RIPNEKYVF IPNEKYVFEKNNKYY YVFEKNNKY PNEKYVFEKNNKYYD YVFEKNNKY NEKYVFEKNNKYYDS YVFEKNNKY EKYVFEKNNKYYDSN YVFEKNNKY ESPKPYFIDMLVHQS YFIDMLVHQ SPKPYFIDMLVHQSF YFIDMLVHQ KPYFIDMLVHQSFIP YFIDMLVHQ PKPYFIDMLVHQSFI YFIDMLVHQ LESPKPYFIDMLVHQ PYFIDMLVH KYVFEKNNKYYDSNE YVFEKNNKY YVFEKNNKYYDSNEV YVFEKNNKY PYFIDMLVHQSFIPV YFIDMLVHQ YFIDMLVHQSFIPVP YFIDMLVHQ

		LDPIKRQDILRQAEE IKRQDILRQ DLELDPIKRQDILRQ DLELDPIKR ELDPIKRQDILRQAE IKRQDILRQ LELDPIKRQDILRQA IKRQDILRQ DPIKRQDILRQAEEI IKRQDILRQ EEITFYTTNDSSTAY YTTNDSSTA LEEITFYTTNDSSTA ITFYTTNDS EITFYTTNDSSTAYK YTTNDSSTA ITFYTTNDSSTAYKM YTTNDSSTA KLRSDYYSSAVNAIY YYSSAVNAI LRSDYYSSAVNAIYF YYSSAVNAI
	HLA-DRB1*0404	LTFLSIFTQGYTQFS FLSIFTQGY ADPLTFLSIFTQGYT FLSIFTQGY RKSYLRILNKETGSK YLRILNKET KSYLRILNKETGSKY ILNKETGSK YADPLTFLSIFTQGY PLTFLSIFT VNAIYFYAFNTHIKP YFYAFNTHI DPLTFLSIFTQGYTQ FLSIFTQGY AIYFYAFNTHIKPLD YFYAFNTHI AVNAIYFYAFNTHIK YFYAFNTHI NAIYFYAFNTHIKPL YFYAFNTHI PLTFLSIFTQGYTQF FLSIFTQGY SAVNAIYFYAFNTHI IYFYAFNTH SYLRILNKETGSKYV ILNKETGSK
	HLA-DRB1*0405	VTEKYGQNWTSPENM GQNWTSPEN HVTEKYGQNWTSPEN YGQNWTSPE TEKYGQNWTSPENMV GQNWTSPEN EKYGQNWTSPENMVT GQNWTSPEN KYGQNWTSPENMVTS GQNWTSPEN RNDKWTGWNTNILER WTGWNTNIL LFRNDKWTGWNTNIL DKWTGWNTN FRNDKWTGWNTNILE WTGWNTNIL NDKWTGWNTNILERF WTGWNTNIL DKWTGWNTNILERFD WTGWNTNIL YGQNWTSPENMVTSG GQNWTSPEN VSFKISLGAEPSSLD VSFKISLGA SFKISLGAEPSSLDP LGAEPSSLD FKISLGAEPSSLDPQ LGAEPSSLD ISLGAEPSSLDPQLA LGAEPSSLD KISLGAEPSSLDPQL LGAEPSSLD FNLREKITWSDGVAI LREKITWSD ELENEEWTTYLNTKA NEEWTTYLN TVYTFNLREKITWSD TVYTFNLRE SLGAEPSSLDPQLAE LGAEPSSLD LGAEPSSLDPQLAED LGAEPSSLD YTFNLREKITWSDGV LREKITWSD LENEEWTTYLNTKAN NEEWTTYLN TFNLREKITWSDGVA LREKITWSD IYFYAFNTHIKPLDN FNTHIKPLD VYTFNLREKITWSDG LREKITWSD KWTGWNTNILERFDL WTGWNTNIL AIYFYAFNTHIKPLD FYAFNTHIK EELDAIFGSIPPDLI DAIFGSIPP ELDAIFGSIPPDLIK FGSIPPDLI GQNWTSPENMVTSGP GQNWTSPEN EFIQNQWKKNLNIDV QNQWKKNLN

		ELEEITFYTTNDSST ITFYTTNDS VELENEEWTTYLNTK NEEWTTYLN LEEITFYTTNDSSTA ITFYTTNDS IDVELENEEWTTYLN ENEEWTTYL DVELENEEWTTYLNT NEEWTTYLN LVHQSFIPVPVHVTE HQSFIPVPV MLVHQSFIPVPVHVT HQSFIPVPV EVELEEITFYTTNDS EITFYTTND VELEEITFYTTNDSS ITFYTTNDS FIQNQWKKNLNIDVE QNQWKKNLN LDAIFGSIPPDLIKN FGSIPPDLI WTGWNTNILERFDLS WTGWNTNIL DAIFGSIPPDLIKNL FGSIPPDLI YFYAFNTHIKPLDNV FNTHIKPLD FYAFNTHIKPLDNVK FNTHIKPLD EEITFYTTNDSSTAY ITFYTTNDS ENEEWTTYLNTKANG NEEWTTYLN NEEWTTYLNTKANGN NEEWTTYLN
	HLA-DRB1*0701	LFRNDKWTGWNTNIL NDKWTGWNT FRNDKWTGWNTNILE WTGWNTNIL RSDYYSSAVNAIYFY YYSSAVNAI SDYYSSAVNAIYFYA YYSSAVNAI KLRSDYYSSAVNAIY YYSSAVNAI LRSDYYSSAVNAIYF YYSSAVNAI NDKWTGWNTNILERF WTGWNTNIL RNDKWTGWNTNILER WTGWNTNIL PLDNVKIRKALTLAI VKIRKALTL DKWTGWNTNILERFD WTGWNTNIL LDNVKIRKALTLAID IRKALTLAI DNVKIRKALTLAIDR IRKALTLAI MLVHQSFIPVPVHVT SFIPVPVHV LVHQSFIPVPVHVTE FIPVPVHVT LKLRSDYYSSAVNAI RSDYYSSAV VHQSFIPVPVHVTEK FIPVPVHVT NVKIRKALTLAIDRE IRKALTLAI HQSFIPVPVHVTEKY FIPVPVHVT VKIRKALTLAIDRET IRKALTLAI DYYSSAVNAIYFYAF YYSSAVNAI QSFIPVPVHVTEKYG FIPVPVHVT MKLQRSLFLIIFFLT MKLQRSLFL
	HLA-DRB1*0802	PLDNVKIRKALTLAI VKIRKALTL LDNVKIRKALTLAID IRKALTLAI DNVKIRKALTLAIDR IRKALTLAI NVKIRKALTLAIDRE IRKALTLAI
	HLA-DRB1*0901	None
	HLA-DRB1*1101	SDGTVYTFNLREKIT YTFNLREKI GTVYTFNLREKITWS YTFNLREKI DGTVYTFNLREKITW YTFNLREKI SSDGTVYTFNLREKI GTVYTFNLR TVYTFNLREKITWSD YTFNLREKI SGPFKLKERIPNEKY FKLKERIPN MVTSGPFKLKERIPN VTSGPFKLK VTSGPFKLKERIPNE FKLKERIPN GPFKLKERIPNEKYV FKLKERIPN TSGPFKLKERIPNEK FKLKERIPN
	HLA-DRB1*1302	SKYVEMVKSVIKNGQ VEMVKSVIK

		KYVEMVKSVIKNGQK VKSVIKNGQ
		EMVKSVIKNGQKYFD VKSVIKNGQ
		YVEMVKSVIKNGQKY VKSVIKNGQ
		ETLTYKVLDNGTTPT YKVLDNGTT
		TLTYKVLDNGTTPTR VLDNGTTPT
		LTYKVLDNGTTPTRR VLDNGTTPT
		VEMVKSVIKNGQKYF VKSVIKNGQ
		PDLIKNLKLRSDYYS LIKNLKLRS
		SIPPDLIKNLKLRSD LIKNLKLRS
		IPPDLIKNLKLRSDY LIKNLKLRS
		PPDLIKNLKLRSDYY LIKNLKLRS
		TYKVLDNGTTPTRRA VLDNGTTPT
		YKVLDNGTTPTRRAT VLDNGTTPT
		NDKWTGWNTNILERF WTGWNTNIL
		DKWTGWNTNILERFD WNTNILERF
		KSYLRILNKETGSKY LRILNKETG
		DLIKNLKLRSDYYSS IKNLKLRSD
		SYLRILNKETGSKYV LRILNKETG
		MVKSVIKNGQKYFDG VKSVIKNGQ
		VKSVIKNGQKYFDGQ VKSVIKNGQ
		GSKYVEMVKSVIKNG VEMVKSVIK
		KWTGWNTNILERFDL WNTNILERF
		WTGWNTNILERFDLS WNTNILERF
		GSIPPDLIKNLKLRS PPDLIKNLK
		LIKNLKLRSDYYSSA LIKNLKLRS
		TGSKYVEMVKSVIKN VEMVKSVIK
		ETGSKYVEMVKSVIK YVEMVKSVI
		MKLQRSLFLIIFFLT LQRSLFLII
		EFIQNQWKKNLNIDV IQNQWKKNL
		LQRSLFLIIFFLTFL LFLIIFFLT
		YLRILNKETGSKYVE LRILNKETG
		RKSYLRILNKETGSK LRILNKETG
		IRKSYLRILNKETGS LRILNKETG
		LRILNKETGSKYVEM LRILNKETG
		GIRKSYLRILNKETG YLRILNKET
		WTSPENMVTSGPFKL ENMVTSGPF
		TSPENMVTSGPFKLK MVTSGPFKL
		IKPLDNVKIRKALTL LDNVKIRKA
		QRSLFLIIFFLTFLC LFLIIFFLT
		FIQNQWKKNLNIDVE IQNQWKKNL
		RSLFLIIFFLTFLCC LFLIIFFLT
		KLQRSLFLIIFFLTF LFLIIFFLT
		IQNQWKKNLNIDVEL IQNQWKKNL
		IAPIYIYGNSYLFRN IYIYGNSYL
		APIYIYGNSYLFRND YGNSYLFRN
		PLDNVKIRKALTLAI VKIRKALTL
		SPENMVTSGPFKLKE MVTSGPFKL
		LDNVKIRKALTLAID VKIRKALTL
		PYFIDMLVHQSFIPV FIDMLVHQS
		TGWNTNILERFDLSQ WNTNILERF
		YAFNTHIKPLDNVKI FNTHIKPLD
		KVLDNGTTPTRRATP VLDNGTTPT
		KPLDNVKIRKALTLA VKIRKALTL
		IKNLKLRSDYYSSAV LKLRSDYYS
	HLA-DRB1*1501	RKSYLRILNKETGSK LRILNKETG
		KSYLRILNKETGSKY LRILNKETG
		SYLRILNKETGSKYV LRILNKETG

		GIRKSYLRILNKETG YLRILNKET IRKSYLRILNKETGS LRILNKETG YLRILNKETGSKYVE LRILNKETG LRILNKETGSKYVEM LRILNKETG PPDLIKNLKLRSDYY IKNLKLRSD PDLIKNLKLRSDYYS IKNLKLRSD DLIKNLKLRSDYYSS IKNLKLRSD SIPPDLIKNLKLRSD DLIKNLKLR IPPDLIKNLKLRSDY IKNLKLRSD LIKNLKLRSDYYSSA IKNLKLRSD IKNLKLRSDYYSSAV IKNLKLRSD GTVYTFNLREKITWS VYTFNLREK IAPIYIYGNSYLFRN IYGNSYLFR YGNSYLFRNDKWTGW LFRNDKWTG PIAPIYIYGNSYLFR IYIYGNSYL
	HLA-DRB3*0101	None
	HLA-DRB4*0101	FKLKERIPNEKYVFE LKERIPNEK PFKLKERIPNEKYVF LKERIPNEK GPFKLKERIPNEKYV LKERIPNEK SGPFKLKERIPNEKY LKERIPNEK TSGPFKLKERIPNEK TSGPFKLKE VNAIYFYAFNTHIKP IYFYAFNTH SAVNAIYFYAFNTHI IYFYAFNTH SSAVNAIYFYAFNTH VNAIYFYAF NAIYFYAFNTHIKPL IYFYAFNTH AVNAIYFYAFNTHIK IYFYAFNTH YFIDMLVHQSFIPVP IDMLVHQSF PYFIDMLVHQSFIPV IDMLVHQSF AIYFYAFNTHIKPLD IYFYAFNTH IYFYAFNTHIKPLDN IYFYAFNTH FIDMLVHQSFIPVPV LVHQSFIPV IDMLVHQSFIPVPVH LVHQSFIPV KLKERIPNEKYVFEK LKERIPNEK LKERIPNEKYVFEKN LKERIPNEK FLIIFFLTFLCCNNK IFFLTFLCC RSLFLIIFFLTFLCC IIFFLTFLC SLFLIIFFLTFLCCN IFFLTFLCC
	HLA-DRB5*0101	LTYKVLDNGTTPTRR LDNGTTPTR YKVLDNGTTPTRRAT LDNGTTPTR TYKVLDNGTTPTRRA LDNGTTPTR AKSLELFNPEIAKTL LFNPEIAKT KSLELFNPEIAKTLL FNPEIAKTL SLELFNPEIAKTLLA FNPEIAKTL LELFNPEIAKTLLAE FNPEIAKTL ELFNPEIAKTLLAEA FNPEIAKTL TLTYKVLDNGTTPTR YKVLDNGTT KVLDNGTTPTRRATP LDNGTTPTR KSYLRILNKETGSKY ILNKETGSK
AAC44381.1| outer membrane porin protein Oms28 precursor Seq25	HLA-DRB1*0101	
		VKKFVGSMSLMSDVA FVGSMSLMS GVVKKFVGSMSLMSD FVGSMSLMS VVKKFVGSMSLMSDV FVGSMSLMS KKFVGSMSLMSDVAK FVGSMSLMS AGVVKKFVGSMSLMS AGVVKKFVG FVGSMSLMSDVAKGT FVGSMSLMS KFVGSMSLMSDVAKG FVGSMSLMS

		KKDVRKAISNVVKVA VRKAISNVV
		AKCSGMVAEGANKVV MVAEGANKV
		VLAKKDVRKAISNVV LAKKDVRKA
		LAKKDVRKAISNVVK VRKAISNVV
		AKKDVRKAISNVVKV VRKAISNVV
		KDVRKAISNVVKVAQ VRKAISNVV
		KCSGMVAEGANKVVE MVAEGANKV
		CSGMVAEGANKVVEM MVAEGANKV
		VAKCSGMVAEGANKV CSGMVAEGA
		AKGTVVASQEATIVA VASQEATIV
		VAKGTVVASQEATIV GTVVASQEA
		KGTVVASQEATIVAK VASQEATIV
		GTVVASQEATIVAKC VASQEATIV
		SGMVAEGANKVVEMS MVAEGANKV
		ARDLTKVMAISLYMR LTKVMAISL
		TVVASQEATIVAKCS VASQEATIV
		ATIVAKCSGMVAEGA IVAKCSGMV
		SQEATIVAKCSGMVA IVAKCSGMV
		EATIVAKCSGMVAEG IVAKCSGMV
		MSLMSDVAKGTVVAS LMSDVAKGT
		QEATIVAKCSGMVAE IVAKCSGMV
		TQKAVSVAGEATFLI SVAGEATFL
		QKAVSVAGEATFLIE VAGEATFLI
		AVSVAGEATFLIEKQ VAGEATFLI
		KAVSVAGEATFLIEK VAGEATFLI
		LMSDVAKGTVVASQE VAKGTVVAS
		SLMSDVAKGTVVASQ VAKGTVVAS
		GARDLTKVMAISLYM LTKVMAISL
		MSDVAKGTVVASQEA VAKGTVVAS
		ASQEATIVAKCSGMV EATIVAKCS
		TIVAKCSGMVAEGAN IVAKCSGMV
		VSVAGEATFLIEKQI VAGEATFLI
		DVRKAISNVVKVAQG VRKAISNVV
		GMVAEGANKVVEMSK MVAEGANKV
		VRKAISNVVKVAQGA VRKAISNVV
		SDVAKGTVVASQEAT VAKGTVVAS
		SMSLMSDVAKGTVVA LMSDVAKGT
		VVASQEATIVAKCSG VASQEATIV
		IVAKCSGMVAEGANK IVAKCSGMV
		VASQEATIVAKCSGM VASQEATIV
		MVAEGANKVVEMSKK MVAEGANKV
		SNNANILKPQSNVLE ILKPQSNVL
		NNANILKPQSNVLEH ILKPQSNVL
		LIINGLLFGFVSLNV INGLLFGFV
		NANILKPQSNVLEHS ILKPQSNVL
		ANILKPQSNVLEHSD ILKPQSNVL
		VGSMSLMSDVAKGTV LMSDVAKGT
		QGARDLTKVMAISLY LTKVMAISL
		AQGARDLTKVMAISL ARDLTKVMA
		MTKIFSNLIINGLLF FSNLIINGL
		GSMSLMSDVAKGTVV LMSDVAKGT
		INGLLFGFVSLNVFA LFGFVSLNV
		IINGLLFGFVSLNVF LFGFVSLNV
		DVAKGTVVASQEATI VAKGTVVAS
		KIFSNLIINGLLFGF FSNLIINGL
		TKIFSNLIINGLLFG FSNLIINGL
		VKETLMASERALDET ETLMASERA

		EVKETLMASERALDE ETLMASERA FSNLIINGLLFGFVS INGLLFGFV IFSNLIINGLLFGFV LIINGLLFG ANKVVEMSKKAVQET VVEMSKKAV NILKPQSNVLEHSDQ LKPQSNVLE NKVVEMSKKAVQETQ MSKKAVQET NGLLFGFVSLNVFAD LFGFVSLNV GLLFGFVSLNVFADS LFGFVSLNV SVAGEATFLIEKQIM VAGEATFLI SNLIINGLLFGFVSL INGLLFGFV DSNNANILKPQSNVL ANILKPQSN VVEMSKKAVQETQKA MSKKAVQET NLIINGLLFGFVSLN INGLLFGFV KVVEMSKKAVQETQK MSKKAVQET VAGEATFLIEKQIML VAGEATFLI ISNVVKVAQGARDLT VKVAQGARD QETQKAVSVAGEATF TQKAVSVAG DEVKETLMASERALD ETLMASERA SNVVKVAQGARDLTK VKVAQGARD VQETQKAVSVAGEAT TQKAVSVAG NVVKVAQGARDLTKV VKVAQGARD VDEVKETLMASERAL ETLMASERA QKVLNMVNGLNPSNK MVNGLNPSN LIEKQIMLNKSPNNK IMLNKSPNN KAVQETQKAVSVAGE TQKAVSVAG KKAVQETQKAVSVAG QETQKAVSV KVDEVKETLMASERA VKETLMASE VEMSKKAVQETQKAV MSKKAVQET AVQETQKAVSVAGEA TQKAVSVAG KVLNMVNGLNPSNKD MVNGLNPSN SKLEGVRESSLELVE VRESSLELV SSKLEGVRESSLELV LEGVRESSL KETLMASERALDETV ETLMASERA LEGVRESSLELVESN VRESSLELV VLNMVNGLNPSNKDQ MVNGLNPSN KLEGVRESSLELVES VRESSLELV AISNVVKVAQGARDL VKVAQGARD ETQKAVSVAGEATFL TQKAVSVAG ILKPQSNVLEHSDQK ILKPQSNVL ETLMASERALDETVQ ETLMASERA LNMVNGLNPSNKDQV MVNGLNPSN AQKVLNMVNGLNPSN VLNMVNGLN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	AGVVKKFVGSMSLMS VKKFVGSMS GVVKKFVGSMSLMSD FVGSMSLMS VVKKFVGSMSLMSDV FVGSMSLMS KKFVGSMSLMSDVAK FVGSMSLMS VKKFVGSMSLMSDVA FVGSMSLMS KFVGSMSLMSDVAKG FVGSMSLMS FVGSMSLMSDVAKGT FVGSMSLMS LAKKDVRKAISNVVK VRKAISNVV VLAKKDVRKAISNVV AKKDVRKAI KDVRKAISNVVKVAQ VRKAISNVV AKKDVRKAISNVVKV VRKAISNVV KKDVRKAISNVVKVA VRKAISNVV MTKIFSNLIINGLLF MTKIFSNLI INGLLFGFVSLNVFA LFGFVSLNV

		NGLLFGFVSLNVFAD LFGFVSLNV GLLFGFVSLNVFADS LFGFVSLNV
	HLA-DRB1*0404	QKVLNMVNGLNPSNK VLNMVNGLN EAQKVLNMVNGLNPS VLNMVNGLN QEAQKVLNMVNGLNP VLNMVNGLN AQKVLNMVNGLNPSN VLNMVNGLN VQEAQKVLNMVNGLN QKVLNMVNG KVLNMVNGLNPSNKD VLNMVNGLN VLNMVNGLNPSNKDQ VLNMVNGLN LIINGLLFGFVSLNV LLFGFVSLN INGLLFGFVSLNVFA LFGFVSLNV NGLLFGFVSLNVFAD LFGFVSLNV IINGLLFGFVSLNVF LFGFVSLNV IEKQIMLNKSPNNKE IMLNKSPNN LIEKQIMLNKSPNNK IMLNKSPNN EKQIMLNKSPNNKEL IMLNKSPNN KQIMLNKSPNNKELE IMLNKSPNN GLLFGFVSLNVFADS LFGFVSLNV
	HLA-DRB1*0405	IEKQIMLNKSPNNKE IMLNKSPNN EKQIMLNKSPNNKEL LNKSPNNKE KQIMLNKSPNNKELE LNKSPNNKE QIMLNKSPNNKELEL LNKSPNNKE IMLNKSPNNKELELT LNKSPNNKE LNKSPNNKELELTKE LNKSPNNKE MLNKSPNNKELELTK LNKSPNNKE
	HLA-DRB1*0701	VLAKKDVRKAISNVV VLAKKDVRK AKKDVRKAISNVVKV VRKAISNVV KKDVRKAISNVVKVA VRKAISNVV LAKKDVRKAISNVVK VRKAISNVV KDVRKAISNVVKVAQ VRKAISNVV DVRKAISNVVKVAQG VRKAISNVV VRKAISNVVKVAQGA VRKAISNVV
	HLA-DRB1*0802	None
	HLA-DRB1*0901	KDVRKAISNVVKVAQ VRKAISNVV KKDVRKAISNVVKVA VRKAISNVV AKKDVRKAISNVVKV VRKAISNVV LAKKDVRKAISNVVK VRKAISNVV VLAKKDVRKAISNVV AKKDVRKAI VVKKFVGSMSLMSDV FVGSMSLMS AGVVKKFVGSMSLMS KKFVGSMSL GVVKKFVGSMSLMSD FVGSMSLMS
	HLA-DRB1*1101	None
	HLA-DRB1*1302	TKIFSNLIINGLLFG FSNLIINGL KIFSNLIINGLLFGF FSNLIINGL IFSNLIINGLLFGFV FSNLIINGL FSNLIINGLLFGFVS FSNLIINGL MTKIFSNLIINGLLF FSNLIINGL EAQKVLNMVNGLNPS LNMVNGLNP AQKVLNMVNGLNPSN LNMVNGLNP QEAQKVLNMVNGLNP KVLNMVNGL QKVLNMVNGLNPSNK LNMVNGLNP KVLNMVNGLNPSNKD LNMVNGLNP KDVRKAISNVVKVAQ VRKAISNVV VLNMVNGLNPSNKDQ LNMVNGLNP GLLFGFVSLNVFADS FGFVSLNVF

		IEKQIMLNKSPNNKE MLNKSPNNK EKQIMLNKSPNNKEL MLNKSPNNK DVRKAISNVVKVAQG ISNVVKVAQ VRKAISNVVKVAQGA ISNVVKVAQ LLFGFVSLNVFADSN FGFVSLNVF LIEKQIMLNKSPNNK QIMLNKSPN NGLLFGFVSLNVFAD FGFVSLNVF SNLIINGLLFGFVSL LIINGLLFG KAISNVVKVAQGARD ISNVVKVAQ VQEAQKVLNMVNGLN KVLNMVNGL IINGLLFGFVSLNVF IINGLLFGF KQIMLNKSPNNKELE MLNKSPNNK QIMLNKSPNNKELEL MLNKSPNNK GVVKKFVGSMSLMSD VKKFVGSMS INGLLFGFVSLNVFA FGFVSLNVF RKAISNVVKVAQGAR ISNVVKVAQ ARDLTKVMAISLYMR TKVMAISLY LFGFVSLNVFADSNN FGFVSLNVF LNMVNGLNPSNKDQV LNMVNGLNP FGFVSLNVFADSNNA FGFVSLNVF AGVVKKFVGSMSLMS VKKFVGSMS ISNVVKVAQGARDLT ISNVVKVAQ DAGVVKKFVGSMSLM VKKFVGSMS NDAGVVKKFVGSMSL VKKFVGSMS SNDAGVVKKFVGSMS AGVVKKFVG VVKKFVGSMSLMSDV VKKFVGSMS VKKFVGSMSLMSDVA VKKFVGSMS AISNVVKVAQGARDL ISNVVKVAQ NLIINGLLFGFVSLN LIINGLLFG GARDLTKVMAISLYM TKVMAISLY KKDVRKAISNVVKVA VRKAISNVV IMLNKSPNNKELELT MLNKSPNNK QGARDLTKVMAISLY LTKVMAISL
	HLA-DRB1*1501	ARDLTKVMAISLYMR KVMAISLYM INGLLFGFVSLNVFA LFGFVSLNV IINGLLFGFVSLNVF LFGFVSLNV NGLLFGFVSLNVFAD LFGFVSLNV GLLFGFVSLNVFADS LFGFVSLNV LIINGLLFGFVSLNV INGLLFGFV VLAKKDVRKAISNVV VLAKKDVRK LLFGFVSLNVFADSN LFGFVSLNV LFGFVSLNVFADSNN LFGFVSLNV LAKKDVRKAISNVVK VRKAISNVV KKDVRKAISNVVKVA VRKAISNVV AKKDVRKAISNVVKV VRKAISNVV KDVRKAISNVVKVAQ VRKAISNVV QKVLNMVNGLNPSNK VLNMVNGLN AGVVKKFVGSMSLMS VKKFVGSMS GVVKKFVGSMSLMSD FVGSMSLMS LIEKQIMLNKSPNNK IMLNKSPNN KVLNMVNGLNPSNKD VNGLNPSNK IEKQIMLNKSPNNKE MLNKSPNNK EKQIMLNKSPNNKEL MLNKSPNNK KQIMLNKSPNNKELE MLNKSPNNK VLNMVNGLNPSNKDQ VNGLNPSNK VVKKFVGSMSLMSDV FVGSMSLMS QIMLNKSPNNKELEL MLNKSPNNK

		VKKFVGSMSLMSDVA FVGSMSLMS
	HLA-DRB3*0101	None
	HLA-DRB4*0101	LIEKQIMLNKSPNNK LIEKQIMLN EKQIMLNKSPNNKEL MLNKSPNNK IEKQIMLNKSPNNKE MLNKSPNNK KQIMLNKSPNNKELE MLNKSPNNK QIMLNKSPNNKELEL MLNKSPNNK IMLNKSPNNKELELT MLNKSPNNK MLNKSPNNKELELTK MLNKSPNNK
	HLA-DRB5*0101	IEKQIMLNKSPNNKE MLNKSPNNK
CAA49829.1| p93 [Borrelia burgdorferi] Seq26	HLA-DRB1*0101	IDPITNLGTLQLIDL ITNLGTLQL LEVIDPITNLGTLQL VIDPITNLG EVIDPITNLGTLQLI ITNLGTLQL VIDPITNLGTLQLID ITNLGTLQL DPITNLGTLQLIDLN ITNLGTLQL DYYKGFYIEPALKSL FYIEPALKS YKGFYIEPALKSLTK FYIEPALKS YYKGFYIEPALKSLT FYIEPALKS KGFYIEPALKSLTKE FYIEPALKS LDYYKGFYIEPALKS YKGFYIEPA ITNLGTLQLIDLNTG ITNLGTLQL PITNLGTLQLIDLNT ITNLGTLQL EKLKDFVNMDLEFVN FVNMDLEFV LKDFVNMDLEFVNYK FVNMDLEFV KDFVNMDLEFVNYKG FVNMDLEFV KLKDFVNMDLEFVNY FVNMDLEFV KEKLKDFVNMDLEFV KEKLKDFVN FLIFLNGFPLNARKV FLNGFPLNA LIFLNGFPLNARKVD FLNGFPLNA DELKNLVILDVNTLK LKNLVILDV QDELKNLVILDVNTL LKNLVILDV EEEITKGKSRASLGD ITKGKSRAS LQDELKNLVILDVNT LKNLVILDV KEEEITKGKSRASLG ITKGKSRAS EEITKGKSRASLGDL ITKGKSRAS YLQDELKNLVILDVN LKNLVILDV VKEEEITKGKSRASL ITKGKSRAS EFLARPLTNSNSNSS FLARPLTNS IYLQDELKNLVILDV IYLQDELKN KVKEEEITKGKSRAS EITKGKSRA IGEFLARPLTNSNSN FLARPLTNS GEFLARPLTNSNSNS FLARPLTNS FLARPLTNSNSNSSY LTNSNSNSS FFLIFLNGFPLNARK FLNGFPLNA VGIGEFLARPLTNSN FLARPLTNS GIGEFLARPLTNSNS FLARPLTNS SFFLIFLNGFPLNAR FLNGFPLNA GFYIEPALKSLTKEN FYIEPALKS FYIEPALKSLTKENA FYIEPALKS NFEINKNSSLYVDSK INKNSSLYV SNFEINKNSSLYVDS INKNSSLYV IVGIGEFLARPLTNS IGEFLARPL IFLNGFPLNARKVDK FLNGFPLNA ESNFEINKNSSLYVD INKNSSLYV SESNFEINKNSSLYV EINKNSSLY

		FEINKNSSLYVDSKM	INKNSSLYV
		LARPLTNSNSNSSYY	LTNSNSNSS
		FSFFLIFLNGFPLNA	FFLIFLNGF
		ARPLTNSNSNSSYYG	LTNSNSNSS
		DFVNMDLEFVNYKGP	FVNMDLEFV
		FVNMDLEFVNYKGPY	FVNMDLEFV
		RPLTNSNSNSSYYGK	LTNSNSNSS
		FLNGFPLNARKVDKE	FLNGFPLNA
		LKNLVILDVNTLKKV	LKNLVILDV
		ELKNLVILDVNTLKK	LKNLVILDV
		LVVIKMDSGKAKLQI	VIKMDSGKA
		DLVVIKMDSGKAKLQ	VIKMDSGKA
		DSILNLRRILTGYII	ILNLRRILT
		LDSILNLRRILTGYI	ILNLRRILT
		EDLDKDLTTMSIDSS	DKDLTTMSI
		EITKGKSRASLGDLN	ITKGKSRAS
		DLDKDLTTMSIDSSS	LTTMSIDSS
		ITKGKSRASLGDLNN	ITKGKSRAS
		KDLVVIKMDSGKAKL	VIKMDSGKA
		IDSLVTDKVIAALLS	LVTDKVIAA
		EKDLVVIKMDSGKAK	VIKMDSGKA
		DSLVTDKVIAALLSE	DKVIAALLS
		ILNLRRILTGYIIKS	LRRILTGYI
		DKDLTTMSIDSSSPV	LTTMSIDSS
		MKKMLLIFSFFLIFL	MKKMLLIFS
		LVTDKVIAALLSENE	DKVIAALLS
		LDKDLTTMSIDSSSP	LTTMSIDSS
		DLTTMSIDSSSPVFL	LTTMSIDSS
		LTTMSIDSSSPVFLE	IDSSSPVFL
		VTDKVIAALLSENEA	DKVIAALLS
		LNLRRILTGYIIKSF	LRRILTGYI
		SLVTDKVIAALLSEN	DKVIAALLS
		KDLTTMSIDSSSPVF	LTTMSIDSS
		TNLGTLQLIDLNTGV	LGTLQLIDL
		SILNLRRILTGYIIK	LRRILTGYI
		VVIKMDSGKAKLQIL	IKMDSGKAK
		SELDSILNLRRILTG	ILNLRRILT
		ENKILPFTSFSVRKN	ILPFTSFSV
		LGTLQLIDLNTGVRL	LQLIDLNTG
		EINKNSSLYVDSKMI	INKNSSLYV
		NKILPFTSFSVRKNF	FTSFSVRKN
		ELDSILNLRRILTGY	ILNLRRILT
		SLYVDSKMILAAVRD	YVDSKMILA
		INKNSSLYVDSKMIL	INKNSSLYV
		LYVDSKMILAAVRDK	SKMILAAVR
		NLRRILTGYIIKSFD	ILTGYIIKS
		IDIDSLVTDKVIAAL	LVTDKVIAA
		VIKMDSGKAKLQILN	VIKMDSGKA
		KSELDSILNLRRILT	LDSILNLRR
		TDKVIAALLSENEAG	IAALLSENE
		DKVIAALLSENEAGV	IAALLSENE
		SSLYVDSKMILAAVR	YVDSKMILA
		PVFLEVIDPITNLGT	VIDPITNLG
		PLTNSNSNSSYYGKY	LTNSNSNSS
		VFLEVIDPITNLGTL	VIDPITNLG
		LQILNKLENLKVVSE	LNKLENLKV
		LTNSNSNSSYYGKYF	LTNSNSNSS

		LRRILTGYIIKSFDY ILTGYIIKS
		EELLKSKDGKVSKDY LKSKDGKVS
		RDEELLKSKDGKVSK LKSKDGKVS
		QILNKLENLKVVSES LNKLENLKV
		TTMSIDSSSPVFLEV IDSSSPVFL
		KRDEELLKSKDGKVS EELLKSKDG
		FLEVIDPITNLGTLQ VIDPITNLG
		ELLKSKDGKVSKDYE LKSKDGKVS
		KNLVILDVNTLKKVK LVILDVNTL
		YVDSKMILAAVRDKD MILAAVRDK
		NEDLDKDLTTMSIDS LDKDLTTMS
		LNGFPLNARKVDKEK GFPLNARKV
		DEELLKSKDGKVSKD LKSKDGKVS
		IDLNTGVRLKESTQQ IDLNTGVRL
		LNEDLDKDLTTMSID DKDLTTMSI
		SLNEDLDKDLTTMSI LDKDLTTMS
		TMSIDSSSPVFLEVI IDSSSPVFL
		LEFVNYKGPYDSTNT VNYKGPYDS
		GTLQLIDLNTGVRLK LQLIDLNTG
		NLGTLQLIDLNTGVR LQLIDLNTG
		VDSKMILAAVRDKDD MILAAVRDK
		EFVNYKGPYDSTNTY VNYKGPYDS
		DLNTGVRLKESTQQG VRLKESTQQ
		KSLTKENAGLSRVYS LTKENAGLS
		MSIDSSSPVFLEVID IDSSSPVFL
		DIDSLVTDKVIAALL LVTDKVIAA
		DPKVKDQTTSLNEDL VKDQTTSLN
		LKSLTKENAGLSRVY LTKENAGLS
		NTGVRLKESTQQGIQ VRLKESTQQ
		DIDIDSLVTDKVIAA IDSLVTDKV
		LNTGVRLKESTQQGI VRLKESTQQ
		ILPFTSFSVRKNFIY FTSFSVRKN
		LSENKILPFTSFSVR ILPFTSFSV
		SENKILPFTSFSVRK ILPFTSFSV
		IDPKVKDQTTSLNED VKDQTTSLN
		QKIDPKVKDQTTSLN KVKDQTTSL
		KIDPKVKDQTTSLNE VKDQTTSLN
		KILPFTSFSVRKNFI FTSFSVRKN
		ALKSLTKENAGLSRV LTKENAGLS
		REKDLVVIKMDSGKA LVVIKMDSG
		PKVKDQTTSLNEDLD VKDQTTSLN
		RRILTGYIIKSFDYD ILTGYIIKS
		SFDYDRSSAELIAKV YDRSSAELI
		TGVRLKESTQQGIQR VRLKESTQQ
		IKSFDYDRSSAELIA YDRSSAELI
		AGLSRVYSQWAGKTQ LSRVYSQWA
		KSFDYDRSSAELIAK YDRSSAELI
		FDYDRSSAELIAKVI YDRSSAELI
		SRVYSQWAGKTQIFI VYSQWAGKT
		NSSLYVDSKMILAAV YVDSKMILA
		AKLQILNKLENLKVV LNKLENLKV
		IKMDSGKAKLQILNK MDSGKAKLQ
		ILSENKILPFTSFSV NKILPFTSF
		EQIVGIGEFLARPLT IGEFLARPL
		IIKSFDYDRSSAELI DYDRSSAEL
		YEQIVGIGEFLARPL IVGIGEFLA
		LSRVYSQWAGKTQIF VYSQWAGKT

		KLQILNKLENLKVVS LNKLENLKV NAGLSRVYSQWAGKT LSRVYSQWA KAKLQILNKLENLKV LQILNKLEN LQLIDLNTGVRLKES IDLNTGVRL DLEFVNYKGPYDSTN VNYKGPYDS GLSRVYSQWAGKTQI VYSQWAGKT ILNKLENLKVVSESN LENLKVVSE PALKSLTKENAGLSR LTKENAGLS ELIAKVITIYNAVYR IAKVITIYN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	EFLARPLTNSNSNSS LARPLTNSN FLARPLTNSNSNSSY LTNSNSNSS LARPLTNSNSNSSYY LTNSNSNSS ARPLTNSNSNSSYYG LTNSNSNSS RPLTNSNSNSSYYGK LTNSNSNSS LDYYKGFYIEPALKS YKGFYIEPA DYYKGFYIEPALKSL FYIEPALKS VNFARDITDIQGETH FARDITDIQ NEAGVNFARDITDIQ NEAGVNFAR GVNFARDITDIQGET FARDITDIQ EAGVNFARDITDIQG FARDITDIQ AGVNFARDITDIQGE FARDITDIQ YKGFYIEPALKSLTK FYIEPALKS YYKGFYIEPALKSLT FYIEPALKS KGFYIEPALKSLTKE FYIEPALKS LTNSNSNSSYYGKYF LTNSNSNSS PLTNSNSNSSYYGKY LTNSNSNSS NFARDITDIQGETHK FARDITDIQ FARDITDIQGETHKA FARDITDIQ FYIEPALKSLTKENA FYIEPALKS GFYIEPALKSLTKEN FYIEPALKS FSFFLIFLNGFPLNA FFLIFLNGF FFLIFLNGFPLNARK FLNGFPLNA SFFLIFLNGFPLNAR FLNGFPLNA
	HLA-DRB1*0404	SFFLIFLNGFPLNAR FLIFLNGFP FSFFLIFLNGFPLNA FLIFLNGFP LEVIDPITNLGTLQL VIDPITNLG SPVFLEVIDPITNLG VFLEVIDPI PVFLEVIDPITNLGT VIDPITNLG VFLEVIDPITNLGTL VIDPITNLG FLEVIDPITNLGTLQ VIDPITNLG FFLIFLNGFPLNARK FLNGFPLNA FLIFLNGFPLNARKV FLNGFPLNA IFSFFLIFLNGFPLN FLIFLNGFP LLIFSFFLIFLNGFP SFFLIFLNG LIFSFFLIFLNGFPL FLIFLNGFP EVIDPITNLGTLQLI VIDPITNLG VIDPITNLGTLQLID VIDPITNLG LIFLNGFPLNARKVD FLNGFPLNA EFLARPLTNSNSNSS LARPLTNSN ELKNLVILDVNTLKK VILDVNTLK LKNLVILDVNTLKKV ILDVNTLKK EKDLVVIKMDSGKAK VIKMDSGKA REKDLVVIKMDSGKA LVVIKMDSG FLARPLTNSNSNSSY LTNSNSNSS KNLVILDVNTLKKVK ILDVNTLKK

		KDLVVIKMDSGKAKL VIKMDSGKA LARPLTNSNSNSSYY LTNSNSNSS GTLQLIDLNTGVRLK LIDLNTGVR NLGTLQLIDLNTGVR LQLIDLNTG IFLNGFPLNARKVDK FLNGFPLNA LGTLQLIDLNTGVRL LIDLNTGVR IGEFLARPLTNSNSN LARPLTNSN GEFLARPLTNSNSNS LARPLTNSN GIGEFLARPLTNSNS LARPLTNSN DLVVIKMDSGKAKLQ VIKMDSGKA LVVIKMDSGKAKLQI VIKMDSGKA TLQLIDLNTGVRLKE LIDLNTGVR VGIGEFLARPLTNSN FLARPLTNS LQLIDLNTGVRLKES LIDLNTGVR
	HLA-DRB1*0405	ELIAKVITIYNAVYR IAKVITIYN AELIAKVITIYNAVY IAKVITIYN LDYYKGFYIEPALKS YKGFYIEPA DYYKGFYIEPALKSL FYIEPALKS YYKGFYIEPALKSLT FYIEPALKS YKGFYIEPALKSLTK FYIEPALKS IDPKVKDQTTSLNED VKDQTTSLN PKVKDQTTSLNEDLD VKDQTTSLN INEINKEKNLPKPGD INKEKNLPK DPKVKDQTTSLNEDL VKDQTTSLN NEINKEKNLPKPGDV INKEKNLPK KGFYIEPALKSLTKE FYIEPALKS SFFLIFLNGFPLNAR IFLNGFPLN FFLIFLNGFPLNARK LNGFPLNAR IAKVITIYNAVYRGD IAKVITIYN FLIFLNGFPLNARKV LNGFPLNAR RSSAELIAKVITIYN LIAKVITIY SSAELIAKVITIYNA IAKVITIYN SAELIAKVITIYNAV IAKVITIYN LIAKVITIYNAVYRG IAKVITIYN LIFLNGFPLNARKVD LNGFPLNAR IFLNGFPLNARKVDK LNGFPLNAR QKIDPKVKDQTTSLN QKIDPKVKD KIDPKVKDQTTSLNE VKDQTTSLN EINKEKNLPKPGDVS EKNLPKPGD INKEKNLPKPGDVSS EKNLPKPGD SNITETIENLRDQLE TETIENLRD NAWRLAKFSPKNLDE AKFSPKNLD
	HLA-DRB1*0701	LSENKILPFTSFSVR ILPFTSFSV SENKILPFTSFSVRK ILPFTSFSV ENKILPFTSFSVRKN ILPFTSFSV NKILPFTSFSVRKNF ILPFTSFSV ILSENKILPFTSFSV ILSENKILP ILPFTSFSVRKNFIY ILPFTSFSV KILPFTSFSVRKNFI ILPFTSFSV LARPLTNSNSNSSYY LTNSNSNSS ARPLTNSNSNSSYYG LTNSNSNSS RPLTNSNSNSSYYGK LTNSNSNSS SESNFEINKNSSLYV EINKNSSLY LPFTSFSVRKNFIYL FSVRKNFIY ESNFEINKNSSLYVD INKNSSLYV
	HLA-DRB1*0802	None

	HLA-DRB1*0901	FDYDRSSAELIAKVI YDRSSAELI SFDYDRSSAELIAKV YDRSSAELI KSFDYDRSSAELIAK YDRSSAELI IKSFDYDRSSAELIA YDRSSAELI IIKSFDYDRSSAELI IIKSFDYDR SVDVFSISSKSELDS FSISSKSEL VDVFSISSKSELDSI FSISSKSEL ASVDVFSISSKSELD FSISSKSEL DVFSISSKSELDSIL FSISSKSEL KASVDVFSISSKSEL DVFSISSKS YDRSSAELIAKVITI YDRSSAELI DYDRSSAELIAKVIT YDRSSAELI
	HLA-DRB1*1101	None
	HLA-DRB1*1302	SPVFLEVIDPITNLG VFLEVIDPI LNKLENLKVVSESNF LENLKVVSE IAKVITIYNAVYRGD ITIYNAVYR AKVITIYNAVYRGDL ITIYNAVYR ILNKLENLKVVSESN LENLKVVSE GDLNNDKNLMLPEDQ LNNDKNLML SKEEVDNKAINLQKI VDNKAINLQ EINKNSSLYVDSKMI INKNSSLYV KDLVVIKMDSGKAKL IKMDSGKAK KEEVDNKAINLQKID VDNKAINLQ INKNSSLYVDSKMIL INKNSSLYV VFLEVIDPITNLGTL VIDPITNLG KVITIYNAVYRGDLD ITIYNAVYR PVFLEVIDPITNLGT VIDPITNLG NKLENLKVVSESNFE LKVVSESNF IFSFFLIFLNGFPLN LIFLNGFPL FSFFLIFLNGFPLNA LIFLNGFPL EFILSENKILPFTSF ILSENKILP AINLQKIDPKVKDQT INLQKIDPK DLVVIKMDSGKAKLQ IKMDSGKAK MKKMLLIFSFFLIFL LLIFSFFLI DKDLTTMSIDSSSPV LTTMSIDSS SRASLGDLNNDKNLM LGDLNNDKN FLIFLNGFPLNARKV LIFLNGFPL
	HLA-DRB1*1501	SFFLIFLNGFPLNAR FLIFLNGFP FFLIFLNGFPLNARK LNGFPLNAR FLIFLNGFPLNARKV LNGFPLNAR LIFLNGFPLNARKVD LNGFPLNAR SENKILPFTSFSVRK ILPFTSFSV ENKILPFTSFSVRKN ILPFTSFSV LSENKILPFTSFSVR ILPFTSFSV NKILPFTSFSVRKNF ILPFTSFSV LDSILNLRRILTGYI LNLRRILTG DSILNLRRILTGYII LRRILTGYI IFLNGFPLNARKVDK LNGFPLNAR SILNLRRILTGYIIK LRRILTGYI KILPFTSFSVRKNFI LPFTSFSVR ILNLRRILTGYIIKS LRRILTGYI SELDSILNLRRILTG LDSILNLRR ELDSILNLRRILTGY LNLRRILTG LGTLQLIDLNTGVRL LIDLNTGVR GTLQLIDLNTGVRLK LIDLNTGVR LNLRRILTGYIIKSF LRRILTGYI

		NLGTLQLIDLNTGVR LQLIDLNTG EKDLVVIKMDSGKAK LVVIKMDSG KDLVVIKMDSGKAKL LVVIKMDSG ILPFTSFSVRKNFIY ILPFTSFSV FLNGFPLNARKVDKE LNGFPLNAR QQGIQRYGIYEREKD IQRYGIYER QGIQRYGIYEREKDL IQRYGIYER TQQGIQRYGIYEREK IQRYGIYER TLQLIDLNTGVRLKE LIDLNTGVR ESTQQGIQRYGIYER QGIQRYGIY NSSYYGKYFINRFID YYGKYFINR SSYYGKYFINRFIDD YYGKYFINR LQLIDLNTGVRLKES LIDLNTGVR STQQGIQRYGIYERE IQRYGIYER SNSSYYGKYFINRFI YYGKYFINR DELKNLVILDVNTLK LKNLVILDV LNGFPLNARKVDKEK LNGFPLNAR SNAWRLAKFSPKNLD WRLAKFSPK DSNAWRLAKFSPKNL WRLAKFSPK NAWRLAKFSPKNLDE WRLAKFSPK DLVVIKMDSGKAKLQ VIKMDSGKA FSFFLIFLNGFPLNA LIFLNGFPL IFSFFLIFLNGFPLN LIFLNGFPL QDELKNLVILDVNTL LKNLVILDV LIFSFFLIFLNGFPL FFLIFLNGF REKDLVVIKMDSGKA LVVIKMDSG ILSENKILPFTSFSV SENKILPFT LVVIKMDSGKAKLQI VIKMDSGKA LLIFSFFLIFLNGFP LLIFSFFLI NSNSSYYGKYFINRF YYGKYFINR ELIAKVITIYNAVYR VITIYNAVY LIAKVITIYNAVYRG ITIYNAVYR
	HLA-DRB3*0101	DLTTMSIDSSSPVFL MSIDSSSPV LTTMSIDSSSPVFLE MSIDSSSPV TTMSIDSSSPVFLEV MSIDSSSPV KDLTTMSIDSSSPVF MSIDSSSPV DKDLTTMSIDSSSPV TMSIDSSSP
	HLA-DRB4*0101	None
	HLA-DRB5*0101	AINLQKIDPKVKDQT LQKIDPKVK INLQKIDPKVKDQTT LQKIDPKVK KSELDSILNLRRILT LDSILNLRR SELDSILNLRRILTG LDSILNLRR VNYKGPYDSTNTYEQ VNYKGPYDS KKEFKPVSEVEKLDK FKPVSEVEK LDGKKEFKPVSEVEK LDGKKEFKP KEFKPVSEVEKLDKI FKPVSEVEK DGKKEFKPVSEVEKL FKPVSEVEK GKKEFKPVSEVEKLD FKPVSEVEK
NP_212375.1| glycerol kinase (glpK) [Borrelia burgdorferi B31] Seq27	HLA-DRB1*0101	VYFVPAFVGLGAPHW FVPAFVGLG YFVPAFVGLGAPHWD FVGLGAPHW FVPAFVGLGAPHWDS FVGLGAPHW VPAFVGLGAPHWDSY FVGLGAPHW PAFVGLGAPHWDSYA FVGLGAPHW AAYLAGLATGYWQSA YLAGLATGY

		QKEFTQIYPQPSWVE FTQIYPQPS
		KEFTQIYPQPSWVEH FTQIYPQPS
		ALGAAYLAGLATGYW YLAGLATGY
		LGAAYLAGLATGYWQ YLAGLATGY
		GAAYLAGLATGYWQS YLAGLATGY
		AYLAGLATGYWQSAE LAGLATGYW
		FAQKEFTQIYPQPSW FTQIYPQPS
		GFAQKEFTQIYPQPS FAQKEFTQI
		TALGAAYLAGLATGY LGAAYLAGL
		AQKEFTQIYPQPSWV FTQIYPQPS
		ACLKKGMAKNTYGTG LKKGMAKNT
		AFVGLGAPHWDSYAR FVGLGAPHW
		QACLKKGMAKNTYGT LKKGMAKNT
		EFTQIYPQPSWVEHD FTQIYPQPS
		FVGLGAPHWDSYARG FVGLGAPHW
		FGQACLKKGMAKNTY LKKGMAKNT
		FTQIYPQPSWVEHDP FTQIYPQPS
		KVVRPKITETTALGA VRPKITETT
		YLAGLATGYWQSAEE YLAGLATGY
		TFGQACLKKGMAKNT FGQACLKKG
		GQACLKKGMAKNTYG LKKGMAKNT
		EGSVFIGGAVIQWLR FIGGAVIQW
		GSVFIGGAVIQWLRD FIGGAVIQW
		LEGSVFIGGAVIQWL FIGGAVIQW
		CKVVRPKITETTALG VRPKITETT
		LECKVVRPKITETTA VRPKITETT
		ECKVVRPKITETTAL VRPKITETT
		LLECKVVRPKITETT CKVVRPKIT
		TETTALGAAYLAGLA TTALGAAYL
		ITETTALGAAYLAGL TTALGAAYL
		SVFIGGAVIQWLRDG FIGGAVIQW
		ETTALGAAYLAGLAT LGAAYLAGL
		TTALGAAYLAGLATG LGAAYLAGL
		LAGLATGYWQSAEEI LATGYWQSA
		KALFGAEIPIAGIAG FGAEIPIAG
		DKALFGAEIPIAGIA FGAEIPIAG
		KTDKALFGAEIPIAG LFGAEIPIA
		TDKALFGAEIPIAGI FGAEIPIAG
		GVITEAMANARILPN ITEAMANAR
		QLGVITEAMANARIL ITEAMANAR
		LGVITEAMANARILP ITEAMANAR
		NGGVYFVPAFVGLGA FVPAFVGLG
		GGVYFVPAFVGLGAP FVPAFVGLG
		SVTYVLEGSVFIGGA YVLEGSVFI
		PKITETTALGAAYLA TTALGAAYL
		TEIWGSQLGVITEAM WGSQLGVIT
		KSVTYVLEGSVFIGG YVLEGSVFI
		VTYVLEGSVFIGGAV YVLEGSVFI
		GSTKAHITRAALESI TKAHITRAA
		KKSVTYVLEGSVFIG YVLEGSVFI
		PTEIWGSQLGVITEA WGSQLGVIT
		DQFAATFGQACLKKG FAATFGQAC
		RKKSVTYVLEGSVFI VTYVLEGSV
		VFIGGAVIQWLRDGL IGGAVIQWL
		DPTEIWGSQLGVITE WGSQLGVIT
		VLEGSVFIGGAVIQW VFIGGAVIQ
		DNGGVYFVPAFVGLG YFVPAFVGL

		HDPTEIWGSQLGVIT IWGSQLGVI
		ALFGAEIPIAGIAGD FGAEIPIAG
		GVYFVPAFVGLGAPH FVPAFVGLG
		LCFGTIDTWILWNLT FGTIDTWIL
		SQLGVITEAMANARI ITEAMANAR
		RPKITETTALGAAYL ITETTALGA
		CLKKGMAKNTYGTGC LKKGMAKNT
		VITEAMANARILPNE MANARILPN
		VRPKITETTALGAAY VRPKITETT
		KITETTALGAAYLAG TTALGAAYL
		LKKGMAKNTYGTGCF LKKGMAKNT
		FAATFGQACLKKGMA FGQACLKKG
		QFAATFGQACLKKGM FGQACLKKG
		KAHITRAALESIAFQ ITRAALESI
		ELCFGTIDTWILWNL FGTIDTWIL
		IQELRVDGGASQNNL VDGGASQNN
		ENGELCFGTIDTWIL LCFGTIDTW
		GELCFGTIDTWILWN FGTIDTWIL
		QELRVDGGASQNNLL VDGGASQNN
		NGELCFGTIDTWILW FGTIDTWIL
		DELLSILNVPRAILP LSILNVPRA
		EIQELRVDGGASQNN LRVDGGASQ
		IYNAIVWQDRRTAKI IVWQDRRTA
		AATFGQACLKKGMAK FGQACLKKG
		ELRVDGGASQNNLLM VDGGASQNN
		ELLSILNVPRAILPE LNVPRAILP
		ITEAMANARILPNEI MANARILPN
		ATFGQACLKKGMAKN FGQACLKKG
		LRVDGGASQNNLLMQ VDGGASQNN
		YNAIVWQDRRTAKIC WQDRRTAKI
		AHITRAALESIAFQS ITRAALESI
		GSQLGVITEAMANAR VITEAMANA
		YVLEGSVFIGGAVIQ YVLEGSVFI
		RGTIIGITRGSTKAH GITRGSTKA
		LLSILNVPRAILPEL LNVPRAILP
		LSILNVPRAILPELK LNVPRAILP
		AGLATGYWQSAEEIV LATGYWQSA
		KNTYGTGCFLTVNIG YGTGCFLTV
		GMAKNTYGTGCFLTV GMAKNTYGT
		WGSQLGVITEAMANA WGSQLGVIT
		YILSIDQGTTSSRAM IDQGTTSSR
		GTIIGITRGSTKAHI ITRGSTKAH
		NAIVWQDRRTAKICD WQDRRTAKI
		NTYGTGCFLTVNIGK YGTGCFLTV
		TIIGITRGSTKAHIT ITRGSTKAH
		AKNTYGTGCFLTVNI YGTGCFLTV
		MAKNTYGTGCFLTVN YGTGCFLTV
		IIGITRGSTKAHITR ITRGSTKAH
		DKLLTSIAWGRKKSV LLTSIAWGR
		SILNVPRAILPELKE LNVPRAILP
		HATDYSNASRTLLLN YSNASRTLL
		ATDYSNASRTLLLNI YSNASRTLL
		EHATDYSNASRTLLL YSNASRTLL
		KYILSIDQGTTSSRA IDQGTTSSR
		GTIDTWILWNLTQKK DTWILWNLT
		TDYSNASRTLLLNIK YSNASRTLL
		LSIDQGTTSSRAMVF IDQGTTSSR

		TIDTWILWNLTQKKE ILWNLTQKK
		IGITRGSTKAHITRA ITRGSTKAH
		FIGGAVIQWLRDGLE FIGGAVIQW
		TEAMANARILPNEID MANARILPN
		ILSIDQGTTSSRAMV IDQGTTSSR
		AIVWQDRRTAKICDQ WQDRRTAKI
		LFGAEIPIAGIAGDQ FGAEIPIAG
		GITRGSTKAHITRAA ITRGSTKAH
		KEHATDYSNASRTLL DYSNASRTL
		LATGYWQSAEEIVSL LATGYWQSA
		IVWQDRRTAKICDQL WQDRRTAKI
		GLATGYWQSAEEIVS LATGYWQSA
		RAILPELKESSTIYG LPELKESST
		LLTSIAWGRKKSVTY IAWGRKKSV
		AILPELKESSTIYGK LKESSTIYG
		HITRAALESIAFQSF ITRAALESI
		ITRGSTKAHITRAAL TKAHITRAA
		ILPELKESSTIYGKT LKESSTIYG
		LPELKESSTIYGKTD LKESSTIYG
		IDTWILWNLTQKKEH ILWNLTQKK
		DTWILWNLTQKKEHA ILWNLTQKK
		LTSIAWGRKKSVTYV IAWGRKKSV
		ISHDKLLTSIAWGRK LLTSIAWGR
		TSIAWGRKKSVTYVL IAWGRKKSV
		IWGSQLGVITEAMAN WGSQLGVIT
		FGTIDTWILWNLTQK FGTIDTWIL
		IISHDKLLTSIAWGR DKLLTSIAW
		TQIYPQPSWVEHDPT IYPQPSWVE
		GKTDKALFGAEIPIA DKALFGAEI
		TYVLEGSVFIGGAVI YVLEGSVFI
		ITRAALESIAFQSFD ITRAALESI
		KPIYNAIVWQDRRTA YNAIVWQDR
		SHDKLLTSIAWGRKK LLTSIAWGR
		CFGTIDTWILWNLTQ FGTIDTWIL
		PELKESSTIYGKTDK LKESSTIYG
		KLLTSIAWGRKKSVT IAWGRKKSV
		TWILWNLTQKKEHAT ILWNLTQKK
		SDNGGVYFVPAFVGL VYFVPAFVG
		DDELLSILNVPRAIL LSILNVPRA
		SSDAEALASSVSDNG AEALASSVS
		SIDQGTTSSRAMVFD DQGTTSSRA
		EAMANARILPNEIDA MANARILPN
		FRKSSDAEALASSVS FRKSSDAEA
		SDAEALASSVSDNGG AEALASSVS
		FGAEIPIAGIAGDQF FGAEIPIAG
		PIYNAIVWQDRRTAK YNAIVWQDR
		MKYILSIDQGTTSSR MKYILSIDQ
		HDKLLTSIAWGRKKS LLTSIAWGR
		WDDELLSILNVPRAI LSILNVPRA
		VDGGASQNNLLMQFQ VDGGASQNN
		EWDDELLSILNVPRA LLSILNVPR
		RVDGGASQNNLLMQF VDGGASQNN
		SIAFQSFDILNTMKK FQSFDILNT
		DYSNASRTLLLNIKT YSNASRTLL
		IAFQSFDILNTMKKS FQSFDILNT
		LKESSTIYGKTDKAL LKESSTIYG
		AIGITNQRETTVIWE ITNQRETTV

		IDQGTTSSRAMVFDK IDQGTTSSR ENWNKAVGKAKSWIQ WNKAVGKAK DAIGITNQRETTVIW ITNQRETTV IGITNQRETTVIWEK ITNQRETTV ILNVPRAILPELKES LNVPRAILP IDAIGITNQRETTVI ITNQRETTV SIAWGRKKSVTYVLE WGRKKSVTY RGSTKAHITRAALES TKAHITRAA WDSYARGTIIGITRG YARGTIIGI IAWGRKKSVTYVLEG WGRKKSVTY EIDAIGITNQRETTV IDAIGITNQ DSYARGTIIGITRGS YARGTIIGI LNVPRAILPELKESS LNVPRAILP TYGTGCFLTVNIGKE YGTGCFLTV NTGKPIYNAIVWQDR IYNAIVWQD IYPQPSWVEHDPTEI IYPQPSWVE
	HLA-DRB1*0301	None
	HLA-DRB1*0401	TQKKEHATDYSNASR HATDYSNAS QKKEHATDYSNASRT HATDYSNAS LTQKKEHATDYSNAS QKKEHATDY KKEHATDYSNASRTL HATDYSNAS KEHATDYSNASRTLL HATDYSNAS EHATDYSNASRTLLL HATDYSNAS HATDYSNASRTLLLN HATDYSNAS FDILNTMKKSIPNFE FDILNTMKK MKYILSIDQGTTSSR MKYILSIDQ DILNTMKKSIPNFEI MKKSIPNFE ILNTMKKSIPNFEIQ MKKSIPNFE LNTMKKSIPNFEIQE MKKSIPNFE
	HLA-DRB1*0404	VYFVPAFVGLGAPHW FVPAFVGLG YFVPAFVGLGAPHWD FVGLGAPHW FVPAFVGLGAPHWDS FVGLGAPHW TIDTWILWNLTQKKE ILWNLTQKK DTWILWNLTQKKEHA ILWNLTQKK GTIDTWILWNLTQKK DTWILWNLT IDTWILWNLTQKKEH ILWNLTQKK TWILWNLTQKKEHAT ILWNLTQKK NGGVYFVPAFVGLGA FVPAFVGLG GVYFVPAFVGLGAPH FVPAFVGLG GGVYFVPAFVGLGAP FVPAFVGLG DNGGVYFVPAFVGLG GVYFVPAFV NASRTLLLNIKTLEW LLLNIKTLE ASRTLLLNIKTLEWD LLNIKTLEW SRTLLLNIKTLEWDD LLNIKTLEW RTLLLNIKTLEWDDE LLNIKTLEW TKIMWILDNVEGARQ IMWILDNVE GTKIMWILDNVEGAR IMWILDNVE EWDDELLSILNVPRA LLSILNVPR DDELLSILNVPRAIL LSILNVPRA WDDELLSILNVPRAI LSILNVPRA DELLSILNVPRAILP LSILNVPRA TLLLNIKTLEWDDEL LLNIKTLEW AAYLAGLATGYWQSA LAGLATGYW AYLAGLATGYWQSAE LAGLATGYW GSQLGVITEAMANAR VITEAMANA VPAFVGLGAPHWDSY FVGLGAPHW

		LGVITEAMANARILP VITEAMANA WILWNLTQKKEHATD ILWNLTQKK SQLGVITEAMANARI VITEAMANA ILWNLTQKKEHATDY ILWNLTQKK QLGVITEAMANARIL VITEAMANA ELLSILNVPRAILPE LSILNVPRA PAFVGLGAPHWDSYA FVGLGAPHW SDAEALASSVSDNGG LASSVSDNG SGTKIMWILDNVEGA IMWILDNVE
	HLA-DRB1*0405	QKEFTQIYPQPSWVE FTQIYPQPS KEFTQIYPQPSWVEH IYPQPSWVE EFTQIYPQPSWVEHD IYPQPSWVE FTQIYPQPSWVEHDP IYPQPSWVE TEAMANARILPNEID MANARILPN EAMANARILPNEIDA ARILPNEID TQIYPQPSWVEHDPT IYPQPSWVE AMANARILPNEIDAI ARILPNEID MANARILPNEIDAIG ARILPNEID IYPQPSWVEHDPTEI IYPQPSWVE ANARILPNEIDAIGI ARILPNEID QIYPQPSWVEHDPTE IYPQPSWVE GVITEAMANARILPN ITEAMANAR GTIDTWILWNLTQKK WILWNLTQK ITEAMANARILPNEI MANARILPN FGTIDTWILWNLTQK TWILWNLTQ TIDTWILWNLTQKKE WILWNLTQK FAQKEFTQIYPQPSW FTQIYPQPS FIGGAVIQWLRDGLE GAVIQWLRD VITEAMANARILPNE MANARILPN IYNAIVWQDRRTAKI IYNAIVWQD SGTKIMWILDNVEGA IMWILDNVE IDTWILWNLTQKKEH WILWNLTQK IGGAVIQWLRDGLEF IQWLRDGLE NARILPNEIDAIGIT ARILPNEID FSGTKIMWILDNVEG IMWILDNVE ARILPNEIDAIGITN ARILPNEID AQKEFTQIYPQPSWV FTQIYPQPS YPQPSWVEHDPTEIW WVEHDPTEI TKIMWILDNVEGARQ IMWILDNVE NTGKPIYNAIVWQDR IYNAIVWQD GTKIMWILDNVEGAR IMWILDNVE GGAVIQWLRDGLEFF IQWLRDGLE PQPSWVEHDPTEIWG VEHDPTEIW GFAQKEFTQIYPQPS QKEFTQIYP
	HLA-DRB1*0701	EHATDYSNASRTLLL YSNASRTLL HATDYSNASRTLLLN YSNASRTLL ATDYSNASRTLLLNI YSNASRTLL TDYSNASRTLLLNIK YSNASRTLL DAIGITNQRETTVIW ITNQRETTV LSIDQGTTSSRAMVF DQGTTSSRA IDAIGITNQRETTVI ITNQRETTV AIGITNQRETTVIWE ITNQRETTV IGITNQRETTVIWEK ITNQRETTV SIDQGTTSSRAMVFD TTSSRAMVF TSIAWGRKKSVTYVL WGRKKSVTY SIAWGRKKSVTYVLE RKKSVTYVL IAWGRKKSVTYVLEG RKKSVTYVL

		KEHATDYSNASRTLL DYSNASRTL IDQGTTSSRAMVFDK TTSSRAMVF AWGRKKSVTYVLEGS RKKSVTYVL KEFTQIYPQPSWVEH IYPQPSWVE QKEFTQIYPQPSWVE QIYPQPSWV EFTQIYPQPSWVEHD IYPQPSWVE WGRKKSVTYVLEGSV RKKSVTYVL TQIYPQPSWVEHDPT IYPQPSWVE DQGTTSSRAMVFDKN TTSSRAMVF FTQIYPQPSWVEHDP IYPQPSWVE EIDAIGITNQRETTV IGITNQRET QGTTSSRAMVFDKNA TTSSRAMVF
	HLA-DRB1*0802	EKLLENWNKAVGKAK LENWNKAVG KLLENWNKAVGKAKS WNKAVGKAK LLENWNKAVGKAKSW WNKAVGKAK LENWNKAVGKAKSWI WNKAVGKAK ENWNKAVGKAKSWIQ WNKAVGKAK DKLLTSIAWGRKKSV SIAWGRKKS KLLTSIAWGRKKSVT SIAWGRKKS LLTSIAWGRKKSVTY SIAWGRKKS LTSIAWGRKKSVTYV SIAWGRKKS IDTWILWNLTQKKEH WILWNLTQK
	HLA-DRB1*0901	LATGYWQSAEEIVSL YWQSAEEIV GLATGYWQSAEEIVS YWQSAEEIV ATGYWQSAEEIVSLW YWQSAEEIV TGYWQSAEEIVSLWQ YWQSAEEIV AGLATGYWQSAEEIV GYWQSAEEI HATDYSNASRTLLLN YSNASRTLL EHATDYSNASRTLLL YSNASRTLL WQVDKIFEPSMPKNQ IFEPSMPKN ATDYSNASRTLLLNI YSNASRTLL TDYSNASRTLLLNIK YSNASRTLL GLEFFRKSSDAEALA FRKSSDAEA LEFFRKSSDAEALAS FRKSSDAEA DGLEFFRKSSDAEAL FRKSSDAEA QVDKIFEPSMPKNQK FEPSMPKNQ VDKIFEPSMPKNQKE FEPSMPKNQ DKIFEPSMPKNQKEK FEPSMPKNQ KEHATDYSNASRTLL TDYSNASRT EFFRKSSDAEALASS FRKSSDAEA RDGLEFFRKSSDAEA FFRKSSDAE GYWQSAEEIVSLWQV YWQSAEEIV KIFEPSMPKNQKEKL FEPSMPKNQ PHWDSYARGTIIGIT WDSYARGTI APHWDSYARGTIIGI WDSYARGTI
	HLA-DRB1*1101	KLLENWNKAVGKAKS LENWNKAVG EKLLENWNKAVGKAK LENWNKAVG IYNAIVWQDRRTAKI IVWQDRRTA
	HLA-DRB1*1302	FDILNTMKKSIPNFE LNTMKKSIP TDYSNASRTLLLNIK YSNASRTLL FQSFDILNTMKKSIP FDILNTMKK QSFDILNTMKKSIPN LNTMKKSIP DILNTMKKSIPNFEI LNTMKKSIP ATDYSNASRTLLLNI YSNASRTLL EHATDYSNASRTLLL YSNASRTLL HATDYSNASRTLLLN YSNASRTLL

		SFDILNTMKKSIPNF LNTMKKSIP ASRTLLLNIKTLEWD LLLNIKTLE KEHATDYSNASRTLL HATDYSNAS SRTLLLNIKTLEWDD LLLNIKTLE RTLLLNIKTLEWDDE LLLNIKTLE NASRTLLLNIKTLEW LLLNIKTLE SNASRTLLLNIKTLE SRTLLLNIK DELLSILNVPRAILP LSILNVPRA ELLSILNVPRAILPE LSILNVPRA ILNTMKKSIPNFEIQ LNTMKKSIP DDELLSILNVPRAIL LSILNVPRA DYSNASRTLLLNIKT YSNASRTLL YSNASRTLLLNIKTL YSNASRTLL LNTMKKSIPNFEIQE LNTMKKSIP LLSILNVPRAILPEL ILNVPRAIL TLLLNIKTLEWDDEL LLLNIKTLE TGCFLTVNIGKEPII LTVNIGKEP LSILNVPRAILPELK ILNVPRAIL GCFLTVNIGKEPIIS LTVNIGKEP LLLNIKTLEWDDELL LLLNIKTLE AFQSFDILNTMKKSI FDILNTMKK CFLTVNIGKEPIISH LTVNIGKEP GTGCFLTVNIGKEPI LTVNIGKEP WDDELLSILNVPRAI LSILNVPRA EIWGSQLGVITEAMA WGSQLGVIT TEIWGSQLGVITEAM WGSQLGVIT HDPTEIWGSQLGVIT TEIWGSQLG DPTEIWGSQLGVITE WGSQLGVIT PTEIWGSQLGVITEA WGSQLGVIT EWDDELLSILNVPRA ELLSILNVP KLLENWNKAVGKAKS LENWNKAVG YGTGCFLTVNIGKEP FLTVNIGKE FLTVNIGKEPIISHD LTVNIGKEP IDAIGITNQRETTVI IGITNQRET DAIGITNQRETTVIW IGITNQRET IAFQSFDILNTMKKS FDILNTMKK IAWGRKKSVTYVLEG WGRKKSVTY SIAWGRKKSVTYVLE WGRKKSVTY EKLLENWNKAVGKAK LENWNKAVG TSIAWGRKKSVTYVL WGRKKSVTY LLTSIAWGRKKSVTY LTSIAWGRK YARGTIIGITRGSTK RGTIIGITR SIAFQSFDILNTMKK FQSFDILNT
	HLA-DRB1*1501	IDTWILWNLTQKKEH WILWNLTQK DTWILWNLTQKKEHA WILWNLTQK TIDTWILWNLTQKKE WILWNLTQK GTIDTWILWNLTQKK WILWNLTQK FGTIDTWILWNLTQK IDTWILWNL DKLLTSIAWGRKKSV LLTSIAWGR HDKLLTSIAWGRKKS LLTSIAWGR ISHDKLLTSIAWGRK LLTSIAWGR SHDKLLTSIAWGRKK LLTSIAWGR TWILWNLTQKKEHAT WILWNLTQK LLTSIAWGRKKSVTY LTSIAWGRK WILWNLTQKKEHATD WILWNLTQK KLLTSIAWGRKKSVT LTSIAWGRK LTSIAWGRKKSVTYV WGRKKSVTY

		WDDELLSILNVPRAI LLSILNVPR DDELLSILNVPRAIL LLSILNVPR EWDDELLSILNVPRA LLSILNVPR DELLSILNVPRAILP LLSILNVPR IISHDKLLTSIAWGR KLLTSIAWG TSIAWGRKKSVTYVL WGRKKSVTY EKLLENWNKAVGKAK LENWNKAVG QKEKLLENWNKAVGK LENWNKAVG NQKEKLLENWNKAVG LLENWNKAV SIAWGRKKSVTYVLE WGRKKSVTY KEKLLENWNKAVGKA LENWNKAVG VYFVPAFVGLGAPHW VYFVPAFVG AFVGLGAPHWDSYAR FVGLGAPHW LEWDDELLSILNVPR DELLSILNV
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EEIVSLWQVDKIFEP VSLWQVDKI AEEIVSLWQVDKIFE VSLWQVDKI EIVSLWQVDKIFEPS VSLWQVDKI SAEEIVSLWQVDKIF VSLWQVDKI FSGTKIMWILDNVEG KIMWILDNV SGTKIMWILDNVEGA KIMWILDNV GTKIMWILDNVEGAR KIMWILDNV YFSGTKIMWILDNVE KIMWILDNV IDTWILWNLTQKKEH WILWNLTQK DTWILWNLTQKKEHA WILWNLTQK IVSLWQVDKIFEPSM VSLWQVDKI TIDTWILWNLTQKKE WILWNLTQK GTIDTWILWNLTQKK WILWNLTQK VSLWQVDKIFEPSMP VSLWQVDKI QSAEEIVSLWQVDKI AEEIVSLWQ TKIMWILDNVEGARQ IMWILDNVE AALESIAFQSFDILN IAFQSFDIL RAALESIAFQSFDIL LESIAFQSF TWILWNLTQKKEHAT WILWNLTQK KIMWILDNVEGARQR KIMWILDNV LESIAFQSFDILNTM IAFQSFDIL ALESIAFQSFDILNT IAFQSFDIL
	HLA-DRB5*0101	EKLLENWNKAVGKAK LENWNKAVG KLLENWNKAVGKAKS WNKAVGKAK LENWNKAVGKAKSWI WNKAVGKAK LLENWNKAVGKAKSW WNKAVGKAK ENWNKAVGKAKSWIQ WNKAVGKAK PIYNAIVWQDRRTAK YNAIVWQDR KPIYNAIVWQDRRTA YNAIVWQDR GKPIYNAIVWQDRRT YNAIVWQDR TGKPIYNAIVWQDRR YNAIVWQDR NTGKPIYNAIVWQDR GKPIYNAIV IYNAIVWQDRRTAKI YNAIVWQDR YNAIVWQDRRTAKIC YNAIVWQDR HDKLLTSIAWGRKKS LTSIAWGRK DKLLTSIAWGRKKSV LTSIAWGRK SHDKLLTSIAWGRKK LTSIAWGRK DKIFEPSMPKNQKEK FEPSMPKNQ IDTWILWNLTQKKEH WILWNLTQK KIFEPSMPKNQKEKL FEPSMPKNQ DTWILWNLTQKKEHA WILWNLTQK

		NWNKAVGKAKSWIQN WNKAVGKAK WNKAVGKAKSWIQNS WNKAVGKAK GTIDTWILWNLTQKK WILWNLTQK ISHDKLLTSIAWGRK LLTSIAWGR KLLTSIAWGRKKSVT LTSIAWGRK TIDTWILWNLTQKKE WILWNLTQK QVDKIFEPSMPKNQK FEPSMPKNQ VDKIFEPSMPKNQKE FEPSMPKNQ KEFTQIYPQPSWVEH IYPQPSWVE
NP_212342.1| hypothetical protein BB0208 [Borrelia burgdorferi B31] Seq28	HLA-DRB1*0101	GTTYKLKSSNFLKLI YKLKSSNFL LGTTYKLKSSNFLKL YKLKSSNFL TTYKLKSSNFLKLIE YKLKSSNFL KLGTTYKLKSSNFLK YKLKSSNFL KKLGTTYKLKSSNFL LGTTYKLKS DIYKQIILNFSSNIN YKQIILNFS KDIYKQIILNFSSNI YKQIILNFS KKDIYKQIILNFSSN YKQIILNFS EKKDIYKQIILNFSS YKQIILNFS QEKKDIYKQIILNFS IYKQIILNF TYKLKSSNFLKLIEI YKLKSSNFL EQTIDILVAVRNRNK IDILVAVRN YKLKSSNFLKLIEIQ YKLKSSNFL QTIDILVAVRNRNKI IDILVAVRN SEFYDSLATLKKHIN YDSLATLKK DSEFYDSLATLKKHI YDSLATLKK DSLEQTIDILVAVRN LEQTIDILV KDSEFYDSLATLKKH YDSLATLKK KKDSEFYDSLATLKK FYDSLATLK SLEQTIDILVAVRNR IDILVAVRN LEQTIDILVAVRNRN IDILVAVRN IYKQIILNFSSNINI YKQIILNFS YKQIILNFSSNINID YKQIILNFS EFYDSLATLKKHINK YDSLATLKK FLKLIEIQNSPYYSQ LKLIEIQNS LKLIEIQNSPYYSQE IQNSPYYSQ KVLKYSISSQLYKLE LKYSISSQL LIEIQNSPYYSQEKK IQNSPYYSQ KLIEIQNSPYYSQEK IQNSPYYSQ EEKVLKYSISSQLYK LKYSISSQL EKVLKYSISSQLYKL LKYSISSQL IEEKVLKYSISSQLY LKYSISSQL IDILVAVRNRNKIKI IDILVAVRN IEIQNSPYYSQEKKD IQNSPYYSQ TIDILVAVRNRNKIK IDILVAVRN ECYYKNTQNEAIKKW YKNTQNEAI YIEEKVLKYSISSQL KVLKYSISS CYYKNTQNEAIKKWI YKNTQNEAI YDSLATLKKHINKYI YDSLATLKK KQIILNFSSNINIDS ILNFSSNIN FYDSLATLKKHINKY YDSLATLKK EECYYKNTQNEAIKK YKNTQNEAI LEECYYKNTQNEAIK YKNTQNEAI SLEECYYKNTQNEAI YYKNTQNEA QIILNFSSNINIDSL ILNFSSNIN
	HLA-DRB1*0301	None

	HLA-DRB1*0401	EECYYKNTQNEAIKK YYKNTQNEA ECYYKNTQNEAIKKW YYKNTQNEA LEECYYKNTQNEAIK YYKNTQNEA SLEECYYKNTQNEAI YYKNTQNEA TSLEECYYKNTQNEA TSLEECYYK DIYKQIILNFSSNIN YKQIILNFS KKDIYKQIILNFSSN YKQIILNFS QEKKDIYKQIILNFS IYKQIILNF EKKDIYKQIILNFSS YKQIILNFS KDIYKQIILNFSSNI YKQIILNFS SNFLKLIEIQNSPYY LIEIQNSPY NFLKLIEIQNSPYYS IEIQNSPYY FLKLIEIQNSPYYSQ IEIQNSPYY LKLIEIQNSPYYSQE IEIQNSPYY IYKQIILNFSSNINI YKQIILNFS CYYKNTQNEAIKKWI YYKNTQNEA KLIEIQNSPYYSQEK IEIQNSPYY YYKNTQNEAIKKWIL YYKNTQNEA YKQIILNFSSNINID YKQIILNFS KKLGTTYKLKSSNFL LGTTYKLKS LGTTYKLKSSNFLKL YKLKSSNFL KLGTTYKLKSSNFLK YKLKSSNFL TTYKLKSSNFLKLIE YKLKSSNFL GTTYKLKSSNFLKLI YKLKSSNFL
	HLA-DRB1*0404	DIYKQIILNFSSNIN IILNFSSNI IYKQIILNFSSNINI ILNFSSNIN YKQIILNFSSNINID ILNFSSNIN KQIILNFSSNINIDS ILNFSSNIN QIILNFSSNINIDSL ILNFSSNIN EQTIDILVAVRNRNK ILVAVRNRN QTIDILVAVRNRNKI ILVAVRNRN TIDILVAVRNRNKIK ILVAVRNRN LEQTIDILVAVRNRN TIDILVAVR IDILVAVRNRNKIKI ILVAVRNRN KDIYKQIILNFSSNI YKQIILNFS IILNFSSNINIDSLE ILNFSSNIN
	HLA-DRB1*0405	KQIILNFSSNINIDS ILNFSSNIN DIYKQIILNFSSNIN YKQIILNFS QIILNFSSNINIDSL ILNFSSNIN YKQIILNFSSNINID ILNFSSNIN IYKQIILNFSSNINI ILNFSSNIN ILNFSSNINIDSLEQ ILNFSSNIN IILNFSSNINIDSLE ILNFSSNIN
	HLA-DRB1*0701	GTTYKLKSSNFLKLI YKLKSSNFL LGTTYKLKSSNFLKL YKLKSSNFL KKLGTTYKLKSSNFL TYKLKSSNF KLGTTYKLKSSNFLK YKLKSSNFL TTYKLKSSNFLKLIE YKLKSSNFL
	HLA-DRB1*0802	None
	HLA-DRB1*0901	GTTYKLKSSNFLKLI YKLKSSNFL TTYKLKSSNFLKLIE YKLKSSNFL LGTTYKLKSSNFLKL YKLKSSNFL EKVLKYSISSQLYKL LKYSISSQL EEKVLKYSISSQLYK LKYSISSQL KVLKYSISSQLYKLE LKYSISSQL KLGTTYKLKSSNFLK YKLKSSNFL

		KKLGTTYKLKSSNFL LGTTYKLKS IEEKVLKYSISSQLY LKYSISSQL YIEEKVLKYSISSQL VLKYSISSQ VLKYSISSQLYKLEK YSISSQLYK IYKQIILNFSSNINI ILNFSSNIN YKQIILNFSSNINID LNFSSNINI TYKLKSSNFLKLIEI YKLKSSNFL KQIILNFSSNINIDS LNFSSNINI QIILNFSSNINIDSL LNFSSNINI YKLKSSNFLKLIEIQ YKLKSSNFL LKYSISSQLYKLEKP YSISSQLYK
	HLA-DRB1*1101	None
	HLA-DRB1*1302	RNKIKILNILNKNLK IKILNILNK VRNRNKIKILNILNK VRNRNKIKI ILVAVRNRNKIKILN VRNRNKIKI NRNKIKILNILNKNL IKILNILNK DILVAVRNRNKIKIL VRNRNKIKI DIYKQIILNFSSNIN YKQIILNFS IDILVAVRNRNKIKI VAVRNRNKI RNRNKIKILNILNKN IKILNILNK IYKQIILNFSSNINI ILNFSSNIN VAVRNRNKIKILNIL VRNRNKIKI YKQIILNFSSNINID ILNFSSNIN LVAVRNRNKIKILNI VRNRNKIKI KQIILNFSSNINIDS ILNFSSNIN QIILNFSSNINIDSL ILNFSSNIN AVRNRNKIKILNILN VRNRNKIKI KDIYKQIILNFSSNI YKQIILNFS QTIDILVAVRNRNKI ILVAVRNRN TIDILVAVRNRNKIK VAVRNRNKI IILNFSSNINIDSLE ILNFSSNIN LGTTYKLKSSNFLKL YKLKSSNFL KKDIYKQIILNFSSN YKQIILNFS QEKKDIYKQIILNFS IYKQIILNF EKKDIYKQIILNFSS YKQIILNFS KEANLNTKKLGTTYK ANLNTKKLG ISKEANLNTKKLGTT ANLNTKKLG KKLGTTYKLKSSNFL LGTTYKLKS GTTYKLKSSNFLKLI YKLKSSNFL SKEANLNTKKLGTTY ANLNTKKLG TTYKLKSSNFLKLIE YKLKSSNFL ILNFSSNINIDSLEQ ILNFSSNIN EANLNTKKLGTTYKL LNTKKLGTT KLGTTYKLKSSNFLK YKLKSSNFL ANLNTKKLGTTYKLK LNTKKLGTT KWILEIVRNKNFIQI IVRNKNFIQ ILEIVRNKNFIQISK VRNKNFIQI TYKLKSSNFLKLIEI YKLKSSNFL WILEIVRNKNFIQIS IVRNKNFIQ YKLKSSNFLKLIEIQ YKLKSSNFL LEIVRNKNFIQISKE VRNKNFIQI FLKLIEIQNSPYYSQ IEIQNSPYY LEQTIDILVAVRNRN IDILVAVRN IQISKEANLNTKKLG EANLNTKKL LKLIEIQNSPYYSQE IEIQNSPYY DSLATLKKHINKYIE LATLKKHIN YDSLATLKKHINKYI LATLKKHIN

		NLNTKKLGTTYKLKS LNTKKLGTT EQTIDILVAVRNRNK ILVAVRNRN LNTKKLGTTYKLKSS LNTKKLGTT
	HLA-DRB1*1501	RNKIKILNILNKNLK IKILNILNK NRNKIKILNILNKNL IKILNILNK VRNRNKIKILNILNK VRNRNKIKI RNRNKIKILNILNKN IKILNILNK IDILVAVRNRNKIKI LVAVRNRNK DILVAVRNRNKIKIL LVAVRNRNK NEAIKKWILEIVRNK IKKWILEIV EAIKKWILEIVRNKN IKKWILEIV KWILEIVRNKNFIQI IVRNKNFIQ WILEIVRNKNFIQIS VRNKNFIQI QNEAIKKWILEIVRN IKKWILEIV TIDILVAVRNRNKIK LVAVRNRNK LVAVRNRNKIKILNI LVAVRNRNK ILVAVRNRNKIKILN LVAVRNRNK QTIDILVAVRNRNKI LVAVRNRNK TQNEAIKKWILEIVR IKKWILEIV NTQNEAIKKWILEIV EAIKKWILE ILEIVRNKNFIQISK VRNKNFIQI
	HLA-DRB3*0101	None
	HLA-DRB4*0101	SISSQLYKLEKPEII LYKLEKPEI SQLYKLEKPEIIELI YKLEKPEII SSQLYKLEKPEIIEL YKLEKPEII ISSQLYKLEKPEIIE YKLEKPEII
	HLA-DRB5*0101	EQTIDILVAVRNRNK ILVAVRNRN QTIDILVAVRNRNKI LVAVRNRNK IDILVAVRNRNKIKI LVAVRNRNK TIDILVAVRNRNKIK LVAVRNRNK IKISNDYEKEKNAFN ISNDYEKEK
NP_045482.1| hypothetical protein BBG22 [Borrelia burgdorferi B31] Seq29	HLA-DRB1*0101	
		GTLTAKFAMEGSILT LTAKFAMEG LTAKFAMEGSILTRS FAMEGSILT TAKFAMEGSILTRSK FAMEGSILT AKFAMEGSILTRSKL FAMEGSILT TLTAKFAMEGSILTR FAMEGSILT KRMTMIYRSADTWYT KRMTMIYRS RMTMIYRSADTWYTW YRSADTWYT

		PVGTLTAKFAMEGSI LTAKFAMEG FLEKTPVGTLTAKFA FLEKTPVGT LEKTPVGTLTAKFAM VGTLTAKFA EKTPVGTLTAKFAME VGTLTAKFA YAYKVLGISSAPKLS YKVLGISSA
	HLA-DRB1*0301	None
	HLA-DRB1*0401	TAKFAMEGSILTRSK FAMEGSILT AKFAMEGSILTRSKL FAMEGSILT LTAKFAMEGSILTRS FAMEGSILT TLTAKFAMEGSILTR FAMEGSILT GTLTAKFAMEGSILT GTLTAKFAM EHMILFFLEKTPVGT FFLEKTPVG LEHMILFFLEKTPVG LFFLEKTPV HMILFFLEKTPVGTL FFLEKTPVG MILFFLEKTPVGTLT FFLEKTPVG ILFFLEKTPVGTLTA FFLEKTPVG KFAMEGSILTRSKLI FAMEGSILT FAMEGSILTRSKLIQ FAMEGSILT RKEYEITKNAPSLDS YEITKNAPS KEYEITKNAPSLDSL YEITKNAPS TRSKLIQAFTNTNKF LIQAFTNTN RSKLIQAFTNTNKFC LIQAFTNTN FKGKLVKRMTMIYRS LVKRMTMIY NFKGKLVKRMTMIYR LVKRMTMIY KGKLVKRMTMIYRSA LVKRMTMIY SKLIQAFTNTNKFCI LIQAFTNTN GKLVKRMTMIYRSAD LVKRMTMIY IDNRKEYEITKNAPS EYEITKNAP DNRKEYEITKNAPSL YEITKNAPS NRKEYEITKNAPSLD YEITKNAPS LFFLEKTPVGTLTAK FFLEKTPVG INFKGKLVKRMTMIY FKGKLVKRM
	HLA-DRB1*0404	LTRSKLIQAFTNTNK LIQAFTNTN TRSKLIQAFTNTNKF LIQAFTNTN RSKLIQAFTNTNKFC LIQAFTNTN ILTRSKLIQAFTNTN KLIQAFTNT SKLIQAFTNTNKFCI LIQAFTNTN KLIQAFTNTNKFCIP LIQAFTNTN IDPEYLLPPFTSQSG LLPPFTSQS PEYLLPPFTSQSGSK LLPPFTSQS DPEYLLPPFTSQSGS LLPPFTSQS LIQAFTNTNKFCIPD LIQAFTNTN EYLLPPFTSQSGSKE LLPPFTSQS EIDPEYLLPPFTSQS YLLPPFTSQ LEHMILFFLEKTPVG ILFFLEKTP EHMILFFLEKTPVGT FFLEKTPVG HMILFFLEKTPVGTL FFLEKTPVG YLLPPFTSQSGSKET LLPPFTSQS
	HLA-DRB1*0405	YRSADTWYTWYWAEE YRSADTWYT KRMTMIYRSADTWYT MTMIYRSAD ADTWYTWYWAEEIMS WYTWYWAEE RKEYEITKNAPSLDS YEITKNAPS KEYEITKNAPSLDSL YEITKNAPS RSADTWYTWYWAEEI WYTWYWAEE RMTMIYRSADTWYTW YRSADTWYT MTMIYRSADTWYTWY YRSADTWYT

		TMIYRSADTWYTWYW YRSADTWYT DTWYTWYWAEEIMSP WYWAEEIMS MIYRSADTWYTWYWA YRSADTWYT TRSKLIQAFTNTNKF IQAFTNTNK LTRSKLIQAFTNTNK LIQAFTNTN RSKLIQAFTNTNKFC IQAFTNTNK SKLIQAFTNTNKFCI IQAFTNTNK SADTWYTWYWAEEIM YTWYWAEEI TWYTWYWAEEIMSPF YTWYWAEEI EYEITKNAPSLDSLI TKNAPSLDS YEITKNAPSLDSLIE TKNAPSLDS KLIQAFTNTNKFCIP IQAFTNTNK WYTWYWAEEIMSPFI WYWAEEIMS IYRSADTWYTWYWAE YRSADTWYT NRKEYEITKNAPSLD YEITKNAPS IDNRKEYEITKNAPS EYEITKNAP DNRKEYEITKNAPSL YEITKNAPS LIQAFTNTNKFCIPD IQAFTNTNK GKLVKRMTMIYRSAD VKRMTMIYR KLVKRMTMIYRSADT VKRMTMIYR YTWYWAEEIMSPFIT WYWAEEIMS
	HLA-DRB1*0701	SKLIQAFTNTNKFCI IQAFTNTNK KLIQAFTNTNKFCIP FTNTNKFCI LIQAFTNTNKFCIPD FTNTNKFCI IQAFTNTNKFCIPDG FTNTNKFCI QAFTNTNKFCIPDGR FTNTNKFCI IKKKLENTKTRIQFR LENTKTRIQ KKKLENTKTRIQFRN LENTKTRIQ KKLENTKTRIQFRNG LENTKTRIQ EIKKKLENTKTRIQF LENTKTRIQ TEIKKKLENTKTRIQ KLENTKTRI KFAMEGSILTRSKLI GSILTRSKL MEGSILTRSKLIQAF SILTRSKLI AMEGSILTRSKLIQA SILTRSKLI FAMEGSILTRSKLIQ SILTRSKLI EGSILTRSKLIQAFT SILTRSKLI RMTMIYRSADTWYTW YRSADTWYT
	HLA-DRB1*0802	None
	HLA-DRB1*0901	YAYKVLGISSAPKLS LGISSAPKL AYKVLGISSAPKLSG LGISSAPKL YKVLGISSAPKLSGR LGISSAPKL CYAYKVLGISSAPKL VLGISSAPK KVLGISSAPKLSGRF LGISSAPKL VLGISSAPKLSGRFL LGISSAPKL LGISSAPKLSGRFLR LGISSAPKL
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NFKGKLVKRMTMIYR LVKRMTMIY FKGKLVKRMTMIYRS VKRMTMIYR KGKLVKRMTMIYRSA VKRMTMIYR GKLVKRMTMIYRSAD VKRMTMIYR KLVKRMTMIYRSADT VKRMTMIYR INFKGKLVKRMTMIY GKLVKRMTM CYAYKVLGISSAPKL YKVLGISSA YAYKVLGISSAPKLS LGISSAPKL LVKRMTMIYRSADTW VKRMTMIYR TRIQFRNGNKIDSLG IQFRNGNKI

		SRINFKGKLVKRMTM INFKGKLVK AYKVLGISSAPKLSG LGISSAPKL YKVLGISSAPKLSGR LGISSAPKL IQFRNGNKIDSLGYQ FRNGNKIDS RINFKGKLVKRMTMI GKLVKRMTM VKRMTMIYRSADTWY VKRMTMIYR KTRIQFRNGNKIDSL IQFRNGNKI RIQFRNGNKIDSLGY IQFRNGNKI TKTRIQFRNGNKIDS IQFRNGNKI FSRINFKGKLVKRMT INFKGKLVK SKLIQAFTNTNKFCI IQAFTNTNK KEYEITKNAPSLDSL ITKNAPSLD RKEYEITKNAPSLDS ITKNAPSLD KLIQAFTNTNKFCIP FTNTNKFCI FAMEGSILTRSKLIQ FAMEGSILT EYEITKNAPSLDSLI ITKNAPSLD YEITKNAPSLDSLIE ITKNAPSLD NCYAYKVLGISSAPK YKVLGISSA
	HLA-DRB1*1501	FKGKLVKRMTMIYRS VKRMTMIYR KLVKRMTMIYRSADT VKRMTMIYR GKLVKRMTMIYRSAD VKRMTMIYR NFKGKLVKRMTMIYR FKGKLVKRM KGKLVKRMTMIYRSA VKRMTMIYR VKRMTMIYRSADTWY VKRMTMIYR LVKRMTMIYRSADTW VKRMTMIYR NCYAYKVLGISSAPK YKVLGISSA YAYKVLGISSAPKLS VLGISSAPK CYAYKVLGISSAPKL VLGISSAPK AYKVLGISSAPKLSG VLGISSAPK LEHMILFFLEKTPVG LFFLEKTPV YKVLGISSAPKLSGR VLGISSAPK EHMILFFLEKTPVGT LFFLEKTPV HMILFFLEKTPVGTL LFFLEKTPV MILFFLEKTPVGTLT LFFLEKTPV DFSRINFKGKLVKRM INFKGKLVK FSRINFKGKLVKRMT INFKGKLVK LDFSRINFKGKLVKR INFKGKLVK YLEHMILFFLEKTPV ILFFLEKTP SRINFKGKLVKRMTM INFKGKLVK LSGRFLRHYDSGGST LRHYDSGGS KLSGRFLRHYDSGGS FLRHYDSGG SGRFLRHYDSGGSTD LRHYDSGGS GRFLRHYDSGGSTDS LRHYDSGGS DLDFSRINFKGKLVK RINFKGKLV ILFFLEKTPVGTLTA LFFLEKTPV RINFKGKLVKRMTMI INFKGKLVK RFLRHYDSGGSTDSD LRHYDSGGS LTRSKLIQAFTNTNK LIQAFTNTN
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	FSRINFKGKLVKRMT FKGKLVKRM DFSRINFKGKLVKRM INFKGKLVK SRINFKGKLVKRMTM FKGKLVKRM RINFKGKLVKRMTMI FKGKLVKRM INFKGKLVKRMTMIY FKGKLVKRM FKGKLVKRMTMIYRS FKGKLVKRM

		NFKGKLVKRMTMIYR FKGKLVKRM KRMTMIYRSADTWYT MTMIYRSAD AKFAMEGSILTRSKL FAMEGSILT TAKFAMEGSILTRSK FAMEGSILT RMTMIYRSADTWYTW YRSADTWYT MTMIYRSADTWYTWY YRSADTWYT TMIYRSADTWYTWYW YRSADTWYT MIYRSADTWYTWYWA YRSADTWYT LTAKFAMEGSILTRS FAMEGSILT TLTAKFAMEGSILTR FAMEGSILT
NP_212885.1| hypothetical protein BB0751 [Borrelia burgdorferi B31] Seq30	HLA-DRB1*0101	KILIIVVLTSTFLLG IVVLTSTFL IKILIIVVLTSTFLL IVVLTSTFL ILIIVVLTSTFLLGI IVVLTSTFL LIIVVLTSTFLLGII IVVLTSTFL KIKILIIVVLTSTFL IKILIIVVL IIVVLTSTFLLGIIF IVVLTSTFL IVVLTSTFLLGIIFS IVVLTSTFL KEKIKILIIVVLTST IKILIIVVL EKIKILIIVVLTSTF IKILIIVVL NKEKIKILIIVVLTS IKILIIVVL INKEKIKILIIVVLT IKILIIVVL SINKEKIKILIIVVL INKEKIKIL KIETELEGTLTKLGK LEGTLTKLG SKIETELEGTLTKLG ETELEGTLT IETELEGTLTKLGKD LEGTLTKLG ETELEGTLTKLGKDW LEGTLTKLG TELEGTLTKLGKDWI LEGTLTKLG NKNKGVFMTKPKIFS VFMTKPKIF NKGVFMTKPKIFSIN FMTKPKIFS KGVFMTKPKIFSINK FMTKPKIFS KNKGVFMTKPKIFSI FMTKPKIFS KDEYYYTTSKWTFFD YYYTTSKWT DKDEYYYTTSKWTFF YYYTTSKWT DEYYYTTSKWTFFDV YYYTTSKWT GVFMTKPKIFSINKE FMTKPKIFS LEGTLTKLGKDWILT LEGTLTKLG ELEGTLTKLGKDWIL LEGTLTKLG KQINKNKGVFMTKPK INKNKGVFM EKQINKNKGVFMTKP INKNKGVFM KEKQINKNKGVFMTK INKNKGVFM LNNQKMTKERPLNII MTKERPLNI EKEKQINKNKGVFMT INKNKGVFM
	HLA-DRB1*0301	None
	HLA-DRB1*0401	YNLQYKIEVKWSNKS YKIEVKWSN LQYKIEVKWSNKSVN IEVKWSNKS QYKIEVKWSNKSVNN IEVKWSNKS NLQYKIEVKWSNKSV IEVKWSNKS YKIEVKWSNKSVNNI IEVKWSNKS KIEVKWSNKSVNNIE IEVKWSNKS IEVKWSNKSVNNIEV IEVKWSNKS DKDEYYYTTSKWTFF YYYTTSKWT FLLGIIFSNENKVAR LGIIFSNEN KDEYYYTTSKWTFFD YYYTTSKWT DEYYYTTSKWTFFDV YYYTTSKWT

		KDKDEYYYTTSKWTF YYYTTSKWT
	HLA-DRB1*0404	KILIIVVLTSTFLLG IIVVLTSTF
		ILIIVVLTSTFLLGI VLTSTFLLG
		TFLLGIIFSNENKVA LLGIIFSNE
		STFLLGIIFSNENKV LLGIIFSNE
		FLLGIIFSNENKVAR LLGIIFSNE
		TSTFLLGIIFSNENK LLGIIFSNE
		LTSTFLLGIIFSNEN LLGIIFSNE
		KIKILIIVVLTSTFL ILIIVVLTS
		IKILIIVVLTSTFLL ILIIVVLTS
		LIIVVLTSTFLLGII VLTSTFLLG
		VLTSTFLLGIIFSNE VLTSTFLLG
		LLGIIFSNENKVARI LLGIIFSNE
	HLA-DRB1*0405	KDWILTYNKQNIPVD WILTYNKQN
		DWILTYNKQNIPVDN YNKQNIPVD
		WILTYNKQNIPVDNK YNKQNIPVD
		LQYKIEVKWSNKSVN IEVKWSNKS
		QYKIEVKWSNKSVNN IEVKWSNKS
		YKIEVKWSNKSVNNI IEVKWSNKS
		IEVKWSNKSVNNIEV IEVKWSNKS
		ILTYNKQNIPVDNKK YNKQNIPVD
		KIEVKWSNKSVNNIE IEVKWSNKS
		LTYNKQNIPVDNKKV YNKQNIPVD
		NLQYKIEVKWSNKSV IEVKWSNKS
		YNLQYKIEVKWSNKS YKIEVKWSN
		TKLGKDWILTYNKQN KDWILTYNK
		KFFDFDFNLISKIET FDFDFNLIS
		KLGKDWILTYNKQNI WILTYNKQN
		LGKDWILTYNKQNIP WILTYNKQN
		IGENPSFKLFDNNNK ENPSFKLFD
		GKDWILTYNKQNIPV WILTYNKQN
	HLA-DRB1*0701	LIIVVLTSTFLLGII IVVLTSTFL
		ILIIVVLTSTFLLGI IVVLTSTFL
		IKILIIVVLTSTFLL IVVLTSTFL
		KILIIVVLTSTFLLG IVVLTSTFL
		DEYYYTTSKWTFFDV YYTTSKWTF
		DKDEYYYTTSKWTFF YYTTSKWTF
		KDEYYYTTSKWTFFD YYTTSKWTF
		KIKILIIVVLTSTFL IIVVLTSTF
		EYYYTTSKWTFFDVF YYTTSKWTF
		IIVVLTSTFLLGIIF IVVLTSTFL
		KDKDEYYYTTSKWTF YYYTTSKWT
		IVVLTSTFLLGIIFS IVVLTSTFL
		YYYTTSKWTFFDVFD YTTSKWTFF
		YYTTSKWTFFDVFDL YYTTSKWTF
		KNKGVFMTKPKIFSI VFMTKPKIF
		NKGVFMTKPKIFSIN VFMTKPKIF
		KGVFMTKPKIFSINK VFMTKPKIF
		INKNKGVFMTKPKIF INKNKGVFM
		KKDKDEYYYTTSKWT EYYYTTSKW
		NKNKGVFMTKPKIFS VFMTKPKIF
	HLA-DRB1*0802	None
	HLA-DRB1*0901	DKDEYYYTTSKWTFF YYYTTSKWT
		KDEYYYTTSKWTFFD YYYTTSKWT
		DEYYYTTSKWTFFDV YYYTTSKWT
		KDKDEYYYTTSKWTF YYYTTSKWT

	HLA-DRB1*1101	DENVYLTKNIFLSYK LTKNIFLSY SDENVYLTKNIFLSY NVYLTKNIF ENVYLTKNIFLSYKG LTKNIFLSY NVYLTKNIFLSYKGN LTKNIFLSY
	HLA-DRB1*1302	EKIKILIIVVLTSTF IKILIIVVL KEKIKILIIVVLTST IKILIIVVL SINKEKIKILIIVVL EKIKILIIV INKEKIKILIIVVLT IKILIIVVL NKEKIKILIIVVLTS IKILIIVVL IKILIIVVLTSTFLL IKILIIVVL KIKILIIVVLTSTFL IKILIIVVL DGLYFLNNQKMTKER LNNQKMTKE KILIIVVLTSTFLLG LIIVVLTST SFKLFDNNNKLLTEI FDNNNKLLT FKLFDNNNKLLTEIF FDNNNKLLT KDGLYFLNNQKMTKE YFLNNQKMT PSFKLFDNNNKLLTE FDNNNKLLT NPSFKLFDNNNKLLT LFDNNNKLL KLFDNNNKLLTEIFV FDNNNKLLT GLYFLNNQKMTKERP LNNQKMTKE EKEKQINKNKGVFMT INKNKGVFM KEKQINKNKGVFMTK INKNKGVFM KQINKNKGVFMTKPK INKNKGVFM EKQINKNKGVFMTKP INKNKGVFM LYFLNNQKMTKERPL LNNQKMTKE ILIIVVLTSTFLLGI IIVVLTSTF LIIVVLTSTFLLGII VVLTSTFLL YFLNNQKMTKERPLN LNNQKMTKE YKIEVKWSNKSVNNI VKWSNKSVN QINKNKGVFMTKPKI INKNKGVFM LEKEKQINKNKGVFM QINKNKGVF IEVKWSNKSVNNIEV WSNKSVNNI LFDNNNKLLTEIFVG FDNNNKLLT KIEVKWSNKSVNNIE WSNKSVNNI FDFDFNLISKIETEL FNLISKIET KFFDFDFNLISKIET FDFNLISKI FFDFDFNLISKIETE FNLISKIET FDNNNKLLTEIFVGK FDNNNKLLT KENENNINNNYEIIS NENNINNNY DFDFNLISKIETELE FNLISKIET FDFNLISKIETELEG FNLISKIET SKDGLYFLNNQKMTK YFLNNQKMT VKWSNKSVNNIEVYF WSNKSVNNI IIVVLTSTFLLGIIF VVLTSTFLL EVKWSNKSVNNIEVY WSNKSVNNI INKNKGVFMTKPKIF INKNKGVFM ENENNINNNYEIISK INNNYEIIS NENNINNNYEIISKD INNNYEIIS NNINNNYEIISKDGL INNNYEIIS ENNINNNYEIISKDG INNNYEIIS LENLSFKIIRKLNKE FKIIRKLNK KLENLSFKIIRKLNK LENLSFKII SDENVYLTKNIFLSY YLTKNIFLS FLNNQKMTKERPLNI LNNQKMTKE DENVYLTKNIFLSYK YLTKNIFLS EKNTKLENLSFKIIR LENLSFKII QEKNTKLENLSFKII KNTKLENLS

		ENVYLTKNIFLSYKG YLTKNIFLS KNTKLENLSFKIIRK LENLSFKII NTKLENLSFKIIRKL LENLSFKII KWSNKSVNNIEVYFN WSNKSVNNI TKLENLSFKIIRKLN LENLSFKII PVDNKKVNSLIKALD KKVNSLIKA NVYLTKNIFLSYKGN YLTKNIFLS WSNKSVNNIEVYFNK WSNKSVNNI VDNKKVNSLIKALDE VNSLIKALD INNNYEIISKDGLYF INNNYEIIS DWILTYNKQNIPVDN LTYNKQNIP ISKDGLYFLNNQKMT LYFLNNQKM KDWILTYNKQNIPVD LTYNKQNIP IVVLTSTFLLGIIFS VVLTSTFLL NINNNYEIISKDGLY INNNYEIIS FNLISKIETELEGTL FNLISKIET DFNLISKIETELEGT FNLISKIET LQYKIEVKWSNKSVN IEVKWSNKS GSDENVYLTKNIFLS VYLTKNIFL WILTYNKQNIPVDNK LTYNKQNIP GKDWILTYNKQNIPV LTYNKQNIP VYLTKNIFLSYKGNS YLTKNIFLS DNKKVNSLIKALDEL VNSLIKALD KALDELQKNKLVSRD LQKNKLVSR QYKIEVKWSNKSVNN VKWSNKSVN LGKDWILTYNKQNIP ILTYNKQNI FLLGIIFSNENKVAR LGIIFSNEN IKALDELQKNKLVSR LDELQKNKL LGIIFSNENKVARIL FSNENKVAR LLGIIFSNENKVARI FSNENKVAR YLTKNIFLSYKGNSY YLTKNIFLS LDELQKNKLVSRDQK LQKNKLVSR IPVDNKKVNSLIKAL VDNKKVNSL VVLTSTFLLGIIFSN VVLTSTFLL NIPVDNKKVNSLIKA VDNKKVNSL ALDELQKNKLVSRDQ LQKNKLVSR NKKVNSLIKALDELQ VNSLIKALD LNNQKMTKERPLNII LNNQKMTKE
	HLA-DRB1*1501	KILIIVVLTSTFLLG IVVLTSTFL KIKILIIVVLTSTFL ILIIVVLTS IKILIIVVLTSTFLL IVVLTSTFL ILIIVVLTSTFLLGI IVVLTSTFL KLENLSFKIIRKLNK NLSFKIIRK LENLSFKIIRKLNKE FKIIRKLNK YLTKNIFLSYKGNSY TKNIFLSYK LIIVVLTSTFLLGII IVVLTSTFL ENLSFKIIRKLNKEN FKIIRKLNK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	YKIEVKWSNKSVNNI IEVKWSNKS
	HLA-DRB5*0101	FLLGIIFSNENKVAR LGIIFSNEN LLGIIFSNENKVARI FSNENKVAR LGIIFSNENKVARIL FSNENKVAR GIIFSNENKVARILE FSNENKVAR IIFSNENKVARILEE FSNENKVAR LQYKIEVKWSNKSVN YKIEVKWSN YNLQYKIEVKWSNKS YKIEVKWSN

		NLQYKIEVKWSNKSV YKIEVKWSN DKDEYYYTTSKWTFF YYYTTSKWT KDEYYYTTSKWTFFD YYYTTSKWT DEYYYTTSKWTFFDV YYYTTSKWT KDGLYFLNNQKMTKE LYFLNNQKM DGLYFLNNQKMTKER LYFLNNQKM KDKDEYYYTTSKWTF YYYTTSKWT DYNLQYKIEVKWSNK YKIEVKWSN SKDGLYFLNNQKMTK LYFLNNQKM DDYNLQYKIEVKWSN YNLQYKIEV FSNENKVARILEEKF FSNENKVAR IFSNENKVARILEEK FSNENKVAR EYYYTTSKWTFFDVF YYYTTSKWT YKIEVKWSNKSVNNI YKIEVKWSN QYKIEVKWSNKSVNN YKIEVKWSN GLYFLNNQKMTKERP LYFLNNQKM ENLSFKIIRKLNKEN FKIIRKLNK NLSFKIIRKLNKENE FKIIRKLNK LSFKIIRKLNKENEN FKIIRKLNK LYFLNNQKMTKERPL LYFLNNQKM KKDKDEYYYTTSKWT DEYYYTTSK KLENLSFKIIRKLNK LSFKIIRKL LENLSFKIIRKLNKE FKIIRKLNK
AAC67038.1| predicted coding region BB0689 [Borrelia burgdorferi B31] Seq31	HLA-DRB1*0101	THTLFGTTPMQRIHK FGTTPMQRI HTLFGTTPMQRIHKY FGTTPMQRI TITHTLFGTTPMQRI LFGTTPMQR ITHTLFGTTPMQRIH FGTTPMQRI TLFGTTPMQRIHKYD FGTTPMQRI KEDMKILYSEIAELR MKILYSEIA EDMKILYSEIAELRK MKILYSEIA IDTKEDMKILYSEIA IDTKEDMKI TKEDMKILYSEIAEL MKILYSEIA DTKEDMKILYSEIAE MKILYSEIA IIFTLFLSQACNLST FLSQACNLS IFTLFLSQACNLSTM LSQACNLST IIIFTLFLSQACNLS IFTLFLSQA KKLIIIFTLFLSQAC IFTLFLSQA LFGTTPMQRIHKYDQ FGTTPMQRI TLFLSQACNLSTMHK LSQACNLST MKKLIIIFTLFLSQA LIIIFTLFL FTLFLSQACNLSTMH LSQACNLST DMKILYSEIAELRKK MKILYSEIA MKILYSEIAELRKKL MKILYSEIA LIIIFTLFLSQACNL IFTLFLSQA KLIIIFTLFLSQACN IFTLFLSQA NRVVNAWLNSPSHKE VVNAWLNSP FGTTPMQRIHKYDQS FGTTPMQRI RTITHTLFGTTPMQR THTLFGTTP LFLSQACNLSTMHKI LSQACNLST RVVNAWLNSPSHKEA WLNSPSHKE VVNAWLNSPSHKEAL WLNSPSHKE VNAWLNSPSHKEALI WLNSPSHKE TDKIGGYRLKTTDNI IGGYRLKTT DKIGGYRLKTTDNID IGGYRLKTT VAKEYAIKLGENRTI VAKEYAIKL NAWLNSPSHKEALIN WLNSPSHKE

		FLSQACNLSTMHKID LSQACNLST TDTDKIGGYRLKTTD IGGYRLKTT DTDKIGGYRLKTTDN IGGYRLKTT NTDTDKIGGYRLKTT TDKIGGYRL IELNRVVNAWLNSPS VVNAWLNSP LSQACNLSTMHKIDT LSQACNLST KIGGYRLKTTDNIDI IGGYRLKTT FNLTREILASGIELN LTREILASG IGGYRLKTTDNIDIF IGGYRLKTT LNRVVNAWLNSPSHK VVNAWLNSP ELNRVVNAWLNSPSH VVNAWLNSP EYAIKLGENRTITHT IKLGENRTI DQSFNLTREILASGI LTREILASG KEYAIKLGENRTITH IKLGENRTI QSFNLTREILASGIE LTREILASG EKVAKEYAIKLGENR VAKEYAIKL YAIKLGENRTITHTL IKLGENRTI GIELNRVVNAWLNSP IELNRVVNA LTREILASGIELNRV ILASGIELN SFNLTREILASGIEL LTREILASG DTLEKVAKEYAIKLG VAKEYAIKL LEKVAKEYAIKLGEN VAKEYAIKL
	HLA-DRB1*0301	None
	HLA-DRB1*0401	KEDMKILYSEIAELR MKILYSEIA EDMKILYSEIAELRK MKILYSEIA IDTKEDMKILYSEIA TKEDMKILY DTKEDMKILYSEIAE MKILYSEIA TKEDMKILYSEIAEL MKILYSEIA DMKILYSEIAELRKK MKILYSEIA MKILYSEIAELRKKL MKILYSEIA IIIFTLFLSQACNLS IIFTLFLSQ IIFTLFLSQACNLST FLSQACNLS IFTLFLSQACNLSTM FLSQACNLS FTLFLSQACNLSTMH FLSQACNLS TLFLSQACNLSTMHK FLSQACNLS
	HLA-DRB1*0404	NRVVNAWLNSPSHKE VVNAWLNSP ELNRVVNAWLNSPSH VVNAWLNSP LNRVVNAWLNSPSHK VVNAWLNSP GIELNRVVNAWLNSP ELNRVVNAW IELNRVVNAWLNSPS VVNAWLNSP RVVNAWLNSPSHKEA VVNAWLNSP VVNAWLNSPSHKEAL VVNAWLNSP IIIFTLFLSQACNLS IFTLFLSQA IIFTLFLSQACNLST FLSQACNLS RTITHTLFGTTPMQR ITHTLFGTT TLFLSQACNLSTMHK FLSQACNLS MKKLIIIFTLFLSQA LIIIFTLFL KKLIIIFTLFLSQAC LIIIFTLFL IFTLFLSQACNLSTM FLSQACNLS HKEALINTDTDKIGG LINTDTDKI FTLFLSQACNLSTMH FLSQACNLS SHKEALINTDTDKIG LINTDTDKI NRTITHTLFGTTPMQ ITHTLFGTT TITHTLFGTTPMQRI ITHTLFGTT PSHKEALINTDTDKI EALINTDTD

		KEALINTDTDKIGGY LINTDTDKI EALINTDTDKIGGYR LINTDTDKI GENRTITHTLFGTTP ITHTLFGTT
	HLA-DRB1*0405	IELNRVVNAWLNSPS NRVVNAWLN ELNRVVNAWLNSPSH VNAWLNSPS NRVVNAWLNSPSHKE VNAWLNSPS LNRVVNAWLNSPSHK VNAWLNSPS RVVNAWLNSPSHKEA VNAWLNSPS VVNAWLNSPSHKEAL VNAWLNSPS VNAWLNSPSHKEALI VNAWLNSPS IIIFTLFLSQACNLS FTLFLSQAC KKLIIIFTLFLSQAC IIIFTLFLS IIFTLFLSQACNLST FLSQACNLS GIELNRVVNAWLNSP NRVVNAWLN KLIIIFTLFLSQACN IIIFTLFLS HKYDQSFNLTREILA YDQSFNLTR FTLFLSQACNLSTMH FLSQACNLS IFTLFLSQACNLSTM FLSQACNLS
	HLA-DRB1*0701	None
	HLA-DRB1*0802	None
	HLA-DRB1*0901	VNAWLNSPSHKEALI WLNSPSHKE VVNAWLNSPSHKEAL WLNSPSHKE NAWLNSPSHKEALIN WLNSPSHKE RVVNAWLNSPSHKEA WLNSPSHKE NRVVNAWLNSPSHKE VNAWLNSPS
	HLA-DRB1*1101	None
	HLA-DRB1*1302	MKKLIIIFTLFLSQA IIIFTLFLS KKLIIIFTLFLSQAC IIIFTLFLS IELNRVVNAWLNSPS VVNAWLNSP KLIIIFTLFLSQACN IIIFTLFLS ELNRVVNAWLNSPSH VVNAWLNSP LNRVVNAWLNSPSHK VVNAWLNSP NRVVNAWLNSPSHKE VVNAWLNSP GIELNRVVNAWLNSP LNRVVNAWL IIIFTLFLSQACNLS IIIFTLFLS RVVNAWLNSPSHKEA VNAWLNSPS LIIIFTLFLSQACNL IIIFTLFLS DNIDIFVVLFGKRKY IFVVLFGKR
	HLA-DRB1*1501	NIDIFVVLFGKRKYK IFVVLFGKR DNIDIFVVLFGKRKY IFVVLFGKR IDIFVVLFGKRKYKN IFVVLFGKR LNRVVNAWLNSPSHK VNAWLNSPS ELNRVVNAWLNSPSH VNAWLNSPS NRVVNAWLNSPSHKE VNAWLNSPS TDNIDIFVVLFGKRK IFVVLFGKR RVVNAWLNSPSHKEA VNAWLNSPS IELNRVVNAWLNSPS LNRVVNAWL KKLIIIFTLFLSQAC IIIFTLFLS KLIIIFTLFLSQACN IIIFTLFLS MKKLIIIFTLFLSQA IIIFTLFLS SEIAELRKKLNLNHL LRKKLNLNH YSEIAELRKKLNLNH ELRKKLNLN EIAELRKKLNLNHLE LRKKLNLNH IAELRKKLNLNHLEI LRKKLNLNH AELRKKLNLNHLEID LRKKLNLNH TTDNIDIFVVLFGKR DIFVVLFGK

		VVNAWLNSPSHKEAL VNAWLNSPS RTITHTLFGTTPMQR ITHTLFGTT LIIIFTLFLSQACNL IIIFTLFLS TITHTLFGTTPMQRI LFGTTPMQR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	None
	HLA-DRB5*0101	HTLFGTTPMQRIHKY LFGTTPMQR THTLFGTTPMQRIHK LFGTTPMQR
NP_045709.1| lipoprotein BBA36[Borrelia burgdorferi B31] Seq32	HLA-DRB1*0101	SLTPEEAEKLESLKV LTPEEAEKL MQRISILLMLLAVFS MQRISILLM ISILLMLLAVFSCKQ LLMLLAVFS QRISILLMLLAVFSC LLMLLAVFS RISILLMLLAVFSCK LLMLLAVFS SILLMLLAVFSCKQF LLMLLAVFS ILLMLLAVFSCKQFG LLMLLAVFS LLMLLAVFSCKQFGD LLMLLAVFS ISSFDNISSIVSKAV FDNISSIVS SSFDNISSIVSKAVD FDNISSIVS KEFISSFDNISSIVS FISSFDNIS FISSFDNISSIVSKA FDNISSIVS SLKVFLKDAMSVNGR LKDAMSVNG LKVFLKDAMSVNGRE LKDAMSVNG EFISSFDNISSIVSK FDNISSIVS ESLKVFLKDAMSVNG VFLKDAMSV KVFLKDAMSVNGREE LKDAMSVNG FDNISSIVSKAVDAS ISSIVSKAV VFLKDAMSVNGREEA LKDAMSVNG SFDNISSIVSKAVDA ISSIVSKAV MMQRISILLMLLAVF MMQRISILL DNISSIVSKAVDASK ISSIVSKAV LESLKVFLKDAMSVN VFLKDAMSV KLESLKVFLKDAMSV SLKVFLKDA DVVKDLIPKEISLTP VKDLIPKEI IPKEISLTPEEAEKL IPKEISLTP SDVVKDLIPKEISLT VKDLIPKEI PKEISLTPEEAEKLE LTPEEAEKL EISLTPEEAEKLESL LTPEEAEKL FLKDAMSVNGREEAL LKDAMSVNG KEISLTPEEAEKLES LTPEEAEKL ISLTPEEAEKLESLK LTPEEAEKL VVKDLIPKEISLTPE LIPKEISLT VKDLIPKEISLTPEE LIPKEISLT ISSIVSKAVDASKKR ISSIVSKAV NISSIVSKAVDASKK ISSIVSKAV EEIFKVIKKVLTESE FKVIKKVLT EIFKVIKKVLTESES FKVIKKVLT LKDAMSVNGREEALK LKDAMSVNG VCYKIKNSKGEALSL IKNSKGEAL KDLIPKEISLTPEEA LIPKEISLT YKIKNSKGEALSLFF IKNSKGEAL CYKIKNSKGEALSLF IKNSKGEAL NEEIFKVIKKVLTES FKVIKKVLT YVCYKIKNSKGEALS IKNSKGEAL EYVCYKIKNSKGEAL YKIKNSKGE IDSGNGIPLVVSDVV GNGIPLVVS

		LTEIDSGNGIPLVVS IDSGNGIPL TEIDSGNGIPLVVSD GNGIPLVVS VSDVVKDLIPKEISL VKDLIPKEI VVSDVVKDLIPKEIS VKDLIPKEI CNEEIFKVIKKVLTE FKVIKKVLT KCNEEIFKVIKKVLT IFKVIKKVL LVVSDVVKDLIPKEI LVVSDVVKD LTPEEAEKLESLKVF LTPEEAEKL YKEFFDWLSKDVNRQ FFDWLSKDV IFKVIKKVLTESESN FKVIKKVLT FKVIKKVLTESESNN FKVIKKVLT KEFFDWLSKDVNRQK WLSKDVNRQ DSGNGIPLVVSDVVK GNGIPLVVS DLIPKEISLTPEEAE LIPKEISLT EIDSGNGIPLVVSDV GNGIPLVVS ESNNELKNLKNYGNV LKNLKNYGN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	KEFISSFDNISSIVS FISSFDNIS EIFKVIKKVLTESES FKVIKKVLT EEIFKVIKKVLTESE FKVIKKVLT NEEIFKVIKKVLTES FKVIKKVLT NRQKEFISSFDNISS FISSFDNIS RQKEFISSFDNISSI FISSFDNIS QKEFISSFDNISSIV FISSFDNIS
	HLA-DRB1*0404	ISILLMLLAVFSCKQ MLLAVFSCK SLFFQKVVDAFGADP FQKVVDAFG LFFQKVVDAFGADPY VVDAFGADP FQKVVDAFGADPYKK VVDAFGADP FFQKVVDAFGADPYK VVDAFGADP SILLMLLAVFSCKQF LLAVFSCKQ ILLMLLAVFSCKQFG LLAVFSCKQ QKVVDAFGADPYKKD VVDAFGADP ESLKVFLKDAMSVNG FLKDAMSVN SLKVFLKDAMSVNGR LKDAMSVNG LKVFLKDAMSVNGRE LKDAMSVNG
	HLA-DRB1*0405	KSYKEFFDWLSKDVN YKEFFDWLS EKSYKEFFDWLSKDV YKEFFDWLS YEKSYKEFFDWLSKD YKEFFDWLS YKEFFDWLSKDVNRQ YKEFFDWLS EYEKSYKEFFDWLSK YKEFFDWLS AEYEKSYKEFFDWLS YEKSYKEFF SYKEFFDWLSKDVNR YKEFFDWLS KEFISSFDNISSIVS ISSFDNISS EFISSFDNISSIVSK FDNISSIVS NRQKEFISSFDNISS FISSFDNIS RQKEFISSFDNISSI ISSFDNISS QKEFISSFDNISSIV ISSFDNISS FISSFDNISSIVSKA FDNISSIVS KEFFDWLSKDVNRQK FDWLSKDVN EFFDWLSKDVNRQKE FDWLSKDVN ISSFDNISSIVSKAV FDNISSIVS
	HLA-DRB1*0701	ISSFDNISSIVSKAV SFDNISSIV SSFDNISSIVSKAVD ISSIVSKAV SFDNISSIVSKAVDA ISSIVSKAV FDNISSIVSKAVDAS ISSIVSKAV

		DNISSIVSKAVDASK ISSIVSKAV
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NEEIFKVIKKVLTES FKVIKKVLT EEIFKVIKKVLTESE FKVIKKVLT KCNEEIFKVIKKVLT IFKVIKKVL CNEEIFKVIKKVLTE FKVIKKVLT EIFKVIKKVLTESES FKVIKKVLT IFKVIKKVLTESESN FKVIKKVLT FKVIKKVLTESESNN FKVIKKVLT MQRISILLMLLAVFS MQRISILLM MMQRISILLMLLAVF MQRISILLM SESNNELKNLKNYGN SNNELKNLK QRISILLMLLAVFSC ISILLMLLA ESNNELKNLKNYGNV LKNLKNYGN RISILLMLLAVFSCK ISILLMLLA ISILLMLLAVFSCKQ ISILLMLLA ESLKVFLKDAMSVNG LKVFLKDAM LESLKVFLKDAMSVN LKVFLKDAM EYVCYKIKNSKGEAL YKIKNSKGE ISSFDNISSIVSKAV FDNISSIVS SSFDNISSIVSKAVD FDNISSIVS AEKLESLKVFLKDAM LESLKVFLK EFISSFDNISSIVSK FDNISSIVS YVCYKIKNSKGEALS IKNSKGEAL FISSFDNISSIVSKA FDNISSIVS VCYKIKNSKGEALSL IKNSKGEAL EKLESLKVFLKDAMS LKVFLKDAM LVVSDVVKDLIPKEI VSDVVKDLI NGIPLVVSDVVKDLI LVVSDVVKD KEFISSFDNISSIVS SFDNISSIV
	HLA-DRB1*1501	MQRISILLMLLAVFS ILLMLLAVF RISILLMLLAVFSCK ILLMLLAVF MMQRISILLMLLAVF MMQRISILL ISILLMLLAVFSCKQ ILLMLLAVF QRISILLMLLAVFSC ILLMLLAVF SILLMLLAVFSCKQF LLMLLAVFS
	HLA-DRB3*0101	None
	HLA-DRB4*0101	RISILLMLLAVFSCK ILLMLLAVF ISILLMLLAVFSCKQ MLLAVFSCK SILLMLLAVFSCKQF MLLAVFSCK ILLMLLAVFSCKQFG MLLAVFSCK YKEFFDWLSKDVNRQ FDWLSKDVN KEFFDWLSKDVNRQK FDWLSKDVN
	HLA-DRB5*0101	None
AAT93789.1| lipoprotein BBA36 (homolog 67%)[Borrelia garinii PBi] Seq33	HLA-DRB1*0101	VSFFNNICGIITKAV FNNICGIIT SFFNNICGIITKAVD ICGIITKAV NNELANLKNLNSYNL LANLKNLNS NELANLKNLNSYNLN LKNLNSYNL LANLKNLNSYNLNSN LKNLNSYNL ELANLKNLNSYNLNS LKNLNSYNL ANLKNLNSYNLNSNN LKNLNSYNL FNNICGIITKAVDAS ICGIITKAV FFNNICGIITKAVDA ICGIITKAV

		SEEFERLEALKTFLK FERLEALKT EEFERLEALKTFLKD FERLEALKT NNICGIITKAVDASK ICGIITKAV TSEEFERLEALKTFL FERLEALKT VLTSEEFERLEALKT VLTSEEFER LTSEEFERLEALKTF FERLEALKT KDQIIEKGPVLTSEE IIEKGPVLT DQIIEKGPVLTSEEF IIEKGPVLT MKRISILSILLLLLL ILSILLLLL NLKNLNSYNLNSNNK LKNLNSYNL SKDQIIEKGPVLTSE IIEKGPVLT ESKDQIIEKGPVLTS IIEKGPVLT KRISILSILLLLLLF ILSILLLLL RISILSILLLLLLFS ILSILLLLL ISILSILLLLLLFSC ILSILLLLL FVSFFNNICGIITKA FNNICGIIT EFVSFFNNICGIITK FNNICGIIT YGDVKSLTEVATDLE VKSLTEVAT QYGDVKSLTEVATDL VKSLTEVAT KEFVSFFNNICGIIT VSFFNNICG GDVKSLTEVATDLED VKSLTEVAT KQYGDVKSLTEVATD VKSLTEVAT CKQYGDVKSLTEVAT YGDVKSLTE EFERLEALKTFLKDA FERLEALKT FERLEALKTFLKDAM FERLEALKT SILSILLLLLLFSCK LSILLLLLL NICGIITKAVDASKK ICGIITKAV ICGIITKAVDASKKR ICGIITKAV VESKDQIIEKGPVLT DQIIEKGPV QIIEKGPVLTSEEFE IIEKGPVLT ILSILLLLLLFSCKQ ILLLLLLFS LSILLLLLLFSCKQY ILLLLLLFS IIEKGPVLTSEEFER IIEKGPVLT SLFFQKVADAFGTQE FQKVADAFG DLSLFFQKVADAFGT FQKVADAFG LSLFFQKVADAFGTQ FQKVADAFG DVKSLTEVATDLEDD VKSLTEVAT VKSLTEVATDLEDDN VKSLTEVAT ALKTFLKDAMGVNGR LKDAMGVNG LKTFLKDAMGVNGRE LKDAMGVNG LFFQKVADAFGTQEY FQKVADAFG EALKTFLKDAMGVNG TFLKDAMGV KTFLKDAMGVNGREG LKDAMGVNG TFLKDAMGVNGREGD LKDAMGVNG YKEFFDWLSKDVNRQ FFDWLSKDV DDLSLFFQKVADAFG FFQKVADAF LEDDNSFASGSVESK SFASGSVES EDDNSFASGSVESKD FASGSVESK KEFFDWLSKDVNRQK WLSKDVNRQ DDNSFASGSVESKDQ FASGSVESK DNSFASGSVESKDQI FASGSVESK SENNNELANLKNLNS NNNELANLK
	HLA-DRB1*0301	LGFNEYVCYDIKTRT LGFNEYVCY EYVCYDIKTRTGDDL VCYDIKTRT FNEYVCYDIKTRTGD VCYDIKTRT NEYVCYDIKTRTGDD VCYDIKTRT

		GFNEYVCYDIKTRTG VCYDIKTRT
	HLA-DRB1*0401	None
	HLA-DRB1*0404	ILSILLLLLLFSCKQ ILLLLLLFS SILLLLLLFSCKQYG LLLLFSCKQ ILLLLLLFSCKQYGD LLLLFSCKQ LSILLLLLLFSCKQY LLLLFSCKQ LLLLLLFSCKQYGDV LLLLFSCKQ
	HLA-DRB1*0405	KSYKEFFDWLSKDVN YKEFFDWLS NRQKEFVSFFNNICG FVSFFNNIC VNRQKEFVSFFNNIC QKEFVSFFN RQKEFVSFFNNICGI FVSFFNNIC QKEFVSFFNNICGII FVSFFNNIC KEFVSFFNNICGIIT FVSFFNNIC EKSYKEFFDWLSKDV YKEFFDWLS YEKSYKEFFDWLSKD YKEFFDWLS YKEFFDWLSKDVNRQ YKEFFDWLS EYEKSYKEFFDWLSK YKEFFDWLS AEYEKSYKEFFDWLS YEKSYKEFF SYKEFFDWLSKDVNR YKEFFDWLS EFVSFFNNICGIITK FVSFFNNIC FVSFFNNICGIITKA FVSFFNNIC KVIKRVFTESENNNE IKRVFTESE EIFKVIKRVFTESEN IKRVFTESE KEFFDWLSKDVNRQK FDWLSKDVN FKVIKRVFTESENNN IKRVFTESE IFKVIKRVFTESENN IKRVFTESE EEIFKVIKRVFTESE FKVIKRVFT EFFDWLSKDVNRQKE FDWLSKDVN VIKRVFTESENNNEL IKRVFTESE
	HLA-DRB1*0701	NNELANLKNLNSYNL NLKNLNSYN ANLKNLNSYNLNSNN LKNLNSYNL NELANLKNLNSYNLN LKNLNSYNL ELANLKNLNSYNLNS LKNLNSYNL LANLKNLNSYNLNSN LKNLNSYNL CNEEIFKVIKRVFTE IFKVIKRVF NEEIFKVIKRVFTES IFKVIKRVF KCNEEIFKVIKRVFT IFKVIKRVF EEIFKVIKRVFTESE IFKVIKRVF
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NNELANLKNLNSYNL LANLKNLNS ELANLKNLNSYNLNS LKNLNSYNL LANLKNLNSYNLNSN LKNLNSYNL ANLKNLNSYNLNSNN LKNLNSYNL KEFVSFFNNICGIIT FFNNICGII VSFFNNICGIITKAV FNNICGIIT EFVSFFNNICGIITK FNNICGIIT FVSFFNNICGIITKA FNNICGIIT MKRISILSILLLLLL ISILSILLL SFFNNICGIITKAVD FNNICGIIT KRISILSILLLLLLF ISILSILLL NLKNLNSYNLNSNNK LKNLNSYNL ISILSILLLLLLFSC ISILSILLL RISILSILLLLLLFS ISILSILLL

		NEEIFKVIKRVFTES FKVIKRVFT EEIFKVIKRVFTESE FKVIKRVFT FFNNICGIITKAVDA FNNICGIIT ASKKRYNSNPKSLGF YNSNPKSLG KCNEEIFKVIKRVFT IFKVIKRVF DASKKRYNSNPKSLG KKRYNSNPK CNEEIFKVIKRVFTE FKVIKRVFT SKKRYNSNPKSLGFN YNSNPKSLG FNNICGIITKAVDAS FNNICGIIT EIFKVIKRVFTESEN FKVIKRVFT KKRYNSNPKSLGFNE YNSNPKSLG KRYNSNPKSLGFNEY YNSNPKSLG SILSILLLLLLFSCK LSILLLLLL IFKVIKRVFTESENN FKVIKRVFT FERLEALKTFLKDAM LEALKTFLK ERLEALKTFLKDAMG LEALKTFLK ILSILLLLLLFSCKQ LSILLLLLL ENNNELANLKNLNSY LANLKNLNS NNNELANLKNLNSYN LANLKNLNS LSILLLLLLFSCKQY LSILLLLLL FKVIKRVFTESENNN FKVIKRVFT EALKTFLKDAMGVNG LKTFLKDAM ESKDQIIEKGPVLTS IIEKGPVLT LEALKTFLKDAMGVN LKTFLKDAM
	HLA-DRB1*1501	NNELANLKNLNSYNL LANLKNLNS NELANLKNLNSYNLN LANLKNLNS ELANLKNLNSYNLNS LKNLNSYNL LANLKNLNSYNLNSN LKNLNSYNL ENNNELANLKNLNSY LANLKNLNS NNNELANLKNLNSYN LANLKNLNS ANLKNLNSYNLNSNN LKNLNSYNL LSILLLLLLFSCKQY LLLLLFSCK SENNNELANLKNLNS NELANLKNL SILLLLLLFSCKQYG LLLLLFSCK ILSILLLLLLFSCKQ LLLLLFSCK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	SILSILLLLLLFSCK LLLLLLFSC LSILLLLLLFSCKQY LLLLLFSCK ILSILLLLLLFSCKQ LLLLLFSCK SILLLLLLFSCKQYG LLLLLFSCK ILLLLLLFSCKQYGD LLLLLFSCK YKEFFDWLSKDVNRQ FDWLSKDVN KEFFDWLSKDVNRQK FDWLSKDVN
	HLA-DRB5*0101	None
NP_045739.1| BBA66 antigen, P35, putative [Borrelia burgdorferi B31] Seq34	HLA-DRB1*0101	DGLIANASSNSSLSD IANASSNSS RQADGLIANASSNSS LIANASSNS QADGLIANASSNSSL IANASSNSS ADGLIANASSNSSLS IANASSNSS GLIANASSNSSLSDS IANASSNSS LIRELMISGLGTQIS MISGLGTQI ELMISGLGTQISFEL ISGLGTQIS IRELMISGLGTQISF ISGLGTQIS RELMISGLGTQISFE ISGLGTQIS LMISGLGTQISFELA ISGLGTQIS KQRIPIQAVTTVPGN IQAVTTVPG

		TKQRIPIQAVTTVPG	IPIQAVTTV
		QRIPIQAVTTVPGNT	IQAVTTVPG
		IPIQAVTTVPGNTRT	IQAVTTVPG
		RIPIQAVTTVPGNTR	IQAVTTVPG
		LIANASSNSSLSDSK	IANASSNSS
		IANASSNSSLSDSKS	IANASSNSS
		MISGLGTQISFELAL	ISGLGTQIS
		ISGLGTQISFELALE	ISGLGTQIS
		SNLPKTTAARAASLT	LPKTTAARA
		LSNLPKTTAARAASL	LPKTTAARA
		AKTVAAAPNKGSQNQ	VAAAPNKGS
		SQAAKTVAAAPNKGS	TVAAAPNKG
		AAKTVAAAPNKGSQN	VAAAPNKGS
		QAAKTVAAAPNKGSQ	VAAAPNKGS
		GSKLQTLKNELIRAI	LQTLKNELI
		IQAVTTVPGNTRTFN	IQAVTTVPG
		PIQAVTTVPGNTRTF	IQAVTTVPG
		SKLQTLKNELIRAIS	LKNELIRAI
		ADLSNLPKTTAARAA	LPKTTAARA
		SSAVQTTTSSGSKLQ	VQTTTSSGS
		KNKVKGILNKAADDQ	VKGILNKAA
		TNSSSAVQTTTSSGS	TNSSSAVQT
		NLPKTTAARAASLTK	TTAARAASL
		SAVQTTTSSGSKLQT	VQTTTSSGS
		NKVKGILNKAADDQE	VKGILNKAA
		TMKLKELKSKLNQIL	LKELKSKLN
		SSSAVQTTTSSGSKL	VQTTTSSGS
		MKLKELKSKLNQILD	LKELKSKLN
		NSSSAVQTTTSSGSK	VQTTTSSGS
		KTVAAAPNKGSQNQP	VAAAPNKGS
		LPKTTAARAASLTKQ	TTAARAASL
		SADLSNLPKTTAARA	LSNLPKTTA
		SLTKQRIPIQAVTTV	RIPIQAVTT
		LTKQRIPIQAVTTVP	IPIQAVTTV
		KLQTLKNELIRAISE	LKNELIRAI
		LQTLKNELIRAISEE	LKNELIRAI
		SRQADGLIANASSNS	ADGLIANAS
		DLSNLPKTTAARAAS	LPKTTAARA
		EDYKNKVKGILNKAA	YKNKVKGIL
		YKNKVKGILNKAADD	VKGILNKAA
		DYKNKVKGILNKAAD	VKGILNKAA
		FALNYSFSQPTRQQT	LNYSFSQPT
		MKIKPLIQLKLLGLF	MKIKPLIQL
		TFALNYSFSQPTRQQ	LNYSFSQPT
		QTLKNELIRAISEEK	LKNELIRAI
		SLIRELMISGLGTQI	IRELMISGL
		LKELKSKLNQILDKR	LKSKLNQIL
		KLKELKSKLNQILDK	LKSKLNQIL
		PKTTAARAASLTKQR	TTAARAASL
		PTFALNYSFSQPTRQ	LNYSFSQPT
		KVYDRSYAPQLNSNT	YDRSYAPQL
		LPTFALNYSFSQPTR	LNYSFSQPT
		KGSQNQQAAPSPQLQ	QQAAPSPQL
		GLPTFALNYSFSQPT	LPTFALNYS
		NKGSQNQQAAPSPQL	SQNQQAAPS
		GSQNQQAAPSPQLQS	QQAAPSPQL
		LSFSADLSNLPKTTA	FSADLSNLP

		SQNQQAAPSPQLQSL	QQAAPSPQL
		DSAFELLDVISSAKV	FELLDVISS
		YDQFKMKDSAFELLD	FKMKDSAFE
		TYDQFKMKDSAFELL	FKMKDSAFE
		SAFELLDVISSAKVY	LDVISSAKV
		QNQQAAPSPQLQSLS	QQAAPSPQL
		DQFKMKDSAFELLDV	FKMKDSAFE
		FDFTMKLKELKSKLN	FTMKLKELK
		KVKGILNKAADDQET	VKGILNKAA
		VKGILNKAADDQETT	VKGILNKAA
		DFTMKLKELKSKLNQ	LKELKSKLN
		TVAAAPNKGSQNQPQ	VAAAPNKGS
		FTMKLKELKSKLNQI	LKELKSKLN
		AELKKQSQAAKTVAA	KQSQAAKTV
		FELLDVISSAKVYDR	LDVISSAKV
		IKPLIQLKLLGLFLF	LIQLKLLGL
		VYDRSYAPQLNSNTP	YAPQLNSNT
		KPLIQLKLLGLFLFS	LIQLKLLGL
		ALNYSFSQPTRQQTN	LNYSFSQPT
		LNYSFSQPTRQQTNS	LNYSFSQPT
		SSGSKLQTLKNELIR	LQTLKNELI
		FSADLSNLPKTTAAR	LSNLPKTTA
		ETYDQFKMKDSAFEL	FKMKDSAFE
		SGSKLQTLKNELIRA	LQTLKNELI
		TSSGSKLQTLKNELI	GSKLQTLKN
		AFELLDVISSAKVYD	LDVISSAKV
		ELKKQSQAAKTVAAA	SQAAKTVAA
		AVQTTTSSGSKLQTL	VQTTTSSGS
		SFSADLSNLPKTTAA	LSNLPKTTA
		RETYDQFKMKDSAFE	QFKMKDSAF
		YDRSYAPQLNSNTPE	YAPQLNSNT
		KRYLDNMQNARQSVL	LDNMQNARQ
		RYLDNMQNARQSVLE	MQNARQSVL
		VQTTTSSGSKLQTLK	VQTTTSSGS
		ELLDVISSAKVYDRS	LDVISSAKV
		NSRNSGLPTFALNYS	NSGLPTFAL
		KTTAARAASLTKQRI	TAARAASLT
		ASLTKQRIPIQAVTT	LTKQRIPIQ
		LKKQSQAAKTVAAAP	SQAAKTVAA
		KIKPLIQLKLLGLFL	LIQLKLLGL
		TLKNELIRAISEEKN	LKNELIRAI
		LKNELIRAISEEKNK	LKNELIRAI
		KELKSKLNQILDKRK	LKSKLNQIL
		QAVTTVPGNTRTFNS	VTTVPGNTR
		RTFNSRNSGLPTFAL	FNSRNSGLP
		SRNSGLPTFALNYSF	LPTFALNYS
		YLDNMQNARQSVLEA	MQNARQSVL
		VAAAPNKGSQNQPQT	VAAAPNKGS
		QPTRQQTNSSSAVQT	QQTNSSSAV
		PTRQQTNSSSAVQTT	TNSSSAVQT
		QSQAAKTVAAAPNKG	SQAAKTVAA
		TRQQTNSSSAVQTTT	TNSSSAVQT
		RSYAPQLNSNTPEAE	YAPQLNSNT
		FKMKDSAFELLDVIS	FKMKDSAFE
		LIQLKLLGLFLFSCT	LKLLGLFLF
		KKQSQAAKTVAAAPN	SQAAKTVAA
		LDNMQNARQSVLEAY	MQNARQSVL

		VAAELKKQSQAAKTV KKQSQAAKT KQSQAAKTVAAAPNK SQAAKTVAA DRSYAPQLNSNTPEA YAPQLNSNT AAELKKQSQAAKTVA KQSQAAKTV HSLIRELMISGLGTQ IRELMISGL PLIQLKLLGLFLFSC LKLLGLFLF NSGLPTFALNYSFSQ LPTFALNYS QFKMKDSAFELLDVI FKMKDSAFE RQQTNSSSAVQTTTS TNSSSAVQT NHSLIRELMISGLGT IRELMISGL DNMQNARQSVLEAYI MQNARQSVL TTAARAASLTKQRIP TTAARAASL QQTNSSSAVQTTTSS TNSSSAVQT RNSGLPTFALNYSFS LPTFALNYS AKVYDRSYAPQLNSN YDRSYAPQL TFNSRNSGLPTFALN FNSRNSGLP SLSFSADLSNLPKTT FSADLSNLP FNSRNSGLPTFALNY FNSRNSGLP MKDSAFELLDVISSA FELLDVISS QLQSLSFSADLSNLP LQSLSFSAD IQLKLLGLFLFSCTI LKLLGLFLF LQSLSFSADLSNLPK FSADLSNLP SSAKVYDRSYAPQLN YDRSYAPQL KMKDSAFELLDVISS MKDSAFELL AVTTVPGNTRTFNSR VTTVPGNTR KKRYLDNMQNARQSV LDNMQNARQ NQQAAPSPQLQSLSF QQAAPSPQL NYSFSQPTRQQTNSS FSQPTRQQT IKKRYLDNMQNARQS LDNMQNARQ LKLLGLFLFSCTIDA LLGLFLFSC QSLSFSADLSNLPKT FSADLSNLP NQNHSLIRELMISGL LIRELMISG QNHSLIRELMISGLG IRELMISGL AASLTKQRIPIQAVT LTKQRIPIQ
	HLA-DRB1*0301	None
	HLA-DRB1*0401	GSIMEALYNENQNHS MEALYNENQ SIMEALYNENQNHSL LYNENQNHS MEALYNENQNHSLIR LYNENQNHS IMEALYNENQNHSLI LYNENQNHS EALYNENQNHSLIRE LYNENQNHS RQADGLIANASSNSS LIANASSNS QADGLIANASSNSSL IANASSNSS ADGLIANASSNSSLS IANASSNSS DGLIANASSNSSLSD IANASSNSS GLIANASSNSSLSDS IANASSNSS LSFSADLSNLPKTTA FSADLSNLP LQSLSFSADLSNLPK FSADLSNLP QSLSFSADLSNLPKT FSADLSNLP SLSFSADLSNLPKTT FSADLSNLP QLQSLSFSADLSNLP LSFSADLSN LYNENQNHSLIRELM LYNENQNHS ALYNENQNHSLIREL LYNENQNHS LIANASSNSSLSDSK IANASSNSS IANASSNSSLSDSKS IANASSNSS FSADLSNLPKTTAAR FSADLSNLP SFSADLSNLPKTTAA FSADLSNLP PTFALNYSFSQPTRQ FALNYSFSQ

		LPTFALNYSFSQPTR FALNYSFSQ EIFNQDYLNAKINSF FNQDYLNAK GLPTFALNYSFSQPT FALNYSFSQ SGLPTFALNYSFSQP FALNYSFSQ NSGLPTFALNYSFSQ LPTFALNYS IFNQDYLNAKINSFD YLNAKINSF FALNYSFSQPTRQQT FALNYSFSQ TFALNYSFSQPTRQQ FALNYSFSQ FNQDYLNAKINSFDF YLNAKINSF
	HLA-DRB1*0404	RQADGLIANASSNSS LIANASSNS ADGLIANASSNSSLS IANASSNSS DGLIANASSNSSLSD IANASSNSS QADGLIANASSNSSL IANASSNSS GLIANASSNSSLSDS IANASSNSS DRSYAPQLNSNTPEA YAPQLNSNT RSYAPQLNSNTPEAE QLNSNTPEA SYAPQLNSNTPEAEN QLNSNTPEA HSLIRELMISGLGTQ LIRELMISG LIRELMISGLGTQIS LMISGLGTQ YAPQLNSNTPEAENE QLNSNTPEA LSFSADLSNLPKTTA FSADLSNLP SLIRELMISGLGTQI LMISGLGTQ RELMISGLGTQISFE LMISGLGTQ LIANASSNSSLSDSK IANASSNSS IANASSNSSLSDSKS IANASSNSS IRELMISGLGTQISF LMISGLGTQ APQLNSNTPEAENER QLNSNTPEA LQSLSFSADLSNLPK FSADLSNLP
	HLA-DRB1*0405	RIPIQAVTTVPGNTR IQAVTTVPG IPIQAVTTVPGNTRT IQAVTTVPG KQRIPIQAVTTVPGN IQAVTTVPG TKQRIPIQAVTTVPG KQRIPIQAV QRIPIQAVTTVPGNT IQAVTTVPG PIQAVTTVPGNTRTF IQAVTTVPG IQAVTTVPGNTRTFN IQAVTTVPG SQAAKTVAAAPNKGS AKTVAAAPN AKTVAAAPNKGSQNQ VAAAPNKGS QAAKTVAAAPNKGSQ VAAAPNKGS AAKTVAAAPNKGSQN VAAAPNKGS KTVAAAPNKGSQNQP VAAAPNKGS LQSLSFSADLSNLPK FSADLSNLP
	HLA-DRB1*0701	DNMQNARQSVLEAYI MQNARQSVL KRYLDNMQNARQSVL DNMQNARQS YLDNMQNARQSVLEA MQNARQSVL LDNMQNARQSVLEAY MQNARQSVL RYLDNMQNARQSVLE MQNARQSVL SNLPKTTAARAASLT LPKTTAARA LSNLPKTTAARAASL LPKTTAARA NLPKTTAARAASLTK TTAARAASL LPKTTAARAASLTKQ TTAARAASL ADLSNLPKTTAARAA LPKTTAARA DLSNLPKTTAARAAS LPKTTAARA SADLSNLPKTTAARA LSNLPKTTA MQNARQSVLEAYISI MQNARQSVL NMQNARQSVLEAYIS MQNARQSVL PKTTAARAASLTKQR TTAARAASL

	HLA-DRB1*0802	None
	HLA-DRB1*0901	DNMQNARQSVLEAYI MQNARQSVL LDNMQNARQSVLEAY MQNARQSVL YLDNMQNARQSVLEA MQNARQSVL RYLDNMQNARQSVLE MQNARQSVL KRYLDNMQNARQSVL LDNMQNARQ
	HLA-DRB1*1101	None
	HLA-DRB1*1302	LIQLKLLGLFLFSCT LKLLGLFLF IKPLIQLKLLGLFLF IQLKLLGLF IQLKLLGLFLFSCTI LKLLGLFLF KPLIQLKLLGLFLFS LKLLGLFLF PLIQLKLLGLFLFSC LKLLGLFLF ANLNEDYKNKVKGIL LNEDYKNKV QLKLLGLFLFSCTID LKLLGLFLF NLNEDYKNKVKGILN YKNKVKGIL LNEDYKNKVKGILNK YKNKVKGIL LKLLGLFLFSCTIDA LKLLGLFLF RIPIQAVTTVPGNTR IQAVTTVPG IPIQAVTTVPGNTRT IQAVTTVPG EDYKNKVKGILNKAA YKNKVKGIL NEDYKNKVKGILNKA YKNKVKGIL TKQRIPIQAVTTVPG IPIQAVTTV QRIPIQAVTTVPGNT IQAVTTVPG KQRIPIQAVTTVPGN IQAVTTVPG QADGLIANASSNSSL IANASSNSS ADGLIANASSNSSLS IANASSNSS DGLIANASSNSSLSD IANASSNSS RQADGLIANASSNSS LIANASSNS IQAVTTVPGNTRTFN IQAVTTVPG DYKNKVKGILNKAAD YKNKVKGIL GLIANASSNSSLSDS IANASSNSS PIQAVTTVPGNTRTF IQAVTTVPG YKNKVKGILNKAADD YKNKVKGIL MKIKPLIQLKLLGLF IKPLIQLKL LSFSADLSNLPKTTA FSADLSNLP NQDYLNAKINSFDFT YLNAKINSF SFSADLSNLPKTTAA LSNLPKTTA KRYLDNMQNARQSVL YLDNMQNAR FSADLSNLPKTTAAR LSNLPKTTA ELMISGLGTQISFEL ISGLGTQIS QDYLNAKINSFDFTM YLNAKINSF KIKPLIQLKLLGLFL IQLKLLGLF LIANASSNSSLSDSK IANASSNSS DYLNAKINSFDFTMK YLNAKINSF LIRELMISGLGTQIS IRELMISGL RYLDNMQNARQSVLE MQNARQSVL YLNAKINSFDFTMKL YLNAKINSF SADLSNLPKTTAARA LSNLPKTTA LMISGLGTQISFELA LGTQISFEL IRELMISGLGTQISF ISGLGTQIS ADLSNLPKTTAARAA LSNLPKTTA FNQDYLNAKINSFDF YLNAKINSF IFNQDYLNAKINSFD YLNAKINSF EIFNQDYLNAKINSF FNQDYLNAK YLDNMQNARQSVLEA MQNARQSVL
	HLA-DRB1*1501	IKPLIQLKLLGLFLF LIQLKLLGL

		FTMKLKELKSKLNQI MKLKELKSK FDFTMKLKELKSKLN MKLKELKSK KPLIQLKLLGLFLFS LIQLKLLGL DFTMKLKELKSKLNQ MKLKELKSK LIQLKLLGLFLFSCT LIQLKLLGL PLIQLKLLGLFLFSC LIQLKLLGL SFDFTMKLKELKSKL MKLKELKSK NSFDFTMKLKELKSK TMKLKELKS MKIKPLIQLKLLGLF LIQLKLLGL
	HLA-DRB3*0101	None
	HLA-DRB4*0101	LIQLKLLGLFLFSCT LKLLGLFLF KPLIQLKLLGLFLFS LKLLGLFLF IKPLIQLKLLGLFLF LIQLKLLGL IQLKLLGLFLFSCTI LKLLGLFLF PLIQLKLLGLFLFSC LKLLGLFLF LKLLGLFLFSCTIDA LKLLGLFLF QLKLLGLFLFSCTID LKLLGLFLF SGLPTFALNYSFSQP LPTFALNYS FALNYSFSQPTRQQT YSFSQPTRQ LNYSFSQPTRQQTNS YSFSQPTRQ PTFALNYSFSQPTRQ FALNYSFSQ NSGLPTFALNYSFSQ LPTFALNYS ALNYSFSQPTRQQTN YSFSQPTRQ TFALNYSFSQPTRQQ YSFSQPTRQ SRNSGLPTFALNYSF LPTFALNYS RNSGLPTFALNYSFS LPTFALNYS NSRNSGLPTFALNYS GLPTFALNY
	HLA-DRB5*0101	IKKRYLDNMQNARQS LDNMQNARQ KRYLDNMQNARQSVL LDNMQNARQ KKRYLDNMQNARQSV LDNMQNARQ YIKKRYLDNMQNARQ IKKRYLDNM RYLDNMQNARQSVLE LDNMQNARQ VYDRSYAPQLNSNTP YAPQLNSNT KVYDRSYAPQLNSNT YDRSYAPQL DRSYAPQLNSNTPEA YAPQLNSNT RSYAPQLNSNTPEAE YAPQLNSNT YDRSYAPQLNSNTPE YAPQLNSNT FALNYSFSQPTRQQT YSFSQPTRQ ALNYSFSQPTRQQTN YSFSQPTRQ LNYSFSQPTRQQTNS YSFSQPTRQ TFALNYSFSQPTRQQ YSFSQPTRQ PTFALNYSFSQPTRQ NYSFSQPTR FDFTMKLKELKSKLN FTMKLKELK
AAT93824.1|BBA66 antigen, P35, putative [Borrelia garinii PBi] Seq35	HLA-DRB1*0101	TYDQFKMKDSAFTLL FKMKDSAFT YDQFKMKDSAFTLLD FKMKDSAFT DQFKMKDSAFTLLDV FKMKDSAFT RETYDQFKMKDSAFT RETYDQFKM ETYDQFKMKDSAFTL FKMKDSAFT ASQASQVASSASQAS ASQVASSAS ASQVASSASQASPVA VASSASQAS SQVASSASQASPVAS VASSASQAS SQASQVASSASQASP VASSASQAS QASQVASSASQASPV VASSASQAS QFKMKDSAFTLLDVI FKMKDSAFT FKMKDSAFTLLDVIS FKMKDSAFT

		ATPPKQIASAQAIQT PKQIASAQA TPPKQIASAQAIQTV IASAQAIQT PKQIASAQAIQTVPN IASAQAIQT PPKQIASAQAIQTVP IASAQAIQT KQIASAQAIQTVPNN IASAQAIQT SPATNVQATPPKQIA VQATPPKQI ASPATNVQATPPKQI ATNVQATPP ATNVQATPPKQIASA VQATPPKQI PATNVQATPPKQIAS VQATPPKQI VASSASQASPVASPA VASSASQAS SPLQKLKNNLLRRIA LKNNLLRRI QVASSASQASPVASP VASSASQAS TNVQATPPKQIASAQ VQATPPKQI NSPLQKLKNNLLRRI LQKLKNNLL IASAQAIQTVPNNTS IASAQAIQT PLQKLKNNLLRRIAE LKNNLLRRI LQKLKNNLLRRIAEE LKNNLLRRI QKLKNNLLRRIAEEK LKNNLLRRI QIASAQAIQTVPNNT IASAQAIQT VQATPPKQIASAQAI VQATPPKQI YTFSSSFSQPTSQTN FSSSFSQPT SLIISGLGIQISLES ISGLGIQIS NVQATPPKQIASAQA VQATPPKQI QYTFSSSFSQPTSQT FSSSFSQPT QTNFNNSQSNNVLTN FNNSQSNNV TNFNNSQSNNVLTNY FNNSQSNNV LIISGLGIQISLEST ISGLGIQIS SQTNFNNSQSNNVLT FNNSQSNNV TSQTNFNNSQSNNVL FNNSQSNNV PTSQTNFNNSQSNNV QTNFNNSQS SVFDRGSAPQLSSNT FDRGSAPQL IRSLIISGLGIQISL ISGLGIQIS ISVFDRGSAPQLSSN FDRGSAPQL LIRSLIISGLGIQIS IISGLGIQI PQQYTFSSSFSQPTS FSSSFSQPT QQYTFSSSFSQPTSQ FSSSFSQPT NISVFDRGSAPQLSS FDRGSAPQL KPQQYTFSSSFSQPT YTFSSSFSQ RSLIISGLGIQISLE ISGLGIQIS SNISVFDRGSAPQLS FDRGSAPQL AQAIQTVPNNTSTPN IQTVPNNTS QAIQTVPNNTSTPNQ IQTVPNNTS NQVNPGNPMQIANQA VNPGNPMQI KEWLNYADAIITNTS LNYADAIIT ANQVNPGNPMQIANQ VNPGNPMQI EWLNYADAIITNTSS LNYADAIIT PANQVNPGNPMQIAN VNPGNPMQI NPANQVNPGNPMQIA VNPGNPMQI FSSSFSQPTSQTNFN FSSSFSQPT TFSSSFSQPTSQTNF FSSSFSQPT KKEWLNYADAIITNT LNYADAIIT ASQASPVASPATNVQ ASPVASPAT IISGLGIQISLESTL LGIQISLES ASAQAIQTVPNNTST IQTVPNNTS SQASPVASPATNVQA VASPATNVQ VFDRGSAPQLSSNTP DRGSAPQLS ISGLGIQISLESTLE LGIQISLES

		KLKNNLLRRIAEEKN	LKNNLLRRI
		LNPANQVNPGNPMQI	NQVNPGNPM
		DSAFTLLDVISNISV	FTLLDVISN
		NYRHQTQPSFVVPVY	HQTQPSFVV
		PNQSIIKPQQYTFSS	IKPQQYTFS
		PSFVVPVYSGNSPLQ	VVPVYSGNS
		IIKPQQYTFSSSFSQ	IKPQQYTFS
		SAFTLLDVISNISVF	FTLLDVISN
		TPNQSIIKPQQYTFS	QSIIKPQQY
		QIANQANQANQANQA	IANQANQAN
		IANQANQANQANQAN	IANQANQAN
		IKPQQYTFSSSFSQP	IKPQQYTFS
		YSGNSPLQKLKNNLL	YSGNSPLQK
		YRHQTQPSFVVPVYS	HQTQPSFVV
		PVYSGNSPLQKLKNN	YSGNSPLQK
		IESFNTQYLNTIINS	FNTQYLNTI
		ILYQENQNHSLIRSL	YQENQNHSL
		KIESFNTQYLNTIIN	FNTQYLNTI
		SFNTQYLNTIINSYT	FNTQYLNTI
		PVASPATNVQATPPK	VASPATNVQ
		NLQGLNPANQVNPGN	LQGLNPANQ
		NILYQENQNHSLIRS	YQENQNHSL
		FNTQYLNTIINSYTF	LNTIINSYT
		QTVPNNTSTPNQSII	VPNNTSTPN
		KDSAFTLLDVISNIS	FTLLDVISN
		ESFNTQYLNTIINSY	FNTQYLNTI
		YAMMDFDQAKTTEFG	FDQAKTTEF
		QASQASQASQVASSA	QASQASQVA
		SGNSPLQKLKNNLLR	LQKLKNNLL
		SASQASPVASPATNV	ASPVASPAT
		NQANQASQASQASQV	QASQASQAS
		NQASQASQASQVASS	QASQASQVA
		QATPPKQIASAQAIQ	KQIASAQAI
		KLKELESKLNSILAE	LKELESKLN
		ASQASQASQVASSAS	QASQASQVA
		LKELESKLNSILAEK	LKELESKLN
		KYLDKMQDARQSALD	DKMQDARQS
		KISINTGSNATKNKT	INTGSNATK
		ASSASQASPVASPAT	ASQASPVAS
		NKYLDKMQDARQSAL	DKMQDARQS
		LQGLNPANQVNPGNP	LQGLNPANQ
		SFSQPTSQTNFNNSQ	FSQPTSQTN
		TQYLNTIINSYTFKD	LNTIINSYT
		YLDKMQDARQSALDL	DKMQDARQS
		SERNRLYAMMDFDQA	RNRLYAMMD
		AFTLLDVISNISVFD	LLDVISNIS
		FTLLDVISNISVFDR	LLDVISNIS
		AKISINTGSNATKNK	INTGSNATK
		GNSPLQKLKNNLLRR	LQKLKNNLL
		IKVAGLQKNTQSKKN	IKVAGLQKN
		QAKISINTGSNATKN	INTGSNATK
		DQAKISINTGSNATK	SINTGSNAT
		NIKVAGLQKNTQSKK	IKVAGLQKN
		NRLYAMMDFDQAKTT	YAMMDFDQA
		LYAMMDFDQAKTTEF	YAMMDFDQA
		RLYAMMDFDQAKTTE	YAMMDFDQA
		NTQYLNTIINSYTFK	LNTIINSYT

		SSASQASPVASPATN ASQASPVAS RNRLYAMMDFDQAKT YAMMDFDQA VASPATNVQATPPKQ VASPATNVQ ERNRLYAMMDFDQAK YAMMDFDQA YQENQNHSLIRSLII YQENQNHSL AMMDFDQAKTTEFGS FDQAKTTEF VYSGNSPLQKLKNNL YSGNSPLQK IITNTSSNSKRNDPQ ITNTSSNSK IKNKYLDKMQDARQS IKNKYLDKM QYLNTIINSYTFKDK LNTIINSYT ENQNHSLIRSLIISG NQNHSLIRS
	HLA-DRB1*0301	None
	HLA-DRB1*0401	ESFNTQYLNTIINSY FNTQYLNTI SFNTQYLNTIINSYT YLNTIINSY FNTQYLNTIINSYTF YLNTIINSY TQYLNTIINSYTFKD YLNTIINSY NTQYLNTIINSYTFK YLNTIINSY GSIMNILYQENQNHS MNILYQENQ SIMNILYQENQNHSL LYQENQNHS MNILYQENQNHSLIR LYQENQNHS NILYQENQNHSLIRS LYQENQNHS IMNILYQENQNHSLI LYQENQNHS QYLNTIINSYTFKDK YLNTIINSY YLNTIINSYTFKDKL YLNTIINSY SFVVPVYSGNSPLQK VYSGNSPLQ PSFVVPVYSGNSPLQ VVPVYSGNS VPVYSGNSPLQKLKN VYSGNSPLQ VVPVYSGNSPLQKLK VYSGNSPLQ FVVPVYSGNSPLQKL VYSGNSPLQ SLIISGLGIQISLES ISGLGIQIS LIISGLGIQISLEST LGIQISLES SGLGIQISLESTLEE LGIQISLES ISGLGIQISLESTLE LGIQISLES RETYDQFKMKDSAFT TYDQFKMKD IISGLGIQISLESTL LGIQISLES NYADAIITNTSSNSK IITNTSSNS PTSQTNFNNSQSNNV SQTNFNNSQ YADAIITNTSSNSKR ITNTSSNSK ADAIITNTSSNSKRN ITNTSSNSK ETYDQFKMKDSAFTL FKMKDSAFT TSQTNFNNSQSNNVL FNNSQSNNV TYDQFKMKDSAFTLL FKMKDSAFT SQTNFNNSQSNNVLT FNNSQSNNV QTNFNNSQSNNVLTN FNNSQSNNV DQFKMKDSAFTLLDV FKMKDSAFT TNFNNSQSNNVLTNY FNNSQSNNV YDQFKMKDSAFTLLD FKMKDSAFT DAIITNTSSNSKRND ITNTSSNSK AIITNTSSNSKRNDP ITNTSSNSK ILYQENQNHSLIRSL LYQENQNHS LYQENQNHSLIRSLI LYQENQNHS ANLNKDYKNKVEELL LNKDYKNKV TIDANLNKDYKNKVE LNKDYKNKV CTIDANLNKDYKNKV DANLNKDYK IDANLNKDYKNKVEE LNKDYKNKV DANLNKDYKNKVEEL LNKDYKNKV KPQQYTFSSSFSQPT YTFSSSFSQ

		QQYTFSSSFSQPTSQ YTFSSSFSQ PQQYTFSSSFSQPTS YTFSSSFSQ VYSGNSPLQKLKNNL VYSGNSPLQ FTLLDVISNISVFDR LLDVISNIS
	HLA-DRB1*0404	TQYLNTIINSYTFKD YLNTIINSY SFNTQYLNTIINSYT YLNTIINSY ESFNTQYLNTIINSY SFNTQYLNT FNTQYLNTIINSYTF YLNTIINSY NTQYLNTIINSYTFK YLNTIINSY NKVEELLNSSTDDQA LLNSSTDDQ KNKVEELLNSSTDDQ VEELLNSST KVEELLNSSTDDQAK LLNSSTDDQ VEELLNSSTDDQAKI LLNSSTDDQ EELLNSSTDDQAKIS LLNSSTDDQ QYLNTIINSYTFKDK YLNTIINSY YLNTIINSYTFKDKL YLNTIINSY NYADAIITNTSSNSK IITNTSSNS YADAIITNTSSNSKR ITNTSSNSK ADAIITNTSSNSKRN ITNTSSNSK DAIITNTSSNSKRND ITNTSSNSK AIITNTSSNSKRNDP ITNTSSNSK QAIQTVPNNTSTPNQ TVPNNTSTP ELLNSSTDDQAKISI LLNSSTDDQ GSIMNILYQENQNHS ILYQENQNH LLNSSTDDQAKISIN LLNSSTDDQ FGSIMNILYQENQNH IMNILYQEN AIQTVPNNTSTPNQS TVPNNTSTP LNYADAIITNTSSNS YADAIITNT IQTVPNNTSTPNQSI TVPNNTSTP AQAIQTVPNNTSTPN TVPNNTSTP SIMNILYQENQNHSL ILYQENQNH SAQAIQTVPNNTSTP IQTVPNNTS IMNILYQENQNHSLI ILYQENQNH SQASPVASPATNVQA VASPATNVQ ASQASPVASPATNVQ PVASPATNV ASPVASPATNVQATP VASPATNVQ
	HLA-DRB1*0405	IASAQAIQTVPNNTS AQAIQTVPN ASAQAIQTVPNNTST IQTVPNNTS SAQAIQTVPNNTSTP IQTVPNNTS AQAIQTVPNNTSTPN IQTVPNNTS QAIQTVPNNTSTPNQ IQTVPNNTS AIQTVPNNTSTPNQS IQTVPNNTS IQTVPNNTSTPNQSI IQTVPNNTS ASPATNVQATPPKQI TNVQATPPK SGLGIQISLESTLEE LGIQISLES SPATNVQATPPKQIA VQATPPKQI PATNVQATPPKQIAS VQATPPKQI KMKDSAFTLLDVISN KDSAFTLLD LGIQISLESTLEEIE ISLESTLEE LTNYRHQTQPSFVVP HQTQPSFVV GIQISLESTLEEIEK ISLESTLEE VLTNYRHQTQPSFVV YRHQTQPSF GLGIQISLESTLEEI ISLESTLEE ATNVQATPPKQIASA VQATPPKQI EKKIESFNTQYLNTI IESFNTQYL IQISLESTLEEIEKK ISLESTLEE TNVQATPPKQIASAQ VQATPPKQI

		KKIESFNTQYLNTII IESFNTQYL TNYRHQTQPSFVVPV HQTQPSFVV DQFKMKDSAFTLLDV KDSAFTLLD YDQFKMKDSAFTLLD FKMKDSAFT TQYLNTIINSYTFKD LNTIINSYT
	HLA-DRB1*0701	TQYLNTIINSYTFKD YLNTIINSY NQNHSLIRSLIISGL HSLIRSLII QNHSLIRSLIISGLG HSLIRSLII FNTQYLNTIINSYTF YLNTIINSY NTQYLNTIINSYTFK YLNTIINSY ADAIITNTSSNSKRN ITNTSSNSK NYADAIITNTSSNSK IITNTSSNS YADAIITNTSSNSKR ITNTSSNSK VLTNYRHQTQPSFVV RHQTQPSFV TNYRHQTQPSFVVPV HQTQPSFVV YQENQNHSLIRSLII NHSLIRSLI QENQNHSLIRSLIIS HSLIRSLII SQTNFNNSQSNNVLT FNNSQSNNV DAIITNTSSNSKRND ITNTSSNSK ENQNHSLIRSLIISG HSLIRSLII TSQTNFNNSQSNNVL FNNSQSNNV QTNFNNSQSNNVLTN FNNSQSNNV TNFNNSQSNNVLTNY FNNSQSNNV LTNYRHQTQPSFVVP HQTQPSFVV SFNTQYLNTIINSYT YLNTIINSY PTSQTNFNNSQSNNV NFNNSQSNN
	HLA-DRB1*0802	None
	HLA-DRB1*0901	QQYTFSSSFSQPTSQ YTFSSSFSQ KPQQYTFSSSFSQPT YTFSSSFSQ PQQYTFSSSFSQPTS YTFSSSFSQ IIKPQQYTFSSSFSQ IIKPQQYTF IKPQQYTFSSSFSQP YTFSSSFSQ KKEWLNYADAIITNT WLNYADAII AEKKEWLNYADAIIT WLNYADAII EKKEWLNYADAIITN WLNYADAII KEWLNYADAIITNTS WLNYADAII QYTFSSSFSQPTSQT YTFSSSFSQ YTFSSSFSQPTSQTN YTFSSSFSQ LAEKKEWLNYADAII LAEKKEWLN TPPKQIASAQAIQTV KQIASAQAI ATPPKQIASAQAIQT KQIASAQAI HSLIRSLIISGLGIQ LIRSLIISG PPKQIASAQAIQTVP KQIASAQAI SLIRSLIISGLGIQI LIISGLGIQ LIRSLIISGLGIQIS LIISGLGIQ IRSLIISGLGIQISL LIISGLGIQ RSLIISGLGIQISLE LIISGLGIQ QTNFNNSQSNNVLTN FNNSQSNNV SQTNFNNSQSNNVLT FNNSQSNNV TNFNNSQSNNVLTNY FNNSQSNNV
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NSPLQKLKNNLLRRI LQKLKNNLL SPLQKLKNNLLRRIA LKNNLLRRI PLQKLKNNLLRRIAE LKNNLLRRI LQKLKNNLLRRIAEE LKNNLLRRI QSLGQYIKNKYLDKM LGQYIKNKY

		QKLKNNLLRRIAEEK LKNNLLRRI
		SLGQYIKNKYLDKMQ LGQYIKNKY
		LGQYIKNKYLDKMQD LGQYIKNKY
		PQSLGQYIKNKYLDK LGQYIKNKY
		DPQSLGQYIKNKYLD LGQYIKNKY
		TQYLNTIINSYTFKD LNTIINSYT
		NDPQSLGQYIKNKYL LGQYIKNKY
		FNTQYLNTIINSYTF YLNTIINSY
		RNDPQSLGQYIKNKY PQSLGQYIK
		SFNTQYLNTIINSYT YLNTIINSY
		KLKNNLLRRIAEEKN LKNNLLRRI
		NTQYLNTIINSYTFK YLNTIINSY
		QYLNTIINSYTFKDK LNTIINSYT
		AQAIQTVPNNTSTPN IQTVPNNTS
		QAIQTVPNNTSTPNQ VPNNTSTPN
		LKNNLLRRIAEEKNK LKNNLLRRI
		FTLLDVISNISVFDR LLDVISNIS
		ESFNTQYLNTIINSY FNTQYLNTI
		HSLIRSLIISGLGIQ IRSLIISGL
		YLNTIINSYTFKDKL IINSYTFKD
		SLIISGLGIQISLES LIISGLGIQ
		SLIRSLIISGLGIQI IRSLIISGL
		LIISGLGIQISLEST LGIQISLES
		IQTVPNNTSTPNQSI VPNNTSTPN
		AIQTVPNNTSTPNQS VPNNTSTPN
		TLLDVISNISVFDRG ISNISVFDR
		IISGLGIQISLESTL LGIQISLES
		LLDVISNISVFDRGS ISNISVFDR
		ISGLGIQISLESTLE LGIQISLES
		GNSPLQKLKNNLLRR LQKLKNNLL
		LIRSLIISGLGIQIS LIISGLGIQ
		IRSLIISGLGIQISL LIISGLGIQ
		YADAIITNTSSNSKR IITNTSSNS
		NYADAIITNTSSNSK IITNTSSNS
		RQSALDLYLNITEIR ALDLYLNIT
		ADAIITNTSSNSKRN IITNTSSNS
		SGLGIQISLESTLEE LGIQISLES
		DAIITNTSSNSKRND IITNTSSNS
		SGNSPLQKLKNNLLR LQKLKNNLL
		TEFGSIMNILYQENQ FGSIMNILY
		LNTIINSYTFKDKLK LNTIINSYT
		YSGNSPLQKLKNNLL YSGNSPLQK
		AFTLLDVISNISVFD LLDVISNIS
		QGLNPANQVNPGNPM LNPANQVNP
		TTEFGSIMNILYQEN FGSIMNILY
		DQAKISINTGSNATK ISINTGSNA
		NQNHSLIRSLIISGL LIRSLIISG
		LNYADAIITNTSSNS LNYADAIIT
		KTTEFGSIMNILYQE FGSIMNILY
		DDQAKISINTGSNAT ISINTGSNA
		AKISINTGSNATKNK ISINTGSNA
		QAKISINTGSNATKN ISINTGSNA
		QTVPNNTSTPNQSII VPNNTSTPN
		NHSLIRSLIISGLGI IRSLIISGL
		TNFNNSQSNNVLTNY FNNSQSNNV
		LNPANQVNPGNPMQI NQVNPGNPM
		LDVISNISVFDRGSA ISNISVFDR

		TKNKTNIKVAGLQKN NKTNIKVAG NFNNSQSNNVLTNYR FNNSQSNNV QNHSLIRSLIISGLG IRSLIISGL FNNSQSNNVLTNYRH FNNSQSNNV GQYIKNKYLDKMQDA IKNKYLDKM QYIKNKYLDKMQDAR IKNKYLDKM SAFTLLDVISNISVF LLDVISNIS GLNPANQVNPGNPMQ NQVNPGNPM RSLIISGLGIQISLE LIISGLGIQ AIITNTSSNSKRNDP IITNTSSNS AKTTEFGSIMNILYQ FGSIMNILY KISINTGSNATKNKT ISINTGSNA QTNFNNSQSNNVLTN FNNSQSNNV DSAFTLLDVISNISV LLDVISNIS SQTNFNNSQSNNVLT FNNSQSNNV TSQTNFNNSQSNNVL FNNSQSNNV QAKTTEFGSIMNILY EFGSIMNIL GLGIQISLESTLEEI LGIQISLES LGIQISLESTLEEIE LGIQISLES KDSAFTLLDVISNIS FTLLDVISN EFGSIMNILYQENQN FGSIMNILY NKTNIKVAGLQKNTQ IKVAGLQKN ANLNKDYKNKVEELL LNKDYKNKV PTSQTNFNNSQSNNV NFNNSQSNN DVISNISVFDRGSAP ISNISVFDR PANQVNPGNPMQIAN NQVNPGNPM NPANQVNPGNPMQIA NQVNPGNPM TDDQAKISINTGSNA AKISINTGS SQSNNVLTNYRHQTQ SNNVLTNYR ISINTGSNATKNKTN ISINTGSNA SAQAIQTVPNNTSTP IQTVPNNTS NSQSNNVLTNYRHQT SNNVLTNYR NIKVAGLQKNTQSKK IKVAGLQKN
	HLA-DRB1*1501	NSPLQKLKNNLLRRI QKLKNNLLR SPLQKLKNNLLRRIA QKLKNNLLR HSLIRSLIISGLGIQ LIRSLIISG PLQKLKNNLLRRIAE QKLKNNLLR NQNHSLIRSLIISGL LIRSLIISG GNSPLQKLKNNLLRR LQKLKNNLL QNHSLIRSLIISGLG LIRSLIISG NHSLIRSLIISGLGI LIRSLIISG TQYLNTIINSYTFKD YLNTIINSY
	HLA-DRB3*0101	None
	HLA-DRB4*0101	YSGNSPLQKLKNNLL SPLQKLKNN NSPLQKLKNNLLRRI LQKLKNNLL SPLQKLKNNLLRRIA LQKLKNNLL GNSPLQKLKNNLLRR LQKLKNNLL SGNSPLQKLKNNLLR LQKLKNNLL
	HLA-DRB5*0101	RETYDQFKMKDSAFT YDQFKMKDS ETYDQFKMKDSAFTL FKMKDSAFT TYDQFKMKDSAFTLL FKMKDSAFT YDQFKMKDSAFTLLD FKMKDSAFT DQFKMKDSAFTLLDV FKMKDSAFT
NP_045742.1| hypothetical protein BBA69 [Borrelia	HLA-DRB1*0101	IKINIITMILTLICI IITMILTLI IIKINIITMILTLIC IITMILTLI

burgdorferi B31] Seq36		KINIITMILTLICIS IITMILTLI INIITMILTLICISC IITMILTLI NIIKINIITMILTLI INIITMILT SDEKFMGTTASELKA FMGTTASEL ASDEKFMGTTASELK FMGTTASEL DEKFMGTTASELKAI FMGTTASEL EKFMGTTASELKAIG FMGTTASEL AKITNEESNLLDTYI ITNEESNLL NIITMILTLICISCA IITMILTLI QIAKITNEESNLLDT ITNEESNLL IAKITNEESNLLDTY ITNEESNLL IQIAKITNEESNLLD ITNEESNLL DIQIAKITNEESNLL IAKITNEES GASDEKFMGTTASEL EKFMGTTAS IITMILTLICISCAP IITMILTLI NKYYKDSDSLQSAFY YKDSDSLQS HFNKYYKDSDSLQSA YKDSDSLQS FNKYYKDSDSLQSAF YKDSDSLQS EHFNKYYKDSDSLQS NKYYKDSDS LNIIKINIITMILTL INIITMILT KLNIIKINIITMILT IKINIITMI KFMGTTASELKAIGK FMGTTASEL IAANFLYRIALDIQL IAANFLYRI KITNEESNLLDTYIR ITNEESNLL FMGTTASELKAIGKE FMGTTASEL ITNEESNLLDTYIRA ITNEESNLL PKIAANFLYRIALDI IAANFLYRI ENDPKIAANFLYRIA IAANFLYRI YENDPKIAANFLYRI DPKIAANFL KNQYDIQIAKITNEE YDIQIAKIT NQYDIQIAKITNEES YDIQIAKIT RKNQYDIQIAKITNE YDIQIAKIT NDPKIAANFLYRIAL IAANFLYRI EDRKNQYDIQIAKIT RKNQYDIQI DRKNQYDIQIAKITN YDIQIAKIT DPKIAANFLYRIALD IAANFLYRI AKLNIIKINIITMIL IKINIITMI ANFLYRIALDIQLKL YRIALDIQL AANFLYRIALDIQLK YRIALDIQL NFLYRIALDIQLKLE YRIALDIQL ITMILTLICISCAPF ITMILTLIC ENEKMLLKRFLLSSL MLLKRFLLS EKMLLKRFLLSSLDY MLLKRFLLS FLYRIALDIQLKLEK YRIALDIQL NEKMLLKRFLLSSLD MLLKRFLLS APFNKINPKANENTK INPKANENT CAPFNKINPKANENT FNKINPKAN TMILTLICISCAPFN LTLICISCA FNKINPKANENTKLK INPKANENT KIAANFLYRIALDIQ IAANFLYRI PFNKINPKANENTKL INPKANENT KMLLKRFLLSSLDYK LKRFLLSSL MLLKRFLLSSLDYKK LKRFLLSSL MILTLICISCAPFNK ICISCAPFN LQLQEKFKKTLNKTL KFKKTLNKT LQEKFKKTLNKTLED FKKTLNKTL QLQEKFKKTLNKTLE FKKTLNKTL

		NENEKMLLKRFLLSS MLLKRFLLS QEKFKKTLNKTLEDY FKKTLNKTL
	HLA-DRB1*0301	None
	HLA-DRB1*0401	EDYRKNTNNIQENKV YRKNTNNIQ LEDYRKNTNNIQENK YRKNTNNIQ TLEDYRKNTNNIQEN YRKNTNNIQ KTLEDYRKNTNNIQE YRKNTNNIQ NKTLEDYRKNTNNIQ LEDYRKNTN YRKNTNNIQENKVLA YRKNTNNIQ DYRKNTNNIQENKVL YRKNTNNIQ EHFNKYYKDSDSLQS YYKDSDSLQ HFNKYYKDSDSLQSA YKDSDSLQS FNKYYKDSDSLQSAF YKDSDSLQS NKYYKDSDSLQSAFY YKDSDSLQS EKLINNYENDPKIAA LINNYENDP KLINNYENDPKIAAN YENDPKIAA LINNYENDPKIAANF YENDPKIAA NNYENDPKIAANFLY YENDPKIAA INNYENDPKIAANFL YENDPKIAA DIQIAKITNEESNLL IAKITNEES IQIAKITNEESNLLD ITNEESNLL
	HLA-DRB1*0404	None
	HLA-DRB1*0405	IQIAKITNEESNLLD IAKITNEES DIQIAKITNEESNLL IAKITNEES NQYDIQIAKITNEES QIAKITNEE QYDIQIAKITNEESN IAKITNEES YDIQIAKITNEESNL IAKITNEES IIKINIITMILTLIC INIITMILT IKINIITMILTLICI ITMILTLIC QIAKITNEESNLLDT IAKITNEES KINIITMILTLICIS ITMILTLIC INIITMILTLICISC ITMILTLIC IAKITNEESNLLDTY IAKITNEES NIITMILTLICISCA ITMILTLIC LEDYRKNTNNIQENK YRKNTNNIQ EDYRKNTNNIQENKV YRKNTNNIQ TLEDYRKNTNNIQEN YRKNTNNIQ KTLEDYRKNTNNIQE YRKNTNNIQ EILEKLINNYENDPK LEKLINNYE EKLINNYENDPKIAA INNYENDPK KEILEKLINNYENDP LEKLINNYE LKEILEKLINNYEND LEKLINNYE TLKEILEKLINNYEN LEKLINNYE EHFNKYYKDSDSLQS FNKYYKDSD
	HLA-DRB1*0701	DEKFMGTTASELKAI FMGTTASEL EKFMGTTASELKAIG FMGTTASEL GASDEKFMGTTASEL KFMGTTASE ASDEKFMGTTASELK FMGTTASEL SDEKFMGTTASELKA FMGTTASEL KFMGTTASELKAIGK FMGTTASEL FMGTTASELKAIGKE FMGTTASEL LQLQEKFKKTLNKTL KFKKTLNKT QEKFKKTLNKTLEDY FKKTLNKTL QLQEKFKKTLNKTLE FKKTLNKTL LQEKFKKTLNKTLED FKKTLNKTL

		EKFKKTLNKTLEDYR FKKTLNKTL
	HLA-DRB1*0802	TKLKKNTRLKKPANP LKKNTRLKK
		ENTKLKKNTRLKKPA LKKNTRLKK
		NTKLKKNTRLKKPAN LKKNTRLKK
		ANENTKLKKNTRLKK ENTKLKKNT
		NENTKLKKNTRLKKP LKKNTRLKK
	HLA-DRB1*0901	None
	HLA-DRB1*1101	ENTKLKKNTRLKKPA LKKNTRLKK
		ANENTKLKKNTRLKK ANENTKLKK
		NTKLKKNTRLKKPAN LKKNTRLKK
		NENTKLKKNTRLKKP LKKNTRLKK
		TKLKKNTRLKKPANP LKKNTRLKK
		KLKKNTRLKKPANPG LKKNTRLKK
		LKKNTRLKKPANPGE LKKNTRLKK
	HLA-DRB1*1302	KLNIIKINIITMILT IKINIITMI
		LNIIKINIITMILTL IKINIITMI
		NIIKINIITMILTLI IKINIITMI
		IIKINIITMILTLIC INIITMILT
		IKINIITMILTLICI INIITMILT
		AKLNIIKINIITMIL IKINIITMI
		KAKLNIIKINIITMI LNIIKINII
		KINIITMILTLICIS INIITMILT
		INIITMILTLICISC INIITMILT
		KKAKLNIIKINIITM LNIIKINII
		MKKAKLNIIKINIIT LNIIKINII
		NIITMILTLICISCA IITMILTLI
		IITMILTLICISCAP IITMILTLI
		ANENTKLKKNTRLKK NTKLKKNTR
		NENTKLKKNTRLKKP LKKNTRLKK
		ENTKLKKNTRLKKPA LKKNTRLKK
		NTKLKKNTRLKKPAN LKKNTRLKK
		TKLKKNTRLKKPANP LKKNTRLKK
		RKNQYDIQIAKITNE YDIQIAKIT
		NQYDIQIAKITNEES IQIAKITNE
		KNQYDIQIAKITNEE IQIAKITNE
	HLA-DRB1*1501	KMLLKRFLLSSLDYK LKRFLLSSL
		MLLKRFLLSSLDYKK LKRFLLSSL
		ENEKMLLKRFLLSSL MLLKRFLLS
		NEKMLLKRFLLSSLD LKRFLLSSL
		EKMLLKRFLLSSLDY LKRFLLSSL
		LLKRFLLSSLDYKKE LKRFLLSSL
		LKRFLLSSLDYKKEN LKRFLLSSL
		NENEKMLLKRFLLSS MLLKRFLLS
		INIITMILTLICISC IITMILTLI
	HLA-DRB3*0101	None
	HLA-DRB4*0101	NFLYRIALDIQLKLE LYRIALDIQ
		ANFLYRIALDIQLKL LYRIALDIQ
		IAANFLYRIALDIQL LYRIALDIQ
		AANFLYRIALDIQLK LYRIALDIQ
		KIAANFLYRIALDIQ FLYRIALDI
		LYRIALDIQLKLEKH LYRIALDIQ
		FLYRIALDIQLKLEK LYRIALDIQ
		NKTLEDYRKNTNNIQ LEDYRKNTN
		KTLEDYRKNTNNIQE YRKNTNNIQ
	HLA-DRB5*0101	APFNKINPKANENTK FNKINPKAN
		CAPFNKINPKANENT FNKINPKAN

		CISCAPFNKINPKAN ISCAPFNKI ISCAPFNKINPKANE FNKINPKAN SCAPFNKINPKANEN FNKINPKAN FNKINPKANENTKLK FNKINPKAN
AAT93826.1| conserved hypothetical protein BBA69[Borrelia garinii PBi] Seq37	HLA-DRB1*0101	KLNIIKLNILTTTLT KLNILTTTL LNIIKLNILTTTLTL LNILTTTLT NIIKLNILTTTLTLI LNILTTTLT IIKLNILTTTLTLIC LNILTTTLT IKLNILTTTLTLICI LNILTTTLT KLNILTTTLTLICIS LNILTTTLT LNILTTTLTLICISC LNILTTTLT EPLREKYPEATASKL LREKYPEAT DEKMQMKKIIYSSLN MQMKKIIYS EDEKMQMKKIIYSSL MQMKKIIYS EKMQMKKIIYSSLNY MQMKKIIYS TKLNIIKLNILTTTL IKLNILTTT PEDEKMQMKKIIYSS MQMKKIIYS LPEDEKMQMKKIIYS DEKMQMKKI IKENFKKALNKTIDA FKKALNKTI LREKYPEATASKLET YPEATASKL KTKLNIIKLNILTTT IIKLNILTT KENFKKALNKTIDAY FKKALNKTI PLREKYPEATASKLE YPEATASKL KLETTLKILEAQKEK LKILEAQKE KIKENFKKALNKTID FKKALNKTI SKLETTLKILEAQKE ETTLKILEA LKIKENFKKALNKTI NFKKALNKT ETTLKILEAQKEKEN LKILEAQKE LETTLKILEAQKEKE LKILEAQKE NILTTTLTLICISCA LTTTLTLIC TTLKILEAQKEKENI LKILEAQKE ENFKKALNKTIDAYN FKKALNKTI MQMKKIIYSSLNYET MQMKKIIYS ILTTTLTLICISCAV LTLICISCA LEPLREKYPEATASK LREKYPEAT REKYPEATASKLETT YPEATASKL EKYPEATASKLETTL YPEATASKL KMQMKKIIYSSLNYE MQMKKIIYS DLEPLREKYPEATAS LREKYPEAT KDLEPLREKYPEATA LREKYPEAT NKDLEPLREKYPEAT LEPLREKYP LTTTLTLICISCAVN LTLICISCA KKTKLNIIKLNILTT LNIIKLNIL TTTLTLICISCAVNK LTLICISCA NFKKALNKTIDAYNQ FKKALNKTI
	HLA-DRB1*0301	None
	HLA-DRB1*0401	QEILEKLDKNLQHKK LEKLDKNLQ EILEKLDKNLQHKKI LEKLDKNLQ QIDFLKTFKTDPHDS LKTFKTDPH LQEILEKLDKNLQHK LEKLDKNLQ IIKLNILTTTLTLIC LNILTTTLT NTQIDFLKTFKTDPH FLKTFKTDP IDFLKTFKTDPHDSL LKTFKTDPH ILQEILEKLDKNLQH LEKLDKNLQ

		TQIDFLKTFKTDPHD LKTFKTDPH IKLNILTTTLTLICI LNILTTTLT KILQEILEKLDKNLQ EILEKLDKN KLNIIKLNILTTTLT IIKLNILTT LNIIKLNILTTTLTL LNILTTTLT NIIKLNILTTTLTLI LNILTTTLT DFLKTFKTDPHDSLP LKTFKTDPH INENYKEFNSLKPIY YKEFNSLKP
	HLA-DRB1*0404	IDFLKTFKTDPHDSL FLKTFKTDP NTQIDFLKTFKTDPH FLKTFKTDP TQIDFLKTFKTDPHD FLKTFKTDP QIDFLKTFKTDPHDS FLKTFKTDP DNTQIDFLKTFKTDP IDFLKTFKT DFLKTFKTDPHDSLP FLKTFKTDP IIKLNILTTTLTLIC KLNILTTTL FLKTFKTDPHDSLPE FLKTFKTDP NIIKLNILTTTLTLI KLNILTTTL KLNIIKLNILTTTLT KLNILTTTL LNIIKLNILTTTLTL KLNILTTTL
	HLA-DRB1*0405	KHINENYKEFNSLKP NYKEFNSLK HINENYKEFNSLKPI YKEFNSLKP INENYKEFNSLKPIY YKEFNSLKP ENIKNFVNKFQDLEP IKNFVNKFQ MQMKKIIYSSLNYET KKIIYSSLN
	HLA-DRB1*0701	IIKLNILTTTLTLIC ILTTTLTLI IKLNILTTTLTLICI ILTTTLTLI NIIKLNILTTTLTLI LNILTTTLT EPLREKYPEATASKL LREKYPEAT PLREKYPEATASKLE YPEATASKL LREKYPEATASKLET YPEATASKL REKYPEATASKLETT YPEATASKL EKYPEATASKLETTL YPEATASKL KLNILTTTLTLICIS ILTTTLTLI
	HLA-DRB1*0802	None
	HLA-DRB1*0901	LKIKENFKKALNKTI IKENFKKAL KENFKKALNKTIDAY FKKALNKTI IKENFKKALNKTIDA FKKALNKTI KIKENFKKALNKTID FKKALNKTI ENFKKALNKTIDAYN FKKALNKTI
	HLA-DRB1*1101	None
	HLA-DRB1*1302	KLNIIKLNILTTTLT IKLNILTTT LNIIKLNILTTTLTL LNILTTTLT NIIKLNILTTTLTLI LNILTTTLT IIKLNILTTTLTLIC LNILTTTLT IKLNILTTTLTLICI LNILTTTLT KTKLNIIKLNILTTT LNIIKLNIL TKLNIIKLNILTTTL IKLNILTTT KLNILTTTLTLICIS LNILTTTLT LNILTTTLTLICISC LNILTTTLT KKTKLNIIKLNILTT LNIIKLNIL MKKTKLNIIKLNILT LNIIKLNIL QSRLDIISKVIKNPI LDIISKVIK SRLDIISKVIKNPIK ISKVIKNPI RLDIISKVIKNPIKD ISKVIKNPI DIISKVIKNPIKDEL ISKVIKNPI LDIISKVIKNPIKDE ISKVIKNPI

		IISKVIKNPIKDELQ IKNPIKDEL ISKVIKNPIKDELQI IKNPIKDEL YDIPIIIQSRLDIIS IPIIIQSRL FIYDIPIIIQSRLDI IPIIIQSRL IYDIPIIIQSRLDII IPIIIQSRL IIIQSRLDIISKVIK IIIQSRLDI IPIIIQSRLDIISKV IIIQSRLDI IQSRLDIISKVIKNP LDIISKVIK EDEKMQMKKIIYSSL MQMKKIIYS DIPIIIQSRLDIISK IIIQSRLDI IIQSRLDIISKVIKN LDIISKVIK EKMQMKKIIYSSLNY MQMKKIIYS KNFIYDIPIIIQSRL FIYDIPIII DEKMQMKKIIYSSLN MQMKKIIYS MQMKKIIYSSLNYET MQMKKIIYS KMQMKKIIYSSLNYE MQMKKIIYS PEDEKMQMKKIIYSS MQMKKIIYS NFIYDIPIIIQSRLD IPIIIQSRL LPEDEKMQMKKIIYS EKMQMKKII NPIKDELQILNQKEI IKDELQILN IKDELQILNQKEIEE LQILNQKEI PIKDELQILNQKEIE LQILNQKEI KDELQILNQKEIEEL LQILNQKEI
	HLA-DRB1*1501	IEELLMRIESELKIK LMRIESELK EIEELLMRIESELKI LMRIESELK KEIEELLMRIESELK LLMRIESEL EELLMRIESELKIKE LMRIESELK ELLMRIESELKIKEN LMRIESELK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	ILQEILEKLDKNLQH LEKLDKNLQ LQEILEKLDKNLQHK LEKLDKNLQ QEILEKLDKNLQHKK LEKLDKNLQ EILEKLDKNLQHKKI LEKLDKNLQ KILQEILEKLDKNLQ ILQEILEKL
	HLA-DRB5*0101	LKIKENFKKALNKTI LKIKENFKK NKFQDLEPSKKQNKD FQDLEPSKK VNKFQDLEPSKKQNK FQDLEPSKK ESELKIKENFKKALN LKIKENFKK IESELKIKENFKKAL LKIKENFKK SELKIKENFKKALNK LKIKENFKK RIESELKIKENFKKA LKIKENFKK MRIESELKIKENFKK IESELKIKE KFQDLEPSKKQNKDL LEPSKKQNK
NP_045573.1| hypothetical protein BBI42 [Borrelia burgdorferi B31] Seq38	HLA-DRB1*0101	PEYYRNMPRPTAYQQ YRNMPRPTA SPEYYRNMPRPTAYQ YRNMPRPTA GSPEYYRNMPRPTAY YRNMPRPTA EGSPEYYRNMPRPTA YYRNMPRPT EYYRNMPRPTAYQQY YRNMPRPTA MRILVGVCIIALALL MRILVGVCI YYRNMPRPTAYQQYL YRNMPRPTA LKDPNYRGVVLPVSD YRGVVLPVS DPNYRGVVLPVSDYN YRGVVLPVS SLKDPNYRGVVLPVS LKDPNYRGV KDPNYRGVVLPVSDY YRGVVLPVS PNYRGVVLPVSDYNE YRGVVLPVS

		YRNMPRPTAYQQYLK YRNMPRPTA NKFFLDLGSEQSKDL FLDLGSEQS KFFLDLGSEQSKDLI FLDLGSEQS ILVGVCIIALALLGC VCIIALALL LVGVCIIALALLGCY VCIIALALL RILVGVCIIALALLG VCIIALALL VGVCIIALALLGCYL VCIIALALL EGIFSSLKLYASEHR FSSLKLYAS GIFSSLKLYASEHRL FSSLKLYAS FNKFFLDLGSEQSKD FLDLGSEQS YFNKFFLDLGSEQSK FLDLGSEQS EYFNKFFLDLGSEQS FNKFFLDLG TEGIFSSLKLYASEH FSSLKLYAS GVCIIALALLGCYLP IIALALLGC IVTEGIFSSLKLYAS IVTEGIFSS VTEGIFSSLKLYASE FSSLKLYAS VCIIALALLGCYLPD IIALALLGC VKRYDYNRPVPILPT YNRPVPILP NYRGVVLPVSDYNEE YRGVVLPVS FFLDLGSEQSKDLIK FLDLGSEQS FLDLGSEQSKDLIKL FLDLGSEQS YRGVVLPVSDYNEEY YRGVVLPVS FSSLKLYASEHRLLV FSSLKLYAS IFSSLKLYASEHRLL FSSLKLYAS KVKRYDYNRPVPILP YDYNRPVPI EEGSPEYYRNMPRPT EYYRNMPRP NKFMRIVRWLYSCIE MRIVRWLYS KFMRIVRWLYSCIEE VRWLYSCIE CIIALALLGCYLPDN IIALALLGC SSLKLYASEHRLLVE LKLYASEHR IIALALLGCYLPDNQ IIALALLGC FMRIVRWLYSCIEEL VRWLYSCIE MRIVRWLYSCIEELY VRWLYSCIE QTFFENSESSDMGSD FENSESSDM TFFENSESSDMGSDE FENSESSDM VQTFFENSESSDMGS FENSESSDM AVQTFFENSESSDMG FENSESSDM QAVQTFFENSESSDM TFFENSESS RNMPRPTAYQQYLKV MPRPTAYQQ LDLGSEQSKDLIKLF LGSEQSKDL
	HLA-DRB1*0301	None
	HLA-DRB1*0401	DLIKLFIMVKNEQNN LFIMVKNEQ IKLFIMVKNEQNNNK LFIMVKNEQ KDLIKLFIMVKNEQN LFIMVKNEQ LIKLFIMVKNEQNNN LFIMVKNEQ SKDLIKLFIMVKNEQ IKLFIMVKN PEYYRNMPRPTAYQQ YRNMPRPTA SPEYYRNMPRPTAYQ YRNMPRPTA EGSPEYYRNMPRPTA YYRNMPRPT GSPEYYRNMPRPTAY YRNMPRPTA KLFIMVKNEQNNNKF LFIMVKNEQ EYYRNMPRPTAYQQY YRNMPRPTA LFIMVKNEQNNNKFM LFIMVKNEQ EYFNKFFLDLGSEQS FFLDLGSEQ YYRNMPRPTAYQQYL YRNMPRPTA QNNNKFMRIVRWLYS FMRIVRWLY

		NNNKFMRIVRWLYSC FMRIVRWLY YFNKFFLDLGSEQSK FFLDLGSEQ
	HLA-DRB1*0404	IKLFIMVKNEQNNNK LFIMVKNEQ DLIKLFIMVKNEQNN LFIMVKNEQ LIKLFIMVKNEQNNN LFIMVKNEQ KLFIMVKNEQNNNKF VKNEQNNNK LFIMVKNEQNNNKFM VKNEQNNNK KDLIKLFIMVKNEQN LFIMVKNEQ SKDLIKLFIMVKNEQ IKLFIMVKN
	HLA-DRB1*0405	NKFMRIVRWLYSCIE MRIVRWLYS KFMRIVRWLYSCIEE MRIVRWLYS FMRIVRWLYSCIEEL VRWLYSCIE PEYYRNMPRPTAYQQ YRNMPRPTA SPEYYRNMPRPTAYQ YRNMPRPTA KDLIKLFIMVKNEQN IKLFIMVKN GSPEYYRNMPRPTAY YRNMPRPTA EYYRNMPRPTAYQQY YRNMPRPTA EGSPEYYRNMPRPTA YYRNMPRPT MRIVRWLYSCIEELY VRWLYSCIE DLIKLFIMVKNEQNN FIMVKNEQN IKLFIMVKNEQNNNK FIMVKNEQN LIKLFIMVKNEQNNN FIMVKNEQN KLFIMVKNEQNNNKF FIMVKNEQN RIVRWLYSCIEELYS VRWLYSCIE NNKFMRIVRWLYSCI MRIVRWLYS NNNKFMRIVRWLYSC MRIVRWLYS QNNNKFMRIVRWLYS FMRIVRWLY YYRNMPRPTAYQQYL YRNMPRPTA YRNMPRPTAYQQYLK YRNMPRPTA LFIMVKNEQNNNKFM FIMVKNEQN IVRWLYSCIEELYSP VRWLYSCIE
	HLA-DRB1*0701	NNKFMRIVRWLYSCI FMRIVRWLY NKFMRIVRWLYSCIE FMRIVRWLY QNNNKFMRIVRWLYS FMRIVRWLY NNNKFMRIVRWLYSC FMRIVRWLY KFMRIVRWLYSCIEE MRIVRWLYS
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	EYYRNMPRPTAYQQY YRNMPRPTA PEYYRNMPRPTAYQQ YRNMPRPTA EGSPEYYRNMPRPTA YYRNMPRPT GSPEYYRNMPRPTAY YRNMPRPTA SPEYYRNMPRPTAYQ YRNMPRPTA YYRNMPRPTAYQQYL YRNMPRPTA YRNMPRPTAYQQYLK YRNMPRPTA
	HLA-DRB1*1302	SKDLIKLFIMVKNEQ IKLFIMVKN KDLIKLFIMVKNEQN IKLFIMVKN DLIKLFIMVKNEQNN IKLFIMVKN IKLFIMVKNEQNNNK LFIMVKNEQ HRLLVEIKKTLISLK VEIKKTLIS LIKLFIMVKNEQNNN LFIMVKNEQ EQSKDLIKLFIMVKN SKDLIKLFI RLLVEIKKTLISLKD VEIKKTLIS QSKDLIKLFIMVKNE IKLFIMVKN GSPEYYRNMPRPTAY YYRNMPRPT SPEYYRNMPRPTAYQ YYRNMPRPT

		PEYYRNMPRPTAYQQ YYRNMPRPT LLVEIKKTLISLKDP VEIKKTLIS EHRLLVEIKKTLISL VEIKKTLIS SEHRLLVEIKKTLIS LVEIKKTLI EGSPEYYRNMPRPTA YYRNMPRPT MRILVGVCIIALALL MRILVGVCI EYYRNMPRPTAYQQY YYRNMPRPT IMVKNEQNNNKFMRI EQNNNKFMR GVCIIALALLGCYLP IALALLGCY VCIIALALLGCYLPD LALLGCYLP VKNEQNNNKFMRIVR EQNNNKFMR MVKNEQNNNKFMRIV EQNNNKFMR LVEIKKTLISLKDPN VEIKKTLIS FIMVKNEQNNNKFMR VKNEQNNNK YYRNMPRPTAYQQYL YYRNMPRPT KNEQNNNKFMRIVRW EQNNNKFMR EQNNNKFMRIVRWLY EQNNNKFMR LVGVCIIALALLGCY VCIIALALL CIIALALLGCYLPDN LALLGCYLP VGVCIIALALLGCYL VCIIALALL VEIKKTLISLKDPNY VEIKKTLIS QNNNKFMRIVRWLYS FMRIVRWLY
	HLA-DRB1*1501	NKFMRIVRWLYSCIE MRIVRWLYS NNKFMRIVRWLYSCI MRIVRWLYS KFMRIVRWLYSCIEE MRIVRWLYS NNNKFMRIVRWLYSC MRIVRWLYS QNNNKFMRIVRWLYS FMRIVRWLY FMRIVRWLYSCIEEL MRIVRWLYS MRIVRWLYSCIEELY MRIVRWLYS EGIFSSLKLYASEHR FSSLKLYAS GIFSSLKLYASEHRL LKLYASEHR FSSLKLYASEHRLLV LKLYASEHR IFSSLKLYASEHRLL LKLYASEHR SSLKLYASEHRLLVE LKLYASEHR PNYRGVVLPVSDYNE YRGVVLPVS LKDPNYRGVVLPVSD YRGVVLPVS KDPNYRGVVLPVSDY YRGVVLPVS SLKDPNYRGVVLPVS PNYRGVVLP DPNYRGVVLPVSDYN YRGVVLPVS SKDLIKLFIMVKNEQ LIKLFIMVK KDLIKLFIMVKNEQN LIKLFIMVK EQSKDLIKLFIMVKN LIKLFIMVK QSKDLIKLFIMVKNE LIKLFIMVK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	EIKKTLISLKDPNYR LISLKDPNY KKTLISLKDPNYRGV ISLKDPNYR KTLISLKDPNYRGVV ISLKDPNYR IKKTLISLKDPNYRG ISLKDPNYR TLISLKDPNYRGVVL ISLKDPNYR LISLKDPNYRGVVLP ISLKDPNYR ISLKDPNYRGVVLPV ISLKDPNYR IIALALLGCYLPDNQ LALLGCYLP IALALLGCYLPDNQE LGCYLPDNQ ALALLGCYLPDNQEQ LGCYLPDNQ LALLGCYLPDNQEQA LGCYLPDNQ ALLGCYLPDNQEQAV LGCYLPDNQ

		NKFMRIVRWLYSCIE IVRWLYSCI KFMRIVRWLYSCIEE IVRWLYSCI FMRIVRWLYSCIEEL IVRWLYSCI
	HLA-DRB5*0101	GSPEYYRNMPRPTAY YRNMPRPTA SPEYYRNMPRPTAYQ YRNMPRPTA PEYYRNMPRPTAYQQ YRNMPRPTA EYYRNMPRPTAYQQY YRNMPRPTA EGSPEYYRNMPRPTA YYRNMPRPT IKLFIMVKNEQNNNK LFIMVKNEQ KLFIMVKNEQNNNKF VKNEQNNNK LFIMVKNEQNNNKFM VKNEQNNNK IMVKNEQNNNKFMRI VKNEQNNNK FIMVKNEQNNNKFMR VKNEQNNNK TAYQQYLKVKRYDYN YQQYLKVKR YYRNMPRPTAYQQYL YRNMPRPTA YRNMPRPTAYQQYLK YRNMPRPTA
NP_051318.1| revA protein[Borrelia burgdorferi B31] Seq39	HLA-DRB1*0101	NIFKLFFASMLFVMA FFASMLFVM IFKLFFASMLFVMAC FASMLFVMA FKLFFASMLFVMACK FASMLFVMA KLFFASMLFVMACKA FASMLFVMA LFFASMLFVMACKAY FASMLFVMA NSFQDKLAAKLAALK FQDKLAAKL DKLAAKLAALKAAKN LAAKLAALK SFQDKLAAKLAALKA LAAKLAALK FQDKLAAKLAALKAA LAAKLAALK QNSFQDKLAAKLAAL FQDKLAAKL LQNSFQDKLAAKLAA FQDKLAAKL KLAAKLAALKAAKNT LAALKAAKN NLQNSFQDKLAAKLA FQDKLAAKL FFASMLFVMACKAYV FASMLFVMA FASMLFVMACKAYVE FASMLFVMA QDKLAAKLAALKAAK LAAKLAALK LAAKLAALKAAKNTI LAALKAAKN AKLVGVTVPLLGSNT LVGVTVPLL AAKLAALKAAKNTIE LAALKAAKN EAKLVGVTVPLLGSN LVGVTVPLL LNLQNSFQDKLAAKL LNLQNSFQD SEAKLVGVTVPLLGS LVGVTVPLL KLVGVTVPLLGSNTS LVGVTVPLL AKLAALKAAKNTIEN LAALKAAKN WSEAKLVGVTVPLLG LVGVTVPLL LVGVTVPLLGSNTSG LVGVTVPLL IWSEAKLVGVTVPLL EAKLVGVTV GVTVPLLGSNTSGNG VPLLGSNTS VGVTVPLLGSNTSGN VPLLGSNTS VTVPLLGSNTSGNGD VPLLGSNTS SMLFVMACKAYVEEK FVMACKAYV ASMLFVMACKAYVEE FVMACKAYV MLFVMACKAYVEEKK FVMACKAYV KNIFKLFFASMLFVM FKLFFASML NKNIFKLFFASMLFV FKLFFASML KLAALKAAKNTIENI LAALKAAKN LAALKAAKNTIENIT LAALKAAKN MRNKNIFKLFFASML IFKLFFASM RNKNIFKLFFASMLF FKLFFASML

		TVPLLGSNTSGNGDK VPLLGSNTS VPLLGSNTSGNGDKM VPLLGSNTS LFVMACKAYVEEKKE FVMACKAYV FVMACKAYVEEKKEI FVMACKAYV
	HLA-DRB1*0301	None
	HLA-DRB1*0401	None
	HLA-DRB1*0404	AELKEKLLNLQNSFQ LKEKLLNLQ LKEKLLNLQNSFQDK LLNLQNSFQ ELKEKLLNLQNSFQD LLNLQNSFQ KEKLLNLQNSFQDKL LLNLQNSFQ EKLLNLQNSFQDKLA LLNLQNSFQ KLLNLQNSFQDKLAA LLNLQNSFQ LLNLQNSFQDKLAAK LLNLQNSFQ GVTVPLLGSNTSGNG LLGSNTSGN VTVPLLGSNTSGNGD LLGSNTSGN VGVTVPLLGSNTSGN VPLLGSNTS TVPLLGSNTSGNGDK LLGSNTSGN VPLLGSNTSGNGDKM LLGSNTSGN
	HLA-DRB1*0405	None
	HLA-DRB1*0701	None
	HLA-DRB1*0802	FFASMLFVMACKAYV LFVMACKAY FASMLFVMACKAYVE FVMACKAYV ASMLFVMACKAYVEE FVMACKAYV SMLFVMACKAYVEEK FVMACKAYV MLFVMACKAYVEEKK FVMACKAYV
	HLA-DRB1*0901	KNIFKLFFASMLFVM LFFASMLFV NIFKLFFASMLFVMA LFFASMLFV IFKLFFASMLFVMAC LFFASMLFV FKLFFASMLFVMACK LFFASMLFV NKNIFKLFFASMLFV FKLFFASML KLFFASMLFVMACKA FFASMLFVM
	HLA-DRB1*1101	None
	HLA-DRB1*1302	KLVGVTVPLLGSNTS VGVTVPLLG GVTVPLLGSNTSGNG VPLLGSNTS VTVPLLGSNTSGNGD VPLLGSNTS VGVTVPLLGSNTSGN VPLLGSNTS LVGVTVPLLGSNTSG VPLLGSNTS WSEAKLVGVTVPLLG AKLVGVTVP SEAKLVGVTVPLLGS VGVTVPLLG VPLLGSNTSGNGDKM VPLLGSNTS TVPLLGSNTSGNGDK VPLLGSNTS EAKLVGVTVPLLGSN VGVTVPLLG AKLVGVTVPLLGSNT VGVTVPLLG ELKEKLLNLQNSFQD LLNLQNSFQ LKEKLLNLQNSFQDK LLNLQNSFQ AELKEKLLNLQNSFQ LKEKLLNLQ KEKLLNLQNSFQDKL LLNLQNSFQ EKLLNLQNSFQDKLA LLNLQNSFQ
	HLA-DRB1*1501	MEDVLALVNDSSGGK VLALVNDSS EDVLALVNDSSGGKF VLALVNDSS DVLALVNDSSGGKFK LVNDSSGGK KNIFKLFFASMLFVM IFKLFFASM VLALVNDSSGGKFKD LVNDSSGGK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	AELKEKLLNLQNSFQ LKEKLLNLQ

		DIGNAELKEKLLNLQ DIGNAELKE IGNAELKEKLLNLQN LKEKLLNLQ GNAELKEKLLNLQNS LKEKLLNLQ NAELKEKLLNLQNSF LKEKLLNLQ ELKEKLLNLQNSFQD LKEKLLNLQ LKEKLLNLQNSFQDK LKEKLLNLQ KLVGVTVPLLGSNTS VGVTVPLLG
	HLA-DRB5*0101	None
NP_045737.1| BBA64 antigen, P35 [Borrelia burgdorferi B31] Seq40	HLA-DRB1*0101	IFNLGQILSKLSQDS LGQILSKLS FNLGQILSKLSQDSN LGQILSKLS GKIFNLGQILSKLSQ LGQILSKLS EGKIFNLGQILSKLS IFNLGQILS KIFNLGQILSKLSQD LGQILSKLS LGQILSKLSQDSNYR ILSKLSQDS SKIFFNANSTVHFDS FFNANSTVH KIFFNANSTVHFDSH FNANSTVHF NLGQILSKLSQDSNY ILSKLSQDS FSKIFFNANSTVHFD FFNANSTVH IFSKIFFNANSTVHF FFNANSTVH LIAIFLLHVLTVLIL LLHVLTVLI IFFNANSTVHFDSHE FNANSTVHF DIILDLVNTTTNILA LVNTTTNIL IAIFLLHVLTVLILI LLHVLTVLI NDTLRSKNSRAQFAN LRSKNSRAQ AIFLLHVLTVLILIS LLHVLTVLI LNDTLRSKNSRAQFA LRSKNSRAQ DTLRSKNSRAQFANI LRSKNSRAQ IILDLVNTTTNILAP LVNTTTNIL ILDLVNTTTNILAPI LVNTTTNIL IFLLHVLTVLILISC LLHVLTVLI HDIILDLVNTTTNIL ILDLVNTTT KLIAIFLLHVLTVLI IFLLHVLTV LDLVNTTTNILAPIQ LVNTTTNIL GQILSKLSQDSNYRG ILSKLSQDS EIFSKIFFNANSTVH IFFNANSTV YNTNPDLQTDVSKLN YNTNPDLQT SKLNDTLRSKNSRAQ NDTLRSKNS KETLINRGFSIQLAM INRGFSIQL VKETLINRGFSIQLA INRGFSIQL NKLIAIFLLHVLTVL LIAIFLLHV ETLINRGFSIQLAME INRGFSIQL TLINRGFSIQLAMEE INRGFSIQL KLNDTLRSKNSRAQF LRSKNSRAQ NNKLIAIFLLHVLTV LIAIFLLHV LKNNKLIAIFLLHVL LIAIFLLHV FFNANSTVHFDSHEY FNANSTVHF FLLHVLTVLILISCS LHVLTVLIL TLRSKNSRAQFANIH LRSKNSRAQ LLHVLTVLILISCSL LLHVLTVLI LRSKNSRAQFANIHD LRSKNSRAQ ILKNNKLIAIFLLHV LKNNKLIAI KNNKLIAIFLLHVLT LIAIFLLHV VLTVLILISCSLEVK ILISCSLEV HVLTVLILISCSLEV VLILISCSL LTVLILISCSLEVKD ILISCSLEV

		SNYRGLVKETLINRG YRGLVKETL
		LVKETLINRGFSIQL LINRGFSIQ
		IDEYNTNPDLQTDVS YNTNPDLQT
		DEYNTNPDLQTDVSK YNTNPDLQT
		LHVLTVLILISCSLE VLILISCSL
		DNILKNNKLIAIFLL LKNNKLIAI
		NILKNNKLIAIFLLH LKNNKLIAI
		KDNILKNNKLIAIFL LKNNKLIAI
		LIDEYNTNPDLQTDV YNTNPDLQT
		DLIDEYNTNPDLQTD YNTNPDLQT
		ENIIQISEMDSSRGE ISEMDSSRG
		DSNYRGLVKETLINR YRGLVKETL
		SENIIQISEMDSSRG IIQISEMDS
		DDLIDEYNTNPDLQT LIDEYNTNP
		IIQISEMDSSRGEPN ISEMDSSRG
		LINRGFSIQLAMEEI INRGFSIQL
		NIIQISEMDSSRGEP ISEMDSSRG
		TVLILISCSLEVKDS ILISCSLEV
		QILSKLSQDSNYRGL ILSKLSQDS
		ILSKLSQDSNYRGLV ILSKLSQDS
		LSQDSNYRGLVKETL LSQDSNYRG
		IQISEMDSSRGEPND ISEMDSSRG
		PNDQFGMRAEIFSKI FGMRAEIFS
		VLILISCSLEVKDSN ILISCSLEV
		NDQFGMRAEIFSKIF FGMRAEIFS
		MKDNILKNNKLIAIF LKNNKLIAI
		NPDLQTDVSKLNDTL LQTDVSKLN
		NTNPDLQTDVSKLND LQTDVSKLN
		TNPDLQTDVSKLNDT LQTDVSKLN
		PDLQTDVSKLNDTLR LQTDVSKLN
		INRGFSIQLAMEEIS INRGFSIQL
		NAPKKILDPEVAKLI KKILDPEVA
		APKKILDPEVAKLIQ LDPEVAKLI
		NEGKIFNLGQILSKL IFNLGQILS
		QDSNYRGLVKETLIN YRGLVKETL
		KKILDPEVAKLIQKI LDPEVAKLI
		FNEGKIFNLGQILSK IFNLGQILS
		YRGLVKETLINRGFS YRGLVKETL
		NYRGLVKETLINRGF YRGLVKETL
		PKKILDPEVAKLIQK LDPEVAKLI
		SQDSNYRGLVKETLI YRGLVKETL
		GEPNDQFGMRAEIFS QFGMRAEIF
		EPNDQFGMRAEIFSK FGMRAEIFS
		DQFGMRAEIFSKIFF FGMRAEIFS
		FNANSTVHFDSHEYT FNANSTVHF
		EERRMLYTSLNFNEG RRMLYTSLN
		KILDPEVAKLIQKIL LDPEVAKLI
		VAINNLKNPTKPAAG LKNPTKPAA
		INNLKNPTKPAAGKN LKNPTKPAA
		NNLKNPTKPAAGKNK LKNPTKPAA
		NIHDIILDLVNTTTN ILDLVNTTT
		IHDIILDLVNTTTNI ILDLVNTTT
		AINNLKNPTKPAAGK LKNPTKPAA
		GKVENLLVAINNLKN VENLLVAIN
		LVAINNLKNPTKPAA INNLKNPTK
		ANIHDIILDLVNTTT IILDLVNTT
		LQTDVSKLNDTLRSK LQTDVSKLN

		DLQTDVSKLNDTLRS LQTDVSKLN
	HLA-DRB1*0301	None
	HLA-DRB1*0401	IFSKIFFNANSTVHF FFNANSTVH FSKIFFNANSTVHFD FFNANSTVH SKIFFNANSTVHFDS FFNANSTVH KIFFNANSTVHFDSH FFNANSTVH EIFSKIFFNANSTVH FSKIFFNAN IILDLVNTTTNILAP LVNTTTNIL DIILDLVNTTTNILA LVNTTTNIL LDLVNTTTNILAPIQ LVNTTTNIL ILDLVNTTTNILAPI LVNTTTNIL HDIILDLVNTTTNIL IILDLVNTT IFFNANSTVHFDSHE FFNANSTVH FFNANSTVHFDSHEY FFNANSTVH ETLYNDFEKLTSLKE YNDFEKLTS TLYNDFEKLTSLKEK FEKLTSLKE ENLLVAINNLKNPTK LLVAINNLK LYNDFEKLTSLKEKW FEKLTSLKE VENLLVAINNLKNPT LVAINNLKN SCSLEVKDSNESKKH LEVKDSNES CSLEVKDSNESKKHK LEVKDSNES ISCSLEVKDSNESKK LEVKDSNES LISCSLEVKDSNESK LEVKDSNES KVENLLVAINNLKNP LLVAINNLK YNDFEKLTSLKEKWL FEKLTSLKE GKVENLLVAINNLKN LLVAINNLK ILISCSLEVKDSNES ILISCSLEV NDFEKLTSLKEKWLK FEKLTSLKE EERRMLYTSLNFNEG MLYTSLNFN NLLVAINNLKNPTKP LVAINNLKN
	HLA-DRB1*0404	ENLLVAINNLKNPTK LLVAINNLK HDIILDLVNTTTNIL ILDLVNTTT DIILDLVNTTTNILA ILDLVNTTT VENLLVAINNLKNPT LLVAINNLK KVENLLVAINNLKNP LLVAINNLK GKVENLLVAINNLKN LLVAINNLK KGKVENLLVAINNLK VENLLVAIN ANIHDIILDLVNTTT IILDLVNTT NIHDIILDLVNTTTN ILDLVNTTT IHDIILDLVNTTTNI ILDLVNTTT IILDLVNTTTNILAP LVNTTTNIL ILDLVNTTTNILAPI LVNTTTNIL NLLVAINNLKNPTKP LLVAINNLK LLVAINNLKNPTKPA LLVAINNLK RRMLYTSLNFNEGKI MLYTSLNFN EERRMLYTSLNFNEG MLYTSLNFN ERRMLYTSLNFNEGK MLYTSLNFN DDLIDEYNTNPDLQT LIDEYNTNP EIFSKIFFNANSTVH FSKIFFNAN TDDLIDEYNTNPDLQ LIDEYNTNP KDTDDLIDEYNTNPD LIDEYNTNP GLVKETLINRGFSIQ VKETLINRG DTDDLIDEYNTNPDL LIDEYNTNP LKDTDDLIDEYNTNP LKDTDDLID SNYRGLVKETLINRG LVKETLINR IFSKIFFNANSTVHF FFNANSTVH

		YRGLVKETLINRGFS VKETLINRG NYRGLVKETLINRGF VKETLINRG KLIAIFLLHVLTVLI IFLLHVLTV RGLVKETLINRGFSI VKETLINRG NIIQISEMDSSRGEP ISEMDSSRG FSKIFFNANSTVHFD FFNANSTVH YTEERRMLYTSLNFN ERRMLYTSL IIQISEMDSSRGEPN ISEMDSSRG TEERRMLYTSLNFNE MLYTSLNFN IQISEMDSSRGEPND ISEMDSSRG LIAIFLLHVLTVLIL LLHVLTVLI SENIIQISEMDSSRG IQISEMDSS ENIIQISEMDSSRGE ISEMDSSRG SKIFFNANSTVHFDS FFNANSTVH IAIFLLHVLTVLILI LLHVLTVLI KIFFNANSTVHFDSH FFNANSTVH LDLVNTTTNILAPIQ LVNTTTNIL RMLYTSLNFNEGKIF MLYTSLNFN MLYTSLNFNEGKIFN MLYTSLNFN
	HLA-DRB1*0405	ENLLVAINNLKNPTK LVAINNLKN DDLIDEYNTNPDLQT IDEYNTNPD DLIDEYNTNPDLQTD IDEYNTNPD NLLVAINNLKNPTKP LVAINNLKN GKVENLLVAINNLKN VENLLVAIN KVENLLVAINNLKNP LVAINNLKN VENLLVAINNLKNPT LVAINNLKN ETLYNDFEKLTSLKE YNDFEKLTS TLYNDFEKLTSLKEK FEKLTSLKE IILDLVNTTTNILAP VNTTTNILA KDTDDLIDEYNTNPD LIDEYNTNP DIILDLVNTTTNILA LVNTTTNIL TDDLIDEYNTNPDLQ IDEYNTNPD EERRMLYTSLNFNEG RRMLYTSLN DTDDLIDEYNTNPDL IDEYNTNPD LYNDFEKLTSLKEKW FEKLTSLKE LDLVNTTTNILAPIQ VNTTTNILA ILDLVNTTTNILAPI VNTTTNILA YNDFEKLTSLKEKWL FEKLTSLKE TEERRMLYTSLNFNE RRMLYTSLN HEYTEERRMLYTSLN YTEERRMLY LLVAINNLKNPTKPA LVAINNLKN NDFEKLTSLKEKWLK FEKLTSLKE LIDEYNTNPDLQTDV IDEYNTNPD YTEERRMLYTSLNFN RRMLYTSLN IDEYNTNPDLQTDVS IDEYNTNPD LVAINNLKNPTKPAA LVAINNLKN EYTEERRMLYTSLNF RRMLYTSLN YNTNPDLQTDVSKLN YNTNPDLQT ERRMLYTSLNFNEGK RRMLYTSLN
	HLA-DRB1*0701	EIFSKIFFNANSTVH IFFNANSTV IFSKIFFNANSTVHF FFNANSTVH FSKIFFNANSTVHFD FFNANSTVH SKIFFNANSTVHFDS FFNANSTVH KIFFNANSTVHFDSH FFNANSTVH IFFNANSTVHFDSHE FFNANSTVH FFNANSTVHFDSHEY FFNANSTVH HDIILDLVNTTTNIL DLVNTTTNI

		DIILDLVNTTTNILA LVNTTTNIL ILDLVNTTTNILAPI LVNTTTNIL LDLVNTTTNILAPIQ LVNTTTNIL IILDLVNTTTNILAP LVNTTTNIL LNDTLRSKNSRAQFA LRSKNSRAQ NDTLRSKNSRAQFAN LRSKNSRAQ DTLRSKNSRAQFANI LRSKNSRAQ LIAIFLLHVLTVLIL LLHVLTVLI IAIFLLHVLTVLILI LHVLTVLIL TLRSKNSRAQFANIH SKNSRAQFA LRSKNSRAQFANIHD SKNSRAQFA
	HLA-DRB1*0802	None
	HLA-DRB1*0901	None
	HLA-DRB1*1101	RMLYTSLNFNEGKIF YTSLNFNEG RRMLYTSLNFNEGKI YTSLNFNEG ERRMLYTSLNFNEGK YTSLNFNEG MLYTSLNFNEGKIFN YTSLNFNEG EERRMLYTSLNFNEG MLYTSLNFN
	HLA-DRB1*1302	MKDNILKNNKLIAIF LKNNKLIAI KDNILKNNKLIAIFL LKNNKLIAI DNILKNNKLIAIFLL LKNNKLIAI NILKNNKLIAIFLLH LKNNKLIAI ENLLVAINNLKNPTK AINNLKNPT DIILDLVNTTTNILA LVNTTTNIL HDIILDLVNTTTNIL IILDLVNTT IILDLVNTTTNILAP LVNTTTNIL NLLVAINNLKNPTKP AINNLKNPT VENLLVAINNLKNPT VAINNLKNP ILDLVNTTTNILAPI LVNTTTNIL LLVAINNLKNPTKPA AINNLKNPT LDLVNTTTNILAPIQ LVNTTTNIL GKIFNLGQILSKLSQ IFNLGQILS EGKIFNLGQILSKLS IFNLGQILS ILKNNKLIAIFLLHV LKNNKLIAI LVAINNLKNPTKPAA AINNLKNPT LKNNKLIAIFLLHVL LKNNKLIAI NEGKIFNLGQILSKL IFNLGQILS FNEGKIFNLGQILSK IFNLGQILS NFNEGKIFNLGQILS GKIFNLGQI KVENLLVAINNLKNP LLVAINNLK IFLLHVLTVLILISC LLHVLTVLI AIFLLHVLTVLILIS LLHVLTVLI KIFNLGQILSKLSQD IFNLGQILS IFNLGQILSKLSQDS IFNLGQILS VAINNLKNPTKPAAG AINNLKNPT IAIFLLHVLTVLILI LLHVLTVLI LIAIFLLHVLTVLIL LLHVLTVLI FLLHVLTVLILISCS LLHVLTVLI KLIAIFLLHVLTVLI IAIFLLHVL IFSKIFFNANSTVHF FFNANSTVH FSKIFFNANSTVHFD FNANSTVHF SKIFFNANSTVHFDS FNANSTVHF LLHVLTVLILISCSL LLHVLTVLI KIFFNANSTVHFDSH FNANSTVHF IHDIILDLVNTTTNI IILDLVNTT IFFNANSTVHFDSHE FNANSTVHF

		GKVENLLVAINNLKN LLVAINNLK KGKVENLLVAINNLK VENLLVAIN AINNLKNPTKPAAGK AINNLKNPT GLVKETLINRGFSIQ VKETLINRG NIHDIILDLVNTTTN IILDLVNTT LHVLTVLILISCSLE VLTVLILIS LVKETLINRGFSIQL LINRGFSIQ VKETLINRGFSIQLA LINRGFSIQ ANIHDIILDLVNTTT IILDLVNTT HVLTVLILISCSLEV LTVLILISC KETLINRGFSIQLAM LINRGFSIQ FANIHDIILDLVNTT IHDIILDLV ETLINRGFSIQLAME LINRGFSIQ NKLIAIFLLHVLTVL IAIFLLHVL DKLQQLNKPNLETLY LQQLNKPNL VKDKLQQLNKPNLET LQQLNKPNL NVKDKLQQLNKPNLE LQQLNKPNL VLTVLILISCSLEVK LTVLILISC FFNANSTVHFDSHEY FNANSTVHF KDKLQQLNKPNLETL LQQLNKPNL EEISAKILNVKDKLQ ISAKILNVK DPEVAKLIQKILDRS VAKLIQKIL PEVAKLIQKILDRSE LIQKILDRS ISAKILNVKDKLQQL ISAKILNVK EISAKILNVKDKLQQ ISAKILNVK EVAKLIQKILDRSEN LIQKILDRS LNVKDKLQQLNKPNL DKLQQLNKP
	HLA-DRB1*1501	ENLLVAINNLKNPTK LLVAINNLK NLLVAINNLKNPTKP INNLKNPTK LLVAINNLKNPTKPA INNLKNPTK NKLIAIFLLHVLTVL LIAIFLLHV LIAIFLLHVLTVLIL IFLLHVLTV EIFSKIFFNANSTVH SKIFFNANS IFSKIFFNANSTVHF FFNANSTVH LVAINNLKNPTKPAA INNLKNPTK VAINNLKNPTKPAAG INNLKNPTK IAIFLLHVLTVLILI IFLLHVLTV SNYRGLVKETLINRG LVKETLINR KLIAIFLLHVLTVLI IFLLHVLTV FSKIFFNANSTVHFD FFNANSTVH SKIFFNANSTVHFDS FFNANSTVH YRGLVKETLINRGFS LVKETLINR RGLVKETLINRGFSI LVKETLINR NYRGLVKETLINRGF LVKETLINR NNKLIAIFLLHVLTV LIAIFLLHV DSNYRGLVKETLINR YRGLVKETL AIFLLHVLTVLILIS LHVLTVLIL KIFFNANSTVHFDSH FFNANSTVH IFLLHVLTVLILISC LHVLTVLIL LKNNKLIAIFLLHVL LIAIFLLHV VLTVLILISCSLEVK VLILISCSL GLVKETLINRGFSIQ LVKETLINR LTVLILISCSLEVKD VLILISCSL LVKETLINRGFSIQL LVKETLINR VENLLVAINNLKNPT LLVAINNLK FLLHVLTVLILISCS LHVLTVLIL KVENLLVAINNLKNP LLVAINNLK

		HVLTVLILISCSLEV VLILISCSL LLHVLTVLILISCSL LTVLILISC KNNKLIAIFLLHVLT LIAIFLLHV LHVLTVLILISCSLE VLILISCSL AINNLKNPTKPAAGK INNLKNPTK ILKNNKLIAIFLLHV LKNNKLIAI SKLNDTLRSKNSRAQ TLRSKNSRA
	HLA-DRB3*0101	None
	HLA-DRB4*0101	AKLIQKILDRSENII LIQKILDRS
	HLA-DRB5*0101	VAINNLKNPTKPAAG INNLKNPTK ENLLVAINNLKNPTK LLVAINNLK LVAINNLKNPTKPAA INNLKNPTK NLLVAINNLKNPTKP INNLKNPTK SKLNDTLRSKNSRAQ LNDTLRSKN LLVAINNLKNPTKPA INNLKNPTK KLNDTLRSKNSRAQF LRSKNSRAQ LNDTLRSKNSRAQFA LRSKNSRAQ
AAT93822.1| BBA64 antigen, P35 [Borrelia garinii PBi] Seq41	HLA-DRB1*0101	IFSKIFFNAGSTVTF FFNAGSTVT FSKIFFNAGSTVTFD FFNAGSTVT SKIFFNAGSTVTFDD FFNAGSTVT KIFFNAGSTVTFDDN FFNAGSTVT EIFSKIFFNAGSTVT EIFSKIFFN IFFNAGSTVTFDDNE FFNAGSTVT FFNAGSTVTFDDNEY FFNAGSTVT ILNLGKILSKLSQDS LGKILSKLS LNLGKILSKLSQDSN LGKILSKLS NKILNLGKILSKLSQ LGKILSKLS ENKILNLGKILSKLS ILNLGKILS FLLHILTGLILLSCS LTGLILLSC IFLLHILTGLILLSC ILTGLILLS LGKILSKLSQDSNYR ILSKLSQDS NIILNLINTTTNILA ILNLINTTT NLGKILSKLSQDSNY ILSKLSQDS LHILTGLILLSCSLE ILTGLILLS LLHILTGLILLSCSL ILTGLILLS HNIILNLINTTTNIL ILNLINTTT KILNLGKILSKLSQD LGKILSKLS TDIHNIILNLINTTT IHNIILNLI IILNLINTTTNILAP LINTTTNIL AIFLLHILTGLILLS LHILTGLIL ILNLINTTTNILAPI LINTTTNIL GKILSKLSQDSNYRS ILSKLSQDS DIHNIILNLINTTTN ILNLINTTT IHNIILNLINTTTNI ILNLINTTT HILTGLILLSCSLEV LTGLILLSC VKEILINRGFSIQLA INRGFSIQL IKDYNANPELRTDIS YNANPELRT LVAINTLKNPPKTAG LVAINTLKN KEILINRGFSIQLAI INRGFSIQL DIIKDYNANPELRTD YNANPELRT IIKDYNANPELRTDI YNANPELRT KDYNANPELRTDISK YNANPELRT DDIIKDYNANPELRT DYNANPELR EILINRGFSIQLAIE INRGFSIQL INTLKNPPKTAGKNK LKNPPKTAG

		YNANPELRTDISKLN YNANPELRT
		AINTLKNPPKTAGKN LKNPPKTAG
		LNLINTTTNILAPIQ LINTTTNIL
		NTLKNPPKTAGKNKS LKNPPKTAG
		ILINRGFSIQLAIEE INRGFSIQL
		VAINTLKNPPKTAGK LKNPPKTAG
		LVKEILINRGFSIQL ILINRGFSI
		LIAIFLLHILTGLIL LLHILTGLI
		IAIFLLHILTGLILL LHILTGLIL
		ILTGLILLSCSLEVN ILTGLILLS
		FNAGSTVTFDDNEYV FNAGSTVTF
		PTVDNLLVAINTLKN VDNLLVAIN
		TVDNLLVAINTLKNP LVAINTLKN
		NDYIISKNSKAQFTD SKNSKAQFT
		LNDYIISKNSKAQFT IISKNSKAQ
		DNLLVAINTLKNPPK LVAINTLKN
		VDNLLVAINTLKNPP LVAINTLKN
		DYIISKNSKAQFTDI SKNSKAQFT
		FTDIHNIILNLINTT IHNIILNLI
		LTGLILLSCSLEVNQ LTGLILLSC
		AQFTDIHNIILNLIN IHNIILNLI
		KILSKLSQDSNYRSL ILSKLSQDS
		MKNNKLIAIFLLHIL LIAIFLLHI
		NLLVAINTLKNPPKT LVAINTLKN
		ILSKLSQDSNYRSLV ILSKLSQDS
		QFTDIHNIILNLINT IHNIILNLI
		KAQFTDIHNIILNLI FTDIHNIIL
		NKLIAIFLLHILTGL LIAIFLLHI
		SLVKEILINRGFSIQ VKEILINRG
		NNKLIAIFLLHILTG LIAIFLLHI
		KLIAIFLLHILTGLI IAIFLLHIL
		SNYRSLVKEILINRG YRSLVKEIL
		DYNANPELRTDISKL YNANPELRT
		LINRGFSIQLAIEEI INRGFSIQL
		KNNKLIAIFLLHILT LIAIFLLHI
		YIISKNSKAQFTDIH SKNSKAQFT
		TLKNPPKTAGKNKSN LKNPPKTAG
		NANPELRTDISKLND LRTDISKLN
		RSLVKEILINRGFSI VKEILINRG
		LKNPPKTAGKNKSNS LKNPPKTAG
		PELRTDISKLNDYII LRTDISKLN
		NPELRTDISKLNDYI LRTDISKLN
		ANPELRTDISKLNDY LRTDISKLN
		IISKNSKAQFTDIHN SKNSKAQFT
		KPTVDNLLVAINTLK VDNLLVAIN
		AIEEISLRTLNVKDK EISLRTLNV
		IEEISLRTLNVKDKI LRTLNVKDK
		NENKILNLGKILSKL ILNLGKILS
		YRSLVKEILINRGFS VKEILINRG
		TGLILLSCSLEVNQD ILLSCSLEV
		NYRSLVKEILINRGF VKEILINRG
		INRGFSIQLAIEEIS INRGFSIQL
		FNENKILNLGKILSK ILNLGKILS
		LLVAINTLKNPPKTA LVAINTLKN
		GLILLSCSLEVNQDD ILLSCSLEV
		IQLAIEEISLRTLNV LAIEEISLR
		SKLNDYIISKNSKAQ YIISKNSKA

		KLNDYIISKNSKAQF IISKNSKAQ AKELIQKILERSEDI LIQKILERS EAKELIQKILERSED LIQKILERS PEAKELIQKILERSE LIQKILERS KELIQKILERSEDIV LIQKILERS
	HLA-DRB1*0301	None
	HLA-DRB1*0401	IILNLINTTTNILAP LINTTTNIL NIILNLINTTTNILA LINTTTNIL LNLINTTTNILAPIQ LINTTTNIL ILNLINTTTNILAPI LINTTTNIL HNIILNLINTTTNIL LNLINTTTN DNLLVAINTLKNPPK LVAINTLKN VDNLLVAINTLKNPP LVAINTLKN NLLVAINTLKNPPKT LVAINTLKN TVDNLLVAINTLKNP LVAINTLKN IFSKIFFNAGSTVTF FFNAGSTVT PTVDNLLVAINTLKN LLVAINTLK FSKIFFNAGSTVTFD FFNAGSTVT SKIFFNAGSTVTFDD FFNAGSTVT KIFFNAGSTVTFDDN FFNAGSTVT EIFSKIFFNAGSTVT FSKIFFNAG NEYVNERRILYTSLN YVNERRILY LVAINTLKNPPKTAG LVAINTLKN DIHNIILNLINTTTN IILNLINTT IHNIILNLINTTTNI IILNLINTT LLVAINTLKNPPKTA LVAINTLKN
	HLA-DRB1*0404	HNIILNLINTTTNIL ILNLINTTT NIILNLINTTTNILA ILNLINTTT TDIHNIILNLINTTT IILNLINTT DIHNIILNLINTTTN ILNLINTTT IHNIILNLINTTTNI ILNLINTTT IILNLINTTTNILAP ILNLINTTT KLIAIFLLHILTGLI IFLLHILTG ILNLINTTTNILAPI ILNLINTTT LIAIFLLHILTGLIL LLHILTGLI IAIFLLHILTGLILL LLHILTGLI IFLLHILTGLILLSC LLHILTGLI AIFLLHILTGLILLS LLHILTGLI VDNLLVAINTLKNPP LLVAINTLK DNLLVAINTLKNPPK LLVAINTLK NLLVAINTLKNPPKT LLVAINTLK RRILYTSLNFNENKI ILYTSLNFN ERRILYTSLNFNENK ILYTSLNFN NERRILYTSLNFNEN ILYTSLNFN YVNERRILYTSLNFN ERRILYTSL EIFSKIFFNAGSTVT FSKIFFNAG TVDNLLVAINTLKNP LLVAINTLK VNERRILYTSLNFNE ILYTSLNFN LLVAINTLKNPPKTA LLVAINTLK PTVDNLLVAINTLKN LLVAINTLK FLLHILTGLILLSCS LLHILTGLI LLHILTGLILLSCSL LLHILTGLI LNLINTTTNILAPIQ LINTTTNIL IFSKIFFNAGSTVTF FFNAGSTVT DDIIKDYNANPELRT IIKDYNANP

		KDVDDIIKDYNANPE IIKDYNANP
		VDDIIKDYNANPELR IIKDYNANP
		DVDDIIKDYNANPEL IIKDYNANP
		FSKIFFNAGSTVTFD FFNAGSTVT
		SLVKEILINRGFSIQ VKEILINRG
		KPTVDNLLVAINTLK VDNLLVAIN
		RILYTSLNFNENKIL ILYTSLNFN
	HLA-DRB1*0405	DNLLVAINTLKNPPK LVAINTLKN
		NLLVAINTLKNPPKT LVAINTLKN
		LLVAINTLKNPPKTA LVAINTLKN
		LVAINTLKNPPKTAG LVAINTLKN
		PTVDNLLVAINTLKN VDNLLVAIN
		VDNLLVAINTLKNPP LVAINTLKN
		TVDNLLVAINTLKNP LVAINTLKN
		IILNLINTTTNILAP INTTTNILA
		NIILNLINTTTNILA LNLINTTTN
		LNLINTTTNILAPIQ INTTTNILA
		ILNLINTTTNILAPI INTTTNILA
		NERRILYTSLNFNEN RRILYTSLN
		KTLYHDFNKLIPLKE LYHDFNKLI
		ERRILYTSLNFNENK YTSLNFNEN
		TLYHDFNKLIPLKEK FNKLIPLKE
		RRILYTSLNFNENKI YTSLNFNEN
		HNIILNLINTTTNIL LNLINTTTN
		VNERRILYTSLNFNE RRILYTSLN
		VAINTLKNPPKTAGK INTLKNPPK
		YNANPELRTDISKLN YNANPELRT
		LYHDFNKLIPLKEKW FNKLIPLKE
		NEYVNERRILYTSLN YVNERRILY
	HLA-DRB1*0701	HNIILNLINTTTNIL ILNLINTTT
		NIILNLINTTTNILA LINTTTNIL
		ILNLINTTTNILAPI LINTTTNIL
		LNLINTTTNILAPIQ LINTTTNIL
		IFSKIFFNAGSTVTF FFNAGSTVT
		FSKIFFNAGSTVTFD FFNAGSTVT
		IILNLINTTTNILAP LINTTTNIL
		EIFSKIFFNAGSTVT IFFNAGSTV
		SKIFFNAGSTVTFDD FFNAGSTVT
		KIFFNAGSTVTFDDN FFNAGSTVT
		IFFNAGSTVTFDDNE FFNAGSTVT
		FFNAGSTVTFDDNEY FFNAGSTVT
	HLA-DRB1*0802	NNSSKMKKLSKNAKN MKKLSKNAK
		ENNSSKMKKLSKNAK NSSKMKKLS
		SKMKKLSKNAKNKKP MKKLSKNAK
		NSSKMKKLSKNAKNK MKKLSKNAK
		SSKMKKLSKNAKNKK MKKLSKNAK
		HDFNKLIPLKEKWLK FNKLIPLKE
		YHDFNKLIPLKEKWL FNKLIPLKE
		LYHDFNKLIPLKEKW FNKLIPLKE
		KTLYHDFNKLIPLKE YHDFNKLIP
		TLYHDFNKLIPLKEK FNKLIPLKE
		KMKKLSKNAKNKKPT MKKLSKNAK
		MKKLSKNAKNKKPTV MKKLSKNAK
	HLA-DRB1*0901	IFSKIFFNAGSTVTF FFNAGSTVT
		FSKIFFNAGSTVTFD FFNAGSTVT
		SKIFFNAGSTVTFDD FFNAGSTVT

		KIFFNAGSTVTFDDN FFNAGSTVT EIFSKIFFNAGSTVT KIFFNAGST IFFNAGSTVTFDDNE FFNAGSTVT
	HLA-DRB1*1101	SSKMKKLSKNAKNKK MKKLSKNAK SKMKKLSKNAKNKKP MKKLSKNAK ENNSSKMKKLSKNAK SKMKKLSKN NSSKMKKLSKNAKNK MKKLSKNAK NNSSKMKKLSKNAKN MKKLSKNAK
	HLA-DRB1*1302	NFNENKILNLGKILS NKILNLGKI FNENKILNLGKILSK ILNLGKILS NENKILNLGKILSKL ILNLGKILS ENKILNLGKILSKLS ILNLGKILS NKILNLGKILSKLSQ ILNLGKILS HNIILNLINTTTNIL ILNLINTTT DIHNIILNLINTTTN IILNLINTT IHNIILNLINTTTNI IILNLINTT NIILNLINTTTNILA ILNLINTTT TDIHNIILNLINTTT IHNIILNLI IILNLINTTTNILAP LINTTTNIL FTDIHNIILNLINTT IHNIILNLI ILNLINTTTNILAPI LINTTTNIL KILNLGKILSKLSQD ILNLGKILS ILNLGKILSKLSQDS ILNLGKILS LNLINTTTNILAPIQ LINTTTNIL QFTDIHNIILNLINT IHNIILNLI KAQFTDIHNIILNLI DIHNIILNL AQFTDIHNIILNLIN IHNIILNLI MKNNKLIAIFLLHIL MKNNKLIAI DNLLVAINTLKNPPK VAINTLKNP IFSKIFFNAGSTVTF FFNAGSTVT FSKIFFNAGSTVTFD FFNAGSTVT SLVKEILINRGFSIQ VKEILINRG SKIFFNAGSTVTFDD FFNAGSTVT TVDNLLVAINTLKNP LLVAINTLK VDNLLVAINTLKNPP VAINTLKNP NLLVAINTLKNPPKT VAINTLKNP KIFFNAGSTVTFDDN FFNAGSTVT LVKEILINRGFSIQL LINRGFSIQ VKEILINRGFSIQLA LINRGFSIQ SKMKKLSKNAKNKKP MKKLSKNAK SSKMKKLSKNAKNKK MKKLSKNAK LLVAINTLKNPPKTA VAINTLKNP LVAINTLKNPPKTAG VAINTLKNP KEILINRGFSIQLAI LINRGFSIQ IAIFLLHILTGLILL LHILTGLIL MKKLSKNAKNKKPTV LSKNAKNKK KMKKLSKNAKNKKPT LSKNAKNKK LIAIFLLHILTGLIL LLHILTGLI AIFLLHILTGLILLS LHILTGLIL EIFSKIFFNAGSTVT IFFNAGSTV PTVDNLLVAINTLKN LLVAINTLK ENNSSKMKKLSKNAK SKMKKLSKN NNSSKMKKLSKNAKN MKKLSKNAK NSSKMKKLSKNAKNK MKKLSKNAK IFLLHILTGLILLSC LHILTGLIL IFFNAGSTVTFDDNE FFNAGSTVT LNFNENKILNLGKIL NENKILNLG

		VAINTLKNPPKTAGK LKNPPKTAG SLNFNENKILNLGKI NENKILNLG KLIAIFLLHILTGLI IAIFLLHIL EILINRGFSIQLAIE LINRGFSIQ FLLHILTGLILLSCS LHILTGLIL KKLSKNAKNKKPTVD LSKNAKNKK VKDKIQHLNKPNLKT IQHLNKPNL LNVKDKIQHLNKPNL VKDKIQHLN DKIQHLNKPNLKTLY IQHLNKPNL NEYVNERRILYTSLN YVNERRILY NVKDKIQHLNKPNLK IQHLNKPNL RSLVKEILINRGFSI VKEILINRG KPTVDNLLVAINTLK VDNLLVAIN DNEYVNERRILYTSL YVNERRILY YTSLNFNENKILNLG LNFNENKIL SNYRSLVKEILINRG YRSLVKEIL DDNEYVNERRILYTS YVNERRILY FDDNEYVNERRILYT YVNERRILY TSLNFNENKILNLGK NENKILNLG KDKIQHLNKPNLKTL IQHLNKPNL FFNAGSTVTFDDNEY FFNAGSTVT YRSLVKEILINRGFS VKEILINRG TFDDNEYVNERRILY EYVNERRIL NKLIAIFLLHILTGL IAIFLLHIL KIQHLNKPNLKTLYH IQHLNKPNL LLHILTGLILLSCSL LHILTGLIL IEEISLRTLNVKDKI ISLRTLNVK NYRSLVKEILINRGF VKEILINRG EEISLRTLNVKDKIQ ISLRTLNVK ILINRGFSIQLAIEE LINRGFSIQ YVNERRILYTSLNFN YVNERRILY IQHLNKPNLKTLYHD IQHLNKPNL AINTLKNPPKTAGKN LKNPPKTAG LHILTGLILLSCSLE LHILTGLIL EYVNERRILYTSLNF YVNERRILY KLSKNAKNKKPTVDN LSKNAKNKK LNLGKILSKLSQDSN LGKILSKLS LSKNAKNKKPTVDNL LSKNAKNKK ISLRTLNVKDKIQHL ISLRTLNVK
	HLA-DRB1*1501	IAIFLLHILTGLILL IFLLHILTG LIAIFLLHILTGLIL IFLLHILTG DNLLVAINTLKNPPK LLVAINTLK IFLLHILTGLILLSC IFLLHILTG RSLVKEILINRGFSI LVKEILINR ENKILNLGKILSKLS ILNLGKILS AIFLLHILTGLILLS IFLLHILTG NKILNLGKILSKLSQ ILNLGKILS KLIAIFLLHILTGLI IFLLHILTG NENKILNLGKILSKL ILNLGKILS NKLIAIFLLHILTGL IFLLHILTG FNENKILNLGKILSK ILNLGKILS SLVKEILINRGFSIQ LVKEILINR SNYRSLVKEILINRG LVKEILINR YRSLVKEILINRGFS LVKEILINR NYRSLVKEILINRGF LVKEILINR LVKEILINRGFSIQL LVKEILINR

		TDIHNIILNLINTTT IHNIILNLI NNKLIAIFLLHILTG LIAIFLLHI NLLVAINTLKNPPKT INTLKNPPK LVAINTLKNPPKTAG INTLKNPPK LLVAINTLKNPPKTA INTLKNPPK IHNIILNLINTTTNI ILNLINTTT DSNYRSLVKEILINR YRSLVKEIL DIHNIILNLINTTTN ILNLINTTT KILNLGKILSKLSQD LNLGKILSK VAINTLKNPPKTAGK INTLKNPPK ILNLGKILSKLSQDS ILNLGKILS HNIILNLINTTTNIL ILNLINTTT VDNLLVAINTLKNPP LLVAINTLK NIILNLINTTTNILA ILNLINTTT FLLHILTGLILLSCS LHILTGLIL IQLAIEEISLRTLNV LAIEEISLR
	HLA-DRB3*0101	None
	HLA-DRB4*0101	IEEISLRTLNVKDKI ISLRTLNVK QLAIEEISLRTLNVK IEEISLRTL AIEEISLRTLNVKDK ISLRTLNVK LAIEEISLRTLNVKD ISLRTLNVK EEISLRTLNVKDKIQ ISLRTLNVK EISLRTLNVKDKIQH ISLRTLNVK ISLRTLNVKDKIQHL ISLRTLNVK SLVKEILINRGFSIQ VKEILINRG
	HLA-DRB5*0101	FDDNEYVNERRILYT YVNERRILY
AAL84596.1| BBK32 [Borrelia burgdorferi] Seq42	HLA-DRB1*0101	TLFSTKLTQMYSTRL FSTKLTQMY LFSTKLTQMYSTRLD LTQMYSTRL FSTKLTQMYSTRLDN LTQMYSTRL STKLTQMYSTRLDNL LTQMYSTRL TKLTQMYSTRLDNLA LTQMYSTRL KLTQMYSTRLDNLAK LTQMYSTRL LTQMYSTRLDNLAKA LTQMYSTRL YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT NLYEAYKAIVTSILL YKAIVTSIL SNLYEAYKAIVTSIL YEAYKAIVT YEAYKAIVTSILLMR YKAIVTSIL EAYKAIVTSILLMRD YKAIVTSIL LYEAYKAIVTSILLM YKAIVTSIL KKVKSKYLALGLLFG VKSKYLALG IYDTYTLFSTKLTQM YTLFSTKLT NKIYDTYTLFSTKLT TYTLFSTKL KIYDTYTLFSTKLTQ YTLFSTKLT TYTLFSTKLTQMYST YTLFSTKLT KVKSKYLALGLLFGF YLALGLLFG VKSKYLALGLLFGFI YLALGLLFG KSKYLALGLLFGFIS YLALGLLFG SKYLALGLLFGFISC YLALGLLFG YTLFSTKLTQMYSTR YTLFSTKLT QDEYKGMTQGSLNSL YKGMTQGSL DEYKGMTQGSLNSLS MTQGSLNSL AYKAIVTSILLMRDS YKAIVTSIL YKAIVTSILLMRDSL YKAIVTSIL

		EYKGMTQGSLNSLSG MTQGSLNSL YKGMTQGSLNSLSGE MTQGSLNSL MKKVKSKYLALGLLF VKSKYLALG GMTQGSLNSLSGESG MTQGSLNSL MTQGSLNSLSGESGE LNSLSGESG KGMTQGSLNSLSGES MTQGSLNSL YLALGLLFGFISCDL YLALGLLFG AEIKTLIAKIKEQSN IKTLIAKIK EAEIKTLIAKIKEQS IKTLIAKIK ENIEAEIKTLIAKIK EAEIKTLIA NIEAEIKTLIAKIKE IKTLIAKIK IEAEIKTLIAKIKEQ IKTLIAKIK KYLALGLLFGFISCD YLALGLLFG FKTLLNYIQVSVKTA FKTLLNYIQ QGSLNSLSGESGELK LNSLSGESG TQGSLNSLSGESGEL LNSLSGESG LNYIQVSVKTAANFV YIQVSVKTA LLNYIQVSVKTAANF YIQVSVKTA QSNLYEAYKAIVTSI YEAYKAIVT EQSNLYEAYKAIVTS YEAYKAIVT GSLNSLSGESGELKE LNSLSGESG EKNFKTLLNYIQVSV FKTLLNYIQ TLLNYIQVSVKTAAN YIQVSVKTA KEQSNLYEAYKAIVT LYEAYKAIV KNFKTLLNYIQVSVK FKTLLNYIQ KTLLNYIQVSVKTAA YIQVSVKTA QQDEYKGMTQGSLNS YKGMTQGSL NYIQVSVKTAANFVY YIQVSVKTA DLEKNFKTLLNYIQV FKTLLNYIQ EDLEKNFKTLLNYIQ EKNFKTLLN YIQVSVKTAANFVYI YIQVSVKTA INKIYDTYTLFSTKL YDTYTLFST KAIVTSILLMRDSLK VTSILLMRD EGVKYNVDSAINTIN YNVDSAINT LEKNFKTLLNYIQVS FKTLLNYIQ EPYIHSLKRDSANKS IHSLKRDSA HSLKRDSANKSNFLQ LKRDSANKS IHSLKRDSANKSNFL LKRDSANKS PYIHSLKRDSANKSN LKRDSANKS GVKYNVDSAINTINK YNVDSAINT LEGVKYNVDSAINTI YNVDSAINT YLEGVKYNVDSAINT VKYNVDSAI YIHSLKRDSANKSNF LKRDSANKS
	HLA-DRB1*0301	NEIDITIDSDLRPKS ITIDSDLRP EIDITIDSDLRPKSS ITIDSDLRP IDITIDSDLRPKSSL ITIDSDLRP ITIDSDLRPKSSLQD IDSDLRPKS DITIDSDLRPKSSLQ IDSDLRPKS
	HLA-DRB1*0401	PYIHSLKRDSANKSN LKRDSANKS EPYIHSLKRDSANKS IHSLKRDSA YIHSLKRDSANKSNF LKRDSANKS IHSLKRDSANKSNFL LKRDSANKS HSLKRDSANKSNFLQ LKRDSANKS SLKRDSANKSNFLQK LKRDSANKS LKRDSANKSNFLQKN LKRDSANKS NKIYDTYTLFSTKLT IYDTYTLFS

		AANFVYINDTHAKRK FVYINDTHA
		ANFVYINDTHAKRKL FVYINDTHA
		FKTLLNYIQVSVKTA NYIQVSVKT
		TAANFVYINDTHAKR FVYINDTHA
		TINKIYDTYTLFSTK IYDTYTLFS
		NTINKIYDTYTLFST IYDTYTLFS
		INTINKIYDTYTLFS INKIYDTYT
		INKIYDTYTLFSTKL IYDTYTLFS
		IKTLIAKIKEQSNLY LIAKIKEQS
		KTLIAKIKEQSNLYE KIKEQSNLY
		NFKTLLNYIQVSVKT FKTLLNYIQ
		TLLNYIQVSVKTAAN NYIQVSVKT
		LLNYIQVSVKTAANF NYIQVSVKT
		KTLLNYIQVSVKTAA NYIQVSVKT
		TLIAKIKEQSNLYEA KIKEQSNLY
		LIAKIKEQSNLYEAY KIKEQSNLY
		IAKIKEQSNLYEAYK KIKEQSNLY
	HLA-DRB1*0404	AANFVYINDTHAKRK FVYINDTHA
		ANFVYINDTHAKRKL FVYINDTHA
	HLA-DRB1*0405	EDLEKNFKTLLNYIQ EKNFKTLLN
		DLEKNFKTLLNYIQV EKNFKTLLN
		FTKEDLEKNFKTLLN LEKNFKTLL
		TKEDLEKNFKTLLNY EKNFKTLLN
		NKIYDTYTLFSTKLT IYDTYTLFS
		KEDLEKNFKTLLNYI EKNFKTLLN
		KTLIAKIKEQSNLYE IAKIKEQSN
		TLIAKIKEQSNLYEA IKEQSNLYE
		IAKIKEQSNLYEAYK IKEQSNLYE
		AKIKEQSNLYEAYKA IKEQSNLYE
		LIAKIKEQSNLYEAY IKEQSNLYE
		LEKNFKTLLNYIQVS EKNFKTLLN
		EKNFKTLLNYIQVSV EKNFKTLLN
		IYDTYTLFSTKLTQM YTLFSTKLT
		KIYDTYTLFSTKLTQ YTLFSTKLT
		INTINKIYDTYTLFS INTINKIYD
		YDTYTLFSTKLTQMY YTLFSTKLT
		ITIDSDLRPKSSLQD ITIDSDLRP
		DTYTLFSTKLTQMYS YTLFSTKLT
		IKEQSNLYEAYKAIV IKEQSNLYE
		TIDSDLRPKSSLQDI LRPKSSLQD
		IDSDLRPKSSLQDIA LRPKSSLQD
	HLA-DRB1*0701	YIQVSVKTAANFVYI VKTAANFVY
		LYEAYKAIVTSILLM YKAIVTSIL
		YEAYKAIVTSILLMR YKAIVTSIL
		IQVSVKTAANFVYIN VKTAANFVY
		NYIQVSVKTAANFVY SVKTAANFV
		QVSVKTAANFVYIND VKTAANFVY
		EAYKAIVTSILLMRD YKAIVTSIL
		NLYEAYKAIVTSILL YKAIVTSIL
		SNLYEAYKAIVTSIL AYKAIVTSI
		VSVKTAANFVYINDT VKTAANFVY
		AYKAIVTSILLMRDS YKAIVTSIL
		YKAIVTSILLMRDSL YKAIVTSIL
		SVKTAANFVYINDTH VKTAANFVY
		LNYIQVSVKTAANFV VSVKTAANF
	HLA-DRB1*0802	ESIKKPMNKKGKGKI SIKKPMNKK

	HLA-DRB1*0901	SNLYEAYKAIVTSIL YEAYKAIVT NLYEAYKAIVTSILL YEAYKAIVT QSNLYEAYKAIVTSI YEAYKAIVT EQSNLYEAYKAIVTS YEAYKAIVT KEQSNLYEAYKAIVT LYEAYKAIV YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT YEAYKAIVTSILLMR YEAYKAIVT IYDTYTLFSTKLTQM YTLFSTKLT KIYDTYTLFSTKLTQ YTLFSTKLT LYEAYKAIVTSILLM YEAYKAIVT NKIYDTYTLFSTKLT IYDTYTLFS
	HLA-DRB1*1101	None
	HLA-DRB1*1302	EAYKAIVTSILLMRD YKAIVTSIL YEAYKAIVTSILLMR YKAIVTSIL YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT IYDTYTLFSTKLTQM YTLFSTKLT NKIYDTYTLFSTKLT NKIYDTYTL AYKAIVTSILLMRDS IVTSILLMR YKAIVTSILLMRDSL IVTSILLMR KIYDTYTLFSTKLTQ YTLFSTKLT NYIQVSVKTAANFVY IQVSVKTAA YTLFSTKLTQMYSTR YTLFSTKLT LYEAYKAIVTSILLM YKAIVTSIL TYTLFSTKLTQMYST YTLFSTKLT KTLLNYIQVSVKTAA LLNYIQVSV KNFKTLLNYIQVSVK LLNYIQVSV ENIEAEIKTLIAKIK IEAEIKTLI NLYEAYKAIVTSILL YKAIVTSIL FKTLLNYIQVSVKTA LLNYIQVSV EKNFKTLLNYIQVSV FKTLLNYIQ SNLYEAYKAIVTSIL YEAYKAIVT NFKTLLNYIQVSVKT LNYIQVSVK TLLNYIQVSVKTAAN IQVSVKTAA IEAEIKTLIAKIKEQ IKTLIAKIK NIEAEIKTLIAKIKE IKTLIAKIK DYEEIRLSNRYQSYL IRLSNRYQS KSKYLALGLLFGFIS YLALGLLFG KAIVTSILLMRDSLK IVTSILLMR YEEIRLSNRYQSYLE IRLSNRYQS YIQVSVKTAANFVYI VKTAANFVY DDYEEIRLSNRYQSY IRLSNRYQS EDDYEEIRLSNRYQS EEIRLSNRY SKYLALGLLFGFISC LGLLFGFIS EEIRLSNRYQSYLEG IRLSNRYQS LLNYIQVSVKTAANF IQVSVKTAA EAEIKTLIAKIKEQS IKTLIAKIK AEIKTLIAKIKEQSN IKTLIAKIK EDLEKNFKTLLNYIQ EKNFKTLLN IQVSVKTAANFVYIN VKTAANFVY KYLALGLLFGFISCD LGLLFGFIS VDSAINTINKIYDTY INTINKIYD YNVDSAINTINKIYD SAINTINKI DLEKNFKTLLNYIQV FKTLLNYIQ LALGLLFGFISCDLF LGLLFGFIS SAINTINKIYDTYTL INTINKIYD

		YLALGLLFGFISCDL LGLLFGFIS NVDSAINTINKIYDT INTINKIYD LNYIQVSVKTAANFV IQVSVKTAA DSAINTINKIYDTYT INTINKIYD ANKSNFLQKNVILEE SNFLQKNVI NKSNFLQKNVILEEE SNFLQKNVI LEKNFKTLLNYIQVS FKTLLNYIQ EPYIHSLKRDSANKS IHSLKRDSA
	HLA-DRB1*1501	KAIVTSILLMRDSLK IVTSILLMR IVTSILLMRDSLKEV IVTSILLMR YEAYKAIVTSILLMR YEAYKAIVT AIVTSILLMRDSLKE IVTSILLMR KGKIARKKGKSKVSR IARKKGKSK GKIARKKGKSKVSRK IARKKGKSK EAYKAIVTSILLMRD IVTSILLMR AYKAIVTSILLMRDS IVTSILLMR YKAIVTSILLMRDSL IVTSILLMR KKGKGKIARKKGKSK KKGKGKIAR GKGKIARKKGKSKVS IARKKGKSK KGKGKIARKKGKSKV IARKKGKSK TSILLMRDSLKEVQG ILLMRDSLK VTSILLMRDSLKEVQ ILLMRDSLK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	GKSKVSRKEPYIHSL VSRKEPYIH KSKVSRKEPYIHSLK VSRKEPYIH KKGKSKVSRKEPYIH KKGKSKVSR KGKSKVSRKEPYIHS VSRKEPYIH SKVSRKEPYIHSLKR VSRKEPYIH VSRKEPYIHSLKRDS VSRKEPYIH KVSRKEPYIHSLKRD VSRKEPYIH
	HLA-DRB5*0101	KTELLKEQSETRKEK LLKEQSETR TELLKEQSETRKEKI LLKEQSETR TSEESIKKPMNKKGK IKKPMNKKG SEESIKKPMNKKGKG KKPMNKKGK SLKTELLKEQSETRK LLKEQSETR LKTELLKEQSETRKE LLKEQSETR ESIKKPMNKKGKGKI KKPMNKKGK EESIKKPMNKKGKGK KKPMNKKGK AANFVYINDTHAKRK YINDTHAKR ANFVYINDTHAKRKL INDTHAKRK NFVYINDTHAKRKLE INDTHAKRK FVYINDTHAKRKLEN INDTHAKRK ELLKEQSETRKEKIQ LKEQSETRK
AAL84590.1| BBK32 [Borrelia afzelii] Seq43	HLA-DRB1*0101	YDNYTLLSTKQTQMY YTLLSTKQT VKIYDNYTLLSTKQT YDNYTLLST KIYDNYTLLSTKQTQ YTLLSTKQT DNYTLLSTKQTQMYS YTLLSTKQT IYDNYTLLSTKQTQM YTLLSTKQT DEHKRMLQGSLSFLS KRMLQGSLS EHKRMLQGSLSFLSG LQGSLSFLS HKRMLQGSLSFLSGE LQGSLSFLS KRMLQGSLSFLSGES LQGSLSFLS RMLQGSLSFLSGESG LQGSLSFLS NYTLLSTKQTQMYST YTLLSTKQT YTLLSTKQTQMYSTR YTLLSTKQT

		LLNYIQVSARTATNF YIQVSARTA	
		YLEGVKYNVSSAIKT VKYNVSSAI	
		LEGVKYNVSSAIKTI YNVSSAIKT	
		EGVKYNVSSAIKTIV YNVSSAIKT	
		TLLNYIQVSARTATN YIQVSARTA	
		LNYIQVSARTATNFV YIQVSARTA	
		KTLLNYIQVSARTAT YIQVSARTA	
		LKTLLNYIQVSARTA NYIQVSART	
		GVKYNVSSAIKTIVK YNVSSAIKT	
		VKYNVSSAIKTIVKI YNVSSAIKT	
		NYIQVSARTATNFVY YIQVSARTA	
		MKIKSKCLALGLLFG IKSKCLALG	
		TLLSTKQTQMYSTRL LSTKQTQMY	
		LQGSLSFLSGESGEL LQGSLSFLS	
		MLQGSLSFLSGESGE LQGSLSFLS	
		YIQVSARTATNFVYA YIQVSARTA	
		EDYYYDGETRLSNRY YYDGETRLS	
		EEDYYYDGETRLSNR YYDGETRLS	
		DYYYDGETRLSNRYE YYDGETRLS	
		LEEDYYYDGETRLSN YYDGETRLS	
		LSTKQTQMYSTRLDN QTQMYSTRL	
		KTIVKIYDNYTLLST IYDNYTLLS	
		LLSTKQTQMYSTRLD QTQMYSTRL	
		AIVRSILLMKDSLKI VRSILLMKD	
		VRSILLMKDSLKIIE LLMKDSLKI	
		TKQTQMYSTRLDNLA QTQMYSTRL	
		IVRSILLMKDSLKII LLMKDSLKI	
		RSILLMKDSLKIIEI LLMKDSLKI	
		SLEEDYYYDGETRLS YYYDGETRL	
		KYNVSSAIKTIVKIY YNVSSAIKT	
		TIVKIYDNYTLLSTK YDNYTLLST	
		SILLMKDSLKIIEIV LLMKDSLKI	
		YNVSSAIKTIVKIYD YNVSSAIKT	
		IVKIYDNYTLLSTKQ YDNYTLLST	
		KIKSKCLALGLLFGF IKSKCLALG	
		IKSKCLALGLLFGFI IKSKCLALG	
		STKQTQMYSTRLDNL QTQMYSTRL	
		KSDLQAISGSNSISY LQAISGSNS	
		SDLQAISGSNSISYT LQAISGSNS	
		KQTQMYSTRLDNLAK QTQMYSTRL	
		QTQMYSTRLDNLAKA QTQMYSTRL	
		YYYDGETRLSNRYES YYDGETRLS	
		QDEHKRMLQGSLSFL KRMLQGSLS	
		LRLKSDLQAISGSNS KSDLQAISG	
		RLKSDLQAISGSNSI LQAISGSNS	
		LKSDLQAISGSNSIS LQAISGSNS	
		SEEEILKTKLLRERP LKTKLLRER	
		YYDGETRLSNRYESY YYDGETRLS	
		EEILKTKLLRERPET LKTKLLRER	
		EEEILKTKLLRERPE LKTKLLRER	
		ISEEEILKTKLLRER EEILKTKLL	
		ILLMKDSLKIIEIVI LLMKDSLKI	
		KDLKTLLNYIQVSAR LKTLLNYIQ	
		EILKTKLLRERPETR LKTKLLRER	
		EKDLKTLLNYIQVSA LKTLLNYIQ	
		DLKTLLNYIQVSART LKTLLNYIQ	
		IKTIVKIYDNYTLLS VKIYDNYTL	

		LLMKDSLKIIEIVID LLMKDSLKI	
		ELEKDLKTLLNYIQV LKTLLNYIQ	
		EELEKDLKTLLNYIQ EKDLKTLLN	
		EAYKAIVRSILLMKD YKAIVRSIL	
		LEKDLKTLLNYIQVS LKTLLNYIQ	
		SYLEGVKYNVSSAIK VKYNVSSAI	
		DLYEAYKAIVRSILL YEAYKAIVR	
		DLQAISGSNSISYTD LQAISGSNS	
		SDLYEAYKAIVRSIL YEAYKAIVR	
		LQAISGSNSISYTDE LQAISGSNS	
		QMYSTRLDNLAKAKA YSTRLDNLA	
		ETEIKNLILKIKGQS IKNLILKIK	
		TEIKNLILKIKGQSD IKNLILKIK	
		IETEIKNLILKIKGQ IKNLILKIK	
		AIETEIKNLILKIKG IKNLILKIK	
		QGSLSFLSGESGELK FLSGESGEL	
		AYKAIVRSILLMKDS VRSILLMKD	
		DAIETEIKNLILKIK EIKNLILKI	
		IQVSARTATNFVYAR VSARTATNF	
		YKAIVRSILLMKDSL VRSILLMKD	
		KAIVRSILLMKDSLK VRSILLMKD	
		GSLSFLSGESGELKD FLSGESGEL	
		ESYLEGVKYNVSSAI LEGVKYNVS	
		STRLDNLAKAKAREE LDNLAKAKA	
		TRLDNLAKAKAREEA LDNLAKAKA	
	HLA-DRB1*0301	NEIDFTIDSDLRLKS FTIDSDLRL	
		IDFTIDSDLRLKSDL FTIDSDLRL	
		EIDFTIDSDLRLKSD FTIDSDLRL	
		FTIDSDLRLKSDLQA IDSDLRLKS	
		DFTIDSDLRLKSDLQ IDSDLRLKS	
		ESNEIDFTIDSDLRL NEIDFTIDS	
		SNEIDFTIDSDLRLK FTIDSDLRL	
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		KVEGNAVKKDPFNHH KVEGNAVKK	
		EGNAVKKDPFNHHVK VKKDPFNHH	
		VEGNAVKKDPFNHHV VKKDPFNHH	
		NHHVKRESVNNSNLS VKRESVNNS	
		HHVKRESVNNSNLSQ VKRESVNNS	
		DPFNHHVKRESVNNS FNHHVKRES	
		PFNHHVKRESVNNSN VKRESVNNS	
		VKIYDNYTLLSTKQT IYDNYTLLS	
		IVKIYDNYTLLSTKQ IYDNYTLLS	
		FNHHVKRESVNNSNL VKRESVNNS	
		IKTIVKIYDNYTLLS IVKIYDNYT	
		KTIVKIYDNYTLLST IYDNYTLLS	
		TIVKIYDNYTLLSTK IYDNYTLLS	
		VKKDPFNHHVKRESV VKKDPFNHH	
		AVKKDPFNHHVKRES VKKDPFNHH	
		HVKRESVNNSNLSQK VKRESVNNS	
		VKRESVNNSNLSQKN VKRESVNNS	
	HLA-DRB1*0404	None	
	HLA-DRB1*0405	IKTIVKIYDNYTLLS IKTIVKIYD	
		VKIYDNYTLLSTKQT IYDNYTLLS	
		SSAIKTIVKIYDNYT IKTIVKIYD	
		KTIVKIYDNYTLLST IYDNYTLLS	

		SAIKTIVKIYDNYTL	IKTIVKIYD
	HLA-DRB1*0701	NYIQVSARTATNFVY	VSARTATNF
		YIQVSARTATNFVYA	ARTATNFVY
		IQVSARTATNFVYAR	ARTATNFVY
		DLYEAYKAIVRSILL	YKAIVRSIL
		LYEAYKAIVRSILLM	YKAIVRSIL
		YEAYKAIVRSILLMK	YKAIVRSIL
		SDLYEAYKAIVRSIL	YEAYKAIVR
		QVSARTATNFVYARE	ARTATNFVY
		EAYKAIVRSILLMKD	YKAIVRSIL
		VSARTATNFVYAREI	ARTATNFVY
		LNYIQVSARTATNFV	VSARTATNF
		EGVKYNVSSAIKTIV	VKYNVSSAI
		LLNYIQVSARTATNF	IQVSARTAT
	HLA-DRB1*0802	None	
	HLA-DRB1*0901	EGVKYNVSSAIKTIV	YNVSSAIKT
		LEGVKYNVSSAIKTI	YNVSSAIKT
		GVKYNVSSAIKTIVK	YNVSSAIKT
		VKYNVSSAIKTIVKI	YNVSSAIKT
		YLEGVKYNVSSAIKT	VKYNVSSAI
		KTLLNYIQVSARTAT	YIQVSARTA
		LNYIQVSARTATNFV	YIQVSARTA
		KYNVSSAIKTIVKIY	YNVSSAIKT
		TLLNYIQVSARTATN	YIQVSARTA
		LLNYIQVSARTATNF	YIQVSARTA
		YNVSSAIKTIVKIYD	YNVSSAIKT
	HLA-DRB1*1101	None	
	HLA-DRB1*1302	DAIETEIKNLILKIK	IETEIKNLI
		AIETEIKNLILKIKG	IKNLILKIK
		IETEIKNLILKIKGQ	IKNLILKIK
		ETEIKNLILKIKGQS	IKNLILKIK
		TEIKNLILKIKGQSD	IKNLILKIK
		EIKNLILKIKGQSDL	IKNLILKIK
		IKNLILKIKGQSDLY	IKNLILKIK
		EGVKYNVSSAIKTIV	YNVSSAIKT
		LEGVKYNVSSAIKTI	YNVSSAIKT
		YLEGVKYNVSSAIKT	VKYNVSSAI
		GVKYNVSSAIKTIVK	YNVSSAIKT
		VKYNVSSAIKTIVKI	YNVSSAIKT
		VKIYDNYTLLSTKQT	IYDNYTLLS
		KTLLNYIQVSARTAT	LLNYIQVSA
		EAYKAIVRSILLMKD	YKAIVRSIL
		TLLNYIQVSARTATN	IQVSARTAT
		YEAYKAIVRSILLMK	YKAIVRSIL
		HVKRESVNNSNLSQK	ESVNNSNLS
		VKRESVNNSNLSQKN	VNNSNLSQK
		LLNYIQVSARTATNF	IQVSARTAT
		LNYIQVSARTATNFV	IQVSARTAT
		NYIQVSARTATNFVY	IQVSARTAT
		KIYDNYTLLSTKQTQ	YTLLSTKQT
		IYDNYTLLSTKQTQM	YTLLSTKQT
		YDNYTLLSTKQTQMY	YTLLSTKQT
		KRESVNNSNLSQKNV	VNNSNLSQK
		RESVNNSNLSQKNVI	VNNSNLSQK
		YKAIVRSILLMKDSL	IVRSILLMK
		AYKAIVRSILLMKDS	IVRSILLMK

		DNYTLLSTKQTQMYS YTLLSTKQT KDLKTLLNYIQVSAR LKTLLNYIQ ESVNNSNLSQKNVIS VNNSNLSQK YNVSSAIKTIVKIYD YNVSSAIKT KNLILKIKGQSDLYE LKIKGQSDL LYEAYKAIVRSILLM YKAIVRSIL DLKTLLNYIQVSART LNYIQVSAR EKDLKTLLNYIQVSA LKTLLNYIQ LKTLLNYIQVSARTA LNYIQVSAR LDAIETEIKNLILKI IETEIKNLI KYNVSSAIKTIVKIY YNVSSAIKT KTIVKIYDNYTLLST VKIYDNYTL HHVKRESVNNSNLSQ VKRESVNNS IKTIVKIYDNYTLLS VKIYDNYTL SAIKTIVKIYDNYTL IKTIVKIYD NHHVKRESVNNSNLS VKRESVNNS DLYEAYKAIVRSILL YKAIVRSIL KAIVRSILLMKDSLK IVRSILLMK SYLEGVKYNVSSAIK VKYNVSSAI YIQVSARTATNFVYA IQVSARTAT TIVKIYDNYTLLSTK VKIYDNYTL KLDAIETEIKNLILK IETEIKNLI IQVSARTATNFVYAR IQVSARTAT YTLLSTKQTQMYSTR YTLLSTKQT LALGLLFGFISCDLF LGLLFGFIS ESYLEGVKYNVSSAI LEGVKYNVS SDLYEAYKAIVRSIL EAYKAIVRS NYTLLSTKQTQMYST YTLLSTKQT KSKCLALGLLFGFIS LALGLLFGF SKCLALGLLFGFISC LGLLFGFIS EELEKDLKTLLNYIQ LEKDLKTLL KCLALGLLFGFISCD LGLLFGFIS CLALGLLFGFISCDL LGLLFGFIS AIVRSILLMKDSLKI ILLMKDSLK LEKDLKTLLNYIQVS LKTLLNYIQ IVRSILLMKDSLKII ILLMKDSLK ELEKDLKTLLNYIQV LKTLLNYIQ NLILKIKGQSDLYEA LKIKGQSDL IVKIYDNYTLLSTKQ IYDNYTLLS LILKIKGQSDLYEAY LKIKGQSDL VRSILLMKDSLKIIE ILLMKDSLK SVNNSNLSQKNVISE VNNSNLSQK MKIKSKCLALGLLFG MKIKSKCLA RKLDAIETEIKNLIL IETEIKNLI AIKTIVKIYDNYTLL VKIYDNYTL DPFNHHVKRESVNNS FNHHVKRES KRKLDAIETEIKNLI KLDAIETEI	
	HLA-DRB1*1501	EILKTKLLRERPETR LKTKLLRER ILKTKLLRERPETRK LLRERPETR LKTKLLRERPETRKE LLRERPETR KTKLLRERPETRKEE LLRERPETR TKLLRERPETRKEEI LLRERPETR KAIVRSILLMKDSLK IVRSILLMK YEAYKAIVRSILLMK YEAYKAIVR AIVRSILLMKDSLKI IVRSILLMK IVRSILLMKDSLKII IVRSILLMK AYKAIVRSILLMKDS IVRSILLMK	

		EAYKAIVRSILLMKD IVRSILLMK YKAIVRSILLMKDSL IVRSILLMK KLLRERPETRKEEIQ LLRERPETR ETEIKNLILKIKGQS IKNLILKIK TEIKNLILKIKGQSD IKNLILKIK LLRERPETRKEEIQK LLRERPETR ISEEEILKTKLLRER EILKTKLLR SEEEILKTKLLRERP LKTKLLRER EEEILKTKLLRERPE LKTKLLRER IETEIKNLILKIKGQ IKNLILKIK EEILKTKLLRERPET LKTKLLRER AIETEIKNLILKIKG IKNLILKIK DAIETEIKNLILKIK TEIKNLILK VRSILLMKDSLKIIE LLMKDSLKI RSILLMKDSLKIIEI LLMKDSLKI ATNFVYAREIYSKRK VYAREIYSK TNFVYAREIYSKRKL VYAREIYSK KDLKTLLNYIQVSAR LLNYIQVSA TATNFVYAREIYSKR VYAREIYSK NFVYAREIYSKRKLD VYAREIYSK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	ILKTKLLRERPETRK LLRERPETR LKTKLLRERPETRKE LRERPETRK
	HLA-DRB5*0101	ATNFVYAREIYSKRK YAREIYSKR TNFVYAREIYSKRKL YAREIYSKR NFVYAREIYSKRKLD YAREIYSKR FVYAREIYSKRKLDA YAREIYSKR EILKTKLLRERPETR LKTKLLRER VYAREIYSKRKLDAI YAREIYSKR TATNFVYAREIYSKR VYAREIYSK ILKTKLLRERPETRK LLRERPETR KTKLLRERPETRKEE LLRERPETR LKTKLLRERPETRKE LLRERPETR TKLLRERPETRKEEI LLRERPETR
AAL84595.1| BBK32 [Borrelia garinii] Seq44	HLA-DRB1*0101	TLFSTKLTQMYSTRL FSTKLTQMY LFSTKLTQMYSTRLD LTQMYSTRL FSTKLTQMYSTRLDN LTQMYSTRL STKLTQMYSTRLDNL LTQMYSTRL TKLTQMYSTRLDNLA LTQMYSTRL KLTQMYSTRLDNLAK LTQMYSTRL LTQMYSTRLDNLAKA LTQMYSTRL YSAYKAIVSSILLMR YKAIVSSIL NLYSAYKAIVSSILL YKAIVSSIL LYSAYKAIVSSILLM YKAIVSSIL SAYKAIVSSILLMRD YKAIVSSIL SNLYSAYKAIVSSIL YSAYKAIVS YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT KKVKSKYLALGLLFG VKSKYLALG IYDTYTLFSTKLTQM YTLFSTKLT NKIYDTYTLFSTKLT TYTLFSTKL KIYDTYTLFSTKLTQ YTLFSTKLT TYTLFSTKLTQMYST YTLFSTKLT KVKSKYLALGLLFGF YLALGLLFG VKSKYLALGLLFGFI YLALGLLFG

		KSKYLALGLLFGFIS YLALGLLFG
		SKYLALGLLFGFISC YLALGLLFG
		YTLFSTKLTQMYSTR YTLFSTKLT
		AYKAIVSSILLMRDS YKAIVSSIL
		YKAIVSSILLMRDSL YKAIVSSIL
		HSFKRDAANKSNFLQ FKRDAANKS
		IHSFKRDAANKSNFL FKRDAANKS
		DEYKGMTKGSLNSLS MTKGSLNSL
		PFIHSFKRDAANKSN FKRDAANKS
		MKKVKSKYLALGLLF VKSKYLALG
		QDEYKGMTKGSLNSL YKGMTKGSL
		EPFIHSFKRDAANKS FIHSFKRDA
		FIHSFKRDAANKSNF FKRDAANKS
		GMTKGSLNSLSGESG MTKGSLNSL
		EYKGMTKGSLNSLSG MTKGSLNSL
		YKGMTKGSLNSLSGE MTKGSLNSL
		MTKGSLNSLSGESGE LNSLSGESG
		YLALGLLFGFISCDL YLALGLLFG
		ENIEAKIKTLIAKIK EAKIKTLIA
		NIEAKIKTLIAKIKE IKTLIAKIK
		EAKIKTLIAKIKEKS IKTLIAKIK
		AKIKTLIAKIKEKSN IKTLIAKIK
		IEAKIKTLIAKIKEK IKTLIAKIK
		KYLALGLLFGFISCD YLALGLLFG
		FKTLLNYIQVSVKTA FKTLLNYIQ
		KGSLNSLSGESGELK LNSLSGESG
		LLNYIQVSVKTATNF YIQVSVKTA
		TKGSLNSLSGESGEL LNSLSGESG
		LNYIQVSVKTATNFV YIQVSVKTA
		KGMTKGSLNSLSGES MTKGSLNSL
		GSLNSLSGESGELKE LNSLSGESG
		EKNFKTLLNYIQVSV FKTLLNYIQ
		TLLNYIQVSVKTATN YIQVSVKTA
		KNFKTLLNYIQVSVK FKTLLNYIQ
		KTLLNYIQVSVKTAT YIQVSVKTA
		DLEKNFKTLLNYIQV FKTLLNYIQ
		EDLEKNFKTLLNYIQ EKNFKTLLN
		SFKRDAANKSNFLQK FKRDAANKS
		INKIYDTYTLFSTKL YDTYTLFST
		QQDEYKGMTKGSLNS YKGMTKGSL
		FKRDAANKSNFLQKN FKRDAANKS
		EGVKYNVDSAINTIN YNVDSAINT
		LEKNFKTLLNYIQVS FKTLLNYIQ
		GVKYNVDSAINTINK YNVDSAINT
		LEGVKYNVDSAINTI YNVDSAINT
		YLEGVKYNVDSAINT VKYNVDSAI
		NYIQVSVKTATNFVY YIQVSVKTA
		VKYNVDSAINTINKI YNVDSAINT
		SSLQDIAGSNSISYT IAGSNSISY
		KSSLQDIAGSNSISY LQDIAGSNS
		EKSNLYSAYKAIVSS YSAYKAIVS
		KSNLYSAYKAIVSSI YSAYKAIVS
		ITIDSDLRPKSSLQD DSDLRPKSS
		KEKSNLYSAYKAIVS LYSAYKAIV
		TIDSDLRPKSSLQDI LRPKSSLQD
		DSDLRPKSSLQDIAG LRPKSSLQD
		NFKTLLNYIQVSVKT FKTLLNYIQ

		IDSDLRPKSSLQDIA LRPKSSLQD NTINKIYDTYTLFST INKIYDTYT YIQVSVKTATNFVYI YIQVSVKTA KQQDEYKGMTKGSLN YKGMTKGSL SDLRPKSSLQDIAGS LRPKSSLQD QKQQDEYKGMTKGSL QKQQDEYKG SLQDIAGSNSISYTD IAGSNSISY LRPKSSLQDIAGSNS LRPKSSLQD LQDIAGSNSISYTDE IAGSNSISY KIKTLIAKIKEKSNL IKTLIAKIK IKTLIAKIKEKSNLY IKTLIAKIK TINKIYDTYTLFSTK YDTYTLFST QMYSTRLDNLAKAKA YSTRLDNLA KAIVSSILLMRDSLK IVSSILLMR TNFVYINEMHAKRKL INEMHAKRK ATNFVYINEMHAKRK FVYINEMHA SLNSLSGESGELKET LNSLSGESG LNSLSGESGELKETI LNSLSGESG FVYINEMHAKRKLEN INEMHAKRK NFVYINEMHAKRKLE INEMHAKRK AIVSSILLMRDSLKE VSSILLMRD QDIAGSNSISYTDEI IAGSNSISY
	HLA-DRB1*0301	NEIDITIDSDLRPKS ITIDSDLRP EIDITIDSDLRPKSS ITIDSDLRP IDITIDSDLRPKSSL ITIDSDLRP ITIDSDLRPKSSLQD IDSDLRPKS DITIDSDLRPKSSLQ IDSDLRPKS
	HLA-DRB1*0401	PFIHSFKRDAANKSN FKRDAANKS EPFIHSFKRDAANKS IHSFKRDAA FIHSFKRDAANKSNF FKRDAANKS HSFKRDAANKSNFLQ FKRDAANKS IHSFKRDAANKSNFL FKRDAANKS SFKRDAANKSNFLQK FKRDAANKS FKRDAANKSNFLQKN FKRDAANKS TATNFVYINEMHAKR FVYINEMHA TNFVYINEMHAKRKL FVYINEMHA ATNFVYINEMHAKRK FVYINEMHA KTATNFVYINEMHAK FVYINEMHA VKTATNFVYINEMHA TNFVYINEM KTLIAKIKEKSNLYS KIKEKSNLY IKTLIAKIKEKSNLY LIAKIKEKS TLIAKIKEKSNLYSA KIKEKSNLY LIAKIKEKSNLYSAY KIKEKSNLY IAKIKEKSNLYSAYK KIKEKSNLY NKIYDTYTLFSTKLT IYDTYTLFS FKTLLNYIQVSVKTA NYIQVSVKT TINKIYDTYTLFSTK IYDTYTLFS NTINKIYDTYTLFST IYDTYTLFS INTINKIYDTYTLFS INKIYDTYT INKIYDTYTLFSTKL IYDTYTLFS FVYINEMHAKRKLEN FVYINEMHA NFKTLLNYIQVSVKT FKTLLNYIQ NFVYINEMHAKRKLE FVYINEMHA LLNYIQVSVKTATNF NYIQVSVKT TLLNYIQVSVKTATN NYIQVSVKT

		SAYKAIVSSILLMRD YKAIVSSIL YSAYKAIVSSILLMR YKAIVSSIL KTLLNYIQVSVKTAT NYIQVSVKT
	HLA-DRB1*0404	ATNFVYINEMHAKRK FVYINEMHA TNFVYINEMHAKRKL FVYINEMHA TATNFVYINEMHAKR FVYINEMHA
	HLA-DRB1*0405	EDLEKNFKTLLNYIQ EKNFKTLLN DLEKNFKTLLNYIQV EKNFKTLLN FTKEDLEKNFKTLLN LEKNFKTLL TKEDLEKNFKTLLNY EKNFKTLLN NKIYDTYTLFSTKLT IYDTYTLFS KEDLEKNFKTLLNYI EKNFKTLLN LEKNFKTLLNYIQVS EKNFKTLLN EKNFKTLLNYIQVSV EKNFKTLLN IYDTYTLFSTKLTQM YTLFSTKLT KIYDTYTLFSTKLTQ YTLFSTKLT INTINKIYDTYTLFS INTINKIYD YDTYTLFSTKLTQMY YTLFSTKLT ITIDSDLRPKSSLQD ITIDSDLRP DTYTLFSTKLTQMYS YTLFSTKLT TIDSDLRPKSSLQDI LRPKSSLQD IDSDLRPKSSLQDIA LRPKSSLQD
	HLA-DRB1*0701	LYSAYKAIVSSILLM YKAIVSSIL YSAYKAIVSSILLMR YKAIVSSIL SAYKAIVSSILLMRD YKAIVSSIL NLYSAYKAIVSSILL YKAIVSSIL SNLYSAYKAIVSSIL YSAYKAIVS YIQVSVKTATNFVYI VKTATNFVY IQVSVKTATNFVYIN VKTATNFVY NYIQVSVKTATNFVY SVKTATNFV QVSVKTATNFVYINE VKTATNFVY VSVKTATNFVYINEM VKTATNFVY AYKAIVSSILLMRDS YKAIVSSIL YKAIVSSILLMRDSL YKAIVSSIL SVKTATNFVYINEMH VKTATNFVY LNYIQVSVKTATNFV VSVKTATNF VKTATNFVYINEMHA VKTATNFVY
	HLA-DRB1*0802	ESIKKPMNKKGKGKI SIKKPMNKK
	HLA-DRB1*0901	SNLYSAYKAIVSSIL YSAYKAIVS LYSAYKAIVSSILLM YKAIVSSIL YSAYKAIVSSILLMR AIVSSILLM YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT IYDTYTLFSTKLTQM YTLFSTKLT NLYSAYKAIVSSILL YSAYKAIVS KIYDTYTLFSTKLTQ YTLFSTKLT NKIYDTYTLFSTKLT IYDTYTLFS
	HLA-DRB1*1101	None
	HLA-DRB1*1302	NYIQVSVKTATNFVY IQVSVKTAT KTLLNYIQVSVKTAT LLNYIQVSV YDTYTLFSTKLTQMY YTLFSTKLT DTYTLFSTKLTQMYS YTLFSTKLT TLLNYIQVSVKTATN IQVSVKTAT LLNYIQVSVKTATNF IQVSVKTAT LNYIQVSVKTATNFV IQVSVKTAT IYDTYTLFSTKLTQM YTLFSTKLT

		YIQVSVKTATNFVYI	IQVSVKTAT
		IQVSVKTATNFVYIN	IQVSVKTAT
		NKIYDTYTLFSTKLT	NKIYDTYTL
		ENIEAKIKTLIAKIK	IEAKIKTLI
		KIYDTYTLFSTKLTQ	YTLFSTKLT
		NIEAKIKTLIAKIKE	IKTLIAKIK
		IEAKIKTLIAKIKEK	IKTLIAKIK
		YTLFSTKLTQMYSTR	YTLFSTKLT
		TYTLFSTKLTQMYST	YTLFSTKLT
		SAYKAIVSSILLMRD	IVSSILLMR
		KNFKTLLNYIQVSVK	LLNYIQVSV
		YSAYKAIVSSILLMR	YKAIVSSIL
		FKTLLNYIQVSVKTA	LLNYIQVSV
		EKNFKTLLNYIQVSV	FKTLLNYIQ
		EAKIKTLIAKIKEKS	IKTLIAKIK
		NFKTLLNYIQVSVKT	LNYIQVSVK
		AKIKTLIAKIKEKSN	IKTLIAKIK
		AYKAIVSSILLMRDS	IVSSILLMR
		DYEEIRLSNRYQSYL	IRLSNRYQS
		KSKYLALGLLFGFIS	YLALGLLFG
		YKAIVSSILLMRDSL	IVSSILLMR
		YEEIRLSNRYQSYLE	IRLSNRYQS
		DDYEEIRLSNRYQSY	IRLSNRYQS
		EDDYEEIRLSNRYQS	EEIRLSNRY
		SKYLALGLLFGFISC	LGLLFGFIS
		EEIRLSNRYQSYLEG	IRLSNRYQS
		ANKSNFLQKNVMLEE	SNFLQKNVM
		EDLEKNFKTLLNYIQ	EKNFKTLLN
		NKSNFLQKNVMLEEE	SNFLQKNVM
		KYLALGLLFGFISCD	LGLLFGFIS
		VDSAINTINKIYDTY	INTINKIYD
		YNVDSAINTINKIYD	SAINTINKI
		DLEKNFKTLLNYIQV	FKTLLNYIQ
		LALGLLFGFISCDLF	LGLLFGFIS
		SAINTINKIYDTYTL	INTINKIYD
		KAIVSSILLMRDSLK	IVSSILLMR
		YLALGLLFGFISCDL	LGLLFGFIS
		NVDSAINTINKIYDT	INTINKIYD
		DSAINTINKIYDTYT	INTINKIYD
		RKLENIEAKIKTLIA	IEAKIKTLI
		KLENIEAKIKTLIAK	IEAKIKTLI
		KRKLENIEAKIKTLI	ENIEAKIKT
		LEKNFKTLLNYIQVS	FKTLLNYIQ
		LENIEAKIKTLIAKI	IEAKIKTLI
		LYSAYKAIVSSILLM	YKAIVSSIL
		IKTLIAKIKEKSNLY	IKTLIAKIK
		KSNFLQKNVMLEEES	SNFLQKNVM
	HLA-DRB1*1501	KAIVSSILLMRDSLK	IVSSILLMR
		IVSSILLMRDSLKEV	IVSSILLMR
		AIVSSILLMRDSLKE	IVSSILLMR
		YSAYKAIVSSILLMR	YKAIVSSIL
		SAYKAIVSSILLMRD	IVSSILLMR
		AYKAIVSSILLMRDS	IVSSILLMR
		YKAIVSSILLMRDSL	IVSSILLMR
		KKGKGKIARKNGKSK	KKGKGKIAR
		VSSILLMRDSLKEVQ	ILLMRDSLK
		SSILLMRDSLKEVQY	ILLMRDSLK

		GKGKIARKNGKSKVS IARKNGKSK KGKIARKNGKSKVSG IARKNGKSK
	HLA-DRB3*0101	None
	HLA-DRB4*0101	GKSKVSGKEPFIHSF VSGKEPFIH KNGKSKVSGKEPFIH SKVSGKEPF NGKSKVSGKEPFIHS VSGKEPFIH KSKVSGKEPFIHSFK VSGKEPFIH SKVSGKEPFIHSFKR VSGKEPFIH VSGKEPFIHSFKRDA VSGKEPFIH
	HLA-DRB5*0101	ATNFVYINEMHAKRK YINEMHAKR TNFVYINEMHAKRKL INEMHAKRK NFVYINEMHAKRKLE INEMHAKRK FVYINEMHAKRKLEN INEMHAKRK VYINEMHAKRKLENI INEMHAKRK YINEMHAKRKLENIE INEMHAKRK KTELLKEQSETRKEK LLKEQSETR TELLKEQSETRKEKI LLKEQSETR TSEESIKKPMNKKGK IKKPMNKKG SEESIKKPMNKKGKG KKPMNKKGK SLKTELLKEQSETRK LLKEQSETR LKTELLKEQSETRKE LLKEQSETR ESIKKPMNKKGKGKI KKPMNKKGK EESIKKPMNKKGKGK KKPMNKKGK ELLKEQSETRKEKIQ LKEQSETRK

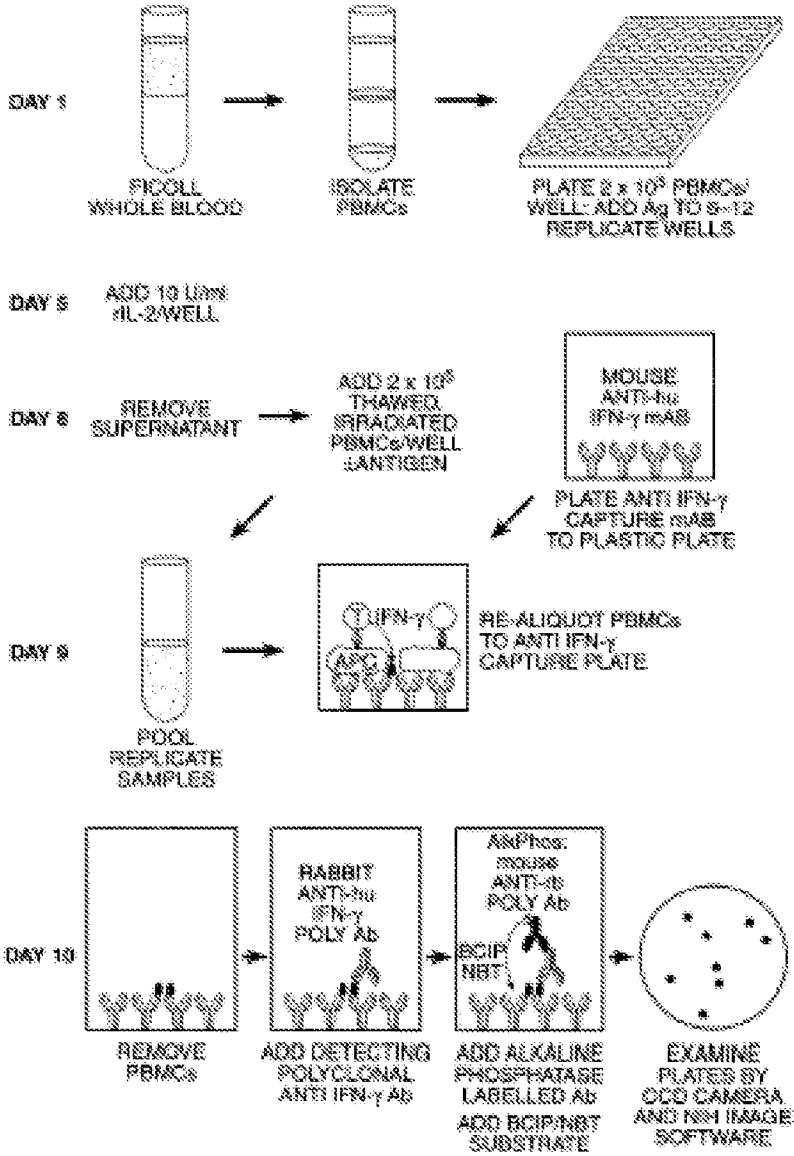

Fig. 35. Summary flow chart ELISPOT

Fig. 36. Prediction of cancer antigen BclX(L) specific MHC class 1, 8-, 9-, 10, 11-mer peptide binders

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
57	HLADSPAV	0.691	28	SB	Sequence	A0201
213	FLTGMTVA	0.687	29	SB	Sequence	A0201
166	AAWMATYL	0.477	285	WB	Sequence	A0201
160	VLVSRIAA	0.463	333	WB	Sequence	A0201
119	YQSFEQVV	0.436	448	WB	Sequence	A0201
147	GALCVESV	0.431	472	WB	Sequence	A0201
223	VLLGSLFS	0.427	494	WB	Sequence	A0201
213	FLTGMTVA	0.777	11	SB	Sequence	A0202
57	HLADSPAV	0.771	11	SB	Sequence	A0202
119	YQSFEQVV	0.590	84	WB	Sequence	A0202
218	TVAGVVLL	0.565	110	WB	Sequence	A0202
11	FLSYKLSQ	0.545	137	WB	Sequence	A0202
82	MAAVKQAL	0.512	195	WB	Sequence	A0202
73	SLDAREVI	0.475	294	WB	Sequence	A0202
192	ELYGNNAA	0.444	410	WB	Sequence	A0202
217	MTVAGVVL	0.440	425	WB	Sequence	A0202
160	VLVSRIAA	0.434	454	WB	Sequence	A0202
1	SQSNRELV	0.434	457	WB	Sequence	A0202
213	FLTGMTVA	0.852	4	SB	Sequence	A0203
57	HLADSPAV	0.831	6	SB	Sequence	A0203
160	VLVSRIAA	0.642	48	SB	Sequence	A0203
158	MQVLVSRI	0.602	74	WB	Sequence	A0203
11	FLSYKLSQ	0.582	92	WB	Sequence	A0203
133	GVNWGRIV	0.581	92	WB	Sequence	A0203
216	GMTVAGVV	0.579	94	WB	Sequence	A0203
119	YQSFEQVV	0.578	96	WB	Sequence	A0203
164	RIAAWMAT	0.573	101	WB	Sequence	A0203
78	EVIPMAAV	0.486	261	WB	Sequence	A0203
1	SQSNRELV	0.481	274	WB	Sequence	A0203
217	MTVAGVVL	0.467	318	WB	Sequence	A0203
147	GALCVESV	0.464	328	WB	Sequence	A0203
221	GVVLLGSL	0.443	412	WB	Sequence	A0203
218	TVAGVVLL	0.440	429	WB	Sequence	A0203
57	HLADSPAV	0.555	122	WB	Sequence	A0204
153	SVDKEMQV	0.431	469	WB	Sequence	A0204
57	HLADSPAV	0.780	10	SB	Sequence	A0206
158	MQVLVSRI	0.733	18	SB	Sequence	A0206
213	FLTGMTVA	0.682	31	SB	Sequence	A0206
1	SQSNRELV	0.677	32	SB	Sequence	A0206
119	YQSFEQVV	0.677	33	SB	Sequence	A0206
138	RIVAFFSF	0.653	42	SB	Sequence	A0206
164	RIAAWMAT	0.575	99	WB	Sequence	A0206
147	GALCVESV	0.568	106	WB	Sequence	A0206
166	AAWMATYL	0.567	108	WB	Sequence	A0206
217	MTVAGVVL	0.563	112	WB	Sequence	A0206
160	VLVSRIAA	0.517	185	WB	Sequence	A0206
42	SEMEIPSA	0.514	191	WB	Sequence	A0206
78	EVIPMAAV	0.496	233	WB	Sequence	A0206
153	SVDKEMQV	0.493	240	WB	Sequence	A0206
57	HLADSPAV	0.955	1	SB	Sequence	A0211
153	SVDKEMQV	0.898	3	SB	Sequence	A0211
213	FLTGMTVA	0.893	3	SB	Sequence	A0211
73	SLDAREVI	0.877	3	SB	Sequence	A0211
192	ELYGNNAA	0.834	6	SB	Sequence	A0211

218	TVAGVVLL	0.797	8	SB	Sequence	A0211
172	YLNDHLEP	0.751	14	SB	Sequence	A0211
78	EVIPMAAV	0.739	16	SB	Sequence	A0211
216	GMTVAGVV	0.718	21	SB	Sequence	A0211
160	VLVSRIAA	0.684	30	SB	Sequence	A0211
223	VLLGSLFS	0.683	30	SB	Sequence	A0211
133	GVNWGRIV	0.668	36	SB	Sequence	A0211
212	WFLTGMTV	0.668	36	SB	Sequence	A0211
144	SFGGALCV	0.591	83	WB	Sequence	A0211
72	SSLDAREV	0.590	84	WB	Sequence	A0211
106	DLTSQLHI	0.564	111	WB	Sequence	A0211
119	YQSFEQVV	0.545	136	WB	Sequence	A0211
81	PMAAVKQA	0.532	158	WB	Sequence	A0211
11	FLSYKLSQ	0.511	198	WB	Sequence	A0211
166	AAWMATYL	0.456	360	WB	Sequence	A0211
1	SQSNRELV	0.439	431	WB	Sequence	A0211
147	GALCVESV	0.439	434	WB	Sequence	A0211
57	HLADSPAV	0.915	2	SB	Sequence	A0212
192	ELYGNNAA	0.813	7	SB	Sequence	A0212
213	FLTGMTVA	0.801	8	SB	Sequence	A0212
153	SVDKEMQV	0.732	18	SB	Sequence	A0212
73	SLDAREVI	0.714	22	SB	Sequence	A0212
160	VLVSRIAA	0.662	38	SB	Sequence	A0212
172	YLNDHLEP	0.662	38	SB	Sequence	A0212
119	YQSFEQVV	0.586	88	WB	Sequence	A0212
78	EVIPMAAV	0.585	88	WB	Sequence	A0212
223	VLLGSLFS	0.582	92	WB	Sequence	A0212
11	FLSYKLSQ	0.573	101	WB	Sequence	A0212
212	WFLTGMTV	0.541	142	WB	Sequence	A0212
216	GMTVAGVV	0.466	321	WB	Sequence	A0212
57	HLADSPAV	0.892	3	SB	Sequence	A0216
153	SVDKEMQV	0.817	7	SB	Sequence	A0216
213	FLTGMTVA	0.761	13	SB	Sequence	A0216
192	ELYGNNAA	0.715	21	SB	Sequence	A0216
78	EVIPMAAV	0.666	37	SB	Sequence	A0216
218	TVAGVVLL	0.657	41	SB	Sequence	A0216
73	SLDAREVI	0.640	49	SB	Sequence	A0216
144	SFGGALCV	0.630	54	WB	Sequence	A0216
216	GMTVAGVV	0.613	65	WB	Sequence	A0216
166	AAWMATYL	0.603	73	WB	Sequence	A0216
160	VLVSRIAA	0.583	91	WB	Sequence	A0216
212	WFLTGMTV	0.565	110	WB	Sequence	A0216
11	FLSYKLSQ	0.488	255	WB	Sequence	A0216
106	DLTSQLHI	0.487	258	WB	Sequence	A0216
133	GVNWGRIV	0.470	308	WB	Sequence	A0216
81	PMAAVKQA	0.469	311	WB	Sequence	A0216
118	AYQSFEQV	0.461	342	WB	Sequence	A0216
223	VLLGSLFS	0.442	417	WB	Sequence	A0216
147	GALCVESV	0.438	436	WB	Sequence	A0216
57	HLADSPAV	0.924	2	SB	Sequence	A0219
213	FLTGMTVA	0.668	36	SB	Sequence	A0219
153	SVDKEMQV	0.597	78	WB	Sequence	A0219
73	SLDAREVI	0.576	98	WB	Sequence	A0219
218	TVAGVVLL	0.517	185	WB	Sequence	A0219
192	ELYGNNAA	0.486	259	WB	Sequence	A0219
212	WFLTGMTV	0.458	352	WB	Sequence	A0219
166	AAWMATYL	0.455	362	WB	Sequence	A0219
106	DLTSQLHI	0.448	390	WB	Sequence	A0219
223	VLLGSLFS	0.431	471	WB	Sequence	A0219
12	LSYKLSQK	0.761	13	SB	Sequence	A0301
8	VVDFLSYK	0.551	128	WB	Sequence	A0301
224	LLGSLFSR	0.487	257	WB	Sequence	A0301

8	VVDFLSYK	0.751	14	SB	Sequence	A1101
12	LSYKLSQK	0.721	20	SB	Sequence	A1101
79	VIPMAAVK	0.509	203	WB	Sequence	A1101
124	QVVNELFR	0.472	302	WB	Sequence	A1101
7	LVVDFLSY	0.457	355	WB	Sequence	A1101
197	NAAAESRK	0.455	363	WB	Sequence	A1101
135	NWGRIVAF	0.600	75	WB	Sequence	A2301
138	RIVAFFSF	0.466	321	WB	Sequence	A2301
222	VVLLGSLF	0.461	339	WB	Sequence	A2301
135	NWGRIVAF	0.617	62	WB	Sequence	A2402
118	AYQSFEQV	0.569	105	WB	Sequence	A2403
78	EVIPMAAV	0.598	77	WB	Sequence	A2601
7	LVVDFLSY	0.541	144	WB	Sequence	A2601
78	EVIPMAAV	0.862	4	SB	Sequence	A2602
7	LVVDFLSY	0.797	9	SB	Sequence	A2602
112	HITPGTAY	0.755	14	SB	Sequence	A2602
97	ELRYRRAF	0.589	85	WB	Sequence	A2602
138	RIVAFFSF	0.529	164	WB	Sequence	A2602
112	HITPGTAY	0.597	78	WB	Sequence	A2902
7	LVVDFLSY	0.480	276	WB	Sequence	A2902
204	KGQERFNR	0.743	16	SB	Sequence	A3101
224	LLGSLFSR	0.697	26	SB	Sequence	A3101
157	EMQVLVSR	0.583	90	WB	Sequence	A3101
70	HSSSLDAR	0.577	97	WB	Sequence	A3101
83	AAVKQALR	0.539	146	WB	Sequence	A3101
95	EFELRYRR	0.509	201	WB	Sequence	A3101
124	QVVNELFR	0.453	369	WB	Sequence	A3101
12	LSYKLSQK	0.447	397	WB	Sequence	A3101
95	EFELRYRR	0.823	6	SB	Sequence	A3301
157	EMQVLVSR	0.738	16	SB	Sequence	A3301
94	DEFELRYR	0.650	43	SB	Sequence	A3301
201	ESRKGQER	0.606	71	WB	Sequence	A3301
224	LLGSLFSR	0.538	148	WB	Sequence	A3301
70	HSSSLDAR	0.463	332	WB	Sequence	A3301
124	QVVNELFR	0.803	8	SB	Sequence	A6801
70	HSSSLDAR	0.775	11	SB	Sequence	A6801
197	NAAAESRK	0.681	31	SB	Sequence	A6801
12	LSYKLSQK	0.647	45	SB	Sequence	A6801
157	EMQVLVSR	0.599	76	WB	Sequence	A6801
196	NNAAAESR	0.585	88	WB	Sequence	A6801
83	AAVKQALR	0.535	153	WB	Sequence	A6801
201	ESRKGQER	0.532	158	WB	Sequence	A6801
165	IAAWMATY	0.532	158	WB	Sequence	A6801
95	EFELRYRR	0.511	198	WB	Sequence	A6801
117	TAYQSFEQ	0.507	208	WB	Sequence	A6801
8	VVDFLSYK	0.481	273	WB	Sequence	A6801
94	DEFELRYR	0.457	357	WB	Sequence	A6801
26	FSDVEENR	0.442	418	WB	Sequence	A6801
224	LLGSLFSR	0.430	476	WB	Sequence	A6801
78	EVIPMAAV	0.888	3	SB	Sequence	A6802
218	TVAGVVLL	0.790	9	SB	Sequence	A6802
215	TGMTVAGV	0.742	16	SB	Sequence	A6802
217	MTVAGVVL	0.697	26	SB	Sequence	A6802
82	MAAVKQAL	0.633	52	WB	Sequence	A6802
57	HLADSPAV	0.549	131	WB	Sequence	A6802
207	ERFNRWFL	0.481	273	WB	Sequence	A6802
60	DSPAVNGA	0.473	300	WB	Sequence	A6802

192	ELYGNNAA	0.447	395	WB	Sequence	A6802
91	EAGDEFEL	0.436	444	WB	Sequence	A6802
78	EVIPMAAV	0.812	7	SB	Sequence	A6901
57	HLADSPAV	0.740	16	SB	Sequence	A6901
192	ELYGNNAA	0.570	104	WB	Sequence	A6901
217	MTVAGVVL	0.544	138	WB	Sequence	A6901
218	TVAGVVLL	0.507	206	WB	Sequence	A6901
91	EAGDEFEL	0.489	252	WB	Sequence	A6901
153	SVDKEMQV	0.437	441	WB	Sequence	A6901
212	WFLTGMTV	0.436	445	WB	Sequence	A6901
61	SPAVNGAT	0.657	41	SB	Sequence	B0702
82	MAAVKQAL	0.468	316	WB	Sequence	B0702
166	AAWMATYL	0.430	477	WB	Sequence	B0702
97	ELRYRRAF	0.589	85	WB	Sequence	B0801
7	LVVDFLSY	0.511	198	WB	Sequence	B1501
138	RIVAFFSF	0.493	240	WB	Sequence	B1501
112	HITPGTAY	0.492	243	WB	Sequence	B1501
165	IAAWMATY	0.473	300	WB	Sequence	B1501
97	ELRYRRAF	0.439	430	WB	Sequence	B1501
222	VVLLGSLF	0.433	461	WB	Sequence	B1501
206	QERFNRWF	0.528	165	WB	Sequence	B1801
5	RELVVDFL	0.517	185	WB	Sequence	B1801
122	FEQVVNEL	0.508	205	WB	Sequence	B1801
210	NRWFLTGM	0.510	200	WB	Sequence	B2705
165	IAAWMATY	0.806	8	SB	Sequence	B3501
7	LVVDFLSY	0.629	55	WB	Sequence	B3501
82	MAAVKQAL	0.591	83	WB	Sequence	B3501
112	HITPGTAY	0.543	140	WB	Sequence	B3501
75	DAREVIPM	0.516	187	WB	Sequence	B3501
142	FFSFGGAL	0.499	226	WB	Sequence	B3501
61	SPAVNGAT	0.478	283	WB	Sequence	B3501
166	AAWMATYL	0.476	289	WB	Sequence	B3501
217	MTVAGVVL	0.470	307	WB	Sequence	B3501
5	RELVVDFL	0.624	58	WB	Sequence	B4001
122	FEQVVNEL	0.618	62	WB	Sequence	B4001
5	RELVVDFL	0.442	420	WB	Sequence	B4002
156	KEMQVLVS	0.430	478	WB	Sequence	B4403
77	REVIPMAA	0.434	456	WB	Sequence	B4501
161	LVSRIAAW	0.626	57	WB	Sequence	B5801
165	IAAWMATY	0.593	81	WB	Sequence	B5801
16	LSQKGYSW	0.586	88	WB	Sequence	B5801
19	KGYSWSQF	0.543	141	WB	Sequence	B5801
138	RIVAFFSF	0.467	320	WB	Sequence	B5801
49	AINGNPSW	0.447	394	WB	Sequence	B5801
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104	FSDLTSQLH	0.482	270	WB	Sequence	A0101
143	FSFGGALCV	0.518	183	WB	Sequence	A0201
217	MTVAGVVLL	0.478	282	WB	Sequence	A0201
172	YLNDHLEPW	0.739	16	SB	Sequence	A0202
217	MTVAGVVLL	0.604	72	WB	Sequence	A0202
165	IAAWMATYL	0.568	107	WB	Sequence	A0202

213	FLTGMTVAG	0.564	111	WB	Sequence	A0202
11	FLSYKLSQK	0.520	179	WB	Sequence	A0202
161	LVSRIAAWM	0.450	382	WB	Sequence	A0202
8	VVDFLSYKL	0.449	387	WB	Sequence	A0202
192	ELYGNNAAA	0.447	394	WB	Sequence	A0202
81	PMAAVKQAL	0.437	441	WB	Sequence	A0202
216	GMTVAGVVL	0.436	448	WB	Sequence	A0202
214	LTGMTVAGV	0.691	28	SB	Sequence	A0203
217	MTVAGVVLL	0.609	69	WB	Sequence	A0203
165	IAAWMATYL	0.530	161	WB	Sequence	A0203
84	AVKQALREA	0.518	183	WB	Sequence	A0203
110	QLHITPGIA	0.507	206	WB	Sequence	A0203
172	YLNDHLEPW	0.493	240	WB	Sequence	A0203
117	TAYQSFEQV	0.473	300	WB	Sequence	A0203
11	FLSYKLSQK	0.447	396	WB	Sequence	A0203
214	LTGMTVAGV	0.504	213	WB	Sequence	A0204
217	MTVAGVVLL	0.475	291	WB	Sequence	A0204
109	SQLHITPGT	0.712	22	SB	Sequence	A0206
217	MTVAGVVLL	0.675	33	SB	Sequence	A0206
117	TAYQSFEQV	0.650	43	SB	Sequence	A0206
1	SQSNRELVV	0.648	45	SB	Sequence	A0206
143	FSFGGALCV	0.584	90	WB	Sequence	A0206
77	REVIPMAAV	0.572	103	WB	Sequence	A0206
165	IAAWMATYL	0.551	128	WB	Sequence	A0206
158	MQVLVSRIA	0.544	138	WB	Sequence	A0206
214	LTGMTVAGV	0.492	244	WB	Sequence	A0206
172	YLNDHLEPW	0.464	331	WB	Sequence	A0206
42	SEMETPSAI	0.440	426	WB	Sequence	A0206
192	ELYGNNAAA	0.863	4	SB	Sequence	A0211
143	FSFGGALCV	0.797	8	SB	Sequence	A0211
81	PMAAVKQAL	0.794	9	SB	Sequence	A0211
172	YLNDHLEPW	0.715	21	SB	Sequence	A0211
153	SVDKEMQVL	0.703	24	SB	Sequence	A0211
8	VVDFLSYKL	0.696	26	SB	Sequence	A0211
217	MTVAGVVLL	0.634	52	WB	Sequence	A0211
112	HITPGTAYQ	0.618	62	WB	Sequence	A0211
117	TAYQSFEQV	0.617	63	WB	Sequence	A0211
223	VLLGSLFSR	0.581	93	WB	Sequence	A0211
213	FLTGMTVAG	0.581	93	WB	Sequence	A0211
133	GVNWGRIVA	0.575	99	WB	Sequence	A0211
216	GMTVAGVVL	0.553	126	WB	Sequence	A0211
185	GGWDTFVEL	0.550	130	WB	Sequence	A0211
103	AFSDLTSQL	0.472	302	WB	Sequence	A0211
176	HLEPWIQEN	0.427	493	WB	Sequence	A0211
192	ELYGNNAAA	0.845	5	SB	Sequence	A0212
81	PMAAVKQAL	0.789	9	SB	Sequence	A0212
143	FSFGGALCV	0.702	25	SB	Sequence	A0212
172	YLNDHLEPW	0.673	34	SB	Sequence	A0212
223	VLLGSLFSR	0.573	101	WB	Sequence	A0212
8	VVDFLSYKL	0.561	115	WB	Sequence	A0212
153	SVDKEMQVL	0.535	153	WB	Sequence	A0212
213	FLTGMTVAG	0.521	178	WB	Sequence	A0212
118	AYQSFEQVV	0.476	290	WB	Sequence	A0212
192	ELYGNNAAA	0.741	16	SB	Sequence	A0216
81	PMAAVKQAL	0.710	22	SB	Sequence	A0216
143	FSFGGALCV	0.652	42	SB	Sequence	A0216
117	TAYQSFEQV	0.593	81	WB	Sequence	A0216
112	HITPGTAYQ	0.512	196	WB	Sequence	A0216
216	GMTVAGVVL	0.430	479	WB	Sequence	A0216
81	PMAAVKQAL	0.675	33	SB	Sequence	A0219

143	FSFGGALCV	0.652	43	SB	Sequence	A0219
192	ELYGNNAAA	0.541	142	WB	Sequence	A0219
117	TAYQSFEQV	0.497	232	WB	Sequence	A0219
172	YLNDHLEPW	0.459	348	WB	Sequence	A0219
223	VLLGSLFSR	0.456	361	WB	Sequence	A0219
214	LTGMTVAGV	0.450	384	WB	Sequence	A0219
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224	LLGSLFSRK	0.762	13	SB	Sequence	A0301
11	FLSYKLSQK	0.710	23	SB	Sequence	A0301
164	RIAAWMATY	0.698	26	SB	Sequence	A0301
223	VLLGSLFSR	0.615	64	WB	Sequence	A0301
7	LVVDFLSYK	0.497	231	WB	Sequence	A0301
7	LVVDFLSYK	0.767	12	SB	Sequence	A1101
224	LLGSLFSRK	0.612	66	WB	Sequence	A1101
223	VLLGSLFSR	0.595	79	WB	Sequence	A1101
164	RIAAWMATY	0.575	99	WB	Sequence	A1101
148	ALCVESVDK	0.529	163	WB	Sequence	A1101
78	EVIPMAAVK	0.509	201	WB	Sequence	A1101
11	FLSYKLSQK	0.430	477	WB	Sequence	A1101
99	RYRRAFSDL	0.690	28	SB	Sequence	A2301
135	NWGRIVAFF	0.644	47	SB	Sequence	A2301
137	GRIVAFFSF	0.459	346	WB	Sequence	A2301
135	NWGRIVAFF	0.739	16	SB	Sequence	A2402
99	RYRRAFSDL	0.550	129	WB	Sequence	A2402
99	RYRRAFSDL	0.748	15	SB	Sequence	A2403
121	SFEQVVNEL	0.557	120	WB	Sequence	A2403
118	AYQSFEQVV	0.487	256	WB	Sequence	A2403
6	ELVVDFLSY	0.532	158	WB	Sequence	A2601
164	RIAAWMATY	0.495	235	WB	Sequence	A2601
164	RIAAWMATY	0.923	2	SB	Sequence	A2602
6	ELVVDFLSY	0.873	3	SB	Sequence	A2602
161	LVSRIAAWM	0.677	32	SB	Sequence	A2602
153	SVDKEMQVL	0.639	49	SB	Sequence	A2602
78	EVIPMAAVK	0.496	234	WB	Sequence	A2602
217	MTVAGVVLL	0.481	273	WB	Sequence	A2602
111	LHITPGTAY	0.553	125	WB	Sequence	A2902
6	ELVVDFLSY	0.539	146	WB	Sequence	A2902
164	RIAAWMATY	0.463	334	WB	Sequence	A3002
82	MAAVKQALR	0.766	12	SB	Sequence	A3101
223	VLLGSLFSR	0.686	30	SB	Sequence	A3101
7	LVVDFLSYK	0.573	101	WB	Sequence	A3101
156	KEMQVLVSR	0.474	296	WB	Sequence	A3101
94	DEFELRYRR	0.721	20	SB	Sequence	A3301
82	MAAVKQALR	0.665	37	SB	Sequence	A3301
97	ELRYRRAFS	0.614	65	WB	Sequence	A3301
223	VLLGSLFSR	0.581	92	WB	Sequence	A3301
91	EAGDEFELR	0.532	157	WB	Sequence	A3301
25	QFSDVEENR	0.531	159	WB	Sequence	A3301
78	EVIPMAAVK	0.848	5	SB	Sequence	A6801
82	MAAVKQALR	0.813	7	SB	Sequence	A6801
7	LVVDFLSYK	0.786	10	SB	Sequence	A6801
91	EAGDEFELR	0.710	23	SB	Sequence	A6801
123	EQVVNELFR	0.635	51	WB	Sequence	A6801
11	FLSYKLSQK	0.558	119	WB	Sequence	A6801
94	DEFELRYRR	0.544	139	WB	Sequence	A6801
25	QFSDVEENR	0.540	145	WB	Sequence	A6801

196	NNAAAESRK	0.474	295	WB	Sequence	A6801
223	VLLGSLFSR	0.430	477	WB	Sequence	A6801
217	MTVAGVVLL	0.796	9	SB	Sequence	A6802
117	TAYQSFEQV	0.729	18	SB	Sequence	A6802
215	TGMTVAGVV	0.654	42	SB	Sequence	A6802
0	MSQSNRELV	0.587	86	WB	Sequence	A6802
21	YSWSQFSDV	0.549	131	WB	Sequence	A6802
143	FSFGGALCV	0.526	169	WB	Sequence	A6802
152	ESVDKEMQV	0.525	171	WB	Sequence	A6802
169	MATYLNDHL	0.520	180	WB	Sequence	A6802
192	ELYGNNAAA	0.509	202	WB	Sequence	A6802
140	VAFFSFGGA	0.500	222	WB	Sequence	A6802
214	LTGMTVAGV	0.464	330	WB	Sequence	A6802
165	IAAWMATYL	0.451	378	WB	Sequence	A6802
217	MTVAGVVLL	0.705	24	SB	Sequence	A6901
117	TAYQSFEQV	0.623	58	WB	Sequence	A6901
192	ELYGNNAAA	0.604	72	WB	Sequence	A6901
143	FSFGGALCV	0.589	85	WB	Sequence	A6901
214	LTGMTVAGV	0.557	120	WB	Sequence	A6901
21	YSWSQFSDV	0.489	252	WB	Sequence	A6901
36	APEGTESEM	0.519	181	WB	Sequence	B0702
61	SPAVNGATG	0.454	369	WB	Sequence	B0702
114	TPGTAYQSF	0.450	382	WB	Sequence	B0702
96	FELRYRRAF	0.497	229	WB	Sequence	B0801
164	RIAAWMATY	0.586	87	WB	Sequence	B1501
88	ALREAGDEF	0.520	180	WB	Sequence	B1501
96	FELRYRRAF	0.752	14	SB	Sequence	B1801
206	QERFNRWFL	0.592	82	WB	Sequence	B1801
122	FEQVVNELF	0.523	174	WB	Sequence	B1801
182	QENGGWDTF	0.476	290	WB	Sequence	B1801
137	GRIVAFFSF	0.554	124	WB	Sequence	B2705
101	RRAFSDLTS	0.434	459	WB	Sequence	B2705
114	TPGTAYQSF	0.705	24	SB	Sequence	B3501
165	IAAWMATYL	0.649	44	SB	Sequence	B3501
36	APEGTESEM	0.540	144	WB	Sequence	B3501
6	ELVVDFLSY	0.531	159	WB	Sequence	B3501
111	LHITPGTAY	0.437	441	WB	Sequence	B3501
53	NPSWHLADS	0.429	480	WB	Sequence	B3501
164	RIAAWMATY	0.428	485	WB	Sequence	B3501
90	REAGDEFEL	0.788	9	SB	Sequence	B4001
206	QERFNRWFL	0.597	78	WB	Sequence	B4001
182	QENGGWDTF	0.525	170	WB	Sequence	B4001
122	FEQVVNELF	0.453	370	WB	Sequence	B4001
96	FELRYRRAF	0.446	399	WB	Sequence	B4001
42	SEMETPSAI	0.504	215	WB	Sequence	B4002
96	FELRYRRAF	0.473	299	WB	Sequence	B4002
182	QENGGWDTF	0.434	455	WB	Sequence	B4402
42	SEMETPSAI	0.467	319	WB	Sequence	B4403
5	RELVVDFLS	0.444	407	WB	Sequence	B4403
77	REVIPMAAV	0.438	438	WB	Sequence	B4501
165	IAAWMATYL	0.442	416	WB	Sequence	B5301
80	IPMAAVKQA	0.716	21	SB	Sequence	B5401

48	SAINGNPSW	0.641	48	SB	Sequence B5801
15	KLSQKGYSW	0.596	79	WB	Sequence B5801
165	IAAWMATYL	0.559	118	WB	Sequence B5801
172	YLNDHLEPW	0.506	208	WB	Sequence B5801
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104	FSDLTSQLHI	0.427	492	WB	Sequence A0101
172	YLNDHLEPWI	0.866	4	SB	Sequence A0201
213	FLTGMTVAGV	0.841	5	SB	Sequence A0201
164	RIAAWMATYL	0.651	43	SB	Sequence A0201
168	WMATYLNDHL	0.573	101	WB	Sequence A0201
7	LVVDFLSYKL	0.524	173	WB	Sequence A0201
73	SLDAREVIPM	0.491	246	WB	Sequence A0201
160	VLVSRIAAWM	0.486	259	WB	Sequence A0201
153	SVDKEMQVLV	0.473	298	WB	Sequence A0201
216	GMTVAGVVLL	0.444	411	WB	Sequence A0201
213	FLTGMTVAGV	0.811	7	SB	Sequence A0202
168	WMATYLNDHL	0.772	11	SB	Sequence A0202
164	RIAAWMATYL	0.763	13	SB	Sequence A0202
7	LVVDFLSYKL	0.651	43	SB	Sequence A0202
102	RAFSDLTSQL	0.617	63	WB	Sequence A0202
73	SLDAREVIPM	0.616	63	WB	Sequence A0202
172	YLNDHLEPWI	0.587	87	WB	Sequence A0202
216	GMTVAGVVLL	0.496	233	WB	Sequence A0202
145	FGGALCVESV	0.480	276	WB	Sequence A0202
160	VLVSRIAAWM	0.430	476	WB	Sequence A0202
213	FLTGMTVAGV	0.936	2	SB	Sequence A0203
172	YLNDHLEPWI	0.891	3	SB	Sequence A0203
164	RIAAWMATYL	0.837	5	SB	Sequence A0203
168	WMATYLNDHL	0.647	45	SB	Sequence A0203
160	VLVSRIAAWM	0.613	66	WB	Sequence A0203
139	IVAFFSFGGA	0.596	79	WB	Sequence A0203
7	LVVDFLSYKL	0.581	92	WB	Sequence A0203
125	VVNELFRDGV	0.570	105	WB	Sequence A0203
216	GMTVAGVVLL	0.476	289	WB	Sequence A0203
102	RAFSDLTSQL	0.470	308	WB	Sequence A0203
214	LTGMTVAGVV	0.468	315	WB	Sequence A0203
116	GTAYQSFEQV	0.463	335	WB	Sequence A0203
213	FLTGMTVAGV	0.697	26	SB	Sequence A0204
172	YLNDHLEPWI	0.664	37	SB	Sequence A0204
73	SLDAREVIPM	0.477	287	WB	Sequence A0204
164	RIAAWMATYL	0.476	290	WB	Sequence A0204
7	LVVDFLSYKL	0.468	317	WB	Sequence A0204
49	AINGNPSWHL	0.452	374	WB	Sequence A0204
213	FLTGMTVAGV	0.869	4	SB	Sequence A0206
164	RIAAWMATYL	0.809	7	SB	Sequence A0206
172	YLNDHLEPWI	0.722	20	SB	Sequence A0206
158	MQVLVSRIAA	0.689	28	SB	Sequence A0206
7	LVVDFLSYKL	0.684	30	SB	Sequence A0206
168	WMATYLNDHL	0.680	31	SB	Sequence A0206
109	SQLHITPGTA	0.652	43	SB	Sequence A0206
116	GTAYQSFEQV	0.572	102	WB	Sequence A0206
153	SVDKEMQVLV	0.558	119	WB	Sequence A0206
102	RAFSDLTSQL	0.543	140	WB	Sequence A0206
156	KEMQVLVSRI	0.508	204	WB	Sequence A0206
181	IQENGGWDTF	0.508	205	WB	Sequence A0206
139	IVAFFSFGGA	0.495	235	WB	Sequence A0206
125	VVNELFRDGV	0.483	269	WB	Sequence A0206
117	TAYQSFEQVV	0.450	383	WB	Sequence A0206

213	FLTGMTVAGV	0.966	1	SB	Sequence	A0211
172	YLNDHLEPWI	0.951	1	SB	Sequence	A0211
153	SVDKEMQVLV	0.905	2	SB	Sequence	A0211
73	SLDAREVIPM	0.826	6	SB	Sequence	A0211
216	GMTVAGVVLL	0.737	17	SB	Sequence	A0211
7	LVVDFLSYKL	0.730	18	SB	Sequence	A0211
164	RIAAWMATYL	0.711	22	SB	Sequence	A0211
125	VVNELFRDGV	0.687	29	SB	Sequence	A0211
49	AINGNPSWHL	0.686	29	SB	Sequence	A0211
168	WMATYLNDHL	0.685	30	SB	Sequence	A0211
117	TAYQSFEQVV	0.633	52	WB	Sequence	A0211
160	VLVSRIAAWM	0.632	53	WB	Sequence	A0211
142	FFSFGGALCV	0.567	107	WB	Sequence	A0211
223	VLLGSLFSRK	0.498	228	WB	Sequence	A0211
102	RAFSDLTSQL	0.453	372	WB	Sequence	A0211
116	GTAYQSFEQV	0.429	481	WB	Sequence	A0211
213	FLTGMTVAGV	0.932	2	SB	Sequence	A0212
172	YLNDHLEPWI	0.916	2	SB	Sequence	A0212
153	SVDKEMQVLV	0.742	16	SB	Sequence	A0212
168	WMATYLNDHL	0.697	26	SB	Sequence	A0212
125	VVNELFRDGV	0.695	27	SB	Sequence	A0212
7	LVVDFLSYKL	0.648	45	SB	Sequence	A0212
160	VLVSRIAAWM	0.604	72	WB	Sequence	A0212
73	SLDAREVIPM	0.594	80	WB	Sequence	A0212
49	AINGNPSWHL	0.570	104	WB	Sequence	A0212
164	RIAAWMATYL	0.550	129	WB	Sequence	A0212
142	FFSFGGALCV	0.494	238	WB	Sequence	A0212
223	VLLGSLFSRK	0.487	258	WB	Sequence	A0212
117	TAYQSFEQVV	0.482	270	WB	Sequence	A0212
192	ELYGNNAAAE	0.475	293	WB	Sequence	A0212
216	GMTVAGVVLL	0.440	426	WB	Sequence	A0212
213	FLTGMTVAGV	0.911	2	SB	Sequence	A0216
172	YLNDHLEPWI	0.869	4	SB	Sequence	A0216
153	SVDKEMQVLV	0.772	11	SB	Sequence	A0216
168	WMATYLNDHL	0.696	26	SB	Sequence	A0216
164	RIAAWMATYL	0.695	27	SB	Sequence	A0216
49	AINGNPSWHL	0.680	31	SB	Sequence	A0216
160	VLVSRIAAWM	0.657	41	SB	Sequence	A0216
7	LVVDFLSYKL	0.643	47	SB	Sequence	A0216
73	SLDAREVIPM	0.617	62	WB	Sequence	A0216
216	GMTVAGVVLL	0.588	85	WB	Sequence	A0216
117	TAYQSFEQVV	0.530	161	WB	Sequence	A0216
142	FFSFGGALCV	0.487	256	WB	Sequence	A0216
116	GTAYQSFEQV	0.444	408	WB	Sequence	A0216
213	FLTGMTVAGV	0.927	2	SB	Sequence	A0219
172	YLNDHLEPWI	0.884	3	SB	Sequence	A0219
168	WMATYLNDHL	0.611	67	WB	Sequence	A0219
49	AINGNPSWHL	0.543	140	WB	Sequence	A0219
7	LVVDFLSYKL	0.539	146	WB	Sequence	A0219
153	SVDKEMQVLV	0.533	156	WB	Sequence	A0219
164	RIAAWMATYL	0.449	387	WB	Sequence	A0219
73	SLDAREVIPM	0.445	404	WB	Sequence	A0219
160	VLVSRIAAWM	0.441	421	WB	Sequence	A0219
223	VLLGSLFSRK	0.767	12	SB	Sequence	A0301
6	ELVVDFLSYK	0.504	213	WB	Sequence	A0301
147	GALCVESVDK	0.488	253	WB	Sequence	A0301
222	VVLLGSLFSR	0.457	356	WB	Sequence	A0301
77	REVIPMAAVK	0.453	372	WB	Sequence	A0301
223	VLLGSLFSRK	0.742	16	SB	Sequence	A1101
222	VVLLGSLFSR	0.681	31	SB	Sequence	A1101
147	GALCVESVDK	0.515	190	WB	Sequence	A1101
24	SQFSDVEENR	0.470	310	WB	Sequence	A1101

121 SFEQVVNELF	0.581	92	WB	Sequence	A2301
171 TYLNDHLEPW	0.547	134	WB	Sequence	A2301
121 SFEQVVNELF	0.528	165	WB	Sequence	A2402
171 TYLNDHLEPW	0.520	180	WB	Sequence	A2402
113 ITPGTAYQSF	0.460	343	WB	Sequence	A2402
171 TYLNDHLEPW	0.739	16	SB	Sequence	A2403
121 SFEQVVNELF	0.546	136	WB	Sequence	A2403
113 ITPGTAYQSF	0.508	204	WB	Sequence	A2403
35 EAPEGTESEM	0.448	390	WB	Sequence	A2601
164 RIAAWMATYL	0.626	57	WB	Sequence	A2602
113 ITPGTAYQSF	0.581	92	WB	Sequence	A2602
160 VLVSRIAAWM	0.553	126	WB	Sequence	A2602
35 EAPEGTESEM	0.507	207	WB	Sequence	A2602
152 ESVDKEMQVL	0.490	249	WB	Sequence	A2602
95 EFELRYRRAF	0.483	268	WB	Sequence	A2602
110 QLHITPGTAY	0.506	209	WB	Sequence	A2902
222 VVLLGSLFSR	0.683	30	SB	Sequence	A3101
129 LFRDGVNWGR	0.667	36	SB	Sequence	A3101
202 SRKGQERFNR	0.608	69	WB	Sequence	A3101
81 PMAAVKQALR	0.521	177	WB	Sequence	A3101
222 VVLLGSLFSR	0.572	103	WB	Sequence	A3301
129 LFRDGVNWGR	0.553	126	WB	Sequence	A3301
10 DFLSYKLSQK	0.470	308	WB	Sequence	A3301
6 ELVVDFLSYK	0.702	25	SB	Sequence	A6801
24 SQFSDVEENR	0.532	158	WB	Sequence	A6801
222 VVLLGSLFSR	0.516	188	WB	Sequence	A6801
194 YGNNAAAESR	0.493	240	WB	Sequence	A6801
78 EVIPMAAVKQ	0.454	368	WB	Sequence	A6801
169 MATYLNDHLE	0.448	394	WB	Sequence	A6801
139 IVAFFSFGGA	0.742	16	SB	Sequence	A6802
116 GTAYQSFEQV	0.673	34	SB	Sequence	A6802
7 LVVDFLSYKL	0.659	39	SB	Sequence	A6802
120 QSFEQVVNEL	0.618	62	WB	Sequence	A6802
213 FLTGMTVAGV	0.577	96	WB	Sequence	A6802
117 TAYQSFEQVV	0.561	115	WB	Sequence	A6802
164 RIAAWMATYL	0.519	182	WB	Sequence	A6802
65 NGATGHSSSL	0.496	234	WB	Sequence	A6802
218 TVAGVVLLGS	0.491	246	WB	Sequence	A6802
145 FGGALCVESV	0.474	294	WB	Sequence	A6802
125 VVNELFRDGV	0.465	328	WB	Sequence	A6802
161 LVSRIAAWMA	0.451	380	WB	Sequence	A6802
215 TGMTVAGVVL	0.450	382	WB	Sequence	A6802
153 SVDKEMQVLV	0.534	155	WB	Sequence	A6901
213 FLTGMTVAGV	0.527	166	WB	Sequence	A6901
117 TAYQSFEQVV	0.466	324	WB	Sequence	A6901
7 LVVDFLSYKL	0.451	378	WB	Sequence	A6901
164 RIAAWMATYL	0.443	412	WB	Sequence	A6901
116 GTAYQSFEQV	0.427	493	WB	Sequence	A6901
80 IPMAAVKQAL	0.704	24	SB	Sequence	B0702
17 SQKGYSWSQF	0.572	102	WB	Sequence	B1501
110 QLHITPGTAY	0.557	121	WB	Sequence	B1501
133 GVNWGRIVAF	0.548	132	WB	Sequence	B1501
181 IQENGGWDTF	0.522	175	WB	Sequence	B1501
12 LSYKLSQKGY	0.455	364	WB	Sequence	B1501

5	RELVVDFLSY	0.759	13	SB	Sequence	B1801
163	SRIAAWMATY	0.588	86	WB	Sequence	B2705
101	RRAFSDLTSQ	0.461	340	WB	Sequence	B2705
80	IPMAAVKQAL	0.609	69	WB	Sequence	B3501
178	EPWIQENGGW	0.604	72	WB	Sequence	B3501
91	EAGDEFELRY	0.566	109	WB	Sequence	B3501
35	EAPEGTESEM	0.563	112	WB	Sequence	B3501
87	QALREAGDEF	0.508	206	WB	Sequence	B3501
61	SPAVNGATGH	0.490	249	WB	Sequence	B3501
46	IPSAINGNPS	0.483	269	WB	Sequence	B3501
133	GVNWGRIVAF	0.455	362	WB	Sequence	B3501
140	VAFFSFGGAL	0.454	367	WB	Sequence	B3501
190	FVELYGNNAA	0.439	430	WB	Sequence	B3501
200	AESRKGQERF	0.453	370	WB	Sequence	B4501
178	EPWIQENGGW	0.603	73	WB	Sequence	B5301
2	QSNRELVVDF	0.474	295	WB	Sequence	B5801
159	QVLVSRIAAW	0.467	320	WB	Sequence	B5801
47	PSAINGNPSW	0.437	444	WB	Sequence	B5801
	11-mers					
213	FLTGMTVAGVV	0.627	56	WB	Sequence	A0201
73	SLDAREVIPMA	0.561	115	WB	Sequence	A0201
160	VLVSRIAAWMA	0.547	135	WB	Sequence	A0201
57	HLADSPAVNGA	0.539	147	WB	Sequence	A0201
172	YLNDHLEPWIQ	0.480	278	WB	Sequence	A0201
88	ALREAGDEFEL	0.470	309	WB	Sequence	A0201
119	YQSFEQVVNEL	0.426	497	WB	Sequence	A0201
57	HLADSPAVNGA	0.763	12	SB	Sequence	A0202
213	FLTGMTVAGVV	0.754	14	SB	Sequence	A0202
119	YQSFEQVVNEL	0.734	17	SB	Sequence	A0202
88	ALREAGDEFEL	0.679	32	SB	Sequence	A0202
172	YLNDHLEPWIQ	0.611	67	WB	Sequence	A0202
139	IVAFFSFGGAL	0.558	119	WB	Sequence	A0202
218	TVAGVVLLGSL	0.537	149	WB	Sequence	A0202
160	VLVSRIAAWMA	0.525	170	WB	Sequence	A0202
15	KLSQKGYSWSQ	0.450	382	WB	Sequence	A0202
6	ELVVDFLSYKL	0.449	387	WB	Sequence	A0202
73	SLDAREVIPMA	0.446	401	WB	Sequence	A0202
213	FLTGMTVAGVV	0.864	4	SB	Sequence	A0203
57	HLADSPAVNGA	0.844	5	SB	Sequence	A0203
138	RIVAFFSFGGA	0.752	14	SB	Sequence	A0203
160	VLVSRIAAWMA	0.649	44	SB	Sequence	A0203
218	TVAGVVLLGSL	0.619	61	WB	Sequence	A0203
88	ALREAGDEFEL	0.604	72	WB	Sequence	A0203
119	YQSFEQVVNEL	0.567	108	WB	Sequence	A0203
172	YLNDHLEPWIQ	0.565	110	WB	Sequence	A0203
49	AINGNPSWHLA	0.562	114	WB	Sequence	A0203
209	FNRWFLTGMTV	0.494	239	WB	Sequence	A0203
139	IVAFFSFGGAL	0.487	257	WB	Sequence	A0203
73	SLDAREVIPMA	0.480	276	WB	Sequence	A0203
82	MAAVKQALREA	0.430	477	WB	Sequence	A0203
124	QVVNELFRDGV	0.426	496	WB	Sequence	A0203
213	FLTGMTVAGVV	0.584	90	WB	Sequence	A0204
88	ALREAGDEFEL	0.526	168	WB	Sequence	A0204
160	VLVSRIAAWMA	0.517	185	WB	Sequence	A0204
172	YLNDHLEPWIQ	0.517	186	WB	Sequence	A0204

73 SLDAREVIPMA	0.485	263	WB	Sequence	A0204
213 FLTGMTVAGVV	0.746	15	SB	Sequence	A0206
138 RIVAFFSFGGA	0.725	19	SB	Sequence	A0206
181 IQENGGWDTFV	0.704	24	SB	Sequence	A0206
119 YQSFEQVVNEL	0.671	35	SB	Sequence	A0206
48 SAINGNPSWHL	0.664	38	SB	Sequence	A0206
124 QVVNELFRDGV	0.619	62	WB	Sequence	A0206
160 VLVSRIAAWMA	0.584	90	WB	Sequence	A0206
86 KQALREAGDEF	0.547	134	WB	Sequence	A0206
57 HLADSPAVNGA	0.509	201	WB	Sequence	A0206
218 TVAGVVLLGSL	0.456	358	WB	Sequence	A0206
88 ALREAGDEFEL	0.442	420	WB	Sequence	A0206
109 SQLHITPGTAY	0.441	422	WB	Sequence	A0206
213 FLTGMTVAGVV	0.943	1	SB	Sequence	A0211
73 SLDAREVIPMA	0.876	3	SB	Sequence	A0211
172 YLNDHLEPWIQ	0.852	4	SB	Sequence	A0211
88 ALREAGDEFEL	0.799	8	SB	Sequence	A0211
57 HLADSPAVNGA	0.787	10	SB	Sequence	A0211
160 VLVSRIAAWMA	0.759	13	SB	Sequence	A0211
15 KLSQKGYSWSQ	0.743	16	SB	Sequence	A0211
6 ELVVDFLSYKL	0.682	31	SB	Sequence	A0211
218 TVAGVVLLGSL	0.628	55	WB	Sequence	A0211
49 AINGNPSWHLA	0.612	66	WB	Sequence	A0211
212 WFLTGMTVAGV	0.577	97	WB	Sequence	A0211
141 AFFSFGGALCV	0.571	103	WB	Sequence	A0211
144 SFGGALCVESV	0.569	105	WB	Sequence	A0211
79 VIPMAAVKQAL	0.568	107	WB	Sequence	A0211
124 QVVNELFRDGV	0.535	152	WB	Sequence	A0211
130 FRDGVNWGRIV	0.516	187	WB	Sequence	A0211
48 SAINGNPSWHL	0.515	189	WB	Sequence	A0211
192 ELYGNNAAAES	0.504	214	WB	Sequence	A0211
150 CVESVDKEMQV	0.489	252	WB	Sequence	A0211
116 GTAYQSFEQVV	0.452	376	WB	Sequence	A0211
139 IVAFFSFGGAL	0.444	411	WB	Sequence	A0211
213 FLTGMTVAGVV	0.824	6	SB	Sequence	A0212
172 YLNDHLEPWIQ	0.812	7	SB	Sequence	A0212
88 ALREAGDEFEL	0.779	10	SB	Sequence	A0212
73 SLDAREVIPMA	0.745	15	SB	Sequence	A0212
57 HLADSPAVNGA	0.714	22	SB	Sequence	A0212
160 VLVSRIAAWMA	0.681	31	SB	Sequence	A0212
79 VIPMAAVKQAL	0.604	72	WB	Sequence	A0212
15 KLSQKGYSWSQ	0.568	107	WB	Sequence	A0212
212 WFLTGMTVAGV	0.504	213	WB	Sequence	A0212
6 ELVVDFLSYKL	0.451	380	WB	Sequence	A0212
130 FRDGVNWGRIV	0.431	473	WB	Sequence	A0212
213 FLTGMTVAGVV	0.862	4	SB	Sequence	A0216
88 ALREAGDEFEL	0.821	6	SB	Sequence	A0216
73 SLDAREVIPMA	0.744	16	SB	Sequence	A0216
160 VLVSRIAAWMA	0.649	44	SB	Sequence	A0216
150 CVESVDKEMQV	0.641	48	SB	Sequence	A0216
57 HLADSPAVNGA	0.595	79	WB	Sequence	A0216
144 SFGGALCVESV	0.591	83	WB	Sequence	A0216
172 YLNDHLEPWIQ	0.581	92	WB	Sequence	A0216
15 KLSQKGYSWSQ	0.561	115	WB	Sequence	A0216
6 ELVVDFLSYKL	0.544	138	WB	Sequence	A0216
218 TVAGVVLLGSL	0.534	154	WB	Sequence	A0216
141 AFFSFGGALCV	0.526	168	WB	Sequence	A0216
181 IQENGGWDTFV	0.497	231	WB	Sequence	A0216
124 QVVNELFRDGV	0.490	249	WB	Sequence	A0216
79 VIPMAAVKQAL	0.487	257	WB	Sequence	A0216
192 ELYGNNAAAES	0.478	283	WB	Sequence	A0216
48 SAINGNPSWHL	0.468	315	WB	Sequence	A0216
212 WFLTGMTVAGV	0.437	441	WB	Sequence	A0216

49	AINGNPSWHLA	0.436	447	WB	Sequence	A0216
213	FLTGMTVAGVV	0.781	10	SB	Sequence	A0219
57	HLADSPAVNGA	0.730	18	SB	Sequence	A0219
172	YLNDHLEPWIQ	0.695	27	SB	Sequence	A0219
73	SLDAREVIPMA	0.609	68	WB	Sequence	A0219
88	ALREAGDEFEL	0.549	131	WB	Sequence	A0219
212	WFLTGMTVAGV	0.524	172	WB	Sequence	A0219
160	VLVSRIAAWMA	0.499	225	WB	Sequence	A0219
222	VVLLGSLFSRK	0.688	29	SB	Sequence	A0301
222	VVLLGSLFSRK	0.786	10	SB	Sequence	A1101
221	GVVLLGSLFSR	0.596	78	WB	Sequence	A1101
67	ATGHSSSLDAR	0.505	212	WB	Sequence	A1101
5	RELVVDFLSYK	0.428	489	WB	Sequence	A1101
135	NWGRIVAFFSF	0.695	26	SB	Sequence	A2301
171	TYLNDHLEPWI	0.576	98	WB	Sequence	A2301
167	AWMATYLNDHL	0.534	154	WB	Sequence	A2301
13	SYKLSQKGYSW	0.531	159	WB	Sequence	A2301
135	NWGRIVAFFSF	0.746	15	SB	Sequence	A2402
171	TYLNDHLEPWI	0.746	15	SB	Sequence	A2402
167	AWMATYLNDHL	0.520	180	WB	Sequence	A2402
171	TYLNDHLEPWI	0.660	39	SB	Sequence	A2403
167	AWMATYLNDHL	0.523	174	WB	Sequence	A2403
13	SYKLSQKGYSW	0.523	174	WB	Sequence	A2403
112	HITPGTAYQSF	0.431	473	WB	Sequence	A2403
159	QVLVSRIAAWM	0.640	49	SB	Sequence	A2602
112	HITPGTAYQSF	0.573	101	WB	Sequence	A2602
180	WIQENGGWDTF	0.518	183	WB	Sequence	A2602
11	FLSYKLSQKGY	0.516	188	WB	Sequence	A2602
132	DGVNWGRIVAF	0.462	336	WB	Sequence	A2602
218	TVAGVVLLGSL	0.443	415	WB	Sequence	A2602
109	SQLHITPGTAY	0.516	188	WB	Sequence	A2902
222	VVLLGSLFSRK	0.435	453	WB	Sequence	A3001
99	RYRRAFSDLTS	0.428	486	WB	Sequence	A3001
221	GVVLLGSLFSR	0.598	77	WB	Sequence	A3101
121	SFEQVVNELFR	0.552	127	WB	Sequence	A3101
201	ESRKGQERFNR	0.511	198	WB	Sequence	A3101
67	ATGHSSSLDAR	0.475	292	WB	Sequence	A3101
5	RELVVDFLSYK	0.442	417	WB	Sequence	A3101
193	LYGNNAAAESR	0.435	449	WB	Sequence	A3101
201	ESRKGQERFNR	0.690	28	SB	Sequence	A3301
128	ELFRDGVNWGR	0.634	52	WB	Sequence	A3301
91	EAGDEFELRYR	0.538	148	WB	Sequence	A3301
121	SFEQVVNELFR	0.472	303	WB	Sequence	A3301
221	GVVLLGSLFSR	0.447	396	WB	Sequence	A3301
95	EFELRYRRAFS	0.435	449	WB	Sequence	A3301
128	ELFRDGVNWGR	0.739	16	SB	Sequence	A6801
23	WSQFSDVEENR	0.667	36	SB	Sequence	A6801
201	ESRKGQERFNR	0.666	36	SB	Sequence	A6801
91	EAGDEFELRYR	0.643	47	SB	Sequence	A6801
221	GVVLLGSLFSR	0.638	49	SB	Sequence	A6801
80	IPMAAVKQALR	0.566	109	WB	Sequence	A6801
121	SFEQVVNELFR	0.536	151	WB	Sequence	A6801
218	TVAGVVLLGSL	0.796	9	SB	Sequence	A6802
124	QVVNELFRDGV	0.712	22	SB	Sequence	A6802

139	IVAFFSFGGAL	0.684	30	SB	Sequence A6802
152	ESVDKEMQVLV	0.613	65	WB	Sequence A6802
215	TGMTVAGVVLL	0.561	116	WB	Sequence A6802
6	ELVVDFLSYKL	0.551	129	WB	Sequence A6802
138	RIVAFFSFGGA	0.548	132	WB	Sequence A6802
188	DTFVELYGNNA	0.530	161	WB	Sequence A6802
78	EVIPMAAVKQA	0.516	188	WB	Sequence A6802
116	GTAYQSFEQVV	0.514	191	WB	Sequence A6802
75	DAREVIPMAAV	0.509	203	WB	Sequence A6802
57	HLADSPAVNGA	0.508	206	WB	Sequence A6802
217	MTVAGVVLLGS	0.480	277	WB	Sequence A6802
45	ETPSAINGNPS	0.479	279	WB	Sequence A6802
213	FLTGMTVAGVV	0.470	308	WB	Sequence A6802
70	HSSSLDAREVI	0.447	397	WB	Sequence A6802
48	SAINGNPSWHL	0.541	143	WB	Sequence A6901
75	DAREVIPMAAV	0.527	166	WB	Sequence A6901
152	ESVDKEMQVLV	0.511	199	WB	Sequence A6901
57	HLADSPAVNGA	0.485	263	WB	Sequence A6901
54	PSWHLADSPAV	0.469	312	WB	Sequence A6901
212	WFLTGMTVAGV	0.453	369	WB	Sequence A6901
78	EVIPMAAVKQA	0.442	417	WB	Sequence A6901
6	ELVVDFLSYKL	0.442	417	WB	Sequence A6901
218	TVAGVVLLGSL	0.430	475	WB	Sequence A6901
188	DTFVELYGNNA	0.427	494	WB	Sequence A6901
139	IVAFFSFGGAL	0.518	183	WB	Sequence B0702
53	NPSWHLADSPA	0.499	224	WB	Sequence B0702
61	SPAVNGATGHS	0.457	355	WB	Sequence B0702
109	SQLHITPGTAY	0.605	72	WB	Sequence B1501
86	KQALREAGDEF	0.567	108	WB	Sequence B1501
1	SQSNRELVVDF	0.540	144	WB	Sequence B1501
119	YQSFEQVVNEL	0.515	189	WB	Sequence B1501
158	MQVLVSRIAAW	0.512	196	WB	Sequence B1501
162	VSRIAAWMATY	0.477	285	WB	Sequence B1501
11	FLSYKLSQKGY	0.474	294	WB	Sequence B1501
180	WIQENGGWDTF	0.473	299	WB	Sequence B1501
120	QSFEQVVNELF	0.450	386	WB	Sequence B1501
112	HITPGTAYQSF	0.447	394	WB	Sequence B1501
133	GVNWGRIVAFF	0.433	463	WB	Sequence B1501
94	DEFELRYRRAF	0.829	6	SB	Sequence B1801
90	REAGDEFELRY	0.560	116	WB	Sequence B1801
109	SQLHITPGTAY	0.539	146	WB	Sequence B1801
151	VESVDKEMQVL	0.476	288	WB	Sequence B1801
177	LEPWIQENGGW	0.466	321	WB	Sequence B1801
209	FNRWFLTGMTV	0.444	409	WB	Sequence B1801
101	RRAFSDLTSQL	0.563	113	WB	Sequence B2705
163	SRIAAWMATYL	0.470	310	WB	Sequence B2705
53	NPSWHLADSPA	0.623	59	WB	Sequence B3501
46	TPSAINGNPSW	0.485	263	WB	Sequence B3501
180	WIQENGGWDTF	0.474	297	WB	Sequence B3501
132	DGVNWGRIVAF	0.442	419	WB	Sequence B3501
119	YQSFEQVVNEL	0.610	68	WB	Sequence B3901
151	VESVDKEMQVL	0.492	243	WB	Sequence B4001
40	TESEMETPSAI	0.446	402	WB	Sequence B4002
30	EENRTEAPEGT	0.498	228	WB	Sequence B4501
46	TPSAINGNPSW	0.772	11	SB	Sequence B5301

53 NPSWHLADSPA	0.430	474	WB	Sequence	B5401
170 ATYLNDHLEPW	0.540	145	WB	Sequence	B5701
170 ATYLNDHLEPW	0.537	150	WB	Sequence	B5801
120 QSFEQVVNELF	0.495	235	WB	Sequence	B5801

Fig. 37. Prediction of cancer antigen BclX(L) specific MHC class 2, 15-mer peptide binders.

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	Identity
DRB1_0101	212	RWFLTGMTVAGVVLL	LTGMTVAGV	0.8028	8	SB	BclX(L)
DRB1_0101	209	RFNRWFLTGMTVAGV	FLTGMTVAG	0.7932	9	SB	BclX(L)
DRB1_0101	210	FNRWFLTGMTVAGVV	LTGMTVAGV	0.7940	9	SB	BclX(L)
DRB1_0101	211	NRWFLTGMTVAGVVL	LTGMTVAGV	0.7970	9	SB	BclX(L)
DRB1_0101	213	WFLTGMTVAGVVLLG	LTGMTVAGV	0.7753	11	SB	BclX(L)
DRB1_0101	76	DAREVIPMAAVKQAL	VIPMAAVKQ	0.7755	11	SB	BclX(L)
DRB1_0101	77	AREVIPMAAVKQALR	VIPMAAVKQ	0.7788	11	SB	BclX(L)
DRB1_0101	78	REVIPMAAVKQALRE	VIPMAAVKQ	0.7772	11	SB	BclX(L)
DRB1_0101	75	LDAREVIPMAAVKQA	VIPMAAVKQ	0.7730	12	SB	BclX(L)
DRB1_0101	157	KEMQVLVSRIAAWMA	MQVLVSRIA	0.7458	16	SB	BclX(L)
DRB1_0101	108	LTSQLHITPGTAYQS	LHITPGTAY	0.7338	18	SB	BclX(L)
DRB1_0101	109	TSQLHITPGTAYQSF	ITPGTAYQS	0.7313	18	SB	BclX(L)
DRB1_0101	74	SLDAREVIPMAAVKQ	AREVIPMAA	0.7348	18	SB	BclX(L)
DRB1_0101	110	SQLHITPGTAYQSFE	ITPGTAYQS	0.7287	19	SB	BclX(L)
DRB1_0101	214	FLTGMTVAGVVLLGS	LTGMTVAGV	0.7282	19	SB	BclX(L)
DRB1_0101	156	DKEMQVLVSRIAAWM	MQVLVSRIA	0.7226	20	SB	BclX(L)
DRB1_0101	111	QLHITPGTAYQSFEQ	ITPGTAYQS	0.7202	21	SB	BclX(L)
DRB1_0101	112	LHITPGTAYQSFEQV	ITPGTAYQS	0.7189	21	SB	BclX(L)
DRB1_0101	154	SVDKEMQVLVSRIAA	MQVLVSRIA	0.7165	21	SB	BclX(L)
DRB1_0101	79	EVIPMAAVKQALREA	IPMAAVKQA	0.7208	21	SB	BclX(L)
DRB1_0101	153	ESVDKEMQVLVSRIA	VDKEMQVLV	0.7145	22	SB	BclX(L)
DRB1_0101	155	VDKEMQVLVSRIAAW	MQVLVSRIA	0.7141	22	SB	BclX(L)
DRB1_0101	215	LTGMTVAGVVLLGSL	LTGMTVAGV	0.7090	23	SB	BclX(L)
DRB1_0101	208	ERFNRWFLTGMTVAG	FNRWFLTGM	0.7077	24	SB	BclX(L)
DRB1_0101	46	ETPSAINGNPSWHLA	INGNPSWHL	0.7051	24	SB	BclX(L)
DRB1_0101	47	TPSAINGNPSWHLAD	INGNPSWHL	0.7051	24	SB	BclX(L)
DRB1_0101	48	PSAINGNPSWHLADS	INGNPSWHL	0.7076	24	SB	BclX(L)
DRB1_0101	49	SAINGNPSWHLADSP	INGNPSWHL	0.7072	24	SB	BclX(L)
DRB1_0101	45	METPSAINGNPSWHL	PSAINGNPS	0.7034	25	SB	BclX(L)
DRB1_0101	158	EMQVLVSRIAAWMAT	MQVLVSRIA	0.6845	30	SB	BclX(L)
DRB1_0101	80	VIPMAAVKQALREAG	VIPMAAVKQ	0.6856	30	SB	BclX(L)
DRB1_0101	159	MQVLVSRIAAWMATY	MQVLVSRIA	0.6834	31	SB	BclX(L)
DRB1_0101	161	VLVSRIAAWMATYLN	IAAWMATYL	0.6838	31	SB	BclX(L)
DRB1_0101	217	GMTVAGVVLLGSLFS	MTVAGVVLL	0.6800	32	SB	BclX(L)
DRB1_0101	218	MTVAGVVLLGSLFSR	VVLLGSLFS	0.6800	32	SB	BclX(L)
DRB1_0101	51	INGNPSWHLADSPAV	INGNPSWHL	0.6778	33	SB	BclX(L)
DRB1_0101	192	VELYGNNAAAESRKG	YGNNAAAES	0.6693	36	SB	BclX(L)
DRB1_0101	219	TVAGVVLLGSLFSRK	VVLLGSLFS	0.6677	36	SB	BclX(L)
DRB1_0101	160	QVLVSRIAAWMATYL	VSRIAAWMA	0.6652	37	SB	BclX(L)
DRB1_0101	191	FVELYGNNAAAESRK	YGNNAAAES	0.6658	37	SB	BclX(L)
DRB1_0101	193	ELYGNNAAAESRKGQ	YGNNAAAES	0.6661	37	SB	BclX(L)
DRB1_0101	99	LRYRRAFSDLTSQLH	YRRAFSDLT	0.6657	37	SB	BclX(L)
DRB1_0101	162	LVSRIAAWMATYLND	IAAWMATYL	0.6627	38	SB	BclX(L)
DRB1_0101	190	TFVELYGNNAAAESR	YGNNAAAES	0.6628	38	SB	BclX(L)
DRB1_0101	189	DTFVELYGNNAAAES	FVELYGNNA	0.6613	39	SB	BclX(L)
DRB1_0101	54	NPSWHLADSPAVNGA	WHLADSPAV	0.6617	39	SB	BclX(L)
DRB1_0101	55	PSWHLADSPAVNGAT	WHLADSPAV	0.6611	39	SB	BclX(L)
DRB1_0101	216	TGMTVAGVVLLGSLF	MTVAGVVLL	0.6543	42	SB	BclX(L)
DRB1_0101	163	VSRIAAWMATYLNDH	IAAWMATYL	0.6531	43	SB	BclX(L)
DRB1_0101	53	GNPSWHLADSPAVNG	WHLADSPAV	0.6532	43	SB	BclX(L)
DRB1_0101	59	LADSPAVNGATGHSS	LADSPAVNG	0.6361	51	WB	BclX(L)
DRB1_0101	98	ELRYRRAFSDLTSQL	YRRAFSDLT	0.6357	51	WB	BclX(L)
DRB1_0101	164	SRIAAWMATYLNDHL	IAAWMATYL	0.6357	52	WB	BclX(L)
DRB1_0101	97	FELRYRRAFSDLTSQ	YRRAFSDLT	0.6337	53	WB	BclX(L)
DRB1_0101	96	EFELRYRRAFSDLTS	YRRAFSDLT	0.6321	54	WB	BclX(L)
DRB1_0101	95	DEFELRYRRAFSDLT	LRYRRAFSD	0.6294	55	WB	BclX(L)
DRB1_0101	140	IVAFFSFGGALCVES	FSFGGALCV	0.6203	61	WB	BclX(L)
DRB1_0101	56	SWHLADSPAVNGATG	LADSPAVNG	0.6196	61	WB	BclX(L)
DRB1_0101	61	DSPAVNGATGHSSSL	VNGATGHSS	0.6197	61	WB	BclX(L)
DRB1_0101	62	SPAVNGATGHSSSLD	VNGATGHSS	0.6205	61	WB	BclX(L)

DRB1_0101	141	VAFFSFGGALCVESV	FSFGGALCV	0.6191	62	WB	BclX(L)
DRB1_0101	60	ADSPAVNGATGHSSS	VNGATGHSS	0.6174	63	WB	BclX(L)
DRB1_0101	142	AFFSFGGALCVESVD	FSFGGALCV	0.6153	64	WB	BclX(L)
DRB1_0101	57	WHLADSPAVNGATGH	LADSPAVNG	0.6162	64	WB	BclX(L)
DRB1_0101	113	HITPGTAYQSFEQVV	ITPGTAYQS	0.6121	66	WB	BclX(L)
DRB1_0101	114	ITPGTAYQSFEQVVN	ITPGTAYQS	0.6131	66	WB	BclX(L)
DRB1_0101	50	AINGNPSWHLADSPA	INGNPSWHL	0.6133	66	WB	BclX(L)
DRB1_0101	63	PAVNGATGHSSSLDA	VNGATGHSS	0.6078	70	WB	BclX(L)
DRB1_0101	100	RYRRAFSDLTSQLHI	YRRAFSDLT	0.6026	74	WB	BclX(L)
DRB1_0101	101	YRRAFSDLTSQLHIT	YRRAFSDLT	0.6021	74	WB	BclX(L)
DRB1_0101	52	NGNPSWHLADSPAVN	WHLADSPAV	0.6004	75	WB	BclX(L)
DRB1_0101	138	GRIVAFFSFGGALCV	IVAFFSFGG	0.5864	88	WB	BclX(L)
DRB1_0101	194	LYGNNAAAESRKGQE	YGNNAAAES	0.5808	93	WB	BclX(L)
DRB1_0101	165	RIAAWMATYLNDHLE	AAWMATYLN	0.5762	98	WB	BclX(L)
DRB1_0101	195	YGNNAAAESRKGQER	YGNNAAAES	0.5731	101	WB	BclX(L)
DRB1_0101	139	RIVAFFSFGGALCVE	FSFGGALCV	0.5729	102	WB	BclX(L)
DRB1_0101	131	FRDGVNWGRIVAFFS	VNWGRIVAF	0.5627	114	WB	BclX(L)
DRB1_0101	143	FFSFGGALCVESVDK	FSFGGALCV	0.5613	115	WB	BclX(L)
DRB1_0101	144	FSFGGALCVESVDKE	FSFGGALCV	0.5583	119	WB	BclX(L)
DRB1_0101	132	RDGVNWGRIVAFFSF	VNWGRIVAF	0.5561	122	WB	BclX(L)
DRB1_0101	133	DGVNWGRIVAFFSFG	VNWGRIVAF	0.5558	122	WB	BclX(L)
DRB1_0101	81	IPMAAVKQALREAGD	IPMAAVKQA	0.5527	126	WB	BclX(L)
DRB1_0101	102	RRAFSDLTSQLHITP	FSDLTSQLH	0.5334	156	WB	BclX(L)
DRB1_0101	103	RAFSDLTSQLHITPG	FSDLTSQLH	0.5314	159	WB	BclX(L)
DRB1_0101	58	HLADSPAVNGATGHS	LADSPAVNG	0.5293	163	WB	BclX(L)
DRB1_0101	134	GVNWGRIVAFFSFGG	VNWGRIVAF	0.5282	165	WB	BclX(L)
DRB1_0101	166	IAAWMATYLNDHLEP	IAAWMATYL	0.5271	167	WB	BclX(L)
DRB1_0101	64	AVNGATGHSSSLDAR	VNGATGHSS	0.5266	168	WB	BclX(L)
DRB1_0101	135	VNWGRIVAFFSFGGA	VNWGRIVAF	0.5248	171	WB	BclX(L)
DRB1_0101	7	ELVVDFLSYKLSQKG	VVDFLSYKL	0.5243	172	WB	BclX(L)
DRB1_0101	129	ELFRDGVNWGRIVAF	FRDGVNWGR	0.5154	189	WB	BclX(L)
DRB1_0101	65	VNGATGHSSSLDARE	VNGATGHSS	0.5156	189	WB	BclX(L)
DRB1_0101	130	LFRDGVNWGRIVAFF	VNWGRIVAF	0.5023	218	WB	BclX(L)
DRB1_0101	8	LVVDFLSYKLSQKGY	LSYKLSQKG	0.4921	244	WB	BclX(L)
DRB1_0101	9	VVDFLSYKLSQKGYS	LSYKLSQKG	0.4892	251	WB	BclX(L)
DRB1_0101	207	QERFNRWFLTGMTVA	FNRWFLTGM	0.4845	264	WB	BclX(L)
DRB1_0101	42	ESEMETPSAINGNPS	METPSAING	0.4626	335	WB	BclX(L)
DRB1_0101	40	GTESEMETPSAINGN	METPSAING	0.4622	337	WB	BclX(L)
DRB1_0101	107	DLTSQLHITPGTAYQ	LHITPGTAY	0.4593	347	WB	BclX(L)
DRB1_0101	39	EGTESEMETPSAING	ESEMETPSA	0.4591	348	WB	BclX(L)
DRB1_0101	43	SEMETPSAINGNPSW	METPSAING	0.4590	348	WB	BclX(L)
DRB1_0101	106	SDLTSQLHITPGTAY	SQLHITPGT	0.4569	356	WB	BclX(L)
DRB1_0101	10	VDFLSYKLSQKGYSW	LSYKLSQKG	0.4565	358	WB	BclX(L)
DRB1_0101	41	TESEMETPSAINGNP	METPSAING	0.4564	358	WB	BclX(L)
DRB1_0101	167	AAWMATYLNDHLEPW	AAWMATYLN	0.4556	361	WB	BclX(L)
DRB1_0101	11	DFLSYKLSQKGYSWS	LSYKLSQKG	0.4515	378	WB	BclX(L)
DRB1_0101	104	AFSDLTSQLHITPGT	FSDLTSQLH	0.4453	404	WB	BclX(L)
DRB1_0101	105	FSDLTSQLHITPGTA	FSDLTSQLH	0.4451	405	WB	BclX(L)
DRB1_0101	137	WGRIVAFFSFGGALC	IVAFFSFGG	0.4311	471	WB	BclX(L)
DRB1_0101	206	GQERFNRWFLTGMTV	FNRWFLTGM	0.4277	489	WB	BclX(L)
DRB1_0401	99	LRYRRAFSDLTSQLH	YRRAFSDLT	0.5618	115	WB	BclX(L)
DRB1_0401	97	FELRYRRAFSDLTSQ	YRRAFSDLT	0.5300	162	WB	BclX(L)
DRB1_0401	96	EFELRYRRAFSDLTS	YRRAFSDLT	0.5284	164	WB	BclX(L)
DRB1_0401	95	DEFELRYRRAFSDLT	DEFELRYRR	0.5275	166	WB	BclX(L)
DRB1_0401	98	ELRYRRAFSDLTSQL	YRRAFSDLT	0.5259	169	WB	BclX(L)
DRB1_0401	185	NGGWDTFVELYGNNA	WDTFVELYG	0.5189	182	WB	BclX(L)
DRB1_0401	186	GGWDTFVELYGNNAA	FVELYGNNA	0.5180	184	WB	BclX(L)
DRB1_0401	188	WDTFVELYGNNAAAE	FVELYGNNA	0.5159	188	WB	BclX(L)
DRB1_0401	187	GWDTFVELYGNNAAA	FVELYGNNA	0.5157	189	WB	BclX(L)
DRB1_0401	189	DTFVELYGNNAAAES	FVELYGNNA	0.5154	189	WB	BclX(L)
DRB1_0401	100	RYRRAFSDLTSQLHI	YRRAFSDLT	0.4844	265	WB	BclX(L)
DRB1_0401	101	YRRAFSDLTSQLHIT	YRRAFSDLT	0.4813	274	WB	BclX(L)
DRB1_0401	153	ESVDKEMQVLVSRIA	KEMQVLVSR	0.4561	360	WB	BclX(L)
DRB1_0401	155	VDKEMQVLVSRIAAW	MQVLVSRIA	0.4519	376	WB	BclX(L)
DRB1_0401	208	ERFNRWFLTGMTVAG	WFLTGMTVA	0.4512	379	WB	BclX(L)
DRB1_0401	154	SVDKEMQVLVSRIAA	MQVLVSRIA	0.4495	386	WB	BclX(L)

DRB1_0401	209	RFNRWFLTGMTVAGV	FLTGMTVAG	0.4467	398	WB	BclX(L)
DRB1_0401	210	FNRWFLTGMTVAGVV	FLTGMTVAG	0.4427	416	WB	BclX(L)
DRB1_0401	157	KEMQVLVSRIAAWMA	MQVLVSRIA	0.4419	419	WB	BclX(L)
DRB1_0401	156	DKEMQVLVSRIAAWM	MQVLVSRIA	0.4413	422	WB	BclX(L)
DRB1_0401	211	NRWFLTGMTVAGVVL	FLTGMTVAG	0.4327	463	WB	BclX(L)
DRB1_0404	167	AAWMATYLNDHLEPW	WMATYLNDH	0.5484	132	WB	BclX(L)
DRB1_0404	164	SRIAAWMATYLNDHL	WMATYLNDH	0.5424	141	WB	BclX(L)
DRB1_0404	165	RIAAWMATYLNDHLE	WMATYLNDH	0.5417	142	WB	BclX(L)
DRB1_0404	166	IAAWMATYLNDHLEP	WMATYLNDH	0.5330	156	WB	BclX(L)
DRB1_0404	163	VSRIAAWMATYLNDH	AAWMATYLN	0.5217	177	WB	BclX(L)
DRB1_0404	219	TVAGVVLLGSLFSRK	VVLLGSLFS	0.5094	202	WB	BclX(L)
DRB1_0404	209	RFNRWFLTGMTVAGV	FLTGMTVAG	0.4902	249	WB	BclX(L)
DRB1_0404	210	FNRWFLTGMTVAGVV	FLTGMTVAG	0.4853	262	WB	BclX(L)
DRB1_0404	211	NRWFLTGMTVAGVVL	FLTGMTVAG	0.4826	270	WB	BclX(L)
DRB1_0404	208	ERFNRWFLTGMTVAG	WFLTGMTVA	0.4761	290	WB	BclX(L)
DRB1_0404	168	AWMATYLNDHLEPWI	WMATYLNDH	0.4694	311	WB	BclX(L)
DRB1_0404	212	RWFLTGMTVAGVVLL	FLTGMTVAG	0.4547	365	WB	BclX(L)
DRB1_0404	189	DTFVELYGNNAAAES	FVELYGNNA	0.4505	382	WB	BclX(L)
DRB1_0404	187	GWDTFVELYGNNAAA	FVELYGNNA	0.4498	385	WB	BclX(L)
DRB1_0404	169	WMATYLNDHLEPWIQ	WMATYLNDH	0.4478	393	WB	BclX(L)
DRB1_0404	188	WDTFVELYGNNAAAE	FVELYGNNA	0.4462	400	WB	BclX(L)
DRB1_0404	186	GGWDTFVELYGNNAA	FVELYGNNA	0.4437	411	WB	BclX(L)
DRB1_0404	185	NGGWDTFVELYGNNA	GWDTFVELY	0.4388	434	WB	BclX(L)
DRB1_0405	118	TAYQSFEQVVNELFR	YQSFEQVVN	0.5794	95	WB	BclX(L)
DRB1_0405	117	GTAYQSFEQVVNELF	YQSFEQVVN	0.5772	97	WB	BclX(L)
DRB1_0405	115	TPGTAYQSFEQVVNE	YQSFEQVVN	0.5541	124	WB	BclX(L)
DRB1_0405	116	PGTAYQSFEQVVNEL	YQSFEQVVN	0.5538	125	WB	BclX(L)
DRB1_0405	114	ITPGTAYQSFEQVVN	AYQSFEQVV	0.5505	129	WB	BclX(L)
DRB1_0405	163	VSRIAAWMATYLNDH	AAWMATYLN	0.5510	129	WB	BclX(L)
DRB1_0405	162	LVSRIAAWMATYLND	AAWMATYLN	0.5473	134	WB	BclX(L)
DRB1_0405	161	VLVSRIAAWMATYLN	IAAWMATYL	0.5442	139	WB	BclX(L)
DRB1_0405	164	SRIAAWMATYLNDHL	AAWMATYLN	0.5402	145	WB	BclX(L)
DRB1_0405	99	LRYRRAFSDLTSQLH	YRRAFSDLT	0.5100	201	WB	BclX(L)
DRB1_0405	97	FELRYRRAFSDLTSQ	YRRAFSDLT	0.5085	204	WB	BclX(L)
DRB1_0405	96	EFELRYRRAFSDLTS	YRRAFSDLT	0.5069	208	WB	BclX(L)
DRB1_0405	165	RIAAWMATYLNDHLE	AAWMATYLN	0.5055	211	WB	BclX(L)
DRB1_0405	119	AYQSFEQVVNELFRD	YQSFEQVVN	0.4974	230	WB	BclX(L)
DRB1_0405	120	YQSFEQVVNELFRDG	YQSFEQVVN	0.4968	231	WB	BclX(L)
DRB1_0405	98	ELRYRRAFSDLTSQL	YRRAFSDLT	0.4923	243	WB	BclX(L)
DRB1_0405	18	SQKGYSWSQFSDVEE	GYSWSQFSD	0.4575	354	WB	BclX(L)
DRB1_0405	95	DEFELRYRRAFSDLT	LRYRRAFSD	0.4574	355	WB	BclX(L)
DRB1_0405	19	QKGYSWSQFSDVEEN	WSQFSDVEE	0.4562	359	WB	BclX(L)
DRB1_0405	100	RYRRAFSDLTSQLHI	YRRAFSDLT	0.4475	395	WB	BclX(L)
DRB1_0405	20	KGYSWSQFSDVEENR	WSQFSDVEE	0.4430	414	WB	BclX(L)
DRB1_0405	166	IAAWMATYLNDHLEP	AAWMATYLN	0.4423	418	WB	BclX(L)
DRB1_0405	21	GYSWSQFSDVEENRT	WSQFSDVEE	0.4353	450	WB	BclX(L)
DRB1_0701	157	KEMQVLVSRIAAWMA	VLVSRIAAW	0.5228	175	WB	BclX(L)
DRB1_0701	159	MQVLVSRIAAWMATY	VLVSRIAAW	0.5194	181	WB	BclX(L)
DRB1_0701	158	EMQVLVSRIAAWMAT	VLVSRIAAW	0.5191	182	WB	BclX(L)
DRB1_0701	156	DKEMQVLVSRIAAWM	VLVSRIAAW	0.4971	231	WB	BclX(L)
DRB1_0701	160	QVLVSRIAAWMATYL	VLVSRIAAW	0.4833	268	WB	BclX(L)
DRB1_0701	46	ETPSAINGNPSWHLA	INGNPSWHL	0.4783	283	WB	BclX(L)
DRB1_0701	45	METPSAINGNPSWHL	AINGNPSWH	0.4779	284	WB	BclX(L)
DRB1_0701	155	VDKEMQVLVSRIAAW	MQVLVSRIA	0.4772	286	WB	BclX(L)
DRB1_0701	47	TPSAINGNPSWHLAD	INGNPSWHL	0.4774	286	WB	BclX(L)
DRB1_0701	48	PSAINGNPSWHLADS	INGNPSWHL	0.4764	289	WB	BclX(L)
DRB1_0701	161	VLVSRIAAWMATYLN	VLVSRIAAW	0.4745	295	WB	BclX(L)
DRB1_0701	49	SAINGNPSWHLADSP	INGNPSWHL	0.4718	303	WB	BclX(L)
DRB1_0701	99	LRYRRAFSDLTSQLH	YRRAFSDLT	0.4627	335	WB	BclX(L)
DRB1_0701	100	RYRRAFSDLTSQLHI	FSDLTSQLH	0.4416	420	WB	BclX(L)
DRB1_0701	101	YRRAFSDLTSQLHIT	FSDLTSQLH	0.4344	455	WB	BclX(L)
DRB1_0701	51	INGNPSWHLADSPAV	INGNPSWHL	0.4291	481	WB	BclX(L)
DRB1_0901	55	PSWHLADSPAVNGAT	WHLADSPAV	0.5482	133	WB	BclX(L)

DRB1_0901	54	NPSWHLADSPAVNGA	WHLADSPAV	0.5414	143	WB	BclX(L)
DRB1_0901	53	GNPSWHLADSPAVNG	WHLADSPAV	0.5408	144	WB	BclX(L)
DRB1_0901	51	INGNPSWHLADSPAV	SWHLADSPA	0.5289	164	WB	BclX(L)
DRB1_0901	52	NGNPSWHLADSPAVN	WHLADSPAV	0.5284	164	WB	BclX(L)
DRB1_0901	56	SWHLADSPAVNGATG	WHLADSPAV	0.4678	317	WB	BclX(L)
DRB1_0901	57	WHLADSPAVNGATGH	WHLADSPAV	0.4636	331	WB	BclX(L)
DRB1_0901	212	RWFLTGMTVAGVVLL	FLTGMTVAG	0.4483	391	WB	BclX(L)
DRB1_0901	213	WFLTGMTVAGVVLLG	MTVAGVVLL	0.4445	408	WB	BclX(L)
DRB1_0901	214	FLTGMTVAGVVLLGS	MTVAGVVLL	0.4327	463	WB	BclX(L)
DRB1_1101	157	KEMQVLVSRIAAWMA	MQVLVSRIA	0.4319	467	WB	BclX(L)
DRB1_1101	131	FRDGVNWGRIVAFFS	GVNWGRIVA	0.4310	472	WB	BclX(L)
DRB1_1101	156	DKEMQVLVSRIAAWM	MQVLVSRIA	0.4308	473	WB	BclX(L)
DRB1_1101	155	VDKEMQVLVSRIAAW	MQVLVSRIA	0.4292	481	WB	BclX(L)
DRB1_1101	132	RDGVNWGRIVAFFSF	GVNWGRIVA	0.4283	486	WB	BclX(L)
DRB1_1101	154	SVDKEMQVLVSRIAA	MQVLVSRIA	0.4267	494	WB	BclX(L)
DRB1_1302	218	MTVAGVVLLGSLFSR	VVLLGSLFS	0.4945	237	WB	BclX(L)
DRB1_1302	216	TGMTVAGVVLLGSLF	MTVAGVVLL	0.4855	262	WB	BclX(L)
DRB1_1302	214	FLTGMTVAGVVLLGS	MTVAGVVLL	0.4842	265	WB	BclX(L)
DRB1_1302	217	GMTVAGVVLLGSLFS	MTVAGVVLL	0.4840	266	WB	BclX(L)
DRB1_1302	212	RWFLTGMTVAGVVLL	FLTGMTVAG	0.4832	268	WB	BclX(L)
DRB1_1302	215	LTGMTVAGVVLLGSL	MTVAGVVLL	0.4775	285	WB	BclX(L)
DRB1_1302	213	WFLTGMTVAGVVLLG	MTVAGVVLL	0.4716	304	WB	BclX(L)
DRB1_1302	189	DTFVELYGNNAAAES	VELYGNNAA	0.4688	313	WB	BclX(L)
DRB1_1302	190	TFVELYGNNAAAESR	YGNNAAAES	0.4615	339	WB	BclX(L)
DRB1_1302	191	FVELYGNNAAAESRK	YGNNAAAES	0.4526	373	WB	BclX(L)
DRB1_1302	192	VELYGNNAAAESRKG	YGNNAAAES	0.4415	421	WB	BclX(L)
DRB1_1302	219	TVAGVVLLGSLFSRK	VVLLGSLFS	0.4384	436	WB	BclX(L)
DRB1_1302	193	ELYGNNAAAESRKGQ	YGNNAAAES	0.4275	490	WB	BclX(L)
DRB1_1501	219	TVAGVVLLGSLFSRK	VLLGSLFSR	0.6681	36	SB	BclX(L)
DRB1_1501	218	MTVAGVVLLGSLFSR	VVLLGSLFS	0.6441	47	SB	BclX(L)
DRB1_1501	6	RELVVDFLSYKLSQK	LVVDFLSYK	0.5208	179	WB	BclX(L)
DRB1_1501	7	ELVVDFLSYKLSQKG	FLSYKLSQK	0.5009	221	WB	BclX(L)
DRB1_1501	157	KEMQVLVSRIAAWMA	MQVLVSRIA	0.4968	231	WB	BclX(L)
DRB1_1501	156	DKEMQVLVSRIAAWM	MQVLVSRIA	0.4965	232	WB	BclX(L)
DRB1_1501	209	RFNRWFLTGMTVAGV	FNRWFLTGM	0.4870	257	WB	BclX(L)
DRB1_1501	164	SRIAAWMATYLNDHL	WMATYLNDH	0.4849	263	WB	BclX(L)
DRB1_1501	210	FNRWFLTGMTVAGVV	LTGMTVAGV	0.4836	267	WB	BclX(L)
DRB1_1501	8	LVVDFLSYKLSQKGY	FLSYKLSQK	0.4778	284	WB	BclX(L)
DRB1_1501	5	NRELVVDFLSYKLSQ	LVVDFLSYK	0.4777	285	WB	BclX(L)
DRB1_1501	135	VNWGRIVAFFSFGGA	IVAFFSFGG	0.4756	291	WB	BclX(L)
DRB1_1501	4	SNRELVVDFLSYKLS	LVVDFLSYK	0.4755	291	WB	BclX(L)
DRB1_1501	159	MQVLVSRIAAWMATY	LVSRIAAWM	0.4693	312	WB	BclX(L)
DRB1_1501	163	VSRIAAWMATYLNDH	IAAWMATYL	0.4691	312	WB	BclX(L)
DRB1_1501	158	EMQVLVSRIAAWMAT	VLVSRIAAW	0.4683	315	WB	BclX(L)
DRB1_1501	165	RIAAWMATYLNDHLE	WMATYLNDH	0.4685	315	WB	BclX(L)
DRB1_1501	128	NELFRDGVNWGRIVA	LFRDGVNWG	0.4675	318	WB	BclX(L)
DRB1_1501	125	QVVNELFRDGVNWGR	LFRDGVNWG	0.4668	320	WB	BclX(L)
DRB1_1501	126	VVNELFRDGVNWGRI	LFRDGVNWG	0.4668	320	WB	BclX(L)
DRB1_1501	166	IAAWMATYLNDHLEP	WMATYLNDH	0.4649	327	WB	BclX(L)
DRB1_1501	137	WGRIVAFFSFGGALC	IVAFFSFGG	0.4643	329	WB	BclX(L)
DRB1_1501	136	NWGRIVAFFSFGGAL	IVAFFSFGG	0.4638	331	WB	BclX(L)
DRB1_1501	207	QERFNRWFLTGMTVA	FNRWFLTGM	0.4608	342	WB	BclX(L)
DRB1_1501	208	ERFNRWFLTGMTVAG	FNRWFLTGM	0.4602	344	WB	BclX(L)
DRB1_1501	138	GRIVAFFSFGGALCV	IVAFFSFGG	0.4587	350	WB	BclX(L)
DRB1_1501	9	VVDFLSYKLSQKGYS	FLSYKLSQK	0.4584	351	WB	BclX(L)
DRB1_1501	155	VDKEMQVLVSRIAAW	MQVLVSRIA	0.4570	356	WB	BclX(L)
DRB1_1501	167	AAWMATYLNDHLEPW	WMATYLNDH	0.4551	364	WB	BclX(L)
DRB1_1501	3	QSNRELVVDFLSYKL	LVVDFLSYK	0.4543	367	WB	BclX(L)
DRB1_1501	127	VNELFRDGVNWGRIV	LFRDGVNWG	0.4431	414	WB	BclX(L)
DRB1_1501	134	GVNWGRIVAFFSFGG	VNWGRIVAF	0.4391	432	WB	BclX(L)
DRB1_1501	129	ELFRDGVNWGRIVAF	LFRDGVNWG	0.4390	433	WB	BclX(L)
DRB1_1501	217	GMTVAGVVLLGSLFS	VAGVVLLGS	0.4377	439	WB	BclX(L)
DRB1_1501	124	EQVVNELFRDGVNWG	VVNELFRDG	0.4373	441	WB	BclX(L)
DRB1_1501	139	RIVAFFSFGGALCVE	IVAFFSFGG	0.4300	477	WB	BclX(L)

DRB1_1501	211	NRWFLTGMTVAGVVL	LTGMTVAGV	0.4264	496	WB	BclX(L)
DRB4_0101	99	LRYRRAFSDLTSQLH	YRRAFSDLT	0.4654	325	WB	BclX(L)
DRB4_0101	100	RYRRAFSDLTSQLHI	FSDLTSQLH	0.4328	463	WB	BclX(L)

Fig. 38.

Antigen	Sequence
<ABX71745 CRASP-2,Borrelia Burgdorferi> Seq45	<ABX71745 CRASP-2;Protein;Borrelia burgdorferi> mkksflsiymlisislscdvsrlnqrnidelkifvekakyysikldaiyseytgayndimtyimtysegts sdkskvnqaisilkkdnkivnkfkelekiieeykpmflskliddfaieldqavdndvsnarhvadsye klrksvalayiesfdvisskfvdskfveaskkfvnkakefveendlialkcivktigdmvndreinsrsry nnfykkeadflgaavelegaykaikqtll
<CAH10086 CRASP-1,Borrelia garinii> Seq 46	<CAH10086 CRASP-1;Protein;Borrelia garinii> mkktklniiklnilttiltliciscavdkidpesksktntkdfenksqdlepsntknkdlepleknsketiiskl ekmikdledqkdqedteiakitntqidflenfksephdtisediemkikriiysslnyeiekintlkeildkl yknhkykttarnfilnisikiqfqienalelmkeeiedaseilnqeryeillkhvepslnlkqkfekilnetik aynqdldniksnedqlahmdenykefdplnldy
<AAU07022 4-alpha-glucanotransferase,Borrelia garinii PBi> Seq 47	<AAU07022 4-alpha-glucanotransferase;Protein;Borrelia garinii PBi> Mkykkirinlnlkrksgillnisslpskygigdlgkgaykfidflfassqsywqmfayspidftrsppysif safagnvyyidlealdkfidsdlnllkenetrysdlkklsfkdkflkeaalnfinrasvdevrsfekfkkks sywlldfasfvafkeyflkdsrdafnvlfdrgilirnekdlfklrnilskeikvqevlqyfffsqfqalkryand kgielvmnlplfiaydsadvwahqkyfklrfdaskdkvagispdyfleqeqawdspayswnvlknv kyewwakrigilrkyidvikidhfrgfvstwevgvgeayafnglwvkspgrdffnfilneikdlkiwvedf endledvsrlrdffnfpgmrimklafdfdsdnqnlphnyikncivytgigdnstirefvnslddlhkkyif dylntnedfvvwdmirsamssvsdsviipmqdyinlgnefranipkntlnnwifrllesdldatlsknis fitrlygrt
<CAA59725 outer surface protein A,Borrelia afzelii> Seq 48	<CAA59725 outer surface protein A;Protein;Borrelia afzelii> mkkyllgiglilaliackqnvssldeknsasvdlpgemkvlvskekdkdgkyslkatvdkielkgtsdk dngsgvlegtkddkskakltiaddlskttfelfkedgktlvsrkvsskdktstdemfnekgelsaktmtr engtkleytemksdgtgkakevlknftlegkvandkvtlevkegtvtlskeiaksgevtvalndtnttq atkktgawdsktstltisvnskkttqlvftkqdtitvqkydsagtnlegtaveiktldelknalk
<CAA59727 outer surface protein A,Borrelia garinii> Seq 49	<CAA59727 outer surface protein A;Protein;Borrelia garinii> Mkkyllgiglilaliackqnvssldeknsvsvdlpggmkvlvskekdkdgkyslmatveklelkgtsd knngsgtlegektdkskvkltiaedlskttfeifkedgktlvskkvtlkdkssteekfnekgeisektivra ngtrleytdiksdgsgkakevlkdftlegtlaadgkttlkvtegtvvlsknilksgeitvalddsdttqatkkt gkwdsktstltisvnsqktknlvftkedtitvqkydsagtnlegkaveittleklkdalk
<YP_853838 outer surface protein B,Borrelia afzelii PKo> Seq 50	<YP_853838 outer surface protein B;Protein;Borrelia afzelii PKo> Mkqyllvfalvlaliacsqkgtepkstsqdhndqeiinsdntpkdskkdltvlaeensvplfngnkifvs keknsagkyelratvdtvelkgvsdknngsgklegtkadktkvamtiaddlntitvetydasnkktgs evvkkqgsvikesykankldskkitrenettleysemtdssnatkavetlkngiklegslvggkttvklt egtitltreieqdgkvkiylndttsgstkktatwnettntltisadskktkdfvfltdgtitvqaydtagtkleg nsseikdlaalkaalk
<NP_045689 outer surface protein B,Borrelia burgdorferi	<NP_045689 outer surface protein B;Protein;Borrelia burgdorferi B31> mrlligfalalaligcaqkgaesigsqkendlnledsskkshqnakqdlpavtedsvslfngnkifvsk eknssgkydlratidqvelkgtsdknngsgtlegskpdkskvkltvsadlntvtleafdasnqkisskv tkkqgsitxetlkankldskkltrsngttleysqitdadnatkavetlknsiklegslvggkttveikegtvtl kreiekdgkvkvflndtagsnkktgkwedststltisadskktkdlvfltdgtitvqqyntagtslegsas

B31> Seq 51	eiknlselknalk
AAN87995 OspC,Borrelia garinii> Seq 52	<AAN87995 Outer Surface Protein C;Protein;Borrelia garinii> ilmtlflfiscnnsggdtastnpdesakgpnltviskkitdsnafvlavkevealissidelankaigkvihqnnglnanagqngsllagayaistliteklsklknseelnkkieeaknhseaftnrlkgshaqlgvaaatddhakeailksnptkdkgakelkdlsesveslakaaqealansvkeltnpvvaespk
<NP_047005 outer surface protein C, Borrelia burgdorferi B31> Seq 53	<NP_047005 outer surface protein C;Protein;Borrelia burgdorferi B31> Mkkntlsailmtlflfiscnnsgkdgntsansadesvkgpnlteiskkitdsnavllavkeveallssideiaakaigkkihqnngldtennhngsllagayaistlikqkldglkneglkekidaakkcsetftnklkekhtdlgkegvtdadakeailktngtktkgaeelgklfesvevlskaakemlansvkeltspvvaespkkp
<CAF34024 outer surface protein VlsE,Borrelia garinii> Seq 54	<CAF34024 outer surface protein VlsE;Protein;Borrelia garinii> mkkissaifivaflaligcknnvggddkkdtaasifyqsiinlgngfievfnafsglvadafskadpkksdvktyfdsitktlkdtktklediskektggektpavegiaevvktvgewldglikaaegggkaadgggsdkignvaagggagadkesvngiagaikgiveaakkvegvkfapkaaadaaaadgnkkagklfgtaagadagdvkdaaaavgavsgeqilnaivtaagqagqagkkadeaknaieaaigaagdadfgddikkkndqiaaalvlrgvakdgkfaga
<CAF34027 outer surface protein VlsE,Borrelia afzelii PKo> Seq 55	<CAF34027 outer surface protein VlsE;Protein;Borrelia afzelii PKo> Mkkissaifltallvfincknnavgkgnddkdsvktfyesiinlgngfidvfnafsglvadtffksdpkksdvktyfesisstlkatkgkldelvsakkgeggsvkasvesavdevskwleemikaaeeaakvggtggdgkigdsaanhgakadkdsvkgiakgikgivdaagkalgekgalkdvkaaaddeanadagklfagnanaavgaaadiakaagavtavsgeqilkaiveaagdpanqagkkaeeaknpiaaaigtddngaafkdemkksdkiaaaivlrgvakdgkfavk

Fig. 39.

<ABX71745 CRASP-2;Protein;Borrelia burgdorferi>

8 mers:
mkksflsi;kksflsiy;ksflsiym;sflsiyml;flsiymli;lsiymlis;siymlisi;iymlisis;ymlisisl;mlisisll;lisislls;isisllsc;sisllscd;isllscdv;sllscdvs;llscdvsr;lscdvsrl;scdvsrln;cdvsrlnq;dvsrlnqr;vsrlnqrn;srlnqrni;rlnqrnid;lnqrnide;nqrnidel;qrnidelk;rnidelki;nidelkif;idelkifv;delkifve;elkifvek;lkifveka;kifvekak;ifvekaky;fvekakyy;vekakyys;ekakyysi;kakyysik;akyysikl;kyysikld;yysiklda;ysikldai;sikldaiy;ikldaiys;kldaiyse;ldaiysey;daiyseyt;aiyseytg;iyseytga;yseytgay;seytgayn;eytgaynd;ytgayndi;tgayndim;gayndimt;ayndimty;yndimtyi;ndimtyim;dimtyimt;imtyimty;mtyimtys;tyimtyse;yimtyseg;imtysegt;mtysegts;tysegtss;ysegtssd;segtssdk;egtssdks;gtssdksk;tssdkskv;ssdkskvn;sdkskvnq;dkskvnqa;kskvnqai;skvnqais;kvnqaisi;vnqaisil;nqaisilk;qaisilkk;aisilkkd;isilkkdn;silkkdnk;ilkkdnki;lkkdnkiv;kkdnkivn;kdnkivnk;dnkivnkf;nkivnkfk;kivnkfke;ivnkfkel;vnkfkele;nkfkelek;kfkeleki;fkelekii;kelekiie;elekiiee;lekiieey;ekiieeyk;kiieeykp;iieeykpm;ieeykpmf;eeykpmfl;eykpmfls;ykpmflsk;kpmflskl;pmflskli;mflsklid;flsklidd;lskliddf;skliddfa;kliddfai;liddfaie;iddfaiel;ddfaield;dfaieldq;faieldqa;aieldqav;ieldqavd;eldqavdn;ldqavdnd;dqavdndv;qavdndvs;avdndvsn;vdndvsna;dndvsnar;ndvsnarh;dvsnarhv;vsnarhva;snarhvad;narhvads;arhvadsy;rhvadsye;hvadsyek;vadsyekl;adsyeklr;dsyeklrk;syeklrks;yeklrksv;eklrksva;klrksval;lrksvala;rksvalay;ksvalayi;svalayie;valayies;alayiesf;layiesfd;ayiesfdv;yiesfdvi;iesfdvis;esfdviss;sfdvissk;fdvisskf;dvisskfv;visskfvd;isskfvds;sskfvdsk;skfvdskf;kfvdskfv;fvdskfve;vdskfvea;dskfveas;skfveask;kfveaskk;fveaskkf;veaskkfv;easkkfvn;askkfvnk;skkfvnka;kkfvnkak;kfvnkake;fvnkakef;vnkakefv;nkakefve;kakefvee;akefveen;kefveend;efveendl;fveendli;veendlia;eendlial;endlialk;ndlialkc;dlialkci;lialkciv;ialkcivk;alkcivkt;lkcivkti;kcivktig;civktigd;ivktigdm;vktigdmv;ktigdmvn;tigdmvnd;igdmvndr;gdmvndre;dmvndrei;mvndrein;vndreins;ndreinsr;dreinsrs;reinsrsr;einsrsry;insrsryn;nsrsrynn;srsrynnf;rsrynnfy;srynnfyk;rynnfykk;ynnfykke;nnfykkea;nfykkead;fykkeadf;ykkeadfl;kkeadflg;keadflga;eadflgaa;adflgaav;dflgaave;flgaavel;lgaavele;gaaveleg;aavelega;avelegay;velegayk;elegayka;legaykai;egaykaik;gaykaikq;aykaikqt;ykaikqtl;kaikqtll;

9 mers:
mkksflsiy;kksflsiym;ksflsiyml;sflsiymli;flsiymlis;lsiymlisi;siymlisis;iymlisisl;ymlisisll;mlisislls;lisisllsc;isisllscd;sisllscdv;isllscdvs;sllscdvsr;llscdvsrl;lscdvsrln;scdvsrlnq;cdvsrlnqr;dvsrlnqrn;vsrlnqrni;srlnqrnid;rlnqrnide;lnqrnidel;nqrnidelk;qrnidelki;rnidelkif;nidelkifv;idelkifve;delkifvek;elkifveka;lkifvekak;kifvekaky;ifvekakyy;fvekakyys;vekakyysi;ekakyysik;kakyysikl;akyysikld;kyysiklda;yysikldai;ysikldaiy;sikldaiys;ikldaiyse;kldaiysey;ldaiyseyt;daiyseytg;aiyseytga;iyseytgay;yseytgayn;seytgaynd;eytgayndi;ytgayndim;tgayndimt;gayndimty;ayndimtyi;yndimtyim;ndimtyimt;dimtyimty;imtyimtys;mtyimtyse;tyimtyseg;yimtysegt;imtysegts;mtysegtss;tysegtssd;ysegtssdk;segtssdks;egtssdksk;gtssdkskv;tssdkskvn;ssdkskvnq;sdkskvnqa;dkskvnqai;kskvnqais;skvnqaisi;kvnqaisil;vnqaisilk;nqaisilkk;qaisilkkd;aisilkkdn;isilkkdnk;silkkdnki;ilkkdnkiv;lkkdnkivn;kkdnkivnk;kdnkivnkf;dnkivnkfk;nkivnkfke;kivnkfkel;ivnkfkele;vnkfkelek;nkfkeleki;kfkelekii;fkelekiie;kelekiiee;elekiieey;lekiieeyk;ekiieeykp;kiieeykpm;iieeykpmf;ieeykpmfl;eeykpmfls;eykpmflsk;ykpmflskl;kpmflskli;pmflsklid;mflsklidd;flskliddf;lskliddfa;skliddfai;kliddfaie;liddfaiel;iddfaield;ddfaieldq;dfaieldqa;faieldqav;aieldqavd;ieldqavdn;eldqavdnd;ldqavdndv;dqavdndvs;qavdn

dvsn;avdndvsna;vdndvsnar;dndvsnarh;ndvsnarhv;dvsnarhva;vsnarhvad;snarhvads;narhvadsy;arhvadsye;rhvadsyek;hvadsyekl;vadsyeklr;adsyeklrk;dsyeklrks;syeklrksv;yeklrksva;eklrksval;klrksvala;lrksvalay;rksvalayi;ksvalayie;svalayies;valayiesf;alayiesfd;layiesfdv;ayiesfdvi;yiesfdvis;iesfdviss;esfdvissk;sfdvisskf;fdvisskfv;dvisskfvd;visskfvds;isskfvdsk;sskfvdskf;skfvdskfv;kfvdskfve;fvdskfvea;vdskfveas;dskfveask;skfveaskk;kfveaskkf;fveaskkfv;veaskkfvn;easkkfvnk;askkfvnka;skkfvnkak;kkfvnkake;kfvnkakef;fvnkakefv;vnkakefve;nkakefvee;kakefveen;akefveend;kefveendl;efveendli;fveendlia;veendlial;eendlialk;endlialkc;ndlialkci;dlialkciv;lialkcivk;ialkcivkt;alkcivkti;lkcivktig;kcivktigd;civktigdm;ivktigdmv;vktigdmvn;ktigdmvnd;tigdmvndr;igdmvndre;gdmvndrei;dmvndrein;mvndreins;vndreinsr;ndreinsrs;dreinsrsr;reinsrsry;einsrsryn;insrsrynn;nsrsrynnf;srsrynnfy;rsrynnfyk;srynnfykk;rynnfykke;ynnfykkea;nnfykkead;nfykkeadf;fykkeadfl;ykkeadflg;kkeadflga;keadflgaa;eadflgaav;adflgaave;dflgaavel;flgaavele;lgaaveleg;gaavelega;aavelegay;avelegayk;velegayka;elegaykai;legaykaik;egaykaikq;gaykaikqt;aykaikqtl;ykaikqtll;

10 mers:
mkksflsiym;kksflsiyml;ksflsiymli;sflsiymlis;flsiymlisi;lsiymlisis;siymlisisl;iymlisisll;ymlisislls;mlisisllsc;lisisllscd;isisllscdv;sisllscdvs;isllscdvsr;sllscdvsrl;llscdvsrln;lscdvsrlnq;scdvsrlnqr;cdvsrlnqrn;dvsrlnqrni;vsrlnqrnid;srlnqrnide;rlnqrnidel;lnqrnidelk;nqrnidelki;qrnidelkif;rnidelkifv;nidelkifve;idelkifvek;delkifveka;elkifvekak;lkifvekaky;kifvekakyy;ifvekakyys;fvekakyysi;vekakyysik;ekakyysikl;kakyysikld;akyysiklda;kyysikldai;yysikldaiy;ysikldaiys;sikldaiyse;ikldaiysey;kldaiyseyt;ldaiyseytg;daiyseytga;aiyseytgay;iyseytgayn;yseytgaynd;seytgayndi;eytgayndim;ytgayndimt;tgayndimty;gayndimtyi;ayndimtyim;yndimtyimt;ndimtyimty;dimtyimtys;imtyimtyse;mtyimtyseg;tyimtysegt;yimtysegts;imtysegtss;mtysegtssd;tysegtssdk;ysegtssdks;segtssdksk;egtssdkskv;gtssdkskvn;tssdkskvnq;ssdkskvnqa;sdkskvnqai;dkskvnqais;kskvnqaisi;skvnqaisil;kvnqaisilk;vnqaisilkk;nqaisilkkd;qaisilkkdn;aisilkkdnk;isilkkdnki;silkkdnkiv;ilkkdnkivn;lkkdnkivnk;kkdnkivnkf;kdnkivnkfk;dnkivnkfke;nkivnkfkel;kivnkfkele;ivnkfkelek;vnkfkeleki;nkfkelekii;kfkelekiie;fkelekiiee;kelekiieey;elekiieeyk;lekiieeykp;ekiieeykpm;kiieeykpmf;iieeykpmfl;ieeykpmfls;eeykpmflsk;eykpmflskl;ykpmflskli;kpmflsklid;pmflsklidd;mflskliddf;flskliddfa;lskliddfai;skliddfaie;kliddfaiel;liddfaield;iddfaieldq;ddfaieldqa;dfaieldqav;faieldqavd;aieldqavdn;ieldqavdnd;eldqavdndv;ldqavdndvs;dqavdndvsn;qavdndvsna;avdndvsnar;vdndvsnarh;dndvsnarhv;ndvsnarhva;dvsnarhvad;vsnarhvads;snarhvadsy;narhvadsye;arhvadsyek;rhvadsyekl;hvadsyeklr;vadsyeklrk;adsyeklrks;dsyeklrksv;syeklrksva;yeklrksval;eklrksvala;klrksvalay;lrksvalayi;rksvalayie;ksvalayies;svalayiesf;valayiesfd;alayiesfdv;layiesfdvi;ayiesfdvis;yiesfdviss;iesfdvissk;esfdvisskf;sfdvisskfv;fdvisskfvd;dvisskfvds;visskfvdsk;isskfvdskf;sskfvdskfv;skfvdskfve;kfvdskfvea;fvdskfveas;vdskfveask;dskfveaskk;skfveaskkf;kfveaskkfv;fveaskkfvn;veaskkfvnk;easkkfvnka;askkfvnkak;skkfvnkake;kkfvnkakef;kfvnkakefv;fvnkakefve;vnkakefvee;nkakefveen;kakefveend;akefveendl;kefveendli;efveendlia;fveendlial;veendlialk;eendlialkc;endlialkci;ndlialkciv;dlialkcivk;lialkcivkt;ialkcivkti;alkcivktig;lkcivktigd;kcivktigdm;civktigdmv;ivktigdmvn;vktigdmvnd;ktigdmvndr;tigdmvndre;igdmvndrei;gdmvndrein;dmvndreins;mvndreinsr;vndreinsrs;ndreinsrsr;dreinsrsry;reinsrsryn;einsrsrynn;insrsrynnf;nsrsrynnfy;srsrynnfyk;rsrynnfykk;srynnfykke;rynnfykkea;ynnfykkead;nnfykkeadf;nfykkeadfl;fykkeadflg;ykkeadflga;kkeadflgaa;keadflgaav;eadflgaave;adflgaavel;dflgaavele;flgaaveleg;lgaavelega;gaavelegay;aavelegayk;avelegayka;velegaykai;elegaykaik;legaykaikq;egaykaikqt;gaykaikqtl;aykaikqtll;

11 mers:
mkksflsiyml;kksflsiymli;ksflsiymlis;sflsiymlisi;flsiymlisis;lsiymlisisl;siymlisisll;iymlisisl
ls;ymlisisllsc;mlisisllscd;lisisllscdv;isisllscdvs;sisllscdvsr;isllscdvsrl;sllscdvsrln;llscdvsrln
q;lscdvsrlnqr;scdvsrlnqrn;cdvsrlnqrni;dvsrlnqrnid;vsrlnqrnide;srlnqrnidel;rlnqrnidelk;lnqr
nidelki;nqrnidelkif;qrnidelkifv;rnidelkifve;nidelkifvek;idelkifveka;delkifvekak;elkifvekak
y;lkifvekakyy;kifvekakyys;ifvekakyysi;fvekakyysik;vekakyysikl;ekakyysikld;kakyysikld
a;akyysikldai;kyysikldaiy;yysikldaiys;ysikldaiyse;sikldaiysey;ikldaiyseyt;kldaiyseytg;ldai
yseytga;daiyseytgay;aiyseytgayn;iyseytgaynd;yseytgayndi;seytgayndim;eytgayndimt;ytg
ayndimty;tgayndimtyi;gayndimtyim;ayndimtyimt;yndimtyimty;ndimtyimtys;dimtyimtyse
;imtyimtyseg;mtyimtysegt;tyimtysegts;yimtysegtss;imtysegtssd;mtysegtssdk;tysegtssdks;
ysegtssdksk;segtssdkskv;egtssdkskvn;gtssdkskvnq;tssdkskvnqa;ssdkskvnqai;sdkskvnqais
;dkskvnqaisi;kskvnqaisil;skvnqaisilk;kvnqaisilkk;vnqaisilkkd;nqaisilkkdn;qaisilkkdnk;ais
ilkkdnki;isilkkdnkiv;silkkdnkivn;ilkkdnkivnk;lkkdnkivnkf;kkdnkivnkfk;kdnkivnkfke;dnk
ivnkfkel;nkivnkfkele;kivnkfkelek;ivnkfkeleki;vnkfkelekii;nkfkelekiie;kfkelekiiee;fkelekii
eey;kelekiieeyk;elekiieeykp;lekiieeykpm;ekiieeykpmf;kiieeykpmfl;iieeykpmfls;ieeykpmf
lsk;eeykpmflskl;eykpmflskli;ykpmflsklid;kpmflsklidd;pmflskliddf;mflskliddfa;flskliddfai
;lskliddfaie;skliddfaiel;kliddfaield;liddfaieldq;iddfaieldqa;ddfaieldqav;dfaieldqavd;faield
qavdn;aieldqavdnd;ieldqavdndv;eldqavdndvs;ldqavdndvsn;dqavdndvsna;qavdndvsnar;av
dndvsnarh;vdndvsnarhv;dndvsnarhva;ndvsnarhvad;dvsnarhvads;vsnarhvadsy;snarhvadsy
e;narhvadsyek;arhvadsyekl;rhvadsyeklr;hvadsyeklrk;vadsyeklrks;adsyeklrksv;dsyeklrksv
a;syeklrksval;yeklrksvala;eklrksvalay;klrksvalayi;lrksvalayie;rksvalayies;ksvalayiesf;sval
ayiesfd;valayiesfdv;alayiesfdvi;layiesfdvis;ayiesfdviss;yiesfdvissk;iesfdvisskf;esfdvisskfv
;sfdvisskfvd;fdvisskfvds;dvisskfvdsk;visskfvdskf;isskfvdskfv;sskfvdskfve;skfvdskfvea;kf
vdskfveas;fvdskfveask;vdskfveaskk;dskfveaskkf;skfveaskkfv;kfveaskkfvn;fveaskkfvnk;v
easkkfvnka;easkkfvnkak;askkfvnkake;skkfvnkakef;kkfvnkakefv;kfvnkakefve;fvnkakefve
e;vnkakefveen;nkakefveend;kakefveendl;akefveendli;kefveendlia;efveendlial;fveendlialk
;veendlialkc;eendlialkci;endlialkciv;ndlialkcivk;dlialkcivkt;lialkcivkti;ialkcivktig;alkcivkt
igd;lkcivktigdm;kcivktigdmv;civktigdmvn;ivktigdmvnd;vktigdmvndr;ktigdmvndre;tigdm
vndrei;igdmvndrein;gdmvndreins;dmvndreinsr;mvndreinsrs;vndreinsrsr;ndreinsrsry;drein
srsryn;reinsrsrynn;einsrsrynnf;insrsrynnfy;nsrsrynnfyk;srsrynnfykk;rsrynnfykke;srynnfyk
kea;rynnfykkead;ynnfykkeadf;nnfykkeadfl;nfykkeadflg;fykkeadflga;ykkeadflgaa;kkeadfl
gaav;keadflgaave;eadflgaavel;adflgaavele;dflgaaveleg;flgaavelega;lgaavelegay;gaavelega
yk;aavelegayka;avelegaykai;velegaykaik;elegaykaikq;legaykaikqt;egaykaikqtl;gaykaikqtl
l;

13 mers:
mkksflsiymlis;kksflsiymlisi;ksflsiymlisis;sflsiymlisisl;flsiymlisisll;lsiymlisislls;siymlisisl
lsc;iymlisisllscd;ymlisisllscdv;mlisisllscdvs;lisisllscdvsr;isisllscdvsrl;sisllscdvsrln;isllscd
vsrlnq;sllscdvsrlnqr;llscdvsrlnqrn;lscdvsrlnqrni;scdvsrlnqrnid;cdvsrlnqrnide;dvsrlnqrnidel
;vsrlnqrnidelk;srlnqrnidelki;rlnqrnidelkif;lnqrnidelkifv;nqrnidelkifve;qrnidelkifvek;rnidel
kifveka;nidelkifvekak;idelkifvekaky;delkifvekakyy;elkifvekakyys;lkifvekakyysi;kifvekak
yysik;ifvekakyysikl;fvekakyysikld;vekakyysiklda;ekakyysikldai;kakyysikldaiy;akyysikld
aiys;kyysikldaiyse;yysikldaiysey;ysikldaiyseyt;sikldaiyseytg;ikldaiyseytga;kldaiyseytgay;
ldaiyseytgayn;daiyseytgaynd;aiyseytgayndi;iyseytgayndim;yseytgayndimt;seytgayndimty
;eytgayndimtyi;ytgayndimtyim;tgayndimtyimt;gayndimtyimty;ayndimtyimtys;yndimtyim
tyse;ndimtyimtyseg;dimtyimtysegt;imtyimtysegts;mtyimtysegtss;tyimtysegtssd;yimtysegt

ssdk;imtysegtssdks;mtysegtssdksk;tysegtssdkskv;ysegtssdkskvn;segtssdkskvnq;egtssdksk
vnqa;gtssdkskvnqai;tssdkskvnqais;ssdkskvnqaisi;sdkskvnqaisil;dkskvnqaisilk;kskvnqaisil
kk;skvnqaisilkkd;kvnqaisilkkdn;vnqaisilkkdnk;nqaisilkkdnki;qaisilkkdnkiv;aisilkkdnkivn
;isilkkdnkivnk;silkkdnkivnkf;ilkkdnkivnkfk;lkkdnkivnkfke;kkdnkivnkfkel;kdnkivnkfkele
;dnkivnkfkelek;nkivnkfkeleki;kivnkfkelekii;ivnkfkelekiie;vnkfkelekiiee;nkfkelekiieey;kf
kelekiieeyk;fkelekiieeykp;kelekiieeykpm;elekiieeykpmf;lekiieeykpmfl;ekiieeykpmfls;kii
eeykpmflsk;iieeykpmflskl;ieeykpmflskli;eeykpmflsklid;eykpmflsklidd;ykpmflskliddf;kp
mflskliddfa;pmflskliddfai;mflskliddfaie;flskliddfaiel;lskliddfaield;skliddfaieldq;kliddfaiel
dqa;liddfaieldqav;iddfaieldqavd;ddfaieldqavdn;dfaieldqavdnd;faieldqavdndv;aieldqavdnd
vs;ieldqavdndvsn;eldqavdndvsna;ldqavdndvsnar;dqavdndvsnarh;qavdndvsnarhv;avdndvs
narhva;vdndvsnarhvad;dndvsnarhvads;ndvsnarhvadsy;dvsnarhvadsye;vsnarhvadsyek;sna
rhvadsyekl;narhvadsyeklr;arhvadsyeklrk;rhvadsyeklrks;hvadsyeklrksv;vadsyeklrksva;ads
yeklrksval;dsyeklrksvala;syeklrksvalay;yeklrksvalayi;eklrksvalayie;klrksvalayies;lrksvala
yiesf;rksvalayiesfd;ksvalayiesfdv;svalayiesfdvi;valayiesfdvis;alayiesfdviss;layiesfdvissk;
ayiesfdvisskf;yiesfdvisskfv;iesfdvisskfvd;esfdvisskfvds;sfdvisskfvdsk;fdvisskfvdskf;dvis
skfvdskfv;visskfvdskfve;isskfvdskfvea;sskfvdskfveas;skfvdskfveask;kfvdskfveaskk;fvds
kfveaskkf;vdskfveaskkfv;dskfveaskkfvn;skfveaskkfvnk;kfveaskkfvnka;fveaskkfvnkak;ve
askkfvnkake;easkkfvnkakef;askkfvnkakefv;skkfvnkakefve;kkfvnkakefvee;kfvnkakefveen
;fvnkakefveend;vnkakefveendl;nkakefveendli;kakefveendlia;akefveendlial;kefveendlialk;
efveendlialkc;fveendlialkci;veendlialkciv;eendlialkcivk;endlialkcivkt;ndlialkcivkti;dlialk
civktig;lialkcivktigd;ialkcivktigdm;alkcivktigdmv;lkcivktigdmvn;kcivktigdmvnd;civktigd
mvndr;ivktigdmvndre;vktigdmvndrei;ktigdmvndrein;tigdmvndreins;igdmvndreinsr;gdmv
ndreinsrs;dmvndreinsrsr;mvndreinsrsry;vndreinsrsryn;ndreinsrsrynn;dreinsrsrynnf;reinsrs
rynnfy;einsrsrynnfyk;insrsrynnfykk;nsrsrynnfykke;srsrynnfykkea;rsrynnfykkead;srynnfy
kkeadf;rynnfykkeadfl;ynnfykkeadflg;nnfykkeadflga;nfykkeadflgaa;fykkeadflgaav;ykkead
flgaave;kkeadflgaavel;keadflgaavele;eadflgaaveleg;adflgaavelega;dflgaavelegay;flgaavel
egayk;lgaavelegayka;gaavelegaykai;aavelegaykaik;avelegaykaikq;velegaykaikqt;elegayk
aikqtl;legaykaikqtll;

14 mers:
mkksflsiymlisi;kksflsiymlisis;ksflsiymlisisl;sflsiymlisisll;flsiymlisislls;lsiymlisisllsc;siym
lisisllscd;iymlisisllscdv;ymlisisllscdvs;mlisisllscdvsr;lisisllscdvsrl;isisllscdvsrln;sisllscdvs
rlnq;isllscdvsrlnqr;sllscdvsrlnqrn;llscdvsrlnqrni;lscdvsrlnqrnid;scdvsrlnqrnide;cdvsrlnqrni
del;dvsrlnqrnidelk;vsrlnqrnidelki;srlnqrnidelkif;rlnqrnidelkifv;lnqrnidelkifve;nqrnidelkifv
ek;qrnidelkifveka;rnidelkifvekak;nidelkifvekaky;idelkifvekakyy;delkifvekakyys;elkifvek
akyysi;lkifvekakyysik;kifvekakyysikl;ifvekakyysikld;fvekakyysiklda;vekakyysikldai;eka
kyysikldaiy;kakyysikldaiys;akyysikldaiyse;kyysikldaiysey;yysikldaiyseyt;ysikldaiyseytg;
sikldaiyseytga;ikldaiyseytgay;kldaiyseytgayn;ldaiyseytgaynd;daiyseytgayndi;aiyseytgayn
dim;iyseytgayndimt;yseytgayndimty;seytgayndimtyi;eytgayndimtyim;ytgayndimtyimt;tg
ayndimtyimty;gayndimtyimtys;ayndimtyimtyse;yndimtyimtyseg;ndimtyimtysegt;dimtyi
mtysegts;imtyimtysegtss;mtyimtysegtssd;tyimtysegtssdk;yimtysegtssdks;imtysegtssdksk;
mtysegtssdkskv;tysegtssdkskvn;ysegtssdkskvnq;segtssdkskvnqa;egtssdkskvnqai;gtssdksk
vnqais;tssdkskvnqaisi;ssdkskvnqaisil;sdkskvnqaisilk;dkskvnqaisilkk;kskvnqaisilkkd;skvn
qaisilkkdn;kvnqaisilkkdnk;vnqaisilkkdnki;nqaisilkkdnkiv;qaisilkkdnkivn;aisilkkdnkivnk;
isilkkdnkivnkf;silkkdnkivnkfk;ilkkdnkivnkfke;lkkdnkivnkfkel;kkdnkivnkfkele;kdnkivnkf
kelek;dnkivnkfkeleki;nkivnkfkelekii;kivnkfkelekiie;ivnkfkelekiiee;vnkfkelekiieey;nkfkel

ekiieeyk;kfkelekiieeykp;fkelekiieeykpm;kelekiieeykpmf;elekiieeykpmfl;lekiieeykpmfls;e
kiieeykpmflsk;kiieeykpmflskl;iieeykpmflskli;ieeykpmflsklid;eeykpmflsklidd;eykpmflskli
ddf;ykpmflskliddfa;kpmflskliddfai;pmflskliddfaie;mflskliddfaiel;flskliddfaield;lskliddfaie
ldq;skliddfaieldqa;kliddfaieldqav;liddfaieldqavd;iddfaieldqavdn;ddfaieldqavdnd;dfaieldq
avdndv;faieldqavdndvs;aieldqavdndvsn;ieldqavdndvsna;eldqavdndvsnar;ldqavdndvsnarh;
dqavdndvsnarhv;qavdndvsnarhva;avdndvsnarhvad;vdndvsnarhvads;dndvsnarhvadsy;ndvs
narhvadsye;dvsnarhvadsyek;vsnarhvadsyekl;snarhvadsyeklr;narhvadsyeklrk;arhvadsyeklr
ks;rhvadsyeklrksv;hvadsyeklrksva;vadsyeklrksval;adsyeklrksvala;dsyeklrksvalay;syeklrk
svalayi;yeklrksvalayie;eklrksvalayies;klrksvalayiesf;lrksvalayiesfd;rksvalayiesfdv;ksvala
yiesfdvi;svalayiesfdvis;valayiesfdviss;alayiesfdvissk;layiesfdvisskf;ayiesfdvisskfv;yiesfd
visskfvd;iesfdvisskfvds;esfdvisskfvdsk;sfdvisskfvdskf;fdvisskfvdskfv;dvisskfvdskfve;vis
skfvdskfvea;isskfvdskfveas;sskfvdskfveask;skfvdskfveaskk;kfvdskfveaskkf;fvdskfveaskk
fv;vdskfveaskkfvn;dskfveaskkfvnk;skfveaskkfvnka;kfveaskkfvnkak;fveaskkfvnkake;veas
kkfvnkakef;easkkfvnkakefv;askkfvnkakefve;skkfvnkakefvee;kkfvnkakefveen;kfvnkakefv
eend;fvnkakefveendl;vnkakefveendli;nkakefveendlia;kakefveendlial;akefveendlialk;kefv
eendlialkc;efveendlialkci;fveendlialkciv;veendlialkcivk;eendlialkcivkt;endlialkcivkti;ndli
alkcivktig;dlialkcivktigd;lialkcivktigdm;ialkcivktigdmv;alkcivktigdmvn;lkcivktigdmvnd;
kcivktigdmvndr;civktigdmvndre;ivktigdmvndrei;vktigdmvndrein;ktigdmvndreins;tigdmv
ndreinsr;igdmvndreinsrs;gdmvndreinsrsr;dmvndreinsrsry;mvndreinsrsryn;vndreinsrsrynn;
ndreinsrsrynnf;dreinsrsrynnfy;reinsrsrynnfyk;einsrsrynnfykk;insrsrynnfykke;nsrsrynnfyk
kea;srsrynnfykkead;rsrynnfykkeadf;srynnfykkeadfl;rynnfykkeadflg;ynnfykkeadflga;nnfy
kkeadflgaa;nfykkeadflgaav;fykkeadflgaave;ykkeadflgaavel;kkeadflgaavele;keadflgaavele
g;eadflgaavelega;adflgaavelegay;dflgaavelegayk;flgaavelegayka;lgaavelegaykai;gaaveleg
aykaik;aavelegaykaikq;avelegaykaikqt;velegaykaikqtl;elegaykaikqtll;

15 mers:
mkksflsiymlisis;kksflsiymlisisl;ksflsiymlisisll;sflsiymlisislls;flsiymlisisllsc;lsiymlisisllscd
;siymlisisllscdv;iymlisisllscdvs;ymlisisllscdvsr;mlisisllscdvsrl;lisisllscdvsrln;isisllscdvsrl
nq;sisllscdvsrlnqr;isllscdvsrlnqrn;sllscdvsrlnqrni;llscdvsrlnqrnid;lscdvsrlnqrnide;scdvsrln
qrnidel;cdvsrlnqrnidelk;dvsrlnqrnidelki;vsrlnqrnidelkif;srlnqrnidelkifv;rlnqrnidelkifve;ln
qrnidelkifvek;nqrnidelkifveka;qrnidelkifvekak;rnidelkifvekaky;nidelkifvekakyy;idelkifve
kakyys;delkifvekakyysi;elkifvekakyysik;lkifvekakyysikl;kifvekakyysikld;ifvekakyysikld
a;fvekakyysikldai;vekakyysikldaiy;ekakyysikldaiys;kakyysikldaiyse;akyysikldaiysey;kyy
sikldaiyseyt;yysikldaiyseytg;ysikldaiyseytga;sikldaiyseytgay;ikldaiyseytgayn;kldaiyseytg
aynd;ldaiyseytgayndi;daiyseytgayndim;aiyseytgayndimt;iyseytgayndimty;yseytgayndimt
yi;seytgayndimtyim;eytgayndimtyimt;ytgayndimtyimty;tgayndimtyimtys;gayndimtyimty
se;ayndimtyimtyseg;yndimtyimtysegt;ndimtyimtysegts;dimtyimtysegtss;imtyimtysegtssd
;mtyimtysegtssdk;tyimtysegtssdks;yimtysegtssdksk;imtysegtssdkskv;mtysegtssdkskvn;ty
segtssdkskvnq;ysegtssdkskvnqa;segtssdkskvnqai;egtssdkskvnqais;gtssdkskvnqaisi;tssdks
kvnqaisil;ssdkskvnqaisilk;sdkskvnqaisilkk;dkskvnqaisilkkd;kskvnqaisilkkdn;skvnqaisilk
kdnk;kvnqaisilkkdnki;vnqaisilkkdnkiv;nqaisilkkdnkivn;qaisilkkdnkivnk;aisilkkdnkivnkf;i
silkkdnkivnkfk;silkkdnkivnkfke;ilkkdnkivnkfkel;lkkdnkivnkfkele;kkdnkivnkfkelek;kdnki
vnkfkeleki;dnkivnkfkelekii;nkivnkfkelekiie;kivnkfkelekiiee;ivnkfkelekiieey;vnkfkelekiie
eyk;nkfkelekiieeykp;kfkelekiieeykpm;fkelekiieeykpmf;kelekiieeykpmfl;elekiieeykpmfls;l
ekiieeykpmflsk;ekiieeykpmflskl;kiieeykpmflskli;iieeykpmflsklid;ieeykpmflsklidd;eeykp
mflskliddf;eykpmflskliddfa;ykpmflskliddfai;kpmflskliddfaie;pmflskliddfaiel;mflskliddfai

eld;flskliddfaieldq;lskliddfaieldqa;skliddfaieldqav;kliddfaieldqavd;liddfaieldqavdn;iddfai
eldqavdnd;ddfaieldqavdndv;dfaieldqavdndvs;faieldqavdndvsn;aieldqavdndvsna;ieldqavd
ndvsnar;eldqavdndvsnarh;ldqavdndvsnarhv;dqavdndvsnarhva;qavdndvsnarhvad;avdndvs
narhvads;vdndvsnarhvadsy;dndvsnarhvadsye;ndvsnarhvadsyek;dvsnarhvadsyekl;vsnarhv
adsyeklr;snarhvadsyeklrk;narhvadsyeklrks;arhvadsyeklrksv;rhvadsyeklrksva;hvadsyeklrk
sval;vadsyeklrksvala;adsyeklrksvalay;dsyeklrksvalayi;syeklrksvalayie;yeklrksvalayies;ek
lrksvalayiesf;klrksvalayiesfd;lrksvalayiesfdv;rksvalayiesfdvi;ksvalayiesfdvis;svalayiesfdv
iss;valayiesfdvissk;alayiesfdvisskf;layiesfdvisskfv;ayiesfdvisskfvd;yiesfdvisskfvds;iesfdv
isskfvdsk;esfdvisskfvdskf;sfdvisskfvdskfv;fdvisskfvdskfve;dvisskfvdskfvea;visskfvdskfv
eas;isskfvdskfveask;sskfvdskfveaskk;skfvdskfveaskkf;kfvdskfveaskkfv;fvdskfveaskkfvn;
vdskfveaskkfvnk;dskfveaskkfvnka;skfveaskkfvnkak;kfveaskkfvnkake;fveaskkfvnkakef;v
easkkfvnkakefv;easkkfvnkakefve;askkfvnkakefvee;skkfvnkakefveen;kkfvnkakefveend;kf
vnkakefveendl;fvnkakefveendli;vnkakefveendlia;nkakefveendlial;kakefveendlialk;akefve
endlialkc;kefveendlialkci;efveendlialkciv;fveendlialkcivk;veendlialkcivkt;eendlialkcivkti;
endlialkcivktig;ndlialkcivktigd;dlialkcivktigdm;lialkcivktigdmv;ialkcivktigdmvn;alkcivkt
igdmvnd;lkcivktigdmvndr;kcivktigdmvndre;civktigdmvndrei;ivktigdmvndrein;vktigdmv
ndreins;ktigdmvndreinsr;tigdmvndreinsrs;igdmvndreinsrsr;gdmvndreinsrsry;dmvndreinsr
sryn;mvndreinsrsrynn;vndreinsrsrynnf;ndreinsrsrynnfy;dreinsrsrynnfyk;reinsrsrynnfykk;e
insrsrynnfykke;insrsrynnfykkea;nsrsrynnfykkead;srsrynnfykkeadf;rsrynnfykkeadfl;srynnf
ykkeadflg;rynnfykkeadflga;ynnfykkeadflgaa;nnfykkeadflgaav;nfykkeadflgaave;fykkeadfl
gaavel;ykkeadflgaavele;kkeadflgaaveleg;keadflgaavelega;eadflgaavelegay;adflgaavelega
yk;dflgaavelegayka;flgaavelegaykai;lgaavelegaykaik;gaavelegaykaikq;aavelegaykaikqt;a
velegaykaikqtl;velegaykaikqtll;

16 mers:
mkksflsiymlisisl;kksflsiymlisisll;ksflsiymlisislls;sflsiymlisisllsc;flsiymlisisllscd;lsiymlisis
llscdv;siymlisisllscdvs;iymlisisllscdvsr;ymlisisllscdvsrl;mlisisllscdvsrln;lisisllscdvsrlnq;is
isllscdvsrlnqr;sisllscdvsrlnqrn;isllscdvsrlnqrni;sllscdvsrlnqrnid;llscdvsrlnqrnide;lscdvsrln
qrnidel;scdvsrlnqrnidelk;cdvsrlnqrnidelki;dvsrlnqrnidelkif;vsrlnqrnidelkifv;srlnqrnidelkif
ve;rlnqrnidelkifvek;lnqrnidelkifveka;nqrnidelkifvekak;qrnidelkifvekaky;rnidelkifvekakyy
;nidelkifvekakyys;idelkifvekakyysi;delkifvekakyysik;elkifvekakyysikl;lkifvekakyysikld;k
ifvekakyysiklda;ifvekakyysikldai;fvekakyysikldaiy;vekakyysikldaiys;ekakyysikldaiyse;k
akyysikldaiysey;akyysikldaiyseyt;kyysikldaiyseytg;yysikldaiyseytga;ysikldaiyseytgay;sik
ldaiyseytgayn;ikldaiyseytgaynd;kldaiyseytgayndi;ldaiyseytgayndim;daiyseytgayndimt;ai
yseytgayndimty;iyseytgayndimtyi;yseytgayndimtyim;seytgayndimtyimt;eytgayndimtyimt
y;ytgayndimtyimtys;tgayndimtyimtyse;gayndimtyimtyseg;ayndimtyimtysegt;yndimtyimt
ysegts;ndimtyimtysegtss;dimtyimtysegtssd;imtyimtysegtssdk;mtyimtysegtssdks;tyimtyse
gtssdksk;yimtysegtssdkskv;imtysegtssdkskvn;mtysegtssdkskvnq;tysegtssdkskvnqa;ysegts
sdkskvnqai;segtssdkskvnqais;egtssdkskvnqaisi;gtssdkskvnqaisil;tssdkskvnqaisilk;ssdkskv
nqaisilkk;sdkskvnqaisilkkd;dkskvnqaisilkkdn;kskvnqaisilkkdnk;skvnqaisilkkdnki;kvnqai
silkkdnkiv;vnqaisilkkdnkivn;nqaisilkkdnkivnk;qaisilkkdnkivnkf;aisilkkdnkivnkfk;isilkkd
nkivnkfke;silkkdnkivnkfkel;ilkkdnkivnkfkele;lkkdnkivnkfkelek;kkdnkivnkfkeleki;kdnkiv
nkfkelekii;dnkivnkfkelekiie;nkivnkfkelekiiee;kivnkfkelekiieey;ivnkfkelekiieeyk;vnkfkele
kiieeykp;nkfkelekiieeykpm;kfkelekiieeykpmf;fkelekiieeykpmfl;kelekiieeykpmfls;elekiiee
ykpmflsk;lekiieeykpmflskl;ekiieeykpmflskli;kiieeykpmflsklid;iieeykpmflsklidd;ieeykpmf
lskliddf;eeykpmflskliddfa;eykpmflskliddfai;ykpmflskliddfaie;kpmflskliddfaiel;pmflsklid

dfaield;mflskliddfaieldq;flskliddfaieldqa;lskliddfaieldqav;skliddfaieldqavd;kliddfaieldqav
dn;liddfaieldqavdnd;iddfaieldqavdndv;ddfaieldqavdndvs;dfaieldqavdndvsn;faieldqavdnd
vsna;aieldqavdndvsnar;ieldqavdndvsnarh;eldqavdndvsnarhv;ldqavdndvsnarhva;dqavdndv
snarhvad;qavdndvsnarhvads;avdndvsnarhvadsy;vdndvsnarhvadsye;dndvsnarhvadsyek;nd
vsnarhvadsyekl;dvsnarhvadsyeklr;vsnarhvadsyeklrk;snarhvadsyeklrks;narhvadsyeklrksv;
arhvadsyeklrksva;rhvadsyeklrksval;hvadsyeklrksvala;vadsyeklrksvalay;adsyeklrksvalayi;
dsyeklrksvalayie;syeklrksvalayies;yeklrksvalayiesf;eklrksvalayiesfd;klrksvalayiesfdv;lrks
valayiesfdvi;rksvalayiesfdvis;ksvalayiesfdviss;svalayiesfdvissk;valayiesfdvisskf;alayiesfd
visskfv;layiesfdvisskfvd;ayiesfdvisskfvds;yiesfdvisskfvdsk;iesfdvisskfvdskf;esfdvisskfvd
skfv;sfdvisskfvdskfve;fdvisskfvdskfvea;dvisskfvdskfveas;visskfvdskfveask;isskfvdskfvea
skk;sskfvdskfveaskkf;skfvdskfveaskkfv;kfvdskfveaskkfvn;fvdskfveaskkfvnk;vdskfveask
kfvnka;dskfveaskkfvnkak;skfveaskkfvnkake;kfveaskkfvnkakef;fveaskkfvnkakefv;veaskk
fvnkakefve;easkkfvnkakefvee;askkfvnkakefveen;skkfvnkakefveend;kkfvnkakefveendl;kf
vnkakefveendli;fvnkakefveendlia;vnkakefveendlial;nkakefveendlialk;kakefveendlialkc;a
kefveendlialkci;kefveendlialkciv;efveendlialkcivk;fveendlialkcivkt;veendlialkcivkti;eendl
ialkcivktig;endlialkcivktigd;ndlialkcivktigdm;dlialkcivktigdmv;lialkcivktigdmvn;ialkcivk
tigdmvnd;alkcivktigdmvndr;lkcivktigdmvndre;kcivktigdmvndrei;civktigdmvndrein;ivktig
dmvndreins;vktigdmvndreinsr;ktigdmvndreinsrs;tigdmvndreinsrsr;igdmvndreinsrsry;gdm
vndreinsrsryn;dmvndreinsrsrynn;mvndreinsrsrynnf;vndreinsrsrynnfy;ndreinsrsrynnfyk;dr
einsrsrynnfykk;reinsrsrynnfykke;einsrsrynnfykkea;insrsrynnfykkead;nsrsrynnfykkeadf;sr
srynnfykkeadfl;rsrynnfykkeadflg;srynnfykkeadflga;rynnfykkeadflgaa;ynnfykkeadflgaav;
nnfykkeadflgaave;nfykkeadflgaavel;fykkeadflgaavele;ykkeadflgaaveleg;kkeadflgaaveleg
a;keadflgaavelegay;eadflgaavelegayk;adflgaavelegayka;dflgaavelegaykai;flgaavelegaykai
k;lgaavelegaykaikq;gaavelegaykaikqt;aavelegaykaikqtl;avelegaykaikqtll;

<CAH10086 CRASP-1;Protein;Borrelia garinii>

8 mers:
mkktklni;kktklnii;ktklniik;tklniikl;klniikln;lniiklni;niiklnil;iiklnilt;iklniltt;klniltti;lnilttil;ni
lttilt;ilttiltl;lttiltli;ttiltlic;tiltlici;iltlicis;ltlicisc;tlicisca;liciscav;iciscavd;ciscavdk;iscavdki;s
cavdkid;cavdkidp;avdkidpe;vdkidpes;dkidpesk;kidpesks;idpesksk;dpeskskt;peskskt n;esks
ktnt;sksktntk;ksktntkd;sktntkdf;ktntkdfe;tntkdfen;ntkdfenk;tkdfenks;kdfenksq;dfenksqd;f
enksqdl;enksqdle;nksqdlep;ksqdleps;sqdlepsn;qdlepsnt;dlepsntk;lepsntkn;epsntknk;psntk
nkd;sntknkdl;ntknkdle;tknkdlep;knkdlepl;nkdleple;kdleplek;dleplekn;leplekns;epleknsk;p
leknske;leknsket;eknsketi;knsketii;nsketiis;sketiisk;ketiiskl;etiiskle;tiisklek;iisklekm;iskle
kmi;sklekmik;klekmikd;lekmikdl;ekmikdle;kmikdled;mikdledq;ikdledqk;kdledqkd;dledq
kdq;ledqkdqe;edqkdqed;dqkdqedt;qkdqedte;kdqedtei;dqedteia;qedteiak;edteiaki;dteiakit;t
eiakitn;eiakitnt;iakitntq;akitntqi;kitntqid;itntqidf;tntqidfl;ntqidfle;tqidflen;qidflenf;idflenf
k;dflenfks;flenfkse;lenfksep;enfkseph;nfksephd;fksephdt;ksephdti;sephdtis;ephdtise;phdti
sed;hdtisedi;dtisedie;tisediem;isediemk;sediemki;ediemkik;diemkikr;iemkikri;emkikrii;m
kikriiy;kikriiys;ikriiyss;kriiyssl;riiyssln;iiysslny;iysslnye;ysslnyei;sslnyeie;slnyeiek;lnyeie
ki;nyeiekin;yeiekint;eiekintl;iekintlk;ekintlke;kintlkei;intlkeil;ntlkeild;tlkeildk;lkeildkl;ke
ildkly;eildklyk;ildklykn;ldklyknh;dklyknhk;klyknhky;lyknhkyk;yknhkykt;knhkyktt;nhky
ktta;hkykttar;kykttarn;ykttarnf;kttarnfi;ttarnfil;tarnfiln;arnfilni;rnfilnis;nfilnisi;filnisik;ilni
siki;lnisikiq;nisikiqf;isikiqfq;sikiqfqi;ikiqfqie;kiqfqien;iqfqiena;qfqienal;fqienale;qienalel
;ienalelm;enalelmk;nalelmke;alelmkee;lelmkeei;elmkeeie;lmkeeied;mkeeieda;keeiedas;e

eiedase;eiedasei;iedaseil;edaseiln;daseilnq;aseilnqe;seilnqer;eilnqery;ilnqerye;lnqeryei;nqeryeil;qeryeill;eryeillk;ryeillkh;yeillkhv;eillkhve;illkhvep;llkhveps;lkhvepsl;khvepsln;hvepslnl;vepslnlk;epslnlkq;pslnlkqk;slnlkqkf;lnlkqkfe;nlkqkfek;lkqkfeki;kqkfekil;qkfekiln;kfekilne;fekilnet;ekilneti;kilnetik;ilnetika;lnetikay;netikayn;etikaynq;tikaynqd;ikaynqdl;kaynqdld;aynqdldn;ynqdldni;nqdldnik;qdldniks;dldniksn;ldniksne;dniksned;niksnedq;iksnedql;ksnedqla;snedqlah;nedqlahm;edqlahmd;dqlahmde;qlahmden;lahmdeny;ahmdenyk;hmdenyke;mdenykef;denykefd;enykefdp;nykefdpl;ykefdpln;kefdplnl;efdplnld;fdplnldy;

9 mers:
mkktklnii;kktklniik;ktklniikl;tklniikln;klniiklni;lniiklnil;niiklnilt;iiklniltt;iklniltti;klnilttil;lnilttilt;nilttiltl;ilttiltli;ltttiltlic;ttiltlici;tiltlicis;iltlicisc;ltlicisca;tliciscav;liciscavd;iciscavdk;ciscavdki;iscavdkid;scavdkidp;cavdkidpe;avdkidpes;vdkidpesk;dkidpesks;kidpesksk;idpeskskt;dpeskskt;peskskt;eskskntk;skskntkd;kskntkdf;sktntkdfe;ktntkdfen;tntkdfenk;ntkdfenks;tkdfenksq;kdfenksqd;dfenksqdl;fenksqdle;enksqdlep;nksqdleps;ksqdlepsn;sqdlepsnt;qdlepsntk;dlepsntkn;lepsntknk;epsntknkd;psntknkdl;sntknkdle;ntknkdlep;tknkdlepl;knkdleple;nkdleplek;kdleplekn;dleplekns;lepleknsk;epleknske;pleknsket;leknsketi;eknsketii;knsketiis;nsketiisk;sketiiskl;ketiiskle;etiisklek;tiisklekm;iisklekmi;isklekmik;sklekmikd;klekmikdl;lekmikdle;ekmikdled;kmikdledq;mikdledqk;ikdledqkd;kdledqkdq;dledqkdqe;ledqkdqed;edqkdqedt;dqkdqedte;qkdqedtei;kdqedteia;dqedteiak;qedteiaki;edteiakit;dteiakitn;teiakitnt;eiakitntq;iakitntqi;akitntqid;kitntqidf;itntqidfl;tntqidfle;ntqidflen;tqidflenf;qidflenfk;idflenfks;dflenfkse;flenfksep;lenfkseph;enfksephd;nfksephdt;fksephdti;ksephdtis;sephdtise;ephdtised;phdtisedi;hdtisedie;dtisediem;tisediemk;isediemki;sediemkik;ediemkikr;diemkikri;iemkikrii;emkikriiy;mkikriiys;kikriiyss;ikriiyssl;kriiyssln;riiysslny;iiysslnye;iysslnyei;ysslnyeie;sslnyeiek;slnyeieki;lnyeiekin;nyeiekint;yeiekintl;eiekintlk;iekintlke;ekintlkei;kintlkeil;intlkeild;ntlkeildk;tlkeildkl;lkeildkly;keildklyk;eildklykn;ildklyknh;ldklyknhk;dklyknhky;klyknhkyk;lyknhkykt;yknhkyktt;knhkyktta;nhkykttar;hkykttarn;kykttarnf;ykttarnfi;kttarnfil;ttarnfiln;tarnfilni;arnfilnis;rnfilnisi;nfilnisik;filnisiki;ilnisikiq;lnisikiqf;nisikiqfq;isikiqfqi;sikiqfqie;ikiqfqien;kiqfqiena;iqfqienal;qfqienale;fqienalel;qienalelm;ienalelmk;enalelmke;nalelmkee;alelmkeei;lelmkeeie;elmkeeied;lmkeeieda;mkeeiedas;keeiedase;eeiedasei;eiedaseil;iedaseiln;edaseilnq;daseilnqe;aseilnqer;seilnqery;eilnqerye;ilnqeryei;lnqeryeil;nqeryeill;qeryeillk;eryeillkh;ryeillkhv;yeillkhve;eillkhvep;illkhveps;llkhvepsl;lkhvepsln;khvepslnl;hvepslnlk;vepslnlkq;epslnlkqk;pslnlkqkf;slnlkqkfe;lnlkqkfek;nlkqkfeki;lkqkfekil;kqkfekiln;qkfekilne;kfekilnet;fekilneti;ekilnetik;kilnetika;ilnetikay;lnetikayn;netikaynq;etikaynqd;tikaynqdl;ikaynqdld;kaynqdldn;aynqdldni;ynqdldnik;nqdldniks;qdldniksn;dldniksne;ldniksned;dniksnedq;niksnedql;iksnedqla;ksnedqlah;snedqlahm;nedqlahmd;edqlahmde;dqlahmden;qlahmdeny;lahmdenyk;ahmdenyke;hmdenykef;mdenykefd;denykefdp;enykefdpl;nykefdpln;ykefdplnl;kefdplnld;efdplnldy;

10 mers:
mkktklniik;kktklniikl;ktklniikln;tklniiklni;klniiklnil;lniiklnilt;niiklniltt;iiklniltti;iklnilttil;klnilttilt;lnilttiltl;nilttiltli;ilttiltlic;lttiltlici;ttiltlicis;tiltlicisc;iltlicisca;ltliciscav;tliciscavd;liciscavdk;iciscavdki;ciscavdkid;iscavdkidp;scavdkidpe;cavdkidpes;avdkidpesk;vdkidpesks;dkidpesksk;kidpeskskt;idpeskskt;dpeskskt;peskskntk;eskskntkd;skskntkdf;ksktntkdfe;sktntkdfen;ktntkdfenk;tntkdfenks;ntkdfenksq;tkdfenksqd;kdfenksqdl;dfenksqdle;fenksqdlep;enksqdleps;nksqdlepsn;ksqdlepsnt;sqdlepsntk;qdlepsntkn;dlepsntknk;lepsntknkd;epsntknkdl;psntknkdle;sntknkdlep;ntknkdlepl;tknkdleple;knkdleplek;nkdleplekn;kdleplekns;

dlepleknsk;lepleknske;epleknsket;pleknsketi;leknsketii;eknsketiis;knsketiisk;nsketiiskl;sketiiskle;ketiisklek;etiisklekm;tiisklekmi;iisklekmik;isklekmikd;sklekmikdl;klekmikdle;lekmikdled;ekmikdledq;kmikdledqk;mikdledqkd;ikdledqkdq;kdledqkdqe;dledqkdqed;ledqkdqedt;edqkdqedte;dqkdqedtei;qkdqedteia;kdqedteiak;dqedteiaki;qedteiakit;edteiakitn;dteiakitnt;teiakitntq;eiakitntqi;iakitntqid;akitntqidf;kitntqidfl;itntqidfle;tntqidflen;ntqidflenf;tqidflenfk;qidflenfks;idflenfkse;dflenfksep;flenfkseph;lenfksephd;enfksephdt;nfksephdti;fksephdtis;ksephdtise;sephdtised;ephdtisedi;phdtisedie;hdtisediem;dtisediemk;tisediemki;isediemkik;sediemkikr;ediemkikri;diemkikrii;iemkikriiy;emkikriiys;mkikriiyss;kikriiyssl;ikriiyssln;kriiyssln;riiysslnye;iiysslnyei;iysslnyeie;ysslnyeiek;sslnyeieki;slnyeiekin;lnyeiekint;nyeiekintl;yeiekintlk;eiekintlke;iekintlkei;ekintlkeil;kintlkeild;intlkeildk;ntlkeildkl;tlkeildkly;lkeildklyk;keildklykn;eildklyknh;ildklyknhk;ldklyknhky;dklyknhkyk;klyknhkykt;lyknhkyktt;yknhkyktta;knhkykttar;nhkykttarn;hkykttarnf;kykttarnfi;ykttarnfil;kttarnfiln;ttarnfilni;tarnfilnis;arnfilnisi;rnfilnisik;nfilnisiki;filnisikiq;ilnisikiqf;lnisikiqfq;nisikiqfqi;isikiqfqie;sikiqfqien;ikiqfqiena;kiqfqienal;iqfqienale;qfqienalel;fqienalelm;qienalelmk;ienalelmke;enalelmkee;nalelmkeei;alelmkeeie;lelmkeeied;elmkeeieda;lmkeeiedas;mkeeiedase;keeiedasei;eeiedaseil;eiedaseiln;iedaseilnq;edaseilnqe;daseilnqer;aseilnqery;seilnqerye;eilnqeryei;ilnqeryeil;lnqeryeill;nqeryeillk;qeryeillkh;eryeillkhv;ryeillkhve;yeillkhvep;eillkhveps;illkhvepsl;llkhvepsln;lkhvepslnl;khvepslnlk;hvepslnlkq;vepslnlkqk;epslnlkqkf;pslnlkqkfe;slnlkqkfek;lnlkqkfeki;nlkqkfekil;lkqkfekiln;kqkfekilne;qkfekilnet;kfekilneti;fekilnetik;ekilnetika;kilnetikay;ilnetikayn;lnetikaynq;netikaynqd;etikaynqdl;tikaynqdld;ikaynqdldn;kaynqdldni;aynqdldnik;ynqdldniks;nqdldniksn;qdldniksne;dldniksned;ldniksnedq;dniksnedql;niksnedqla;iksnedqlah;ksnedqlahm;snedqlahmd;nedqlahmde;edqlahmden;dqlahmdeny;qlahmdenyk;lahmdenyke;ahmdenykef;hmdenykefd;mdenykefdp;denykefdpl;enykefdpln;nykefdplnl;ykefdplnld;kefdplnldy;

11 mers:
mkktklniikl;kktklniikln;ktklniiklni;tklniiklnil;klniiklnilt;lniiklniltt;niiklniltti;iiklnilttil;iklnilttilt;klnilttiltl;lnilttiltli;nilttiltlic;ilttiltlici;lttiltlicis;ttiltlicisc;tiltlicisca;iltliciscav;ltliciscavd;tliciscavdk;liciscavdki;iciscavdkid;ciscavdkidp;iscavdkidpe;scavdkidpes;cavdkidpesk;avdkidpesks;vdkidpesksk;dkidpeskskt;kidpeskskt;idpeskskt;dpeskskt;peskskt;eskskt;skskt;kskdf;skskt;kskdfe;kskt;kskdfen;skt;kskdfenk;kt;kskdfenks;t;kskdfenksq;k;kskdfenksqd;skdfenksqdl;kdfenksqdle;dfenksqdlep;fenksqdleps;enksqdlepsn;nksqdlepsnt;ksqdlepsntk;sqdlepsntkn;qdlepsntknk;dlepsntknkd;lepsntknkdl;epsntknkdle;psntknkdlep;sntknkdlepl;ntknkdleple;tknkdleplek;knkdleplekn;nkdleplekns;kdlepleknsk;dlepleknske;lepleknsket;epleknsketi;pleknsketii;leknsketiis;eknsketiisk;knsketiiskl;nsketiiskle;sketiisklek;ketiisklekm;etiisklekmi;tiisklekmik;iisklekmikd;isklekmikdl;sklekmikdle;klekmikdled;lekmikdledq;ekmikdledqk;kmikdledqkd;mikdledqkdq;ikdledqkdqe;kdledqkdqed;dledqkdqedt;ledqkdqedte;edqkdqedtei;dqkdqedteia;qkdqedteiak;kdqedteiaki;dqedteiakit;qedteiakitn;edteiakitnt;dteiakitntq;teiakitntqi;eiakitntqid;iakitntqidf;akitntqidfl;kitntqidfle;itntqidflen;tntqidflenf;ntqidflenfk;tqidflenfks;qidflenfkse;idflenfksep;dflenfkseph;flenfksephd;lenfksephdt;enfksephdti;nfksephdtis;fksephdtise;ksephdtised;sephdtisedi;ephdtisedie;phdtisediem;hdtisediemk;dtisediemki;tisediemkik;isediemkikr;sediemkikri;ediemkikrii;diemkikriiy;iemkikriiys;emkikriiyss;mkikriiyssl;kikriiyssln;ikriiyssln;kriiysslnye;riiysslnyei;iiysslnyeie;iysslnyeiek;ysslnyeieki;sslnyeiekin;slnyeiekint;lnyeiekintl;nyeiekintlk;yeiekintlke;eiekintlkei;iekintlkeil;ekintlkeild;kintlkeildk;intlkeildkl;ntlkeildkly;tlkeildklyk;lkeildklykn;keildklyknh;eildklyknhk;ildklyknhky;ldklyknhkyk;dklyknhkykt;klyknhkyktt;lyknhkyktta;yknhkykttar;

knhkykttarn;nhkykttarnf;hkykttarnfi;kykttarnfil;ykttarnfiln;kttarnfilni;ttarnfilnis;tarnfilnis i;arnfilnisik;rnfilnisiki;nfilnisikiq;filnisikiqf;ilnisikiqfq;lnisikiqfqi;nisikiqfqie;isikiqfqien; sikiqfqiena;ikiqfqienal;kiqfqienale;iqfqienalel;qfqienalelm;fqienalelmk;qienalelmke;ienal elmkee;enalelmkeei;nalelmkeeie;alelmkeeied;lelmkeeieda;elmkeeiedas;lmkeeiedase;mke eiedasei;keeiedaseil;eeiedaseiln;eiedaseilnq;iedaseilnqe;edaseilnqer;daseilnqery;aseilnqer ye;seilnqeryei;eilnqeryeil;ilnqeryeill;lnqeryeillk;nqeryeillkh;qeryeillkhv;eryeillkhve;ryeill khvep;yeillkhveps;eillkhvepsl;illkhvepsln;llkhvepslnl;lkhvepslnlk;khvepslnlkq;hvepslnlk qk;vepslnlkqkf;epslnlkqkfe;pslnlkqkfek;slnlkqkfeki;lnlkqkfekil;nlkqkfekiln;lkqkfekilne;k qkfekilnet;qkfekilneti;kfekilnetik;fekilnetika;ekilnetikay;kilnetikayn;ilnetikaynq;lnetikay nqd;netikaynqdl;etikaynqdld;tikaynqdldn;ikaynqdldni;kaynqdldnik;aynqdldniks;ynqdldni ksn;nqdldniksne;qdldniksned;dldniksnedq;ldniksnedql;dniksnedqla;niksnedqlah;iksnedql ahm;ksnedqlahmd;snedqlahmde;nedqlahmden;edqlahmdeny;dqlahmdenyk;qlahmdenyke; lahmdenykef;ahmdenykefd;hmdenykefdp;mdenykefdpl;denykefdpln;enykefdplnl;nykefd plnld;ykefdplnldy;

13 mers:
mkktklniiklni;kktklniiklnil;ktklniiklnilt;tklniiklniltt;klniiklniltti;lniiklnilttil;niiklnilttilt;iikl nilttiltl;iklnilttiltli;klnilttiltlic;lnilttiltlici;nilttiltlicis;ilttiltlicisc;lttiltlicisca;ttiltliciscav;tiltli ciscavd;iltliciscavdk;ltliciscavdki;tliciscavdkid;liciscavdkidp;iciscavdkidpe;ciscavdkidpes ;iscavdkidpesk;scavdkidpesks;cavdkidpesksk;avdkidpeskskt;vdkidpesksktn;dkidpesksktn t;kidpesksktntk;idpesksktntkd;dpesksktntkdf;pesksktntkdfe;esksktntkdfen;sksktntkdfenk; ksktntkdfenks;sktntkdfenksq;ktntkdfenksqd;tntkdfenksqdl;ntkdfenksqdle;tkdfenksqdlep;k dfenksqdleps;dfenksqdlepsn;fenksqdlepsnt;enksqdlepsntk;nksqdlepsntkn;ksqdlepsntknk;s qdlepsntknkd;qdlepsntknkdl;dlepsntknkdle;lepsntknkdlep;epsntknkdlepl;psntknkdleple;s ntknkdleplek;ntknkdleplekn;tknkdleplekns;knkdlepleknsk;nkdlepleknske;kdlepleknsket;d lepleknsketi;lepleknsketii;epleknsketiis;pleknsketiisk;leknsketiiskl;eknsketiiskle;knsketiis klek;nsketiisklekm;sketiisklekmi;ketiisklekmik;etiisklekmikd;tiisklekmikdl;iisklekmikdle ;isklekmikdled;sklekmikdledq;klekmikdledqk;lekmikdledqkd;ekmikdledqkdq;kmikdledq kdqe;mikdledqkdqed;ikdledqkdqedt;kdledqkdqedte;dledqkdqedtei;ledqkdqedteia;edqkdq edteiak;dqkdqedteiaki;qkdqedteiakit;kdqedteiakitn;dqedteiakitnt;qedteiakitntq;edteiakitnt qi;dteiakitntqid;teiakitntqidf;eiakitntqidfl;iakitntqidfle;akitntqidflen;kitntqidflenf;itntqidfl enfk;tntqidflenfks;ntqidflenfkse;tqidflenfksep;qidflenfkseph;idflenfksephd;dflenfksephdt; flenfksephdti;lenfksephdtis;enfksephdtise;nfksephdtised;fksephdtisedi;ksephdtisedie;seph dtisediem;ephdtisediemk;phdtisediemki;hdtisediemkik;dtisediemkikr;tisediemkikri;isedie mkikrii;sediemkikriiy;ediemkikriiys;diemkikriiyss;iemkikriiyssl;emkikriiyssln;mkikriiyss lny;kikriiysslnye;ikriiysslnyei;kriiysslnyeie;riiysslnyeiek;iiysslnyeieki;iysslnyeiekin;yssln yeiekint;sslnyeiekintl;slnyeiekintlk;lnyeiekintlke;nyeiekintlkei;yeiekintlkeil;eiekintlkeild; iekintlkeildk;ekintlkeildkl;kintlkeildkly;intlkeildklyk;ntlkeildklykn;tlkeildklyknh;lkeildkl yknhk;keildklyknhky;eildklyknhkyk;ildklyknhkykt;ldklyknhkyktt;dklyknhkyktta;klyknhk ykttar;lyknhkykttarn;yknhkykttarnf;knhkykttarnfi;nhkykttarnfil;hkykttarnfiln;kykttarnfiln i;ykttarnfilnis;kttarnfilnisi;ttarnfilnisik;tarnfilnisiki;arnfilnisikiq;rnfilnisikiqf;nfilnisikiqfq; filnisikiqfqi;ilnisikiqfqie;lnisikiqfqien;nisikiqfqiena;isikiqfqienal;sikiqfqienale;ikiqfqienal el;kiqfqienalelm;iqfqienalelmk;qfqienalelmke;fqienalelmkee;qienalelmkeei;ienalelmkeei e;enalelmkeeied;nalelmkeeieda;alelmkeeiedas;lelmkeeiedase;elmkeeiedasei;lmkeeiedasei l;mkeeiedaseiln;keeiedaseilnq;eeiedaseilnqe;eiedaseilnqer;iedaseilnqery;edaseilnqerye;da seilnqeryei;aseilnqeryeil;seilnqeryeill;eilnqeryeillk;ilnqeryeillkh;lnqeryeillkhv;nqeryeillk

hve;qeryeillkhvep;eryeillkhveps;ryeillkhvepsl;yeillkhvepsln;eillkhvepslnl;illkhvepslnlk;ll
khvepslnlkq;lkhvepslnlkqk;khvepslnlkqkf;hvepslnlkqkfe;vepslnlkqkfek;epslnlkqkfeki;psl
nlkqkfekil;slnlkqkfekiln;lnlkqkfekilne;nlkqkfekilnet;lkqkfekilneti;kqkfekilnetik;qkfekilne
tika;kfekilnetikay;fekilnetikayn;ekilnetikaynq;kilnetikaynqd;ilnetikaynqdl;lnetikaynqdld;
netikaynqdldn;etikaynqdldni;tikaynqdldnik;ikaynqdldniks;kaynqdldniksn;aynqdldniksne;
ynqdldniksned;nqdldniksnedq;qdldniksnedql;dldniksnedqla;ldniksnedqlah;dniksnedqlah
m;niksnedqlahmd;iksnedqlahmde;ksnedqlahmden;snedqlahmdeny;nedqlahmdenyk;edqla
hmdenyke;dqlahmdenykef;qlahmdenykefd;lahmdenykefdp;ahmdenykefdpl;hmdenykefdp
ln;mdenykefdplnl;denykefdplnld;enykefdplnldy;

14 mers:
mkktklniiklnil;kktklniiklnilt;ktklniiklniltt;tklniiklniltti;klniiklnilttil;lniiklnilttilt;niiklnilttil
tl;iiklnilttiltli;iklnilttiltlic;klnilttiltlici;lnilttiltlicis;nilttiltlicisc;ilttiltlicisca;lttiltliciscav;ttiltl
iciscavd;tiltliciscavdk;iltliciscavdki;ltliciscavdkid;tliciscavdkidp;liciscavdkidpe;iciscavdk
idpes;ciscavdkidpesk;iscavdkidpesks;scavdkidpesksk;cavdkidpesksk t;avdkidpesksktn;vd
kidpesksktnt;dkidpesksktntk;kidpesksktntkd;idpesksktntkdf;dpesksktntkdfe;pesksktntkdf
en;esksktntkdfenk;sksktntkdfenks;ksktntkdfenksq;sktntkdfenksqd;ktntkdfenksqdl;tntkdfe
nksqdle;ntkdfenksqdlep;tkdfenksqdleps;kdfenksqdlepsn;dfenksqdlepsnt;fenksqdlepsntk;e
nksqdlepsntkn;nksqdlepsntknk;ksqdlepsntknkd;sqdlepsntknkdl;qdlepsntknkdle;dlepsntkn
kdlep;lepsntknkdlepl;epsntknkdleple;psntknkdleplek;sntknkdleplekn;ntknkdleplekns;tknk
dlepleknsk;knkdlepleknske;nkdlepleknsket;kdlepleknsketi;dlepleknsketii;lepleknsketiis;e
pleknsketiisk;pleknsketiiskl;leknsketiiskle;eknsketiisklek;knsketiisklekm;nsketiisklekmi;s
ketiisklekmik;ketiisklekmikd;etiisklekmikdl;tiisklekmikdle;iisklekmikdled;isklekmikdled
q;sklekmikdledqk;klekmikdledqkd;lekmikdledqkdq;ekmikdledqkdqe;kmikdledqkdqed;mi
kdledqkdqedt;ikdledqkdqedte;kdledqkdqedtei;dledqkdqedteia;ledqkdqedteiak;edqkdqedte
iaki;dqkdqedteiakit;qkdqedteiakitn;kdqedteiakitnt;dqedteiakitntq;qedteiakitntqi;edteiakitn
tqid;dteiakitntqidf;teiakitntqidfl;eiakitntqidfle;iakitntqidflen;akitntqidflenf;kitntqidflenfk;i
tntqidflenfks;tntqidflenfkse;ntqidflenfksep;tqidflenfkseph;qidflenfksephd;idflenfksephdt;
dflenfksephdti;flenfksephdtis;lenfksephdtise;enfksephdtised;nfksephdtisedi;fksephdtisedi
e;ksephdtisediem;sephdtisediemk;ephdtisediemki;phdtisediemkik;hdtisediemkikr;dtisedie
mkikri;tisediemkikrii;isediemkikriiy;sediemkikriiys;ediemkikriiyss;diemkikriiyssl;iemkik
riiyssln;emkikriiysslny;mkikriiysslnye;kikriiysslnyei;ikriiysslnyeie;kriiysslnyeiek;riiyssln
yeieki;iiysslnyeiekin;iysslnyeiekint;ysslnyeiekintl;sslnyeiekintlk;slnyeiekintlke;lnyeiekint
lkei;nyeiekintlkeil;yeiekintlkeild;eiekintlkeildk;iekintlkeildkl;ekintlkeildkly;kintlkeildkly
k;intlkeildklykn;ntlkeildklyknh;tlkeildklyknhk;lkeildklyknhky;keildklyknhkyk;eildklykn
hkykt;ildklyknhkyktt;ldklyknhkyktta;dklyknhkykttar;klyknhkykttarn;lyknhkykttarnf;ykn
hkykttarnfi;knhkykttarnfil;nhkykttarnfiln;hkykttarnfilni;kykttarnfilnis;ykttarnfilnisi;kttarn
filnisik;ttarnfilnisiki;tarnfilnisikiq;arnfilnisikiqf;rnfilnisikiqfq;nfilnisikiqfqi;filnisikiqfqie;
ilnisikiqfqien;lnisikiqfqiena;nisikiqfqienal;isikiqfqienale;sikiqfqienalel;ikiqfqienalelm;kiq
fqienalelmk;iqfqienalelmke;qfqienalelmkee;fqienalelmkeei;qienalelmkeeie;ienalelmkeeie
d;enalelmkeeieda;nalelmkeeiedas;alelmkeeiedase;lelmkeeiedasei;elmkeeiedaseil;lmkeeie
daseiln;mkeeiedaseilnq;keeiedaseilnqe;eeiedaseilnqer;eiedaseilnqery;iedaseilnqerye;edas
eilnqeryei;daseilnqeryeil;aseilnqeryeill;seilnqeryeillk;eilnqeryeillkh;ilnqeryeillkhv;lnqery
eillkhve;nqeryeillkhvep;qeryeillkhveps;eryeillkhvepsl;ryeillkhvepsln;yeillkhvepslnl;eillk
hvepslnlk;illkhvepslnlkq;llkhvepslnlkqk;lkhvepslnlkqkf;khvepslnlkqkfe;hvepslnlkqkfek;
vepslnlkqkfeki;epslnlkqkfekil;pslnlkqkfekiln;slnlkqkfekilne;lnlkqkfekilnet;nlkqkfekilneti

;lkqkfekilnetik;kqkfekilnetika;qkfekilnetikay;kfekilnetikayn;fekilnetikaynq;ekilnetikaynq
d;kilnetikaynqdl;ilnetikaynqdld;lnetikaynqdldn;netikaynqdldni;etikaynqdldnik;tikaynqdld
niks;ikaynqdldniksn;kaynqdldniksne;aynqdldniksned;ynqdldniksnedq;nqdldniksnedql;qdl
dniksnedqla;dldniksnedqlah;ldniksnedqlahm;dniksnedqlahmd;niksnedqlahmde;iksnedqla
hmden;ksnedqlahmdeny;snedqlahmdenyk;nedqlahmdenyke;edqlahmdenykef;dqlahmden
ykefd;qlahmdenykefdp;lahmdenykefdpl;ahmdenykefdpln;hmdenykefdplnl;mdenykefdpln
ld;denykefdplnldy;

15 mers:
mkktklniiklnilt;kktklniiklniltt;ktklniiklniltti;tklniiklnilttil;klniiklnilttilt;lniiklnilttiltl;niikln
ilttiltli;iiklnilttiltlic;iklnilttiltlici;klnilttiltlicis;lnilttiltlicisc;nilttiltlicisca;ilttiltliciscav;ltiltli
ciscavd;ttiltliciscavdk;tiltliciscavdki;iltliciscavdkid;ltliciscavdkidp;tliciscavdkidpe;licisca
vdkidpes;iciscavdkidpesk;ciscavdkidpesks;iscavdkidpesksk;scavdkidpeskskt;cavdkidpesk
sktn;avdkidpesksktnt;vdkidpesksktntk;dkidpesksktntkd;kidpesksktntkdf;idpesksktntkdfe;
dpesksktntkdfen;pesksktntkdfenk;eskstntkdfenks;sksktntkdfenksq;ksktntkdfenksqd;sktnt
kdfenksqdl;ktntkdfenksqdle;tntkdfenksqdlep;ntkdfenksqdleps;tkdfenksqdlepsn;kdfenksqd
lepsnt;dfenksqdlepsntk;fenksqdlepsntkn;enksqdlepsntknk;nksqdlepsntknkd;ksqdlepsntkn
kdl;sqdlepsntknkdle;qdlepsntknkdlep;dlepsntknkdlepl;lepsntknkdleple;epsntknkdleplek;p
sntknkdleplekn;sntknkdleplekns;ntknkdlepleknsk;tknkdlepleknske;knkdlepleknsket;nkdle
pleknsketi;kdlepleknsketii;dlepleknsketiis;lepleknsketiisk;epleknsketiiskl;pleknsketiiskle;
leknsketiisklek;eknsketiisklekm;knsketiisklekmi;nsketiisklekmik;sketiisklekmikd;ketiiskl
ekmikdl;etiisklekmikdle;tiisklekmikdled;iisklekmikdledq;isklekmikdledqk;sklekmikdled
qkd;klekmikdledqkdq;lekmikdledqkdqe;ekmikdledqkdqed;kmikdledqkdqedt;mikdledqkd
qedte;ikdledqkdqedtei;kdledqkdqedteia;dledqkdqedteiak;ledqkdqedteiaki;edqkdqedteiakit
;dqkdqedteiakitn;qkdqedteiakitnt;kdqedteiakitntq;dqedteiakitntqi;qedteiakitntqid;edteiakit
ntqidf;dteiakitntqidfl;teiakitntqidfle;eiakitntqidflen;iakitntqidflenf;akitntqidflenfk;kitntqid
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ikriiyssl;diemkikriiyssln;iemkikriiysslny;emkikriiysslnye;mkikriiysslnyei;kikriiysslnyeie;
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lk;sslnyeiekintlke;slnyeiekintlkei;lnyeiekintlkeil;nyeiekintlkeild;yeiekintlkeildk;eiekintlk
eildkl;iekintlkeildkly;ekintlkeildklyk;kintlkeildklykn;intlkeildklyknh;ntlkeildklyknhk;tlke
ildklyknhky;lkeildklyknhkyk;keildklyknhkykt;eildklyknhkyktt;ildklyknhkyktta;ldklyknh
kykttar;dklyknhkykttarn;klyknhkykttarnf;lyknhkykttarnfi;yknhkykttarnfil;knhkykttarnfiln
;nhkykttarnfilni;hkykttarnfilnis;kykttarnfilnisi;ykttarnfilnisik;kttarnfilnisiki;ttarnfilnisikiq
;tarnfilnisikiqf;arnfilnisikiqfq;rnfilnisikiqfqi;nfilnisikiqfqie;filnisikiqfqien;ilnisikiqfqiena;
lnisikiqfqienal;nisikiqfqienale;isikiqfqienalel;sikiqfqienalelm;ikiqfqienalelmk;kiqfqienale
lmke;iqfqienalelmkee;qfqienalelmkeei;fqienalelmkeeie;qienalelmkeeied;ienalelmkeeieda;
enalelmkeeiedas;nalelmkeeiedase;alelmkeeiedasei;lelmkeeiedaseil;elmkeeiedaseiln;lmke
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lahmdenykefdpln;ahmdenykefdplnl;hmdenykefdplnld;mdenykefdplnldy;

16 mers:
mkktklniiklniltt;kktklniiklniltti;ktklniiklnilttil;tklniiklnilttilt;klniiklnilttiltl;lniiklnilttiltli;ni
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scavd;lttiltliciscavdk;ttiltliciscavdki;tiltliciscavdkid;iltliciscavdkidp;ltliciscavdkidpe;tlicis
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iqfqienalelmkeei;qfqienalelmkeeie;fqienalelmkeeied;qienalelmkeeieda;ienalelmkeeiedas;
enalelmkeeiedase;nalelmkeeiedasei;alelmkeeiedaseil;lelmkeeiedaseiln;elmkeeiedaseilnq;l
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daseilnqeryeil;edaseilnqeryeill;daseilnqeryeillk;aseilnqeryeillkh;seilnqeryeillkhv;eilnqery
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dniksnedqlah;qdldniksnedqlahm;dldniksnedqlahmd;ldniksnedqlahmde;dniksnedqlahmde
n;niksnedqlahmdeny;iksnedqlahmdenyk;ksnedqlahmdenyke;snedqlahmdenykef;nedqlah
mdenykefd;edqlahmdenykefdp;dqlahmdenykefdpl;qlahmdenykefdpln;lahmdenykefdplnl;
ahmdenykefdplnld;hmdenykefdplnldy;

<AAU07022 4-alpha-glucanotransferase;Protein;Borrelia garinii PBi>

8 mers:
mkykkiri;kykkirin;ykkirinl;kkirinln;kirinlnl;irinlnlk;rinlnlkr;inlnlkrk;nlnlkrks;lnlkrksg;nl
krksgi;lkrksgil;krksgill;rksgilln;ksgillni;sgillnis;gillniss;illnissl;llnisslp;lnisslps;nisslpsk;is
slpsky;sslpskyg;slpskygi;lpskygig;pskygigd;skygigdl;kygigdlg;ygigdlgk;gigdlgkg;igdlgk
ga;gdlgkgay;dlgkgayk;lgkgaykf;gkgaykfi;kgaykfid;gaykfidf;aykfidfl;ykfidflf;kfidflfa;fidf
lfas;idflfass;dflfassq;flfassqs;lfassqsy;fassqsyw;assqsywq;ssqsywqm;sqsywqmf;qsywqmf
a;sywqmfay;ywqmfays;wqmfaysp;qmfayspi;mfayspid;fayspidf;ayspidft;yspidftr;spidftrs;
pidftrsp;idftrspp;dftrsppy;ftrsppys;trsppysi;rsppysif;sppysifs;ppysifsa;pysifsaf;ysifsafa;sif
safag;ifsafagn;fsafagnv;safagnvy;afagnvyy;fagnvyyi;agnvyyid;gnvyyidl;nvyyidle;vyyidle
a;yyidleal;yidleald;idlealdk;dlealdkf;lealdkfi;ealdkfid;aldkfids;ldkfidsd;dkfidsdl;kfidsdln;
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etrysd;netrysdl;etrysdlk;trysdlkk;rysdlkkl;ysdlkkls;sdlkklsf;dlkklsfk;lkklsfkd;kklsfkdk;kls
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lnfin;aalnfinr;alnfinra;lnfinras;nfinrasv;finrasvd;inrasvde;nrasvdev;rasvdevr;asvdevrs;svd
evrsf;vdevrsfe;devrsfek;evrsfekf;vrsfekfk;rsfekfkk;sfekfkkk;fekfkkks;ekfkkkss;kfkkkssy;
fkkkssyw;kkkssywl;kkssywll;kssywlld;ssywlldf;sywlldfa;ywlldfas;wlldfasf;lldfasfv;ldfas
fva;dfasfvaf;fasfvafk;asfvafke;sfvafkey;fvafkeyf;vafkeyfl;afkeyflk;fkeyflkd;keyflkds;eyfl
kdsr;yflkdsrd;flkdsrda;lkdsrdaf;kdsrdafn;dsrdafnv;srdafnvl;rdafnvlf;dafnvlfd;afnvlfdr;fnv
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nekdlfk;nekdlfkl;ekdlfklr;kdlfklrn;dlfklrni;lfklrnil;fklrnils;klrnilsk;lrnilske;rnilskei;nilskei
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v;payswnvl;ayswnvlk;yswnvlkn;swnvlknv;wnvlknvk;nvlknvky;vlknvkye;lknvkyew;knvk
yeww;nvkyewwa;vkyewwak;kyewwakr;yewwakri;ewwakrig;wwakrigi;wakrigil;akrigilr;
krigilrk;rigilrky;igilrkyi;gilrkyid;ilrkyidv;lrkyidvi;rkyidvik;kyidviki;yidvikid;idvikidh;dvi
kidhf;vikidhfr;ikidhfrg;kidhfrgf;idhfrgfv;dhfrgfvs;hfrgfvst;frgfvstw;rgfvstwe;gfvstwev;fv

stwevg;vstwevgv;stwevgvg;twevgvge;wevgvgea;evgvgeay;vgvgeaya;gvgeayaf;vgeayafn;geayafng;eayafngl;ayafnglw;yafnglwv;afnglwvk;fnglwvks;nglwvksp;glwvkspg;lwvkspgr;wvkspgrd;vkspgrdf;kspgrdff;spgrdffn;pgrdffnf;grdffnfi;rdffnfil;dffnfiln;ffnfilne;fnfilnei;nfilneik;filneikd;ilneikdl;lneikdlk;neikdlki;eikdlkiw;ikdlkiwv;kdlkiwve;dlkiwved;lkiwvedf;kiwvedfe;iwvedfen;wvedfend;vedfendl;edfendle;dfendled;fendledv;endledvs;ndledvsr;dledvsrl;ledvsrlr;edvsrlrd;dvsrlrdf;vsrlrdff;srlrdffn;rlrdffnf;lrdffnfp;rdffnfpg;dffnfpgm;ffnfpgmr;fnfpgmri;nfpgmrim;fpgmrimk;pgmrimkl;gmrimkla;mrimklaf;rimklafd;imklafdf;mklafdfd;klafdfds;lafdfdsd;afdfdsdn;fdfdsdnq;dfdsdnqn;fdsdnqnl;dsdnqnlp;sdnqnlph;dnqnlphn;nqnlphny;qnlphnyi;nlphnyik;lphnyikn;phnyiknc;hnyiknci;nyiknciv;yikncivy;ikncivyt;kncivytg;ncivytgi;civytgig;ivytgigd;vytgigdn;ytgigdns;tgigdnst;gigdnsti;igdnstir;gdnstire;dnstiref;nstirefv;stirefvn;tirefvns;irefvnsl;refvnsld;efvnsldd;fvnslddl;vnslddlh;nslddlhk;slddlhkk;lddlhkky;ddlhkkyi;dlhkkyif;lhkkyifd;hkkyifdy;kkyifdyl;kyifdyln;yifdylnt;ifdylntn;fdylntne;dylntned;ylntnedf;lntnedfv;ntnedfvv;tnedfvvw;nedfvvwd;edfvvwdm;dfvvwdmi;fvvwdmir;vvwdmirs;vwdmirsa;wdmirsam;dmirsams;mirsamss;irsamssv;rsamssvs;samssvsd;amssvsds;mssvsdsv;ssvsdsvi;svsdsvii;vsdsviip;sdsviipm;dsviipmq;sviipmqd;viipmqdy;iipmqdyi;ipmqdyin;pmqdyinl;mqdyinlg;qdyinlgn;dyinlgne;yinlgnef;inlgnefr;nlgnefra;lgnefran;gnefrani;nefranip;efranipk;franipkn;ranipknt;anipkntl;nipkntln;ipkntlnn;pkntlnnw;kntlnnwi;ntlnnwif;tlnnwifr;lnnwifrl;nnwifrll;nwifrlle;wifrlles;ifrllesd;frllesdl;rllesdld;llesdlda;lesdldat;esdldatl;sdldatls;dldatlsk;ldatlskn;datlskni;atlsknis;tlsknisf;lsknisfi;sknisfit;knisfitr;nisfitrl;isfitrly;sfitrlyg;fitrlygr;itrlygrt;

9 mers:
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yfk;wahqkyfkl;ahqkyfklr;hqkyfklrf;qkyfklrfd;kyfklrfda;yfklrfdas;fklrfdask;klrfdaskd;lrfd
askdk;rfdaskdkv;fdaskdkva;daskdkvag;askdkvagi;skdkvagis;kdkvagisp;dkvagispd;kvagis
pdy;vagispdyf;agispdyfl;gispdyfle;ispdyfleq;spdyfleqe;pdyfleqeq;dyfleqeqa;yfleqeqaw;fl
eqeqawd;leqeqawds;eqeqawdsp;qeqawdspa;eqawdspay;qawdspays;awdspaysw;wdspays
wn;dspayswnv;spayswnvl;payswnvlk;ayswnvlkn;yswnvlknv;swnvlknvk;wnvlknvky;nvlk
nvkye;vlknvkyew;lknvkyeww;knvkyewwa;nvkyewwak;vkyewwakr;kyewwakri;yewwakr
ig;ewwakrigi;wwakrigil;wakrigilr;akrigilrk;krigilrky;rigilrkyi;igilrkyid;gilrkyidv;ilrkyidvi
;lrkyidvik;rkyidviki;kyidvikid;yidvikidh;idvikidhf;dvikidhfr;vikidhfrg;ikidhfrgf;kidhfrgfv
;idhfrgfvs;dhfrgfvst;hfrgfvstw;frgfvstwe;rgfvstwev;gfvstwevg;fvstwevgv;vstwevgvg;stw
evgvge;twevgvgea;wevgvgeay;evgvgeaya;vgvgeayaf;gvgeayafn;vgeayafng;geayafngl;ea
yafnglw;ayafnglwv;yafnglwvk;afnglwvks;fnglwvksp;nglwvkspg;glwvkspgr;lwvkspgrd;w
vkspgrdf;vkspgrdff;kspgrdffn;spgrdffnf;pgrdffnfi;grdffnfil;rdffnfiln;dffnfilne;ffnfilnei;fnf
ilneik;nfilneikd;filneikdl;ilneikdlk;lneikdlki;neikdlkiw;eikdlkiwv;ikdlkiwve;kdlkiwved;dl
kiwvedf;lkiwvedfe;kiwvedfen;iwvedfend;wvedfendl;vedfendle;edfendled;dfendledv;fend
ledvs;endledvsr;ndledvsrl;dledvsrlr;ledvsrlrd;edvsrlrdf;dvsrlrdff;vsrlrdffn;srlrdffnf;rlrdffn
fp;lrdffnfpg;rdffnfpgm;dffnfpgmr;ffnfpgmri;fnfpgmrim;nfpgmrimk;fpgmrimkl;pgmrimkl
a;gmrimklaf;mrimklafd;rimklafdf;imklafdfd;mklafdfds;klafdfdsd;lafdfdsdn;afdfdsdnq;fdf
dsdnqn;dfdsdnqnl;fdsdnqnlp;dsdnqnlph;sdnqnlphn;dnqnlphny;nqnlphnyi;qnlphnyik;nlph
nyikn;lphnyiknc;phnyiknci;hnyiknciv;nyiknciv y;yiknciv yt;iknciv ytg;knciv ytgi;nciv ytgig;
civytgigd;ivytgigdn;vytgigdns;ytgigdnst;tgigdnsti;gigdnstir;igdnstire;gdnstiref;dnstirefv;n
stirefvn;stirefvns;tirefvnsl;irefvnsld;refvnsldd;efvnslddl;fvnslddlh;vnslddlhk;nslddlhkk;sl
ddlhkky;lddlhkkyi;ddlhkkyif;dlhkkyifd;lhkkyifdy;hkkyifdyl;kkyifdyln;kyifdylnt;yifdylnt
n;ifdylntne;fdylntned;dylntnedf;ylntnedfv;lntnedfvv;ntnedfvvw;tnedfvvwd;nedfvvwdm;e
dfvvwdmi;dfvvwdmir;fvvwdmirs;vvwdmirsa;vwdmirsam;wdmirsams;dmirsamss;mirsam
ssv;irsamssvs;rsamssvsd;samssvsds;amssvsdsv;mssvsdsvi;ssvsdsvii;svsdsviip;vsdsviipm;
sdsviipmq;dsviipmqd;sviipmqdy;viipmqdyi;iipmqdyin;ipmqdyinl;pmqdyinlg;mqdyinlgn;
qdyinlgne;dyinlgnef;yinlgnefr;inlgnefra;nlgnefran;lgnefrani;gnefranip;nefranipk;efranipk
n;franipknt;ranipkntl;anipkntln;nipkntlnn;ipkntlnnw;pkntlnnwi;kntlnnwif;ntlnnwifr;tlnnw
ifrl;lnnwifrll;nnwifrlle;nwifrlles;wifrllesd;ifrllesdl;frllesdld;rllesdlda;llesdldat;lesdldatl;es
dldatls;sdldatlsk;dldatlskn;ldatlskni;datlsknis;atlsknisf;tlsknisfi;lsknisfit;sknisfitr;knisfitrl;
nisfitrly;isfitrlyg;sfitrlygr;fitrlygrt;

10 mers:
mkykkirinl;kykkirinln;ykkirinlnl;kkirinlnlk;kirinlnlkr;irinlnlkrk;rinlnlkrks;inlnlkrksg;nlnl
krksgi;lnlkrksgil;nlkrksgill;lkrksgilln;krksgillni;rksgillnis;ksgillniss;sgillnissl;gillnisslp;ill
nisslps;llnisslpsk;lnisslpsky;nisslpskyg;isslpskygi;sslpskygig;slpskygigd;lpskygigdl;psky
gigdlg;skygigdlgk;kygigdlgkg;ygigdlgkga;gigdlgkgay;igdlgkgayk;gdlgkgaykf;dlgkgaykfi
;lgkgaykfid;gkgaykfidf;kgaykfidfl;gaykfidflf;aykfidflfa;ykfidflfas;kfidflfass;fidflfassq;idf
lfassqs;dflfassqsy;flfassqsyw;lfassqsywq;fassqsywqm;assqsywqmf;ssqsywqmfa;sqsywq
mfay;qsywqmfays;sywqmfaysp;ywqmfayspi;wqmfayspid;qmfayspidf;mfayspidft;fayspid
ftr;ayspidftrs;yspidftrsp;spidftrspp;pidftrsppy;idftrsppys;dftrsppysi;ftrsppysif;trsppysifs;rs
ppysifsa;sppysifsaf;ppysifsafa;pysifsafag;ysifsafagn;sifsafagnv;ifsafagnvy;fsafagnvyy;saf
agnvyyi;afagnvyyid;fagnvyyidl;agnvyyidle;gnvyyidlea;nvyyidleal;vyyidleald;yyidlealdk;

yidlealdkf;idlealdkfi;dlealdkfid;lealdkfids;ealdkfidsd;aldkfidsdl;ldkfidsdln;dkfidsdlnl;kfid
sdlnll;fidsdlnllk;idsdlnllke;dsdlnllken;sdlnllkene;dlnllkenet;lnllkenetr;nllkenetry;llkenetry
s;lkenetrysd;kenetrysdl;enetrysdlk;netrysdlkk;etrysdlkkl;trysdlkkls;rysdlkklsf;ysdlkklsfk;
sdlkklsfkd;dlkklsfkdk;lkklsfkdkf;kklsfkdkfl;klsfkdkflk;lsfkdkflke;sfkdkflkea;fkdkflkeaa;
kdkflkeaal;dkflkeaaln;kflkeaalnf;flkeaalnfi;lkeaalnfin;keaalnfinr;eaalnfinra;aalnfinras;aln
finrasv;lnfinrasvd;nfinrasvde;finrasvdev;inrasvdevr;nrasvdevrs;rasvdevrsf;asvdevrsfe;svd
evrsfek;vdevrsfekf;devrsfekfk;evrsfekfkk;vrsfekfkkk;rsfekfkkks;sfekfkkkss;fekfkkkssy;e
kfkkkssyw;kfkkkssywl;fkkkssywll;kkkssywlld;kkssywlldf;kssywlldfa;ssywlldfas;sywlldf
asf;ywlldfasfv;wlldfasfva;lldfasfvaf;ldfasfvafk;dfasfvafke;fasfvafkey;asfvafkeyf;sfvafkey
fl;fvafkeyflk;vafkeyflkd;afkeyflkds;fkeyflkdsr;keyflkdsrd;eyflkdsrda;yflkdsrdaf;flkdsrdaf
n;lkdsrdafnv;kdsrdafnvl;dsrdafnvlf;srdafnvlfd;rdafnvlfdr;dafnvlfdrg;afnvlfdrgi;fnvlfdrgil;
nvlfdrgili;vlfdrgilir;lfdrgilirn;fdrgilirne;drgilirnek;rgilirnekd;gilirnekdl;ilirnekdlf;lirnekdlf
k;irnekdlfkl;rnekdlfklr;nekdlfklrn;ekdlfklrni;kdlfklrnil;dlfklrnils;lfklrnilsk;fklrnilske;klrni
lskei;lrnilskeik;rnilskeikv;nilskeikvq;ilskeikvqe;lskeikvqev;skeikvqevl;keikvqevlq;eikvqe
vlqy;ikvqevlqyf;kvqevlqyff;vqevlqyfff;qevlqyffffs;evlqyfffsq;vlqyfffsqf;lqyfffsqfq;qyffffs
qfqa;yfffsqfqal;fffsqfqalk;ffsqfqalkr;fsqfqalkry;sqfqalkrya;qfqalkryan;fqalkryand;qalkrya
ndk;alkryandkg;lkryandkgi;kryandkgie;ryandkgiel;yandkgielv;andkgielvm;ndkgielvmn;d
kgielvmnl;kgielvmnlp;gielvmnlpl;ielvmnlplf;elvmnlplfi;lvmnlplfia;vmnlplfiay;mnlplfiay
d;nlplfiayds;lplfiaydsa;plfiaydsad;lfiaydsadv;fiaydsadvw;iaydsadvwa;aydsadvwah;ydsad
vwahq;dsadvwahqk;sadvwahqky;advwahqkyf;dvwahqkyfk;vwahqkyfkl;wahqkyfklr;ahqk
yfklrf;hqkyfklrfd;qkyfklrfda;kyfklrfdas;yfklrfdask;fklrfdaskd;klrfdaskdk;lrfdaskdkv;rfdas
kdkva;fdaskdkvag;daskdkvagi;askdkvagis;skdkvagisp;kdkvagispd;dkvagispdy;kvagispdy
f;vagispdyfl;agispdyfle;gispdyfleq;ispdyfleqe;spdyfleqeq;pdyfleqeqa;dyfleqeqaw;yfleqeq
awd;fleqeqawds;leqeqawdsp;eqeqawdspa;qeqawdspay;eqawdspays;qawdspaysw;awdspa
yswn;wdspayswnv;dspayswnvl;spayswnvlk;payswnvlkn;ayswnvlknv;yswnvlknvk;swnvl
knvky;wnvlknvkye;nvlknvkyew;vlknvkyeww;lknvkyewwa;knvkyewwak;nvkyewwakr;v
kyewwakri;kyewwakrig;yewwakrigi;ewwakrigil;wwakrigilr;wakrigilrk;akrigilrky;krigilr
kyi;rigilrkyid;igilrkyidv;gilrkyidvi;ilrkyidvik;lrkyidviki;rkyidvikid;kyidvikidh;yidvikidhf;
idvikidhfr;dvikidhfrg;vikidhfrgf;ikidhfrgfv;kidhfrgfvs;idhfrgfvst;dhfrgfvstw;hfrgfvstwe;f
rgfvstwev;rgfvstwevg;gfvstwevgv;fvstwevgvg;vstwevgvge;stwevgvgea;twevgvgeay;wev
gvgeaya;evgvgeayaf;vgvgeayafn;gvgeayafng;vgeayafngl;geayafnglw;eayafnglwv;ayafngl
wvk;yafnglwvks;afnglwvksp;fnglwvkspg;nglwvkspgr;glwvkspgrd;lwvkspgrdf;wvkspgrdf
f;vkspgrdffn;kspgrdffnf;spgrdffnfi;pgrdffnfil;grdffnfiln;rdffnfilne;dffnfilnei;ffnfilneik;fnf
ilneikd;nfilneikdl;filneikdlk;ilneikdlki;lneikdlkiw;neikdlkiwv;eikdlkiwve;ikdlkiwved;kdl
kiwvedf;dlkiwvedfe;lkiwvedfen;kiwvedfend;iwvedfendl;wvedfendle;vedfendled;edfendle
dv;dfendledvs;fendledvsr;endledvsrl;ndledvsrlr;dledvsrlrd;ledvsrlrdf;edvsrlrdff;dvsrlrdffn
;vsrlrdffnf;srlrdffnfp;rlrdffnfpg;lrdffnfpgm;rdffnfpgmr;dffnfpgmri;ffnfpgmrim;fnfpgmri
mk;nfpgmrimkl;fpgmrimkla;pgmrimklaf;gmrimklafd;mrimklafdf;rimklafdfd;imklafdfds;
mklafdfdsd;klafdfdsdn;lafdfdsdnq;afdfdsdnqn;fdfdsdnqnl;dfdsdnqnlp;fdsdnqnlph;dsdnqn
lphn;sdnqnlphny;dnqnlphnyi;nqnlphnyik;qnlphnyikn;nlphnyiknc;lphnyiknci;phnyiknciv;
hnyiknciv;nyiknciv yt;yiknciv ytg;iknciv ytgi;knciv ytgig;nciv ytgigd;civytgigdn;ivytgigdn
s;vytgigdnst;ytgigdnsti;tgigdnstir;gigdnstire;igdnstiref;gdnstirefv;dnstirefvn;nstirefvns;sti
refvnsl;tirefvnsld;irefvnsldd;refvnsldd l;efvnsldd lh;fvnsldd lhk;vnsldd lhkk;nsldd lhkky;sldd
lhkkyi;lddlhkkyif;ddlhkkyifd;dlhkkyifdy;lhkkyifdyl;hkkyifdyln;kkyifdylnt;kyifdylntn;yif
dylntne;ifdylntned;fdylntnedf;dylntnedfv;ylntnedfvv;lntnedfvvw;ntnedfvvwd;tnedfvvwd
m;nedfvvwdmi;edfvvwdmir;dfvvwdmirs;fvvwdmirsa;vvwdmirsam;vwdmirsams;wdmirs

amss;dmirsamssv;mirsamssvs;irsamssvsd;rsamssvsds;samssvsdsv;amssvsdsvi;mssvsdsvii;ssvsdsviip;svsdsviipm;vsdsviipmq;sdsviipmqd;dsviipmqdy;sviipmqdyi;viipmqdyin;iipmqdyinl;ipmqdyinlg;pmqdyinlgn;mqdyinlgne;qdyinlgnef;dyinlgnefr;yinlgnefra;inlgnefran;nlgnefrani;lgnefranip;gnefranipk;nefranipkn;efranipknt;franipkntl;ranipkntln;anipkntlnn;nipkntlnnw;ipkntlnnwi;pkntlnnwif;kntlnnwifr;ntlnnwifrl;tlnnwifrll;lnnwifrlle;nnwifrlles;nwifrllesd;wifrllesdl;ifrllesdld;frllesdlda;rllesdldat;llesdldatl;lesdldatls;esdldatlsk;sdldatlskn;dldatlskni;ldatlsknis;datlsknisf;atlsknisfi;tlsknisfit;lsknisfitr;sknisfitrl;knisfitrly;nisfitrlyg;isfitrlygr;sfitrlygrt;

11 mers:
mkykkirinln;kykkirinlnl;ykkirinlnlk;kkirinlnlkr;kirinlnlkrk;irinlnlkrks;rinlnlkrksg;inlnlkrksgi;nlnlkrksgil;lnlkrksgill;nlkrksgilln;lkrksgillni;krksgillnis;rksgillniss;ksgillnissl;sgillnisslp;gillnisslps;illnisslpsk;llnisslpsky;lnisslpskyg;nisslpskygi;isslpskygig;sslpskygigd;slpskygigdl;lpskygigdlg;pskygigdlgk;skygigdlgkg;kygigdlgkga;ygigdlgkgay;gigdlgkgayk;igdlgkgaykf;gdlgkgaykfi;dlgkgaykfid;lgkgaykfidf;gkgaykfidfl;kgaykfidflf;gaykfidflfa;aykfidflfas;ykfidflfass;kfidflfassq;fidflfassqs;idflfassqsy;dflfassqsyw;flfassqsywq;lfassqsywqm;fassqsywqmf;assqsywqmfa;ssqsywqmfay;sqsywqmfays;qsywqmfaysp;sywqmfayspi;ywqmfayspid;wqmfayspidf;qmfayspidft;mfayspidftr;fayspidftrs;ayspidftrsp;yspidftrspp;spidftrsppy;pidftrsppys;idftrsppysi;dftrsppysif;ftrsppysifs;trsppysifsa;rsppysifsaf;sppysifsafa;ppysifsafag;pysifsafagn;ysifsafagnv;sifsafagnvy;ifsafagnvyy;fsafagnvyyi;safagnvyyid;afagnvyyidl;fagnvyyidle;agnvyyidlea;gnvyyidleal;nvyyidleald;vyyidlealdk;yyidlealdkf;yidlealdkfi;idlealdkfid;dlealdkfids;lealdkfidsd;ealdkfidsdl;aldkfidsdln;ldkfidsdlnl;dkfidsdlnll;kfidsdlnllk;fidsdlnllke;idsdlnllken;dsdlnllkene;sdlnllkenet;dlnllkenetr;lnllkenetry;nllkenetrys;llkenetrysd;lkenetrysdl;kenetrysdlk;enetrysdlkk;netrysdlkkl;etrysdlkkls;trysdlkklsf;rysdlkklsfk;ysdlkklsfkd;sdlkklsfkdk;dlkklsfkdkf;lkklsfkdkfl;kklsfkdkflk;klsfkdkflke;lsfkdkflkea;sfkdkflkeaa;fkdkflkeaal;kdkflkeaaln;dkflkeaalnf;kflkeaalnfi;flkeaalnfin;lkeaalnfinr;keaalnfinra;eaalnfinras;aalnfinrasv;alnfinrasvd;lnfinrasvde;nfinrasvdev;finrasvdevr;inrasvdevrs;nrasvdevrsf;rasvdevrsfe;asvdevrsfek;svdevrsfekf;vdevrsfekfk;devrsfekfkk;evrsfekfkkk;vrsfekfkkks;rsfekfkkkss;sfekfkkkssy;fekfkkkssyw;ekfkkkssywl;kfkkkssywll;fkkkssywlld;kkkssywlldf;kkssywlldfa;kssywlldfas;ssywlldfasf;sywlldfasfv;ywlldfasfva;wlldfasfvaf;lldfasfvafk;ldfasfvafke;dfasfvafkey;fasfvafkeyf;asfvafkeyfl;sfvafkeyflk;fvafkeyflkd;vafkeyflkds;afkeyflkdsr;fkeyflkdsrd;keyflkdsrda;eyflkdsrdaf;yflkdsrdafn;flkdsrdafnv;lkdsrdafnvl;kdsrdafnvlf;dsrdafnvlfd;srdafnvlfdr;rdafnvlfdrg;dafnvlfdrgi;afnvlfdrgil;fnvlfdrgili;nvlfdrgilir;vlfdrgilirn;lfdrgilirne;fdrgilirnek;drgilirnekd;rgilirnekdl;gilirnekdlf;ilirnekdlfk;lirnekdlfkl;irnekdlfklr;rnekdlfklrn;nekdlfklrni;ekdlfklrnil;kdlfklrnils;dlfklrnilsk;lfklrnilske;fklrnilskei;klrnilskeik;lrnilskeikv;rnilskeikvq;nilskeikvqe;ilskeikvqev;lskeikvqevl;skeikvqevlq;keikvqevlqy;eikvqevlqyf;ikvqevlqyff;kvqevlqyfff;vqevlqyffffs;qevlqyfffsq;evlqyfffsqf;vlqyfffsqfq;lqyfffsqfqa;qyfffsqfqal;yfffsqfqalk;fffsqfqalkr;ffsqfqalkry;fsqfqalkrya;sqfqalkryan;qfqalkryand;fqalkryandk;qalkryandkg;alkryandkgi;lkryandkgie;kryandkgiel;ryandkgielv;yandkgielvm;andkgielvmn;ndkgielvmnl;dkgielvmnlp;kgielvmnlpl;gielvmnlplf;ielvmnlplfi;elvmnlplfia;lvmnlplfiay;vmnlplfiayd;mnlplfiayds;nlplfiaydsa;lplfiaydsad;plfiaydsadv;lfiaydsadvw;fiaydsadvwa;iaydsadvwah;aydsadvwahq;ydsadvwahqk;dsadvwahqky;sadvwahqkyf;advwahqkyfk;dvwahqkyfkl;vwahqkyfklr;wahqkyfklrf;ahqkyfklrfd;hqkyfklrfda;qkyfklrfdas;kyfklrfdask;yfklrfdaskd;fklrfdaskdk;klrfdaskdkv;lrfdaskdkva;rfdaskdkvag;fdaskdkvagi;daskdkvagis;askdkvagisp;skdkvagispd;kdkvagispdy;dkvagispdyf;kvagispdyfl;vagispdyfle;agispdyfleq;gispdyfleqe;ispdyfleqeq;spdyfleqeqa;pdyfleqeqaw;dyfleqeqawd;

yfleqeqawds;fleqeqawdsp;leqeqawdspa;eqeqawdspay;qeqawdspays;eqawdspaysw;qawds
payswn;awdspayswnv;wdspayswnvl;dspayswnvlk;spayswnvlkn;payswnvlknv;ayswnvlkn
vk;yswnvlknvky;swnvlknvkye;wnvlknvkyew;nvlknvkyeww;vlknvkyewwa;lknvkyewwak
;knvkyewwakr;nvkyewwakri;vkyewwakrig;kyewwakrigi;yewwakrigil;ewwakrigilr;wwak
rigilrk;wakrigilrky;akrigilrkyi;krigilrkyid;rigilrkyidv;igilrkyidvi;gilrkyidvik;ilrkyidviki;lr
kyidvikid;rkyidvikidh;kyidvikidhf;yidvikidhfr;idvikidhfrg;dvikidhfrgf;vikidhfrgfv;ikidhfr
gfvs;kidhfrgfvst;idhfrgfvstw;dhfrgfvstwe;hfrgfvstwev;frgfvstwevg;rgfvstwevgv;gfvstwev
gvg;fvstwevgvge;vstwevgvgea;stwevgvgeay;twevgvgeaya;wevgvgeayaf;evgvgeayafn;vg
vgeayafng;gvgeayafngl;vgeayafnglw;geayafnglwv;eayafnglwvk;ayafnglwvks;yafnglwvk
sp;afnglwvkspg;fnglwvkspgr;nglwvkspgrd;glwvkspgrdf;lwvkspgrdff;wvkspgrdffn;vkspg
rdffnf;kspgrdffnfi;spgrdffnfil;pgrdffnfiln;grdffnfilne;rdffnfilnei;dffnfilneik;ffnfilneikd;fnf
ilneikdl;nfilneikdlk;filneikdlki;ilneikdlkiw;lneikdlkiwv;neikdlkiwve;eikdlkiwved;ikdlkiw
vedf;kdlkiwvedfe;dlkiwvedfen;lkiwvedfend;kiwvedfendl;iwvedfendle;wvedfendled;vedf
endledv;edfendledvs;dfendledvsr;fendledvsrl;endledvsrlr;ndledvsrlrd;dledvsrlrdf;ledvsrlr
dff;edvsrlrdffn;dvsrlrdffnf;vsrlrdffnfp;srlrdffnfpg;rlrdffnfpgm;lrdffnfpgmr;rdffnfpgmri;df
fnfpgmrim;ffnfpgmrimk;fnfpgmrimkl;nfpgmrimkla;fpgmrimklaf;pgmrimklafd;gmrimklaf
df;mrimklafdfd;rimklafdfds;imklafdfdsd;mklafdfdsdn;klafdfdsdnq;lafdfdsdnqn;afdfdsdnq
nl;fdfdsdnqnlp;dfdsdnqnlph;fdsdnqnlphn;dsdnqnlphny;sdnqnlphnyi;dnqnlphnyik;nqnlph
nyikn;qnlphnyiknc;nlphnyiknci;lphnyiknciv;phnyiknciv y;hnyiknciv yt;nyiknciv ytg;yiknci
vytgi;iknciv ytgig;knciv ytgigd;nciv ytgigdn;civytgigdns;ivytgigdnst;vytgigdnsti;ytgigdnsti
r;tgigdnstire;gigdnstiref;igdnstirefv;gdnstirefvn;dnstirefvns;nstirefvnsl;stirefvnsld;tirefvns
ldd;irefvnslddl;refvnslddlh;efvnslddlhk;fvnslddlhkk;vnslddlhkky;nslddlhkkyi;slddlhkkyif
;lddlhkkyifd;ddlhkkyifdy;dlhkkyifdyl;lhkkyifdyln;hkkyifdylnt;kkyifdylntn;kyifdylntne;yi
fdylntned;ifdylntnedf;fdylntnedfv;dylntnedfvv;ylntnedfvvw;lntnedfvvwd;ntnedfvvwdm;t
nedfvvwdmi;nedfvvwdmir;edfvvwdmirs;dfvvwdmirsa;fvvwdmirsam;vvwdmirsams;vwd
mirsamss;wdmirsamssv;dmirsamssvs;mirsamssvsd;irsamssvsds;rsamssvsdsv;samssvsdsv
i;amssvsdsvii;mssvsdsviip;ssvsdsviipm;svsdsviipmq;vsdsviipmqd;sdsviipmqdy;dsviipmq
dyi;sviipmqdyin;viipmqdyinl;iipmqdyinlg;ipmqdyinlgn;pmqdyinlgne;mqdyinlgnef;qdyin
lgnefr;dyinlgnefra;yinlgnefran;inlgnefrani;nlgnefranip;lgnefranipk;gnefranipkn;nefranipk
nt;efranipkntl;franipkntln;ranipkntlnn;anipkntlnnw;nipkntlnnwi;ipkntlnnwif;pkntlnnwifr;
kntlnnwifrl;ntlnnwifrll;tlnnwifrlle;lnnwifrlles;nnwifrllesd;nwifrllesdl;wifrllesdld;ifrllesdl
da;frllesdldat;rllesdldatl;llesdldatls;lesdldatlsk;esdldatlskn;sdldatlskni;dldatlsknis;ldatlskn
isf;datlsknisfi;atlsknisfit;tlsknisfitr;lsknisfitrl;sknisfitrly;knisfitrlyg;nisfitrlygr;isfitrlygrt;

13 mers:
mkykkirinlnlk;kykkirinlnlkr;ykkirinlnlkrk;kkirinlnlkrks;kirinlnlkrksg;irinlnlkrksgi;rinlnlk
rksgil;inlnlkrksgill;nlnlkrksgilln;lnlkrksgillni;nlkrksgillnis;lkrksgillniss;krksgillnissl;rksgi
llnisslp;ksgillnisslps;sgillnisslpsk;gillnisslpsky;illnisslpskyg;llnisslpskygi;lnisslpskygig;ni
sslpskygigd;isslpskygigdl;sslpskygigdlg;slpskygigdlgk;lpskygigdlgkg;pskygigdlgkga;sky
gigdlgkgay;kygigdlgkgayk;ygigdlgkgaykf;gigdlgkgaykfi;igdlgkgaykfid;gdlgkgaykfidf;dl
gkgaykfidfl;lgkgaykfidflf;gkgaykfidflfa;kgaykfidflfas;gaykfidflfass;aykfidflfassq;ykfidflf
assqs;kfidflfassqsy;fidflfassqsyw;idflfassqsywq;dflfassqsywqm;flfassqsywqmf;lfassqsyw
qmfa;fassqsywqmfay;assqsywqmfays;ssqsywqmfaysp;sqsywqmfayspi;qsywqmfayspid;sy
wqmfayspidf;ywqmfayspidft;wqmfayspidftr;qmfayspidftrs;mfayspidftrsp;fayspidftrspp;a
yspidftrsppy;yspidftrsppys;spidftrsppysi;pidftrsppysif;idftrsppysifs;dftrsppysifsa;ftrsppysi
fsaf;trsppysifsafa;rsppysifsafag;sppysifsafagn;ppysifsafagnv;pysifsafagnvy;ysifsafagnvyy

;sifsafagnvyyi;ifsafagnvyyid;fsafagnvyyidl;safagnvyyidle;afagnvyyidlea;fagnvyyidleal;a
gnvyyidleald;gnvyyidlealdk;nvyyidlealdkf;vyyidlealdkfi;yyidlealdkfid;yidlealdkfids;idlea
ldkfidsd;dlealdkfidsdl;lealdkfidsdln;ealdkfidsdlnl;aldkfidsdlnll;ldkfidsdlnllk;dkfidsdlnllk
e;kfidsdlnllken;fidsdlnllkene;idsdlnllkenet;dsdlnllkenetr;sdlnllkenetry;dlnllkenetrys;lnllke
netrysd;nllkenetrysdl;llkenetrysdlk;lkenetrysdlkk;kenetrysdlkkl;enetrysdlkkls;netrysdlkkl
sf;etrysdlkklsfk;trysdlkklsfkd;rysdlkklsfkdk;ysdlkklsfkdkf;sdlkklsfkdkfl;dlkklsfkdkflk;lk
klsfkdkflke;kklsfkdkflkea;klsfkdkflkeaa;lsfkdkflkeaal;sfkdkflkeaaln;fkdkflkeaalnf;kdkflk
eaalnfi;dkflkeaalnfin;kflkeaalnfinr;flkeaalnfinra;lkeaalnfinras;keaalnfinrasv;eaalnfinrasvd
;aalnfinrasvde;alnfinrasvdev;lnfinrasvdevr;nfinrasvdevrs;finrasvdevrsf;inrasvdevrsfe;nras
vdevrsfek;rasvdevrsfekf;asvdevrsfekfk;svdevrsfekfkk;vdevrsfekfkkk;devrsfekfkkks;evrsf
ekfkkkss;vrsfekfkkkssy;rsfekfkkkssyw;sfekfkkkssywl;fekfkkkssywll;ekfkkkssywlld;kfkk
kssywlldf;fkkkssywlldfa;kkkssywlldfas;kkssywlldfasf;kssywlldfasfv;ssywlldfasfva;sywll
dfasfvaf;ywlldfasfvafk;wlldfasfvafke;lldfasfvafkey;ldfasfvafkeyf;dfasfvafkeyfl;fasfvafke
yflk;asfvafkeyflkd;sfvafkeyflkds;fvafkeyflkdsr;vafkeyflkdsrd;afkeyflkdsrda;fkeyflkdsrda
f;keyflkdsrdafn;eyflkdsrdafnv;yflkdsrdafnvl;flkdsrdafnvlf;lkdsrdafnvlfd;kdsrdafnvlfdr;ds
rdafnvlfdrg;srdafnvlfdrgi;rdafnvlfdrgil;dafnvlfdrgili;afnvlfdrgilir;fnvlfdrgilirn;nvlfdrgilir
ne;vlfdrgilirnek;lfdrgilirnekd;fdrgilirnekdl;drgilirnekdlf;rgilirnekdlfk;gilirnekdlfkl;ilirnek
dlfklr;lirnekdlfklrn;irnekdlfklrni;rnekdlfklrnil;nekdlfklrnils;ekdlfklrnilsk;kdlfklrnilske;dlf
klrnilskei;lfklrnilskeik;fklrnilskeikv;klrnilskeikvq;lrnilskeikvqe;rnilskeikvqev;nilskeikvqe
vl;ilskeikvqevlq;lskeikvqevlqy;skeikvqevlqyf;keikvqevlqyff;eikvqevlqyfff;ikvqevlqyffs;
kvqevlqyffsq;vqevlqyffsqf;qevlqyffsqfq;evlqyffsqfqa;vlqyffsqfqal;lqyffsqfqalk;qyfff
sqfqalkr;yffsqfqalkry;ffsqfqalkrya;fsqfqalkryan;fsqfqalkryand;sqfqalkryandk;qfqalkrya
ndkg;fqalkryandkgi;qalkryandkgie;alkryandkgiel;lkryandkgielv;kryandkgielvm;ryandkgi
elvmn;yandkgielvmnl;andkgielvmnlp;ndkgielvmnlpl;dkgielvmnlplf;kgielvmnlplfi;gielvm
nlplfia;ielvmnlplfiay;elvmnlplfiayd;lvmnlplfiayds;vmnlplfiaydsa;mnlplfiaydsad;nlplfiayd
sadv;lplfiaydsadvw;plfiaydsadvwa;lfiaydsadvwah;fiaydsadvwahq;iaydsadvwahqk;aydsad
vwahqky;ydsadvwahqkyf;dsadvwahqkyfk;sadvwahqkyfkl;advwahqkyfklr;dvwahqkyfklrf
;vwahqkyfklrfd;wahqkyfklrfda;ahqkyfklrfdas;hqkyfklrfdask;qkyfklrfdaskd;kyfklrfdaskdk
;yfklrfdaskdkv;fklrfdaskdkva;klrfdaskdkvag;lrfdaskdkvagi;rfdaskdkvagis;fdaskdkvagisp;
daskdkvagispd;askdkvagispdy;skdkvagispdyf;kdkvagispdyfl;dkvagispdyfle;kvagispdyfle
q;vagispdyfleqe;agispdyfleqeq;gispdyfleqeqa;ispdyfleqeqaw;spdyfleqeqawd;pdyfleqeqa
wds;dyfleqeqawdsp;yfleqeqawdspa;fleqeqawdspay;leqeqawdspays;eqeqawdspaysw;qeqa
wdspayswn;eqawdspayswnv;qawdspayswnvl;awdspayswnvlk;wdspayswnvlkn;dspayswn
vlknv;spayswnvlknvk;payswnvlknvky;ayswnvlknvkye;yswnvlknvkyew;swnvlknvkyeww
;wnvlknvkyewwa;nvlknvkyewwak;vlknvkyewwakr;lknvkyewwakri;knvkyewwakrig;nvk
yewwakrigi;vkyewwakrigil;kyewwakrigilr;yewwakrigilrk;ewwakrigilrky;wwakrigilrkyi;
wakrigilrkyid;akrigilrkyidv;krigilrkyidvi;rigilrkyidvik;igilrkyidviki;gilrkyidvikid;ilrkyidv
ikidh;lrkyidvikidhf;rkyidvikidhfr;kyidvikidhfrg;yidvikidhfrgf;idvikidhfrgfv;dvikidhfrgfvs
;vikidhfrgfvst;ikidhfrgfvstw;kidhfrgfvstwe;idhfrgfvstwev;dhfrgfvstwevg;hfrgfvstwevgv;f
rgfvstwevgvg;rgfvstwevgvge;gfvstwevgvgea;fvstwevgvgeay;vstwevgvgeaya;stwevgvgea
yaf;twevgvgeayafn;wevgvgeayafng;evgvgeayafngl;vgvgeayafnglw;gvgeayafnglwv;vgeay
afnglwvk;geayafnglwvks;eayafnglwvksp;ayafnglwvkspg;yafnglwvkspgr;afnglwvkspgrd;f
nglwvkspgrdf;nglwvkspgrdff;glwvkspgrdffn;lwvkspgrdffnf;wvkspgrdffnfi;vkspgrdffnfil;
kspgrdffnfiln;spgrdffnfilne;pgrdffnfilnei;grdffnfilneik;rdffnfilneikd;dffnfilneikdl;ffnfilnei
kdlk;fnfilneikdlki;nfilneikdlkiw;filneikdlkiwv;ilneikdlkiwve;lneikdlkiwved;neikdlkiwved
f;eikdlkiwvedfe;ikdlkiwvedfen;kdlkiwvedfend;dlkiwvedfendl;lkiwvedfendle;kiwvedfendl

ed;iwvedfendledv;wvedfendledvs;vedfendledvsr;edfendledvsrl;dfendledvsrlr;fendledvsrlr
d;endledvsrlrdf;ndledvsrlrdff;dledvsrlrdffn;ledvsrlrdffnf;edvsrlrdffnfp;dvsrlrdffnfpg;vsrlr
dffnfpgm;srlrdffnfpgmr;rlrdffnfpgmri;lrdffnfpgmrim;rdffnfpgmrimk;dffnfpgmrimkl;ffnfp
gmrimkla;fnfpgmrimklaf;nfpgmrimklafd;fpgmrimklafdf;pgmrimklafdfd;gmrimklafdfds;
mrimklafdfdsd;rimklafdfdsdn;imklafdfdsdnq;mklafdfdsdnqn;klafdfdsdnqnl;lafdfdsdnqnlp
;afdfdsdnqnlph;fdfdsdnqnlphn;dfdsdnqnlphny;fdsdnqnlphnyi;dsdnqnlphnyik;sdnqnlphnyi
kn;dnqnlphnyiknc;nqnlphnyiknci;qnlphnyiknciv;nlphnyiknciv y;lphnyiknciv yt;phnyiknci
vytg;hnyiknciv ytgi;nyiknciv ytgig;yiknciv ytgigd;iknciv ytgigdn;kncivytgigdns;ncivytgigd
nst;civytgigdnsti;ivytgigdnstir;vytgigdnstire;ytgigdnstiref;tgigdnstirefv;gigdnstirefvn;igd
nstirefvns;gdnstirefvnsl;dnstirefvnsld;nstirefvnsldd;stirefvnsldd l;tirefvnsldd lh;irefvnsldd l
hk;refvnsldd lhkk;efvnsldd lhkky;fvnsldd lhkkyi;vnsldd lhkkyif;nsldd lhkkyifd;sldd lhkkyifd
y;lddlhkkyifdyl;ddlhkkyifdyln;dlhkkyifdylnt;lhkkyifdylntn;hkkyifdylntne;kkyifdylntned;
kyifdylntnedf;yifdylntnedfv;ifdylntnedfvv;fdylntnedfvvw;dylntnedfvvwd;ylntnedfvvwdm
;lntnedfvvwdmi;ntnedfvvwdmir;tnedfvvwdmirs;nedfvvwdmirsa;edfvvwdmirsam;dfvvwd
mirsams;fvvwdmirsamss;vvwdmirsamssv;vwdmirsamssvs;wdmirsamssvsd;dmirsamssvs
ds;mirsamssvsdsv;irsamssvsdsvi;rsamssvsdsvii;samssvsdsviip;amssvsdsviipm;mssvsdsvii
pmq;ssvsdsviipmqd;svsdsviipmqdy;vsdsviipmqdyi;sdsviipmqdyin;dsviipmqdyinl;sviipm
qdyinlg;viipmqdyinlgn;iipmqdyinlgne;ipmqdyinlgnef;pmqdyinlgnefr;mqdyinlgnefra;qdyi
nlgnefran;dyinlgnefrani;yinlgnefranip;inlgnefranipk;nlgnefranipkn;lgnefranipknt;gnefrani
pkntl;nefranipkntln;efranipkntlnn;franipkntlnnw;ranipkntlnnwi;anipkntlnnwif;nipkntlnnw
ifr;ipkntlnnwifrl;pkntlnnwifrll;kntlnnwifrlle;ntlnnwifrlles;tlnnwifrllesd;lnnwifrllesdl;nnwi
frllesdld;nwifrllesdlda;wifrllesdldat;ifrllesdldatl;frllesdldatls;rllesdldatlsk;llesdldatlskn;les
dldatlskni;esdldatlsknis;sdldatlsknisf;dldatlsknisfi;ldatlsknisfit;datlsknisfitr;atlsknisfitrl;tl
sknisfitrly;lsknisfitrlyg;sknisfitrlygr;knisfitrlygrt;

14 mers:
mkykkirinlnlkr;kykkirinlnlkrk;ykkirinlnlkrks;kkirinlnlkrksg;kirinlnlkrksgi;irinlnlkrksgil;r
inlnlkrksgill;inlnlkrksgilln;nlnlkrksgillni;lnlkrksgillnis;nlkrksgillniss;lkrksgillnissl;krksgil
lnisslp;rksgillnisslps;ksgillnisslpsk;sgillnisslpsky;gillnisslpskyg;illnisslpskygi;llnisslpsky
gig;lnisslpskygigd;nisslpskygigdl;isslpskygigdlg;sslpskygigdlgk;slpskygigdlgkg;lpskygig
dlgkga;pskygigdlgkgay;skygigdlgkgayk;kygigdlgkgaykf;ygigdlgkgaykfi;gigdlgkgaykfid;i
gdlgkgaykfidf;gdlgkgaykfidfl;dlgkgaykfidflf;lgkgaykfidflfa;gkgaykfidflfas;kgaykfidflfas
s;gaykfidflfassq;aykfidflfassqs;ykfidflfassqsy;kfidflfassqsyw;fidflfassqsywq;idflfassqsyw
qm;dflfassqsywqmf;flfassqsywqmfa;lfassqsywqmfay;fassqsywqmfays;assqsywqmfaysp;s
sqsywqmfayspi;sqsywqmfayspid;qsywqmfayspidf;sywqmfayspidft;ywqmfayspidftr;wqm
fayspidftrs;qmfayspidftrsp;mfayspidftrspp;fayspidftrsppy;ayspidftrsppys;yspidftrsppysi;s
pidftrsppysif;pidftrsppysifs;idftrsppysifsa;dftrsppysifsaf;ftrsppysifsafa;trsppysifsafag;rspp
ysifsafagn;sppysifsafagnv;ppysifsafagnvy;pysifsafagnvyy;ysifsafagnvyyi;sifsafagnvyyid;
ifsafagnvyyidl;fsafagnvyyidle;safagnvyyidlea;afagnvyyidleal;fagnvyyidleald;agnvyyidlea
ldk;gnvyyidlealdkf;nvyyidlealdkfi;vyyidlealdkfid;yyidlealdkfids;yidlealdkfidsd;idlealdkfi
dsdl;dlealdkfidsdln;lealdkfidsdlnl;ealdkfidsdlnll;aldkfidsdlnllk;ldkfidsdlnllke;dkfidsdlnllk
en;kfidsdlnllkene;fidsdlnllkenet;idsdlnllkenetr;dsdlnllkenetry;sdlnllkenetrys;dlnllkenetrys
d;lnllkenetrysdl;nllkenetrysdlk;llkenetrysdlkk;lkenetrysdlkkl;kenetrysdlkkls;enetrysdlkkls
f;netrysdlkklsfk;etrysdlkklsfkd;trysdlkklsfkdk;rysdlkklsfkdkf;ysdlkklsfkdkfl;sdlkklsfkdkf
lk;dlkklsfkdkflke;lkklsfkdkflkea;kklsfkdkflkeaa;klsfkdkflkeaal;lsfkdkflkeaaln;sfkdkflkea
alnf;fkdkflkeaalnfi;kdkflkeaalnfin;dkflkeaalnfinr;kflkeaalnfinra;flkeaalnfinras;lkeaalnfinr

asv;keaalnfinrasvd;eaalnfinrasvde;aalnfinrasvdev;alnfinrasvdevr;lnfinrasvdevrs;nfinrasvd
evrsf;finrasvdevrsfe;inrasvdevrsfek;nrasvdevrsfekf;rasvdevrsfekfk;asvdevrsfekfkk;svdevr
sfekfkkk;vdevrsfekfkkks;devrsfekfkkkss;evrsfekfkkkssy;vrsfekfkkkssyw;rsfekfkkkssywl;
sfekfkkkssywll;fekfkkkssywlld;ekfkkkssywlldf;kfkkkssywlldfa;fkkkssywlldfas;kkkssywl
ldfasf;kkssywlldfasfv;kssywlldfasfva;ssywlldfasfvaf;sywlldfasfvafk;ywlldfasfvafke;wlldf
asfvafkey;lldfasfvafkeyf;ldfasfvafkeyfl;dfasfvafkeyflk;fasfvafkeyflkd;asfvafkeyflkds;sfva
fkeyflkdsr;fvafkeyflkdsrd;vafkeyflkdsrda;afkeyflkdsrdaf;fkeyflkdsrdafn;keyflkdsrdafnv;e
yflkdsrdafnvl;yflkdsrdafnvlf;flkdsrdafnvlfd;lkdsrdafnvlfdr;kdsrdafnvlfdrg;dsrdafnvlfdrgi;
srdafnvlfdrgil;rdafnvlfdrgili;dafnvlfdrgilir;afnvlfdrgilirn;fnvlfdrgilirne;nvlfdrgilirnek;vlfd
rgilirnekd;lfdrgilirnekdl;fdrgilirnekdlf;drgilirnekdlfk;rgilirnekdlfkl;gilirnekdlfklr;ilirnekdl
fklrn;lirnekdlfklrni;irnekdlfklrnil;rnekdlfklrnils;nekdlfklrnilsk;ekdlfklrnilske;kdlfklrnilske
i;dlfklrnilskeik;lfklrnilskeikv;fklrnilskeikvq;klrnilskeikvqe;lrnilskeikvqev;rnilskeikvqevl;
nilskeikvqevlq;ilskeikvqevlqy;lskeikvqevlqyf;skeikvqevlqyff;keikvqevlqyfff;eikvqevlqyf
ffs;ikvqevlqyfffsq;kvqevlqyfffsqf;vqevlqyfffsqfq;qevlqyfffsqfqa;evlqyfffsqfqal;vlqyfffsq
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yandk;sqfqalkryandkg;qfqalkryandkgi;fqalkryandkgie;qalkryandkgiel;alkryandkgielv;lkr
yandkgielvm;kryandkgielvmn;ryandkgielvmnl;yandkgielvmnlp;andkgielvmnlpl;ndkgielv
mnlplf;dkgielvmnlplfi;kgielvmnlplfia;gielvmnlplfiay;ielvmnlplfiayd;elvmnlplfiayds;lvmn
lplfiaydsa;vmnlplfiaydsad;mnlplfiaydsadv;nlplfiaydsadvw;lplfiaydsadvwa;plfiaydsadvwa
h;lfiaydsadvwahq;fiaydsadvwahqk;iaydsadvwahqky;aydsadvwahqkyf;ydsadvwahqkyfk;d
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fklrfdaskdkvag;klrfdaskdkvagi;lrfdaskdkvagis;rfdaskdkvagisp;fdaskdkvagispd;daskdkvag
ispdy;askdkvagispdyf;skdkvagispdyfl;kdkvagispdyfle;dkvagispdyfleq;kvagispdyfleqe;va
gispdyfleqeq;agispdyfleqeqa;gispdyfleqeqaw;ispdyfleqeqawd;spdyfleqeqawds;pdyfleqeq
awdsp;dyfleqeqawdspa;yfleqeqawdspay;fleqeqawdspays;leqeqawdspaysw;eqeqawdspays
wn;qeqawdspayswnv;eqawdspayswnvl;qawdspayswnvlk;awdspayswnvlkn;wdspayswnvl
knv;dspayswnvlknvk;spayswnvlknvky;payswnvlknvkye;ayswnvlknvkyew;yswnvlknvkye
ww;swnvlknvkyewwa;wnvlknvkyewwak;nvlknvkyewwakr;vlknvkyewwakri;lknvkyeww
akrig;knvkyewwakrigi;nvkyewwakrigil;vkyewwakrigilr;kyewwakrigilrk;yewwakrigilrky;
ewwakrigilrkyi;wwakrigilrkyid;wakrigilrkyidv;akrigilrkyidvi;krigilrkyidvik;rigilrkyidviki
;igilrkyidvikid;gilrkyidvikidh;ilrkyidvikidhf;lrkyidvikidhfr;rkyidvikidhfrg;kyidvikidhfrgf;
yidvikidhfrgfv;idvikidhfrgfvs;dvikidhfrgfvst;vikidhfrgfvstw;ikidhfrgfvstwe;kidhfrgfvstw
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ayafngl;evgvgeayafnglw;vgvgeayafnglwv;gvgeayafnglwvk;vgeayafnglwvks;geayafnglw
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nglwvkspgrdffn;glwvkspgrdffnf;lwvkspgrdffnfi;wvkspgrdffnfil;vkspgrdffnfiln;kspgrdffnf
ilne;spgrdffnfilnei;pgrdffnfilneik;grdffnfilneikd;rdffnfilneikdl;dffnfilneikdlk;ffnfilneikdlk
i;fnfilneikdlkiw;nfilneikdlkiwv;filneikdlkiwve;ilneikdlkiwved;lneikdlkiwvedf;neikdlkiwv
edfe;eikdlkiwvedfen;ikdlkiwvedfend;kdlkiwvedfendl;dlkiwvedfendle;lkiwvedfendled;ki
wvedfendledv;iwvedfendledvs;wvedfendledvsr;vedfendledvsrl;edfendledvsrlr;dfendledvs
rlrd;fendledvsrlrdf;endledvsrlrdff;ndledvsrlrdffn;dledvsrlrdffnf;ledvsrlrdffnfp;edvsrlrdffn
fpg;dvsrlrdffnfpgm;vsrlrdffnfpgmr;srlrdffnfpgmri;rlrdffnfpgmrim;lrdffnfpgmrimk;rdffnfp
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15 mers:
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16 mers:
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hnyikncivy;nqnlphnyikncivyt;qnlphnyikncivytg;nlphnyikncivytgi;lphnyikncivytgig;phnyi
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efvns;tgigdnstirefvnsl;gigdnstirefvnsld;igdnstirefvnsldd;gdnstirefvnsldd;dnstirefvnsldlh
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wdmirsamssvsds;vwdmirsamssvsdsv;wdmirsamssvsdsvi;dmirsamssvsdsvii;mirsamssvsds
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ldatlsknis;llesdldatlsknisf;lesdldatlsknisfi;esdldatlsknisfit;sdldatlsknisfitr;dldatlsknisfitrl;l
datlsknisfitrly;datlsknisfitrlyg;atlsknisfitrlygr;tlsknisfitrlygrt;

<CAA59725 outer surface protein A;Protein;Borrelia afzelii>

8 mers:
mkkyllgi;kkyllgig;kyllgigl;yllgigli;llgiglil;lgiglila;giglilal;iglilali;glilalia;lilaliac;ilaliack;l
aliackq;aliackqn;liackqnv;iackqnvs;ackqnvss;ckqnvssl;kqnvssld;qnvsslde;nvssldek;vsslde
kn;ssldekns;sldeknsa;ldeknsas;deknsasv;eknsasvd;knsasvdl;nsasvdlp;sasvdlpg;asvdlpge;s
vdlpgem;vdlpgemk;dlpgemkv;lpgemkvl;pgemkvlv;gemkvlvs;emkvlvsk;mkvlvske;kvlvsk
ek;vlvskekd;lvskekdk;vskekdkd;skekdkdg;kekdkdgk;ekdkdgky;kdkdgkys;dkdgkysl;kdgk
yslk;dgkyslka;gkyslkat;kyslkatv;yslkatvd;slkatvdk;lkatvdki;katvdkie;atvdkiel;tvdkielk;vd
kielkg;dkielkgt;kielkgts;ielkgtsd;elkgtsdk;lkgtsdkd;kgtsdkdn;gtsdkdng;tsdkdngs;sdkdngs
g;dkdngsgv;kdngsgvl;dngsgvle;ngsgvleg;gsgvlegt;sgvlegtk;gvlegtkd;vlegtkdd;legtkddk;e
gtkddks;gtkddksk;tkddkska;kddkskak;ddkskakl;dkskaklt;kskaklti;skakltia;kakltiad;akltiad
d;kltiaddl;ltiaddls;tiaddlsk;iaddlskt;addlsktt;ddlskttf;dlskttfe;lskttfel;skttfelf;kttfelfk;ttfelf

ke;tfelfked;felfkedg;elfkedgk;lfkedgkt;fkedgktl;kedgktlv;edgktlvs;dgktlvsr;gktlvsrk;ktlvs
rkv;tlvsrkvs;lvsrkvss;vsrkvssk;srkvsskd;rkvsskdk;kvsskdkt;vsskdkts;sskdktst;skdktstd;kd
ktstde;dktstdem;ktstdemf;tstdemfn;stdemfne;tdemfnek;demfnekg;emfnekge;mfnekgel;fne
kgels;nekgelsa;ekgelsak;kgelsakt;gelsaktm;elsaktmt;lsaktmtr;saktmtre;aktmtren;ktmtreng
;tmtrengt;mtrengtk;trengtkl;rengtkle;engtkley;ngtkleyt;gtkleyte;tkleytem;kleytemk;leyte
mks;eytemksd;ytemksdg;temksdgt;emksdgtg;mksdgtgk;ksdgtgka;sdgtgkak;dgtgkake;gtg
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vtlev;dkvtlevk;kvtlevke;vtlevkeg;tlevkegt;levkegtv;evkegtvt;vkegtvtl;kegtvtls;egtvtlsk;gt
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gevtva;sgevtval;gevtvaln;evtvalnd;vtvalndt;tvalndtn;valndtnt;alndtntt;lndtnttq;ndtnttqa;dt
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;tgawdskt;gawdskts;awdsktst;wdsktstl;dsktstlt;sktstlti;ktstltis;tstltisv;stltisvn;tltisvns;ltisv
nsk;tisvnskk;isvnskkt;svnskktt;vnskkttq;nskkttql;skkttqlv;kkttqlvf;kttqlvft;ttqlvftk;tqlvftk
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;tvqkydsa;vqkydsag;qkydsagt;kydsagtn;ydsagtnl;dsagtnle;sagtnleg;agtnlegt;gtnlegta;tnleg
tav;nlegtave;legtavei;egtaveik;gtaveikt;taveiktl;aveiktld;veiktlde;eiktldel;iktldelk;ktldelkn
;tldelkna;ldelknal;delknalk;

9 mers:
mkkyllgig;kkyllgigl;kyllgigli;yllgiglil;llgiglila;lgiglilal;giglilali;iglilalia;glilaliac;lilaliack;
ilaliackq;laliackqn;aliackqnv;liackqnvs;iackqnvss;ackqnvssl;ckqnvssld;kqnvsslde;qnvssld
ek;nvssldekn;vssldekns;ssldeknsa;sldeknsas;ldeknsasv;deknsasvd;eknsasvdl;knsasvdlp;ns
asvdlpg;sasvdlpge;asvdlpgem;svdlpgemk;vdlpgemkv;dlpgemkvl;lpgemkvlv;pgemkvlvs;g
emkvlvsk;emkvlvske;mkvlvskek;kvlvskekd;vlvskekdk;lvskekdkd;vskekdkdg;skekdkdgk;
kekdkdgky;ekdkdgkys;kdkdgkysl;dkdgkyslk;kdgkyslka;dgkyslkat;gkyslkatv;kyslkatvd;ys
lkatvdk;slkatvdki;lkatvdkie;katvdkiel;atvdkielk;tvdkielkg;vdkielkgt;dkielkgts;kielkgtsd;ie
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sgvle;dngsgvleg;ngsgvlegt;gsgvlegtk;sgvlegtkd;gvlegtkdd;vlegtkddk;legtkddks;egtkddks
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addl;kltiaddls;ltiaddlsk;tiaddlskt;iaddlsktt;addlskttf;ddlskttfe;dlskttfel;lskttfelf;skttfelfk;kt
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vsskdktst;sskdktstd;skdktstde;kdktstdem;dktstdemf;ktstdemfn;tstdemfne;stdemfnek;tdem
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mt;elsaktmtr;lsaktmtre;saktmtren;aktmtreng;ktmtrengt;tmtrengtk;mtrengtkl;trengtkle;reng
tkley;engtkleyt;ngtkleyte;gtkleytem;tkleytemk;kleytemks;leytemksd;eytemksdg;ytemksd
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10 mers:
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11 mers:
mkkyllgigli;kkyllgiglil;kyllgiglila;yllgiglilal;llgiglilali;lgiglilalia;giglilaliac;iglilaliack;glilaliackq;lilaliackqn;ilaliackqnv;laliackqnvs;aliackqnvss;liackqnvssl;iackqnvssld;ackqnvsslde;ckqnvssldek;kqnvssldekn;qnvssldekns;nvssldeknsa;vssldeknsas;ssldeknsasv;sldeknsas

vd;ldeknsasvdl;deknsasvdlp;eknsasvdlpg;knsasvdlpge;nsasvdlpgem;sasvdlpgemk;asvdlp
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;emkvlvskekd;mkvlvskekdk;kvlvskekdkd;vlvskekdkdg;lvskekdkdgk;vskekdkdgky;skekd
kdgkys;kekdkdgkysl;ekdkdgkyslk;kdkdgkyslka;dkdgkyslkat;kdgkyslkatv;dgkyslkatvd;gk
yslkatvdk;kyslkatvdki;yslkatvdkie;slkatvdkiel;lkatvdkielk;katvdkielkg;atvdkielkgt;tvdkiel
kgts;vdkielkgtsd;dkielkgtsdk;kielkgtsdkd;ielkgtsdkdn;elkgtsdkdng;lkgtsdkdngs;kgtsdkdn
gsg;gtsdkdngsgv;tsdkdngsgvl;sdkdngsgvle;dkdngsgvleg;kdngsgvlegt;dngsgvlegtk;ngsgvl
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d;lvsrkvsskdk;vsrkvsskdkt;srkvsskdkts;rkvsskdktst;kvsskdktstd;vsskdktstde;sskdktstdem;
skdktstdemf;kdktstdemfn;dktstdemfne;ktstdemfnek;tstdemfnekg;stdemfnekge;tdemfnekg
el;demfnekgels;emfnekgelsa;mfnekgelsak;fnekgelsakt;nekgelsaktm;ekgelsaktmt;kgelsakt
mtr;gelsaktmtre;elsaktmtren;lsaktmtreng;saktmtrengt;aktmtrengtk;ktmtrengtkl;tmtrengtkl
e;mtrengtkley;trengtkleyt;rengtkleyte;engtkleytem;ngtkleytemk;gtkleytemks;tkleytemksd
;kleytemksdg;leytemksdgt;eytemksdgtg;ytemksdgtgk;temksdgtgka;emksdgtgkak;mksdgt
gkake;ksdgtgkakev;sdgtgkakevl;dgtgkakevlk;gtgkakevlkn;tgkakevlknf;gkakevlknft;kake
vlknftl;akevlknftle;kevlknftleg;evlknftlegk;vlknftlegkv;lknftlegkva;knftlegkvan;nftlegkva
nd;ftlegkvandk;tlegkvandkv;legkvandkvt;egkvandkvtl;gkvandkvtle;kvandkvtlev;vandkvtl
evk;andkvtlevke;ndkvtlevkeg;dkvtlevkegt;kvtlevkegtv;vtlevkegtvt;tlevkegtvtl;levkegtvtls
;evkegtvtlsk;vkegtvtlske;kegtvtlskei;egtvtlskeia;gtvtlskeiak;tvtlskeiaks;vtlskeiaksg;tlskeia
ksge;lskeiaksgev;skeiaksgevt;keiaksgevtv;eiaksgevtva;iaksgevtval;aksgevtvaln;ksgevtval
nd;sgevtvalndt;gevtvalndtn;evtvalndtnt;vtvalndtntt;tvalndtnttq;valndtnttqa;alndtnttqat;lnd
tnttqatk;ndtnttqatkk;dtnttqatkkt;tnttqatkktg;nttqatkktga;ttqatkktgaw;tqatkktgawd;qatkktga
wds;atkktgawdsk;tkktgawdskt;kktgawdskts;ktgawdsktst;tgawdsktstl;gawdsktstlt;awdsktst
lti;wdsktstltis;dsktstltisv;sktstltisvn;ktstltisvns;tstltisvnsk;stltisvnskk;tltisvnskkt;ltisvnskkt
t;tisvnskkttq;isvnskkttql;svnskkttqlv;vnskkttqlvf;nskkttqlvft;skkttqlvftk;kkttqlvftkq;kttqlv
ftkqd;ttqlvftkqdt;tqlvftkqdti;qlvftkqdtit;lvftkqdtitv;vftkqdtitvq;ftkqdtitvqk;tkqdtitvqky;kq
dtitvqkyd;qdtitvqkyds;dtitvqkydsa;titvqkydsag;itvqkydsagt;tvqkydsagtn;vqkydsagtnl;qky
dsagtnle;kydsagtnleg;ydsagtnlegt;dsagtnlegta;sagtnlegtav;agtnlegtave;gtnlegtavei;tnlegta
veik;nlegtaveikt;legtaveiktl;egtaveiktld;gtaveiktlde;taveiktldel;aveiktldelk;veiktldelkn;eik
tldelkna;iktldelknal;ktldelknalk;

13 mers:
mkkyllgiglila;kkyllgiglilal;kyllgiglilali;yllgiglilalia;llgiglilaliac;lgiglilaliack;giglilaliackq;
iglilaliackqn;glilaliackqnv;lilaliackqnvs;ilaliackqnvss;laliackqnvssl;aliackqnvssld;liackqn
vsslde;iackqnvssldek;ackqnvssldekn;ckqnvssldekns;kqnvssldeknsa;qnvssldeknsas;nvssld
eknsasv;vssldeknsasvd;ssldeknsasvdl;sldeknsasvdlp;ldeknsasvdlpg;deknsasvdlpge;eknsas
vdlpgem;knsasvdlpgemk;nsasvdlpgemkv;sasvdlpgemkvl;asvdlpgemkvlv;svdlpgemkvlvs;
vdlpgemkvlvsk;dlpgemkvlvske;lpgemkvlvskek;pgemkvlvskekd;gemkvlvskekdk;emkvlvs
kekdkd;mkvlvskekdkdg;kvlvskekdkdgk;vlvskekdkdgky;lvskekdkdgkys;vskekdkdgkysl;s
kekdkdgkyslk;kekdkdgkyslka;ekdkdgkyslkat;kdkdgkyslkatv;dkdgkyslkatvd;kdgkyslkatv
dk;dgkyslkatvdki;gkyslkatvdkie;kyslkatvdkiel;yslkatvdkielk;slkatvdkielkg;lkatvdkielkgt;
katvdkielkgts;atvdkielkgtsd;tvdkielkgtsdk;vdkielkgtsdkd;dkielkgtsdkdn;kielkgtsdkdng;iel

kgtsdkdngs;elkgtsdkdngsg;lkgtsdkdngsgv;kgtsdkdngsgvl;gtsdkdngsgvle;tsdkdngsgvleg;sdkdngsgvlegt;dkdngsgvlegtk;kdngsgvlegtkd;dngsgvlegtkdd;ngsgvlegtkddk;gsgvlegtkddks;sgvlegtkddksk;gvlegtkddkska;vlegtkddkskak;legtkddkskakl;egtkddkskaklt;gtkddkskakltt;tkddkskakltia;kddkskakltiad;ddkskakltiadd;dkskakltiaddl;kskakltiaddls;skakltiaddlsk;kakltiaddlskt;akltiaddlsktt;kltiaddlskttf;ltiaddlskttfe;tiaddlskttfel;iaddlskttfelf;addlskttfelfk;dlskttfelfke;dlskttfelfked;lskttfelfkedg;skttfelfkedgk;kttfelfkedgkt;ttfelfkedgktl;tfelfkedgktlv;felfkedgktlvs;elfkedgktlvsr;lfkedgktlvsrk;fkedgktlvsrkv;kedgktlvsrkvs;edgktlvsrkvss;dgktlvsrkvssk;gktlvsrkvsskd;ktlvsrkvsskdk;tlvsrkvsskdkt;lvsrkvsskdkts;vsrkvsskdktst;srkvsskdktstd;rkvsskdktstde;kvsskdktstdem;vsskdktstdemf;sskdktstdemfn;skdktstdemfne;kdktstdemfnek;dktstdemfnekg;ktstdemfnekge;tstdemfnekgel;stdemfnekgels;tdemfnekgelsa;demfnekgelsak;emfnekgelsakt;mfnekgelsaktm;fnekgelsaktmt;nekgelsaktmtr;ekgelsaktmtre;kgelsaktmtren;gelsaktmtreng;elsaktmtrengt;lsaktmtrengtk;saktmtrengtkl;aktmtrengtkle;ktmtrengtkley;tmtrengtkleyt;mtrengtkleyte;trengtkleytem;rengtkleytemk;engtkleytemks;ngtkleytemksd;gtkleytemksdg;tkleytemksdgt;kleytemksdgtg;leytemksdgtgk;eytemksdgtgka;ytemksdgtgkak;temksdgtgkake;emksdgtgkakev;mksdgtgkakevl;ksdgtgkakevlk;sdgtgkakevlkn;dgtgkakevlknf;gtgkakevlknft;tgkakevlknftl;gkakevlknftle;kakevlknftleg;akevlknftlegk;kevlknftlegkv;evlknftlegkva;vlknftlegkvan;lknftlegkvand;knftlegkvandk;nftlegkvandkv;ftlegkvandkvt;tlegkvandkvtl;legkvandkvtle;egkvandkvtlev;gkvandkvtlevk;kvandkvtlevke;vandkvtlevkeg;andkvtlevkegt;ndkvtlevkegtv;dkvtlevkegtvt;kvtlevkegtvtl;vtlevkegtvtls;tlevkegtvtlsk;levkegtvtlske;evkegtvtlskei;vkegtvtlskeia;kegtvtlskeiak;egtvtlskeiaks;gtvtlskeiaksg;tvtlskeiaksge;vtlskeiaksgev;tlskeiaksgevt;lskeiaksgevtv;skeiaksgevtva;keiaksgevtval;eiaksgevtvaln;iaksgevtvalnd;aksgevtvalndt;ksgevtvalndtn;sgevtvalndtnt;gevtvalndtntt;evtvalndtnttq;vtvalndtnttqa;tvalndtnttqat;valndtnttqatk;alndtnttqatkk;lndtnttqatkkt;ndtnttqatkktg;dtnttqatkktga;tnttqatkktgaw;nttqatkktgawd;ttqatkktgawds;tqatkktgawdsk;qatkktgawdskt;atkktgawdskts;tkktgawdsktst;kktgawdsktstl;ktgawdsktstlt;tgawdsktstlti;gawdsktstltis;awdsktstltisv;wdsktstltisvn;dsktstltisvns;sktstltisvnsk;ktstltisvnskk;tstltisvnskkt;stltisvnskktt;tltisvnskkttq;ltisvnskkttql;tisvnskkttqlv;isvnskkttqlvf;svnskkttqlvft;vnskkttqlvftk;nskkttqlvftkq;skkttqlvftkqd;kkttqlvftkqdt;kttqlvftkqdti;ttqlvftkqdtit;tqlvftkqdtitv;qlvftkqdtitvq;lvftkqdtitvqk;vftkqdtitvqky;ftkqdtitvqkyd;tkqdtitvqkyds;kqdtitvqkydsa;qdtitvqkydsag;dtitvqkydsagt;titvqkydsagtn;itvqkydsagtnl;tvqkydsagtnle;vqkydsagtnleg;qkydsagtnlegt;kydsagtnlegta;ydsagtnlegtav;dsagtnlegtave;sagtnlegtavei;agtnlegtaveik;gtnlegtaveikt;tnlegtaveiktl;nlegtaveiktld;legtaveiktlde;egtaveiktldel;gtaveiktldelk;taveiktldelkn;aveiktldelkna;veiktldelknal;eiktldelknalk;

14 mers:
mkkyllgiglilal;kkyllgiglilali;kyllgiglilalia;yllgiglilaliac;llgiglilaliack;lgiglilaliackq;giglilaliackqn;iglilaliackqnv;glilaliackqnvs;lilaliackqnvss;ilaliackqnvssl;laliackqnvssld;aliackqnvsslde;liackqnvssldek;iackqnvssldekn;ackqnvssldekns;ckqnvssldeknsa;kqnvssldeknsas;qnvssldeknsasv;nvssldeknsasvd;vssldeknsasvdl;ssldeknsasvdlp;sldeknsasvdlpg;ldeknsasvdlpge;deknsasvdlpgem;eknsasvdlpgemk;knsasvdlpgemkv;nsasvdlpgemkvl;sasvdlpgemkvlv;asvdlpgemkvlvs;svdlpgemkvlvsk;vdlpgemkvlvske;dlpgemkvlvskek;lpgemkvlvskekd;pgemkvlvskekdk;gemkvlvskekdkd;emkvlvskekdkdg;mkvlvskekdkdgk;kvlvskekdkdgky;vlvskekdkdgkys;lvskekdkdgkysl;vskekdkdgkyslk;skekdkdgkyslka;kekdkdgkyslkat;ekdkdgkyslkatv;kdkdgkyslkatvd;dkdgkyslkatvdk;kdgkyslkatvdki;dgkyslkatvdkie;gkyslkatvdkiel;kyslkatvdkielk;yslkatvdkielkg;slkatvdkielkgt;lkatvdkielkgts;katvdkielkgtsd;atvdkielkgtsdk;tvdkielkgtsdkd;vdkielkgtsdkdn;dkielkgtsdkdng;kielkgtsdkdngs;ielkgtsdkdngsg;elkgtsdk

dngsgv;lkgtsdkdngsgvl;kgtsdkdngsgvle;gtsdkdngsgvleg;tsdkdngsgvlegt;sdkdngsgvlegtk;dkdngsgvlegtkd;kdngsgvlegtkdd;dngsgvlegtkddk;ngsgvlegtkddks;gsgvlegtkddksk;sgvlegtkddkska;gvlegtkddkskak;vlegtkddkskakl;legtkddkskaklt;egtkddkskaklti;gtkddkskakltia;tkddkskakltiad;kddkskakltiadd;ddkskakltiaddl;dkskakltiaddls;kskakltiaddlsk;skakltiaddlskt;kakltiaddlsktt;akltiaddlskttf;kltiaddlskttfe;ltiaddlskttfel;tiaddlskttfelf;iaddlskttfelfk;addlskttfelfke;ddlskttfelfked;dlskttfelfkedg;lskttfelfkedgk;skttfelfkedgkt;kttfelfkedgktl;ttfelfkedgktlv;tfelfkedgktlvs;felfkedgktlvsr;elfkedgktlvsrk;lfkedgktlvsrkv;fkedgktlvsrkvs;kedgktlvsrkvss;edgktlvsrkvssk;dgktlvsrkvsskd;gktlvsrkvsskdk;ktlvsrkvsskdkt;tlvsrkvsskdkts;lvsrkvsskdktst;vsrkvsskdktstd;srkvsskdktstde;rkvsskdktstdem;kvsskdktstdemf;vsskdktstdemfn;sskdktstdemfne;skdktstdemfnek;kdktstdemfnekg;dktstdemfnekge;ktstdemfnekgel;tstdemfnekgels;stdemfnekgelsa;tdemfnekgelsak;demfnekgelsakt;emfnekgelsaktm;mfnekgelsaktmt;fnekgelsaktmtr;nekgelsaktmtre;ekgelsaktmtren;kgelsaktmtreng;gelsaktmtrengt;elsaktmtrengtk;lsaktmtrengtkl;saktmtrengtkle;aktmtrengtkley;ktmtrengtkleyt;tmtrengtkleyte;mtrengtkleytem;trengtkleytemk;rengtkleytemks;engtkleytemksd;ngtkleytemksdg;gtkleytemksdgt;tkleytemksdgtg;kleytemksdgtgk;leytemksdgtgka;eytemksdgtgkak;ytemksdgtgkake;temksdgtgkakev;emksdgtgkakevl;mksdgtgkakevlk;ksdgtgkakevlkn;sdgtgkakevlknf;dgtgkakevlknft;gtgkakevlknftl;tgkakevlknftle;gkakevlknftleg;kakevlknftlegk;akevlknftlegkv;kevlknftlegkva;evlknftlegkvan;vlknftlegkvand;lknftlegkvandk;knftlegkvandkv;nftlegkvandkvt;ftlegkvandkvtl;tlegkvandkvtle;legkvandkvtlev;egkvandkvtlevk;gkvandkvtlevke;kvandkvtlevkeg;vandkvtlevkegt;andkvtlevkegtv;ndkvtlevkegtvt;dkvtlevkegtvtl;kvtlevkegtvtls;vtlevkegtvtlsk;tlevkegtvtlske;levkegtvtlskei;evkegtvtlskeia;vkegtvtlskeiak;kegtvtlskeiaks;egtvtlskeiaksg;gtvtlskeiaksge;tvtlskeiaksgev;vtlskeiaksgevt;tlskeiaksgevtv;lskeiaksgevtva;skeiaksgevtval;keiaksgevtvaln;eiaksgevtvalnd;iaksgevtvalndt;aksgevtvalndtn;ksgevtvalndtnt;sgevtvalndtntt;gevtvalndtnttq;evtvalndtnttqa;vtvalndtnttqat;tvalndtnttqatk;valndtnttqatkk;alndtnttqatkkt;lndtnttqatkktg;ndtnttqatkktga;dtnttqatkktgaw;tnttqatkktgawd;nttqatkktgawds;ttqatkktgawdsk;tqatkktgawdskt;qatkktgawdskts;atkktgawdsktst;tkktgawdsktstl;kktgawdsktstlt;ktgawdsktstlti;tgawdsktstltis;gawdsktstltisv;awdsktstltisvn;wdsktstltisvns;dsktstltisvnsk;sktstltisvnskk;ktstltisvnskkt;tstltisvnskktt;stltisvnskkttq;tltisvnskkttql;ltisvnskkttqlv;tisvnskkttqlvf;isvnskkttqlvft;svnskkttqlvftk;vnskkttqlvftkq;nskkttqlvftkqd;skkttqlvftkqdt;kkttqlvftkqdti;kttqlvftkqdtit;ttqlvftkqdtitv;tqlvftkqdtitvq;qlvftkqdtitvqk;lvftkqdtitvqky;vftkqdtitvqkyd;ftkqdtitvqkyds;tkqdtitvqkydsa;kqdtitvqkydsag;qdtitvqkydsagt;dtitvqkydsagtn;titvqkydsagtnl;itvqkydsagtnle;tvqkydsagtnleg;vqkydsagtnlegt;qkydsagtnlegta;kydsagtnlegtav;ydsagtnlegtave;dsagtnlegtavei;sagtnlegtaveik;agtnlegtaveikt;gtnlegtaveiktl;tnlegtaveiktld;nlegtaveiktlde;legtaveiktldel;egtaveiktldelk;gtaveiktldelkn;taveiktldelkna;aveiktldelknal;veiktldelknalk;

15 mers:
mkkyllgiglilali;kkyllgiglilalia;kyllgiglilaliac;yllgiglilaliack;llgiglilaliackq;lgiglilaliackqn;giglilaliackqnv;iglilaliackqnvs;glilaliackqnvss;lilaliackqnvssl;ilaliackqnvssld;laliackqnvsslde;aliackqnvssldek;liackqnvssldekn;iackqnvssldekns;ackqnvssldeknsa;ckqnvssldeknsas;kqnvssldeknsasv;qnvssldeknsasvd;nvssldeknsasvdl;vssldeknsasvdlp;ssldeknsasvdlpg;sldeknsasvdlpge;ldeknsasvdlpgem;deknsasvdlpgemk;eknsasvdlpgemkv;knsasvdlpgemkvl;nsasvdlpgemkvlv;sasvdlpgemkvlvs;asvdlpgemkvlvsk;svdlpgemkvlvske;vdlpgemkvlvskek;dlpgemkvlvskekd;lpgemkvlvskekdk;pgemkvlvskekdkd;gemkvlvskekdkdg;emkvlvskekdkdgk;mkvlvskekdkdgky;kvlvskekdkdgkys;vlvskekdkdgkysl;lvskekdkdgkyslk;vskekdkdgkyslka;skekdkdgkyslkat;kekdkdgkyslkatv;ekdkdgkyslkatvd;kdkdgkyslkatvdk;dkdgkyslkatv

dki;kdgkyslkatvdkie;dgkyslkatvdkiel;gkyslkatvdkielk;kyslkatvdkielkg;yslkatvdkielkgt;sl
katvdkielkgts;lkatvdkielkgtsd;katvdkielkgtsdk;atvdkielkgtsdkd;tvdkielkgtsdkdn;vdkielkgt
sdkdng;dkielkgtsdkdngs;kielkgtsdkdngsg;ielkgtsdkdngsgv;elkgtsdkdngsgvl;lkgtsdkdngsg
vle;kgtsdkdngsgvleg;gtsdkdngsgvlegt;tsdkdngsgvlegtk;sdkdngsgvlegtkd;dkdngsgvlegtkd
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skakltiadd;kddkskakltiaddl;ddkskakltiaddls;dkskakltiaddlsk;kskakltiaddlskt;skakltiaddlsk
tt;kakltiaddlskttf;akltiaddlskttfe;kltiaddlskttfel;ltiaddlskttfelf;tiaddlskttfelfk;iaddlskttfelfk
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gktlv;ttfelfkedgktlvs;tfelfkedgktlvsr;felfkedgktlvsrk;elfkedgktlvsrkv;lfkedgktlvsrkvs;fked
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kdkts;tlvsrkvsskdktst;lvsrkvsskdktstd;vsrkvsskdktstde;srkvsskdktstdem;rkvsskdktstdemf;
kvsskdktstdemfn;vsskdktstdemfne;sskdktstdemfnek;skdktstdemfnekg;kdktstdemfnekge;d
ktstdemfnekgel;ktstdemfnekgels;tstdemfnekgelsa;stdemfnekgelsak;tdemfnekgelsakt;demf
nekgelsaktm;emfnekgelsaktmt;mfnekgelsaktmtr;fnekgelsaktmtre;nekgelsaktmtren;ekgels
aktmtreng;kgelsaktmtrengt;gelsaktmtrengtk;elsaktmtrengtkl;lsaktmtrengtkle;saktmtrengtk
ley;aktmtrengtkleyt;ktmtrengtkleyte;tmtrengtkleytem;mtrengtkleytemk;trengtkleytemks;r
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kevlknftle;tgkakevlknftleg;gkakevlknftlegk;kakevlknftlegkv;akevlknftlegkva;kevlknftleg
kvan;evlknftlegkvand;vlknftlegkvandk;lknftlegkvandkv;knftlegkvandkvt;nftlegkvandkvtl
;ftlegkvandkvtle;tlegkvandkvtlev;legkvandkvtlevk;egkvandkvtlevke;gkvandkvtlevkeg;kv
andkvtlevkegt;vandkvtlevkegtv;andkvtlevkegtvt;ndkvtlevkegtvtl;dkvtlevkegtvtls;kvtlevk
egtvtlsk;vtlevkegtvtlske;tlevkegtvtlskei;levkegtvtlskeia;evkegtvtlskeiak;vkegtvtlskeiaks;k
egtvtlskeiaksg;egtvtlskeiaksge;gtvtlskeiaksgev;tvtlskeiaksgevt;vtlskeiaksgevtv;tlskeiaksg
evtva;lskeiaksgevtval;skeiaksgevtvaln;keiaksgevtvalnd;eiaksgevtvalndt;iaksgevtvalndtn;a
ksgevtvalndtnt;ksgevtvalndtntt;sgevtvalndtnttq;gevtvalndtnttqa;evtvalndtnttqat;vtvalndtnt
tqatk;tvalndtnttqatkk;valndtnttqatkkt;alndtnttqatkktg;lndtnttqatkktga;ndtnttqatkktgaw;dtnt
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wdsktst;atkktgawdsktstl;tkktgawdsktstlt;kktgawdsktstlti;ktgawdsktstltis;tgawdsktstltisv;g
awdsktstltisvn;awdsktstltisvns;wdsktstltisvnsk;dsktstltisvnskk;sktstltisvnskkt;ktstltisvnsk
ktt;tstltisvnskkttq;stltisvnskkttql;tltisvnskkttqlv;ltisvnskkttqlvf;tisvnskkttqlvft;isvnskkttql
vftk;svnskkttqlvftkq;vnskkttqlvftkqd;nskkttqlvftkqdt;skkttqlvftkqdti;kkttqlvftkqdtit;kttqlv
ftkqdtitv;ttqlvftkqdtitvq;tqlvftkqdtitvqk;qlvftkqdtitvqky;lvftkqdtitvqkyd;vftkqdtitvqkyds;f
tkqdtitvqkydsa;tkqdtitvqkydsag;kqdtitvqkydsagt;qdtitvqkydsagtn;dtitvqkydsagtnl;titvqky
dsagtnle;itvqkydsagtnleg;tvqkydsagtnlegt;vqkydsagtnlegta;qkydsagtnlegtav;kydsagtnlegt
ave;ydsagtnlegtavei;dsagtnlegtaveik;sagtnlegtaveikt;agtnlegtaveiktl;gtnlegtaveiktld;tnlegt
aveiktlde;nlegtaveiktldel;legtaveiktldelk;egtaveiktldelkn;gtaveiktldelkna;taveiktldelknal;a
veiktldelknalk;

16 mers:
mkkyllgiglilalia;kkyllgiglilalaiac;kyllgiglilalaiack;yllgiglilalaiackq;llgiglilalaiackqn;lgiglilalia
ckqnv;giglilalaiackqnvs;iglilalaiackqnvss;glilalaiackqnvssl;lilalaiackqnvssld;ilalaiackqnvsslde;
laliackqnvssldek;aliackqnvssldekn;liackqnvssldekns;iackqnvssldeknsa;ackqnvssldeknsas;
ckqnvssldeknsasv;kqnvssldeknsasvd;qnvssldeknsasvdl;nvssldeknsasvdlp;vssldeknsasvdlp

g;ssldeknsasvdlpge;sldeknsasvdlpgem;ldeknsasvdlpgemk;deknsasvdlpgemkv;eknsasvdlp
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nalk;

<CAA59727 outer surface protein A;Protein;Borrelia garinii>

8 mers:
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ke;tfeifked;feifkedg;eifkedgk;ifkedgkt;fkedgktl;kedgktlv;edgktlvs;dgktlvsk;gktlvskk;ktlv
skkv;tlvskkvt;lvskkvtl;vskkvtlk;skkvtlkd;kkvtlkdk;kvtlkdks;vtlkdkss;tlkdksst;lkdksste;kd
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;nekgeise;ekgeisek;kgeisekt;geisekti;eisektiv;isektivr;sektivra;ektivran;ktivrang;tivrangt;i
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agt;kydsagtn;ydsagtnl;dsagtnle;sagtnleg;agtnlegk;gtnlegka;tnlegkav;nlegkave;legkavei;eg
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9 mers:
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ktivr;isektivra;sektivran;ektivrang;ktivrangt;tivrangtr;ivrangtrl;vrangtrle;rangtrley;angtrle
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10 mers:
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11 mers:
mkkyllgigli;kkyllgiglil;kyllgiglila;yllgiglilal;llgiglilali;lgiglilalia;giglilaliac;iglilaliack;glilaliackq;lilaliackqn;ilaliackqnv;laliackqnvs;aliackqnvss;liackqnvssl;iackqnvssld;ackqnvsslde;ckqnvssldek;kqnvssldekn;qnvssldekns;nvssldeknsv;vssldeknsvs;ssldeknsvsv;sldeknsvsvd;ldeknsvsvdl;deknsvsvdlp;eknsvsvdlpg;knsvsvdlpgg;nsvsvdlpggm;svsvdlpggmk;vsvdlpggmkv;svdlpggmkvl;vdlpggmkvlv;dlpggmkvlvs;lpggmkvlvsk;pggmkvlvske;ggmkvlvskek;gmkvlvskekd;mkvlvskekdk;kvlvskekdkd;vlvskekdkdg;lvskekdkdgk;vskekdkdgky;skekdkdgkys;kekdkdgkysl;ekdkdgkyslm;kdkdgkyslma;dkdgkyslmat;kdgkyslmatv;dgkyslmatve;gkyslmatvek;kyslmatvekl;yslmatvekle;slmatveklel;lmatveklelk;matveklelkg;atveklelkgt;tveklelkgts;veklelkgtsd;eklelkgtsdk;klelkgtsdkn;lelkgtsdknn;elkgtsdknng;lkgtsdknngs;kgtsdknngsg;gtsdknngsgt;tsdknngsgtl;sdknngsgtle;dknngsgtleg;knngsgtlege;nngsgtlegek;ngsgtlegekt;gsgtlegektd;sgtlegektdk;gtlegektdks;tlegektdksk;legektdkskv;egektdkskvk;gektdkskvkl;ektdkskvklt;ktdkskvklti;tdkskvkltia;dkskvkltiae;kskvkltiaed;skvkltiaedl;kvkltiaedls;vkltiaedlsk;kltiaedlskt;ltiaedlsktt;tiaedlskttf;iaedlskttfe;aedlskttfei;edlskttfeif;dlskttfeifk;lskttfeifke;skttfeifked;kttfeifkedg;ttfeifkedgk;tfeifkedgkt;feifkedgktl;eifkedgktlv;ifkedgktlvs;fkedgktlvsk;kedgktlvskk;edgktlvskkv;dgktlvskkvt;gktlvskkvtl;ktlvskkvtlk;tlvskkvtlkd;lvskkvtlkdk;vskkvtlkdks;skkvtlkdkss;kkvtlkdksst;kvtlkdksste;vtlkdksstee;tlkdksstеek;lkdkssteekf;kdkssteekfn;dkssteekfne;kssteekfnek;ssteekfnekg;steekfnekge;teekfnekgei;eekfnekgeis;ekfnekgeise;kfnekgeisek;fnekgeisekt;nekgeisekti;ekgeisektiv;kgeisektivr;geisektivra;eisektivran;isektivrang;sektivrangt;ektivrangtr;ktivrangtrl;tivrangtrle;ivrangtrley;vrangtrleyt;rangtrleytd;angtrleytdi;ngtrleytdik;gtrleytdiks;trleytdiksd;rleytdiksdg;leytdiksdgs;eytdiksdgsg;ytdiksdgsgk;tdiksdgsgka;diksdgsgkak;iksdgsgkake;ksdgsgkakev;sdgsgkakevl;dgsgkakevlk;gsgkakevlkd;sgkakevlkdf;gkakevlkdft;kakevlkdftl;akevlkdftle;kevlkdftleg;evlkdftlegt;vlkdftlegtl;lkdftlegtla;kdftlegtlaa;dftlegtlaad;ftlegtlaadg;tlegtlaadgk;legtlaadgkt;egtlaadgktt;gtlaadgkttl;tlaadgkttlk;laadgkttlkv;aadgkttlkvt;adgkttlkvte;dgkttlkvteg;gkttlkvtegt;kttlkvtegtv;ttlkvtegtvv;tlkvtegtvvl;lkvtegtvvls;kvtegtvvlsk;vtegtvvlskn;tegtvvlskni;egtvvlsknil;gtvvlsknilk;tvvlsknilks;vvlsknilksg;vlsknilksge;lsknilksgei;sknilksgeit;knilksgeitv;nilksgeitva;ilksgeitval;lksgeitvald;ksgeitvaldd;sgeitvaldds;geitvalddsd;eitvalddsdt;itvalddsdtt;tvalddsdttq;valddsdttqa;alddsdttqat;lddsdttqatk;ddsdttqatkk;dsdttqatkkt;sdttqatkktg;dttqatkktgk;ttqatkktgkw;tqatkktgkwd;qatkktgkwds;atkktgkwdsk;tkktgkwdskt;kktgkwdskts;ktgkwdsktst;tgkwdsktstl;gkwdsktstlt;kwdsktstlti;wdsktstltis;dsktstltisv;sktstltisvn;ktstltisvns;tstltisvnsq;stltisvnsqk;tltisvnsqkt;ltisvnsqktk;tisvnsqktkn;isvnsqktknl;svnsqktknlv;vnsqktknlvf;nsqktknlvft;sqktknlvftk;qktknlvftke;ktknlvftked;tknlvftkedt;knlvftkedti;nlvftkedtit;lvftkedtitv;vftkedtitvq;ftkedtitvqk;tkedtitvqky;kedtitvqkyd;edtitvqkyds;dtitvqk

ydsa;titvqkydsag;itvqkydsagt;tvqkydsagtn;vqkydsagtnl;qkydsagtnle;kydsagtnleg;ydsagtnl
egk;dsagtnlegka;sagtnlegkav;agtnlegkave;gtnlegkavei;tnlegkaveit;nlegkaveitt;legkaveittl;
egkaveittle;gkaveittlek;kaveittlekl;aveittleklk;veittleklkd;eittleklkda;ittleklkdal;ttleklkdal
k;

13 mers:
mkkyllgiglila;kkyllgiglilal;kyllgiglilali;yllgiglilalia;llgiglilaliac;lgiglilaliack;giglilaliackq;
iglilaliackqn;glilaliackqnv;lilaliackqnvs;ilaliackqnvss;laliackqnvssl;aliackqnvssld;liackqn
vsslde;iackqnvssldek;ackqnvssldekn;ckqnvssldekns;kqnvssldeknsv;qnvssldeknsvs;nvssld
eknsvsv;vssldeknsvsvd;ssldeknsvsvdl;sldeknsvsvdlp;ldeknsvsvdlpg;deknsvsvdlpgg;ekns
vsvdlpggm;knsvsvdlpggmk;nsvsvdlpggmkv;svsvdlpggmkvl;vsvdlpggmkvlv;svdlpggmkv
lvs;vdlpggmkvlvsk;dlpggmkvlvske;lpggmkvlvskek;pggmkvlvskekd;ggmkvlvskekdk;gmk
vlvskekdkd;mkvlvskekdkdg;kvlvskekdkdgk;vlvskekdkdgky;lvskekdkdgkys;vskekdkdgky
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slmatvek;dgkyslmatvekl;gkyslmatvekle;kyslmatveklel;yslmatveklelk;slmatveklelkg;lmat
veklelkgt;matveklelkgts;atveklelkgtsd;tveklelkgtsdk;veklelkgtsdkn;eklelkgtsdknn;klelkgt
sdknng;lelkgtsdknngs;elkgtsdknngsg;lkgtsdknngsgt;kgtsdknngsgtl;gtsdknngsgtle;tsdknng
sgtleg;sdknngsgtlege;dknngsgtlegek;knngsgtlegekt;nngsgtlegektd;ngsgtlegektdk;gsgtlege
ktdks;sgtlegektdksk;gtlegektdkskv;tlegektdkskvk;legektdkskvkl;egektdkskvklt;gektdkskv
klti;ektdkskvkltia;ktdkskvkltiae;tdkskvkltiaed;dkskvkltiaedl;kskvkltiaedls;skvkltiaedlsk;k
vkltiaedlskt;vkltiaedlsktt;kltiaedlskttf;ltiaedlskttfe;tiaedlskttfei;iaedlskttfeif;aedlskttfeifk;e
dlskttfeifke;dlskttfeifked;lskttfeifkedg;skttfeifkedgk;kttfeifkedgkt;ttfeifkedgktl;tfeifkedgk
tlv;feifkedgktlvs;eifkedgktlvsk;ifkedgktlvskk;fkedgktlvskkv;kedgktlvskkvt;edgktlvskkvtl
;dgktlvskkvtlk;gktlvskkvtlkd;ktlvskkvtlkdk;tlvskkvtlkdks;lvskkvtlkdkss;vskkvtlkdksst;sk
kvtlkdksste;kkvtlkdksstee;kvtlkdkssteek;vtlkdkssteekf;tlkdkssteekfn;lkdkssteekfne;kdksst
eekfnek;dkssteekfnekg;kssteekfnekge;ssteekfnekgei;steekfnekgeis;teekfnekgeise;eekfnek
geisek;ekfnekgeisekt;kfnekgeisekti;fnekgeisektiv;nekgeisektivr;ekgeisektivra;kgeisektivr
an;geisektivrang;eisektivrangt;isektivrangtr;sektivrangtrl;ektivrangtrle;ktivrangtrley;tivra
ngtrleyt;ivrangtrleytd;vrangtrleytdi;rangtrleytdik;angtrleytdiks;ngtrleytdiksd;gtrleytdiksd
g;trleytdiksdgs;rleytdiksdgsg;leytdiksdgsgk;eytdiksdgsgka;ytdiksdgsgkak;tdiksdgsgkake;
diksdgsgkakev;iksdgsgkakevl;ksdgsgkakevlk;sdgsgkakevlkd;dgsgkakevlkdf;gsgkakevlkd
ft;sgkakevlkdftl;gkakevlkdftle;kakevlkdftleg;akevlkdftlegt;kevlkdftlegtl;evlkdftlegtla;vlk
dftlegtlaa;lkdftlegtlaad;kdftlegtlaadg;dftlegtlaadgk;ftlegtlaadgkt;tlegtlaadgktt;legtlaadgktt
l;egtlaadgkttlk;gtlaadgkttlkv;tlaadgkttlkvt;laadgkttlkvte;aadgkttlkvteg;adgkttlkvtegt;dgktt
lkvtegtv;gkttlkvtegtvv;kttlkvtegtvvl;ttlkvtegtvvls;tlkvtegtvvlsk;lkvtegtvvlskn;kvtegtvvlsk
ni;vtegtvvlsknil;tegtvvlsknilk;egtvvlsknilks;gtvvlsknilksg;tvvlsknilksge;vvlsknilksgei;vls
knilksgeit;lsknilksgeitv;sknilksgeitva;knilksgeitval;nilksgeitvald;ilksgeitvaldd;lksgeitvald
ds;ksgeitvalddsd;sgeitvalddsdt;geitvalddsdtt;eitvalddsdttq;itvalddsdttqa;tvalddsdttqat;vald
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tgkwd;ttqatkktgkwds;tqatkktgkwdsk;qatkktgkwdskt;atkktgkwdskts;tkktgkwdsktst;kktgk
wdsktstl;ktgkwdsktstlt;tgkwdsktstlti;gkwdsktstltis;kwdsktstltisv;wdsktstltisvn;dsktstltisvn
s;sktstltisvnsq;ktstltisvnsqk;tstltisvnsqkt;stltisvnsqktk;tltisvnsqktkn;ltisvnsqktknl;tisvnsqk
tknlv;isvnsqktknlvf;svnsqktknlvft;vnsqktknlvftk;nsqktknlvftke;sqktknlvftked;qktknlvftke
dt;ktknlvftkedti;tknlvftkedtit;knlvftkedtitv;nlvftkedtitvq;lvftkedtitvqk;vftkedtitvqky;ftked
titvqkyd;tkedtitvqkyds;kedtitvqkydsa;edtitvqkydsag;dtitvqkydsagt;titvqkydsagtn;itvqkyds
agtnl;tvqkydsagtnle;vqkydsagtnleg;qkydsagtnlegk;kydsagtnlegka;ydsagtnlegkav;dsagtnle

gkave;sagtnlegkavei;agtnlegkaveit;gtnlegkaveitt;tnlegkaveittl;nlegkaveittle;legkaveittlek;
egkaveittlekl;gkaveittleklk;kaveittleklkd;aveittleklkda;veittleklkdal;eittleklkdalk;

14 mers:
mkkyllgiglilal;kkyllgiglilali;kyllgiglilalia;yllgiglilaliac;llgiglilaliack;lgiglilaliackq;giglilal
iackqn;iglilaliackqnv;glilaliackqnvs;lilaliackqnvss;ilaliackqnvssl;laliackqnvssld;aliackqn
vsslde;liackqnvssldek;iackqnvssldekn;ackqnvssldekns;ckqnvssldeknsv;kqnvssldeknsvs;q
nvssldeknsvsv;nvssldeknsvsvd;vssldeknsvsvdl;ssldeknsvsvdlp;sldeknsvsvdlpg;ldeknsvsv
dlpgg;deknsvsvdlpggm;eknsvsvdlpggmk;knsvsvdlpggmkv;nsvsvdlpggmkvl;svsvdlpggm
kvlv;vsvdlpggmkvlvs;svdlpggmkvlvsk;vdlpggmkvlvske;dlpggmkvlvskek;lpggmkvlvskek
d;pggmkvlvskekdk;ggmkvlvskekdkd;gmkvlvskekdkdg;mkvlvskekdkdgk;kvlvskekdkdgk
y;vlvskekdkdgkys;lvskekdkdgkysl;vskekdkdgkyslm;skekdkdgkyslma;kekdkdgkyslmat;ek
dkdgkyslmatv;kdkdgkyslmatve;dkdgkyslmatvek;kdgkyslmatvekl;dgkyslmatvekle;gkyslm
atveklel;kyslmatveklelk;yslmatveklelkg;slmatveklelkgt;lmatveklelkgts;matveklelkgtsd;at
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sg;elkgtsdknngsgt;lkgtsdknngsgtl;kgtsdknngsgtle;gtsdknngsgtleg;tsdknngsgtlege;sdknngs
gtlegek;dknngsgtlegekt;knngsgtlegektd;nngsgtlegektdk;ngsgtlegektdks;gsgtlegektdksk;sg
tlegektdkskv;gtlegektdkskvk;tlegektdkskvkl;legektdkskvklt;egektdkskvklti;gektdkskvklti
a;ektdkskvkltiae;ktdkskvkltiaed;tdkskvkltiaedl;dkskvkltiaedls;kskvkltiaedlsk;skvkltiaedls
kt;kvkltiaedlsktt;vkltiaedlskttf;kltiaedlskttfe;ltiaedlskttfei;tiaedlskttfeif;iaedlskttfeifk;aedl
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dgktlv;tfeifkedgktlvs;feifkedgktlvsk;eifkedgktlvskk;ifkedgktlvskkv;fkedgktlvskkvt;kedgk
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kkvtlkdksst;vskkvtlkdksste;skkvtlkdksstee;kkvtlkdkssteek;kvtlkdkssteekf;vtlkdkssteekfn;
tlkdkssteekfne;lkdkssteekfnek;kdkssteekfnekg;dkssteekfnekge;kssteekfnekgei;ssteekfnek
geis;steekfnekgeise;teekfnekgeisek;eekfnekgeisekt;ekfnekgeisekti;kfnekgeisektiv;fnekgei
sektivr;nekgeisektivra;ekgeisektivran;kgeisektivrang;geisektivrangt;eisektivrangtr;isektiv
rangtrl;sektivrangtrle;ektivrangtrley;ktivrangtrleyt;tivrangtrleytd;ivrangtrleytdi;vrangtrley
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egtlaadgkttlkv;gtlaadgkttlkvt;tlaadgkttlkvte;laadgkttlkvteg;aadgkttlkvtegt;adgkttlkvtegtv;
dgkttlkvtegtvv;gkttlkvtegtvvl;kttlkvtegtvvls;ttlkvtegtvvlsk;tlkvtegtvvlskn;lkvtegtvvlskni;
kvtegtvvlsknil;vtegtvvlsknilk;tegtvvlsknilks;egtvvlsknilksg;gtvvlsknilksge;tvvlsknilksgei
;vvlsknilksgeit;vlsknilksgeitv;lsknilksgeitva;sknilksgeitval;knilksgeitvald;nilksgeitvaldd;i
lksgeitvaldds;lksgeitvalddsd;ksgeitvalddsdt;sgeitvalddsdtt;geitvalddsdttq;eitvalddsdttqa;it
valddsdttqat;tvalddsdttqatk;valddsdttqatkk;alddsdttqatkkt;lddsdttqatkktg;ddsdttqatkktgk;d
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dskts;atkktgkwdsktst;tkktgkwdsktstl;kktgkwdsktstlt;ktgkwdsktstlti;tgkwdsktstltis;gkwdsk
tstltisv;kwdsktstltisvn;wdsktstltisvns;dsktstltisvnsq;sktstltisvnsqk;ktstltisvnsqkt;tstltisvns
qktk;stltisvnsqktkn;tltisvnsqktknl;ltisvnsqktknlv;tisvnsqktknlvf;isvnsqktknlvft;svnsqktknl
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kydsa;kedtitvqkydsag;edtitvqkydsagt;dtitvqkydsagtn;titvqkydsagtnl;itvqkydsagtnle;tvqky

dsagtnleg;vqkydsagtnlegk;qkydsagtnlegka;kydsagtnlegkav;ydsagtnlegkave;dsagtnlegkav
ei;sagtnlegkaveit;agtnlegkaveitt;gtnlegkaveittl;tnlegkaveittle;nlegkaveittlek;legkaveittlekl
;egkaveittleklk;gkaveittleklkd;kaveittleklkda;aveittleklkdal;veittleklkdalk;

15 mers:
mkkyllgiglilali;kkyllgiglilalia;kyllgiglilaliac;yllgiglilaliack;llgiglilaliackq;lgiglilaliackqn;
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lde;aliackqnvssldek;liackqnvssldekn;iackqnvssldekns;ackqnvssldeknsv;ckqnvssldeknsvs;
kqnvssldeknsvsv;qnvssldeknsvsvd;nvssldeknsvsvdl;vssldeknsvsvdlp;ssldeknsvsvdlpg;sld
eknsvsvdlpgg;ldeknsvsvdlpggm;deknsvsvdlpggmk;eknsvsvdlpggmkv;knsvsvdlpggmkvl;
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veklelkgt;slmatveklelkgts;lmatveklelkgtsd;matveklelkgtsdk;atveklelkgtsdkn;tveklelkgtsd
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kskvk;gtlegektdkskvkl;tlegektdkskvklt;legektdkskvklti;egektdkskvkltia;gektdkskvkltiae;e
ktdkskvkltiaed;ktdkskvkltiaedl;tdkskvkltiaedls;dkskvkltiaedlsk;kskvkltiaedlskt;skvkltiaed
lsktt;kvkltiaedlskttf;vkltiaedlskttfe;kltiaedlskttfei;ltiaedlskttfeif;tiaedlskttfeifk;iaedlskttfei
fke;aedlskttfeifked;edlskttfeifkedg;dlskttfeifkedgk;lskttfeifkedgkt;skttfeifkedgktl;kttfeifke
dgktlv;ttfeifkedgktlvs;tfeifkedgktlvsk;feifkedgktlvskk;eifkedgktlvskkv;ifkedgktlvskkvt;fk
edgktlvskkvtl;kedgktlvskkvtlk;edgktlvskkvtlkd;dgktlvskkvtlkdk;gktlvskkvtlkdks;ktlvskk
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sekti;ekfnekgeisektiv;kfnekgeisektivr;fnekgeisektivra;nekgeisektivran;ekgeisektivrang;kg
eisektivrangt;geisektivrangtr;eisektivrangtrl;isektivrangtrle;sektivrangtrley;ektivrangtrleyt
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gtvvlsknil;kvtegtvvlsknilk;vtegtvvlsknilks;tegtvvlsknilksg;egtvvlsknilksge;gtvvlsknilksge
i;tvvlsknilksgeit;vvlsknilksgeitv;vlsknilksgeitva;lsknilksgeitval;sknilksgeitvald;knilksgeit
valdd;nilksgeitvaldds;ilksgeitvalddsd;lksgeitvalddsdt;ksgeitvalddsdtt;sgeitvalddsdttq;geit
valddsdttqa;eitvalddsdttqat;itvalddsdttqatk;tvalddsdttqatkk;valddsdttqatkkt;alddsdttqatkkt
g;lddsdttqatkktgk;ddsdttqatkktgkw;dsdttqatkktgkwd;sdttqatkktgkwds;dttqatkktgkwdsk;ttq
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vqkydsagtnlegka;qkydsagtnlegkav;kydsagtnlegkave;ydsagtnlegkavei;dsagtnlegkaveit;sag
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;egkaveittleklkd;gkaveittleklkda;kaveittleklkdal;aveittleklkdalk;

16 mers:
mkkyllgiglilalia;kkyllgiglilaliac;kyllgiglilaliack;yllgiglilaliackq;llgiglilaliackqn;lgiglilalia
ckqnv;giglilaliackqnvs;iglilaliackqnvss;glilaliackqnvssl;lilaliackqnvssld;ilaliackqnvsslde;
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ssteekfnekge;kdkssteekfnekgei;dkssteekfnekgeis;kssteekfnekgeise;ssteekfnekgeisek;steek
fnekgeisekt;teekfnekgeisekti;eekfnekgeisektiv;ekfnekgeisektivr;kfnekgeisektivra;fnekgei
sektivran;nekgeisektivrang;ekgeisektivrangt;kgeisektivrangtr;geisektivrangtrl;eisektivran
gtrle;isektivrangtrley;sektivrangtrleyt;ektivrangtrleytd;ktivrangtrleytdi;tivrangtrleytdik;ivr
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;gtvvlsknilksgeit;tvvlsknilksgeitv;vvlsknilksgeitva;vlsknilksgeitval;lsknilksgeitvald;sknil

ksgeitvaldd;knilksgeitvaldds;nilksgeitvalddsd;ilksgeitvalddsdt;lksgeitvalddsdtt;ksgeitvald
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gkaveittl;agtnlegkaveittle;gtnlegkaveittlek;tnlegkaveittlekl;nlegkaveittleklk;legkaveittlekl
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<YP_853838 outer surface protein B;Protein;Borrelia afzelii PKo>

8 mers:
mkqyllvf;kqyllvfa;qyllvfal;yllvfalv;llvfalvl;lvfalvla;vfalvlal;falvlali
;alvlalia;lvlaliac;vlaliacs;laliacsq;aliacsqk;liacsqkg;iacsqkgt;acsqkgt
e;csqkgtep;sqkgtepk;qkgtepks;kgtepkst;gtepksts;tepkstsq;epkstsqd;pkstsq
dh;kstsqdhn;stsqdhnd;tsqdhndq;sqdhndqe;qdhndqei;dhndqeii;hndqeiin;ndqei
ins;dqeiinsd;qeiinsdn;eiinsdnt;iinsdntp;insdntpk;nsdntpkd;sdntpkds;dntp
kdsk;ntpkdskk;tpkdskkd;pkdskkdl;kdskkdlt;dskkdltv;skkdltvl;kkdltvla;kdl
tvlae;dltvlaee;ltvlaeen;tvlaeens;vlaeensv;laeensvp;aeensvpl;eensvplf;en
svplfn;nsvplfng;svplfngn;vplfngnk;plfngnki;lfngnkif;fngnkifv;ngnkifvs;g
nkifvsk;nkifvske;kifvskek;ifvskekn;fvskekns;vskeknsa;skeknsag;keknsagk;
eknsagky;knsagkye;nsagkyel;sagkyelr;agkyelra;gkyelrat;kyelratv;yelratvd
;elratvdt;lratvdtv;ratvdtve;atvdtvel;tvdtvelk;vdtvelkg;dtvelkgv;tvelkgv
s;velkgvsd;elkgvsdk;lkgvsdkn;kgvsdknn;gvsdknng;vsdknngs;sdknngsg;dknngs
gk;knngsgkl;nngsgkle;ngsgkleg;gsgklegt;sgklegtk;gklegtka;klegtkad;legtk
adk;egtkadkt;gtkadktk;tkadktkv;kadktkva;adktkvam;dktkvamt;ktkvamti;tkva
mtia;kvamtiad;vamtiadd;amtiaddl;mtiaddln;tiaddlnt;iaddlnti;addlntit;ddl
ntitv;dlntitve;lntitvet;ntitvety;titvetyd;itvetyda;tvetydas;vetydasn;et
ydasnk;tydasnkk;ydasnkkt;dasnkktg;asnkktgs;snkktgse;nkktgsev;kktgsevv;k
tgsevvk;tgsevvkk;gsevvkkq;sevvkkqg;evvkkqgs;vvkkqgsv;vkkqgsvi;kkqgsvik;
kqgsvike;qgsvikes;gsvikesy;svikesyk;vikesyka;ikesykan;kesykank;esykankl
;sykankld;ykankldk;kankldsk;ankldskk;nkldskki;kldskkit;ldskkitr;dskkitr
e;skkitren;kkitrene;kitrenet;itrenett;trenettl;renettle;enettley;nettle
ys;ettleyse;ttleysem;tleysemt;leysemtd;eysemtds;ysemtdss;semtdssn;emtds
sna;mtdssnat;tdssnatk;dssnatka;ssnatkav;snatkave;natkavet;atkavetl;tkav
etlk;kavetlkn;avetlkng;vetlkngi;etlkngik;tlkngikl;lkngikle;kngikleg;ngi
klegs;giklegsl;iklegslv;klegslvg;legslvgg;egslvggk;gslvggkt;slvggktt;lv
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ltreieqd;treieqdg;reieqdgk;eieqdgkv;ieqdgkvk;eqdgkvki;qdgkvkiy;dgkvkiyl
;gkvkiyln;kvkiylnd;vkiylndt;kiylndtt;iylndtts;ylndttsg;lndttsgs;ndttsgs
t;dttsgstk;ttsgstkk;tsgstkkt;sgstkkta;gstkktat;stkktatw;tkktatwn;kktatw
ne;ktatwnet;tatwnett;atwnettn;twnettnt;wnettntl;nettntlt;ettntlti;ttntl
tis;tntltisa;ntltisad;tltisads;ltisadsk;tisadskk;isadskkt;sadskktk;adsk
ktkd;dskktkdf;skktkdfv;kktkdfvf;ktkdfvfl;tkdfvflt;kdfvfltd;dfvfltdg;fvf
ltdgt;vfltdgti;fltdgtit;ltdgtitv;tdgtitvq;dgtitvqa;gtitvqay;titvqayd;it
vqaydt;tvqaydta;vqaydtag;qaydtagt;aydtagtk;ydtagtkl;dtagtkle;tagtkleg;a

gtklegn;gtklegns;tklegnss;klegnsse;legnssei;egnsseik;gnsseikd;nsseikdl;
sseikdla;seikdlaa;eikdlaal;ikdlaalk;kdlaalka;dlaalkaa;laalkaal;aalkaalk
;

9 mers:
mkqyllvfa;kqyllvfal;qyllvfalv;yllvfalvl;llvfalvla;lvfalvlal;vfalvlali;f
alvlalia;alvlaliac;lvlaliacs;vlaliacsq;laliacsqk;aliacsqkg;liacsqkgt;ia
csqkgte;acsqkgtep;csqkgtepk;sqkgtepks;qkgtepkst;kgtepksts;gtepkstsq;tep
kstsqd;epkstsqdh;pkstsqdhn;kstsqdhnd;stsqdhndq;tsqdhndqe;sqdhndqei;qdhn
dqeii;dhndqeiin;hndqeiins;ndqeiinsd;dqeiinsdn;qeiinsdnt;eiinsdntp;iinsd
ntpk;insdntpkd;nsdntpkds;sdntpkdsk;dntpkdskk;ntpkdskkd;tpkdskkdl;pkdskk
dlt;kdskkdltv;dskkdltvl;skkdltvla;kkdltvlae;kdltvlaee;dltvlaeen;ltvlaee
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;nkifvskek;kifvskekn;ifvskekns;fvskeknsa;vskeknsag;skeknsagk;keknsagky;
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kqgsvikes;qgsvikesy;gsvikesyk;svikesyka;vikesykan;ikesykank;kesykankl;e
sykankld;sykanklds;ykankldsk;kankldskk;ankldskki;nkldskkit;kldskkitr;ld
skkitre;dskkitren;skkitrene;kkitrenet;kitrenett;itrenettl;trenettle;ren
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10 mers:
mkqyllvfal;kqyllvfalv;qyllvfalvl;yllvfalvla;llvfalvlal;lvfalvlali;vfalv
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;liacsqkgte;iacsqkgtep;acsqkgtepk;csqkgtepks;sqkgtepkst;qkgtepksts;kgte
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ddlntitv;addlntitve;ddlntitvet;dlntitvety;lntitvetyd;ntitvetyda;titvety
das;itvetydasn;tvetydasnk;vetydasnkk;etydasnkkt;tydasnkktg;ydasnkktgs;d
asnkktgse;asnkktgsev;snkktgsevv;nkktgsevvk;kktgsevvkk;ktgsevvkkq;tgsevv
kkqg;gsevvkkqgs;sevvkkqgsv;evvkkqgsvi;vvkkqgsvik;vkkqgsvike;kkqgsvikes;
kqgsvikesy;qgsvikesyk;gsvikesyka;svikesykan;vikesykank;ikesykankl;kesyk
ankld;esykankld s;sykankldsk;ykankldskk;kankldskki;ankldskkit;nkldskkitr
;kldskkitre;ldskkitren;dskkitrene;skkitrenet;kkitrenett;kitrenettl;itre
nettle;trenettley;renettleys;enettleyse;nettleysem;ettleysemt;ttleysemt
d;tleysemtds;leysemtdss;eysemtdssn;ysemtdssna;semtdssnat;emtdssnatk;mtd
ssnatka;tdssnatkav;dssnatkave;ssnatkavet;snatkavetl;natkavetlk;atkavetl
kn;tkavetlkng;kavetlkngi;avetlkngik;vetlkngikl;etlkngikle;tlkngikleg;lk
ngiklegs;kngiklegsl;ngiklegslv;giklegslvg;iklegslvgg;klegslvggk;legslvg
gkt;egslvggktt;gslvggkttv;slvggkttvk;lvggkttvkl;vggkttvklt;ggkttvklte;g
kttvklteg;kttvkltegt;ttvkltegti;tvkltegtit;vkltegtitl;kltegtitlt;ltegti
tltr;tegtitltre;egtitltrei;gtitltreie;titltreieq;itltreieqd;tltreieqdg;
ltreieqdgk;treieqdgkv;reieqdgkvk;eieqdgkvki;ieqdgkvkiy;eqdgkvkiyl;qdgkv
kiyln;dgkvkiylnd;gkvkiylndt;kvkiylndtt;vkiylndtts;kiylndttsg;iylndttsgs
;ylndttsgst;lndttsgstk;ndttsgstkk;dttsgstkkt;ttsgstkkta;tsgstkktat;sgst
kktatw;gstkktatwn;stkktatwne;tkktatwnet;kktatwnett;ktatwnettn;tatwnettn
t;atwnettntl;twnettntlt;wnettntlti;nettntltis;ettntltisa;ttntltisad;tnt
ltisads;ntltisadsk;tltisadskk;ltisadskkt;tisadskktk;isadskktkd;sadskktk
df;adskktkdfv;dskktkdfvf;skktkdfvfl;kktkdfvflt;ktkdfvfltd;tkdfvfltdg;kd
fvfltdgt;dfvfltdgti;fvfltdgtit;vfltdgtitv;fltdgtitvq;ltdgtitvqa;tdgtitv
qay;dgtitvqayd;gtitvqaydt;titvqaydta;itvqaydtag;tvqaydtagt;vqaydtagtk;q
aydtagtkl;aydtagtkle;ydtagtkleg;dtagtklegn;tagtklegns;agtklegnss;gtkleg
nsse;tklegnssei;klegnsseik;legnsseikd;egnsseikdl;gnsseikdla;nsseikdlaa;
sseikdlaal;seikdlaalk;eikdlaalka;ikdlaalkaa;kdlaalkaal;dlaalkaalk;

11 mers:
mkqyllvfalv;kqyllvfalvl;qyllvfalvla;yllvfalvlal;llvfalvlali;lvfalvlalia
;vfalvlaliac;falvlaliacs;alvlaliacsq;lvlaliacsqk;vlaliacsqkg;laliacsqkg
t;aliacsqkgte;liacsqkgtep;iacsqkgtepk;acsqkgtepks;csqkgtepkst;sqkgtepks
ts;qkgtepkstsq;kgtepkstsqd;gtepkstsqdh;tepkstsqdhn;epkstsqdhnd;pkstsqdh
ndq;kstsqdhndqe;stsqdhndqei;tsqdhndqeii;sqdhndqeiin;qdhndqeiins;dhndqei
insd;hndqeiinsdn;ndqeiinsdnt;dqeiinsdntp;qeiinsdntpk;eiinsdntpkd;iinsdn
tpkds;insdntpkdsk;nsdntpkdskk;sdntpkdskkd;dntpkdskkdl;ntpkdskkdlt;tpkds
kkdltv;pkdskkdltvl;kdskkdltvla;dskkdltvlae;skkdltvlaee;kkdltvlaeen;kdlt
vlaeens;dltvlaeensv;ltvlaeensvp;tvlaeensvpl;vlaeensvplf;laeensvplfn;aee
nsvplfng;eensvplfngn;ensvplfngnk;nsvplfngnki;svplfngnkif;vplfngnkifv;pl
fngnkifvs;lfngnkifvsk;fngnkifvske;ngnkifvskek;gnkifvskekn;nkifvskekns;k
ifvskeknsa;ifvskeknsag;fvskeknsagk;vskeknsagky;skeknsagkye;keknsagkyel;
eknsagkyelr;knsagkyelra;nsagkyelrat;sagkyelratv;agkyelratvd;gkyelratvdt
;kyelratvdtv;yelratvdtve;elratvdtvel;lratvdtvelk;ratvdtvelkg;atvdtvelkg
v;tvdtvelkgvs;vdtvelkgvsd;dtvelkgvsdk;tvelkgvsdkn;velkgvsdknn;elkgvsdkn
ng;lkgvsdknngs;kgvsdknngsg;gvsdknngsgk;vsdknngsgkl;sdknngsgkle;dknngsgk
leg;knngsgklegt;nngsgklegtk;ngsgklegtka;gsgklegtkad;sgklegtkadk;gklegtk
adkt;klegtkadktk;legtkadktkv;egtkadktkva;gtkadktkvam;tkadktkvamt;kadktk
vamti;adktkvamtia;dktkvamtiad;ktkvamtiadd;tkvamtiaddl;kvamtiaddln;vamti

addlnt;amtiaddlnti;mtiaddlntit;tiaddlntitv;iaddlntitve;addlntitvet;ddln
titvety;dlntitvetyd;lntitvetyda;ntitvetydas;titvetydasn;itvetydasnk;tve
tydasnkk;vetydasnkkt;etydasnkktg;tydasnkktgs;ydasnkktgse;dasnkktgsev;as
nkktgsevv;snkktgsevvk;nkktgsevvkk;kktgsevvkkq;ktgsevvkkqg;tgsevvkkqgs;g
sevvkkqgsv;sevvkkqgsvi;evvkkqgsvik;vvkkqgsvike;vkkqgsvikes;kkqgsvikesy;
kqgsvikesyk;qgsvikesyka;gsvikesykan;svikesykank;vikesykankl;ikesykankld
;kesykankld s;esykankldsk;sykankldskk;ykankldskki;kankldskkit;ankldskkit
r;nkldskkitre;kldskkitren;ldskkitrene;dskkitrenet;skkitrenett;kkitrenet
tl;kitrenettle;itrenettley;trenettleys;renettleyse;enettleysem;nettleys
emt;ettleysemtd;ttleysemtds;tleysemtdss;leysemtdssn;eysemtdssna;ysemtds
snat;semtdssnatk;emtdssnatka;mtdssnatkav;tdssnatkave;dssnatkavet;ssnatk
avetl;snatkavetlk;natkavetlkn;atkavetlkng;tkavetlkngi;kavetlkngik;avetl
kngikl;vetlkngikle;etlkngikleg;tlkngiklegs;lkngiklegsl;kngiklegslv;ngik
legslvg;giklegslvgg;iklegslvggk;klegslvggkt;legslvggktt;egslvggkttv;gsl
vggkttvk;slvggkttvkl;lvggkttvklt;vggkttvklte;ggkttvklteg;gkttvkltegt;kt
tvkltegti;ttvkltegtit;tvkltegtitl;vkltegtitlt;kltegtitltr;ltegtitltre;t
egtitltrei;egtitltreie;gtitltreieq;titltreieqd;itltreieqdg;tltreieqdgk;
ltreieqdgkv;treieqdgkvk;reieqdgkvki;eieqdgkvkiy;ieqdgkvkiyl;eqdgkvkiyln
;qdgkvkiylnd;dgkvkiylndt;gkvkiylndtt;kvkiylndtts;vkiylndttsg;kiylndttsg
s;iylndttsgst;ylndttsgstk;lndttsgstkk;ndttsgstkkt;dttsgstkkta;ttsgstkkt
at;tsgstkktatw;sgstkktatwn;gstkktatwne;stkktatwnet;tkktatwnett;kktatwne
ttn;ktatwnettnt;tatwnettntl;atwnettntlt;twnettntlti;wnettntltis;nettntl
tisa;ettntltisad;ttntltisads;tntltisadsk;ntltisadskk;tltisadskkt;ltisad
skktk;tisadskktkd;isadskktkdf;sadskktkdfv;adskktkdfvf;dskktkdfvfl;skktk
dfvflt;kktkdfvfltd;ktkdfvfltdg;tkdfvfltdgt;kdfvfltdgti;dfvfltdgtit;fvfl
tdgtitv;vfltdgtitvq;fltdgtitvqa;ltdgtitvqay;tdgtitvqayd;dgtitvqaydt;gti
tvqaydta;titvqaydtag;itvqaydtagt;tvqaydtagtk;vqaydtagtkl;qaydtagtkle;ay
dtagtkleg;ydtagtklegn;dtagtklegns;tagtklegnss;agtklegnsse;gtklegnssei;t
klegnsseik;klegnsseikd;legnsseikdl;egnsseikdla;gnsseikdlaa;nsseikdlaal;
sseikdlaalk;seikdlaalka;eikdlaalkaa;ikdlaalkaal;kdlaalkaalk;

13 mers:
mkqyllvfalvla;kqyllvfalvlal;qyllvfalvlali;yllvfalvlalia;llvfalvlaliac;l
vfalvlaliacs;vfalvlaliacsq;falvlaliacsqk;alvlaliacsqkg;lvlaliacsqkgt;vl
aliacsqkgte;laliacsqkgtep;aliacsqkgtepk;liacsqkgtepks;iacsqkgtepkst;acs
qkgtepksts;csqkgtepkstsq;sqkgtepkstsqd;qkgtepkstsqdh;kgtepkstsqdhn;gtep
kstsqdhnd;tepkstsqdhndq;epkstsqdhndqe;pkstsqdhndqei;kstsqdhndqeii;stsqd
hndqeiin;tsqdhndqeiins;sqdhndqeiinsd;qdhndqeiinsdn;dhndqeiinsdnt;hndqei
insdntp;ndqeiinsdntpk;dqeiinsdntpkd;qeiinsdntpkds;eiinsdntpkdsk;iinsdnt
pkdskk;insdntpkdskkd;nsdntpkdskkdl;sdntpkdskkdlt;dntpkdskkdltv;ntpkdskk
dltvl;tpkdskkdltvla;pkdskkdltvlae;kdskkdltvlaee;dskkdltvlaeen;skkdltvla
eens;kkdltvlaeensv;kdltvlaeensvp;dltvlaeensvpl;ltvlaeensvplf;tvlaeensvp
lfn;vlaeensvplfng;laeensvplfngn;aeensvplfngnk;eensvplfngnki;ensvplfngnk
if;nsvplfngnkifv;svplfngnkifvs;vplfngnkifvsk;plfngnkifvske;lfngnkifvske
k;fngnkifvskekn;ngnkifvskekns;gnkifvskeknsa;nkifvskeknsag;kifvskeknsagk
;ifvskeknsagky;fvskeknsagkye;vskeknsagkyel;skeknsagkyelr;keknsagkyelra;
eknsagkyelrat;knsagkyelratv;nsagkyelratvd;sagkyelratvdt;agkyelratvdtv;g
kyelratvdtve;kyelratvdtvel;yelratvdtvelk;elratvdtvelkg;lratvdtvelkgv;ra
tvdtvelkgvs;atvdtvelkgvsd;tvdtvelkgvsdk;vdtvelkgvsdkn;dtvelkgvsdknn;tve
lkgvsdknng;velkgvsdknngs;elkgvsdknngsg;lkgvsdknngsgk;kgvsdknngsgkl;gvsd
knngsgkle;vsdknngsgkleg;sdknngsgklegt;dknngsgklegtk;knngsgklegtka;nngsg
klegtkad;ngsgklegtkadk;gsgklegtkadkt;sgklegtkadktk;gklegtkadktkv;klegtk
adktkva;legtkadktkvam;egtkadktkvamt;gtkadktkvamti;tkadktkvamtia;kadktkv
amtiad;adktkvamtiadd;dktkvamtiaddl;ktkvamtiaddln;tkvamtiaddlnt;kvamtiad
dlnti;vamtiaddlntit;amtiaddlntitv;mtiaddlntitve;tiaddlntitvet;iaddlntit
vety;addlntitvetyd;ddlntitvetyda;dlntitvetydas;lntitvetydasn;ntitvetyda
snk;titvetydasnkk;itvetydasnkkt;tvetydasnkktg;vetydasnkktgs;etydasnkktg

se;tydasnkktgsev;ydasnkktgsevv;dasnkktgsevvk;asnkktgsevvkk;snkktgsevvkk
q;nkktgsevvkkqg;kktgsevvkkqgs;ktgsevvkkqgsv;tgsevvkkqgsvi;gsevvkkqgsvik
;sevvkkqgsvike;evvkkqgsvikes;vvkkqgsvikesy;vkkqgsvikesyk;kkqgsvikesyka;
kqgsvikesykan;qgsvikesykank;gsvikesykankl;svikesykankld;vikesykanklds;i
kesykankldsk;kesykankldskk;esykankldskki;sykankldskkit;ykankldskkitr;ka
nkldskkitre;ankldskkitren;nkldskkitrene;kldskkitrenet;ldskkitrenett;dsk
kitrenettl;skkitrenettle;kkitrenettley;kitrenettleys;itrenettleyse;tren
ettleysem;renettleysemt;enettleysemtd;nettleysemtds;ettleysemtdss;ttley
semtdssn;tleysemtdssna;leysemtdssnat;eysemtdssnatk;ysemtdssnatka;semtds
snatkav;emtdssnatkave;mtdssnatkavet;tdssnatkavetl;dssnatkavetlk;ssnatka
vetlkn;snatkavetlkng;natkavetlkngi;atkavetlkngik;tkavetlkngikl;kavetlkn
gikle;avetlkngikleg;vetlkngiklegs;etlkngiklegsl;tlkngiklegslv;lkngikleg
slvg;kngiklegslvgg;ngiklegslvggk;giklegslvggkt;iklegslvggktt;klegslvggk
ttv;legslvggkttvk;egslvggkttvkl;gslvggkttvklt;slvggkttvklte;lvggkttvklt
eg;vggkttvkltegt;ggkttvkltegti;gkttvkltegtit;kttvkltegtitl;ttvkltegtitl
t;tvkltegtitltr;vkltegtitltre;kltegtitltrei;ltegtitltreie;tegtitltreieq
;egtitltreieqd;gtitltreieqdg;titltreieqdgk;itltreieqdgkv;tltreieqdgkvk;
ltreieqdgkvki;treieqdgkvkiy;reieqdgkvkiyl;eieqdgkvkiyln;ieqdgkvkiylnd;e
qdgkvkiylndt;qdgkvkiylndtt;dgkvkiylndtts;gkvkiylndttsg;kvkiylndttsgs;vk
iylndttsgst;kiylndttsgstk;iylndttsgstkk;ylndttsgstkkt;lndttsgstkkta;ndt
tsgstkktat;dttsgstkktatw;ttsgstkktatwn;tsgstkktatwne;sgstkktatwnet;gstk
ktatwnett;stkktatwnettn;tkktatwnettnt;kktatwnettntl;ktatwnettntlt;tatwn
ettntlti;atwnettntltis;twnettntltisa;wnettntltisad;nettntltisads;ettntl
tisadsk;ttntltisadskk;tntltisadskkt;ntltisadskktk;tltisadskktkd;ltisads
kktkdf;tisadskktkdfv;isadskktkdfvf;sadskktkdfvfl;adskktkdfvflt;dskktkdf
vfltd;skktkdfvfltdg;kktkdfvfltdgt;ktkdfvfltdgti;tkdfvfltdgtit;kdfvfltdg
titv;dfvfltdgtitvq;fvfltdgtitvqa;vfltdgtitvqay;fltdgtitvqayd;ltdgtitvqa
ydt;tdgtitvqaydta;dgtitvqaydtag;gtitvqaydtagt;titvqaydtagtk;itvqaydtagt
kl;tvqaydtagtkle;vqaydtagtkleg;qaydtagtklegn;aydtagtklegns;ydtagtklegns
s;dtagtklegnsse;tagtklegnssei;agtklegnsseik;gtklegnsseikd;tklegnsseikdl
;klegnsseikdla;legnsseikdlaa;egnsseikdlaal;gnsseikdlaalk;nsseikdlaalka;
sseikdlaalkaa;seikdlaalkaal;eikdlaalkaalk;

14 mers:
mkqyllvfalvlal;kqyllvfalvlali;qyllvfalvlalia;yllvfalvlaliac;llvfalvlali
acs;lvfalvlaliacsq;vfalvlaliacsqk;falvlaliacsqkg;alvlaliacsqkgt;lvlalia
csqkgte;vlaliacsqkgtep;laliacsqkgtepk;aliacsqkgtepks;liacsqkgtepkst;iac
sqkgtepksts;acsqkgtepkstsq;csqkgtepkstsqd;sqkgtepkstsqdh;qkgtepkstsqdhn
;kgtepkstsqdhnd;gtepkstsqdhndq;tepkstsqdhndqe;epkstsqdhndqei;pkstsqdhnd
qeii;kstsqdhndqeiin;stsqdhndqeiins;tsqdhndqeiinsd;sqdhndqeiinsdn;qdhndq
eiinsdnt;dhndqeiinsdntp;hndqeiinsdntpk;ndqeiinsdntpkd;dqeiinsdntpkds;qe
iinsdntpkdsk;eiinsdntpkdskk;iinsdntpkdskkd;insdntpkdskkdl;nsdntpkdskkdl
t;sdntpkdskkdltv;dntpkdskkdltvl;ntpkdskkdltvla;tpkdskkdltvlae;pkdskkdlt
vlaee;kdskkdltvlaeen;dskkdltvlaeens;skkdltvlaeensv;kkdltvlaeensvp;kdltv
laeensvpl;dltvlaeensvplf;ltvlaeensvplfn;tvlaeensvplfng;vlaeensvplfngn;l
aeensvplfngnk;aeensvplfngnki;eensvplfngnkif;ensvplfngnkifv;nsvplfngnkif
vs;svplfngnkifvsk;vplfngnkifvske;plfngnkifvskek;lfngnkifvskekn;fngnkifv
skekns;ngnkifvskeknsa;gnkifvskeknsag;nkifvskeknsagk;kifvskeknsagky;ifvs
keknsagkye;fvskeknsagkyel;vskeknsagkyelr;skeknsagkyelra;keknsagkyelrat;
eknsagkyelratv;knsagkyelratvd;nsagkyelratvdt;sagkyelratvdtv;agkyelratvd
tve;gkyelratvdtvel;kyelratvdtvelk;yelratvdtvelkg;elratvdtvelkgv;lratvdt
velkgvs;ratvdtvelkgvsd;atvdtvelkgvsdk;tvdtvelkgvsdkn;vdtvelkgvsdknn;dtv
elkgvsdknng;tvelkgvsdknngs;velkgvsdknngsg;elkgvsdknngsgk;lkgvsdknngsgkl
;kgvsdknngsgkle;gvsdknngsgkleg;vsdknngsgklegt;sdknngsgklegtk;dknngsgkle
gtka;knngsgklegtkad;nngsgklegtkadk;ngsgklegtkadkt;gsgklegtkadktk;sgkleg
tkadktkv;gklegtkadktkva;klegtkadktkvam;legtkadktkvamt;egtkadktkvamti;gt
kadktkvamtia;tkadktkvamtiad;kadktkvamtiadd;adktkvamtiaddl;dktkvamtiaddl

n;ktkvamtiaddlnt;tkvamtiaddlnti;kvamtiaddlntit;vamtiaddlntitv;amtiaddln
titve;mtiaddlntitvet;tiaddlntitvety;iaddlntitvetyd;addlntitvetyda;ddlnt
itvetydas;dlntitvetydasn;lntitvetydasnk;ntitvetydasnkk;titvetydasnkkt;i
tvetydasnkktg;tvetydasnkktgs;vetydasnkktgse;etydasnkktgsev;tydasnkktgse
vv;ydasnkktgsevvk;dasnkktgsevvkk;asnkktgsevvkkq;snkktgsevvkkqg;nkktgsev
vkkqgs;kktgsevvkkqgsv;ktgsevvkkqgsvi;tgsevvkkqgsvik;gsevvkkqgsvike;sevv
kkqgsvikes;evvkkqgsvikesy;vvkkqgsvikesyk;vkkqgsvikesyka;kkqgsvikesykan;
kqgsvikesykank;qgsvikesykankl;gsvikesykankld;svikesykanklds;vikesykankl
dsk;ikesykankldskk;kesykankldskki;esykankldskkit;sykankldskkitr;ykankld
skkitre;kankldskkitren;ankldskkitrene;nkldskkitrenet;kldskkitrenett;lds
kkitrenettl;dskkitrenettle;skkitrenettley;kkitrenettleys;kitrenettleyse
;itrenettleysem;trenettleysemt;renettleysemtd;enettleysemtds;nettleysem
tdss;ettleysemtdssn;ttleysemtdssna;tleysemtdssnat;leysemtdssnatk;eysemt
dssnatka;ysemtdssnatkav;semtdssnatkave;emtdssnatkavet;mtdssnatkavetl;td
ssnatkavetlk;dssnatkavetlkn;ssnatkavetlkng;snatkavetlkngi;natkavetlkngi
k;atkavetlkngikl;tkavetlkngikle;kavetlkngikleg;avetlkngiklegs;vetlkngik
legsl;etlkngiklegslv;tlkngiklegslvg;lkngiklegslvgg;kngiklegslvggk;ngikl
egslvggkt;giklegslvggktt;iklegslvggkttv;klegslvggkttvk;legslvggkttvkl;e
gslvggkttvklt;gslvggkttvklte;slvggkttvklteg;lvggkttvkltegt;vggkttvklteg
ti;ggkttvkltegtit;gkttvkltegtitl;kttvkltegtitlt;ttvkltegtitltr;tvkltegt
itltre;vkltegtitltrei;kltegtitltreie;ltegtitltreieq;tegtitltreieqd;egti
tltreieqdg;gtitltreieqdgk;titltreieqdgkv;itltreieqdgkvk;tltreieqdgkvki;
ltreieqdgkvkiy;treieqdgkvkiyl;reieqdgkvkiyln;eieqdgkvkiylnd;ieqdgkvkiyl
ndt;eqdgkvkiylndtt;qdgkvkiylndtts;dgkvkiylndttsg;gkvkiylndttsgs;kvkiyln
dttsgst;vkiylndttsgstk;kiylndttsgstkk;iylndttsgstkkt;ylndttsgstkkta;lnd
ttsgstkktat;ndttsgstkktatw;dttsgstkktatwn;ttsgstkktatwne;tsgstkktatwnet
;sgstkktatwnett;gstkktatwnettn;stkktatwnettnt;tkktatwnettntl;kktatwnett
ntlt;ktatwnettntlti;tatwnettntltis;atwnettntltisa;twnettntltisad;wnettn
tltisads;nettntltisadsk;ettntltisadskk;ttntltisadskkt;tntltisadskktk;nt
ltisadskktkd;tltisadskktkdf;ltisadskktkdfv;tisadskktkdfvf;isadskktkdfvf
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tdgti;ktkdfvfltdgtit;tkdfvfltdgtitv;kdfvfltdgtitvq;dfvfltdgtitvqa;fvflt
dgtitvqay;vfltdgtitvqayd;fltdgtitvqaydt;ltdgtitvqaydta;tdgtitvqaydtag;d
gtitvqaydtagt;gtitvqaydtagtk;titvqaydtagtkl;itvqaydtagtkle;tvqaydtagtkl
eg;vqaydtagtklegn;qaydtagtklegns;aydtagtklegnss;ydtagtklegnsse;dtagtkle
gnssei;tagtklegnsseik;agtklegnsseikd;gtklegnsseikdl;tklegnsseikdla;kleg
nsseikdlaa;legnsseikdlaal;egnsseikdlaalk;gnsseikdlaalka;nsseikdlaalkaa;
sseikdlaalkaal;seikdlaalkaalk;

15 mers:
mkqyllvfalvlali;kqyllvfalvlalia;qyllvfalvlaliac;yllvfalvlaliacs;llvfalv
laliacsq;lvfalvlaliacsqk;vfalvlaliacsqkg;falvlaliacsqkgt;alvlaliacsqkgt
e;lvlaliacsqkgtep;vlaliacsqkgtepk;laliacsqkgtepks;aliacsqkgtepkst;liacs
qkgtepksts;iacsqkgtepkstsq;acsqkgtepkstsqd;csqkgtepkstsqdh;sqkgtepkstsq
dhn;qkgtepkstsqdhnd;kgtepkstsqdhndq;gtepkstsqdhndqe;tepkstsqdhndqei;epk
stsqdhndqeii;pkstsqdhndqeiin;kstsqdhndqeiins;stsqdhndqeiinsd;tsqdhndqei
insdn;sqdhndqeiinsdnt;qdhndqeiinsdntp;dhndqeiinsdntpk;hndqeiinsdntpkd;n
dqeiinsdntpkds;dqeiinsdntpkdsk;qeiinsdntpkdskk;eiinsdntpkdskkd;iinsdntp
kdskkdl;insdntpkdskkdlt;nsdntpkdskkdltv;sdntpkdskkdltvl;dntpkdskkdltvla
;ntpkdskkdltvlae;tpkdskkdltvlaee;pkdskkdltvlaeen;kdskkdltvlaeens;dskkdl
tvlaeensv;skkdltvlaeensvp;kkdltvlaeensvpl;kdltvlaeensvplf;dltvlaeensvpl
fn;ltvlaeensvplfng;tvlaeensvplfngn;vlaeensvplfngnk;laeensvplfngnki;aeen
svplfngnkif;eensvplfngnkifv;ensvplfngnkifvs;nsvplfngnkifvsk;svplfngnkif
vske;vplfngnkifvskek;plfngnkifvskekn;lfngnkifvskekns;fngnkifvskeknsa;ng
nkifvskeknsag;gnkifvskeknsagk;nkifvskeknsagky;kifvskeknsagkye;ifvskekns
agkyel;fvskeknsagkyelr;vskeknsagkyelra;skeknsagkyelrat;keknsagkyelratv;
eknsagkyelratvd;knsagkyelratvdt;nsagkyelratvdtv;sagkyelratvdtve;agkyelr

atvdtvel;gkyelratvdtvelk;kyelratvdtvelkg;yelratvdtvelkgv;elratvdtvelkgv
s;lratvdtvelkgvsd;ratvdtvelkgvsdk;atvdtvelkgvsdkn;tvdtvelkgvsdknn;vdtve
lkgvsdknng;dtvelkgvsdknngs;tvelkgvsdknngsg;velkgvsdknngsgk;elkgvsdknngs
gkl;lkgvsdknngsgkle;kgvsdknngsgkleg;gvsdknngsgklegt;vsdknngsgklegtk;sdk
nngsgklegtka;dknngsgklegtkad;knngsgklegtkadk;nngsgklegtkadkt;ngsgklegtk
adktk;gsgklegtkadktkv;sgklegtkadktkva;gklegtkadktkvam;klegtkadktkvamt;l
egtkadktkvamti;egtkadktkvamtia;gtkadktkvamtiad;tkadktkvamtiadd;kadktkva
mtiaddl;adktkvamtiaddln;dktkvamtiaddlnt;ktkvamtiaddlnti;tkvamtiaddlntit
;kvamtiaddlntitv;vamtiaddlntitve;amtiaddlntitvet;mtiaddlntitvety;tiaddl
ntitvetyd;iaddlntitvetyda;addlntitvetydas;ddlntitvetydasn;dlntitvetydas
nk;lntitvetydasnkk;ntitvetydasnkkt;titvetydasnkktg;itvetydasnkktgs;tvet
ydasnkktgse;vetydasnkktgsev;etydasnkktgsevv;tydasnkktgsevvk;ydasnkktgse
vvkk;dasnkktgsevvkkq;asnkktgsevvkkqg;snkktgsevvkkqgs;nkktgsevvkkqgsv;kk
tgsevvkkqgsvi;ktgsevvkkqgsvik;tgsevvkkqgsvike;gsevvkkqgsvikes;sevvkkqgs
vikesy;evvkkqgsvikesyk;vvkkqgsvikesyka;vkkqgsvikesykan;kkqgsvikesykank;
kqgsvikesykankl;qgsvikesykankld;gsvikesykanklds;svikesykankldsk;vikesyk
ankldskk;ikesykankldskki;kesykankldskkit;esykankldskkitr;sykankldskkitr
e;ykankldskkitren;kankldskkitrene;ankldskkitrenet;nkldskkitrenett;kldsk
kitrenettl;ldskkitrenettle;dskkitrenettley;skkitrenettleys;kkitrenettle
yse;kitrenettleysem;itrenettleysemt;trenettleysemtd;renettleysemtds;ene
ttleysemtdss;nettleysemtdssn;ettleysemtdssna;ttleysemtdssnat;tleysemtds
snatk;leysemtdssnatka;eysemtdssnatkav;ysemtdssnatkave;semtdssnatkavet;e
mtdssnatkavetl;mtdssnatkavetlk;tdssnatkavetlkn;dssnatkavetlkng;ssnatkav
etlkngi;snatkavetlkngik;natkavetlkngikl;atkavetlkngikle;tkavetlkngikleg
;kavetlkngiklegs;avetlkngiklegsl;vetlkngiklegslv;etlkngiklegslvg;tlkngi
klegslvgg;lkngiklegslvggk;kngiklegslvggkt;ngiklegslvggktt;giklegslvggkt
tv;iklegslvggkttvk;klegslvggkttvkl;legslvggkttvklt;egslvggkttvklte;gslv
ggkttvklteg;slvggkttvkltegt;lvggkttvkltegti;vggkttvkltegtit;ggkttvklteg
titl;gkttvkltegtitlt;kttvkltegtitltr;ttvkltegtitltre;tvkltegtitltrei;vk
ltegtitltreie;kltegtitltreieq;ltegtitltreieqd;tegtitltreieqdg;egtitltre
ieqdgk;gtitltreieqdgkv;titltreieqdgkvk;itltreieqdgkvki;tltreieqdgkvkiy;
ltreieqdgkvkiyl;treieqdgkvkiyln;reieqdgkvkiylnd;eieqdgkvkiylndt;ieqdgkv
kiylndtt;eqdgkvkiylndtts;qdgkvkiylndttsg;dgkvkiylndttsgs;gkvkiylndttsgs
t;kvkiylndttsgstk;vkiylndttsgstkk;kiylndttsgstkkt;iylndttsgstkkta;ylndt
tsgstkktat;lndttsgstkktatw;ndttsgstkktatwn;dttsgstkktatwne;ttsgstkktatw
net;tsgstkktatwnett;sgstkktatwnettn;gstkktatwnettnt;stkktatwnettntl;tkk
tatwnettntlt;kktatwnettntlti;ktatwnettntltis;tatwnettntltisa;atwnettntl
tisad;twnettntltisads;wnettntltisadsk;nettntltisadskk;ettntltisadskkt;t
tntltisadskktk;tntltisadskktkd;ntltisadskktkdf;tltisadskktkdfv;ltisadsk
ktkdfvf;tisadskktkdfvfl;isadskktkdfvflt;sadskktkdfvfltd;adskktkdfvfltdg
;dskktkdfvfltdgt;skktkdfvfltdgti;kktkdfvfltdgtit;ktkdfvfltdgtitv;tkdfvf
ltdgtitvq;kdfvfltdgtitvqa;dfvfltdgtitvqay;fvfltdgtitvqayd;vfltdgtitvqay
dt;fltdgtitvqaydta;ltdgtitvqaydtag;tdgtitvqaydtagt;dgtitvqaydtagtk;gtit
vqaydtagtkl;titvqaydtagtkle;itvqaydtagtkleg;tvqaydtagtklegn;vqaydtagtkl
egns;qaydtagtklegnss;aydtagtklegnsse;ydtagtklegnssei;dtagtklegnsseik;ta
gtklegnsseikd;agtklegnsseikdl;gtklegnsseikdla;tklegnsseikdlaa;klegnssei
kdlaal;legnsseikdlaalk;egnsseikdlaalka;gnsseikdlaalkaa;nsseikdlaalkaal;
sseikdlaalkaalk;

16 mers:
mkqyllvfalvlalia;kqyllvfalvlaliac;qyllvfalvlaliacs;yllvfalvlaliacsq;llv
falvlaliacsqk;lvfalvlaliacsqkg;vfalvlaliacsqkgt;falvlaliacsqkgte;alvlal
iacsqkgtep;lvlaliacsqkgtepk;vlaliacsqkgtepks;laliacsqkgtepkst;aliacsqkg
tepksts;liacsqkgtepkstsq;iacsqkgtepkstsqd;acsqkgtepkstsqdh;csqkgtepksts
qdhn;sqkgtepkstsqdhnd;qkgtepkstsqdhndq;kgtepkstsqdhndqe;gtepkstsqdhndqe
i;tepkstsqdhndqeii;epkstsqdhndqeiin;pkstsqdhndqeiins;kstsqdhndqeiinsd;s
tsqdhndqeiinsdn;tsqdhndqeiinsdnt;sqdhndqeiinsdntp;qdhndqeiinsdntpk;dhnd

qeiinsdntpkd;hndqeiinsdntpkds;ndqeiinsdntpkdsk;dqeiinsdntpkdskk;qeiinsd
ntpkdskkd;eiinsdntpkdskkdl;iinsdntpkdskkdlt;insdntpkdskkdltv;nsdntpkdsk
kdltvl;sdntpkdskkdltvla;dntpkdskkdltvlae;ntpkdskkdltvlaee;tpkdskkdltvla
een;pkdskkdltvlaeens;kdskkdltvlaeensv;dskkdltvlaeensvp;skkdltvlaeensvpl
;kkdltvlaeensvplf;kdltvlaeensvplfn;dltvlaeensvplfng;ltvlaeensvplfngn;tv
laeensvplfngnk;vlaeensvplfngnki;laeensvplfngnkif;aeensvplfngnkifv;eensv
plfngnkifvs;ensvplfngnkifvsk;nsvplfngnkifvske;svplfngnkifvskek;vplfngnk
ifvskekn;plfngnkifvskekns;lfngnkifvskeknsa;fngnkifvskeknsag;ngnkifvskek
nsagk;gnkifvskeknsagky;nkifvskeknsagkye;kifvskeknsagkyel;ifvskeknsagkye
lr;fvskeknsagkyelra;vskeknsagkyelrat;skeknsagkyelratv;keknsagkyelratvd;
eknsagkyelratvdt;knsagkyelratvdtv;nsagkyelratvdtve;sagkyelratvdtvel;agk
yelratvdtvelk;gkyelratvdtvelkg;kyelratvdtvelkgv;yelratvdtvelkgvs;elratv
dtvelkgvsd;lratvdtvelkgvsdk;ratvdtvelkgvsdkn;atvdtvelkgvsdknn;tvdtvelkg
vsdknng;vdtvelkgvsdknngs;dtvelkgvsdknngsg;tvelkgvsdknngsgk;velkgvsdknng
sgkl;elkgvsdknngsgkle;lkgvsdknngsgkleg;kgvsdknngsgklegt;gvsdknngsgklegt
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ngsgklegtkadktk;ngsgklegtkadktkv;gsgklegtkadktkva;sgklegtkadktkvam;gkle
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vet;amtiaddlntitvety;mtiaddlntitvetyd;tiaddlntitvetyda;iaddlntitvetydas
;addlntitvetydasn;ddlntitvetydasnk;dlntitvetydasnkk;lntitvetydasnkkt;nt
itvetydasnkktg;titvetydasnkktgs;itvetydasnkktgse;tvetydasnkktgsev;vetyd
asnkktgsevv;etydasnkktgsevvk;tydasnkktgsevvkk;ydasnkktgsevvkkq;dasnkktg
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yk;evvkkqgsvikesyka;vvkkqgsvikesykan;vkkqgsvikesykank;kkqgsvikesykankl;
kqgsvikesykankld;qgsvikesykankld s;gsvikesykankldsk;svikesykankldskk;vik
esykankldskki;ikesykankldskkit;kesykankldskkitr;esykankldskkitre;sykank
ldskkitren;ykankldskkitrene;kankldskkitrenet;ankldskkitrenett;nkldskkit
renettl;kldskkitrenettle;ldskkitrenettley;dskkitrenettleys;skkitrenettl
eyse;kkitrenettleysem;kitrenettleysemt;itrenettleysemtd;trenettleysemtd
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tleysemtdssnatk;tleysemtdssnatka;leysemtdssnatkav;eysemtdssnatkave;ysem
tdssnatkavet;semtdssnatkavetl;emtdssnatkavetlk;mtdssnatkavetlkn;tdssnat
kavetlkng;dssnatkavetlkngi;ssnatkavetlkngik;snatkavetlkngikl;natkavetlk
ngikle;atkavetlkngikleg;tkavetlkngiklegs;kavetlkngiklegsl;avetlkngikleg
slv;vetlkngiklegslvg;etlkngiklegslvgg;tlkngiklegslvggk;lkngiklegslvggkt
;kngiklegslvggktt;ngiklegslvggkttv;giklegslvggkttvk;iklegslvggkttvkl;kl
egslvggkttvklt;legslvggkttvklte;egslvggkttvklteg;gslvggkttvkltegt;slvgg
kttvkltegti;lvggkttvkltegtit;vggkttvkltegtitl;ggkttvkltegtitlt;gkttvklt
egtitltr;kttvkltegtitltre;ttvkltegtitltrei;tvkltegtitltreie;vkltegtitlt
reieq;kltegtitltreieqd;ltegtitltreieqdg;tegtitltreieqdgk;egtitltreieqdg
kv;gtitltreieqdgkvk;titltreieqdgkvki;itltreieqdgkvkiy;tltreieqdgkvkiyl;
ltreieqdgkvkiyln;treieqdgkvkiylnd;reieqdgkvkiylndt;eieqdgkvkiylndtt;ieq
dgkvkiylndtts;eqdgkvkiylndttsg;qdgkvkiylndttsgs;dgkvkiylndttsgst;gkvkiy
lndttsgstk;kvkiylndttsgstkk;vkiylndttsgstkkt;kiylndttsgstkkta;iylndttsg
stkktat;ylndttsgstkktatw;lndttsgstkktatwn;ndttsgstkktatwne;dttsgstkktat
wnet;ttsgstkktatwnett;tsgstkktatwnettn;sgstkktatwnettnt;gstkktatwnettnt
l;stkktatwnettntlt;tkktatwnettntlti;kktatwnettntltis;ktatwnettntltisa;t
atwnettntltisad;atwnettntltisads;twnettntltisadsk;wnettntltisadskk;nett
ntltisadskkt;ettntltisadskktk;ttntltisadskktkd;tntltisadskktkdf;ntltisa
dskktkdfv;tltisadskktkdfvf;ltisadskktkdfvfl;tisadskktkdfvflt;isadskktkd
fvfltd;sadskktkdfvfltdg;adskktkdfvfltdgt;dskktkdfvfltdgti;skktkdfvfltdg
tit;kktkdfvfltdgtitv;ktkdfvfltdgtitvq;tkdfvfltdgtitvqa;kdfvfltdgtitvqay
;dfvfltdgtitvqayd;fvfltdgtitvqaydt;vfltdgtitvqaydta;fltdgtitvqaydtag;lt
dgtitvqaydtagt;tdgtitvqaydtagtk;dgtitvqaydtagtkl;gtitvqaydtagtkle;titvq

aydtagtkleg;itvqaydtagtklegn;tvqaydtagtklegns;vqaydtagtklegnss;qaydtagt
klegnsse;aydtagtklegnssei;ydtagtklegnsseik;dtagtklegnsseikd;tagtklegnss
eikdl;agtklegnsseikdla;gtklegnsseikdlaa;tklegnsseikdlaal;klegnsseikdlaa
lk;legnsseikdlaalka;egnsseikdlaalkaa;gnsseikdlaalkaal;nsseikdlaalkaalk;

<NP_045689 outer surface protein B;Protein;Borrelia burgdorferi B31>

8 mers:
mrlligfa;rlligfal;lligfala;ligfalal;igfalala;gfalalal;falalali;alalalig
;lalaligc;alaligca;laligcaq;aligcaqk;ligcaqkg;igcaqkga;gcaqkgae;caqkgae
s;aqkgaesi;qkgaesig;kgaesigs;gaesigsq;aesigsqk;esigsqke;sigsqken;igsqke
nd;gsqkendl;sqkendln;qkendlnl;kendlnle;endlnled;ndlnleds;dlnledss;lnled
ssk;nledsskk;ledsskks;edsskksh;dsskkshq;sskkshqn;skkshqna;kkshqnak;kshq
nakq;shqnakqd;hqnakqdl;qnakqdlp;nakqdlpa;akqdlpav;kqdlpavt;qdlpavte;dlp
avted;lpavteds;pavtedsv;avtedsvs;vtedsvsl;tedsvslf;edsvslfn;dsvslfng;sv
slfngn;vslfngnk;slfngnki;lfngnkif;fngnkifv;ngnkifvs;gnkifvsk;nkifvske;k
ifvskek;ifvskekn;fvskekns;vskeknss;skeknssg;keknssgk;eknssgky;knssgkyd;
nssgkydl;ssgkydlr;sgkydlra;gkydlrat;kydlrati;ydlratid;dlratidq;lratidqv
;ratidqve;atidqvel;tidqvelk;idqvelkg;dqvelkgt;qvelkgts;velkgtsd;elkgtsd
k;lkgtsdkn;kgtsdknn;gtsdknng;tsdknngs;sdknngsg;dknngsgt;knngsgtl;nngsgt
le;ngsgtleg;gsgtlegs;sgtlegsk;gtlegskp;tlegskpd;legskpdk;egskpdks;gskpd
ksk;skpdkskv;kpdkskvk;pdkskvkl;dkskvklt;kskvkltv;skvkltvs;kvkltvsa;vklt
vsad;kltvsadl;ltvsadln;tvsadlnt;vsadlntv;sadlntvt;adlntvtl;dlntvtle;lnt
vtlea;ntvtleaf;tvtleafd;vtleafda;tleafdas;leafdasn;eafdasnq;afdasnqk;fd
asnqki;dasnqkis;asnqkiss;snqkissk;nqkisskv;qkisskvt;kisskvtk;isskvtkk;s
skvtkkq;skvtkkqg;kvtkkqgs;vtkkqgsi;tkkqgsit;kkqgsitx;kqgsitxe;qgsitxet;
gsitxetl;sitxetlk;itxetlka;txetlkan;xetlkank;etlkankl;tlkankld;lkankds
;kankldsk;ankldskk;nkldskkl;kldskklt;ldskkltr;dskkltrs;skkltrsn;kkltrsn
g;kltrsngt;ltrsngtt;trsngttl;rsngttle;sngttley;ngttleys;gttleysq;ttleys
qi;tleysqit;leysqitd;eysqitda;ysqitdad;sqitdadn;qitdadna;itdadnat;tdadn
atk;dadnatka;adnatkav;dnatkave;natkavet;atkavetl;tkavetlk;kavetlkn;avet
lkns;vetlknsi;etlknsik;tlknsikl;lknsikle;knsikleg;nsiklegs;siklegsl;ikl
egslv;klegslvg;legslvgg;egslvggk;gslvggkt;slvggktt;lvggkttv;vggkttve;gg
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egtvtlk;egtvtlkr;gtvtlkre;tvtlkrei;vtlkreie;tlkreiek;lkreiekd;kreiekdg;
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;vkvflndt;kvflndta;vflndtag;flndtags;lndtagsn;ndtagsnk;dtagsnkk;tagsnkk
t;agsnkktg;gsnkktgk;snkktgkw;nkktgkwe;kktgkwed;ktgkweds;tgkwedst;gkweds
ts;kwedstst;wedststl;edststlt;dststlti;ststltis;tstltisa;stltisad;tltis
ads;ltisadsk;tisadskk;isadskkt;sadskktk;adskktkd;dskktkdl;skktkdlv;kktk
dlvf;ktkdlvfl;tkdlvflt;kdlvfltd;dlvfltdg;lvfltdgt;vfltdgti;fltdgtit;ltd
gtitv;tdgtitvq;dgtitvqq;gtitvqqy;titvqqyn;itvqqynt;tvqqynta;vqqyntag;qq
yntagt;qyntagts;yntagtsl;ntagtsle;tagtsleg;agtslegs;gtslegsa;tslegsas;s
legsase;legsasei;egsaseik;gsaseikn;saseiknl;aseiknls;seiknlse;eiknlsel;
iknlselk;knlselkn;nlselkna;lselknal;selknalk;

9 mers:
mrlligfal;rlligfala;lligfalal;ligfalala;igfalalal;gfalalali;falalalig;a
lalaligc;lalaligca;alaligcaq;laligcaqk;aligcaqkg;ligcaqkga;igcaqkgae;gc
aqkgaes;caqkgaesi;aqkgaesig;qkgaesigs;kgaesigsq;gaesigsqk;aesigsqke;esi
gsqken;sigsqkend;igsqkendl;gsqkendln;sqkendlnl;qkendlnle;kendlnled;endl
nleds;ndlnledss;dlnledssk;lnledsskk;nledsskks;ledsskksh;edsskkshq;dsskk
shqn;sskkshqna;skkshqnak;kkshqnakq;kshqnakqd;shqnakqdl;hqnakqdlp;qnakqd
lpa;nakqdlpav;akqdlpavt;kqdlpavte;qdlpavted;dlpavteds;lpavtedsv;pavteds
vs;avtedsvsl;vtedsvslf;tedsvslfn;edsvslfng;dsvslfngn;svslfngnk;vslfngnk

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;ifvskekns;fvskeknss;vskeknssg;skeknssgk;keknssgky;eknssgkyd;knssgkydl;
nssgkydlr;ssgkydlra;sgkydlrat;gkydlrati;kydlratid;ydlratidq;dlratidqv;l
ratidqve;ratidqvel;atidqvelk;tidqvelkg;idqvelkgt;dqvelkgts;qvelkgtsd;ve
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da;vtleafdas;tleafdasn;leafdasnq;eafdasnqk;afdasnqki;fdasnqkis;dasnqkis
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kltrsng;kkltrsngt;kltrsngtt;ltrsngttl;trsngttle;rsngttley;sngttleys;ngt
tleysq;gttleysqi;ttleysqit;tleysqitd;leysqitda;eysqitdad;ysqitdadn;sqit
dadna;qitdadnat;itdadnatk;tdadnatka;dadnatkav;adnatkave;dnatkavet;natka
vetl;atkavetlk;tkavetlkn;kavetlkns;avetlknsi;vetlknsik;etlknsikl;tlknsi
kle;lknsikleg;knsiklegs;nsiklegsl;siklegslv;iklegslvg;klegslvgg;legslvg
gk;egslvggkt;gslvggktt;slvggkttv;lvggkttve;vggkttvei;ggkttveik;gkttveik
e;kttveikeg;ttveikegt;tveikegtv;veikegtvt;eikegtvtl;ikegtvtlk;kegtvtlkr
;egtvtlkre;gtvtlkrei;tvtlkreie;vtlkreiek;tlkreiekd;lkreiekdg;kreiekdgk;
reiekdgkv;eiekdgkvk;iekdgkvkv;ekdgkvkvf;kdgkvkvfl;dgkvkvfln;gkvkvflnd;k
vkvflndt;vkvflndta;kvflndtag;vflndtags;flndtagsn;lndtagsnk;ndtagsnkk;dt
agsnkkt;tagsnkktg;agsnkktgk;gsnkktgkw;snkktgkwe;nkktgkwed;kktgkweds;ktg
kwedst;tgkwedsts;gkwedstst;kwedststl;wedststlt;edststlti;dststltis;stst
ltisa;tstltisad;stltisads;tltisadsk;ltisadskk;tisadskkt;isadskktk;sadsk
ktkd;adskktkdl;dskktkdlv;skktkdlvf;kktkdlvfl;ktkdlvflt;tkdlvfltd;kdlvfl
tdg;dlvfltdgt;lvfltdgti;vfltdgtit;fltdgtitv;ltdgtitvq;tdgtitvqq;dgtitvq
qy;gtitvqqyn;titvqqynt;itvqqynta;tvqqyntag;vqqyntagt;qqyntagts;qyntagts
l;yntagtsle;ntagtsleg;tagtslegs;agtslegsa;gtslegsas;tslegsase;slegsasei
;legsaseik;egsaseikn;gsaseiknl;saseiknls;aseiknlse;seiknlsel;eiknlselk;
iknlselkn;knlselkna;nlselknal;lselknalk;

10 mers:
mrlligfala;rlligfalal;lligfalala;ligfalalal;igfalalali;gfalalalig;falal
aligc;alalaligca;lalaligcaq;alaligcaqk;laligcaqkg;aligcaqkga;ligcaqkgae
;igcaqkgaes;gcaqkgaesi;caqkgaesig;aqkgaesigs;qkgaesigsq;kgaesigsqk;gaes
igsqke;aesigsqken;esigsqkend;sigsqkendl;igsqkendln;gsqkendlnl;sqkendlnl
e;qkendlnled;kendlnleds;endlnledss;ndlnledssk;dlnledsskk;lnledsskks;nle
dsskksh;ledsskkshq;edsskkshqn;dsskkshqna;sskkshqnak;skkshqnakq;kkshqnak
qd;kshqnakqdl;shqnakqdlp;hqnakqdlpa;qnakqdlpav;nakqdlpavt;akqdlpavte;kq
dlpavted;qdlpavteds;dlpavtedsv;lpavtedsvs;pavtedsvsl;avtedsvslf;vtedsvs
lfn;tedsvslfng;edsvslfngn;dsvslfngnk;svslfngnki;vslfngnkif;slfngnkifv;l
fngnkifvs;fngnkifvsk;ngnkifvske;gnkifvskek;nkifvskekn;kifvskekns;ifvske
knss;fvskeknssg;vskeknssgk;skeknssgky;keknssgkyd;eknssgkydl;knssgkydlr;
nssgkydlra;ssgkydlrat;sgkydlrati;gkydlratid;kydlratidq;ydlratidqv;dlrat
idqve;lratidqvel;ratidqvelk;atidqvelkg;tidqvelkgt;idqvelkgts;dqvelkgtsd
;qvelkgtsdk;velkgtsdkn;elkgtsdknn;lkgtsdknng;kgtsdknngs;gtsdknngsg;tsdk
nngsgt;sdknngsgtl;dknngsgtle;knngsgtleg;nngsgtlegs;ngsgtlegsk;gsgtlegsk
p;sgtlegskpd;gtlegskpdk;tlegskpdks;legskpdksk;egskpdkskv;gskpdkskvk;skp
dkskvkl;kpdkskvklt;pdkskvkltv;dkskvkltvs;kskvkltvsa;skvkltvsad;kvkltvsa
dl;vkltvsadln;kltvsadlnt;ltvsadlntv;tvsadlntvt;vsadlntvtl;sadlntvtle;ad
lntvtlea;dlntvtleaf;lntvtleafd;ntvtleafda;tvtleafdas;vtleafdasn;tleafda
snq;leafdasnqk;eafdasnqki;afdasnqkis;fdasnqkiss;dasnqkissk;asnqkisskv;s
nqkisskvt;nqkisskvtk;qkisskvtkk;kisskvtkkq;isskvtkkqg;sskvtkkqgs;skvtkk
qgsi;kvtkkqgsit;vtkkqgsitx;tkkqgsitxe;kkqgsitxet;kqgsitxetl;qgsitxetlk;

gsitxetlka;sitxetlkan;itxetlkank;txetlkankl;xetlkankld;etlkanklds;tlkan
kldsk;lkankldskk;kankldskkl;ankldskklt;nkldskkltr;kldskkltrs;ldskkltrsn
;dskkltrsng;skkltrsngt;kkltrsngtt;kltrsngttl;ltrsngttle;trsngttley;rsng
ttleys;sngttleysq;ngttleysqi;gttleysqit;ttleysqitd;tleysqitda;leysqitda
d;eysqitdadn;ysqitdadna;sqitdadnat;qitdadnatk;itdadnatka;tdadnatkav;dad
natkave;adnatkavet;dnatkavetl;natkavetlk;atkavetlkn;tkavetlkns;kavetlkn
si;avetlknsik;vetlknsikl;etlknsikle;tlknsikleg;lknsiklegs;knsiklegsl;ns
iklegslv;siklegslvg;iklegslvgg;klegslvggk;legslvggkt;egslvggktt;gslvggk
ttv;slvggkttve;lvggkttvei;vggkttveik;ggkttveike;gkttveikeg;kttveikegt;t
tveikegtv;tveikegtvt;veikegtvtl;eikegtvtlk;ikegtvtlkr;kegtvtlkre;egtvtl
krei;gtvtlkreie;tvtlkreiek;vtlkreiekd;tlkreiekdg;lkreiekdgk;kreiekdgkv;
reiekdgkvk;eiekdgkvkv;iekdgkvkvf;ekdgkvkvfl;kdgkvkvfln;dgkvkvflnd;gkvkv
flndt;kvkvflndta;vkvflndtag;kvflndtags;vflndtagsn;flndtagsnk;lndtagsnkk
;ndtagsnkkt;dtagsnkktg;tagsnkktgk;agsnkktgkw;gsnkktgkwe;snkktgkwed;nkkt
gkweds;kktgkwedst;ktgkwedsts;tgkwedstst;gkwedststl;kwedststlt;wedststlt
i;edststltis;dststltisa;ststltisad;tstltisads;stltisadsk;tltisadskk;lti
sadskkt;tisadskktk;isadskktkd;sadskktkdl;adskktkdlv;dskktkdlvf;skktkdlv
fl;kktkdlvflt;ktkdlvfltd;tkdlvfltdg;kdlvfltdgt;dlvfltdgti;lvfltdgtit;vf
ltdgtitv;fltdgtitvq;ltdgtitvqq;tdgtitvqqy;dgtitvqqyn;gtitvqqynt;titvqqy
nta;itvqqyntag;tvqqyntagt;vqqyntagts;qqyntagtsl;qyntagtsle;yntagtsleg;n
tagtslegs;tagtslegsa;agtslegsas;gtslegsase;tslegsasei;slegsaseik;legsas
eikn;egsaseiknl;gsaseiknls;saseiknlse;aseiknlsel;seiknlselk;eiknlselkn;
iknlselkna;knlselknal;nlselknalk;

11 mers:
mrlligfalal;rlligfalala;lligfalalal;ligfalalali;igfalalalig;gfalalaligc
;falalaligca;alalaligcaq;lalaligcaqk;alaligcaqkg;laligcaqkga;aligcaqkga
e;ligcaqkgaes;igcaqkgaesi;gcaqkgaesig;caqkgaesigs;aqkgaesigsq;qkgaesigs
qk;kgaesigsqke;gaesigsqken;aesigsqkend;esigsqkendl;sigsqkendln;igsqkend
lnl;gsqkendlnle;sqkendlnled;qkendlnleds;kendlnledss;endlnledssk;ndlnled
sskk;dlnledsskks;lnledsskksh;nledsskkshq;ledsskkshqn;edsskkshqna;dsskks
hqnak;sskkshqnakq;skkshqnakqd;kkshqnakqdl;kshqnakqdlp;shqnakqdlpa;hqnak
qdlpav;qnakqdlpavt;nakqdlpavte;akqdlpavted;kqdlpavteds;qdlpavtedsv;dlpa
vtedsvs;lpavtedsvsl;pavtedsvslf;avtedsvslfn;vtedsvslfng;tedsvslfngn;eds
vslfngnk;dsvslfngnki;svslfngnkif;vslfngnkifv;slfngnkifvs;lfngnkifvsk;fn
gnkifvske;ngnkifvskek;gnkifvskekn;nkifvskekns;kifvskeknss;ifvskeknssg;f
vskeknssgk;vskeknssgky;skeknssgkyd;keknssgkydl;eknssgkydlr;knssgkydlra;
nssgkydlrat;ssgkydlrati;sgkydlratid;gkydlratidq;kydlratidqv;ydlratidqve
;dlratidqvel;lratidqvelk;ratidqvelkg;atidqvelkgt;tidqvelkgts;idqvelkgts
d;dqvelkgtsdk;qvelkgtsdkn;velkgtsdknn;elkgtsdknng;lkgtsdknngs;kgtsdknng
sg;gtsdknngsgt;tsdknngsgtl;sdknngsgtle;dknngsgtleg;knngsgtlegs;nngsgtle
gsk;ngsgtlegskp;gsgtlegskpd;sgtlegskpdk;gtlegskpdks;tlegskpdksk;legskpd
kskv;egskpdkskvk;gskpdkskvkl;skpdkskvklt;kpdkskvkltv;pdkskvkltvs;dkskvk
ltvsa;kskvkltvsad;skvkltvsadl;kvkltvsadln;vkltvsadlnt;kltvsadlntv;ltvsa
dlntvt;tvsadlntvtl;vsadlntvtle;sadlntvtlea;adlntvtleaf;dlntvtleafd;lntv
tleafda;ntvtleafdas;tvtleafdasn;vtleafdasnq;tleafdasnqk;leafdasnqki;eaf
dasnqkis;afdasnqkiss;fdasnqkissk;dasnqkisskv;asnqkisskvt;snqkisskvtk;nq
kisskvtkk;qkisskvtkkq;kisskvtkkqg;isskvtkkqgs;sskvtkkqgsi;skvtkkqgsit;k
vtkkqgsitx;vtkkqgsitxe;tkkqgsitxet;kkqgsitxetl;kqgsitxetlk;qgsitxetlka;
gsitxetlkan;sitxetlkank;itxetlkankl;txetlkankld;xetlkanklds;etlkankldsk
;tlkankldskk;lkankldskkl;kankldskklt;ankldskkltr;nkldskkltrs;kldskkltrs
n;ldskkltrsng;dskkltrsngt;skkltrsngtt;kkltrsngttl;kltrsngttle;ltrsngttl
ey;trsngttleys;rsngttleysq;sngttleysqi;ngttleysqit;gttleysqitd;ttleysqi
tda;tleysqitdad;leysqitdadn;eysqitdadna;ysqitdadnat;sqitdadnatk;qitdadn
atka;itdadnatkav;tdadnatkave;dadnatkavet;adnatkavetl;dnatkavetlk;natkav
etlkn;atkavetlkns;tkavetlknsi;kavetlknsik;avetlknsikl;vetlknsikle;etlkn
sikleg;tlknsiklegs;lknsiklegsl;knsiklegslv;nsiklegslvg;siklegslvgg;ikle

gslvggk;klegslvggkt;legslvggktt;egslvggkttv;gslvggkttve;slvggkttvei;lvg
gkttveik;vggkttveike;ggkttveikeg;gkttveikegt;kttveikegtv;ttveikegtvt;tv
eikegtvtl;veikegtvtlk;eikegtvtlkr;ikegtvtlkre;kegtvtlkrei;egtvtlkreie;g
tvtlkreiek;tvtlkreiekd;vtlkreiekdg;tlkreiekdgk;lkreiekdgkv;kreiekdgkvk;
reiekdgkvkv;eiekdgkvkvf;iekdgkvkvfl;ekdgkvkvfln;kdgkvkvflnd;dgkvkvflndt
;gkvkvflndta;kvkvflndtag;vkvflndtags;kvflndtagsn;vflndtagsnk;flndtagsnk
k;lndtagsnkkt;ndtagsnkktg;dtagsnkktgk;tagsnkktgkw;agsnkktgkwe;gsnkktgkw
ed;snkktgkweds;nkktgkwedst;kktgkwedsts;ktgkwedstst;tgkwedststl;gkwedsts
tlt;kwedststlti;wedststltis;edststltisa;dststltisad;ststltisads;tstltis
adsk;stltisadskk;tltisadskkt;ltisadskktk;tisadskktkd;isadskktkdl;sadskk
tkdlv;adskktkdlvf;dskktkdlvfl;skktkdlvflt;kktkdlvfltd;ktkdlvfltdg;tkdlv
fltdgt;kdlvfltdgti;dlvfltdgtit;lvfltdgtitv;vfltdgtitvq;fltdgtitvqq;ltdg
titvqqy;tdgtitvqqyn;dgtitvqqynt;gtitvqqynta;titvqqyntag;itvqqyntagt;tvq
qyntagts;vqqyntagtsl;qqyntagtsle;qyntagtsleg;yntagtslegs;ntagtslegsa;ta
gtslegsas;agtslegsase;gtslegsasei;tslegsaseik;slegsaseikn;legsaseiknl;e
gsaseiknls;gsaseiknlse;saseiknlsel;aseiknlselk;seiknlselkn;eiknlselkna;
iknlselknal;knlselknalk;

13 mers:
mrlligfalalal;rlligfalalali;lligfalalalig;ligfalalaligc;igfalalaligca;g
falalaligcaq;falalaligcaqk;alalaligcaqkg;lalaligcaqkga;alaligcaqkgae;la
ligcaqkgaes;aligcaqkgaesi;ligcaqkgaesig;igcaqkgaesigs;gcaqkgaesigsq;caq
kgaesigsqk;aqkgaesigsqke;qkgaesigsqken;kgaesigsqkend;gaesigsqkendl;aesi
gsqkendln;esigsqkendlnl;sigsqkendlnle;igsqkendlnled;gsqkendlnleds;sqken
dlnledss;qkendlnledssk;kendlnledsskk;endlnledsskks;ndlnledsskksh;dlnled
sskkshq;lnledsskkshqn;nledsskkshqna;ledsskkshqnak;edsskkshqnakq;dsskksh
qnakqd;sskkshqnakqdl;skkshqnakqdlp;kkshqnakqdlpa;kshqnakqdlpav;shqnakqd
lpavt;hqnakqdlpavte;qnakqdlpavted;nakqdlpavteds;akqdlpavtedsv;kqdlpavte
dsvs;qdlpavtedsvsl;dlpavtedsvslf;lpavtedsvslfn;pavtedsvslfng;avtedsvslf
ngn;vtedsvslfngnk;tedsvslfngnki;edsvslfngnkif;dsvslfngnkifv;svslfngnkif
vs;vslfngnkifvsk;slfngnkifvske;lfngnkifvskek;fngnkifvskekn;ngnkifvskekn
s;gnkifvskeknss;nkifvskeknssg;kifvskeknssgk;ifvskeknssgky;fvskeknssgkyd
;vskeknssgkydl;skeknssgkydlr;keknssgkydlra;eknssgkydlrat;knssgkydlrati;
nssgkydlratid;ssgkydlratidq;sgkydlratidqv;gkydlratidqve;kydlratidqvel;y
dlratidqvelk;dlratidqvelkg;lratidqvelkgt;ratidqvelkgts;atidqvelkgtsd;ti
dqvelkgtsdk;idqvelkgtsdkn;dqvelkgtsdknn;qvelkgtsdknng;velkgtsdknngs;elk
gtsdknngsg;lkgtsdknngsgt;kgtsdknngsgtl;gtsdknngsgtle;tsdknngsgtleg;sdkn
ngsgtlegs;dknngsgtlegsk;knngsgtlegskp;nngsgtlegskpd;ngsgtlegskpdk;gsgtl
egskpdks;sgtlegskpdksk;gtlegskpdkskv;tlegskpdkskvk;legskpdkskvkl;egskpd
kskvklt;gskpdkskvkltv;skpdkskvkltvs;kpdkskvkltvsa;pdkskvkltvsad;dkskvkl
tvsadl;kskvkltvsadln;skvkltvsadlnt;kvkltvsadlntv;vkltvsadlntvt;kltvsadl
ntvtl;ltvsadlntvtle;tvsadlntvtlea;vsadlntvtleaf;sadlntvtleafd;adlntvtle
afda;dlntvtleafdas;lntvtleafdasn;ntvtleafdasnq;tvtleafdasnqk;vtleafdasn
qki;tleafdasnqkis;leafdasnqkiss;eafdasnqkissk;afdasnqkisskv;fdasnqkissk
vt;dasnqkisskvtk;asnqkisskvtkk;snqkisskvtkkq;nqkisskvtkkqg;qkisskvtkkqg
s;kisskvtkkqgsi;isskvtkkqgsit;sskvtkkqgsitx;skvtkkqgsitxe;kvtkkqgsitxet
;vtkkqgsitxetl;tkkqgsitxetlk;kkqgsitxetlka;kqgsitxetlkan;qgsitxetlkank;
gsitxetlkankl;sitxetlkankld;itxetlkanklds;txetlkankldsk;xetlkankldskk;e
tlkankldskkl;tlkankldskklt;lkankldskkltr;kankldskkltrs;ankldskkltrsn;nk
ldskkltrsng;kldskkltrsngt;ldskkltrsngtt;dskkltrsngttl;skkltrsngttle;kkl
trsngttley;kltrsngttleys;ltrsngttleysq;trsngttleysqi;rsngttleysqit;sngt
tleysqitd;ngttleysqitda;gttleysqitdad;ttleysqitdadn;tleysqitdadna;leysq
itdadnat;eysqitdadnatk;ysqitdadnatka;sqitdadnatkav;qitdadnatkave;itdadn
atkavet;tdadnatkavetl;dadnatkavetlk;adnatkavetlkn;dnatkavetlkns;natkave
tlknsi;atkavetlknsik;tkavetlknsikl;kavetlknsikle;avetlknsikleg;vetlknsi
klegs;etlknsiklegsl;tlknsiklegslv;lknsiklegslvg;knsiklegslvgg;nsiklegsl
vggk;siklegslvggkt;iklegslvggktt;klegslvggkttv;legslvggkttve;egslvggktt

vei;gslvggkttveik;slvggkttveike;lvggkttveikeg;vggkttveikegt;ggkttveikeg
tv;gkttveikegtvt;kttveikegtvtl;ttveikegtvtlk;tveikegtvtlkr;veikegtvtlkr
e;eikegtvtlkrei;ikegtvtlkreie;kegtvtlkreiek;egtvtlkreiekd;gtvtlkreiekdg
;tvtlkreiekdgk;vtlkreiekdgkv;tlkreiekdgkvk;lkreiekdgkvkv;kreiekdgkvkvf;
reiekdgkvkvfl;eiekdgkvkvfln;iekdgkvkvflnd;ekdgkvkvflndt;kdgkvkvflndta;d
gkvkvflndtag;gkvkvflndtags;kvkvflndtagsn;vkvflndtagsnk;kvflndtagsnkk;vf
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snkktgkwed;agsnkktgkweds;gsnkktgkwedst;snkktgkwedsts;nkktgkwedstst;kktg
kwedststl;ktgkwedststlt;tgkwedststlti;gkwedststltis;kwedststltisa;wedst
stltisad;edststltisads;dststltisadsk;ststltisadskk;tstltisadskkt;stltis
adskktk;tltisadskktkd;ltisadskktkdl;tisadskktkdlv;isadskktkdlvf;sadskkt
kdlvfl;adskktkdlvflt;dskktkdlvfltd;skktkdlvfltdg;kktkdlvfltdgt;ktkdlvfl
tdgti;tkdlvfltdgtit;kdlvfltdgtitv;dlvfltdgtitvq;lvfltdgtitvqq;vfltdgtit
vqqy;fltdgtitvqqyn;ltdgtitvqqynt;tdgtitvqqynta;dgtitvqqyntag;gtitvqqynt
agt;titvqqyntagts;itvqqyntagtsl;tvqqyntagtsle;vqqyntagtsleg;qqyntagtsle
gs;qyntagtslegsa;yntagtslegsas;ntagtslegsase;tagtslegsasei;agtslegsasei
k;gtslegsaseikn;tslegsaseiknl;slegsaseiknls;legsaseiknlse;egsaseiknlsel
;gsaseiknlselk;saseiknlselkn;aseiknlselkna;seiknlselknal;eiknlselknalk;

14 mers:
mrlligfalalali;rlligfalalalig;lligfalalaligc;ligfalalaligca;igfalalalig
caq;gfalalaligcaqk;falalaligcaqkg;alalaligcaqkga;lalaligcaqkgae;alaligc
aqkgaes;laligcaqkgaesi;aligcaqkgaesig;ligcaqkgaesigs;igcaqkgaesigsq;gca
qkgaesigsqk;caqkgaesigsqke;aqkgaesigsqken;qkgaesigsqkend;kgaesigsqkendl
;gaesigsqkendln;aesigsqkendlnl;esigsqkendlnle;sigsqkendlnled;igsqkendln
leds;gsqkendlnledss;sqkendlnledssk;qkendlnledsskk;kendlnledsskks;endlnl
edsskksh;ndlnledsskkshq;dlnledsskkshqn;lnledsskkshqna;nledsskkshqnak;le
dsskkshqnakq;edsskkshqnakqd;dsskkshqnakqdl;sskkshqnakqdlp;skkshqnakqdlp
a;kkshqnakqdlpav;kshqnakqdlpavt;shqnakqdlpavte;hqnakqdlpavted;qnakqdlpa
vteds;nakqdlpavtedsv;akqdlpavtedsvs;kqdlpavtedsvsl;qdlpavtedsvslf;dlpav
tedsvslfn;lpavtedsvslfng;pavtedsvslfngn;avtedsvslfngnk;vtedsvslfngnki;t
edsvslfngnkif;edsvslfngnkifv;dsvslfngnkifvs;svslfngnkifvsk;vslfngnkifvs
ke;slfngnkifvskek;lfngnkifvskekn;fngnkifvskekns;ngnkifvskeknss;gnkifvsk
eknssg;nkifvskeknssgk;kifvskeknssgky;ifvskeknssgkyd;fvskeknssgkydl;vske
knssgkydlr;skeknssgkydlra;keknssgkydlrat;eknssgkydlrati;knssgkydlratid;
nssgkydlratidq;ssgkydlratidqv;sgkydlratidqve;gkydlratidqvel;kydlratidqv
elk;ydlratidqvelkg;dlratidqvelkgt;lratidqvelkgts;ratidqvelkgtsd;atidqve
lkgtsdk;tidqvelkgtsdkn;idqvelkgtsdknn;dqvelkgtsdknng;qvelkgtsdknngs;vel
kgtsdknngsg;elkgtsdknngsgt;lkgtsdknngsgtl;kgtsdknngsgtle;gtsdknngsgtleg
;tsdknngsgtlegs;sdknngsgtlegsk;dknngsgtlegskp;knngsgtlegskpd;nngsgtlegs
kpdk;ngsgtlegskpdks;gsgtlegskpdksk;sgtlegskpdkskv;gtlegskpdkskvk;tlegsk
pdkskvkl;legskpdkskvklt;egskpdkskvkltv;gskpdkskvkltvs;skpdkskvkltvsa;kp
dkskvkltvsad;pdkskvkltvsadl;dkskvkltvsadln;kskvkltvsadlnt;skvkltvsadlnt
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as;yntagtslegsase;ntagtslegsasei;tagtslegsaseik;agtslegsaseikn;gtslegsa
seiknl;tslegsaseiknls;slegsaseiknlse;legsaseiknlsel;egsaseiknlselk;gsas
eiknlselkn;saseiknlselkna;aseiknlselknal;seiknlselknalk;

15 mers:
mrlligfalalalig;rlligfalalaligc;lligfalalaligca;ligfalalaligcaq;igfalal
aligcaqk;gfalalaligcaqkg;falalaligcaqkga;alalaligcaqkgae;lalaligcaqkgae
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flndtags;dgkvkvflndtagsn;gkvkvflndtagsnk;kvkvflndtagsnkk;vkvflndtagsnkk
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adskk;dststltisadskkt;ststltisadskktk;tstltisadskktkd;stltisadskktkdl;t
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16 mers:
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gsaseikn;tagtslegsaseiknl;agtslegsaseiknls;gtslegsaseiknlse;tslegsaseik
nlsel;slegsaseiknlselk;legsaseiknlselkn;egsaseiknlselkna;gsaseiknlselkn
al;saseiknlselknalk;

<AAN87995 Outer Surface Protein C;Protein;Borrelia garinii>

8 mers:
ilmtlflf;lmtlflfi;mtlflfis;tlflfisc;lflfiscn;flfiscnn;lfiscnns;fiscnnsg
;iscnnsgg;scnnsggd;cnnsggdt;nnsggdta;nsggdtas;sggdtast;ggdtastn;gdtastn
p;dtastnpd;tastnpde;astnpdes;stnpdesa;tnpdesak;npdesakg;pdesakgp;desakg
pn;esakgpnl;sakgpnlt;akgpnltv;kgpnltvi;gpnltvis;pnltvisk;nltviskk;ltvis
kki;tviskkit;viskkitd;iskkitds;skkitdsn;kkitdsna;kitdsnaf;itdsnafv;tdsn
afvl;dsnafvla;snafvlav;nafvlavk;afvlavke;fvlavkev;vlavkeve;lavkevea;avk
eveal;vkeveali;kevealis;evealiss;vealissi;ealissid;alisside;lissidel;is

sidela;ssidelan;sidelank;idelanka;delankai;elankaig;lankaigk;ankaigkv;n
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hqnnglna;qnnglnan;nnglnana;nglnanag;glnanagq;lnanagqn;nanagqng;anagqngs
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qea;akaaqeal;kaaqeala;aaqealan;aqealans;qealansv;ealansvk;alansvke;lans
vkel;ansvkelt;nsvkeltn;svkeltnp;vkeltnpv;keltnpvv;eltnpvva;ltnpvvae;tnp
vvaes;npvvaesp;pvvaespk;

9 mers:
ilmtlflfi;lmtlflfis;mtlflfisc;tlflfiscn;lflfiscnn;flfiscnns;lfiscnnsg;f
iscnnsgg;iscnnsggd;scnnsggdt;cnnsggdta;nnsggdtas;nsggdtast;sggdtastn;gg
dtastnp;gdtastnpd;dtastnpde;tastnpdes;astnpdesa;stnpdesak;tnpdesakg;npd
esakgp;pdesakgpn;desakgpnl;esakgpnlt;sakgpnltv;akgpnltvi;kgpnltvis;gpnl
tvisk;pnltviskk;nltviskki;ltviskkit;tviskkitd;viskkitds;iskkitdsn;skkit
dsna;kkitdsnaf;kitdsnafv;itdsnafvl;tdsnafvla;dsnafvlav;snafvlavk;nafvla
vke;afvlavkev;fvlavkeve;vlavkevea;lavkeveal;avkeveali;vkevealis;keveali
ss;evealissi;vealissid;ealisside;alissidel;lissidela;issidelan;ssidelan
k;sidelanka;idelankai;delankaig;elankaigk;lankaigkv;ankaigkvi;nkaigkvih
;kaigkvihq;aigkvihqn;igkvihqnn;gkvihqnng;kvihqnngl;vihqnngln;ihqnnglna;
hqnnglnan;qnnglnana;nnglnanag;nglnanagq;glnanagqn;lnanagqng;nanagqngs;a
nagqngsl;nagqngsll;agqngslla;gqngsllag;qngsllaga;ngsllagay;gsllagaya;sl
lagayai;llagayais;lagayaist;agayaistl;gayaistli;ayaistlit;yaistlite;ais
tlitek;istlitekl;stlitekls;tliteklsk;liteklskl;iteklsklk;teklsklkn;ekls
klkns;klsklknse;lsklknsee;sklknseel;klknseeln;lknseelnk;knseelnkk;nseel
nkki;seelnkkie;eelnkkiee;elnkkieea;lnkkieeak;nkkieeakn;kkieeaknh;kieeak
nhs;ieeaknhse;eeaknhsea;eaknhseaf;aknhseaft;knhseaftn;nhseaftnr;hseaftn
rl;seaftnrlk;eaftnrlkg;aftnrlkgs;ftnrlkgsh;tnrlkgsha;nrlkgshaq;rlkgshaq
l;lkgshaqlg;kgshaqlgv;gshaqlgva;shaqlgvaa;haqlgvaaa;aqlgvaaat;qlgvaaatd
;lgvaaatdd;gvaaatddh;vaaatddha;aaatddhak;aatddhake;atddhakea;tddhakeai;
ddhakeail;dhakeailk;hakeailks;akeailksn;keailksnp;eailksnpt;ailksnptk;i
lksnptkd;lksnptkdk;ksnptkdkg;snptkdkga;nptkdkgak;ptkdkgake;tkdkgakel;kd
kgakelk;dkgakelkd;kgakelkdl;gakelkdls;akelkdlse;kelkdlses;elkdlsesv;lkd
lsesve;kdlsesves;dlsesvesl;lsesvesla;sesveslak;esveslaka;sveslakaa;vesl
akaaq;eslakaaqe;slakaaqea;lakaaqeal;akaaqeala;kaaqealan;aaqealans;aqeal
ansv;qealansvk;ealansvke;alansvkel;lansvkelt;ansvkeltn;nsvkeltnp;svkelt
npv;vkeltnpvv;keltnpvva;eltnpvvae;ltnpvvaes;tnpvvaesp;npvvaespk;

10 mers:
ilmtlflfis;lmtlflfisc;mtlflfiscn;tlflfiscnn;lflfiscnns;flfiscnnsg;lfisc
nnsgg;fiscnnsggd;iscnnsggdt;scnnsggdta;cnnsggdtas;nnsggdtast;nsggdtastn
;sggdtastnp;ggdtastnpd;gdtastnpde;dtastnpdes;tastnpdesa;astnpdesak;stnp
desakg;tnpdesakgp;npdesakgpn;pdesakgpnl;desakgpnlt;esakgpnltv;sakgpnltv
i;akgpnltvis;kgpnltvisk;gpnltviskk;pnltviskki;nltviskkit;ltviskkitd;tvi
skkitds;viskkitdsn;iskkitdsna;skkitdsnaf;kkitdsnafv;kitdsnafvl;itdsnafv
la;tdsnafvlav;dsnafvlavk;snafvlavke;nafvlavkev;afvlavkeve;fvlavkevea;vl
avkeveal;lavkeveali;avkevealis;vkevealiss;kevealissi;evealissid;vealiss

ide;ealissidel;alissidela;lissidelan;issidelank;ssidelanka;sidelankai;i
delankaig;delankaigk;elankaigkv;lankaigkvi;ankaigkvih;nkaigkvihq;kaigkv
ihqn;aigkvihqnn;igkvihqnng;gkvihqnngl;kvihqnngln;vihqnnglna;ihqnnglnan;
hqnnglnana;qnnglnanag;nnglnanagq;nglnanagqn;glnanagqng;lnanagqngs;nanag
qngsl;anagqngsll;nagqngslla;agqngsllag;gqngsllaga;qngsllagay;ngsllagaya
;gsllagayai;sllagayais;llagayaist;lagayaistl;agayaistli;gayaistlit;ayai
stlite;yaistlitek;aistlitekl;istlitekls;stliteklsk;tliteklskl;liteklskl
k;iteklsklkn;teklsklkns;eklsklknse;klsklknsee;lsklknseel;sklknseeln;klk
nseelnk;lknseelnkk;knseelnkki;nseelnkkie;seelnkkiee;eelnkkieea;elnkkiee
ak;lnkkieeakn;nkkieeaknh;kkieeaknhs;kieeaknhse;ieeaknhsea;eeaknhseaf;ea
knhseaft;aknhseaftn;knhseaftnr;nhseaftnrl;hseaftnrlk;seaftnrlkg;eaftnrl
kgs;aftnrlkgsh;ftnrlkgsha;tnrlkgshaq;nrlkgshaql;rlkgshaqlg;lkgshaqlgv;k
gshaqlgva;gshaqlgvaa;shaqlgvaaa;haqlgvaaat;aqlgvaaatd;qlgvaaatdd;lgvaaa
tddh;gvaaatddha;vaaatddhak;aaatddhake;aatddhakea;atddhakeai;tddhakeail;
ddhakeailk;dhakeailks;hakeailksn;akeailksnp;keailksnpt;eailksnptk;ailks
nptkd;ilksnptkdk;lksnptkdkg;ksnptkdkga;snptkdkgak;nptkdkgake;ptkdkgakel
;tkdkgakelk;kdkgakelkd;dkgakelkdl;kgakelkdls;gakelkdlse;akelkdlses;kelk
dlsesv;elkdlsesve;lkdlsesves;kdlsesvesl;dlsesvesla;lsesveslak;sesveslak
a;esveslakaa;sveslakaaq;veslakaaqe;eslakaaqea;slakaaqeal;lakaaqeala;aka
aqealan;kaaqealans;aaqealansv;aqealansvk;qealansvke;ealansvkel;alansvke
lt;lansvkeltn;ansvkeltnp;nsvkeltnpv;svkeltnpvv;vkeltnpvva;keltnpvvae;el
tnpvvaes;ltnpvvaesp;tnpvvaespk;

11 mers:
ilmtlflfisc;lmtlflfiscn;mtlflfiscnn;tlflfiscnns;lflfiscnnsg;flfiscnnsgg
;lfiscnnsggd;fiscnnsggdt;iscnnsggdta;scnnsggdtas;cnnsggdtast;nnsggdtast
n;nsggdtastnp;sggdtastnpd;ggdtastnpde;gdtastnpdes;dtastnpdesa;tastnpdes
ak;astnpdesakg;stnpdesakgp;tnpdesakgpn;npdesakgpnl;pdesakgpnlt;desakgpn
ltv;esakgpnltvi;sakgpnltvis;akgpnltvisk;kgpnltviskk;gpnltviskki;pnltvis
kkit;nltviskkitd;ltviskkitds;tviskkitdsn;viskkitdsna;iskkitdsnaf;skkitd
snafv;kkitdsnafvl;kitdsnafvla;itdsnafvlav;tdsnafvlavk;dsnafvlavke;snafv
lavkev;nafvlavkeve;afvlavkevea;fvlavkeveal;vlavkeveali;lavkevealis;avke
vealiss;vkevealissi;kevealissid;evealisside;vealissidel;ealissidela;ali
ssidelan;lissidelank;issidelanka;ssidelankai;sidelankaig;idelankaigk;de
lankaigkv;elankaigkvi;lankaigkvih;ankaigkvihq;nkaigkvihqn;kaigkvihqnn;a
igkvihqnng;igkvihqnngl;gkvihqnngln;kvihqnnglna;vihqnnglnan;ihqnnglnana;
hqnnglnanag;qnnglnanagq;nnglnanagqn;nglnanagqng;glnanagqngs;lnanagqngsl
;nanagqngsll;anagqngslla;nagqngsllag;agqngsllaga;gqngsllagay;qngsllagay
a;ngsllagayai;gsllagayais;sllagayaist;llagayaistl;lagayaistli;agayaistl
it;gayaistlite;ayaistlitek;yaistlitekl;aistlitekls;istliteklsk;stliteklsk
skl;tliteklsklk;liteklsklkn;iteklsklkns;teklsklknse;eklsklknsee;klsklkn
seel;lsklknseeln;sklknseelnk;klknseelnkk;lknseelnkki;knseelnkkie;nseeln
kkiee;seelnkkieea;eelnkkieeak;elnkkieeakn;lnkkieeaknh;nkkieeaknhs;kkiee
aknhse;kieeaknhsea;ieeaknhseaf;eeaknhseaft;eaknhseaftn;aknhseaftnr;knhs
eaftnrl;nhseaftnrlk;hseaftnrlkg;seaftnrlkgs;eaftnrlkgsh;aftnrlkgsha;ftn
rlkgshaq;tnrlkgshaql;nrlkgshaqlg;rlkgshaqlgv;lkgshaqlgva;kgshaqlgvaa;gs
haqlgvaaa;shaqlgvaaat;haqlgvaaatd;aqlgvaaatdd;qlgvaaatddh;lgvaaatddha;g
vaaatddhak;vaaatddhake;aaatddhakea;aatddhakeai;atddhakeail;tddhakeailk;
ddhakeailks;dhakeailksn;hakeailksnp;akeailksnpt;keailksnptk;eailksnptkd
;ailksnptkdk;ilksnptkdkg;lksnptkdkga;ksnptkdkgak;snptkdkgake;nptkdkgake
l;ptkdkgakelk;tkdkgakelkd;kdkgakelkdl;dkgakelkdls;kgakelkdlse;gakelkdls
es;akelkdlsesv;kelkdlsesve;elkdlsesves;lkdlsesvesl;kdlsesvesla;dlsesves
lak;lsesveslaka;sesveslakaa;esveslakaaq;sveslakaaqe;veslakaaqea;eslakaa
qeal;slakaaqeala;lakaaqealan;akaaqealans;kaaqealansv;aaqealansvk;aqeala
nsvke;qealansvkel;ealansvkelt;alansvkeltn;lansvkeltnp;ansvkeltnpv;nsvke
ltnpvv;svkeltnpvva;vkeltnpvvae;keltnpvvaes;eltnpvvaesp;ltnpvvaespk;

13 mers:
ilmtlflfiscnn;lmtlflfiscnns;mtlflfiscnnsg;tlflfiscnnsgg;lflfiscnnsggd;f
lfiscnnsggdt;lfiscnnsggdta;fiscnnsggdtas;iscnnsggdtast;scnnsggdtastn;cn
nsggdtastnp;nnsggdtastnpd;nsggdtastnpde;sggdtastnpdes;ggdtastnpdesa;gdt
astnpdesak;dtastnpdesakg;tastnpdesakgp;astnpdesakgpn;stnpdesakgpnl;tnpd
esakgpnlt;npdesakgpnltv;pdesakgpnltvi;desakgpnltvis;esakgpnltvisk;sakgp
nltviskk;akgpnltviskki;kgpnltviskkit;gpnltviskkitd;pnltviskkitds;nltvis
kkitdsn;ltviskkitdsna;tviskkitdsnaf;viskkitdsnafv;iskkitdsnafvl;skkitds
nafvla;kkitdsnafvlav;kitdsnafvlavk;itdsnafvlavke;tdsnafvlavkev;dsnafvla
vkeve;snafvlavkevea;nafvlavkeveal;afvlavkeveali;fvlavkevealis;vlavkevea
liss;lavkevealissi;avkevealissid;vkevealisside;kevealissidel;evealissid
ela;vealissidelan;ealissidelank;alissidelanka;lissidelankai;issidelanka
ig;ssidelankaigk;sidelankaigkv;idelankaigkvi;delankaigkvih;elankaigkvih
q;lankaigkvihqn;ankaigkvihqnn;nkaigkvihqnng;kaigkvihqnngl;aigkvihqnngln
;igkvihqnnglna;gkvihqnnglnan;kvihqnnglnana;vihqnnglnanag;ihqnnglnanagq;
hqnnglnanagqn;qnnglnanagqng;nnglnanagqngs;nglnanagqngsl;glnanagqngsll;l
nanagqngslla;nanagqngsllag;anagqngsllaga;nagqngsllagay;agqngsllagaya;gq
ngsllagayai;qngsllagayais;ngsllagayaist;gsllagayaistl;sllagayaistli;lla
gayaistlit;lagayaistlite;agayaistlitek;gayaistlitekl;ayaistliteklsyais
tliteklsk;aistliteklskl;istliteklsklk;stliteklsklkn;tliteklsklkns;litek
lsklknse;iteklsklknsee;teklsklknseel;eklsklknseeln;klsklknseelnk;lsklkn
seelnkk;sklknseelnkki;klknseelnkkie;lknseelnkkiee;knseelnkkieea;nseelnk
kieeak;seelnkkieeakn;eelnkkieeaknh;elnkkieeaknhs;lnkkieeaknhse;nkkieeak
nhsea;kkieeaknhseaf;kieeaknhseaft;ieeaknhseaftn;eeaknhseaftnr;eaknhseaf
tnrl;aknhseaftnrlk;knhseaftnrlkg;nhseaftnrlkgs;hseaftnrlkgsh;seaftnrlkg
sha;eaftnrlkgshaq;aftnrlkgshaql;ftnrlkgshaqlg;tnrlkgshaqlgv;nrlkgshaqlg
va;rlkgshaqlgvaa;lkgshaqlgvaaa;kgshaqlgvaaat;gshaqlgvaaatd;shaqlgvaaatd
d;haqlgvaaatddh;aqlgvaaatddha;qlgvaaatddhak;lgvaaatddhake;gvaaatddhakea
;vaaatddhakeai;aaatddhakeail;aatddhakeailk;atddhakeailks;tddhakeailksn;
ddhakeailksnp;dhakeailksnpt;hakeailksnptk;akeailksnptkd;keailksnptkdk;e
ailksnptkdkg;ailksnptkdkga;ilksnptkdkgak;lksnptkdkgake;ksnptkdkgakel;sn
ptkdkgakelk;nptkdkgakelkd;ptkdkgakelkdl;tkdkgakelkdls;kdkgakelkdlse;dkg
akelkdlses;kgakelkdlsesv;gakelkdlsesve;akelkdlsesves;kelkdlsesvesl;elkd
lsesvesla;lkdlsesveslak;kdlsesveslaka;dlsesveslakaa;lsesveslakaaq;sesve
slakaaqe;esveslakaaqea;sveslakaaqeal;veslakaaqeala;eslakaaqealan;slakaa
qealans;lakaaqealansv;akaaqealansvk;kaaqealansvke;aaqealansvkel;aqealan
svkelt;qealansvkeltn;ealansvkeltnp;alansvkeltnpv;lansvkeltnpvv;ansvkelt
npvva;nsvkeltnpvvae;svkeltnpvvaes;vkeltnpvvaesp;keltnpvvaespk;

14 mers:
ilmtlflfiscnns;lmtlflfiscnnsg;mtlflfiscnnsgg;tlflfiscnnsggd;lflfiscnnsg
gdt;flfiscnnsggdta;lfiscnnsggdtas;fiscnnsggdtast;iscnnsggdtastn;scnnsgg
dtastnp;cnnsggdtastnpd;nnsggdtastnpde;nsggdtastnpdes;sggdtastnpdesa;ggd
tastnpdesak;gdtastnpdesakg;dtastnpdesakgp;tastnpdesakgpn;astnpdesakgpnl
;stnpdesakgpnlt;tnpdesakgpnltv;npdesakgpnltvi;pdesakgpnltvis;desakgpnlt
visk;esakgpnltviskk;sakgpnltviskki;akgpnltviskkit;kgpnltviskkitd;gpnltv
iskkitds;pnltviskkitdsn;nltviskkitdsna;ltviskkitdsnaf;tviskkitdsnafv;vi
skkitdsnafvl;iskkitdsnafvla;skkitdsnafvlav;kkitdsnafvlavk;kitdsnafvlavk
e;itdsnafvlavkev;tdsnafvlavkeve;dsnafvlavkevea;snafvlavkeveal;nafvlavke
veali;afvlavkevealis;fvlavkevealiss;vlavkevealissi;lavkevealissid;avkev
ealisside;vkevealissidel;kevealissidela;evealissidelan;vealissidelank;e
alissidelanka;alissidelankai;lissidelankaig;issidelankaigk;ssidelankaig
kv;sidelankaigkvi;idelankaigkvih;delankaigkvihq;elankaigkvihqn;lankaigk
vihqnn;ankaigkvihqnng;nkaigkvihqnngl;kaigkvihqnngln;aigkvihqnnglna;igkv
ihqnnglnan;gkvihqnnglnana;kvihqnnglnanag;vihqnnglnanagq;ihqnnglnanagqn;
hqnnglnanagqng;qnnglnanagqngs;nnglnanagqngsl;nglnanagqngsll;glnanagqngs
lla;lnanagqngsllag;nanagqngsllaga;anagqngsllagay;nagqngsllagaya;agqngsl

lagayai;gqngsllagayais;qngsllagayaist;ngsllagayaistl;gsllagayaistli;sll
agayaistlit;llagayaistlite;lagayaistlitek;agayaistlitekl;gayaistliteklk
;ayaistliteklsk;yaistliteklskl;aistliteklsklk;istliteklsklkn;stliteklsk
lkns;tliteklsklknse;liteklsklknsee;iteklsklknseel;teklsklknseeln;eklskl
knseelnk;klsklknseelnkk;lsklknseelnkki;sklknseelnkkie;klknseelnkkiee;lk
nseelnkkieea;knseelnkkieeak;nseelnkkieeakn;seelnkkieeaknh;eelnkkieeaknh
s;elnkkieeaknhse;lnkkieeaknhsea;nkkieeaknhseaf;kkieeaknhseaft;kieeaknhs
eaftn;ieeaknhseaftnr;eeaknhseaftnrl;eaknhseaftnrlk;aknhseaftnrlkg;knhse
aftnrlkgs;nhseaftnrlkgsh;hseaftnrlkgsha;seaftnrlkgshaq;eaftnrlkgshaql;a
ftnrlkgshaqlg;ftnrlkgshaqlgv;tnrlkgshaqlgva;nrlkgshaqlgvaa;rlkgshaqlgva
aa;lkgshaqlgvaaat;kgshaqlgvaaatd;gshaqlgvaaatdd;shaqlgvaaatddh;haqlgvaa
atddha;aqlgvaaatddhak;qlgvaaatddhake;lgvaaatddhakea;gvaaatddhakeai;vaaa
tddhakeail;aaatddhakeailk;aatddhakeailks;atddhakeailksn;tddhakeailksnp;
ddhakeailksnpt;dhakeailksnptk;hakeailksnptkd;akeailksnptkdk;keailksnptk
dkg;eailksnptkdkga;ailksnptkdkgak;ilksnptkdkgake;lksnptkdkgakel;ksnptkd
kgakelk;snptkdkgakelkd;nptkdkgakelkdl;ptkdkgakelkdls;tkdkgakelkdlse;kdk
gakelkdlses;dkgakelkdlsesv;kgakelkdlsesve;gakelkdlsesves;akelkdlsesvesl
;kelkdlsesvesla;elkdlsesveslak;lkdlsesveslaka;kdlsesveslakaa;dlsesvesla
kaaq;lsesveslakaaqe;sesveslakaaqea;esveslakaaqeal;sveslakaaqeala;veslak
aaqealan;eslakaaqealans;slakaaqealansv;lakaaqealansvk;akaaqealansvke;ka
aqealansvkel;aaqealansvkelt;aqealansvkeltn;qealansvkeltnp;ealansvkeltnp
v;alansvkeltnpvv;lansvkeltnpvva;ansvkeltnpvvae;nsvkeltnpvvaes;svkeltnpv
vaesp;vkeltnpvvaespk;

15 mers:
ilmtlflfiscnnsg;lmtlflfiscnnsgg;mtlflfiscnnsggd;tlflfiscnnsggdt;lflfisc
nnsggdta;flfiscnnsggdtas;lfiscnnsggdtast;fiscnnsggdtastn;iscnnsggdtastn
p;scnnsggdtastnpd;cnnsggdtastnpde;nnsggdtastnpdes;nsggdtastnpdesa;sggdt
astnpdesak;ggdtastnpdesakg;gdtastnpdesakgp;dtastnpdesakgpn;tastnpdesakg
pnl;astnpdesakgpnlt;stnpdesakgpnltv;tnpdesakgpnltvi;npdesakgpnltvis;pde
sakgpnltvisk;desakgpnltviskk;esakgpnltviskki;sakgpnltviskkit;akgpnltvis
kkitd;kgpnltviskkitds;gpnltviskkitdsn;pnltviskkitdsna;nltviskkitdsnaf;l
tviskkitdsnafv;tviskkitdsnafvl;viskkitdsnafvla;iskkitdsnafvlav;skkitdsn
afvlavk;kkitdsnafvlavke;kitdsnafvlavkev;itdsnafvlavkeve;tdsnafvlavkevea
;dsnafvlavkeveal;snafvlavkeveali;nafvlavkevealis;afvlavkevealiss;fvlavk
evealissi;vlavkevealissid;lavkevealisside;avkevealissidel;vkevealisside
la;kevealissidelan;evealissidelank;vealissidelanka;ealissidelankai;alis
sidelankaig;lissidelankaigk;issidelankaigkv;ssidelankaigkvi;sidelankaig
kvih;idelankaigkvihq;delankaigkvihqn;elankaigkvihqnn;lankaigkvihqnng;an
kaigkvihqnngl;nkaigkvihqnngln;kaigkvihqnnglna;aigkvihqnnglnan;igkvihqnn
glnana;gkvihqnnglnanag;kvihqnnglnanagq;vihqnnglnanagqn;ihqnnglnanagqng;
hqnnglnanagqngs;qnnglnanagqngsl;nnglnanagqngsll;nglnanagqngslla;glnanag
qngsllag;lnanagqngsllaga;nanagqngsllagay;anagqngsllagaya;nagqngsllagaya
i;agqngsllagayais;gqngsllagayaist;qngsllagayaistl;ngsllagayaistli;gslla
gayaistlit;sllagayaistlite;llagayaistlitek;lagayaistlitekl;agayaistlite
kls;gayaistliteklsk;ayaistliteklskl;yaistliteklsklk;aistliteklsklkn;ist
liteklsklkns;stliteklsklknse;tliteklsklknsee;liteklsklknseel;iteklsklkn
seeln;teklsklknseelnk;eklsklknseelnkk;klsklknseelnkki;lsklknseelnkkie;s
klknseelnkkiee;klknseelnkkieea;lknseelnkkieeak;knseelnkkieeakn;nseelnkk
ieeaknh;seelnkkieeaknhs;eelnkkieeaknhse;elnkkieeaknhsea;lnkkieeaknhseaf
;nkkieeaknhseaft;kkieeaknhseaftn;kieeaknhseaftnr;ieeaknhseaftnrl;eeaknh
seaftnrlk;eaknhseaftnrlkg;aknhseaftnrlkgs;knhseaftnrlkgsh;nhseaftnrlkgs
ha;hseaftnrlkgshaq;seaftnrlkgshaql;eaftnrlkgshaqlg;aftnrlkgshaqlgv;ftnr
lkgshaqlgva;tnrlkgshaqlgvaa;nrlkgshaqlgvaaa;rlkgshaqlgvaaat;lkgshaqlgva
aatd;kgshaqlgvaaatdd;gshaqlgvaaatddh;shaqlgvaaatddha;haqlgvaaatddhak;aq
lgvaaatddhake;qlgvaaatddhakea;lgvaaatddhakeai;gvaaatddhakeail;vaaatddha
keailk;aaatddhakeailks;aatddhakeailksn;atddhakeailksnp;tddhakeailksnpt;

ddhakeailksnptk;dhakeailksnptkd;hakeailksnptkdk;akeailksnptkdkg;keailks
nptkdkga;eailksnptkdkgak;ailksnptkdkgake;ilksnptkdkgakel;lksnptkdkgakel
k;ksnptkdkgakelkd;snptkdkgakelkdl;nptkdkgakelkdls;ptkdkgakelkdlse;tkdkg
akelkdlses;kdkgakelkdlsesv;dkgakelkdlsesve;kgakelkdlsesves;gakelkdlsesv
esl;akelkdlsesvesla;kelkdlsesveslak;elkdlsesveslaka;lkdlsesveslakaa;kdl
sesveslakaaq;dlsesveslakaaqe;lsesveslakaaqea;sesveslakaaqeal;esveslakaa
qeala;sveslakaaqealan;veslakaaqealans;eslakaaqealansv;slakaaqealansvk;l
akaaqealansvke;akaaqealansvkel;kaaqealansvkelt;aaqealansvkeltn;aqealans
vkeltnp;qealansvkeltnpv;ealansvkeltnpvv;alansvkeltnpvva;lansvkeltnpvvae
;ansvkeltnpvvaes;nsvkeltnpvvaesp;svkeltnpvvaespk;

16 mers:
ilmtlflfiscnnsgg;lmtlflfiscnnsggd;mtlflfiscnnsggdt;tlflfiscnnsggdta;lfl
fiscnnsggdtas;flfiscnnsggdtast;lfiscnnsggdtastn;fiscnnsggdtastnp;iscnns
ggdtastnpd;scnnsggdtastnpde;cnnsggdtastnpdes;nnsggdtastnpdesa;nsggdtast
npdesak;sggdtastnpdesakg;ggdtastnpdesakgp;gdtastnpdesakgpn;dtastnpdesak
gpnl;tastnpdesakgpnlt;astnpdesakgpnltv;stnpdesakgpnltvi;tnpdesakgpnltvi
s;npdesakgpnltvisk;pdesakgpnltviskk;desakgpnltviskki;esakgpnltviskkit;s
akgpnltviskkitd;akgpnltviskkitds;kgpnltviskkitdsn;gpnltviskkitdsna;pnlt
viskkitdsnaf;nltviskkitdsnafv;ltviskkitdsnafvl;tviskkitdsnafvla;viskkit
dsnafvlav;iskkitdsnafvlavk;skkitdsnafvlavke;kkitdsnafvlavkev;kitdsnafvl
avkeve;itdsnafvlavkevea;tdsnafvlavkeveal;dsnafvlavkeveali;snafvlavkevea
lis;nafvlavkevealiss;afvlavkevealissi;fvlavkevealissid;vlavkevealisside
;lavkevealissidel;avkevealissidela;vkevealissidelan;kevealissidelank;ev
ealissidelanka;vealissidelankai;ealissidelankaig;alissidelankaigk;lissi
delankaigkv;issidelankaigkvi;ssidelankaigkvih;sidelankaigkvihq;idelanka
igkvihqn;delankaigkvihqnn;elankaigkvihqnng;lankaigkvihqnngl;ankaigkvihq
nngln;nkaigkvihqnnglna;kaigkvihqnnglnan;aigkvihqnnglnana;igkvihqnnglnan
ag;gkvihqnnglnanagq;kvihqnnglnanagqn;vihqnnglnanagqng;ihqnnglnanagqngs;
hqnnglnanagqngsl;qnnglnanagqngsll;nnglnanagqngslla;nglnanagqngsllag;gln
anagqngsllaga;lnanagqngsllagay;nanagqngsllagaya;anagqngsllagayai;nagqng
sllagayais;agqngsllagayaist;gqngsllagayaistl;qngsllagayaistli;ngsllagay
aistlit;gsllagayaistlite;sllagayaistlitek;llagayaistlitekl;lagayaistlit
ekls;agayaistliteklsk;gayaistliteklskl;ayaistliteklsklk;yaistliteklsklk
n;aistliteklsklkns;istliteklsklknse;stliteklsklknsee;tliteklsklknseel;l
iteklsklknseeln;iteklsklknseelnk;teklsklknseelnkk;eklsklknseelnkki;klsk
lknseelnkkie;lsklknseelnkkiee;sklknseelnkkieea;klknseelnkkieeak;lknseel
nkkieeakn;knseelnkkieeaknh;nseelnkkieeaknhs;seelnkkieeaknhse;eelnkkieea
knhsea;elnkkieeaknhseaf;lnkkieeaknhseaft;nkkieeaknhseaftn;kkieeaknhseaf
tnr;kieeaknhseaftnrl;ieeaknhseaftnrlk;eeaknhseaftnrlkg;eaknhseaftnrlkgs
;aknhseaftnrlkgsh;knhseaftnrlkgsha;nhseaftnrlkgshaq;hseaftnrlkgshaql;se
aftnrlkgshaqlg;eaftnrlkgshaqlgv;aftnrlkgshaqlgva;ftnrlkgshaqlgvaa;tnrlk
gshaqlgvaaa;nrlkgshaqlgvaaat;rlkgshaqlgvaaatd;lkgshaqlgvaaatdd;kgshaqlg
vaaatddh;gshaqlgvaaatddha;shaqlgvaaatddhak;haqlgvaaatddhake;aqlgvaaatdd
hakea;qlgvaaatddhakeai;lgvaaatddhakeail;gvaaatddhakeailk;vaaatddhakeail
ks;aaatddhakeailksn;aatddhakeailksnp;atddhakeailksnpt;tddhakeailksnptk;
ddhakeailksnptkd;dhakeailksnptkdk;hakeailksnptkdkg;akeailksnptkdkga;kea
ilksnptkdkgak;eailksnptkdkgake;ailksnptkdkgakel;ilksnptkdkgakelk;lksnpt
kdkgakelkd;ksnptkdkgakelkdl;snptkdkgakelkdls;nptkdkgakelkdlse;ptkdkgake
lkdlses;tkdkgakelkdlsesv;kdkgakelkdlsesve;dkgakelkdlsesves;kgakelkdlses
vesl;gakelkdlsesvesla;akelkdlsesveslak;kelkdlsesveslaka;elkdlsesveslaka
a;lkdlsesveslakaaq;kdlsesveslakaaqe;dlsesveslakaaqea;lsesveslakaaqeal;s
esveslakaaqeala;esveslakaaqealan;sveslakaaqealans;veslakaaqealansv;esla
kaaqealansvk;slakaaqealansvke;lakaaqealansvkel;akaaqealansvkelt;kaaqeal
ansvkeltn;aaqealansvkeltnp;aqealansvkeltnpv;qealansvkeltnpvv;ealansvkel
tnpvva;alansvkeltnpvvae;lansvkeltnpvvaes;ansvkeltnpvvaesp;nsvkeltnpvvae
spk;

<NP_047005 outer surface protein C;Protein;Borrelia burgdorferi B31>

8 mers:
mkkntlsa;kkntlsai;kntlsail;ntlsailm;tlsailmt;lsailmtl;sailmtlf;ailmtlfl
;ilmtlflf;lmtlflfi;mtlflfis;tlflfisc;lflfiscn;flfiscnn;lfiscnns;fiscnns
g;iscnnsgk;scnnsgkd;cnnsgkdg;nnsgkdgn;nsgkdgnt;sgkdgnts;gkdgntsa;kdgnts
an;dgntsans;gntsansa;ntsansad;tsansade;sansades;ansadesv;nsadesvk;sades
vkg;adesvkgp;desvkgpn;esvkgpnl;svkgpnlt;vkgpnlte;kgpnltei;gpnlteis;pnlt
eisk;nlteiskk;lteiskki;teiskkit;eiskkitd;iskkitds;skkitdsn;kkitdsna;kit
dsnav;itdsnavl;tdsnavll;dsnavlla;snavllav;navllavk;avllavke;vllavkev;ll
avkeve;lavkevea;avkeveal;vkeveall;kevealls;eveallss;veallssi;eallssid;a
llsside;llssidei;lssideia;ssideiaa;sideiaak;ideiaaka;deiaakai;eiaakaig;
iaakaigk;aakaigkk;akaigkki;kaigkkih;aigkkihq;igkkihqn;gkkihqnn;kkihqnng
;kihqnngl;ihqnngld;hqnngldt;qnngldte;nngldten;ngldtenn;gldtennh;ldtennh
n;dtennhng;tennhngs;ennhngsl;nnhngsll;nhngslla;hngsllag;ngsllaga;gsllag
ay;sllagaya;llagayai;lagayais;agayaist;gayaistl;ayaistli;yaistlik;aistl
ikq;istlikqk;stlikqkl;tlikqkld;likqkldg;ikqkldgl;kqkldglk;qkldglkn;kldg
lkne;ldglkneg;dglknegl;glkneglk;lkneglke;kneglkek;neglkeki;eglkekid;glk
ekida;lkekidaa;kekidaak;ekidaakk;kidaakkc;idaakkcs;daakkcse;aakkcset;ak
kcsetf;kkcsetft;kcsetftn;csetftnk;setftnkl;etftnklk;tftnklke;ftnklkek;t
nklkekh;nklkekht;klkekhtd;lkekhtdl;kekhtdlg;ekhtdlgk;khtdlgke;htdlgkeg;
tdlgkegv;dlgkegvt;lgkegvtd;gkegvtda;kegvtdad;egvtdada;gvtdadak;vtdadake
;tdadakea;dadakeai;adakeail;dakeailk;akeailkt;keailktn;eailktng;ailktng
t;ilktngtk;lktngtkt;ktngtktk;tngtktkg;ngtktkga;gtktkgae;tktkgaee;ktkgae
el;tkgaeelg;kgaeelgk;gaeelgkl;aeelgklf;eelgklfe;elgklfes;lgklfesv;gklfe
sve;klfesvev;lfesvevl;fesvevls;esvevlsk;svevlska;vevlskaa;evlskaak;vlsk
aake;lskaakem;skaakeml;kaakemla;aakemlan;akemlans;kemlansv;emlansvk;mla
nsvke;lansvkel;ansvkelt;nsvkelts;svkeltsp;vkeltspv;keltspvv;eltspvva;lt
spvvae;tspvvaes;spvvaesp;pvvaespk;vvaespkk;vaespkkp;

9 mers:
mkkntlsai;kkntlsail;kntlsailm;ntlsailmt;tlsailmtl;lsailmtlf;sailmtlfl;a
ilmtlflf;ilmtlflfi;lmtlflfis;mtlflfisc;tlflfiscn;lflfiscnn;flfiscnns;lf
iscnnsg;fiscnnsgk;iscnnsgkd;scnnsgkdg;cnnsgkdgn;nnsgkdgnt;nsgkdgnts;sgk
dgntsa;gkdgntsan;kdgntsans;dgntsansa;gntsansad;ntsansade;tsansades;sans
adesv;ansadesvk;nsadesvkg;sadesvkgp;adesvkgpn;desvkgpnl;esvkgpnlt;svkgp
nlte;vkgpnltei;kgpnlteis;gpnlteisk;pnlteiskk;nlteiskki;lteiskkit;teiskk
itd;eiskkitds;iskkitdsn;skkitdsna;kkitdsnav;kitdsnavl;itdsnavll;tdsnavl
la;dsnavllav;snavllavk;navllavke;avllavkev;vllavkeve;llavkevea;lavkevea
l;avkeveall;vkevealls;keveallss;eveallssi;veallssid;eallsside;allssidei
;llssideia;lssideiaa;ssideiaak;sideiaaka;ideiaakai;deiaakaig;eiaakaigk;
iaakaigkk;aakaigkki;akaigkkih;kaigkkihq;aigkkihqn;igkkihqnn;gkkihqnng;k
kihqnngl;kihqnngld;ihqnngldt;hqnngldte;qnngldten;nngldtenn;ngldtennh;gl
dtennhn;ldtennhng;dtennhngs;tennhngsl;ennhngsll;nnhngslla;nhngsllag;hng
sllaga;ngsllagay;gsllagaya;sllagayai;llagayais;lagayaist;agayaistl;gaya
istli;ayaistlik;yaistlikq;aistlikqk;istlikqkl;stlikqkld;tlikqkldg;likqk
ldgl;ikqkldglk;kqkldglkn;qkldglkne;kldglkneg;ldglknegl;dglkneglk;glkneg
lke;lkneglkek;kneglkeki;neglkekid;eglkekida;glkekidaa;lkekidaak;kekidaa
kk;ekidaakkc;kidaakkcs;idaakkcse;daakkcset;aakkcsetf;akkcsetft;kkcsetft
n;kcsetftnk;csetftnkl;setftnklk;etftnklke;tftnklkek;ftnklkekh;tnklkekht
;nklkekhtd;klkekhtdl;lkekhtdlg;kekhtdlgk;ekhtdlgke;khtdlgkeg;htdlgkegv;
tdlgkegvt;dlgkegvtd;lgkegvtda;gkegvtdad;kegvtdada;egvtdadak;gvtdadake;v
tdadakea;tdadakeai;dadakeail;adakeailk;dakeailkt;akeailktn;keailktng;ea
ilktngt;ailktngtk;ilktngtkt;lktngtktk;ktngtktkg;tngtktkga;ngtktkgae;gtk
tkgaee;tktkgaeel;ktkgaeelg;tkgaeelgk;kgaeelgkl;gaeelgklf;aeelgklfe;eelg

klfes;elgklfesv;lgklfesve;gklfesvev;klfesvevl;lfesvevls;fesvevlsk;esvev
lska;svevlskaa;vevlskaak;evlskaake;vlskaakem;lskaakeml;skaakemla;kaakem
lan;aakemlans;akemlansv;kemlansvk;emlansvke;mlansvkel;lansvkelt;ansvkel
ts;nsvkeltsp;svkeltspv;vkeltspvv;keltspvva;eltspvvae;ltspvvaes;tspvvaes
p;spvvaespk;pvvaespkk;vvaespkkp;

10 mers:
mkkntlsail;kkntlsailm;kntlsailmt;ntlsailmtl;tlsailmtlf;lsailmtlfl;sailm
tlflf;ailmtlflfi;ilmtlflfis;lmtlflfisc;mtlflfiscn;tlflfiscnn;lflfiscnns
;flfiscnnsg;lfiscnnsgk;fiscnnsgkd;iscnnsgkdg;scnnsgkdgn;cnnsgkdgnt;nnsg
kdgnts;nsgkdgntsa;sgkdgntsan;gkdgntsans;kdgntsansa;dgntsansad;gntsansad
e;ntsansades;tsansadesv;sansadesvk;ansadesvkg;nsadesvkgp;sadesvkgpn;ade
svkgpnl;desvkgpnlt;esvkgpnlte;svkgpnltei;vkgpnlteis;kgpnlteisk;gpnlteis
kk;pnlteiskki;nlteiskkit;lteiskkitd;teiskkitds;eiskkitdsn;iskkitdsna;sk
kitdsnav;kkitdsnavl;kitdsnavll;itdsnavlla;tdsnavllav;dsnavllavk;snavlla
vke;navllavkev;avllavkeve;vllavkevea;llavkeveal;lavkeveall;avkevealls;v
keveallss;keveallssi;eveallssid;veallsside;eallssidei;allssideia;llssid
eiaa;lssideiaak;ssideiaaka;sideiaakai;ideiaakaig;deiaakaigk;eiaakaigkk;
iaakaigkki;aakaigkkih;akaigkkihq;kaigkkihqn;aigkkihqnn;igkkihqnng;gkkih
qnngl;kkihqnngld;kihqnngldt;ihqnngldte;hqnngldten;qnngldtenn;nngldtennh
;ngldtennhn;gldtennhng;ldtennhngs;dtennhngsl;tennhngsll;ennhngslla;nnhn
gsllag;nhngsllaga;hngsllagay;ngsllagaya;gsllagayai;sllagayais;llagayais
t;lagayaistl;agayaistli;gayaistlik;ayaistlikq;yaistlikqk;aistlikqkl;ist
likqkld;stlikqkldg;tlikqkldgl;likqkldglk;ikqkldglkn;kqkldglkne;qkldglkn
eg;kldglknegl;ldglkneglk;dglkneglke;glkneglkek;lkneglkeki;kneglkekid;ne
glkekida;eglkekidaa;glkekidaak;lkekidaakk;kekidaakkc;ekidaakkcs;kidaakk
cse;idaakkcset;daakkcsetf;aakkcsetft;akkcsetftn;kkcsetftnk;kcsetftnkl;c
setftnklk;setftnklke;etftnklkek;tftnklkekh;ftnklkekht;tnklkekhtd;nklkek
htdl;klkekhtdlg;lkekhtdlgk;kekhtdlgke;ekhtdlgkeg;khtdlgkegv;htdlgkegvt;
tdlgkegvtd;dlgkegvtda;lgkegvtdad;gkegvtdada;kegvtdadak;egvtdadake;gvtda
dakea;vtdadakeai;tdadakeail;dadakeailk;adakeailkt;dakeailktn;akeailktng
;keailktngt;eailktngtk;ailktngtkt;ilktngtktk;lktngtktkg;ktngtktkga;tngt
ktkgae;ngtktkgaee;gtktkgaeel;tktkgaeelg;ktkgaeelgk;tkgaeelgkl;kgaeelgkl
f;gaeelgklfe;aeelgklfes;eelgklfesv;elgklfesve;lgklfesvev;gklfesvevl;klf
esvevls;lfesvevlsk;fesvevlska;esvevlskaa;svevlskaak;vevlskaake;evlskaak
em;vlskaakeml;lskaakemla;skaakemlan;kaakemlans;aakemlansv;akemlansvk;ke
mlansvke;emlansvkel;mlansvkelt;lansvkelts;ansvkeltsp;nsvkeltspv;svkelts
pvv;vkeltspvva;keltspvvae;eltspvvaes;ltspvvaesp;tspvvaespk;spvvaespkk;p
vvaespkkp;

11 mers:
mkkntlsailm;kkntlsailmt;kntlsailmtl;ntlsailmtlf;tlsailmtlfl;lsailmtlflf
;sailmtlflfi;ailmtlflfis;ilmtlflfisc;lmtlflfiscn;mtlflfiscnn;tlflfiscnn
s;lflfiscnnsg;flfiscnnsgk;lfiscnnsgkd;fiscnnsgkdg;iscnnsgkdgn;scnnsgkdg
nt;cnnsgkdgnts;nnsgkdgntsa;nsgkdgntsan;sgkdgntsans;gkdgntsansa;kdgntsan
sad;dgntsansade;gntsansades;ntsansadesv;tsansadesvk;sansadesvkg;ansades
vkgp;nsadesvkgpn;sadesvkgpnl;adesvkgpnlt;desvkgpnlte;esvkgpnltei;svkgpn
lteis;vkgpnlteisk;kgpnlteiskk;gpnlteiskki;pnlteiskkit;nlteiskkitd;lteis
kkitds;teiskkitdsn;eiskkitdsna;iskkitdsnav;skkitdsnavl;kkitdsnavll;kitd
snavlla;itdsnavllav;tdsnavllavk;dsnavllavke;snavllavkev;navllavkeve;avl
lavkevea;vllavkeveal;llavkeveall;lavkevealls;avkeveallss;vkeveallssi;ke
veallssid;eveallsside;veallssidei;eallssideia;allssideiaa;llssideiaak;l
ssideiaaka;ssideiaakai;sideiaakaig;ideiaakaigk;deiaakaigkk;eiaakaigkki;
iaakaigkkih;aakaigkkihq;akaigkkihqn;kaigkkihqnn;aigkkihqnng;igkkihqnngl
;gkkihqnngld;kkihqnngldt;kihqnngldte;ihqnngldten;hqnngldtenn;qnngldtenn
h;nngldtennhn;ngldtennhng;gldtennhngs;ldtennhngsl;dtennhngsll;tennhngsl
la;ennhngsllag;nnhngsllaga;nhngsllagay;hngsllagaya;ngsllagayai;gsllagay

ais;sllagayaist;llagayaistl;lagayaistli;agayaistlik;gayaistlikq;ayaistl
ikqk;yaistlikqkl;aistlikqkld;istlikqkldg;stlikqkldgl;tlikqkldglk;likqkl
dglkn;ikqkldglkne;kqkldglkneg;qkldglknegl;kldglkneglk;ldglkneglke;dglkn
eglkek;glkneglkeki;lkneglkekid;kneglkekida;neglkekidaa;eglkekidaak;glke
kidaakk;lkekidaakkc;kekidaakkcs;ekidaakkcse;kidaakkcset;idaakkcsetf;daa
kkcsetft;aakkcsetftn;akkcsetftnk;kkcsetftnkl;kcsetftnklk;csetftnklke;se
tftnklkek;etftnklkekh;tftnklkekht;ftnklkekhtd;tnklkekhtdl;nklkekhtdlg;k
lkekhtdlgk;lkekhtdlgke;kekhtdlgkeg;ekhtdlgkegv;khtdlgkegvt;htdlgkegvtd;
tdlgkegvtda;dlgkegvtdad;lgkegvtdada;gkegvtdadak;kegvtdadake;egvtdadakea
;gvtdadakeai;vtdadakeail;tdadakeailk;dadakeailkt;adakeailktn;dakeailktn
g;akeailktngt;keailktngtk;eailktngtkt;ailktngtktk;ilktngtktkg;lktngtktk
ga;ktngtktkgae;tngtktkgaee;ngtktkgaeel;gtktkgaeelg;tktkgaeelgk;ktkgaeel
gkl;tkgaeelgklf;kgaeelgklfe;gaeelgklfes;aeelgklfesv;eelgklfesve;elgklfe
svev;lgklfesvevl;gklfesvevls;klfesvevlsk;lfesvevlska;fesvevlskaa;esvevl
skaak;svevlskaake;vevlskaakem;evlskaakeml;vlskaakemla;lskaakemlan;skaak
emlans;kaakemlansv;aakemlansvk;akemlansvke;kemlansvkel;emlansvkelt;mlan
svkelts;lansvkeltsp;ansvkeltspv;nsvkeltspvv;svkeltspvva;vkeltspvvae;kel
tspvvaes;eltspvvaesp;ltspvvaespk;tspvvaespkk;spvvaespkkp;

13 mers:
mkkntlsailmtl;kkntlsailmtlf;kntlsailmtlfl;ntlsailmtlflf;tlsailmtlflfi;l
sailmtlflfis;sailmtlflfisc;ailmtlflfiscn;ilmtlflfiscnn;lmtlflfiscnns;mt
lflfiscnnsg;tlflfiscnnsgk;lflfiscnnsgkd;flfiscnnsgkdg;lfiscnnsgkdgn;fis
cnnsgkdgnt;iscnnsgkdgnts;scnnsgkdgntsa;cnnsgkdgntsan;nnsgkdgntsans;nsgk
dgntsansa;sgkdgntsansad;gkdgntsansade;kdgntsansades;dgntsansadesv;gntsa
nsadesvk;ntsansadesvkg;tsansadesvkgp;sansadesvkgpn;ansadesvkgpnl;nsades
vkgpnlt;sadesvkgpnlte;adesvkgpnltei;desvkgpnlteis;esvkgpnlteisk;svkgpnl
teiskk;vkgpnlteiskki;kgpnlteiskkit;gpnlteiskkitd;pnlteiskkitds;nlteiskk
itdsn;lteiskkitdsna;teiskkitdsnav;eiskkitdsnavl;iskkitdsnavll;skkitdsna
vlla;kkitdsnavllav;kitdsnavllavk;itdsnavllavke;tdsnavllavkev;dsnavllavk
eve;snavllavkevea;navllavkeveal;avllavkeveall;vllavkevealls;llavkeveall
ss;lavkeveallssi;avkeveallssid;vkeveallsside;keveallssidei;eveallssidei
a;veallssideiaa;eallssideiaak;allssideiaaka;llssideiaakai;lssideiaakaig
;ssideiaakaigk;sideiaakaigkk;ideiaakaigkki;deiaakaigkkih;eiaakaigkkihq;
iaakaigkkihqn;aakaigkkihqnn;akaigkkihqnng;kaigkkihqnngl;aigkkihqnngld;i
gkkihqnngldt;gkkihqnngldte;kkihqnngldten;kihqnngldtenn;ihqnngldtennh;hq
nngldtennhn;qnngldtennhng;nngldtennhngs;ngldtennhngsl;gldtennhngsll;ldt
ennhngslla;dtennhngsllag;tennhngsllaga;ennhngsllagay;nnhngsllagaya;nhng
sllagayai;hngsllagayais;ngsllagayaist;gsllagayaistl;sllagayaistli;llaga
yaistlik;lagayaistlikq;agayaistlikqk;gayaistlikqkl;ayaistlikqkld;yaistl
ikqkldg;aistlikqkldgl;istlikqkldglk;stlikqkldglkn;tlikqkldglkne;likqkld
glkneg;ikqkldglknegl;kqkldglkneglk;qkldglkneglke;kldglkneglkek;ldglkneg
lkeki;dglkneglkekid;glkneglkekida;lkneglkekidaa;kneglkekidaak;neglkekid
aakk;eglkekidaakkc;glkekidaakkcs;lkekidaakkcse;kekidaakkcset;ekidaakkcs
etf;kidaakkcsetft;idaakkcsetftn;daakkcsetftnk;aakkcsetftnkl;akkcsetftnk
lk;kkcsetftnklke;kcsetftnklkek;csetftnklkekh;setftnklkekht;etftnklkekht
d;tftnklkekhtdl;ftnklkekhtdlg;tnklkekhtdlgk;nklkekhtdlgke;klkekhtdlgkeg
;lkekhtdlgkegv;kekhtdlgkegvt;ekhtdlgkegvtd;khtdlgkegvtda;htdlgkegvtdad;
tdlgkegvtdada;dlgkegvtdadak;lgkegvtdadake;gkegvtdadakea;kegvtdadakeai;e
gvtdadakeail;gvtdadakeailk;vtdadakeailkt;tdadakeailktn;dadakeailktng;ad
akeailktngt;dakeailktngtk;akeailktngtkt;keailktngtktk;eailktngtktkg;ail
ktngtktkga;ilktngtktkgae;lktngtktkgaee;ktngtktkgaeel;tngtktkgaeelg;ngtk
tkgaeelgk;gtktkgaeelgkl;tktkgaeelgklf;ktkgaeelgklfe;tkgaeelgklfes;kgaee
lgklfesv;gaeelgklfesve;aeelgklfesvev;eelgklfesvevl;elgklfesvevls;lgklfe
svevlsk;gklfesvevlska;klfesvevlskaa;lfesvevlskaak;fesvevlskaake;esvevls
kaakem;svevlskaakeml;vevlskaakemla;evlskaakemlan;vlskaakemlans;lskaakem
lansv;skaakemlansvk;kaakemlansvke;aakemlansvkel;akemlansvkelt;kemlansvk

elts;emlansvkeltsp;mlansvkeltspv;lansvkeltspvv;ansvkeltspvva;nsvkeltspv
vae;svkeltspvvaes;vkeltspvvaesp;keltspvvaespk;eltspvvaespkk;ltspvvaespk
kp;

14 mers:
mkkntlsailmtlf;kkntlsailmtlfl;kntlsailmtlflf;ntlsailmtlflfi;tlsailmtlfl
fis;lsailmtlflfisc;sailmtlflfiscn;ailmtlflfiscnn;ilmtlflfiscnns;lmtlflf
iscnnsg;mtlflfiscnnsgk;tlflfiscnnsgkd;lflfiscnnsgkdg;flfiscnnsgkdgn;lfi
scnnsgkdgnt;fiscnnsgkdgnts;iscnnsgkdgntsa;scnnsgkdgntsan;cnnsgkdgntsans
;nnsgkdgntsansa;nsgkdgntsansad;sgkdgntsansade;gkdgntsansades;kdgntsansa
desv;dgntsansadesvk;gntsansadesvkg;ntsansadesvkgp;tsansadesvkgpn;sansad
esvkgpnl;ansadesvkgpnlt;nsadesvkgpnlte;sadesvkgpnltei;adesvkgpnlteis;de
svkgpnlteisk;esvkgpnlteiskk;svkgpnlteiskki;vkgpnlteiskkit;kgpnlteiskkit
d;gpnlteiskkitds;pnlteiskkitdsn;nlteiskkitdsna;lteiskkitdsnav;teiskkitd
snavl;eiskkitdsnavll;iskkitdsnavlla;skkitdsnavllav;kkitdsnavllavk;kitds
navllavke;itdsnavllavkev;tdsnavllavkeve;dsnavllavkevea;snavllavkeveal;n
avllavkeveall;avllavkevealls;vllavkeveallss;llavkeveallssi;lavkeveallss
id;avkeveallsside;vkeveallssidei;keveallssideia;eveallssideiaa;veallssi
deiaak;eallssideiaaka;allssideiaakai;llssideiaakaig;lssideiaakaigk;ssid
eiaakaigkk;sideiaakaigkki;ideiaakaigkkih;deiaakaigkkihq;eiaakaigkkihqn;
iaakaigkkihqnn;aakaigkkihqnng;akaigkkihqnngl;kaigkkihqnngld;aigkkihqnng
ldt;igkkihqnngldte;gkkihqnngldten;kkihqnngldtenn;kihqnngldtennh;ihqnngl
dtennhn;hqnngldtennhng;qnngldtennhngs;nngldtennhngsl;ngldtennhngsll;gld
tennhngslla;ldtennhngsllag;dtennhngsllaga;tennhngsllagay;ennhngsllagaya
;nnhngsllagayai;nhngsllagayais;hngsllagayaist;ngsllagayaistl;gsllagayai
stli;sllagayaistlik;llagayaistlikq;lagayaistlikqk;agayaistlikqkl;gayais
tlikqkld;ayaistlikqkldg;yaistlikqkldgl;aistlikqkldglk;istlikqkldglkn;st
likqkldglkne;tlikqkldglkneg;likqkldglknegl;ikqkldglkneglk;kqkldglkneglk
e;qkldglkneglkek;kldglkneglkeki;ldglkneglkekid;dglkneglkekida;glkneglke
kidaa;lkneglkekidaak;kneglkekidaakk;neglkekidaakkc;eglkekidaakkcs;glkek
idaakkcse;lkekidaakkcset;kekidaakkcsetf;ekidaakkcsetft;kidaakkcsetftn;i
daakkcsetftnk;daakkcsetftnkl;aakkcsetftnklk;akkcsetftnklke;kkcsetftnklk
ek;kcsetftnklkekh;csetftnklkekht;setftnklkekhtd;etftnklkekhtdl;tftnklke
khtdlg;ftnklkekhtdlgk;tnklkekhtdlgke;nklkekhtdlgkeg;klkekhtdlgkegv;lkek
htdlgkegvt;kekhtdlgkegvtd;ekhtdlgkegvtda;khtdlgkegvtdad;htdlgkegvtdada;
tdlgkegvtdadak;dlgkegvtdadake;lgkegvtdadakea;gkegvtdadakeai;kegvtdadake
ail;egvtdadakeailk;gvtdadakeailkt;vtdadakeailktn;tdadakeailktng;dadakea
ilktngt;adakeailktngtk;dakeailktngtkt;akeailktngtktk;keailktngtktkg;eai
lktngtktkga;ailktngtktkgae;ilktngtktkgaee;lktngtktkgaeel;ktngtktkgaeelg
;tngtktkgaeelgk;ngtktkgaeelgkl;gtktkgaeelgklf;tktkgaeelgklfe;ktkgaeelgk
lfes;tkgaeelgklfesv;kgaeelgklfesve;gaeelgklfesvev;aeelgklfesvevl;eelgkl
fesvevls;elgklfesvevlsk;lgklfesvevlska;gklfesvevlskaa;klfesvevlskaak;lf
esvevlskaake;fesvevlskaakem;esvevlskaakeml;svevlskaakemla;vevlskaakemla
n;evlskaakemlans;vlskaakemlansv;lskaakemlansvk;skaakemlansvke;kaakemlan
svkel;aakemlansvkelt;akemlansvkelts;kemlansvkeltsp;emlansvkeltspv;mlans
vkeltspvv;lansvkeltspvva;ansvkeltspvvae;nsvkeltspvvaes;svkeltspvvaesp;v
keltspvvaespk;keltspvvaespkk;eltspvvaespkkp;

15 mers:
mkkntlsailmtlfl;kkntlsailmtlflf;kntlsailmtlflfi;ntlsailmtlflfis;tlsailm
tlflfisc;lsailmtlflfiscn;sailmtlflfiscnn;ailmtlflfiscnns;ilmtlflfiscnns
g;lmtlflfiscnnsgk;mtlflfiscnnsgkd;tlflfiscnnsgkdg;lflfiscnnsgkdgn;flfis
cnnsgkdgnt;lfiscnnsgkdgnts;fiscnnsgkdgntsa;iscnnsgkdgntsan;scnnsgkdgnts
ans;cnnsgkdgntsansa;nnsgkdgntsansad;nsgkdgntsansade;sgkdgntsansades;gkd
gntsansadesv;kdgntsansadesvk;dgntsansadesvkg;gntsansadesvkgp;ntsansades
vkgpn;tsansadesvkgpnl;sansadesvkgpnlt;ansadesvkgpnlte;nsadesvkgpnltei;s
adesvkgpnlteis;adesvkgpnlteisk;desvkgpnlteiskk;esvkgpnlteiskki;svkgpnlt

eiskkit;vkgpnlteiskkitd;kgpnlteiskkitds;gpnlteiskkitdsn;pnlteiskkitdsna
;nlteiskkitdsnav;lteiskkitdsnavl;teiskkitdsnavll;eiskkitdsnavlla;iskkit
dsnavllav;skkitdsnavllavk;kkitdsnavllavke;kitdsnavllavkev;itdsnavllavke
ve;tdsnavllavkevea;dsnavllavkeveal;snavllavkeveall;navllavkevealls;avll
avkeveallss;vllavkeveallssi;llavkeveallssid;lavkeveallsside;avkeveallss
idei;vkeveallssideia;keveallssideiaa;eveallssideiaak;veallssideiaaka;ea
llssideiaakai;allssideiaakaig;llssideiaakaigk;lssideiaakaigkk;ssideiaak
aigkki;sideiaakaigkkih;ideiaakaigkkihq;deiaakaigkkihqn;eiaakaigkkihqnn;
iaakaigkkihqnng;aakaigkkihqnngl;akaigkkihqnngld;kaigkkihqnngldt;aigkkih
qnngldte;igkkihqnngldten;gkkihqnngldtenn;kkihqnngldtennh;kihqnngldtennh
n;ihqnngldtennhng;hqnngldtennhngs;qnngldtennhngsl;nngldtennhngsll;ngldt
ennhngslla;gldtennhngsllag;ldtennhngsllaga;dtennhngsllagay;tennhngsllag
aya;ennhngsllagayai;nnhngsllagayais;nhngsllagayaist;hngsllagayaistl;ngs
llagayaistli;gsllagayaistlik;sllagayaistlikq;llagayaistlikqk;lagayaistl
ikqkl;agayaistlikqkld;gayaistlikqkldg;ayaistlikqkldgl;yaistlikqkldglk;a
istlikqkldglkn;istlikqkldglkne;stlikqkldglkneg;tlikqkldglknegl;likqkldg
lkneglk;ikqkldglkneglke;kqkldglkneglkek;qkldglkneglkeki;kldglkneglkekid
;ldglkneglkekida;dglkneglkekidaa;glkneglkekidaak;lkneglkekidaakk;kneglk
ekidaakkc;neglkekidaakkcs;eglkekidaakkcse;glkekidaakkcset;lkekidaakkcse
tf;kekidaakkcsetft;ekidaakkcsetftn;kidaakkcsetftnk;idaakkcsetftnkl;daak
kcsetftnklk;aakkcsetftnklke;akkcsetftnklkek;kkcsetftnklkekh;kcsetftnklk
ekht;csetftnklkekhtd;setftnklkekhtdl;etftnklkekhtdlg;tftnklkekhtdlgk;ft
nklkekhtdlgke;tnklkekhtdlgkeg;nklkekhtdlgkegv;klkekhtdlgkegvt;lkekhtdlg
kegvtd;kekhtdlgkegvtda;ekhtdlgkegvtdad;khtdlgkegvtdada;htdlgkegvtdadak;
tdlgkegvtdadake;dlgkegvtdadakea;lgkegvtdadakeai;gkegvtdadakeail;kegvtda
dakeailk;egvtdadakeailkt;gvtdadakeailktn;vtdadakeailktng;tdadakeailktng
t;dadakeailktngtk;adakeailktngtkt;dakeailktngtktk;akeailktngtktkg;keail
ktngtktkga;eailktngtktkgae;ailktngtktkgaee;ilktngtktkgaeel;lktngtktkgae
elg;ktngtktkgaeelgk;tngtktkgaeelgkl;ngtktkgaeelgklf;gtktkgaeelgklfe;tkt
kgaeelgklfes;ktkgaeelgklfesv;tkgaeelgklfesve;kgaeelgklfesvev;gaeelgklfe
svevl;aeelgklfesvevls;eelgklfesvevlsk;elgklfesvevlska;lgklfesvevlskaa;g
klfesvevlskaak;klfesvevlskaake;lfesvevlskaakem;fesvevlskaakeml;esvevlsk
aakemla;svevlskaakemlan;vevlskaakemlans;evlskaakemlansv;vlskaakemlansvk
;lskaakemlansvke;skaakemlansvkel;kaakemlansvkelt;aakemlansvkelts;akemla
nsvkeltsp;kemlansvkeltspv;emlansvkeltspvv;mlansvkeltspvva;lansvkeltspvv
ae;ansvkeltspvvaes;nsvkeltspvvaesp;svkeltspvvaespk;vkeltspvvaespkk;kelt
spvvaespkkp;

16 mers:
mkkntlsailmtlflf;kkntlsailmtlflfi;kntlsailmtlflfis;ntlsailmtlflfisc;tls
ailmtlflfiscn;lsailmtlflfiscnn;sailmtlflfiscnns;ailmtlflfiscnnsg;ilmtlf
lfiscnnsgk;lmtlflfiscnnsgkd;mtlflfiscnnsgkdg;tlflfiscnnsgkdgn;lflfiscnn
sgkdgnt;flfiscnnsgkdgnts;lfiscnnsgkdgntsa;fiscnnsgkdgntsan;iscnnsgkdgnt
sans;scnnsgkdgntsansa;cnnsgkdgntsansad;nnsgkdgntsansade;nsgkdgntsansade
s;sgkdgntsansadesv;gkdgntsansadesvk;kdgntsansadesvkg;dgntsansadesvkgp;g
ntsansadesvkgpn;ntsansadesvkgpnl;tsansadesvkgpnlt;sansadesvkgpnlte;ansa
desvkgpnltei;nsadesvkgpnlteis;sadesvkgpnlteisk;adesvkgpnlteiskk;desvkgp
nlteiskki;esvkgpnlteiskkit;svkgpnlteiskkitd;vkgpnlteiskkitds;kgpnlteisk
kitdsn;gpnlteiskkitdsna;pnlteiskkitdsnav;nlteiskkitdsnavl;lteiskkitdsna
vll;teiskkitdsnavlla;eiskkitdsnavllav;iskkitdsnavllavk;skkitdsnavllavke
;kkitdsnavllavkev;kitdsnavllavkeve;itdsnavllavkevea;tdsnavllavkeveal;ds
navllavkeveall;snavllavkevealls;navllavkeveallss;avllavkeveallssi;vllav
keveallssid;llavkeveallsside;lavkeveallssidei;avkeveallssideia;vkeveall
ssideiaa;keveallssideiaak;eveallssideiaaka;veallssideiaakai;eallssideia
akaig;allssideiaakaigk;llssideiaakaigkk;lssideiaakaigkki;ssideiaakaigkk
ih;sideiaakaigkkihq;ideiaakaigkkihqn;deiaakaigkkihqnn;eiaakaigkkihqnng;
iaakaigkkihqnngl;aakaigkkihqnngld;akaigkkihqnngldt;kaigkkihqnngldte;aig

kkihqnngldten;igkkihqnngldtenn;gkkihqnngldtennh;kkihqnngldtennhn;kihqnn
gldtennhng;ihqnngldtennhngs;hqnngldtennhngsl;qnngldtennhngsll;nngldtenn
hngslla;ngldtennhngsllag;gldtennhngsllaga;ldtennhngsllagay;dtennhngslla
gaya;tennhngsllagayai;ennhngsllagayais;nnhngsllagayaist;nhngsllagayaist
l;hngsllagayaistli;ngsllagayaistlik;gsllagayaistlikq;sllagayaistlikqk;l
lagayaistlikqkl;lagayaistlikqkld;agayaistlikqkldg;gayaistlikqkldgl;ayai
stlikqkldglk;yaistlikqkldglkn;aistlikqkldglkne;istlikqkldglkneg;stlikqk
ldglknegl;tlikqkldglkneglk;likqkldglkneglke;ikqkldglkneglkek;kqkldglkne
glkeki;qkldglkneglkekid;kldglkneglkekida;ldglkneglkekidaa;dglkneglkekid
aak;glkneglkekidaakk;lkneglkekidaakkc;kneglkekidaakkcs;neglkekidaakkcse
;eglkekidaakkcset;glkekidaakkcsetf;lkekidaakkcsetft;kekidaakkcsetftn;ek
idaakkcsetftnk;kidaakkcsetftnkl;idaakkcsetftnklk;daakkcsetftnklke;aakkc
setftnklkek;akkcsetftnklkekh;kkcsetftnklkekht;kcsetftnklkekhtd;csetftnk
lkekhtdl;setftnklkekhtdlg;etftnklkekhtdlgk;tftnklkekhtdlgke;ftnklkekhtd
lgkeg;tnklkekhtdlgkegv;nklkekhtdlgkegvt;klkekhtdlgkegvtd;lkekhtdlgkegvt
da;kekhtdlgkegvtdad;ekhtdlgkegvtdada;khtdlgkegvtdadak;htdlgkegvtdadake;
tdlgkegvtdadakea;dlgkegvtdadakeai;lgkegvtdadakeail;gkegvtdadakeailk;keg
vtdadakeailkt;egvtdadakeailktn;gvtdadakeailktng;vtdadakeailktngt;tdadak
eailktngtk;dadakeailktngtkt;adakeailktngtktk;dakeailktngtktkg;akeailktn
gtktkga;keailktngtktkgae;eailktngtktkgaee;ailktngtktkgaeel;ilktngtktkga
eelg;lktngtktkgaeelgk;ktngtktkgaeelgkl;tngtktkgaeelgklf;ngtktkgaeelgklf
e;gtktkgaeelgklfes;tktkgaeelgklfesv;ktkgaeelgklfesve;tkgaeelgklfesvev;k
gaeelgklfesvevl;gaeelgklfesvevls;aeelgklfesvevlsk;eelgklfesvevlska;elgk
lfesvevlskaa;lgklfesvevlskaak;gklfesvevlskaake;klfesvevlskaakem;lfesvev
lskaakeml;fesvevlskaakemla;esvevlskaakemlan;svevlskaakemlans;vevlskaake
mlansv;evlskaakemlansvk;vlskaakemlansvke;lskaakemlansvkel;skaakemlansvk
elt;kaakemlansvkelts;aakemlansvkeltsp;akemlansvkeltspv;kemlansvkeltspvv
;emlansvkeltspvva;mlansvkeltspvvae;lansvkeltspvvaes;ansvkeltspvvaesp;ns
vkeltspvvaespk;svkeltspvvaespkk;vkeltspvvaespkkp;

<CAF34024 outer surface protein VlsE;Protein;Borrelia garinii>

8 mers:
mkkissai;kkissaif;kissaifi;issaifiv;ssaifiva;saifivaf;aifivafl;ifivafla
;fivaflal;ivaflali;vaflalig;aflaligc;flaligck;laligckn;aligcknn;ligcknn
v;igcknnvg;gcknnvgg;cknnvggd;knnvggdd;nnvggddk;nvggddkk;vggddkkd;ggddkk
dt;gddkkdta;ddkkdtaa;dkkdtaas;kkdtaasi;kdtaasif;dtaasify;taasifyq;aasif
yqs;asifyqsi;sifyqsii;ifyqsiin;fyqsiinl;yqsiinlg;qsiinlgn;siinlgng;iinl
gngf;inlgngfi;nlgngfie;lgngfiev;gngfievf;ngfievfn;gfievfna;fievfnaf;iev
fnafs;evfnafsg;vfnafsgl;fnafsglv;nafsglva;afsglvad;fsglvada;sglvadaf;gl
vadafs;lvadafsk;vadafska;adafskad;dafskadp;afskadpk;fskadpkk;skadpkks;k
adpkksd;adpkksdv;dpkksdvk;pkksdvkt;kksdvkty;ksdvktyf;sdvktyfd;dvktyfds;
vktyfdsi;ktyfdsit;tyfdsitk;yfdsitkt;fdsitktl;dsitktlk;sitktlkd;itktlkdt
;tktlkdtk;ktlkdtkt;tlkdtktk;lkdtktkl;kdtktkle;dtktkled;tktkledi;ktkledi
s;tkledisk;klediske;lediskek;ediskekt;diskektg;iskektgg;skektgge;kektgg
ek;ektggekt;ktggektp;tggektpa;ggektpav;gektpave;ektpaveg;ktpavegi;tpave
gia;pavegiae;avegiaev;vegiaevv;egiaevvk;giaevvkt;iaevvktv;aevvktvg;evvk
tvge;vvktvgew;vktvgewl;ktvgewld;tvgewldg;vgewldgl;gewldgli;ewldglik;wld
glika;ldglikaa;dglikaae;glikaaeg;likaaegg;ikaaeggg;kaaegggk;aaegggka;ae
gggkaa;egggkaad;gggkaadg;ggkaadgg;gkaadggg;kaadgggs;aadgggsd;adgggsdk;d
gggsdki;gggsdkig;ggsdkign;gsdkignv;sdkignva;dkignvaa;kignvaag;ignvaagg;
gnvaaggg;nvaaggga;vaagggag;aagggaga;agggagad;gggagadk;ggagadke;gagadkes
;agadkesv;gadkesvn;adkesvng;dkesvngi;kesvngia;esvngiag;svngiaga;vngiaga
i;ngiagaik;giagaikg;iagaikgi;agaikgiv;gaikgive;aikgivea;ikgiveaa;kgivea
ak;giveaakk;iveaakkv;veaakkve;eaakkveg;aakkvegv;akkvegvk;kkvegvkf;kvegv

kfa;vegvkfap;egvkfapk;gvkfapka;vkfapkaa;kfapkaaa;fapkaaad;apkaaada;pkaa
adaa;kaaadaaa;aaadaaaa;aadaaaad;adaaaadg;daaaadgn;aaaadgnk;aaadgnkk;aad
gnkka;adgnkkag;dgnkkagk;gnkkagkl;nkkagklf;kkagklfg;kagklfgt;agklfgta;gk
lfgtaa;klfgtaag;lfgtaaga;fgtaagad;gtaagada;taagadag;aagadagd;agadagdv;g
adagdvk;adagdvkd;dagdvkda;agdvkdaa;gdvkdaaa;dvkdaaaa;vkdaaaav;kdaaaavg;
daaaavga;aaaavgav;aaavgavs;aavgavsg;avgavsge;vgavsgeq;gavsgeqi;avsgeqil
;vsgeqiln;sgeqilna;geqilnai;eqilnaiv;qilnaivt;ilnaivta;lnaivtaa;naivtaa
g;aivtaagq;ivtaagqa;vtaagqag;taagqagq;aagqagqa;agqagqag;gqagqagk;qagqag
kk;agqagkka;gqagkkad;qagkkade;agkkadea;gkkadeak;kkadeakn;kadeakna;adeak
nai;deaknaie;eaknaiea;aknaieaa;knaieaai;naieaaig;aieaaiga;ieaaigaa;eaai
gaag;aaigaagd;aigaagda;igaagdad;gaagdadf;aagdadfg;agdadfgd;gdadfgdd;dad
fgddi;adfgddik;dfgddikk;fgddikkk;gddikkkn;ddikkknd;dikkkndq;ikkkndqi;kk
kndqia;kkndqiaa;kndqiaaa;ndqiaaal;dqiaaalv;qiaaalvl;iaaalvlr;aaalvlrg;a
alvlrgv;alvlrgva;lvlrgvak;vlrgvakd;lrgvakdg;rgvakdgk;gvakdgkf;vakdgkfa;
akdgkfag;kdgkfaga;

9 mers:
mkkissaif;kkissaifi;kissaifiv;issaifiva;ssaifivaf;saifivafl;aifivafla;i
fivaflal;fivaflali;ivaflalig;vaflaligc;aflaligck;flaligckn;laligcknn;al
igcknnv;ligcknnvg;igcknnvgg;gcknnvggd;cknnvggdd;knnvggddk;nnvggddkk;nvg
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evf;gngfievfn;ngfievfna;gfievfnaf;fievfnafs;ievfnafsg;evfnafsgl;vfnafsg
lv;fnafsglva;nafsglvad;afsglvada;fsglvadaf;sglvadafs;glvadafsk;lvadafsk
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tkledis;ktkledisk;tkledisk;kledisk;ledisk;ediskekt;diskektg;diskektgg;isk
ektgge;skektggek;kektggekt;ektggektp;ktggektpa;tggektpav;ggektpave;gekt
paveg;ektpavegi;ktpavegia;tpavegiae;pavegiaev;avegiaevv;vegiaevvk;egiae
vvkt;giaevvktv;iaevvktvg;aevvktvge;evvktvgew;vvktvgewl;vktvgewld;ktvgew
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giveaa;ikgiveaak;kgiveaakk;giveaakkv;iveaakkve;veaakkveg;eaakkvegv;aakk
vegvk;akkvegvkf;kkvegvkfa;kvegvkfap;vegvkfapk;egvkfapka;gvkfapkaa;vkfap
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agqagk;gqagqagkk;qagqagkka;agqagkkad;gqagkkade;qagkkadea;agkkadeak;gkka
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aaig;naieaaiga;aieaaigaa;ieaaigaag;eaaigaagd;aaigaagda;aigaagdad;igaagd
adf;gaagdadfg;aagdadfgd;agdadfgdd;gdadfgddi;dadfgddik;adfgddikk;dfgddik
kk;fgddikkkn;gddikkknd;ddikkkndq;dikkkndqi;ikkkndqia;kkkndqiaa;kkndqiaa
a;kndqiaaal;ndqiaaalv;dqiaaalvl;qiaaalvlr;iaaalvlrg;aaalvlrgv;aalvlrgva

;alvlrgvak;lvlrgvakd;vlrgvakdg;lrgvakdgk;rgvakdgkf;gvakdgkfa;vakdgkfag;
akdgkfaga;

10 mers:
mkkissaifi;kkissaifiv;kissaifiva;issaifivaf;ssaifivafl;saifivafla;aifiv
aflal;ifivaflali;fivaflalig;ivaflaligc;vaflaligck;aflaligckn;flaligcknn
;laligcknnv;aligcknnvg;ligcknnvgg;igcknnvggd;gcknnvggdd;cknnvggddk;knnv
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fyqsiin;sifyqsiinl;ifyqsiinlg;fyqsiinlgn;yqsiinlgng;qsiinlgngf;siinlgng
fi;iinlgngfie;inlgngfiev;nlgngfievf;lgngfievfn;gngfievfna;ngfievfnaf;gf
ievfnafs;fievfnafsg;ievfnafsgl;evfnafsglv;vfnafsglva;fnafsglvad;nafsglv
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dvkt;dpkksdvkty;pkksdvktyf;kksdvktyfd;ksdvktyfds;sdvktyfdsi;dvktyfdsit;
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;dtktkledis;tktkledisk;ktkledиske;tkledиskek;kledиskekt;ledиskektg;edis
kektgg;diskektgge;iskektggek;skektggekt;kektggektp;ektggektpa;ktggektpa
v;tggektpave;ggektpaveg;gektpavegi;ektpavegia;ktpavegiae;tpavegiaev;pav
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wldglika;ewldglikaa;wldglikaae;ldglikaaeg;dglikaaegg;glikaaeggg;likaaeg
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dkesv;gagadkesvn;agadkesvng;gadkesvngi;adkesvngia;dkesvngiag;kesvngiaga
;esvngiagai;svngiagaik;vngiagaikg;ngiagaikgi;giagaikgiv;iagaikgive;agai
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g;veaakkvegv;eaakkvegvk;aakkvegvkf;akkvegvkfa;kkvegvkfap;kvegvkfapk;veg
vkfapka;egvkfapkaa;gvkfapkaaa;vkfapkaaad;kfapkaaada;fapkaaadaa;apkaaada
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aadgnkka;aaadgnkkag;aadgnkkagk;adgnkkagkl;dgnkkagklf;gnkkagklfg;nkkagkl
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kdaa;dagdvkdaaa;agdvkdaaaa;gdvkdaaaav;dvkdaaaavg;vkdaaaavga;kdaaaavgav;
daaaavgavs;aaaavgavsg;aaavgavsge;aavgavsgeq;avgavsgeqi;vgavsgeqil;gavsg
eqiln;avsgeqilna;vsgeqilnai;sgeqilnaiv;geqilnaivt;eqilnaivta;qilnaivtaa
;ilnaivtaag;lnaivtaagq;naivtaagqa;aivtaagqag;ivtaagqagq;vtaagqagqa;taag
qagqag;aagqagqagk;agqagqagkk;gqagqagkka;qagqagkkad;agqagkkade;gqagkkade
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knaieaa;eaknaieaai;aknaieaaig;knaieaaiga;naieaaigaa;aieaaigaag;ieaaigaa
gd;eaaigaagda;aaigaagdad;aigaagdadf;igaagdadfg;gaagdadfgd;aagdadfgdd;ag
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ndq;ddikkkndqi;dikkkndqia;ikkkndqiaa;kkkndqiaaa;kkndqiaaal;kndqiaaalv;n
dqiaaalvl;dqiaaalvlr;qiaaalvlrg;iaaalvlrgv;aaalvlrgva;aalvlrgvak;alvlrg
vakd;lvlrgvakdg;vlrgvakdgk;lrgvakdgkf;rgvakdgkfa;gvakdgkfag;vakdgkfaga;

11 mers:
mkkissaifiv;kkissaifiva;kissaifivaf;issaifivafl;ssaifivafla;saifivaflal
;aifivaflali;ifivaflalig;fivaflaligc;ivaflaligck;vaflaligckn;aflaligckn
n;flaligcknnv;laligcknnvg;aligcknnvgg;ligcknnvggd;igcknnvggdd;gcknnvggd
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aas;gddkkdtaasi;ddkkdtaasif;dkkdtaasify;kkdtaasifyq;kdtaasifyqs;dtaasif
yqsi;taasifyqsii;aasifyqsiin;asifyqsiinl;sifyqsiinlg;ifyqsiinlgn;fyqsii
nlgng;yqsiinlgngf;qsiinlgngfi;siinlgngfie;iinlgngfiev;inlgngfievf;nlgng

fievfn;lgngfievfna;gngfievfnaf;ngfievfnafs;gfievfnafsg;fievfnafsgl;ievf
nafsglv;evfnafsglva;vfnafsglvad;fnafsglvada;nafsglvadaf;afsglvadafs;fsg
lvadafsk;sglvadafska;glvadafskad;lvadafskadp;vadafskadpk;adafskadpkk;da
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ve;iagaikgivea;agaikgiveaa;gaikgiveaak;aikgiveaakk;ikgiveaakkv;kgiveaak
kve;giveaakkveg;iveaakkvegv;veaakkvegvk;eaakkvegvkf;aakkvegvkfa;akkvegv
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13 mers:
mkkissaifivaf;kkissaifivafl;kissaifivafla;issaifivaflal;ssaifivaflali;s
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cknnvggddk;igcknnvggddkk;gcknnvggddkkd;cknnvggddkkdt;knnvggddkkdta;nnvg
gddkkdtaa;nvggddkkdtaas;vggddkkdtaasi;ggddkkdtaasif;gddkkdtaasify;ddkkd
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kdtktkledis;lkdtktkledisk;kdtktkledиske;dtktkledиskek;tktkledиskekt;ktk
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k;iaaalvlrgvakd;aaalvlrgvakdg;aalvlrgvakdgk;alvlrgvakdgkf;lvlrgvakdgkfa
;vlrgvakdgkfag;lrgvakdgkfaga;

14 mers:
mkkissaifivafl;kkissaifivafla;kissaifivaflal;issaifivaflali;ssaifivafla
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15 mers:
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<CAF34027 outer surface protein VlsE;Protein;Borrelia afzelii PKo>

8 mers:
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vfnaf;idvfnafs;dvfnafsg;vfnafsgl;fnafsglv;nafsglva;afsglvad;fsglvadt;sg
lvadtf;glvadtff;lvadtffk;vadtffks;adtffksd;dtffksdp;tffksdpk;ffksdpkk;f
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dvktyfes;vktyfesi;ktyfesis;tyfesiss;yfesisst;fesisstl;esisstlk;sisstlka
;isstlkat;sstlkatk;stlkatkg;tlkatkgk;lkatkgkl;katkgkld;atkgklde;tkgklde
l;kgkldelv;gkldelvs;kldelvsa;ldelvsak;delvsakk;elvsakkg;lvsakkge;vsakkg
eg;sakkgegg;akkgeggs;kkgeggsv;kgeggsvk;geggsvka;eggsvkas;ggsvkasv;gsvka
sve;svkasves;vkasvesa;kasvesav;asvesavd;svesavde;vesavdev;esavdevs;savd
evsk;avdevskw;vdevskwl;devskwle;evskwlee;vskwleem;skwleemi;kwleemik;wle
emika;leemikaa;eemikaae;emikaaee;mikaaeea;ikaaeeaa;kaaeeaak;aaeeaakv;ae
eaakvg;eeaakvgg;eaakvggt;aakvggtg;akvggtgg;kvggtggd;vggtggdg;ggtggdgk;g
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gdsaanhg;dsaanhga;saanhgak;aanhgaka;anhgakad;nhgakadk;hgakadkd;gakadkds
;akadkdsv;kadkdsvk;adkdsvkg;dkdsvkgi;kdsvkgia;dsvkgiak;svkgiakg;vkgiakg
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ag;givdaagk;ivdaagka;vdaagkal;daagkalg;aagkalge;agkalgek;gkalgekg;kalge
kga;algekgal;lgekgalk;gekgalkd;ekgalkdv;kgalkdvk;galkdvka;alkdvkaa;lkdv
kaaa;kdvkaaad;dvkaaadd;vkaaadde;kaaaddea;aaaddean;aaddeana;addeanad;dde
anada;deanadag;eanadagk;anadagkl;nadagklf;adagklfa;dagklfag;agklfagn;gk
lfagna;klfagnan;lfagnana;fagnanaa;agnanaav;gnanaavg;nanaavga;anaavgaa;n
aavgaaa;aavgaaad;avgaaadi;vgaaadia;gaaadiak;aaadiaka;aadiakaa;adiakaag;
diakaaga;iakaagav;akaagavt;kaagavta;aagavtav;agavtavs;gavtavsg;avtavsge
;vtavsgeq;tavsgeqi;avsgeqil;vsgeqilk;sgeqilka;geqilkai;eqilkaiv;qilkaiv
e;ilkaivea;lkaiveaa;kaiveaag;aiveaagd;iveaagdp;veaagdpa;eaagdpan;aagdpa
nq;agdpanqa;gdpanqag;dpanqagk;panqagkk;anqagkka;nqagkkae;qagkkaee;agkka
eea;gkkaeeak;kkaeeakn;kaeeaknp;aeeaknpi;eeaknpia;eaknpiaa;aknpiaaa;knpi
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ddnga;tdddngaa;dddngaaf;ddngaafk;dngaafkd;ngaafkde;gaafkdem;aafkdemk;af
kdemkk;fkdemkks;kdemkksd;demkksdk;emkksdki;mkksdkia;kksdkiaa;ksdkiaaa;s
dkiaaai;dkiaaaiv;kiaaaivl;iaaaivlr;aaaivlrg;aaivlrgv;aivlrgva;ivlrgvak;
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9 mers:
mkkissaif;kkissaifl;kissaiflt;issaiflta;ssaifltal;saifltall;aifltallv;i
fltallvf;fltallvfi;ltallvfin;tallvfinc;allvfinck;llvfinckn;lvfincknn;vf

incknna;fincknnav;incknnavg;ncknnavgk;cknnavgkg;knnavgkgn;nnavgkgnd;nav
gkgndd;avgkgnddk;vgkgnddkd;gkgnddkds;kgnddkdsv;gnddkdsvk;nddkdsvkt;ddkd
svktf;dkdsvktfy;kdsvktfye;dsvktfyes;svktfyesi;vktfyesii;ktfyesiin;tfyes
iinl;fyesiinlg;yesiinlgn;esiinlgng;siinlgngf;iinlgngfi;inlgngfid;nlgngf
idv;lgngfidvf;gngfidvfn;ngfidvfna;gfidvfnaf;fidvfnafs;idvfnafsg;dvfnafs
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isstlkat;isstlkatk;sstlkatkg;stlkatkgk;tlkatkgkl;lkatkgkld;katkgklde;at
kgkldel;tkgkldelv;kgkldelvs;gkldelvsa;kldelvsak;ldelvsakk;delvsakkg;elv
sakkge;lvsakkgeg;vsakkgegg;sakkgeggs;akkgeggsv;kkgeggsvk;kgeggsvka;gegg
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avde;svesavdev;vesavdevs;esavdevsk;savdevskw;avdevskwl;vdevskwle;devskw
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;tggdgkigd;ggdgkigds;gdgkigdsa;dgkigdsaa;gkigdsaan;kigdsaanh;igdsaanhg;
gdsaanhga;dsaanhgak;saanhgaka;aanhgakad;anhgakadk;nhgakadkd;hgakadkds;g
akadkdsv;akadkdsvk;kadkdsvkg;adkdsvkgi;dkdsvkgia;kdsvkgiak;dsvkgiakg;sv
kgiakgi;vkgiakgik;kgiakgikg;giakgikgi;iakgikgiv;akgikgivd;kgikgivda;gik
givdaa;ikgivdaag;kgivdaagk;givdaagka;ivdaagkal;vdaagkalg;daagkalge;aagk
algek;agkalgekg;gkalgekga;kalgekgal;algekgalk;lgekgalkd;gekgalkdv;ekgal
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dea;kaaaddean;aaaddeana;aaddeanad;addeanada;ddeanadag;deanadagk;eanadag
kl;anadagklf;nadagklfa;adagklfag;dagklfagn;agklfagna;gklfagnan;klfagnan
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;aavgaaadi;avgaaadia;vgaaadiak;gaaadiaka;aaadiakaa;aadiakaag;adiakaaga;
diakaagav;iakaagavt;akaagavta;kaagavtav;aagavtavs;agavtavsg;gavtavsge;a
vtavsgeq;vtavsgeqi;tavsgeqil;avsgeqilk;vsgeqilka;sgeqilkai;geqilkaiv;eq
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npia;eeaknpiaa;eaknpiaaa;aknpiaaai;knpiaaaig;npiaaaigt;piaaaigtd;iaaaig
tdd;aaaigtddd;aaigtdddn;aigtdddng;igtdddnga;gtdddngaa;tdddngaaf;dddngaa
fk;ddngaafkd;dngaafkde;ngaafkdem;gaafkdemk;aafkdemkk;afkdemkks;fkdemkks
d;kdemkksdk;demkksdki;emkksdkia;mkksdkiaa;kksdkiaaa;ksdkiaaai;sdkiaaaiv
;dkiaaaivl;kiaaaivlr;iaaaivlrg;aaaivlrgv;aaivlrgva;aivlrgvak;ivlrgvakd;
vlrgvakdg;lrgvakdgk;rgvakdgkf;gvakdgkfa;vakdgkfav;akdgkfavk;

10 mers:
mkkissaifl;kkissaiflt;kissaiflta;issaifltal;ssaifltall;saifltallv;aiflt
allvf;ifltallvfi;fltallvfin;ltallvfinc;tallvfinck;allvfinckn;llvfincknn
;lvfincknna;vfincknnav;fincknnavg;incknnavgk;ncknnavgkg;cknnavgkgn;knna
vgkgnd;nnavgkgndd;navgkgnddk;avgkgnddkd;vgkgnddkds;gkgnddkdsv;kgnddkdsv
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tfyesii;vktfyesiin;ktfyesiinl;tfyesiinlg;fyesiinlgn;yesiinlgng;esiinlgn
gf;siinlgngfi;iinlgngfid;inlgngfidv;nlgngfidvf;lgngfidvfn;gngfidvfna;ng
fidvfnaf;gfidvfnafs;fidvfnafsg;idvfnafsgl;dvfnafsglv;vfnafsglva;fnafsgl
vad;nafsglvadt;afsglvadtf;fsglvadtff;sglvadtffk;glvadtffks;lvadtffksd;v
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sdvk;sdpkksdvkt;dpkksdvkty;pkksdvktyf;kksdvktyfe;ksdvktyfes;sdvktyfesi;
dvktyfesis;vktyfesiss;ktyfesisst;tyfesisstl;yfesisstlk;fesisstlka;esiss
tlkat;sisstlkatk;isstlkatkg;sstlkatkgk;stlkatkgkl;tlkatkgkld;lkatkgklde
;katkgkldel;atkgkldelv;tkgkldelvs;kgkldelvsa;gkldelvsak;kldelvsakk;ldel
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asvesav;vkasvesavd;kasvesavde;asvesavdev;svesavdevs;vesavdevsk;esavdevs
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wleemika;kwleemikaa;wleemikaae;leemikaaee;eemikaaeea;emikaaeeaa;mikaaee
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gdsaanhgak;dsaanhgaka;saanhgakad;aanhgakadk;anhgakadkd;nhgakadkds;hgaka
dkdsv;gakadkdsvk;akadkdsvkg;kadkdsvkgi;adkdsvkgia;dkdsvkgiak;kdsvkgiakg
;dsvkgiakgi;svkgiakgik;vkgiakgikg;kgiakgikgi;giakgikgiv;iakgikgivd;akgi
kgivda;kgikgivdaa;gikgivdaag;ikgivdaagk;kgivdaagka;givdaagkal;ivdaagkal
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ddeanada;addeanadag;ddeanadagk;deanadagkl;eanadagklf;anadagklfa;nadagkl
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agnanaavg;agnanaavga;gnanaavgaa;nanaavgaaa;anaavgaaad;naavgaaadi;aavgaa
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vsgeq;avtavsgeqi;vtavsgeqil;tavsgeqilk;avsgeqilka;vsgeqilkai;sgeqilkaiv
;geqilkaive;eqilkaivea;qilkaiveaa;ilkaiveaag;lkaiveaagd;kaiveaagdp;aive
aagdpa;iveaagdpan;veaagdpanq;eaagdpanqa;aagdpanqag;agdpanqagk;gdpanqagk
k;dpanqagkka;panqagkkae;anqagkkaee;nqagkkaeea;qagkkaeeak;agkkaeeakn;gkk
aeeaknp;kkaeeaknpi;kaeeaknpia;aeeaknpiaa;eeaknpiaaa;eaknpiaaai;aknpiaaa
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gtdddnga;igtdddngaa;gtdddngaaf;tdddngaafk;dddngaafkd;ddngaafkde;dngaafk
dem;ngaafkdemk;gaafkdemkk;aafkdemkks;afkdemkksd;fkdemkksdk;kdemkksdki;d
emkksdkia;emkksdkiaa;mkksdkiaaa;kksdkiaaai;ksdkiaaaiv;sdkiaaaivl;dkiaaa
ivlr;kiaaaivlrg;iaaaivlrgv;aaaivlrgva;aaivlrgvak;aivlrgvakd;ivlrgvakdg;
vlrgvakdgk;lrgvakdgkf;rgvakdgkfa;gvakdgkfav;vakdgkfavk;

11 mers:
mkkissaiflt;kkissaiflta;kissaifltal;issaifltall;ssaifltallv;saifltallvf
;aifltallvfi;ifltallvfin;fltallvfinc;ltallvfinck;tallvfinckn;allvfinckn
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fyes;kdsvktfyesi;dsvktfyesii;svktfyesiin;vktfyesiinl;ktfyesiinlg;tfyesi
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fnafsgl;idvfnafsglv;dvfnafsglva;vfnafsglvad;fnafsglvadt;nafsglvadtf;afs
glvadtff;fsglvadtffk;sglvadtffks;glvadtffksd;lvadtffksdp;vadtffksdpk;ad
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dvktyfesiss;vktyfesisst;ktyfesisstl;tyfesisstlk;yfesisstlka;fesisstlkat
;esisstlkatk;sisstlkatkg;isstlkatkgk;sstlkatkgkl;stlkatkgkld;tlkatkgkld
e;lkatkgkldel;katkgkldelv;atkgkldelvs;tkgkldelvsa;kgkldelvsak;gkldelvsa
kk;kldelvsakkg;ldelvsakkge;delvsakkgeg;elvsakkgegg;lvsakkgeggs;vsakkgeg
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sves;ggsvkasvesa;gsvkasvesav;svkasvesavd;vkasvesavde;kasvesavdev;asvesa
vdevs;svesavdevsk;vesavdevskw;esavdevskwl;savdevskwle;avdevskwlee;vdevs
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mikaaee;leemikaaeea;eemikaaeeaa;emikaaeeaak;mikaaeeaakv;ikaaeeaakvg;kaa
eeaakvgg;aaeeaakvggt;aeeaakvggtg;eeaakvggtgg;eaakvggtggd;aakvggtggdg;ak
vggtggdgk;kvggtggdgki;vggtggdgkig;ggtggdgkigd;gtggdgkigds;tggdgkigdsa;g
gdgkigdsaa;gdgkigdsaan;dgkigdsaanh;gkigdsaanhg;kigdsaanhga;igdsaanhgak;
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vlrgvakdgkf;lrgvakdgkfa;rgvakdgkfav;gvakdgkfavk;

13 mers:
mkkissaifltal;kkissaifltall;kissaifltallv;issaifltallvf;ssaifltallvfi;s
aifltallvfin;aifltallvfinc;ifltallvfinck;fltallvfinckn;ltallvfincknn;ta
llvfincknna;allvfincknnav;llvfincknnavg;lvfincknnavgk;vfincknnavgkg;fin
cknnavgkgn;inckknnavgkgnd;nckknnavgkgndd;cknnavgkgnddk;knnavgkgnddkd;nnav
gkgnddkds;navgkgnddkdsv;avgkgnddkdsvk;vgkgnddkdsvkt;gkgnddkdsvktf;kgndd
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fyesiin;dsvktfyesiinl;svktfyesiinlg;vktfyesiinlgn;ktfyesiinlgng;tfyesii
nlgngf;fyesiinlgngfi;yesiinlgngfid;esiinlgngfidv;siinlgngfidvf;iinlgngf
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fsgl;gfidvfnafsglv;fidvfnafsglva;idvfnafsglvad;dvfnafsglvadt;vfnafsglva
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;dpkksdvktyfes;pkksdvktyfesi;kksdvktyfesis;ksdvktyfesiss;sdvktyfesisst;
dvktyfesisstl;vktyfesisstlk;ktyfesisstlka;tyfesisstlkat;yfesisstlkatk;f
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lkatkgkldel;tlkatkgkldelv;lkatkgkldelvs;katkgkldelvsa;atkgkldelvsak;tkg
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14 mers:
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16 mers:
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wleemi;esavdevskwleemik;savdevskwleemika;avdevskwleemikaa;vdevskwleemik
aae;devskwleemikaaee;evskwleemikaaeea;vskwleemikaaeeaa;skwleemikaaeeaak
;kwleemikaaeeaakv;wleemikaaeeaakvg;leemikaaeeaakvgg;eemikaaeeaakvggt;em
ikaaeeaakvggtg;mikaaeeaakvggtgg;ikaaeeaakvggtggd;kaaeeaakvggtggdg;aaeea
akvggtggdgk;aeeaakvggtggdgki;eeaakvggtggdgkig;eaakvggtggdgkigd;aakvggtg
gdgkigds;akvggtggdgkigdsa;kvggtggdgkigdsaa;vggtggdgkigdsaan;ggtggdgkigd
saanh;gtggdgkigdsaanhg;tggdgkigdsaanhga;ggdgkigdsaanhgak;gdgkigdsaanhga
ka;dgkigdsaanhgakad;gkigdsaanhgakadk;kigdsaanhgakadkd;igdsaanhgakadkds;
gdsaanhgakadkdsv;dsaanhgakadkdsvk;saanhgakadkdsvkg;aanhgakadkdsvkgi;anh
gakadkdsvkgia;nhgakadkdsvkgiak;hgakadkdsvkgiakg;gakadkdsvkgiakgi;akadkd
svkgiakgik;kadkdsvkgiakgikg;adkdsvkgiakgikgi;dkdsvkgiakgikgiv;kdsvkgiak
gikgivd;dsvkgiakgikgivda;svkgiakgikgivdaa;vkgiakgikgivdaag;kgiakgikgivd
aagk;giakgikgivdaagka;iakgikgivdaagkal;akgikgivdaagkalg;kgikgivdaagkalg
e;gikgivdaagkalgek;ikgivdaagkalgekg;kgivdaagkalgekga;givdaagkalgekgal;i
vdaagkalgekgalk;vdaagkalgekgalkd;daagkalgekgalkdv;aagkalgekgalkdvk;agka
lgekgalkdvka;gkalgekgalkdvkaa;kalgekgalkdvkaaa;algekgalkdvkaaad;lgekgal
kdvkaaadd;gekgalkdvkaaadde;ekgalkdvkaaaddea;kgalkdvkaaaddean;galkdvkaaa
ddeana;alkdvkaaaddeanad;lkdvkaaaddeanada;kdvkaaaddeanadag;dvkaaaddeanad
agk;vkaaaddeanadagkl;kaaaddeanadagklf;aaaddeanadagklfa;aaddeanadagklfag
;addeanadagklfagn;ddeanadagklfagna;deanadagklfagnan;eanadagklfagnana;an
adagklfagnanaa;nadagklfagnanaav;adagklfagnanaavg;dagklfagnanaavga;agklf
agnanaavgaa;gklfagnanaavgaaa;klfagnanaavgaaad;lfagnanaavgaaadi;fagnanaa
vgaaadia;agnanaavgaaadiak;gnanaavgaaadiaka;nanaavgaaadiakaa;anaavgaaadi
akaag;naavgaaadiakaaga;aavgaaadiakaagav;avgaaadiakaagavt;vgaaadiakaagav
ta;gaaadiakaagavtav;aaadiakaagavtavs;aadiakaagavtavsg;adiakaagavtavsge;
diakaagavtavsgeq;iakaagavtavsgeqi;akaagavtavsgeqil;kaagavtavsgeqilk;aag
avtavsgeqilka;agavtavsgeqilkai;gavtavsgeqilkaiv;avtavsgeqilkaive;vtavsg
eqilkaivea;tavsgeqilkaiveaa;avsgeqilkaiveaag;vsgeqilkaiveaagd;sgeqilkai
veaagdp;geqilkaiveaagdpa;eqilkaiveaagdpan;qilkaiveaagdpanq;ilkaiveaagdp
anqa;lkaiveaagdpanqag;kaiveaagdpanqagk;aiveaagdpanqagkk;iveaagdpanqagkk
a;veaagdpanqagkkae;eaagdpanqagkkaee;aagdpanqagkkaeea;agdpanqagkkaeeak;g
dpanqagkkaeeakn;dpanqagkkaeeaknp;panqagkkaeeaknpi;anqagkkaeeaknpia;nqag
kkaeeaknpiaa;qagkkaeeaknpiaaa;agkkaeeaknpiaaai;gkkaeeaknpiaaaig;kkaeeak
npiaaaigt;kaeeaknpiaaaigtd;aeeaknpiaaaigtdd;eeaknpiaaaigtddd;eaknpiaaai
gtdddn;aknpiaaaigtdddng;knpiaaaigtdddnga;npiaaaigtdddngaa;piaaaigtdddng
aaf;iaaaigtdddngaafk;aaaigtdddngaafkd;aaigtdddngaafkde;aigtdddngaafkdem
;igtdddngaafkdemk;gtdddngaafkdemkk;tdddngaafkdemkks;dddngaafkdemkksd;dd
ngaafkdemkksdk;dngaafkdemkksdki;ngaafkdemkksdkia;gaafkdemkksdkiaa;aafkd
emkksdkiaaa;afkdemkksdkiaaai;fkdemkksdkiaaaiv;kdemkksdkiaaaivl;demkksdk
iaaaivlr;emkksdkiaaaivlrg;mkksdkiaaaivlrgv;kksdkiaaaivlrgva;ksdkiaaaivl
rgvak;sdkiaaaivlrgvakd;dkiaaaivlrgvakdg;kiaaaivlrgvakdgk;iaaaivlrgvakdg
kf;aaaivlrgvakdgkfa;aaivlrgvakdgkfav;aivlrgvakdgkfavk;

Fig. 40.

A) Borrelia burgdorferi MHC class1 & 2 epitopes

<ABX71745 CRASP-2;Protein;Borrelia burgdorferi>

Class 1

MKKSFLSI;KSFLSIYM;SFLSIYML;FLSIYMLI;SIYMLISI;YMLISISL;MLISISLL;LLSCDVSR;DVSRL
NQR;NIDELKIF;ELKIFVEK;KIFVEKAK;IFVEKAKY;FVEKAKYY;EKAKYYSI;KAKYYSIK;YSIKLDAI
;SIKLDAIY;KLDAIYSE;YSEYTGAY;AYNDIMTY;IMTYIMTY;MTYIMTYS;GTSSDKSK;TSSDKSKV;
KSKVNQAI;KVNQAISI;NQAISILK;QAISILKK;SILKKDNK;EEYKPMFL;KPMFLSKL;PMFLSKLI;KLI
DDFAI;FAIELDQA;AIELDQAV;DVSNARHV;HVADSYEK;DSYEKLRK;KLRKSVAL;KSVALAYI;AL
AYIESF;AYIESFDV;YIESFDVI;ESFDVISS;DVISSKFV;SSKFVDSK;KFVDSKFV;KFVEASKK;ASK
KFVNK;KKFVNKAK;FVNKAKEF;FVEENDLI;EENDLIAL;DLIALKCI;LIALKCIV;IALKCIVK;ALKCIV
KT;REINSRSR;EINSRSRY;RSRYNNFY;SRYNNFYK;RYNNFYKK;FYKKEADF;KEADFLGA;EAD
FLGAA;FLGAAVEL;AAVELEGA;AVELEGAY;ELEGAYKA;EGAYKAIK;YKAIKQTL;KAIKQTLL

KSFLSIYML;SFLSIYMLI;FLSIYMLIS;LSIYMLISI;IYMLISISL;YMLISISLL;MLISISLLS;SISLLSCDV;
SLLSCDVSR;LLSCDVSRL;NIDELKIFV;KIFVEKAKY;EKAKYYSIK;YYSIKLDAI;YSIKLDAIY;KLDA
IYSEY;AIYSEYTGA;IYSEYTGAY;EYTGAYNDI;YTGAYNDIM;GAYNDIMTY;AYNDIMTYI;YNDIMT
YIM;DIMTYIMTY;IMTYIMTYS;MTYIMTYSE;YIMTYSEGT;YSEGTSSDK;KVNQAISIL;VNQAISILK
;NQAISILKK;ISILKKDNK;ILKKDNKIV;KIVNKFKEL;ELEKIIEEY;KIIEEYKPM;IEEYKPMFL;EYKPM
FLSK;KPMFLSKLI;FLSKLIDDF;KLIDDFAIE;LIDDFAIEL;FAIELDQAV;DVSNARHVA;NARHVADS
Y;HVADSYEKL;YEKLRKSVA;KLRKSVALA;VALAYIESF;LAYIESFDV;AYIESFDVI;ESFDVISSK;S
FDVISSKF;ISSKFVDSK;FVDSKFVEA;DSKFVEASK;KFVEASKKF;FVEASKKFV;EASKKFVNK;K
FVNKAKEF;FVNKAKEFV;KEFVEENDL;VEENDLIAL;EENDLIALK;DLIALKCIV;LIALKCIVK;ALKCI
VKTI;IVKTIGDMV;TIGDMVNDR;REINSRSRY;RSRYNNFYK;SRYNNFYKK;NFYKKEADF;FYKKE
ADFL;KEADFLGAA;EADFLGAAV;DFLGAAVEL;FLGAAVELE;AAVELEGAY;AVELEGAYK;VELE
GAYKA;ELEGAYKAI;AYKAIKQTL;YKAIKQTLL

KSFLSIYMLI;FLSIYMLISI;SIYMLISISL;IYMLISISLL;YMLISISLLS;MLISISLLSC;ISLLSCDVSR;SL
LSCDVSRL;RLNQRNIDEL;ELKIFVEKAK;KIFVEKAKYY;FVEKAKYYSI;KYYSIKLDAI;YYSIKLDAI
Y;KLDAIYSEYT;AIYSEYTGAY;SEYTGAYNDI;TGAYNDIMTY;GAYNDIMTYI;AYNDIMTYIM;DIMT
YIMTYS;TYSEGTSSDK;KVNQAISILK;VNQAISILKK;AISILKKDNK;SILKKDNKIV;KDNKIVNKFK;I
VNKFKELEK;KELEKIIEEY;ELEKIIEEYK;KIIEEYKPMF;IIEEYKPMFL;EEYKPMFLSK;EYKPMFLS
KL;MFLSKLIDDF;FLSKLIDDFA;KLIDDFAIEL;ELDQAVDNDV;AVDNDVSNAR;ARHVADSYEK;H
VADSYEKLR;VADSYEKLRK;YEKLRKSVAL;KLRKSVALAY;SVALAYIESF;ALAYIESFDV;LAYIES
FDVI;ESFDVISSKF;SFDVISSKFV;VISSKFVDSK;ISSKFVDSKF;DSKFVEASKK;EASKKFVNKA;A
SKKFVNKAK;KEFVEENDLI;FVEENDLIAL;EENDLIALKC;DLIALKCIVK;CIVKTIGDMV;KTIGDMV
NDR;MVNDREINSR;NSRSRYNNFY;RSRYNNFYKK;KEADFLGAAV;FLGAAVELEG;GAAVELEG
AY;AAVELEGAYK;VELEGAYKAI;ELEGAYKAIK;GAYKAIKQTL;AYKAIKQTLL

SFLSIYMLISI;FLSIYMLISIS;LSIYMLISISL;SIYMLISISLL;IYMLISISLLS;YMLISISLLSC;LISISLLSC
DV;SISLLSCDVSR;LSCDVSRLNQR;RLNQRNIDELK;NQRNIDELKIF;NIDELKIFVEK;ELKIFVEK
AKY;FVEKAKYYSIK;VEKAKYYSIKL;KYYSIKLDAIY;SIKLDAIYSEY;KLDAIYSEYTG;DAIYSEYTG
AY;SEYTGAYNDIM;YTGAYNDIMTY;TGAYNDIMTYI;GAYNDIMTYIM;YNDIMTYIMTY;MTYIMTY
SEGT;YIMTYSEGTSS;MTYSEGTSSDK;KVNQAISILKK;QAISILKKDNK;ILKKDNKIVNK;KIVNKF
KELEK;KIIEEYKPMFL;EEYKPMFLSKL;EYKPMFLSKLI;PMFLSKLIDDF;FLSKLIDDFAI;LIDDFAI
ELDQ;QAVDNDVSNAR;VSNARHVADSY;NARHVADSYEK;HVADSYEKLRK;SYEKLRKSVAL;KL
RKSVALAYI;KSVALAYIESF;VALAYIESFDV;ALAYIESFDVI;YIESFDVISSK;IESFDVISSKF;ESFD
VISSKFV;DVISSKFVDSK;FVDSKFVEASK;FVEASKKFVNK;EASKKFVNKAK;KEFVEENDLIA;EF
VEENDLIAL;FVEENDLIALK;EENDLIALKCI;LIALKCIVKTI;TIGDMVNDREI;DMVNDREINSR;EINS
RSRYNNF;NSRSRYNNFYK;EADFLGAAVEL;FLGAAVELEGA;LGAAVELEGAY;GAAVELEGAYK
;EGAYKAIKQTL;GAYKAIKQTLL

Class 2

ADFLGAAVELEGAYK;FLGAAVELE;ADSYEKLRKSVALAY;EKLRKSVAL;ADSYEKLRKSVALAY;
YEKLRKSVA;AISILKKDNKIVNKF;LKKDNKIVN;AYIESFDVISSKFVD;FDVISSKFV;AYNDIMTYIM
TYSEG;YNDIMTYIM;DAIYSEYTGAYNDIM;IYSEYTGAY;DDFAIELDQAVDNDV;FAIELDQAV;DF
LGAAVELEGAYKA;FLGAAVELE;DIMTYIMTYSEGTSS;IMTYSEGTS;DIMTYIMTYSEGTSS;YIMT
YSEGT;DKSKVNQAISILKKD;VNQAISILK;DLIALKCIVKTIGDM;IALKCIVKT;DQAVDNDVSNARH
VA;VDNDVSNAR;DSKFVEASKKFVNKA;FVEASKKFV;DSYEKLRKSVALAYI;LRKSVALAY;DSY
EKLRKSVALAYI;YEKLRKSVA;EADFLGAAVELEGAY;FLGAAVELE;EENDLIALKCIVKTI;IALKCIV
KT;EEYKPMFLSKLIDDF;YKPMFLSKL;EKIIEEYKPMFLSKL;IEEYKPMFL;EKLRKSVALAYIESF;L
RKSVALAY;ELDQAVDNDVSNARH;VDNDVSNAR;ELEKIIEEYKPMFLS;IEEYKPMFL;ENDLIALK
CIVKTIG;IALKCIVKT;ESFDVISSKFVDSKF;FDVISSKFV;EYKPMFLSKLIDDFA;YKPMFLSKL;EY
TGAYNDIMTYIMT;YNDIMTYIM;FDVISSKFVDSKFVE;FDVISSKFV;FLGAAVELEGAYKAI;VELE
GAYKA;FLSIYMLISISLLSC;FLSIYMLIS;FLSIYMLISISLLSC;IYMLISISL;FLSIYMLISISLLSC;MLIS
ISLLS;FVDSKFVEASKKFVN;FVEASKKFV;GAYNDIMTYIMTYSE;YNDIMTYIM;IALKCIVKTIGDM
VN;IALKCIVKT;IALKCIVKTIGDMVN;LKCIVKTIG;IDDFAIELDQAVDND;FAIELDQAV;IEEYKPMF
LSKLIDD;YKPMFLSKL;IELDQAVDNDVSNAR;IELDQAVDN;IESFDVISSKFVDSK;FDVISSKFV;II
EEYKPMFLSKLID;YKPMFLSKL;IKLDAIYSEYTGAYN;IYSEYTGAY;IKLDAIYSEYTGAYN;LDAIY
SEYT;IMTYIMTYSEGTSSD;IMTYSEGTS;IMTYIMTYSEGTSSD;YIMTYSEGT;ISILKKDNKIVNKF
K;LKKDNKIVN;IYMLISISLLSCDVS;IYMLISISL;IYMLISISLLSCDVS;LISISLLSC;IYMLISISLLSCD
VS;MLISISLLS;KEADFLGAAVELEGA;FLGAAVELE;KELEKIIEEYKPMFL;IIEEYKPMF;KFVDSKF
VEASKKFV;FVDSKFVEA;KIIEEYKPMFLSKLI;IEEYKPMFL;KIIEEYKPMFLSKLI;YKPMFLSKL;KK
EADFLGAAVELEG;FLGAAVELE;KKSFLSIYMLISISL;FLSIYMLIS;KKSFLSIYMLISISL;LSIYMLISI
;KLDAIYSEYTGAYND;IYSEYTGAY;KLDAIYSEYTGAYND;LDAIYSEYT;KLIDDFAIELDQAVD;FAI
ELDQAV;KLRKSVALAYIESFD;LRKSVALAY;KSFLSIYMLISISLL;FLSIYMLIS;KSFLSIYMLISISLL;
IYMLISISL;KSKVNQAISILKKDN;VNQAISILK;KVNQAISILKKDNKI;VNQAISILK;KYYSIKLDAIYSE
YT;YSIKLDAIY;LAYIESFDVISSKFV;SFDVISSKF;LAYIESFDVISSKFV;YIESFDVIS;LDAIYSEYT
GAYNDI;IYSEYTGAY;LDAIYSEYTGAYNDI;LDAIYSEYT;LDQAVDNDVSNARHV;VDNDVSNAR;
LEKIIEEYKPMFLSK;IEEYKPMFL;LIALKCIVKTIGDMV;LKCIVKTIG;LIDDFAIELDQAVDN;FAIELD
QAV;LRKSVALAYIESFDV;LRKSVALAY;LSIYMLISISLLSCD;IYMLISISL;LSIYMLISISLLSCD;MLI
SISLLS;MKKSFLSIYMLISIS;FLSIYMLIS;MLISISLLSCDVSRL;ISLLSCDVS;MLISISLLSCDVSRL;
MLISISLLS;MTYIMTYSEGTSSDK;YIMTYSEGT;MVNDREINSRSRYNN;REINSRSRY;NDIMTYIM
TYSEGTS;IMTYIMTYS;NDIMTYIMTYSEGTS;YIMTYSEGT;NDLIALKCIVKTIGD;IALKCIVKT;ND
REINSRSRYNNFY;REINSRSRY;NQAISILKKDNKIVN;ISILKKDNK;QAISILKKDNKIVNK;ISILKKD
NK;QAVDNDVSNARHVAD;VDNDVSNAR;SDKSKVNQAISILKK;VNQAISILK;SEYTGAYNDIMTYI
M;AYNDIMTYI;SEYTGAYNDIMTYIM;YTGAYNDIM;SFDVISSKFVDSKFV;FDVISSKFV;SFLSIYM
LISISLLS;IYMLISISL;SFLSIYMLISISLLS;YMLISISLL;SIKLDAIYSEYTGAY;LDAIYSEYT;SIYMLISI
SLLSCDV;IYMLISISL;SIYMLISISLLSCDV;MLISISLLS;SIYMLISISLLSCDV;YMLISISLL;SKFVEA
SKKFVNKAK;FVEASKKFV;SKLIDDFAIELDQAV;LIDDFAIEL;SKVNQAISILKKDNK;VNQAISILK;S
SDKSKVNQAISILK;KVNQAISIL;SYEKLRKSVALAYIE;LRKSVALAY;TGAYNDIMTYIMTYS;YNDI
MTYIM;TYIMTYSEGTSSDKS;YIMTYSEGT;VDSKFVEASKKFVNK;FVEASKKFV;VEENDLIALKC
IVKT;ENDLIALKC;VELEGAYKAIKQTLL;VELEGAYKA;VNDREINSRSRYNNF;REINSRSRY;VNQ
AISILKKDNKIV;ISILKKDNK;YEKLRKSVALAYIES;LRKSVALAY;YIESFDVISSKFVDS;FDVISSKF
V;YIMTYSEGTSSDKSK;YIMTYSEGT;YKKEADFLGAAVELE;YKKEADFLG;YKPMFLSKLIDDFAI;
YKPMFLSKL;YMLISISLLSCDVSR;ISLLSCDVS;YMLISISLLSCDVSR;MLISISLLS;YNDIMTYIMTY
SEGT;DIMTYIMTY;YNDIMTYIMTYSEGT;IMTYIMTYS;YNDIMTYIMTYSEGT;YNDIMTYIM;YSIKL
DAIYSEYTGA;LDAIYSEYT;YTGAYNDIMTYIMTY;YNDIMTYIM;YYSIKLDAIYSEYTG;LDAIYSEY
T

<NP_045689 outer surface protein B;Protein;Borrelia burgdorferi B31>

Class 1

RLLIGFAL;LLIGFALA;LIGFALAL;FALALALI;ALALIGCA;ALIGCAQK;AQKGAESI;LPAVTEDS;VSL
FNGNK;SLFNGNKI;LFNGNKIF;KIFVSKEK;KEKNSSGK;SSGKYDLR;KYDLRATI;ATIDQVEL;TID
QVELK;ELKGTSDK;GSKPDKSK;KVKLTVSA;KLTVSADL;VSADLNTV;NTVTLEAF;EAFDASNQ;
NQKISSKV;KISSKVTK;ISSKVTKK;SITXETLK;ETLKANKL;KANKLDSK;KLDSKKLT;TRSNGTTL;

TTLEYSQI;ATKAVETL;ETLKNSIK;TLKNSIKL;SIKLEGSL;IKLEGSLV;SLVGGKTT;LVGGKTTV;IK
EGTVTL;EGTVTLKR;TLKREIEK;FLNDTAGS;DTAGSNKK;GSNKKTGK;WEDSTSTL;TSTLTISA;
LTISADSK;TISADSKK;SADSKKTK;KTKDLVFL;VFLTDGTI;FLTDGTIT;LTDGTITV;GTITVQQY;Q
QYNTAGT;NTAGTSLE;EIKNLSEL;NLSELKNA

MRLLIGFAL;RLLIGFALA;LLIGFALAL;LIGFALALA;ALALALIGC;LALALIGCA;LALIGCAQK;GAESI
GSQK;SQKENDLNL;SKKSHQNAK;LPAVTEDSV;AVTEDSVSL;VTEDSVSLF;SVSLFNGNK;SLF
NGNKIF;LFNGNKIFV;NSSGKYDLR;DLRATIDQV;ATIDQVELK;GSGTLEGSK;KPDKSKVKL;TVS
ADLNTV;SADLNTVTL;DLNTVTLEA;VTLEAFDAS;EAFDASNQK;ASNQKISSK;KISSKVTKK;KQG
SITXET;GSITXETLK;SITXETLKA;KANKLDSKK;KLDSKKLTR;LTRSNGTTL;RSNGTTLEY;TTLEY
SQIT;SQITDADNA;ITDADNATK;DADNATKAV;ATKAVETLK;ETLKNSIKL;SIKLEGSLV;SLVGGK
TTV;TTVEIKEGT;EIKEGTVTL;VTLKREIEK;GSNKKTGKW;STSTLTISA;TLTISADSK;LTISADSKK
;ISADSKKTK;KTKDLVFLT;FLTDGTITV;VQQYNTAGT;QYNTAGTSL;SLEGSASEI;SEIKNLSEL;E
IKNLSELK;NLSELKNAL;LSELKNALK

RLLIGFALAL;LLIGFALALA;LIGFALALAL;IGFALALALI;FALALALIGC;ALALALIGCA;ALALIGCAQ
K;ALIGCAQKGA;DLNLEDSSKK;SSKKSHQNAK;DLPAVTEDSV;LPAVTEDSVS;AVTEDSVSLF;D
SVSLFNGNK;SVSLFNGNKI;VSLFNGNKIF;SLFNGNKIFV;VSKEKNSSGK;RATIDQVELK;GTLEG
SKPDK;GSKPDKSKVK;LTVSADLNTV;DLNTVTLEAF;EAFDASNQKI;DASNQKISSK;KQGSITXE
TL;ITXETLKANK;TLKANKLDSK;KLDSKKLTRS;KLTRSNGTTL;SQITDADNAT;QITDADNATK;NA
TKAVETLK;KAVETLKNSI;AVETLKNSIK;VETLKNSIKL;NSIKLEGSLV;KLEGSLVGGK;SLVGGKT
TVE;LVGGKTTVEI;TTVEIKEGTV;VEIKEGTVTL;EIKEGTVTLK;TVTLKREIEK;EIEKDGKVKV;IEK
DGKVKVF;FLNDTAGSNK;TAGSNKKTGK;WEDSTSTLTI;STLTISADSK;TLTISADSKK;TISADSK
KTK;VFLTDGTITV;FLTDGTITVQ;QQYNTAGTSL;NTAGTSLEGS;SLEGSASEIK;NLSELKNALK

MRLLIGFALAL;RLLIGFALALA;LLIGFALALAL;LIGFALALALI;FALALALIGCA;ALALALIGCAQ;LAL
ALIGCAQK;DSSKKSHQNAK;HQNAKQDLPAV;LPAVTEDSVSL;DSVSLFNGNKI;SVSLFNGNKIF;
SLFNGNKIFVS;LFNGNKIFVSK;FVSKEKNSSGK;VSKEKNSSGKY;KEKNSSGKYDL;DLRATIDQ
VEL;KPDKSKVKLTV;KLTVSADLNTV;TVSADLNTVTL;TLEAFDASNQK;DASNQKISSKV;KQGSI
TXETLK;SITXETLKANK;ETLKANKLDSK;TLKANKLDSKK;LTRSNGTTLEY;TTLEYSQITDA;SQIT
DADNATK;ITDADNATKAV;DNATKAVETLK;KAVETLKNSIK;EGSLVGGKTTV;SLVGGKTTVEI;LV
GGKTTVEIK;EIKEGTVTLKR;GTVTLKREIEK;EIEKDGKVKVF;IEKDGKVKVFL;VFLNDTAGSNK;F
LNDTAGSNKK;DTAGSNKKTGK;KWEDSTSTLTI;TSTLTISADSK;STLTISADSKK;LTISADSKKTK
;SADSKKTKDLV;LVFLTDGTITV;FLTDGTITVQQ;LTDGTITVQQY;VQQYNTAGTSL;NTAGTSLE
GSA;TSLEGSASEIK;LEGSASEIKNL;SASEIKNLSEL;ASEIKNLSELK

Class 2

ALIGCAQKGAESIGS;LIGCAQKGA;ANKLDSKKLTRSNGT;LDSKKLTRS;ASEIKNLSELKNALK;IK
NLSELKN;ASNQKISSKVTKKQG;ISSKVTKKQ;AVETLKNSIKLEGSL;LKNSIKLEG;DASNQKISSK
VTKKQ;NQKISSKVT;DGKVKVFLNDTAGSN;VKVFLNDTA;DGTITVQQYNTAGTS;VQQYNTAGT;
DKSKVKLTVSADLNT;VKLTVSADL;DLVFLTDGTITVQQY;FLTDGTITV;DSVSLFNGNKIFVSK;VS
LFNGNKI;EDSVSLFNGNKIFVS;VSLFNGNKI;EGSASEIKNLSELKN;SASEIKNLS;EGSLVGGKTT
VEIKE;VGGKTTVEI;ETLKNSIKLEGSLVG;KNSIKLEGS;ETLKNSIKLEGSLVG;LKNSIKLEG;FALA
LALIGCAQKGA;FALALALIG;FLTDGTITVQQYNTA;FLTDGTITV;FNGNKIFVSKEKNSS;FNGNKIF
VS;GFALALALIGCAQKG;FALALALIG;GKVKVFLNDTAGSNK;VKVFLNDTA;GKWEDSTSTLTISA
D;WEDSTSTLT;GNKIFVSKEKNSSGK;FVSKEKNSS;GSASEIKNLSELKNA;IKNLSELKN;GSITXE
TLKANKLDS;XETLKANKL;GSLVGGKTTVEIKEG;VGGKTTVEI;GTITVQQYNTAGTSL;VQQYNT
AGT;IGFALALALIGCAQK;FALALALIG;IKLEGSLVGGKTTVE;IKLEGSLVG;ITVQQYNTAGTSLEG
;VQQYNTAGT;ITVQQYNTAGTSLEG;YNTAGTSLE;KANKLDSKKLTRSNG;LDSKKLTRS;KAVET
LKNSIKLEGS;LKNSIKLEG;KDGKVKVFLNDTAGS;VKVFLNDTA;KDLVFLTDGTITVQQ;FLTDGTI
TV;KIFVSKEKNSSGKYD;FVSKEKNSS;KKTGKWEDSTSTLTI;WEDSTSTLT;KLEGSLVGGKTTV
EI;LVGGKTTVE;KLTVSADLNTVTLEA;VSADLNTVT;KNSIKLEGSLVGGKT;IKLEGSLVG;KPDKS
KVKLTVSADL;SKVKLTVSA;KQGSITXETLKANKL;ITXETLKAN;KSKVKLTVSADLNTV;VKLTVSA
DL;KTGKWEDSTSTLTIS;WEDSTSTLT;KTKDLVFLTDGTITV;VFLTDGTIT;KVKLTVSADLNTVTL;
LTVSADLNT;KVKVFLNDTAGSNKK;FLNDTAGSN;KWEDSTSTLTISADS;WEDSTSTLT;LDSKKL

TRSNGTTLE;LTRSNGTTL;LEGSLVGGKTTVEIK;VGGKTTVEI;LIGFALALALIGCAQ;FALALALIG
;LKANKLDSKKLTRSN;LDSKKLTRS;LKNSIKLEGSLVGGK;IKLEGSLVG;LKNSIKLEGSLVGGK;L
KNSIKLEG;LLIGFALALALIGCA;FALALALIG;LLIGFALALALIGCA;IGFALALAL;LTVSADLNTVTLE
AF;VSADLNTVT;LVFLTDGTITVQQYN;FLTDGTITV;LVGGKTTVEIKEGTV;VGGKTTVEI;MRLLIG
FALALALIG;IGFALALAL;MRLLIGFALALALIG;LIGFALALA;NGNKIFVSKEKNSSG;FVSKEKNSS;
NKIFVSKEKNSSGKY;FVSKEKNSS;NKKTGKWEDSTSTLT;GKWEDSTST;NKLDSKKLTRSNGT
T;LDSKKLTRS;NSIKLEGSLVGGKTT;IKLEGSLVG;NTAGTSLEGSASEIK;GTSLEGSAS;PDKSKV
KLTVSADLN;VKLTVSADL;QGSITXETLKANKLD;XETLKANKL;QQYNTAGTSLEGSAS;YNTAGT
SLE;QYNTAGTSLEGSASE;YNTAGTSLE;RLLIGFALALALIGC;FALALALIG;RLLIGFALALALIGC;I
GFALALAL;RLLIGFALALALIGC;LIGFALALA;SASEIKNLSELKNAL;IKNLSELKN;SIKLEGSLVGG
KTTV;IKLEGSLVG;SKVKLTVSADLNTVT;VKLTVSADL;SKVTKKQGSITXETL;VTKKQGSIT;SLV
GGKTTVEIKEGT;VGGKTTVEI;SSKVTKKQGSITXET;VTKKQGSIT;SVSLFNGNKIFVSKE;VSLFN
GNKI;TAGTSLEGSASEIKN;LEGSASEIK;TDGTITVQQYNTAGT;ITVQQYNTA;TEDSVSLFNGNKI
FV;VSLFNGNKI;TGKWEDSTSTLTISA;WEDSTSTLT;TITVQQYNTAGTSLE;VQQYNTAGT;TKAV
ETLKNSIKLEG;VETLKNSIK;TKDLVFLTDGTITVQ;FLTDGTITV;TLKANKLDSKKLTRS;ANKLDSK
KL;TLKNSIKLEGSLVGG;IKLEGSLVG;TLKNSIKLEGSLVGG;LKNSIKLEG;TVQQYNTAGTSLEG
S;YNTAGTSLE;VETLKNSIKLEGSLV;LKNSIKLEG;VFLTDGTITVQQYNT;FLTDGTITV;VGGKTTV
EIKEGTVT;VGGKTTVEI;VKLTVSADLNTVTLE;LTVSADLNT;VKVFLNDTAGSNKKT;FLNDTAGS
N;VQQYNTAGTSLEGSA;YNTAGTSLE;VSLFNGNKIFVSKEK;VSLFNGNKI;VTEDSVSLFNGNKI
F;VSLFNGNKI;WEDSTSTLTISADSK;WEDSTSTLT;YNTAGTSLEGSASEI;YNTAGTSLE

<NP_047005 outer surface protein C;Protein;Borrelia burgdorferi B31>

Class 1

NTLSAILM;TLSAILMT;LSAILMTL;SAILMTLF;AILMTLFL;ILMTLFLF;LMTLFLFI;TLFLFISC;ISCNN
SGK;NSADESVK;NLTEISKK;KITDSNAV;NAVLLAVK;VLLAVKEV;AVKEVEAL;KEVEALLS;LLSSI
DEI;SIDEIAAK;IAAKAIGK;AAKAIGKK;KIHQNNGL;GSLLAGAY;SLLAGAYA;LLAGAYAI;GAYAIST
L;AYAISTLI;YAISTLIK;ISTLIKQK;KQKLDGLK;KLDGLKNE;GLKNEGLK;GLKEKIDA;EKIDAAKK;C
SETFTNK;SETFTNKL;ETFTNKLK;FTNKLKEK;GVTDADAK;DAKEAILK;ILKTNGTK;KTNGTKTK;
AEELGKLF;KLFESVEV;ESVEVLSK;EVLSKAAK;KEMLANSV;EMLANSVK;KELTSPVV;ELTSPV
VA;PVVAESPK;VVAESPKK

MKKNTLSAI;NTLSAILMT;TLSAILMTL;LSAILMTLF;SAILMTLFL;AILMTLFLF;ILMTLFLFI;FLFISC
NNS;FISCNNSGK;SANSADESV;DESVKGPNL;NLTEISKKI;KKITDSNAV;KITDSNAVL;ITDSNAV
LL;DSNAVLLAV;AVLLAVKEV;LLAVKEVEA;LAVKEVEAL;AVKEVEALL;EVEALLSSI;ALLSSIDEI;
LLSSIDEIA;SSIDEIAAK;SIDEIAAKA;EIAAKAIGK;IAAKAIGKK;HQNNGLDTE;TENNHNGSL;NGS
LLAGAY;SLLAGAYAI;LLAGAYAIS;GAYAISTLI;AYAISTLIK;AISTLIKQK;LIKQKLDGL;KLDGLKNE
G;GLKEKIDAA;ETFTNKLKE;KLKEKHTDL;KEKHTDLGK;HTDLGKEGV;AILKTNGTK;ELGKLFES
V;KLFESVEVL;ESVEVLSKA;VLSKAAKEM;MLANSVKEL;SVKELTSPV;LTSPVVAES;PVVAESP
KK

NTLSAILMTL;TLSAILMTLF;LSAILMTLFL;SAILMTLFLF;AILMTLFLFI;ILMTLFLFIS;LMTLFLFISC;
FLFISCNNSG;LFISCNNSGK;TSANSADESV;SANSADESVK;SVKGPNLTEI;KGPNLTEISK;KITD
SNAVLL;DSNAVLLAVK;NAVLLAVKEV;VLLAVKEVEA;LLAVKEVEAL;KEVEALLSSI;EALLSSIDEI
;ALLSSIDEIA;LLSSIDEIAA;LSSIDEIAAK;SSIDEIAAKA;SIDEIAAKAI;EIAAKAIGKK;DTENNHNGS
L;TENNHNGSLL;SLLAGAYAIS;LLAGAYAIST;LAGAYAISTL;AGAYAISTLI;GAYAISTLIK;YAISTLI
KQK;AISTLIKQKL;TLIKQKLDGL;KLDGLKNEGL;GLKNEGLKEK;CSETFTNKLK;ETFTNKLKEK;E
AILKTNGTK;ILKTNGTKTK;KTKGAEELGK;KLFESVEVLS;ESVEVLSKAA;SVEVLSKAAK;EVLSK
AAKEM;VLSKAAKEML;AAKEMLANSV;EMLANSVKEL;MLANSVKELT;NSVKELTSPV;SVKELTS
PVV;TSPVVAESPK

NTLSAILMTLF;TLSAILMTLFL;LSAILMTLFLF;SAILMTLFLFI;ILMTLFLFISC;FLFISCNNSGK;NTS
ANSADESV;TSANSADESVK;ESVKGPNLTEI;KITDSNAVLLA;ITDSNAVLLAV;VLLAVKEVEAL;LL
AVKEVEALL;ALLSSIDEIAA;LLSSIDEIAAK;EIAAKAIGKKI;DTENNHNGSLL;NHNGSLLAGAY;NG
SLLAGAYAI;SLLAGAYAIST;LLAGAYAISTL;LAGAYAISTLI;AYAISTLIKQK;YAISTLIKQKL;TLIKQ

KLDGLK;KLDGLKNEGLK;GLKEKIDAAKK;KCSETFTNKLK;ETFTNKLKEKH;KLKEKHTDLGK;GV
TDADAKEAI;AILKTNGTKTK;AEELGKLFESV;ELGKLFESVEV;KLFESVEVLSK;ESVEVLSKAAK;
VEVLSKAAKEM;EVLSKAAKEML;VLSKAAKEMLA;KAAKEMLANSV;AAKEMLANSVK;KEMLANS
VKEL;MLANSVKELTS;SVKELTSPVVA;LTSPVVAESPK;TSPVVAESPKK

Class 2

ADAKEAILKTNGTKT;EAILKTNGT;ADESVKGPNLTEISK;VKGPNLTEI;AGAYAISTLIKQKLD;ISTL
IKQKL;AGAYAISTLIKQKLD;YAISTLIKQ;AILKTNGTKTKGAEE;LKTNGTKTK;AILMTLFLFISCNN
S;LMTLFLFIS;AKEAILKTNGTKTKG;ILKTNGTKT;AKEAILKTNGTKTKG;LKTNGTKTK;AKEMLAN
SVKELTSP;LANSVKELT;AKEMLANSVKELTSP;MLANSVKEL;ANSVKELTSPVVAES;VKELTSP
VV;AVKEVEALLSSIDEI;VKEVEALLS;AVLLAVKEVEALLSS;VKEVEALLS;AYAISTLIKQKLDGL;I
STLIKQKL;CSETFTNKLKEKHTD;FTNKLKEKH;DAKEAILKTNGTKTK;EAILKTNGT;DESVKGPNL
TEISKK;VKGPNLTEI;DGLKNEGLKEKIDAA;LKNEGLKEK;DLGKEGVTDADAKEA;LGKEGVTDA;
EAILKTNGTKTKGAE;ILKTNGTKT;EAILKTNGTKTKGAE;LKTNGTKTK;EGVTDADAKEAILKT;VT
DADAKEA;EISKKITDSNAVLLA;ITDSNAVLL;EMLANSVKELTSPVV;LANSVKELT;EMLANSVKEL
TSPVV;MLANSVKEL;EMLANSVKELTSPVV;NSVKELTSP;EMLANSVKELTSPVV;SVKELTSPV;
ESVEVLSKAAKEMLA;LSKAAKEML;ESVEVLSKAAKEMLA;VLSKAAKEM;ESVKGPNLTEISKKI;V
KGPNLTEI;ETFTNKLKEKHTDLG;FTNKLKEKH;EVLSKAAKEMLANSV;VLSKAAKEM;FESVEVL
SKAAKEML;EVLSKAAKE;FESVEVLSKAAKEML;VLSKAAKEM;GAYAISTLIKQKLDG;ISTLIKQKL
;GKEGVTDADAKEAIL;VTDADAKEA;GSLLAGAYAISTLIK;LAGAYAIST;HNGSLLAGAYAISTL;LA
GAYAIST;ILKTNGTKTKGAEEL;LKTNGTKTK;ILMTLFLFISCNNSG;FLFISCNNS;ISKKITDSNAVL
LAV;ITDSNAVLL;ITDSNAVLLAVKEVE;ITDSNAVLL;KCSETFTNKLKEKHT;FTNKLKEKH;KEAILK
TNGTKTKGA;ILKTNGTKT;KEAILKTNGTKTKGA;LKTNGTKTK;KEGVTDADAKEAILK;VTDADAK
EA;KELTSPVVAESPKKP;LTSPVVAES;KEMLANSVKELTSPV;LANSVKELT;KEMLANSVKELTS
PV;MLANSVKEL;KITDSNAVLLAVKEV;ITDSNAVLL;KKCSETFTNKLKEKH;KKCSETFTN;KKITD
SNAVLLAVKE;ITDSNAVLL;KKNTLSAILMTLFLF;LSAILMTLF;KLDGLKNEGLKEKID;LKNEGLKE
K;KNTLSAILMTLFLFI;LSAILMTLF;KQKLDGLKNEGLKEK;KQKLDGLKN;KAAKEMLANSVKELT;
AKEMLANSV;KAAKEMLANSVKELT;MLANSVKEL;LAGAYAISTLIKQKL;LAGAYAIST;LAGAYAIS
TLIKQKL;YAISTLIKQ;LANSVKELTSPVVAE;LANSVKELT;LANSVKELTSPVVAE;VKELTSPVV;L
AVKEVEALLSSIDE;VKEVEALLS;LDGLKNEGLKEKIDA;LKNEGLKEK;LFESVEVLSKAAKEM;SV
EVLSKAA;LFLFISCNNSGKDGN;LFISCNNSG;LGKEGVTDADAKEAI;VTDADAKEA;LKTNGTKTK
GAEELG;LKTNGTKTK;LLAGAYAISTLIKQK;LAGAYAIST;LLAVKEVEALLSSID;VKEVEALLS;LM
TLFLFISCNNSGK;LFISCNNSG;LSAILMTLFLFISCN;LMTLFLFIS;LSKAAKEMLANSVKE;AKEML
ANSV;LSSIDEIAAKAIGKK;IDEIAAKAI;MKKNTLSAILMTLFL;KNTLSAILM;MKKNTLSAILMTLFL;
MKKNTLSAI;MLANSVKELTSPVVA;LANSVKELT;MLANSVKELTSPVVA;VKELTSPVV;MTLFLFI
SCNNSGKD;LFISCNNSG;NAVLLAVKEVEALLS;LAVKEVEAL;NGSLLAGAYAISTLI;LAGAYAIST;
NHNGSLLAGAYAIST;LLAGAYAIS;NNHNGSLLAGAYAIS;SLLAGAYAI;NSADESVKGPNLTEI;ES
VKGPNLT;NSVKELTSPVVAESP;VKELTSPVV;NTLSAILMTLFLFIS;LSAILMTLF;QKLDGLKNEG
LKEKI;LKNEGLKEK;SADESVKGPNLTEIS;VKGPNLTEI;SAILMTLFLFISCNN;LMTLFLFIS;SETF
TNKLKEKHTDL;FTNKLKEKH;SKKITDSNAVLLAVK;ITDSNAVLL;SKAAKEMLANSVKEL;AKEML
ANSV;SLLAGAYAISTLIKQ;LAGAYAIST;SSIDEIAAKAIGKKI;IDEIAAKAI;SVEVLSKAAKEMLAN;L
SKAAKEML;SVEVLSKAAKEMLAN;VLSKAAKEM;SVKELTSPVVAESPK;VKELTSPVV;TEISKKIT
DSNAVLL;KKITDSNAV;TLFLFISCNNSGKDG;LFISCNNSG;TLSAILMTLFLFISC;LMTLFLFIS;VE
VLSKAAKEMLANS;VLSKAAKEM;VKELTSPVVAESPKK;VKELTSPVV;VKEVEALLSSIDEIA;VKE
VEALLS;VLLAVKEVEALLSSI;VKEVEALLS;VLSKAAKEMLANSVK;VLSKAAKEM;YAISTLIKQKL
DGLK;ISTLIKQKL;AAKEMLANSVKELTS;LANSVKELT;AAKEMLANSVKELTS;MLANSVKEL

B) Borrelia afzelii MHC class1 & 2 epitopes

<CAA59725 outer surface protein A;Protein;Borrelia afzelii>

Class 1

KYLLGIGL;YLLGIGLI;LLGIGLIL;GIGLILAL;GLILALIA;ILALIACK;LIACKQNV;NVSSLDEK;SLDEK
NSA;SVDLPGEM;DLPGEMKV;LPGEMKVL;EMKVLVSK;KVLVSKEK;SLKATVDK;ATVDKIEL;TV
DKIELK;ELKGTSDK;GTKDDKSK;KLTIADDL;TIADDLSK;KTTFELFK;TTFELFKE;ELFKEDGK;FK

EDGKTL;KEDGKTLV;VSRKVSSK;KTSTDEMF;GELSAKTM;LSAKTMTR;MTRENGTK;TRENGT
KL;KLEYTEMK;GTGKAKEV;EVLKNFTL;FTLEGKVA;VANDKVTL;VKEGTVTL;TLSKEIAK;EIAKS
GEV;ALNDTNTT;NTTQATKK;ATKKTGAW;KTGAWDSK;TSTLTISV;LTISVNSK;TISVNSKK;TTQ
LVFTK;TKQDTITV;DTITVQKY;EGTAVEIK;TAVEIKTL;EIKTLDEL;TLDELKNA

KYLLGIGLI;YLLGIGLIL;LLGIGLILA;GIGLILALI;LILALIACK;ALIACKQNV;SLDEKNSAS;SVDLPGE
MK;VDLPGEMKV;DLPGEMKVL;LPGEMKVLV;GKYSLKATV;YSLKATVDK;SLKATVDKI;ATVDKI
ELK;GSGVLEGTK;LTIADDLSK;TIADDLSKT;DLSKTTFEL;SKTTFELFK;FKEDGKTLV;LVSRKVS
SK;SRKVSSKDK;STDEMFNEK;EMFNEKGEL;ELSAKTMTR;TMTRENGTK;MTRENGTKL;RENG
TKLEY;KSDGTGKAK;TGKAKEVLK;KEVLKNFTL;KVANDKVTL;ANDKVTLEV;TLEVKEGTV;EVK
EGTVTL;VTLSKEIAK;KEIAKSGEV;IAKSGEVTV;KSGEVTVAL;TVALNDTNT;ALNDTNTTQ;DTNT
TQATK;KKTGAWDSK;KTSTLTISV;TLTISVNSK;LTISVNSKK;KTTQLVFTK;FTKQDTITV;KQDTIT
VQK;KYDSAGTNL;GTNLEGTAV;NLEGTAVEI;VEIKTLDEL;EIKTLDELK;TLDELKNAL

KYLLGIGLIL;YLLGIGLILA;LLGIGLILAL;LGIGLILALI;GLILALIACK;KQNVSSLDEK;SLDEKNSASV
;SASVDLPGEM;ASVDLPGEMK;SVDLPGEMKV;DLPGEMKVLV;LPGEMKVLVS;EMKVLVSKEK;
KVLVSKEKDK;KDKDGKYSLK;KYSLKATVDK;KATVDKIELK;KIELKGTSDK;GVLEGTKDDK;GTK
DDKSKAK;KLTIADDLSK;TIADDLSKTT;IADDLSKTTF;DLSKTTFELF;LSKTTFELFK;ELFKEDGK
TL;TLVSRKVSSK;VSRKVSSKDK;TSTDEMFNEK;DEMFNEKGEL;KTMTRENGTK;TMTRENGTK
L;GTKLEYTEMK;GTGKAKEVLK;VLKNFTLEGK;VANDKVTLEV;VTLEVKEGTV;LEVKEGTVTL;T
VTLSKEIAK;EIAKSGEVTV;AKSGEVTVAL;TVALNDTNTT;ALNDTNTTQA;DTNTTQATKK;GAWD
SKTSTL;SKTSTLTISV;STLTISVNSK;TLTISVNSKK;SVNSKKTTQL;KKTTQLVFTK;QLVFTKQDTI
;KTLDELKNAL;TLDELKNALK

YLLGIGLILAL;LLGIGLILALI;ILALIACKQNV;LIACKQNVSSL;NVSSLDEKNSA;SSLDEKNSASV;S
ASVDLPGEMK;SVDLPGEMKVL;VDLPGEMKVLV;LPGEMKVLVSK;LVSKEKDKDGK;KYSLKATV
DKI;SLKATVDKIEL;GTSDKDNGSGV;TIADDLSKTTF;DLSKTTFELFK;TTFELFKEDGK;FELFKED
GKTL;ELFKEDGKTLV;KTLVSRKVSSK;LVSRKVSSKDK;KTSTDEMFNEK;EMFNEKGELSA;MFN
EKGELSAK;KTMTRENGTKL;MTRENGTKLEY;YTEMKSDGTGK;EVLKNFTLEGK;VLKNFTLEGK
V;FTLEGKVANDK;TLEGKVANDKV;KVANDKVTLEV;VANDKVTLEVK;KVTLEVKEGTV;TLEVKE
GTVTL;EVKEGTVTLSK;GTVTLSKEIAK;KEIAKSGEVTV;EIAKSGEVTVA;IAKSGEVTVAL;ALNDT
NTTQAT;TTQATKKTGAW;ATKKTGAWDSK;AWDSKTSTLTI;TSTLTISVNSK;STLTISVNSKK;SV
NSKKTTQLV;SKKTTQLVFTK;TQLVFTKQDTI;LVFTKQDTITV;FTKQDTITVQK;DTITVQKYDSA;V
QKYDSAGTNL;SAGTNLEGTAV;NLEGTAVEIKT;LEGTAVEIKTL;TAVEIKTLDEL;AVEIKTLDELK;
KTLDELKNALK

Class 2

AKEVLKNFTLEGKVA;LKNFTLEGK;AKEVLKNFTLEGKVA;VLKNFTLEG;ALNDTNTTQATKKTG;
NTTQATKKT;AWDSKTSTLTISVNS;WDSKTSTLT;DEMFNEKGELSAKTM;MFNEKGELS;DGKTL
VSRKVSSKDK;GKTLVSRKV;DKVTLEVKEGTVTLS;LEVKEGTVT;DLPGEMKVLVSKEKD;MKVL
VSKEK;DTITVQKYDSAGTNL;VQKYDSAGT;EDGKTLVSRKVSSKD;GKTLVSRKV;ELFKEDGKT
LVSRKV;FKEDGKTLV;EMFNEKGELSAKTMT;EKGELSAKT;EVKEGTVTLSKEIAK;VKEGTVTLS;
EVLKNFTLEGKVAND;LKNFTLEGK;EVTVALNDTNTTQAT;LNDTNTTQA;EVTVALNDTNTTQAT;
VALNDTNTT;EYTEMKSDGTGKAKE;MKSDGTGKA;EYTEMKSDGTGKAKE;YTEMKSDGT;FKE
DGKTLVSRKVSS;GKTLVSRKV;FNEKGELSAKTMTRE;EKGELSAKT;FTKQDTITVQKYDSA;FTK
QDTITV;GAWDSKTSTLTISVN;WDSKTSTLT;GEMKVLVSKEKDKDG;MKVLVSKEK;GEVTVALN
DTNTTQA;VALNDTNTT;GIGLILALIACKQNV;ILALIACKQ;GKAKEVLKNFTLEGK;VLKNFTLEG;G
KTLVSRKVSSKDKT;GKTLVSRKV;GLILALIACKQNVSS;ILALIACKQ;GTKLEYTEMKSDGTG;YT
EMKSDGT;IGLILALIACKQNVS;ILALIACKQ;ISVNSKKTTQLVFTK;ISVNSKKTT;ISVNSKKTTQLV
FTK;VNSKKTTQL;ITVQKYDSAGTNLEG;VQKYDSAGT;ITVQKYDSAGTNLEG;YDSAGTNLE;KA
KEVLKNFTLEGKV;LKNFTLEGK;KAKEVLKNFTLEGKV;VLKNFTLEG;KEDGKTLVSRKVSSK;GK
TLVSRKV;KEVLKNFTLEGKVAN;LKNFTLEGK;KEVLKNFTLEGKVAN;VLKNFTLEG;KKTGAWDS
KTSTLTI;WDSKTSTLT;KKYLLGIGLILALIA;LLGIGLILA;KLEYTEMKSDGTGKA;YTEMKSDGT;KQ
DTITVQKYDSAGT;ITVQKYDSA;KSGEVTVALNDTNTT;EVTVALNDT;KTGAWDSKTSTLTIS;WD
SKTSTLT;KTSTLTISVNSKKTT;LTISVNSKK;KTTQLVFTKQDTITV;KTTQLVFTK;KTTQLVFTKQD

TITV;VFTKQDTIT;KVTLEVKEGTVTLSK;VKEGTVTLS;KYLLGIGLILALIAC;LLGIGLILA;LEVKEGT
VTLSKEIA;VKEGTVTLS;LEYTEMKSDGTGKAK;MKSDGTGKA;LEYTEMKSDGTGKAK;YTEMKS
DGT;LFKEDGKTLVSRKVS;GKTLVSRKV;LGIGLILALIACKQN;IGLILALIA;LKNFTLEGKVANDKV;
LKNFTLEGK;LLGIGLILALIACKQ;IGLILALIA;LNDTNTTQATKKTGA;NTTQATKKT;LPGEMKVLVS
KEKDK;MKVLVSKEK;LTISVNSKKTTQLVF;ISVNSKKTT;LTISVNSKKTTQLVF;VNSKKTTQL;LVF
TKQDTITVQKYD;FTKQDTITV;MKKYLLGIGLILALI;LLGIGLILA;NGTKLEYTEMKSDGT;TKLEYTE
MK;NVSSLDEKNSASVDL;LDEKNSASV;PGEMKVLVSKEKDKD;MKVLVSKEK;QDTITVQKYDSA
GTN;VQKYDSAGT;QKYDSAGTNLEGTAV;YDSAGTNLE;QLVFTKQDTITVQKY;FTKQDTITV;SG
EVTVALNDTNTTQ;VALNDTNTT;SSLDEKNSASVDLPG;EKNSASVDL;STLTISVNSKKTTQL;ISV
NSKKTT;STLTISVNSKKTTQL;TISVNSKKT;SVNSKKTTQLVFTKQ;VNSKKTTQL;TDEMFNEKGE
LSAKT;MFNEKGELS;TEMKSDGTGKAKEVL;MKSDGTGKA;TGAWDSKTSTLTISV;WDSKTSTLT
;TGKAKEVLKNFTLEG;AKEVLKNFT;TISVNSKKTTQLVFT;ISVNSKKTT;TISVNSKKTTQLVFT;VN
SKKTTQL;TITVQKYDSAGTNLE;VQKYDSAGT;TKKTGAWDSKTSTLT;KTGAWDSKT;TKLEYTE
MKSDGTGK;YTEMKSDGT;TLEVKEGTVTLSKEI;VKEGTVTLS;TLTISVNSKKTTQLV;ISVNSKKT
T;TLTISVNSKKTTQLV;VNSKKTTQL;TQLVFTKQDTITVQK;FTKQDTITV;TSTLTISVNSKKTTQ;IS
VNSKKTT;TTQLVFTKQDTITVQ;FTKQDTITV;TVALNDTNTTQATKK;LNDTNTTQA;TVALNDTNT
TQATKK;VALNDTNTT;TVQKYDSAGTNLEGT;VQKYDSAGT;TVQKYDSAGTNLEGT;YDSAGTN
LE;VALNDTNTTQATKKT;LNDTNTTQA;VALNDTNTTQATKKT;VALNDTNTT;VDLPGEMKVLVSK
EK;LPGEMKVLV;VDLPGEMKVLVSKEK;VDLPGEMKV;VFTKQDTITVQKYDS;FTKQDTITV;VKE
GTVTLSKEIAKS;VKEGTVTLS;VLKNFTLEGKVANDK;LKNFTLEGK;VNSKKTTQLVFTKQD;VNS
KKTTQL;VQKYDSAGTNLEGTA;VQKYDSAGT;VQKYDSAGTNLEGTA;YDSAGTNLE;VSSLDEK
NSASVDLP;EKNSASVDL;VTLEVKEGTVTLSKE;VKEGTVTLS;VTVALNDTNTTQATK;LNDTNTT
QA;VTVALNDTNTTQATK;VALNDTNTT;WDSKTSTLTISVNSK;WDSKTSTLT;YLLGIGLILALIACK
;IGLILALIA;YTEMKSDGTGKAKEV;MKSDGTGKA;YTEMKSDGTGKAKEV;YTEMKSDGT

<YP_853838 outer surface protein B;Protein;Borrelia afzelii PKo>

Class 1
KQYLLVFA;QYLLVFAL;YLLVFALV;LLVFALVL;LVFALVLA;VFALVLAL;FALVLALI;ALVLALIA;ALI
ACSQK;SQKGTEPK;NTPKDSKK;VLAEENSV;AEENSVPL;EENSVPLF;PLFNGNKI;LFNGNKIF;K
IFVSKEK;KEKNSAGK;NSAGKYEL;SAGKYELR;ATVDTVEL;TVDTVELK;DTVELKGV;ELKGVSD
K;SGKLEGTK;GTKADKTK;KTKVAMTI;AMTIADDL;IADDLNTI;NTITVETY;ETYDASNK;TYDASN
KK;KTGSEVVK;VVKKQGSV;KKQGSVIK;SVIKESYK;KANKLDSK;KLDSKKIT;TRENETTL;TTLEY
SEM;EMTDSSNA;ATKAVETL;ETLKNGIK;TLKNGIKL;IKLEGSLV;SLVGGKTT;LVGGKTTV;KLTE
GTIT;EGTITLTR;TLTREIEQ;YLNDTTSG;DTTSGSTK;TTSGSTKK;STKKTATW;ETTNTLTI;LTISA
DSK;TISADSKK;SADSKKTK;KTKDFVFL;FVFLTDGT;VFLTDGTI;FLTDGTIT;LTDGTITV;GTITVQ
AY;AYDTAGTK;SEIKDLAA;EIKDLAAL;DLAALKAA;LAALKAAL;AALKAALK

KQYLLVFAL;QYLLVFALV;YLLVFALVL;LLVFALVLA;LVFALVLAL;VFALVLALI;FALVLALIA;VLALI
ACSQ;LALIACSQK;CSQKGTEPK;SQDHNDQEI;IINSDNTPK;TPKDSKKDL;TVLAEENSV;LAEEN
SVPL;AEENSVPLF;EENSVPLFN;SVPLFNGNK;VPLFNGNKI;LFNGNKIFV;FVSKEKNSA;NSAGK
YELR;GKYELRATV;ELRATVDTV;RATVDTVEL;ATVDTVELK;KADKTKVAM;KTKVAMTIA;TIADD
LNTI;ETYDASNKK;KTGSEVVKK;EVVKKQGSV;GSVIKESYK;SVIKESYKA;KANKLDSKK;KLDSK
KITR;ITRENETTL;RENETTLEY;ETTLEYSEM;TTLEYSEMT;EMTDSSNAT;MTDSSNATK;ATKAV
ETLK;ETLKNGIKL;GIKLEGSLV;SLVGGKTTV;LVGGKTTVK;TTVKLTEGT;KLTEGTITL;REIEQD
GKV;IEQDGKVKI;YLNDTTSGS;DTTSGSTKK;GSTKKTATW;TWNETTNTL;NETTNTLTI;TTNTLT
ISA;TLTISADSK;LTISADSKK;ISADSKKTK;KTKDFVFLT;FVFLTDGTI;FLTDGTITV;ITVQAYDTA;
VQAYDTAGT;QAYDTAGTK;AYDTAGTKL;KLEGNSSEI;NSSEIKDLA;SEIKDLAAL;EIKDLAALK;D
LAALKAAL;LAALKAALK

KQYLLVFALV;QYLLVFALVL;YLLVFALVLA;LLVFALVLAL;LVFALVLALI;VLALIACSQK;ACSQKG
TEPK;SQDHNDQEII;EIINSDNTPK;LTVLAEENSV;VLAEENSVPL;LAEENSVPLF;NSVPLFNGNK;
SVPLFNGNKI;VPLFNGNKIF;PLFNGNKIFV;VSKEKNSAGK;KNSAGKYELR;YELRATVDTV;RAT
VDTVELK;TVDTVELKGV;TVELKGVSDK;VSDKNNGSGK;MTIADDLNTI;IADDLNTITV;DLNTITV
ETY;NTITVETYDA;TVETYDASNK;ETYDASNKKT;EVVKKQGSVI;VVKKQGSVIK;KQGSVIKESY;

VIKESYKANK;SYKANKLDSK;KITRENETTL;ETTLEYSEMT;EMTDSSNATK;MTDSSNATKA;NAT
KAVETLK;KAVETLKNGI;AVETLKNGIK;VETLKNGIKL;KLEGSLVGGK;SLVGGKTTVK;LVGGKTT
VKL;TTVKLTEGTI;VKLTEGTITL;KLTEGTITLT;LTEGTITLTR;LTREIEQDGK;IEQDGKVKIY;YLND
TTSGST;SGSTKKTATW;ATWNETTNTL;ETTNTLTISA;NTLTISADSK;TLTISADSKK;TISADSKKT
K;VFLTDGTITV;FLTDGTITVQ;LTDGTITVQA;VQAYDTAGTK;QAYDTAGTKL;KLEGNSSEIK;DLA
ALKAALK

MKQYLLVFALV;KQYLLVFALVL;YLLVFALVLAL;LLVFALVLALI;ALVLALIACSQ;LVLALIACSQK;I
ACSQKGTEPK;STSQDHNDQEI;DLTVLAEENSV;TVLAEENSVPL;VLAEENSVPLF;NSVPLFNGN
KI;SVPLFNGNKIF;VPLFNGNKIFV;LFNGNKIFVSK;FVSKEKNSAGK;VSKEKNSAGKY;KEKNSA
GKYEL;EKNSAGKYELR;SAGKYELRATV;ELRATVDTVEL;ATVDTVELKGV;DTVELKGVSDK;GV
SDKNNGSGK;KLEGTKADKTK;KADKTKVAMTI;AMTIADDLNTI;MTIADDLNTIT;TIADDLNTITV;IT
VETYDASNK;TVETYDASNKK;EVVKKQGSVIK;KQGSVIKESYK;SVIKESYKANK;VIKESYKANKL
;ESYKANKLDSK;SYKANKLDSKK;ITRENETTLEY;EMTDSSNATKA;MTDSSNATKAV;KAVETLK
NGIK;TLKNGIKLEGS;EGSLVGGKTTV;GSLVGGKTTVK;SLVGGKTTVKL;KLTEGTITLTR;TLTRE
IEQDGK;REIEQDGKVKI;EIEQDGKVKIY;IEQDGKVKIYL;YLNDTTSGSTK;TSGSTKKTATW;TAT
WNETTNTL;TWNETTNTLTI;TNTLTISADSK;NTLTISADSKK;LTISADSKKTK;SADSKKTKDFV;FV
FLTDGTITV;FLTDGTITVQA;LTDGTITVQAY;TVQAYDTAGTK;VQAYDTAGTKL;LEGNSSEIKDL;
NSSEIKDLAAL;SSEIKDLAALK

Class 2

AEENSVPLFNGNKIF;VPLFNGNKI;AGKYELRATVDTVEL;YELRATVDT;ALVLALIACSQKGTE;V
LALIACSQ;ATWNETTNTLTISAD;WNETTNTLT;AVETLKNGIKLEGSL;LKNGIKLEG;DASNKKTG
SEVVKKQ;NKKTGSEVV;DFVFLTDGTITVQAY;FLTDGTITV;DGKVKIYLNDTTSGS;IYLNDTTSG;
DGKVKIYLNDTTSGS;VKIYLNDTT;DGTITVQAYDTAGTK;VQAYDTAGT;DKTKVAMTIADDLNT;V
AMTIADDL;DNTPKDSKKDLTVLA;DNTPKDSKK;DQEIINSDNTPKDSK;INSDNTPKD;DSKKDLTV
LAEENSV;SKKDLTVLA;EENSVPLFNGNKIFV;VPLFNGNKI;EGNSSEIKDLAALKA;EGNSSEIKD;
EGSLVGGKTTVKLTE;VGGKTTVKL;EIINSDNTPKDSKKD;INSDNTPKD;ENSVPLFNGNKIFVS;V
PLFNGNKI;ETLKNGIKLEGSLVG;LKNGIKLEG;ETYDASNKKTGSEVV;SNKKTGSEV;EVVKKQG
SVIKESYK;VKKQGSVIK;FALVLALIACSQKGT;LVLALIACS;FLTDGTITVQAYDTA;FLTDGTITV;F
NGNKIFVSKEKNSA;FNGNKIFVS;FVFLTDGTITVQAYD;FLTDGTITV;GGKTTVKLTEGTITL;VKL
TEGTIT;GIKLEGSLVGGKTTV;IKLEGSLVG;GKTTVKLTEGTITLT;VKLTEGTIT;GKVKIYLNDTTS
GST;IYLNDTTSG;GKVKIYLNDTTSGST;YLNDTTSGS;GKYELRATVDTVELK;YELRATVDT;GNK
IFVSKEKNSAGK;FVSKEKNSA;GNSSEIKDLAALKAA;IKDLAALKA;GSEVVKKQGSVIKES;VKKQ
GSVIK;GSLVGGKTTVKLTEG;VGGKTTVKL;GTITVQAYDTAGTKL;VQAYDTAGT;HNDQEIINSD
NTPKD;IINSDNTPK;IINSDNTPKDSKKDL;INSDNTPKD;IKLEGSLVGGKTTVK;IKLEGSLVG;INSD
NTPKDSKKDLT;INSDNTPKD;ITVQAYDTAGTKLEG;VQAYDTAGT;IYLNDTTSGSTKKTA;TTSGS
TKKT;KAVETLKNGIKLEGS;LKNGIKLEG;KDFVFLTDGTITVQA;FLTDGTITV;KDSKKDLTVLAEE
NS;SKKDLTVLA;KIFVSKEKNSAGKYE;FVSKEKNSA;KIYLNDTTSGSTKKT;YLNDTTSGS;KKTA
TWNETTNTLTI;WNETTNTLT;KLEGSLVGGKTTVKL;LVGGKTTVK;KNGIKLEGSLVGGKT;IKLEG
SLVG;KNSAGKYELRATVDT;AGKYELRAT;KQYLLVFALVLALIA;LLVFALVLA;KQYLLVFALVLALI
A;LVFALVLAL;KQYLLVFALVLALIA;VFALVLALI;KTATWNETTNTLTIS;WNETTNTLT;KTGSEVVK
KQGSVIK;VVKKQGSVI;KTKDFVFLTDGTITV;FVFLTDGTI;KTTVKLTEGTITLTR;LTEGTITLT;KV
KIYLNDTTSGSTK;IYLNDTTSG;KVKIYLNDTTSGSTK;YLNDTTSGS;KYELRATVDTVELKG;YEL
RATVDT;LAEENSVPLFNGNKI;ENSVPLFNG;LEGSLVGGKTTVKLT;VGGKTTVKL;LKNGIKLEG
SLVGGK;IKLEGSLVG;LKNGIKLEGSLVGGK;LKNGIKLEG;LLVFALVLALIACSQ;FALVLALIA;LLV
FALVLALIACSQ;LLVFALVLA;LNDTTSGSTKKTATW;TTSGSTKKT;LVFALVLALIACSQK;FALVL
ALIA;LVGGKTTVKLTEGTI;VGGKTTVKL;LVLALIACSQKGTEP;LVLALIACS;MKQYLLVFALVLALI
;LLVFALVLA;MKQYLLVFALVLALI;LVFALVLAL;NDQEIINSDNTPKDS;INSDNTPKD;NGIKLEGSL
VGGKTT;IKLEGSLVG;NGNKIFVSKEKNSAG;FVSKEKNSA;NKIFVSKEKNSAGKY;FVSKEKNSA;
NSAGKYELRATVDTV;YELRATVDT;NSSEIKDLAALKAAL;IKDLAALKA;NSVPLFNGNKIFVSK;VP
LFNGNKI;NTPKDSKKDLTVLAE;SKKDLTVLA;PKDSKKDLTVLAEEN;SKKDLTVLA;QAYDTAGTK
LEGNSS;YDTAGTKLE;QDGKVKIYLNDTTSG;KVKIYLNDT;QDGKVKIYLNDTTSG;VKIYLNDTT;
QEIINSDNTPKDSKK;INSDNTPKD;QYLLVFALVLALIAC;FALVLALIA;QYLLVFALVLALIAC;LLVF
ALVLA;QYLLVFALVLALIAC;LVFALVLAL;SAGKYELRATVDTVE;YELRATVDT;SEVVKKQGSVIK

ESY;VKKQGSVIK;SKKDLTVLAEENSVP;SKKDLTVLA;SLVGGKTTVKLTEGT;VGGKTTVKL;SSE
IKDLAALKAALK;IKDLAALKA;SVPLFNGNKIFVSKE;VPLFNGNKI;TATWNETTNTLTISA;WNETT
NTLT;TDGTITVQAYDTAGT;TITVQAYDT;TGSEVVKKQGSVIKE;VKKQGSVIK;TITVQAYDTAGT
KLE;VQAYDTAGT;TKAVETLKNGIKLEG;VETLKNGIK;TKDFVFLTDGTITVQ;FLTDGTITV;TKKTA
TWNETTNTLT;ATWNETTNT;TKKTATWNETTNTLT;TKKTATWNE;TLKNGIKLEGSLVGG;IKLEG
SLVG;TLKNGIKLEGSLVGG;LKNGIKLEG;TPKDSKKDLTVLAEE;SKKDLTVLA;TTVKLTEGTITLT
RE;LTEGTITLT;TVKLTEGTITLTREI;LTEGTITLT;TVQAYDTAGTKLEGN;VQAYDTAGT;TYDASN
KKTGSEVVK;NKKTGSEVV;VETLKNGIKLEGSLV;LKNGIKLEG;VFALVLALIACSQKG;LVLALIAC
S;VFLTDGTITVQAYDT;FLTDGTITV;VGGKTTVKLTEGTIT;VGGKTTVKL;VKIYLNDTTSGSTKK;Y
LNDTTSGS;VKLTEGTITLTREIE;LTEGTITLT;VLALIACSQKGTEPK;VLALIACSQ;VPLFNGNKIFV
SKEK;VPLFNGNKI;VQAYDTAGTKLEGNS;VQAYDTAGT;YDASNKKTGSEVVKK;NKKTGSEVV;
YELRATVDTVELKGV;YELRATVDT;YLLVFALVLALIACS;FALVLALIA;YLLVFALVLALIACS;LLVF
ALVLA;YLLVFALVLALIACS;LVFALVLAL;YLNDTTSGSTKKTAT;TTSGSTKKT

<CAF34027 outer surface protein VlsE;Protein;Borrelia afzelii PKo>

Class 1

KISSAIFL;SAIFLTAL;AIFLTALL;IFLTALLV;FLTALLVF;LTALLVFI;ALLVFINC;LLVFINCK;FINCKN
NA;FYESIINL;IINLGNGF;FIDVFNAF;FNAFSGLV;GLVADTFF;LVADTFFK;TFFKSDPK;KSDVKTY
F;FESISSTL;ESISSTLK;SISSTLKA;SSTLKATK;TLKATKGK;KLDELVSA;KASVESAV;SAVDEVS
K;KWLEEMIK;WLEEMIKA;MIKAAEEA;KAAEEAAK;DSAANHGA;SAANHGAK;DSVKGIAK;KGIA
KGIK;GIKGIVDA;GIVDAAGK;AGKALGEK;ALGEKGAL;ALKDVKAA;EANADAGK;FAGNANAA;NA
AVGAAA;GAAADIAK;IAKAAGAV;KAAGAVTA;AAGAVTAV;AVSGEQIL;VSGEQILK;ILKAIVEA;D
PANQAGK;AEEAKNPI;DDNGAAFK;AAFKDEMK;AFKDEMKK;KIAAAIVL;IAAAIVLR;AAIVLRGV;I
VLRGVAK;AKDGKFAV

KISSAIFLT;ISSAIFLTA;SSAIFLTAL;SAIFLTALL;AIFLTALLV;IFLTALLVF;FLTALLVFI;ALLVFINC
K;FINCKNNAV;AVGKGNDDK;SVKTFYESI;TFYESIINL;SIINLGNGF;IINLGNGFI;NLGNGFIDV;G
FIDVFNAF;DVFNAFSGL;FSGLVADTF;GLVADTFFK;LVADTFFKS;DTFFKSDPK;TFFKSDPKK;D
VKTYFESI;YFESISSTL;ISSTLKATK;STLKATKGK;TLKATKGKL;ATKGKLDEL;KLDELVSAK;EGG
SVKASV;SVKASVESA;SVESAVDEV;ESAVDEVSK;SAVDEVSKW;AVDEVSKWL;EVSKWLEEM;
WLEEMIKAA;EMIKAAEEA;MIKAAEEAA;KAAEEAAKV;DSAANHGAK;ANHGAKADK;SVKGIAKGI
;GIAKGIKGI;GIKGIVDAA;IVDAAGKAL;AAGKALGEK;ALGEKGALK;ALKDVKAAA;NADAGKLFA;
KLFAGNANA;FAGNANAAV;NANAAVGAA;DIAKAAGAV;KAAGAVTAV;TAVSGEQIL;AVSGEQIL
K;QILKAIVEA;ILKAIVEAA;AGKKAEEAK;AEEAKNPIA;EEAKNPIAA;NPIAAAIGT;TDDDNGAAF;G
AAFKDEMK;AAFKDEMKK;KIAAAIVLR;AAAIVLRGV;AIVLRGVAK;VAKDGKFAV

KISSAIFLTA;ISSAIFLTAL;SSAIFLTALL;SAIFLTALLV;AIFLTALLVF;IFLTALLVFI;FLTALLVFIN;TA
LLVFINCK;DSVKTFYESI;SVKTFYESII;KTFYESIINL;ESIINLGNGF;SIINLGNGFI;NGFIDVFNAF;
DVFNAFSGLV;AFSGLVADTF;FSGLVADTFF;SGLVADTFFK;GLVADTFFKS;ADTFFKSDPK;DTF
FKSDPKK;DPKKSDVKTY;KTYFESISST;TYFESISSTL;YFESISSTLK;SISSTLKATK;SSTLKATKG
K;ATKGKLDELV;KLDELVSAKK;SAKKGEGGSV;SVKASVESAV;ASVESAVDEV;ESAVDEVSKW;
SAVDEVSKWL;EVSKWLEEMI;VSKWLEEMIK;EEMIKAAEEA;MIKAAEEAAK;AEEAAKVGGT;KV
GGTGGDGK;AANHGAKADK;HGAKADKDSV;SVKGIAKGIK;GIAKGIKGIV;GIVDAAGKAL;DAAG
KALGEK;KALGEKGALK;EANADAGKLF;KLFAGNANAA;LFAGNANAAV;NANAAVGAAA;AVGAA
ADIAK;AKAAGAVTAV;TAVSGEQILK;AVSGEQILKA;QILKAIVEAA;AIVEAAGDPA;EAAGDPANQ
A;AEEAKNPIAA;EEAKNPIAAA;EAKNPIAAAI;GTDDDNGAAF;NGAAFKDEMK;GAAFKDEMKK;D
KIAAAIVLR;IAAAIVLRGV;AAIVLRGVAK;VLRGVAKDGK;GVAKDGKFAV;VAKDGKFAVK

KKISSAIFLTA;KISSAIFLTAL;ISSAIFLTALL;SSAIFLTALLV;SAIFLTALLVF;AIFLTALLVFI;FLTALL
VFINC;LTALLVFINCK;LLVFINCKNNA;LVFINCKNNAV;FINCKNNAVGK;YESIINLGNGF;ESIINLG
NGFI;IINLGNGFIDV;FIDVFNAFSGL;DVFNAFSGLVA;NAFSGLVADTF;AFSGLVADTFF;FSGLVA
DTFFK;VADTFFKSDPK;DPKKSDVKTYF;KTYFESISSTL;TYFESISSTLK;ESISSTLKATK;ISSTLK
ATKGK;KATKGKLDELV;KGKLDELVSAK;SAKKGEGGSVK;KASVESAVDEV;SVESAVDEVSK;E
SAVDEVSKWL;EVSKWLEEMIK;EEMIKAAEEAA;EMIKAAEEAAK;MIKAAEEAAKV;KIGDSAANH

GA;SAANHGAKADK;DSVKGIAKGIK;GIKGIVDAAGK;ALGEKGALKDV;DEANADAGKLF;KLFAG
NANAAV;FAGNANAAVGA;AAVGAAADIAK;AAADIAKAAGA;IAKAAGAVTAV;AVTAVSGEQIL;VT
AVSGEQILK;AVSGEQILKAI;AAGDPANQAGK;AEEAKNPIAAA;EEAKNPIAAAI;IGTDDDNGAAF;
GTDDDNGAAFK;NGAAFKDEMKK;AFKDEMKKSDK;KSDKIAAAIVL;KIAAAIVLRGV;IAAAIVLRG
VA;AAAIVLRGVAK;IVLRGVAKDGK;VLRGVAKDGKF;GVAKDGKFAVK

Class 2

ADAGKLFAGNANAAV;LFAGNANAA;ADIAKAAGAVTAVSG;IAKAAGAVT;ADTFFKSDPKKSDVK;
FFKSDPKKS;ADTFFKSDPKKSDVK;FKSDPKKSD;AEEAKNPIAAAIGTD;AKNPIAAAI;AGAVTAV
SGEQILKA;VTAVSGEQI;AGKLFAGNANAAVGA;FAGNANAAV;AGNANAAVGAAADIA;ANAAVG
AAA;AIFLTALLVFINCKN;FLTALLVFI;AIVLRGVAKDGKFAV;LRGVAKDGK;AKGIKGIVDAAGKAL;
IKGIVDAAG;AKAAGAVTAVSGEQI;AKAAGAVTA;ALLVFINCKNNAVGK;FINCKNNAV;ALLVFINC
KNNAVGK;VFINCKNNA;ANAAVGAAADIAKAA;AVGAAADIA;DAGKLFAGNANAAVG;FAGNANA
AV;DGKIGDSAANHGAKA;IGDSAANHG;DIAKAAGAVTAVSGE;AKAAGAVTA;DKIAAAIVLRGVA
KD;IAAAIVLRG;DSVKTFYESIINLGN;FYESIINLG;DSVKTFYESIINLGN;VKTFYESII;DTFFKSDPK
KSDVKT;FFKSDPKKS;DTFFKSDPKKSDVKT;FKSDPKKSD;DVFNAFSGLVADTFF;FNAFSGLVA
;DVFNAFSGLVADTFF;VFNAFSGLV;DVKTYFESISSTLKA;FESISSTLK;DVKTYFESISSTLKA;YF
ESISSTL;EAKNPIAAAIGTDDD;IAAAIGTDD;EEAKNPIAAAIGTDD;AKNPIAAAI;EQILKAIVEAAGD
PA;LKAIVEAAG;ESIINLGNGFIDVFN;IINLGNGFI;FAGNANAAVGAAADI;FAGNANAAV;FESISST
LKATKGKL;FESISSTLK;FIDVFNAFSGLVADT;FNAFSGLVA;FIDVFNAFSGLVADT;VFNAFSGLV
;FKSDPKKSDVKTYFE;FKSDPKKSD;FLTALLVFINCKNNA;FLTALLVFI;FNAFSGLVADTFFKS;F
NAFSGLVA;FYESIINLGNGFIDV;FYESIINLG;FYESIINLGNGFIDV;IINLGNGFI;GAVTAVSGEQIL
KAI;VTAVSGEQI;GDGKIGDSAANHGAK;IGDSAANHG;GEQILKAIVEAAGDP;LKAIVEAAG;GFID
VFNAFSGLVAD;FNAFSGLVA;GFIDVFNAFSGLVAD;VFNAFSGLV;GGDGKIGDSAANHGA;IGDS
AANHG;GIAKGIKGIVDAAGK;IKGIVDAAG;GIKGIVDAAGKALGE;IVDAAGKAL;GIVDAAGKALGE
KGA;IVDAAGKAL;GKIGDSAANHGAKAD;IGDSAANHG;GKLFAGNANAAVGAA;FAGNANAAV;G
LVADTFFKSDPKKS;DTFFKSDPK;GNANAAVGAAADIAK;AVGAAADIA;GNGFIDVFNAFSGLV;FI
DVFNAFS;GAAADIAKAAGAVTA;IAKAAGAVT;IAKGIKGIVDAAGKA;IKGIVDAAG;IAKAAGAVTA
VSGEQ;IAKAAGAVT;IDVFNAFSGLVADTF;FNAFSGLVA;IDVFNAFSGLVADTF;VFNAFSGLV;IF
LTALLVFINCKNN;FLTALLVFI;IKGIVDAAGKALGEK;IVDAAGKAL;ISSAIFLTALLVFIN;FLTALLVF
I;IVDAAGKALGEKGAL;IVDAAGKAL;IAAAIVLRGVAKDGK;AIVLRGVAK;IAAAIVLRGVAKDGK;IA
AAIVLRG;KAEEAKNPIAAAIGT;AKNPIAAAI;KAIVEAAGDPANQAG;AAGDPANQA;KDSVKTFYE
SIINLG;KTFYESIIN;KGIAKGIKGIVDAAG;IAKGIKGIV;KGIKGIVDAAGKALG;IVDAAGKAL;KGIVD
AAGKALGEKG;IVDAAGKAL;KISSAIFLTALLVFI;AIFLTALLV;KIAAAIVLRGVAKDG;IAAAIVLRG;K
KISSAIFLTALLVF;ISSAIFLTA;KKSDKIAAAIVLRGV;IAAAIVLRG;KLFAGNANAAVGAAA;FAGNA
NAAV;KSDKIAAAIVLRGVA;IAAAIVLRG;KSDVKTYFESISSTL;KSDVKTYFE;KTFYESIINLGNGFI
;FYESIINLG;KTFYESIINLGNGFI;YESIINLGN;KTYFESISSTLKATK;FESISSTLK;KTYFESISSTLK
ATK;YFESISSTL;KAAGAVTAVSGEQIL;VTAVSGEQI;LFAGNANAAVGAAAD;FAGNANAAV;LKAI
VEAAGDPANQA;LKAIVEAAG;LLVFINCKNNAVGKG;FINCKNNAV;LLVFINCKNNAVGKG;VFINC
KNNA;LTALLVFINCKNNAV;VFINCKNNA;LVADTFFKSDPKKSD;DTFFKSDPK;LVADTFFKSDPK
KSD;FFKSDPKKS;LVFINCKNNAVGKGN;CKNNAVGKG;LVFINCKNNAVGKGN;FINCKNNAV;M
KKISSAIFLTALLV;MKKISSAIF;MKKSDKIAAAIVLRG;DKIAAAIVL;NADAGKLFAGNANAA;AGKLF
AGNA;NANAAVGAAADIAKA;AVGAAADIA;NGFIDVFNAFSGLVA;FIDVFNAFS;NGFIDVFNAFSG
LVA;VFNAFSGLV;NAAVGAAADIAKAAG;AVGAAADIA;SAIFLTALLVFINCK;FLTALLVFI;SDKIAA
AIVLRGVAK;IAAAIVLRG;SDVKTYFESISSTLK;YFESISSTL;SGEQILKAIVEAAGD;LKAIVEAAG;S
IINLGNGFIDVFNA;IINLGNGFI;SSAIFLTALLVFINC;FLTALLVFI;SVKTFYESIINLGNG;FYESIINL
G;SVKTFYESIINLGNG;YESIINLGN;TALLVFINCKNNAVG;FINCKNNAV;TALLVFINCKNNAVG;V
FINCKNNA;TFFKSDPKKSDVKTY;FKSDPKKSD;TFYESIINLGNGFID;FYESIINLG;TFYESIINLGN
GFID;IINLGNGFI;TFYESIINLGNGFID;YESIINLGN;TGGDGKIGDSAANHG;GKIGDSAAN;TYFESI
SSTLKATKG;FESISSTLK;TYFESISSTLKATKG;YFESISSTL;VADTFFKSDPKKSDV;FFKSDPKK
S;VADTFFKSDPKKSDV;FKSDPKKSD;VFINCKNNAVGKGND;CKNNAVGKG;VFNAFSGLVADTF
FK;VFNAFSGLV;VGAAADIAKAAGAVT;DIAKAAGAV;VKTFYESIINLGNGF;FYESIINLG;VKTFYE
SIINLGNGF;YESIINLGN;VKTYFESISSTLKAT;FESISSTLK;VKTYFESISSTLKAT;YFESISSTL;VS
GEQILKAIVEAAG;ILKAIVEAA;YESIINLGNGFIDVF;IINLGNGFI;YFESISSTLKATKGK;FESISSTL
K;AAADIAKAAGAVTAV;IAKAAGAVT;AAAIVLRGVAKDGKF;LRGVAKDGK;AAAIVLRGVAKDGK

F;VLRGVAKDG;AADIAKAAGAVTAVS;IAKAAGAVT;AAGAVTAVSGEQILK;VTAVSGEQI;AAIVLR
GVAKDGKFA;LRGVAKDGK;AAIVLRGVAKDGKFA;VLRGVAKDG

C) Borrelia garinii MHC class 1 & 2 epitopes

<CAH10086 CRASP-1;Protein;Borrelia garinii>

Class 1

KTKLNIIK;NIIKLNIL;KLNILTTI;ILTTILTL;LTTILTLI;TILTLICI;TLICISCA;LICISCAV;CISCAVDK;NT
KDFENK;FENKSQDL;EPSNTKNK;KETIISKL;TIISKLEK;LEKMIKDL;EIAKITNT;ITNTQIDF;QIDFL
ENF;TISEDIEM;ISEDIEMK;DIEMKIKR;KIKRIIYS;KRIIYSSL;IIYSSLNY;YSSLNYEI;SLNYEIEK;EI
EKINTL;KINTLKEI;TLKEILDK;KEILDKLY;EILDKLYK;KLYKNHKY;LYKNHKYK;HKYKTTAR;TTAR
NFIL;NFILNISI;FILNISIK;ILNISIKI;SIKIQFQI;IQFQIENA;QFQIENAL;FQIENALE;QIENALEL;ENAL
ELMK;IEDASEIL;EILNQERY;NQERYEIL;QERYEILL;ERYEILLK;YEILLKHV;NLKQKFEK;KILNETI
K;ILNETIKA;ETIKAYNQ;LAHMDENY;HMDENYKE;NYKEFDPL;KEFDPLNL

KLNIIKLNI;IKLNILTTI;KLNILTTIL;NILTTILTL;ILTTILTLI;TTILTLICI;ILTLICISC;TLICISCAV;CISCA
VDKI;ESKSKTNTK;NSKETIISK;ETIISKLEK;TIISKLEKM;ISKLEKMIK;MIKDLEDQK;EIAKITNTQ;K
ITNTQIDF;ITNTQIDFL;TQIDFLENF;QIDFLENFK;DTISEDIEM;TISEDIEMK;EDIEMKIKR;EMKIKR
IIY;KIKRIIYSS;RIIYSSLNY;IYSSLNYEI;SSLNYEIEK;SLNYEIEKI;YEIEKINTL;EIEKINTLK;NTLKEI
LDK;TLKEILDKL;LDKLYKNHK;KLYKNHKYK;NHKYKTTAR;KYKTTARNF;KTTARNFIL;NFILNISI
K;FILNISIKI;ISIKIQFQI;KIQFQIENA;IQFQIENAL;FQIENALEL;QIENALELM;ALELMKEEI;LMKEEI
EDA;EEIEDASEI;EIEDASEIL;ASEILNQER;SEILNQERY;ILNQERYEI;LLKHVEPSL;KHVEPSLNL;
HVEPSLNLK;EPSLNLKQK;NLKQKFEKI;KILNETIKA;ILNETIKAY;AYNQDLDNI;QLAHMDENY;LA
HMDENYK;HMDENYKEF;YKEFDPLNL;EFDPLNLDY

KLNIIKLNIL;IIKLNILTTI;KLNILTTILT;NILTTILTLI;ILTTILTLIC;ILTLICISCA;LTLICISCAV;LICISCA
VDK;AVDKIDPESK;KTNTKDFENK;SQDLEPSNTK;KNKDLEPLEK;PLEKNSKETI;ETIISKLEKM;T
IISKLEKMI;IISKLEKMIK;KMIKDLEDQK;EIAKITNTQI;KITNTQIDFL;NTQIDFLENF;TQIDFLENFK;
DTISEDIEMK;TISEDIEMKI;IEMKIKRIIY;KIKRIIYSSL;KRIIYSSLNY;IIYSSLNYEI;YSSLNYEIEK;N
YEIEKINTL;ILDKLYKNHK;KLYKNHKYKT;KNHKYKTTAR;KYKTTARNFI;YKTTARNFIL;TTARNFI
LNI;NFILNISIKI;NISIKIQFQI;QFQIENALEL;FQIENALELM;QIENALELMK;NALELMKEEI;EEIEDA
SEIL;DASEILNQER;ASEILNQERY;EILNQERYEI;ILNQERYEIL;NQERYEILLK;ILLKHVEPSL;EPS
LNLKQKF;SLNLKQKFEK;NLKQKFEKIL;KILNETIKAY;ETIKAYNQDL;KAYNQDLDNI;AYNQDLDN
IK;KSNEDQLAHM;QLAHMDENYK;AHMDENYKEF;NYKEFDPLNL;KEFDPLNLDY

KLNIIKLNILT;NIIKLNILTTI;IIKLNILTTIL;KLNILTTILTL;ILTTILTLICI;ILTLICISCAV;TLICISCAVDK;
CAVDKIDPESK;KSQDLEPSNTK;EPLEKNSKETI;ETIISKLEKMI;TIISKLEKMIK;NTQIDFLENFK;T
QIDFLENFKS;DTISEDIEMKI;TISEDIEMKIK;ISEDIEMKIKR;DIEMKIKRIIY;MKIKRIIYSSL;RIIYSS
LNYEI;IYSSLNYEIEK;NYEIEKINTLK;IEKINTLKEIL;KINTLKEILDK;NTLKEILDKLY;TLKEILDKLYK
;EILDKLYKNHK;ILDKLYKNHKY;KLYKNHKYKTT;KYKTTARNFIL;TTARNFILNIS;FILNISIKIQF;IL
NISIKIQFQ;SIKIQFQIENA;IQFQIENALEL;FQIENALELMK;KEEIEDASEIL;EEIEDASEILN;EDASE
ILNQER;DASEILNQERY;SEILNQERYEI;EILNQERYEIL;ILNQERYEILL;EILLKHVEPSL;LLKHVE
PSLNL;HVEPSLNLKQK;VEPSLNLKQKF;PSLNLKQKFEK;SLNLKQKFEKI;KFEKILNETIK;EKILN
ETIKAY;ILNETIKAYNQ;NETIKAYNQDL;KAYNQDLDNIK;LAHMDENYKEF

Class 2

ARNFILNISIKIQFQ;FILNISIKI;AYNQDLDNIKSNEDQ;LDNIKSNED;DFLENFKSEPHDTIS;LENFK
SEPH;DIEMKIKRIIYSSLN;MKIKRIIYS;DKLYKNHKYKTTARN;YKNHKYKTT;DLDNIKSNEDQLAH
M;IKSNEDQLA;EDIEMKIKRIIYSSL;MKIKRIIYS;EIEKINTLKEILDKL;INTLKEILD;EILDKLYKNHKY
KTT;LDKLYKNHK;EILDKLYKNHKYKTT;LYKNHKYKT;EILLKHVEPSLNLKQ;LKHVEPSLN;EMKI
KRIIYSSLNYE;MKIKRIIYS;ENKSQDLEPSNTKNK;QDLEPSNTK;ERYEILLKHVEPSLN;YEILLKH
VE;ETIKAYNQDLDNIKS;IKAYNQDLD;FILNISIKIQFQIEN;LNISIKIQF;HKYKTTARNFILNIS;YKTT
ARNFI;HMDENYKEFDPLNLD;YKEFDPLNL;IDFLENFKSEPHDTI;LENFKSEPH;IEKINTLKEILDK
LY;INTLKEILD;IEMKIKRIIYSSLNY;MKIKRIIYS;IIKLNILTTILTLIC;ILTTILTLI;IIKLNILTTILTLIC;LNI

LTTILT;IKIQFQIENALELMK;FQIENALEL;IKLNILTTILTLICI;LNILTTILT;ILDKLYKNHKYKTTA;YK
NHKYKTT;ILLKHVEPSLNLKQK;LKHVEPSLN;ILNISIKIQFQIENA;LNISIKIQF;ILTTILTLICISCAV;I
LTTILTLI;ILTTILTLICISCAV;LTLICISCA;IQFQIENALELMKEE;FQIENALEL;ISEDIEMKIKRIIYS;IE
MKIKRII;ISIKIQFQIENALEL;IKIQFQIEN;ISIKIQFQIENALEL;IQFQIENAL;KAYNQDLDNIKSNED;
YNQDLDNIK;KEILDKLYKNHKYKT;LDKLYKNHK;KIQFQIENALELMKE;FQIENALEL;KKTKLNIIK
LNILTT;LNIIKLNIL;KLNIIKLNILTTILT;IIKLNILTT;KLNIIKLNILTTILT;IKLNILTTI;KLNIIKLNILTTILT;
KLNILTTIL;KLNILTTILTLICIS;LNILTTILT;KLYKNHKYKTTARNF;YKNHKYKTT;KNHKYKTTARNF
ILN;YKTTARNFI;KSQDLEPSNTKNKDL;LEPSNTKNK;KTKLNIIKLNILTTI;IIKLNILTT;KTKLNIIKLN
ILTTI;LNIIKLNIL;KTTARNFILNISIKI;ARNFILNIS;KYKTTARNFILNISI;ARNFILNIS;KYKTTARNFIL
NISI;YKTTARNFI;LDKLYKNHKYKTTAR;YKNHKYKTT;LDNIKSNEDQLAHMD;IKSNEDQLA;LNII
KLNILTTILTL;LNILTTILT;LNILTTILTLICISC;LNILTTILT;LNISIKIQFQIENAL;LNISIKIQF;LNYEIEKI
NTLKEIL;IEKINTLKE;LNYEIEKINTLKEIL;YEIEKINTL;LTTILTLICISCAVD;LTLICISCA;LYKNHKY
KTTARNFI;KYKTTARNF;LYKNHKYKTTARNFI;NHKYKTTAR;LYKNHKYKTTARNFI;YKNHKYKT
T;MDENYKEFDPLNLDY;KEFDPLNLD;MKIKRIIYSSLNYEI;KRIIYSSLN;MKIKRIIYSSLNYEI;MKI
KRIIYS;MKKTKLNIIKLNILT;LNIIKLNIL;NFILNISIKIQFQIE;LNISIKIQF;NHKYKTTARNFILNI;YKTT
ARNFI;NIIKLNILTTILTLI;LNILTTILT;NILTTILTLICISCA;ILTTILTLI;NILTTILTLICISCA;LTTILTLIC;
NKSQDLEPSNTKNKD;LEPSNTKNK;NQDLDNIKSNEDQLA;LDNIKSNED;NTQIDFLENFKSEPH;
FLENFKSEP;NTQIDFLENFKSEPH;IDFLENFKS;NYEIEKINTLKEILD;EKINTLKEI;NYEIEKINTLK
EILD;IEKINTLKE;QDLDNIKSNEDQLAH;IKSNEDQLA;QDLEPSNTKNKDLEP;LEPSNTKNK;QIDF
LENFKSEPHDT;LENFKSEPH;RNFILNISIKIQFQI;FILNISIKI;RYEILLKHVEPSLNL;LKHVEPSLN;
SEDIEMKIKRIIYSS;MKIKRIIYS;SIKIQFQIENALELM;FQIENALEL;SLNYEIEKINTLKEI;IEKINTLK
E;SLNYEIEKINTLKEI;YEIEKINTL;SQDLEPSNTKNKDLE;LEPSNTKNK;SSLNYEIEKINTLKE;YEI
EKINTL;TARNFILNISIKIQF;FILNISIKI;TKLNIIKLNILTTIL;IIKLNILTT;TKLNIIKLNILTTIL;IKLNILTTI
;TQIDFLENFKSEPHD;LENFKSEPH;TTARNFILNISIKIQ;FILNISIKI;TTILTLICISCAVDK;LTLICISC
A;YEIEKINTLKEILDK;IEKINTLKE;YEIEKINTLKEILDK;INTLKEILD;YEILLKHVEPSLNLK;LKHVEP
SLN;YKNHKYKTTARNFIL;YKNHKYKTT;YKNHKYKTTARNFIL;YKTTARNFI;YKTTARNFILNISIK;
ARNFILNIS;YNQDLDNIKSNEDQL;LDNIKSNED

<AAU07022 4-alpha-glucanotransferase;Protein;Borrelia garinii PBi>

Class 1

KIRINLNL;RINLNLKR;NLKRKSGI;ILLNISSL;NISSLPSK;SLPSKYGI;GAYKFIDF;AYKFIDFL;KFID
FLFA;FIDFLFAS;FLFASSQS;LFASSQSY;FASSQSYW;SQSYWQMF;QSYWQMFA;SYWQMFAY
;WQMFAYSP;QMFAYSPI;FAYSPIDF;YSPIDFTR;TRSPPYSI;RSPPYSIF;PPYSIFSA;PYSIFSAF;
YSIFSAFA;FSAFAGNV;SAFAGNVY;AFAGNVYY;FAGNVYYI;NVYYIDLE;YYIDLEAL;FIDSDLNL;
LLKENETR;NETRYSDL;ETRYSDLK;RYSDLKKL;DLKKLSFK;SFKDKFLK;KFLKEAAL;KEAALNFI
;AALNFINR;ALNFINRA;NRASVDEV;RASVDEVR;SVDEVRSF;EVRSFEKF;RSFEKFKK;KKSSY
WLL;SSYWLLDF;WLLDFASF;LLDFASFV;DFASFVAF;FASFVAFK;FVAFKEYF;VAFKEYFL;AFK
EYFLK;EYFLKDSR;FLKDSRDA;DSRDAFNV;SRDAFNVL;AFNVLFDR;VLFDRGIL;GILIRNEK;NE
KDLFKL;DLFKLRNI;KLRNILSK;ILSKEIKV;KEIKVQEV;EIKVQEVL;KVQEVLQY;VQEVLQYF;QEV
LQYFF;EVLQYFFF;LQYFFFSQ;QYFFFSQF;FFSQFQAL;FSQFQALK;SQFQALKR;FQALKRYA;
RYANDKGI;ELVMNLPL;LVMNLPLF;VMNLPLFI;NLPLFIAY;LPLFIAYD;IAYDSADV;AYDSADVW;
DVWAHQKY;VWAHQKYF;WAHQKYFK;HQKYFKLR;KLRFDASK;GISPDYFL;QAWDSPAY;SPA
YSWNV;AYSWNVLK;NVLKNVKY;KYEWWAKR;YEWWAKRI;WWAKRIGI;WAKRIGIL;KRIGILRK;
ILRKYIDV;KYIDVIKI;DVIKIDHF;VIKIDHFR;GFVSTWEV;WEVGVGEA;EVGVGEAY;EAYAFNGL;
AYAFNGLW;YAFNGLWV;AFNGLWVK;RDFFNFIL;NFILNEIK;ILNEIKDL;EIKDLKIW;IKDLKIWV;V
EDFENDL;FENDLEDV;DLEDVSRL;DVSRLRDF;RLRDFFNF;FFNFPGMR;GMRIMKLA;MRIMKL
AF;IMKLAFDF;FDSDNQNL;NQNLPHNY;YIKNCIVY;NCIVYTGI;GIGDNSTI;NSTIREFV;IREFVNS
L;FVNSLDDL;NSLDDLHK;SLDDLHKK;YIFDYLNT;YLNTNEDF;NTNEDFVV;FVVWDMIR;MSSVS
DSV;SVSDSVII;VIIPMQDY;PMQDYINL;YINLGNEF;NLGNEFRA;EFRANIPK;NTLNNWIF;TLNNW
IFR;TLSKNISF;KNISFITR;NISFITRL;ISFITRLY;FITRLYGR

KYKKIRINL;KIRINLNLK;IRINLNLKR;RINLNLKRK;NLKRKSGIL;GILLNISSL;NISSLPSKY;KYGIG
DLGK;DLGKGAYKF;GAYKFIDFL;AYKFIDFLF;YKFIDFLFA;FIDFLFASS;FLFASSQSY;LFASSQS
YW;FASSQSYWQ;ASSQSYWQM;SQSYWQMFA;QSYWQMFAY;SYWQMFAYS;WQMFAYSPI;

MFAYSPIDF;FAYSPIDFT;AYSPIDFTR;FTRSPPYSI;SPPYSIFSA;PPYSIFSAF;FSAFAGNVY;SA
FAGNVYY;AFAGNVYYI;NVYYIDLEA;VYYIDLEAL;KFIDSDLNL;FIDSDLNLL;LLKENETRY;ETRY
SDLKK;YSDLKKLSF;KLSFKDKFL;LSFKDKFLK;FLKEAALNF;EAALNFINR;AALNFINRA;ASVDE
VRSF;DEVRSFEKF;EVRSFEKFK;RSFEKFKKK;KFKKKSSYW;KSSYWLLDF;SSYWLLDFA;YWL
LDFASF;WLLDFASFV;LLDFASFVA;LDFASFVAF;DFASFVAFK;FASFVAFKE;ASFVAFKEY;SFV
AFKEYF;FVAFKEYFL;VAFKEYFLK;KEYFLKDSR;FLKDSRDAF;DAFNVLFDR;VLFDRGILI;RGILI
RNEK;ILIRNEKDL;DLFKLRNIL;RNILSKEIK;NILSKEIKV;KEIKVQEVL;IKVQEVLQY;KVQEVLQYF
;VQEVLQYFF;QEVLQYFFF;EVLQYFFFS;VLQYFFFSQ;LQYFFFSQF;FFFSQFQAL;FFSQFQAL
K;FSQFQALKR;SQFQALKRY;ALKRYANDK;YANDKGIEL;ANDKGIELV;IELVMNLPL;ELVMNLPL
F;LVMNLPLFI;VMNLPLFIA;MNLPLFIAY;LPLFIAYDS;PLFIAYDSA;FIAYDSADV;IAYDSADVW;S
ADVWAHQK;DVWAHQKYF;VWAHQKYFK;HQKYFKLRF;ASKDKVAGI;KVAGISPDY;VAGISPDY
F;YFLEQEQAW;EQAWDSPAY;QAWDSPAYS;AWDSPAYSW;DSPAYSWNV;SPAYSWNVL;PAY
SWNVLK;YSWNVLKNV;SWNVLKNVK;NVKYEWWAK;KYEWWAKRI;WWAKRIGIL;WAKRIGILR;
AKRIGILRK;KRIGILRKY;GILRKYIDV;ILRKYIDVI;DVIKIDHFR;KIDHFRGFV;RGFVSTWEV;FVST
WEVGV;WEVGVGEAY;EVGVGEAYA;VGVGEAYAF;GEAYAFNGL;EAYAFNGLW;AYAFNGLWV
;YAFNGLWVK;GLWVKSPGR;WVKSPGRDF;SPGRDFFNF;GRDFFNFIL;FFNFILNEI;FNFILNEIK
;FILNEIKDL;ILNEIKDLK;EIKDLKIWV;WVEDFENDL;DLEDVSRLR;DVSRLRDFF;SRLRDFFNF;R
LRDFFNFP;DFFNFPGMR;NFPGMRIMK;FPGMRIMKL;GMRIMKLAF;RIMKLAFDF;NYIKNCIVY;Y
IKNCIVYT;TGIGDNSTI;DNSTIREFV;TIREFVNSL;EFVNSLDDL;NSLDDLHKK;SLDDLHKKY;HKK
YIFDYL;YIFDYLNTN;DYLNTNEDF;YLNTNEDFV;NTNEDFVVW;EDFVVWDMI;DFVVWDMIR;FV
VWDMIRS;VVWDMIRSA;MIRSAMSSV;AMSSVSDSV;MSSVSDSVI;SVIIPMQDY;VIIPMQDYI;IP
MQDYINL;DYINLGNEF;YINLGNEFR;RANIPKNTL;IPKNTLNNW;NTLNNWIFR;TLNNWIFRL;RLL
ESDLDA;LLESDLDAT;LESDLDATL;SDLDATLSK;ATLSKNISF;TLSKNISFI;NISFITRLY;SFITRLY
GR

KYKKIRINLN;KIRINLNLKR;NLNLKRKSGI;NLKRKSGILL;SGILLNISSL;ILLNISSLPS;LLNISSLPS
K;LPSKYGIGDL;DLGKGAYKFI;GAYKFIDFLF;FIDFLFASSQ;DFLFASSQSY;FLFASSQSYW;FAS
SQSYWQM;ASSQSYWQMF;SQSYWQMFAY;YWQMFAYSPI;QMFAYSPIDF;FAYSPIDFTR;PID
FTRSPPY;FTRSPPYSIF;RSPPYSIFSA;SPPYSIFSAF;PPYSIFSAFA;SIFSAFAGNV;IFSAFAGNV
Y;FSAFAGNVYY;SAFAGNVYYI;FAGNVYYIDL;NVYYIDLEAL;YYIDLEALDK;YIDLEALDKF;ALDK
FIDSDL;KFIDSDLNLL;FIDSDLNLLK;KENETRYSDL;ETRYSDLKKL;RYSDLKKLSF;YSDLKKLSF
K;KLSFKDKFLK;KFLKEAALNF;FLKEAALNFI;EAALNFINRA;ALNFINRASV;FINRASVDEV;RASV
DEVRSF;SVDEVRSFEK;EVRSFEKFKK;KFKKKSSYWL;KSSYWLLDFA;SYWLLDFASF;YWLLD
FASFV;WLLDFASFVA;LLDFASFVAF;LDFASFVAFK;DFASFVAFKE;FASFVAFKEY;ASFVAFKE
YF;SFVAFKEYFL;FVAFKEYFLK;YFLKDSRDAF;RDAFNVLFDR;NVLFDRGILI;VLFDRGILIR;ILIR
NEKDLF;LIRNEKDLFK;LFKLRNILSK;KLRNILSKEI;EIKVQEVLQY;IKVQEVLQYF;KVQEVLQYFF
;VQEVLQYFFF;QEVLQYFFFS;EVLQYFFFSQ;VLQYFFFSQF;YFFFSQFQAL;FFFSQFQALK;FF
SQFQALKR;SQFQALKRYA;RYANDKGIEL;YANDKGIELV;IELVMNLPLF;ELVMNLPLFI;LVMNLP
LFIA;VMNLPLFIAY;LPLFIAYDSA;FIAYDSADVW;DSADVWAHQK;SADVWAHQKY;DVWAHQKY
FK;VWAHQKYFKL;WAHQKYFKLR;AHQKYFKLRF;YFKLRFDASK;KLRFDASKDK;KVAGISPDYF
;GISPDYFLEQ;DYFLEQEQAW;QEQAWDSPAY;QAWDSPAYSW;WDSPAYSWNV;SPAYSWNV
LK;AYSWNVLKNV;YSWNVLKNVK;SWNVLKNVKY;KNVKYEWWAK;NVKYEWWAKR;YEWWAK
RIGI;WWAKRIGILR;WAKRIGILRK;KRIGILRKYI;ILRKYIDVIK;YIDVIKIDHF;VIKIDHFRGF;FRGFV
STWEV;STWEVGVGEA;WEVGVGEAYA;EVGVGEAYAF;GEAYAFNGLW;EAYAFNGLWV;AYAF
NGLWVK;LWVKSPGRDF;WVKSPGRDFF;KSPGRDFFNF;SPGRDFFNFI;DFFNFILNEI;FFNFILN
EIK;NFILNEIKDL;FILNEIKDLK;ILNEIKDLKI;NEIKDLKIWV;IWVEDFENDL;VSRLRDFFNF;RLRDF
FNFPG;FNFPGMRIMK;FPGMRIMKLA;NQNLPHNYIK;LPHNYIKNCI;HNYIKNCIVY;YTGIGDNSTI
;TGIGDNSTIR;STIREFVNSL;REFVNSLDDL;FVNSLDDLHK;SLDDLHKKYI;DLHKKYIFDY;YIFDY
LNTNE;YLNTNEDFVV;EDFVVWDMIR;FVVWDMIRSA;VVWDMIRSAM;DMIRSAMSSV;SAMSSV
SDSV;AMSSVSDSVI;SVSDSVIIPM;DSVIIPMQDY;SVIIPMQDYI;IIPMQDYINL;DYINLGNEFR;YI
NLGNEFRA;NLGNEFRANI;FRANIPKNTL;IPKNTLNNWI;KNTLNNWIFR;NTLNNWIFRL;TLNNWI
FRLL;WIFRLLESDL;RLLESDLDAT;LLESDLDATL;ESDLDATLSK;DLDATLSKNI;ATLSKNISFI;TL
SKNISFIT;LSKNISFITR;ISFITRLYGR

KYKKIRINLNL;KIRINLNLKRK;NLNLKRKSGIL;ILLNISSLPSK;LLNISSLPSKY;NISSLPSKYGI;SLP
SKYGIGDL;YGIGDLGKGAY;GIGDLGKGAYK;KGAYKFIDFLF;IDFLFASSQSY;DFLFASSQSYW;
FLFASSQSYWQ;FASSQSYWQMF;SSQSYWQMFAY;SQSYWQMFAYS;SYWQMFAYSPI;WQM
FAYSPIDF;QMFAYSPIDFT;MFAYSPIDFTR;SPIDFTRSPPY;DFTRSPPYSIF;TRSPPYSIFSA;RS
PPYSIFSAF;YSIFSAFAGNV;SIFSAFAGNVY;IFSAFAGNVYY;FSAFAGNVYYI;AFAGNVYYIDL;V
YYIDLEALDK;YYIDLEALDKF;YIDLEALDKFI;KFIDSDLNLLK;DLNLLKENETR;KENETRYSDLK;N
ETRYSDLKKL;TRYSDLKKLSF;RYSDLKKLSFK;KKLSFKDKFLK;FKDKFLKEAAL;KFLKEAALNFI
;EAALNFINRAS;AALNFINRASV;FINRASVDEVR;ASVDEVRSFEK;SVDEVRSFEKF;EVRSFEKF
KKK;KFKKKSSYWLL;SSYWLLDFASF;SYWLLDFASFV;WLLDFASFVAF;LLDFASFVAFK;DFAS
FVAFKEY;FASFVAFKEYF;SFVAFKEYFLK;AFKEYFLKDSR;EYFLKDSRDAF;FLKDSRDAFNV;D
AFNVLFDRGI;NVLFDRGILIR;VLFDRGILIRN;ILIRNEKDLFK;EKDLFKLRNIL;DLFKLRNILSK;KLR
NILSKEIK;ILSKEIKVQEV;KEIKVQEVLQY;EIKVQEVLQYF;KVQEVLQYFFF;EVLQYFFFSQF;VL
QYFFFSQFQ;LQYFFFSQFQA;QYFFFSQFQAL;YFFFSQFQALK;FFFSQFQALKR;FFSQFQALK
RY;ALKRYANDKGI;KRYANDKGIEL;RYANDKGIELV;YANDKGIELVM;IELVMNLPLFI;ELVMNLP
LFIA;LVMNLPLFIAY;NLPLFIAYDSA;LPLFIAYDSAD;PLFIAYDSADV;LFIAYDSADVW;FIAYDSAD
VWA;IAYDSADVWAH;DSADVWAHQKY;DVWAHQKYFKL;VWAHQKYFKLR;WAHQKYFKLRF;K
YFKLRFDASK;KLRFDASKDKV;KVAGISPDYFL;EQEQAWDSPAY;AWDSPAYSWNV;DSPAYSW
NVLK;PAYSWNVLKNV;AYSWNVLKNVK;YSWNVLKNVKY;VLKNVKYEWWA;KNVKYEWWAKR;
KYEWWAKRIGI;YEWWAKRIGIL;EWWAKRIGILR;WWAKRIGILRK;RIGILRKYIDV;GILRKYIDVIK;
ILRKYIDVIKI;KYIDVIKIDHF;YIDVIKIDHFR;DVIKIDHFRGF;VIKIDHFRGFV;KIDHFRGFVST;HFR
GFVSTWEV;STWEVGVGEAY;WEVGVGEAYAF;GVGEAYAFNGL;GEAYAFNGLWV;EAYAFNGL
WVK;LWVKSPGRDFF;SPGRDFFNFIL;DFFNFILNEIK;NFILNEIKDLK;FILNEIKDLKI;ILNEIKDLKI
W;KIWVEDFENDL;DFENDLEDVSR;FENDLEDVSRL;DVSRLRDFFNF;RLRDFFNFPGM;DFFNF
PGMRIM;FFNFPGMRIMK;FPGMRIMKLAF;GMRIMKLAFDF;KLAFDFDSDNQ;DSDNQNLPHNY;
NLPHNYIKNCI;LPHNYIKNCIV;YIKNCIVYTGI;VYTGIGDNSTI;YTGIGDNSTIR;IGDNSTIREFV;EF
VNSLDDLHK;FVNSLDDLHKK;SLDDLHKKYIF;DLHKKYIFDYL;YIFDYLNTNED;IFDYLNTNEDF;F
DYLNTNEDFV;DYLNTNEDFVV;YLNTNEDFVVW;NTNEDFVVWDM;FVVWDMIRSAM;WDMIRS
AMSSV;RSAMSSVSDSV;SAMSSVSDSVI;AMSSVSDSVII;SSVSDSVIIPM;SVSDSVIIPMQ;DSVII
PMQDYI;VIIPMQDYINL;MQDYINLGNEF;QDYINLGNEFR;LGNEFRANIPK;NIPKNTLNNWI;IPKN
TLNNWIF;NTLNNWIFRLL;TLNNWIFRLLE;NWIFRLLESDL;RLLESDLDATL;DATLSKNISFI;TLSK
NISFITR;NISFITRLYGR

Class 2

AFDFDSDNQNLPHNY;FDSDNQNLP;AFKEYFLKDSRDAFN;FLKDSRDAF;AFKEYFLKDSRDAF
N;YFLKDSRDA;AFNGLWVKSPGRDFF;FNGLWVKSP;AFNVLFDRGILIRNE;FDRGILIRN;AFNVL
FDRGILIRNE;VLFDRGILI;AGNVYYIDLEALDKF;YYIDLEALD;AHQKYFKLRFDASKD;FKLRFDAS
K;AKRIGILRKYIDVIK;AKRIGILRK;AKRIGILRKYIDVIK;IGILRKYID;AKRIGILRKYIDVIK;ILRKYIDV
I;ALDKFIDSDLNLLKE;FIDSDLNLL;ALNFINRASVDEVRS;FINRASVDE;ANIPKNTLNNWIFRL;PK
NTLNNWI;ASSQSYWQMFAYSPI;YWQMFAYSP;ATLSKNISFITRLYG;LSKNISFIT;AWDSPAYS
WNVLKNV;DSPAYSWNV;AYAFNGLWVKSPGRD;FNGLWVKSP;AYAFNGLWVKSPGRD;GLWV
KSPGR;AYKFIDFLFASSQSY;FIDFLFASS;AYKFIDFLFASSQSY;IDFLFASSQ;AYSPIDFTRSPPY
SI;IDFTRSPPY;AYSPIDFTRSPPYSI;YSPIDFTRS;AYSWNVLKNVKYEWW;WNVLKNVKY;CIVYT
GIGDNSTIRE;VYTGIGDNS;CIVYTGIGDNSTIRE;YTGIGDNST;DAFNVLFDRGILIRN;FNVLFDR
GI;DATLSKNISFITRLY;LSKNISFIT;DDLHKKYIFDYLNTN;DDLHKKYIF;DFDSDNQNLPHNYIK;F
DSDNQNLP;DFFNFILNEIKDLKI;ILNEIKDLK;DFFNFPGMRIMKLAF;FPGMRIMKL;DFLFASSQSY
WQMFA;FASSQSYWQ;DFLFASSQSYWQMFA;LFASSQSYW;DFTRSPPYSIFSAFA;FTRSPPYS
I;DFVVWDMIRSAMSSV;FVVWDMIRS;DFVVWDMIRSAMSSV;WDMIRSAMS;DHFRGFVSTWEV
GVG;FRGFVSTWE;DKFLKEAALNFINRA;LKEAALNFI;DKGIELVMNLPLFIA;LVMNLPLFI;DLDAT
LSKNISFITR;LSKNISFIT;DLEALDKFIDSDLNL;LEALDKFID;DLFKLRNILSKEIKV;FKLRNILSK;DL
FKLRNILSKEIKV;LFKLRNILS;DLFKLRNILSKEIKV;LRNILSKEI;DLHKKYIFDYLNTNE;YIFDYLNT
N;DLNLLKENETRYSDL;LKENETRYS;DMIRSAMSSVSDSVI;IRSAMSSVS;DNSTIREFVNSLDDL
;IREFVNSLD;DRGILIRNEKDLFKL;LIRNEKDLF;DSDLNLLKENETRYS;LNLLKENET;DSPAYSW
NVLKNVKY;AYSWNVLKN;DSPAYSWNVLKNVKY;SWNVLKNVK;DSPAYSWNVLKNVKY;YSWN
VLKNV;DVWAHQKYFKLRFDA;WAHQKYFKL;DYFLEQEQAWDSPAY;YFLEQEQAW;EAYAFNG
LWVKSPGR;FNGLWVKSP;EAYAFNGLWVKSPGR;YAFNGLWVK;EDFENDLEDVSRLRD;FEND

LEDVS;EDFVVWDMIRSAMSS;FVVWDMIRS;EDFVVWDMIRSAMSS;WDMIRSAMS;EFRANIPK
NTLNNWI;FRANIPKNT;EKDLFKLRNILSKEI;LFKLRNILS;EKFKKKSSYWLLDFA;FKKKSSYWL;E
LVMNLPLFIAYDSA;VMNLPLFIA;ENETRYSDLKKLSFK;RYSDLKKLS;ETRYSDLKKLSFKDK;RY
SDLKKLS;EVLQYFFFSQFQALK;YFFFSQFQA;EVRSFEKFKKKSSYW;FEKFKKKSS;EWWAKRI
GILRKYID;WAKRIGILR;EYFLKDSRDAFNVLF;FLKDSRDAF;EAALNFINRASVDEV;ALNFINRAS;
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;YSPIDFTRS;FDASKDKVAGISPDY;FDASKDKVA;FDFDSDNQNLPHNYI;FDSDNQNLP;FDRGILI
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FNFILNEIKDLKIW;ILNEIKDLK;FFNFPGMRIMKLAFD;FPGMRIMKL;FFNFPGMRIMKLAFD;GMRI
MKLAF;FFSQFQALKRYANDK;FQALKRYAN;FIAYDSADVWAHQKY;FIAYDSADV;FIDFLFASSQ
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AALNFI;FKEYFLKDSRDAFNV;FLKDSRDAF;FKEYFLKDSRDAFNV;YFLKDSRDA;FKKKSSYWL
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FINRASV;LKEAALNFI;FNFILNEIKDLKIWV;ILNEIKDLK;FNFPGMRIMKLAFDF;FPGMRIMKL;FN
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DRGILI;FPGMRIMKLAFDFDS;FPGMRIMKL;FRANIPKNTLNNWIF;FRANIPKNT;FRGFVSTWEV
GVGEA;FRGFVSTWE;FRLLESDLDATLSKN;FRLLESDLD;FSQFQALKRYANDKG;FQALKRYAN
;FTRSPPYSIFSAFAG;FTRSPPYSI;FVAFKEYFLKDSRDA;FKEYFLKDS;FVVWDMIRSAMSSVS;
MIRSAMSSV;FVVWDMIRSAMSSVS;VWDMIRSAM;FVVWDMIRSAMSSVS;WDMIRSAMS;GDL
GKGAYKFIDFLF;LGKGAYKFI;GDNSTIREFVNSLDD;IREFVNSLD;GEAYAFNGLWVKSPG;AYA
FNGLWV;GEAYAFNGLWVKSPG;FNGLWVKSP;GIELVMNLPLFIAYD;LVMNLPLFI;GIELVMNLP
LFIAYD;VMNLPLFIA;GILLNISSLPSKYGI;ILLNISSLP;GILLNISSLPSKYGI;ISSLPSKYG;GILLNIS
SLPSKYGI;LLNISSLPS;GNEFRANIPKNTLNN;FRANIPKNT;GRDFFNFILNEIKDL;FFNFILNEI;HF
RGFVSTWEVGVGE;FRGFVSTWE;HKKYIFDYLNTNEDF;FDYLNTNED;HKKYIFDYLNTNEDF;YI
FDYLNTN;HNYIKNCIVYTGIGD;IKNCIVYTG;HNYIKNCIVYTGIGD;YIKNCIVYT;IAYDSADVWAH
QKYF;YDSADVWAH;IDFLFASSQSYWQMF;FASSQSYWQ;IDFLFASSQSYWQMF;FLFASSQSY
;IDFTRSPPYSIFSAF;FTRSPPYSI;IDHFRGFVSTWEVGV;FRGFVSTWE;IDLEALDKFIDSDLN;EA
LDKFIDS;IDSDLNLLKENETRY;LNLLKENET;IELVMNLPLFIAYDS;LVMNLPLFI;IELVMNLPLFIAY
DS;VMNLPLFIA;IFDYLNTNEDFVVWD;FDYLNTNED;IFDYLNTNEDFVVWD;YLNTNEDFV;IFRLL
ESDLDATLSK;FRLLESDLD;IFSAFAGNVYYIDLE;FSAFAGNVY;IGDNSTIREFVNSLD;NSTIREF
VN;IGILRKYIDVIKIDH;IGILRKYID;IGILRKYIDVIKIDH;ILRKYIDVI;IIPMQDYINLGNEFR;PMQDYI
NLG;IKIDHFRGFVSTWEV;FRGFVSTWE;IKNCIVYTGIGDNST;IKNCIVYTG;ILLNISSLPSKYGIG;
ILLNISSLP;ILLNISSLPSKYGIG;ISSLPSKYG;ILLNISSLPSKYGIG;LLNISSLPS;ILNEIKDLKIWVE
DF;EIKDLKIWV;ILNEIKDLKIWVEDF;ILNEIKDLK;INLGNEFRANIPKNT;LGNEFRANI;INLNLKRK
SGILLNI;LKRKSGILL;IPKNTLNNWIFRLLE;LNNWIFRLL;IPKNTLNNWIFRLLE;PKNTLNNWI;IPM
QDYINLGNEFRA;YINLGNEFR;IREFVNSLDDLHKKY;FVNSLDDLH;IREFVNSLDDLHKKY;IREFV
NSLD;IRINLNLKRKSGILL;INLNLKRKS;IRINLNLKRKSGILL;IRINLNLKR;IRSAMSSVSDSVIIP;IR
SAMSSVS;ISSLPSKYGIGDLGK;ISSLPSKYG;IVYTGIGDNSTIREF;IGDNSTIRE;IVYTGIGDNSTI
REF;IVYTGIGDN;IVYTGIGDNSTIREF;YTGIGDNST;KDKFLKEAALNFINR;LKEAALNFI;KDKVAG
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NFINRAS;KEAALNFINRASVDE;AALNFINRA;KFIDFLFASSQSYWQ;FLFASSQSY;KFIDSDLNLL
KENET;FIDSDLNLL;KFKKKSSYWLLDFAS;FKKKSSYWL;KFLKEAALNFINRAS;FLKEAALNF;KF
LKEAALNFINRAS;LKEAALNFI;KGIELVMNLPLFIAY;VMNLPLFIA;KIDHFRGFVSTWEVG;FRGFV
STWE;KIRINLNLKRKSGIL;INLNLKRKS;KIRINLNLKRKSGIL;IRINLNLKR;KKIRINLNLKRKSGI;IN
LNLKRKS;KKIRINLNLKRKSGI;IRINLNLKR;KKSSYWLLDFASFVA;WLLDFASFV;KKSSYWLLDF
ASFVA;YWLLDFASF;KKYIFDYLNTNEDFV;FDYLNTNED;KKYIFDYLNTNEDFV;YIFDYLNTN;KL
RNILSKEIKVQEV;LRNILSKEI;KNCIVYTGIGDNSTI;YTGIGDNST;KNTLNNWIFRLLESD;LNNWIF
RLL;KNVKYEWWAKRIGIL;VKYEWWAKR;KNVKYEWWAKRIGIL;YEWWAKRIG;KRIGILRKYIDV
IKI;IGILRKYID;KRIGILRKYIDVIKI;ILRKYIDVI;KRKSGILLNISSLPS;GILLNISSL;KRKSGILLNISSL

PS;ILLNISSLP;KSGILLNISSLPSKY;ILLNISSLP;KSGILLNISSLPSKY;LLNISSLPS;KSSYWLLDFA
SFVAF;LLDFASFVA;KSSYWLLDFASFVAF;WLLDFASFV;KYEWWAKRIGILRKY;WAKRIGILR;K
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NLKRKS;IRINLNLKR;KYKKIRINLNLKRKS;YKKIRINLN;LDATLSKNISFITRL;LSKNISFIT;LDDLH
KKYIFDYLNT;HKKYIFDYL;LEDVSRLRDFFNFPG;LEDVSRLRD;LEDVSRLRDFFNFPG;RLRDFF
NFP;LEQEQAWDSPAYSWN;EQAWDSPAY;LESDLDATLSKNISF;LESDLDATL;LFDRGILIRNEK
DLF;ILIRNEKDL;LFDRGILIRNEKDLF;RGILIRNEK;LFIAYDSADVWAHQK;FIAYDSADV;LFKLRNI
LSKEIKVQ;FKLRNILSK;LFKLRNILSKEIKVQ;LRNILSKEI;LGNEFRANIPKNTLN;FRANIPKNT;LH
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FINRAS;LKNVKYEWWAKRIGI;VKYEWWAKR;LKNVKYEWWAKRIGI;YEWWAKRIG;LKRKSGIL
LNISSLP;GILLNISSL;LKRKSGILLNISSLP;LKRKSGILL;LLDFASFVAFKEYFL;LLDFASFVA;LLES
DLDATLSKNIS;LDATLSKNI;LLNISSLPSKYGIGD;ISSLPSKYG;LLNISSLPSKYGIGD;LLNISSLPS
;LNFINRASVDEVRSF;FINRASVDE;LNISSLPSKYGIGDL;ISSLPSKYG;LNLKRKSGILLNISS;LKR
KSGILL;LNLLKENETRYSDLK;LKENETRYS;LNNWIFRLLESDLDA;FRLLESDLD;LNTNEDFVVW
DMIRS;TNEDFVVWD;LPHNYIKNCIVYTGI;IKNCIVYTG;LPHNYIKNCIVYTGI;LPHNYIKNC;LPHN
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LK;LQYFFFSQFQALKRY;FSQFQALKR;LRDFFNFPGMRIMKL;FFNFPGMRI;LRNILSKEIKVQEV
L;LRNILSKEI;LRNILSKEIKVQEVL;LSKEIKVQE;LSFKDKFLKEAALNF;FKDKFLKEA;LSKEIKVQE
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LPLFIAYDSAD;LVMNLPLFI;LVMNLPLFIAYDSAD;VMNLPLFIA;LWVKSPGRDFFNFIL;LWVKSP
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II;IRSAMSSVS;MKYKKIRINLNLKRK;IRINLNLKR;MKYKKIRINLNLKRK;YKKIRINLN;MNLPLFIAY
DSADVW;FIAYDSADV;MQDYINLGNEFRANI;YINLGNEFR;NCIVYTGIGDNSTIR;YTGIGDNST;N
DKGIELVMNLPLFI;DKGIELVMN;NDKGIELVMNLPLFI;ELVMNLPLF;NDKGIELVMNLPLFI;IELV
MNLPL;NDLEDVSRLRDFFNF;VSRLRDFFN;NEDFVVWDMIRSAMS;FVVWDMIRS;NEDFVVWD
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NETRYSDLKKLSFKD;RYSDLKKLS;NFILNEIKDLKIWVE;FILNEIKDL;NFILNEIKDLKIWVE;ILNEI
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GILLNISSL;LKRKSGILL;NLLKENETRYSDLKK;LKENETRYS;NLNLKRKSGILLNIS;LKRKSGILL;
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DDLH;IREFVNSLD;NTLNNWIFRLLESDL;LNNWIFRLL;NTNEDFVVWDMIRSA;FVVWDMIRS;NV
KYEWWAKRIGILR;VKYEWWAKR;NVKYEWWAKRIGILR;WWAKRIGIL;NVKYEWWAKRIGILR;Y
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G;IKNCIVYTG;PHNYIKNCIVYTGIG;YIKNCIVYT;PIDFTRSPPYSIFSA;FTRSPPYSI;PKNTLNNWI
FRLLES;LNNWIFRLL;PLFIAYDSADVWAHQ;FIAYDSADV;PMQDYINLGNEFRAN;YINLGNEFR;
PPYSIFSAFAGNVYY;IFSAFAGNV;PYSIFSAFAGNVYYI;IFSAFAGNV;QALKRYANDKGIELV;LK
RYANDKG;QAWDSPAYSWNVLKN;QAWDSPAYS;QDYINLGNEFRANIP;LGNEFRANI;QDYINL
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;WQMFAYSPI;QSYWQMFAYSPIDFT;YWQMFAYSP;QYFFFSQFQALKRYA;FFSQFQALK;RDFF
NFILNEIKDLK;FFNFILNEI;RDFFNFPGMRIMKLA;FPGMRIMKL;RGILIRNEKDLFKLR;LIRNEKDL
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S;RLRDFFNFPGMRIMK;FFNFPGMRI;RNEKDLFKLRNILSK;LFKLRNILS;RNILSKEIKVQEVLQ;L
SKEIKVQE;RSFEKFKKKSSYWLL;FKKKSSYWL;RSPPYSIFSAFAGNV;YSIFSAFAG;SDLDATLS
KNISFIT;DATLSKNIS;SDLNLLKENETRYSD;LKENETRYS;SDLNLLKENETRYSD;LNLLKENET;S
FEKFKKKSSYWLLD;FKKKSSYWL;SFKDKFLKEAALNFI;FLKEAALNF;SGILLNISSLPSKYG;ILLN
ISSLP;SGILLNISSLPSKYG;LLNISSLPS;SLPSKYGIGDLGKGA;PSKYGIGDL;SPAYSWNVLKNV
KYE;AYSWNVLKN;SPAYSWNVLKNVKYE;WNVLKNVKY;SPAYSWNVLKNVKYE;YSWNVLKNV;
SPIDFTRSPPYSIFS;FTRSPPYSI;SPPYSIFSAFAGNVY;IFSAFAGNV;SQFQALKRYANDKGI;FQ

ALKRYAN;SQSYWQMFAYSPIDF;WQMFAYSPI;SQSYWQMFAYSPIDF;YWQMFAYSP;SRDAF
NVLFDRGILI;FNVLFDRGI;SRLRDFFNFPGMRIM;FFNFPGMRI;SSQSYWQMFAYSPID;WQMFA
YSPI;SSQSYWQMFAYSPID;YWQMFAYSP;SSYWLLDFASFVAFK;LLDFASFVA;SSYWLLDFAS
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KKSS;VRSFEKFKKKSSYWL;KFKKKSSYW;VRSFEKFKKKSSYWL;VRSFEKFKK;VSRLRDFFNF
PGMRI;LRDFFNFPG;VSRLRDFFNFPGMRI;RLRDFFNFP;VSRLRDFFNFPGMRI;VSRLRDFFN;
VVWDMIRSAMSSVSD;IRSAMSSVS;VVWDMIRSAMSSVSD;MIRSAMSSV;VVWDMIRSAMSSV
SD;WDMIRSAMS;VWAHQKYFKLRFDAS;QKYFKLRFD;VWAHQKYFKLRFDAS;WAHQKYFKL;V
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ALDKFIDS;YIDLEALDK;WAKRIGILRKYIDVI;IGILRKYID;WAKRIGILRKYIDVI;WAKRIGILR;WDMI
RSAMSSVSDSV;IRSAMSSVS;WDMIRSAMSSVSDSV;WDMIRSAMS;WEVGVGEAYAFNGLW;V
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KNVKYEWWAKR;WNVLKNVKY;WQMFAYSPIDFTRSP;MFAYSPIDF;WQMFAYSPIDFTRSP;YS
PIDFTRS;WWAKRIGILRKYIDV;IGILRKYID;YAFNGLWVKSPGRDF;FNGLWVKSP;YDSADVWA
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DYLNTNEDFVVW;YIFDYLNTN;YIFDYLNTNEDFVVW;YLNTNEDFV;YIKNCIVYTGIGDNS;IKNCI
VYTG;YINLGNEFRANIPKN;YINLGNEFR;YKFIDFLFASSQSYW;FIDFLFASS;YKFIDFLFASSQS
YW;FLFASSQSY;YKKIRINLNLKRKSG;INLNLKRKS;YKKIRINLNLKRKSG;IRINLNLKR;YKKIRINL
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WNVLKNVKYEWWA;WNVLKNVKY;YTGIGDNSTIREFVN;IGDNSTIRE;YTGIGDNSTIREFVN;YT
GIGDNST;YWQMFAYSPIDFTRS;MFAYSPIDF;YWQMFAYSPIDFTRS;WQMFAYSPI;YWQMFAY
SPIDFTRS;YWQMFAYSP;AALNFINRASVDEVR;FINRASVDE;AALNFINRASVDEVR;INRASVDE
V

<CAA59727 outer surface protein A;Protein;Borrelia garinii>

Class 1

KYLLGIGL;YLLGIGLI;LLGIGLIL;GIGLILAL;GLILALIA;ILALIACK;LIACKQNV;NVSSLDEK;SLDEK
NSV;SVDLPGGM;DLPGGMKV;LPGGMKVL;GMKVLVSK;KVLVSKEK;KYSLMATV;SLMATVEK;L
MATVEKL;ATVEKLEL;TVEKLELK;ELKGTSDK;KTDKSKVK;KLTIAEDL;TIAEDLSK;AEDLSKTT;K
TTFEIFK;TTFEIFKE;EIFKEDGK;FKEDGKTL;KEDGKTLV;LVSKKVTL;VSKKVTLK;TLKDKSST;K
SSTEEKF;GEISEKTI;EISEKTIV;ISEKTIVR;IVRANGTR;RLEYTDIK;EVLKDFTL;FTLEGTLA;TLE
GTLAA;GTLAADGK;AADGKTTL;KVTEGTVV;EGTVVLSK;TVVLSKNI;VLSKNILK;ALDDSDTT;DT
TQATKK;KTGKWDSK;TSTLTISV;TISVNSQK;SVNSQKTK;SQKTKNLV;TKNLVFTK;EDTITVQK;
DTITVQKY;KAVEITTL;EITTLEKL;ITTLEKLK

KYLLGIGLI;YLLGIGLIL;LLGIGLILA;GIGLILALI;LILALIACK;ALIACKQNV;SSLDEKNSV;SLDEKNS
VS;SVDLPGGMK;VDLPGGMKV;DLPGGMKVL;LPGGMKVLV;GGMKVLVSK;GKYSLMATV;YSL
MATVEK;SLMATVEKL;ATVEKLELK;GSGTLEGEK;LTIAEDLSK;AEDLSKTTF;DLSKTTFEI;FKED
GKTLV;TLVSKKVTL;LVSKKVTLK;KDKSSTEEK;STEEKFNEK;GEISEKTIV;EISEKTIVR;TIVRAN
GTR;IVRANGTRL;RANGTRLEY;KSDGSGKAK;SGKAKEVLK;KEVLKDFTL;VLKDFTLEG;FTLEG

TLAA;LAADGKTTL;AADGKTTLK;TTLKVTEGT;TLKVTEGTV;KVTEGTVVL;VVLSKNILK;VLSKNI
LKS;ILKSGEITV;KSGEITVAL;ALDDSDTTQ;TQATKKTGK;KTSTLTISV;LTISVNSQK;ISVNSQKT
K;SQKTKNLVF;KTKNLVFTK;FTKEDTITV;KYDSAGTNL;SAGTNLEGK;NLEGKAVEI;AVEITTLEK
;VEITTLEKL;EITTLEKLK;TLEKLKDAL

KYLLGIGLIL;YLLGIGLILA;LLGIGLILAL;LGIGLILALI;GLILALIACK;KQNVSSLDEK;SLDEKNSVSV
;SVSVDLPGGM;VSVDLPGGMK;SVDLPGGMKV;VDLPGGMKVL;DLPGGMKVLV;LPGGMKVLV
S;GMKVLVSKEK;KVLVSKEKDK;KYSLMATVEK;YSLMATVEKL;LMATVEKLEL;MATVEKLELK;K
LELKGTSDK;GTLEGEKTDK;KLTIAEDLSK;IAEDLSKTTF;DLSKTTFEIF;LSKTTFEIFK;EIFKEDG
KTL;TLVSKKVTLK;VSKKVTLKDK;SSTEEKFNEK;EEKFNEKGEI;EISEKTIVRA;KTIVRANGTR;TI
VRANGTRL;GTRLEYTDIK;GSGKAKEVLK;VLKDFTLEGT;FTLEGTLAAD;TLAADGKTTL;LAADG
KTTLK;AADGKTTLKV;TTLKVTEGTV;TLKVTEGTVV;VTEGTVVLSK;TVVLSKNILK;NILKSGEITV;
ILKSGEITVA;ALDDSDTTQA;TTQATKKTGK;SKTSTLTISV;TLTISVNSQK;TISVNSQKTK;NSQKT
KNLVF;NLVFTKEDTI;VFTKEDTITV;DSAGTNLEGK;KAVEITTLEK;TTLEKLKDAL;TLEKLKDALK

YLLGIGLILAL;LLGIGLILALI;ILALIACKQNV;LIACKQNVSSL;NVSSLDEKNSV;SSLDEKNSVSV;S
VSVDLPGGMK;SVDLPGGMKVL;VDLPGGMKVLV;LPGGMKVLVSK;LVSKEKDKDGK;KYSLMAT
VEKL;SLMATVEKLEL;LMATVEKLELK;GEKTDKSKVKL;KTDKSKVKLTI;TIAEDLSKTTF;AEDLSK
TTFEI;DLSKTTFEIFK;TTFEIFKEDGK;FEIFKEDGKTL;EIFKEDGKTLV;KTLVSKKVTLK;LVSKKV
TLKDK;TLKDKSSTEEK;KSSTEEKFNEK;KFNEKGEISEK;EKTIVRANGTR;KTIVRANGTRL;IVRA
NGTRLEY;YTDIKSDGSGK;VLKDFTLEGTL;TLEGTLAADGK;TLAADGKTTLK;LAADGKTTLKV;K
TTLKVTEGTV;TTLKVTEGTVV;TLKVTEGTVVL;KVTEGTVVLSK;GTVVLSKNILK;ILKSGEITVAL;
ALDDSDTTQAT;DTTQATKKTGK;ATKKTGKWDSK;KWDSKTSTLTI;STLTISVNSQK;LTISVNSQ
KTK;SVNSQKTKNLV;SQKTKNLVFTK;LVFTKEDTITV;FTKEDTITVQK;DTITVQKYDSA;VQKYDS
AGTNL;NLEGKAVEITT;LEGKAVEITTL;KAVEITTLEKL;AVEITTLEKLK;TTLEKLKDALK

Class 2

ADGKTTLKVTEGTVV;ADGKTTLKV;ADGKTTLKVTEGTVV;TLKVTEGTV;AGTNLEGKAVEITTL;L
EGKAVEIT;AKEVLKDFTLEGTLA;VLKDFTLEG;DFTLEGTLAADGKTT;FTLEGTLAA;DGKTLVSK
KVTLKDK;LVSKKVTLK;DGKTTLKVTEGTVVL;LKVTEGTVV;DGKYSLMATVEKLEL;YSLMATVE
K;DKDGKYSLMATVEKL;YSLMATVEK;DLPGGMKVLVSKEKD;MKVLVSKEK;DSAGTNLEGKAV
EIT;GTNLEGKAV;DTITVQKYDSAGTNL;VQKYDSAGT;EDGKTLVSKKVTLKD;GKTLVSKKV;ED
GKTLVSKKVTLKD;LVSKKVTLK;EDTITVQKYDSAGTN;VQKYDSAGT;EGTVVLSKNILKSGE;TV
VLSKNIL;EGTVVLSKNILKSGE;VLSKNILKS;EIFKEDGKTLVSKKV;FKEDGKTLV;EISEKTIVRAN
GTRL;KTIVRANGT;EKTIVRANGTRLEYT;IVRANGTRL;EVLKDFTLEGTLAAD;FTLEGTLAA;EYT
DIKSDGSGKAKE;IKSDGSGKA;FKEDGKTLVSKKVTL;GKTLVSKKV;FTLEGTLAADGKTTL;FTLE
GTLAA;GGMKVLVSKEKDKDG;MKVLVSKEK;GIGLILALIACKQNV;ILALIACKQ;GKAKEVLKDFTL
EGT;VLKDFTLEG;GKTLVSKKVTLKDKS;LVSKKVTLK;GKTTLKVTEGTVVLS;LKVTEGTVV;GKW
DSKTSTLTISVN;WDSKTSTLT;GKYSLMATVEKLELK;YSLMATVEK;GLILALIACKQNVSS;ILALIA
CKQ;GTNLEGKAVEITTLE;LEGKAVEIT;GTVVLSKNILKSGEI;VVLSKNILK;IFKEDGKTLVSKKVT;
GKTLVSKKV;IGLILALIACKQNVS;ILALIACKQ;ILKSGEITVALDDSD;LKSGEITVA;ISEKTIVRANG
TRLE;IVRANGTRL;ISVNSQKTKNLVFTK;VNSQKTKNL;ITVQKYDSAGTNLEG;VQKYDSAGT;ITV
QKYDSAGTNLEG;YDSAGTNLE;IVRANGTRLEYTDIK;IVRANGTRL;KAKEVLKDFTLEGTL;VLKD
FTLEG;KDFTLEGTLAADGKT;FTLEGTLAA;KDGKYSLMATVEKLE;YSLMATVEK;KDKDGKYSL
MATVEK;KDGKYSLMA;KEDGKTLVSKKVTLK;GKTLVSKKV;KEDTITVQKYDSAGT;ITVQKYDSA
;KEVLKDFTLEGTLAA;LKDFTLEGT;KEVLKDFTLEGTLAA;VLKDFTLEG;KKTGKWDSKTSTLTI;
WDSKTSTLT;KKYLLGIGLILALIA;LLGIGLILA;KNILKSGEITVALDD;LKSGEITVA;KNLVFTKEDTIT
VQK;FTKEDTITV;KTGKWDSKTSTLTIS;WDSKTSTLT;KTIVRANGTRLEYTD;IVRANGTRL;KTKN
LVFTKEDTITV;KTKNLVFTK;KTKNLVFTKEDTITV;VFTKEDTIT;KTTLKVTEGTVVLSK;LKVTEGT
VV;KTTLKVTEGTVVLSK;VTEGTVVLS;KVTEGTVVLSKNILK;TVVLSKNIL;KVTEGTVVLSKNILK;
VTEGTVVLS;KWDSKTSTLTISVNS;WDSKTSTLT;KYLLGIGLILALIAC;LLGIGLILA;LEGTLAADG
KTTLKV;LEGTLAADG;LEYTDIKSDGSGKAK;IKSDGSGKA;LGIGLILALIACKQN;IGLILALIA;LKDF
TLEGTLAADGK;FTLEGTLAA;LKSGEITVALDDSDT;LKSGEITVA;LKVTEGTVVLSKNIL;LKVTEG
TVV;LKVTEGTVVLSKNIL;VTEGTVVLS;LLGIGLILALIACKQ;IGLILALIA;LPGGMKVLVSKEKDK;M
KVLVSKEK;LSKNILKSGEITVAL;LKSGEITVA;LTISVNSQKTKNLVF;VNSQKTKNL;LVFTKEDTIT

VQKYD;FTKEDTITV;MKKYLLGIGLILALI;LLGIGLILA;NILKSGEITVALDDS;LKSGEITVA;NLVFTK
EDTITVQKY;FTKEDTITV;NSVSVDLPGGMKVLV;VDLPGGMKV;PGGMKVLVSKEKDKD;MKVLV
SKEK;QKYDSAGTNLEGKAV;YDSAGTNLE;RLEYTDIKSDGSGKA;YTDIKSDGS;SAGTNLEGKA
VEITT;LEGKAVEIT;SEKTIVRANGTRLEY;IVRANGTRL;SGKAKEVLKDFTLEG;AKEVLKDFT;SK
NILKSGEITVALD;LKSGEITVA;SKVKLTIAEDLSKTT;VKLTIAEDL;STLTISVNSQKTKNL;ISVNSQ
KTK;STLTISVNSQKTKNL;TISVNSQKT;SVDLPGGMKVLVSKE;LPGGMKVLV;SVSVDLPGGMKV
LVS;LPGGMKVLV;TEGTVVLSKNILKSG;TVVLSKNIL;TEGTVVLSKNILKSG;VLSKNILKS;TGKW
DSKTSTLTISV;WDSKTSTLT;TISVNSQKTKNLVFT;VNSQKTKNL;TITVQKYDSAGTNLE;VQKYD
SAGT;TIVRANGTRLEYTDI;VRANGTRLE;TKKTGKWDSKTSTLT;TGKWDSKTS;TKNLVFTKEDT
ITVQ;FTKEDTITV;TLEGTLAADGKTTLK;LEGTLAADG;TLKVTEGTVVLSKNI;VTEGTVVLS;TLTIS
VNSQKTKNLV;VNSQKTKNL;TNLEGKAVEITTLEK;LEGKAVEIT;TTLKVTEGTVVLSKN;LKVTEG
TVV;TTLKVTEGTVVLSKN;VTEGTVVLS;TVQKYDSAGTNLEGK;VQKYDSAGT;TVQKYDSAGTN
LEGK;YDSAGTNLE;TVVLSKNILKSGEIT;TVVLSKNIL;VALDDSDTTQATKKT;LDDSDTTQA;VDL
PGGMKVLVSKEK;LPGGMKVLV;VDLPGGMKVLVSKEK;VDLPGGMKV;VLKDFTLEGTLAADG;F
TLEGTLAA;VLSKNILKSGEITVA;KNILKSGEI;VQKYDSAGTNLEGKA;VQKYDSAGT;VQKYDSAG
TNLEGKA;YDSAGTNLE;VRANGTRLEYTDIKS;VRANGTRLE;VSVDLPGGMKVLVSK;LPGGMKV
LV;VTEGTVVLSKNILKS;TVVLSKNIL;VTEGTVVLSKNILKS;VTEGTVVLS;VVLSKNILKSGEITV;V
VLSKNILK;WDSKTSTLTISVNSQ;WDSKTSTLT;YLLGIGLILALIACK;IGLILALIA;YSLMATVEKLEL
KGT;YSLMATVEK;YTDIKSDGSGKAKEV;IKSDGSGKA

<AAN87995 Outer Surface Protein C;Protein;Borrelia garinii>

Class 1
ILMTLFLF;LMTLFLFI;TLFLFISC;STNPDESA;ESAKGPNL;AKGPNLTV;NLTVISKK;KITDSNAF;IT
DSNAFV;SNAFVLAV;NAFVLAVK;FVLAVKEV;AVKEVEAL;KEVEALIS;LISSIDEL;SIDELANK;DE
LANKAI;LANKAIGK;VIHQNNGL;HQNNGLNA;GQNGSLLA;GSLLAGAY;SLLAGAYA;LLAGAYAI;
GAYAISTL;AYAISTLI;ISTLITEK;LITEKLSK;TEKLSKLK;KLKNSEEL;HSEAFTNR;SEAFTNRL;EA
FTNRLK;RLKGSHAQ;AQLGVAAA;AATDDHAK;DHAKEAIL;HAKEAILK;ILKSNPTK;KSNPTKDK;
PTKDKGAK;ESVESLAK;EALANSVK;KELTNPVV;ELTNPVVA;PVVAESPK

ILMTLFLFI;FLFISCNNS;STNPDESAK;SAKGPNLTV;NLTVISKKI;KITDSNAFV;ITDSNAFVL;DSN
AFVLAV;SNAFVLAVK;VLAVKEVEA;LAVKEVEAL;AVKEVEALI;EVEALISSI;ALISSIDEL;LISSIDE
LA;SSIDELANK;SIDELANKA;ELANKAIGK;LANKAIGKV;KVIHQNNGL;NGSLLAGAY;SLLAGAYAI
;LLAGAYAIS;GAYAISTLI;AISTLITEK;ISTLITEKL;TLITEKLSK;LITEKLSKL;ITEKLSKLK;ELNKKIE
EA;EEAKNHSEA;EAKNHSEAF;HSEAFTNRL;RLKGSHAQL;AQLGVAAAT;AAATDDHAK;ATDDH
AKEA;AILKSNPTK;KDKGAKELK;ELKDLSESV;DLSESVESL;ESVESLAKA;SLAKAAQEA;AQEAL
ANSV;ALANSVKEL;SVKELTNPV

ILMTLFLFIS;LMTLFLFISC;FLFISCNNSG;TASTNPDESA;ASTNPDESAK;ESAKGPNLTV;KGPNL
TVISK;KKITDSNAFV;KITDSNAFVL;DSNAFVLAVK;NAFVLAVKEV;FVLAVKEVEA;VLAVKEVEAL
;LAVKEVEALI;KEVEALISSI;EALISSIDEL;ALISSIDELA;ISSIDELANK;SIDELANKAI;ELANKAIGK
V;HQNNGLNANA;NANAGQNGSL;GQNGSLLAGA;SLLAGAYAIS;LLAGAYAIST;LAGAYAISTL;A
GAYAISTLI;YAISTLITEK;AISTLITEKL;STLITEKLSK;TLITEKLSKL;LITEKLSKLK;KLKNSEELNK;
ELNKKIEEAK;EEAKNHSEAF;NHSEAFTNRL;HSEAFTNRLK;VAAATDDHAK;ATDDHAKEAI;EAI
LKSNPTK;ILKSNPTKDK;KELKDLSESV;DLSESVESLA;LSESVESLAK;SLAKAAQEAL;AAQEALA
NSV;AQEALANSVK;EALANSVKEL;ALANSVKELT;NSVKELTNPV;SVKELTNPVV

ILMTLFLFISC;FLFISCNNSGG;DTASTNPDESA;TASTNPDESAK;ESAKGPNLTVI;ISKKITDSNAF
;KITDSNAFVLA;ITDSNAFVLAV;SNAFVLAVKEV;FVLAVKEVEAL;VLAVKEVEALI;VEALISSIDEL;
EALISSIDELA;LISSIDELANK;ELANKAIGKVI;GQNGSLLAGAY;NGSLLAGAYAI;SLLAGAYAIST;L
LAGAYAISTL;LAGAYAISTLI;AYAISTLITEK;YAISTLITEKL;ISTLITEKLSK;TLITEKLSKLK;KLSKL
KNSEEL;KLKNSEELNKK;EEAKNHSEAFT;RLKGSHAQLGV;GVAAATDDHAK;ATDDHAKEAIL;AI
LKSNPTKDK;KSNPTKDKGAK;NPTKDKGAKEL;PTKDKGAKELK;SLAKAAQEALA;KAAQEALAN
SV;AAQEALANSVK;QEALANSVKEL;SVKELTNPVVA;LTNPVVAESPK

Class 2

AFTNRLKGSHAQLGV;LKGSHAQLG;AFVLAVKEVEALISS;VKEVEALIS;AGAYAISTLITEKLS;IST
LITEKL;AGQNGSLLAGAYAIS;GQNGSLLAG;AIGKVIHQNNGLNAN;IHQNNGLNA;AILKSNPTKD
KGAKE;LKSNPTKDK;AISTLITEKLSKLKN;ISTLITEKL;AKEAILKSNPTKDKG;EAILKSNPT;AKEAI
LKSNPTKDKG;LKSNPTKDK;AKGPNLTVISKKITD;LTVISKKIT;ALANSVKELTNPVVA;LANSVKE
LT;ALANSVKELTNPVVA;SVKELTNPV;ALANSVKELTNPVVA;VKELTNPVV;ANSVKELTNPVVA
ES;SVKELTNPV;ANSVKELTNPVVAES;VKELTNPVV;AQEALANSVKELTNP;LANSVKELT;AQL
GVAAATDDHAKE;LGVAAATDD;AYAISTLITEKLSKL;ISTLITEKL;DELANKAIGKVIHQN;LANKAI
GKV;EAFTNRLKGSHAQLG;TNRLKGSHA;EAILKSNPTKDKGAK;LKSNPTKDK;EALANSVKELT
NPVV;LANSVKELT;EALANSVKELTNPVV;SVKELTNPV;ESLAKAAQEALANSV;LAKAAQEAL;ES
VESLAKAAQEALA;SLAKAAQEA;FTNRLKGSHAQLGVA;LKGSHAQLG;FVLAVKEVEALISSI;VK
EVEALIS;GAYAISTLITEKLSK;ISTLITEKL;GKVIHQNNGLNANAG;HQNNGLNAN;GLNANAGQN
GSLLAG;LNANAGQNG;GPNLTVISKKITDSN;LTVISKKIT;GQNGSLLAGAYAIST;LLAGAYAIS;GS
HAQLGVAAATDDH;LGVAAATDD;GSLLAGAYAISTLIT;LAGAYAIST;HAKEAILKSNPTKDK;EAIL
KSNPT;HAQLGVAAATDDHAK;LGVAAATDD;HQNNGLNANAGQNGS;LNANAGQNG;IDELANKA
IGKVIHQ;LANKAIGKV;IGKVIHQNNGLNANA;HQNNGLNAN;IHQNNGLNANAGQNG;NNGLNAN
AG;ILMTLFLFISCNNSG;FLFISCNNS;ISKKITDSNAFVLAV;ITDSNAFVL;ISSIDELANKAIGKV;IDE
LANKAI;ISTLITEKLSKLKNS;ISTLITEKL;ITDSNAFVLAVKEVE;ITDSNAFVL;KEAILKSNPTKDKG
A;LKSNPTKDK;KGPNLTVISKKITDS;LTVISKKIT;KGSHAQLGVAAATDD;AQLGVAAAT;KITDSN
AFVLAVKEV;ITDSNAFVL;KKITDSNAFVLAVKE;ITDSNAFVL;KVIHQNNGLNANAGQ;HQNNGLN
AN;KAAQEALANSVKELT;EALANSVKE;LAGAYAISTLITEKL;LAGAYAIST;LAGAYAISTLITEKL;Y
AISTLITE;LANSVKELTNPVVAE;LANSVKELT;LANSVKELTNPVVAE;SVKELTNPV;LANSVKELT
NPVVAE;VKELTNPVV;LAVKEVEALISSIDE;VKEVEALIS;LFLFISCNNSGGDTA;LFISCNNSG;LK
GSHAQLGVAAATD;LKGSHAQLG;LLAGAYAISTLITEK;LAGAYAIST;LMTLFLFISCNNSGG;LFIS
CNNSG;LNANAGQNGSLLAGA;LNANAGQNG;LTVISKKITDSNAFV;LTVISKKIT;MTLFLFISCNN
SGGD;LFISCNNSG;NAFVLAVKEVEALIS;LAVKEVEAL;NGLNANAGQNGSLLA;LNANAGQNG;N
GSLLAGAYAISTLI;LAGAYAIST;NLTVISKKITDSNAF;LTVISKKIT;NNGLNANAGQNGSLL;LNANA
GQNG;NRLKGSHAQLGVAAA;LKGSHAQLG;NSVKELTNPVVAESP;LTNPVVAES;NSVKELTNP
VVAESP;VKELTNPVV;PNLTVISKKITDSNA;LTVISKKIT;QEALANSVKELTNPV;LANSVKELT;QN
GSLLAGAYAISTL;LAGAYAIST;QNNGLNANAGQNGSL;LNANAGQNG;RLKGSHAQLGVAAAT;L
KGSHAQLG;SAKGPNLTVISKKIT;KGPNLTVIS;SESVESLAKAAQEAL;SLAKAAQEA;SHAQLGVA
AATDDHA;LGVAAATDD;SIDELANKAIGKVIH;LANKAIGKV;SKKITDSNAFVLAVK;ITDSNAFVL;S
LAKAAQEALANSVK;AQEALANSV;SLLAGAYAISTLITE;LAGAYAIST;SSIDELANKAIGKVI;LANK
AIGKV;SVESLAKAAQEALAN;LAKAAQEAL;SVKELTNPVVAESPK;LTNPVVAES;TLFLFISCNNS
GGDT;LFISCNNSG;TNRLKGSHAQLGVAA;LKGSHAQLG;TVISKKITDSNAFVL;SKKITDSNA;VE
SLAKAAQEALANS;LAKAAQEAL;VISKKITDSNAFVLA;ITDSNAFVL;VLAVKEVEALISSID;VKEVE
ALIS;YAISTLITEKLSKLK;ISTLITEKL;AAQEALANSVKELTN;LANSVKELT

<CAF34024 outer surface protein VlsE;Protein;Borrelia garinii>

Class 1

KISSAIFL;SAIFLTAL;AIFLTALL;IFLTALLV;FLTALLVF;LTALLVFI;ALLVFINC;LLVFINCK;FINCKN
NA;FYESIINL;IINLGNGF;FIDVFNAF;FNAFSGLV;GLVADTFF;LVADTFFK;TFFKSDPK;KSDVKTY
F;FESISSTL;ESISSTLK;SISSTLKA;SSTLKATK;TLKATKGK;KLDELVSA;KASVESAV;SAVDEVS
K;KWLEEMIK;WLEEMIKA;MIKAAEEA;KAAEEAAK;DSAANHGA;SAANHGAK;DSVKGIAK;KGIA
KGIK;GIKGIVDA;GIVDAAGK;AGKALGEK;ALGEKGAL;ALKDVKAA;EANADAGK;FAGNANAA;NA
AVGAAA;GAAADIAK;IAKAAGAV;KAAGAVTA;AAGAVTAV;AVSGEQIL;VSGEQILK;ILKAIVEA;D
PANQAGK;AEEAKNPI;DDNGAAFK;AAFKDEMK;AFKDEMKK;KIAAAIVL;IAAAIVLR;AAIVLRGV;I
VLRGVAK;AKDGKFAV

KISSAIFLT;ISSAIFLTA;SSAIFLTAL;SAIFLTALL;AIFLTALLV;IFLTALLVF;FLTALLVFI;ALLVFINC
K;FINCKNNAV;AVGKGNDDK;SVKTFYESI;TFYESIINL;SIINLGNGF;IINLGNGFI;NLGNGFIDV;G
FIDVFNAF;DVFNAFSGL;FSGLVADTF;GLVADTFFK;LVADTFFKS;DTFFKSDPK;TFFKSDPKK;D
VKTYFESI;YFESISSTL;ISSTLKATK;STLKATKGK;TLKATKGKL;ATKGKLDEL;KLDELVSAK;EGG
SVKASV;SVKASVESA;SVESAVDEV;ESAVDEVSK;SAVDEVSKW;AVDEVSKWL;EVSKWLEEM;

WLEEMIKAA;EMIKAAEEA;MIKAAEEAA;KAAEEAAKV;DSAANHGAK;ANHGAKADK;SVKGIAKGI
;GIAKGIKGI;GIKGIVDAA;IVDAAGKAL;AAGKALGEK;ALGEKGALK;ALKDVKAAA;NADAGKLFA;
KLFAGNANA;FAGNANAAV;NANAAVGAA;DIAKAAGAV;KAAGAVTAV;TAVSGEQIL;AVSGEQIL
K;QILKAIVEA;ILKAIVEAA;AGKKAEEAK;AEEAKNPIA;EEAKNPIAA;NPIAAAIGT;TDDDNGAAF;G
AAFKDEMK;AAFKDEMKK;KIAAAIVLR;AAAIVLRGV;AIVLRGVAK;VAKDGKFAV

KISSAIFLTA;ISSAIFLTAL;SSAIFLTALL;SAIFLTALLV;AIFLTALLVF;IFLTALLVFI;FLTALLVFIN;TA
LLVFINCK;DSVKTFYESI;SVKTFYESII;KTFYESIINL;ESIINLGNGF;SIINLGNGFI;NGFIDVFNAF;
DVFNAFSGLV;AFSGLVADTF;FSGLVADTFF;SGLVADTFFK;GLVADTFFKS;ADTFFKSDPK;DTF
FKSDPKK;DPKKSDVKTY;KTYFESISST;TYFESISSTL;YFESISSTLK;SISSTLKATK;SSTLKATKG
K;ATKGKLDELV;KLDELVSAKK;SAKKGEGGSV;SVKASVESAV;ASVESAVDEV;ESAVDEVSKW;
SAVDEVSKWL;EVSKWLEEMI;VSKWLEEMIK;EEMIKAAEEA;MIKAAEEAAK;AEEAAKVGGT;KV
GGTGGDGK;AANHGAKADK;HGAKADKDSV;SVKGIAKGIK;GIAKGIKGIV;GIVDAAGKAL;DAAG
KALGEK;KALGEKGALK;EANADAGKLF;KLFAGNANAA;LFAGNANAAV;NANAAVGAAA;AVGAA
ADIAK;AKAAGAVTAV;TAVSGEQILK;AVSGEQILKA;QILKAIVEAA;AIVEAAGDPA;EAAGDPANQ
A;AEEAKNPIAA;EEAKNPIAAA;EAKNPIAAAI;GTDDDNGAAF;NGAAFKDEMK;GAAFKDEMKK;D
KIAAAIVLR;IAAAIVLRGV;AAIVLRGVAK;VLRGVAKDGK;GVAKDGKFAV;VAKDGKFAVK

KKISSAIFLTA;KISSAIFLTAL;ISSAIFLTALL;SSAIFLTALLV;SAIFLTALLVF;AIFLTALLVFI;FLTALL
VFINC;LTALLVFINCK;LLVFINCKNNA;LVFINCKNNAV;FINCKNNAVGK;YESIINLGNGF;ESIINLG
NGFI;IINLGNGFIDV;FIDVFNAFSGL;DVFNAFSGLVA;NAFSGLVADTF;AFSGLVADTFF;FSGLVA
DTFFK;VADTFFKSDPK;DPKKSDVKTYF;KTYFESISSTL;TYFESISSTLK;ESISSTLKATK;ISSTLK
ATKGK;KATKGKLDELV;KGKLDELVSAK;SAKKGEGGSVK;KASVESAVDEV;SVESAVDEVSK;E
SAVDEVSKWL;EVSKWLEEMIK;EEMIKAAEEAA;EMIKAAEEAAK;MIKAAEEAAKV;KIGDSAANH
GA;SAANHGAKADK;DSVKGIAKGIK;GIKGIVDAAGK;ALGEKGALKDV;DEANADAGKLF;KLFAG
NANAAV;FAGNANAAVGA;AAVGAAADIAK;AAADIAKAAGA;IAKAAGAVTAV;AVTAVSGEQIL;VT
AVSGEQILK;AVSGEQILKAI;AAGDPANQAGK;AEEAKNPIAAA;EEAKNPIAAAI;IGTDDDNGAAF;
GTDDDNGAAFK;NGAAFKDEMKK;AFKDEMKKSDK;KSDKIAAAIVL;KIAAAIVLRGV;IAAAIVLRG
VA;AAAIVLRGVAK;IVLRGVAKDGK;VLRGVAKDGKF;GVAKDGKFAVK

Class 2

ADAFSKADPKKSDVK;FSKADPKKS;ADAGDVKDAAAAVGA;VKDAAAAVG;ADKESVNGIAGAIK
G;VNGIAGAIK;AFSGLVADAFSKADP;LVADAFSKA;AFSKADPKKSDVKTY;FSKADPKKS;AGDV
KDAAAAVGAVS;VKDAAAAVG;AGKLFGTAAGADAGD;FGTAAGADA;AIFIVAFLALIGCKN;IVAFL
ALIG;AIVTAAGQAGQAGKK;IVTAAGQAG;AKNAIEAAIGAAGDA;IEAAIGAAG;ALVLRGVAKDGK
FAG;LRGVAKDGK;ASIFYQSIINLGNGF;FYQSIINLG;ASIFYQSIINLGNGF;YQSIINLGN;AVSGEQ
ILNAIVTAA;EQILNAIVT;AVSGEQILNAIVTAA;VSGEQILNA;DAFSKADPKKSDVKT;FSKADPKKS;
DAGDVKDAAAAVGAV;VKDAAAAVG;DEAKNAIEAAIGAAG;KNAIEAAIG;DIKKKNDQIAAALVL;IK
KKNDQIA;DKESVNGIAGAIKGI;VNGIAGAIK;DKIGNVAAGGGAGAD;IGNVAAGGG;DQIAAALVL
RGVAKD;IAAALVLRG;DTAASIFYQSIINLG;IFYQSIINL;DTAASIFYQSIINLG;SIFYQSIIN;DVKDA
AAAVGAVSGE;VKDAAAAVG;DAAAAVGAVSGEQIL;VGAVSGEQI;EAKNAIEAAIGAAGD;IEAAIG
AAG;EGVKFAPKAAADAAA;FAPKAAADA;EQILNAIVTAAGQAG;ILNAIVTAA;EQILNAIVTAAGQA
G;LNAIVTAAG;ESVNGIAGAIKGIVE;VNGIAGAIK;EVFNAFSGLVADAFS;FNAFSGLVA;EVFNAF
SGLVADAFS;VFNAFSGLV;FAPKAAADAAAADGN;FAPKAAADA;FGTAAGADAGDVKDA;FGTA
AGADA;FIEVFNAFSGLVADA;FNAFSGLVA;FIEVFNAFSGLVADA;VFNAFSGLV;FIVAFLALIGCK
NNV;IVAFLALIG;FNAFSGLVADAFSKA;FSGLVADAF;FSGLVADAFSKADPK;LVADAFSKA;FSK
ADPKKSDVKTYF;FSKADPKKS;FYQSIINLGNGFIEV;FYQSIINLG;FYQSIINLGNGFIEV;IINLGNG
FI;FYQSIINLGNGFIEV;YQSIINLGN;GADAGDVKDAAAAVG;AGDVKDAAA;GDVKDAAAAVGAVS
G;VKDAAAAVG;GEQILNAIVTAAGQA;ILNAIVTAA;GEQILNAIVTAAGQA;LNAIVTAAG;GFIEVFN
AFSGLVAD;FNAFSGLVA;GFIEVFNAFSGLVAD;VFNAFSGLV;GGGSDKIGNVAAGGG;KIGNVA
AGG;GGSDKIGNVAAGGGA;IGNVAAGGG;GKLFGTAAGADAGDV;FGTAAGADA;GLVADAFSK
ADPKKS;AFSKADPKK;GLVADAFSKADPKKS;VADAFSKAD;GNGFIEVFNAFSGLV;FIEVFNAFS;
GNVAAGGGAGADKES;VAAGGGAGA;GSDKIGNVAAGGGAG;IGNVAAGGG;GVKFAPKAAADA
AAA;FAPKAAADA;IEVFNAFSGLVADAF;FNAFSGLVA;IEVFNAFSGLVADAF;VFNAFSGLV;IFIVA
FLALIGCKNN;IVAFLALIG;IFYQSIINLGNGFIE;FYQSIINLG;IFYQSIINLGNGFIE;IINLGNGFI;IFYQ

SIINLGNGFIE;YQSIINLGN;IGNVAAGGGAGADKE;VAAGGGAGA;IKKKNDQIAAALVLR;DQIAAALVL;ILNAIVTAAGQAGQA;ILNAIVTAA;ILNAIVTAAGQAGQA;IVTAAGQAG;ISSAIFIVAFLALIG;FIVAFLALI;IVAFLALIGCKNNVG;IVAFLALIG;IVTAAGQAGQAGKKA;IVTAAGQAG;IAAALVLRGVAKDGK;ALVLRGVAK;IAAALVLRGVAKDGK;IAAALVLRG;KAGKLFGTAAGADAG;FGTAAGADA;KDAAAAVGAVSGEQI;AAAVGAVSG;KESVNGIAGAIKGIV;VNGIAGAIK;KFAPKAAADAAAADG;FAPKAAADA;KIGNVAAGGGAGADK;VAAGGGAGA;KISSAIFIVAFLALI;IFIVAFLAL;KKAGKLFGTAAGADA;LFGTAAGAD;KKKNDQIAAALVLRG;DQIAAALVL;KKNDQIAAALVLRGV;IAAALVLRG;KLFGTAAGADAGDVK;FGTAAGADA;KNAIEAAIGAAGDAD;IEAAIGAAG;KNDQIAAALVLRGVA;IAAALVLRG;KVEGVKFAPKAAADA;VKFAPKAAA;LFGTAAGADAGDVKD;FGTAAGADA;LNAIVTAAGQAGQAG;IVTAAGQAG;LVADAFSKADPKKSD;FSKADPKKS;MKKISSAIFIVAFLA;MKKISSAIF;NAFSGLVADAFSKAD;FSGLVADAF;NAIEAAIGAAGDADF;IEAAIGAAG;NAIVTAAGQAGQAGK;IVTAAGQAG;NDQIAAALVLRGVAK;IAAALVLRG;NGFIEVFNAFSGLVA;FIEVFNAFS;NGFIEVFNAFSGLVA;VFNAFSGLV;QILNAIVTAAGQAGQ;ILNAIVTAA;QILNAIVTAAGQAGQ;IVTAAGQAG;QIAAALVLRGVAKDG;IAAALVLRG;QSIINLGNGFIEVFN;IINLGNGFI;SAIFIVAFLALIGCK;IVAFLALIG;SDKIGNVAAGGGAGA;IGNVAAGGG;SGEQILNAIVTAAGQ;ILNAIVTAA;SGEQILNAIVTAAGQ;LNAIVTAAG;SIFYQSIINLGNGFI;FYQSIINLG;SIFYQSIINLGNGFI;YQSIINLGN;SIINLGNGFIEVFNA;IINLGNGFI;SSAIFIVAFLALIGC;IVAFLALIG;TAASIFYQSIINLGN;FYQSIINLG;VADAFSKADPKKSDV;FSKADPKKS;VEGVKFAPKAAADAA;FAPKAAADA;VFNAFSGLVADAFSK;VFNAFSGLV;VGAVSGEQILNAIVT;VSGEQILNA;VKDAAAAVGAVSGEQ;VKDAAAAVG;VKFAPKAAADAAAAD;FAPKAAADA;VSGEQILNAIVTAAG;ILNAIVTAA;YQSIINLGNGFIEVF;IINLGNGFI;YQSIINLGNGFIEVF;YQSIINLGN;AAALVLRGVAKDGKF;LRGVAKDGK;AAALVLRGVAKDGKF;VLRGVAKDG;AAAVGAVSGEQILNA;VGAVSGEQI;AALVLRGVAKDGKFA;LRGVAKDGK;AALVLRGVAKDGKFA;VLRGVAKDG;AASIFYQSIINLGNG;FYQSIINLG;AASIFYQSIINLGNG;YQSIINLGN;AAAAVGAVSGEQILN;VGAVSGEQI

Fig. 41.

<CAA59725 outer surface protein A;Protein;Borrelia afzelii>

MHC Type 8-mer

A0101
A0201 YLLGIGLI;SLDEKNSA
A0202 YLLGIGLI;LIACKQNV;LLGIGLIL;KLTIADDL;SLDEKNSA;GIGLILAL;ALNDTNTT
A0203 YLLGIGLI;LIACKQNV;ALNDTNTT;LLGIGLIL;GLILALIA;SLDEKNSA
A0204 LLGIGLIL;ATVDKIEL;LIACKQNV
A0206 YLLGIGLI;ATVDKIEL;FTLEGKVA;LIACKQNV
A0211
YLLGIGLI;DLPGEMKV;SLDEKNSA;TLDELKNA;LLGIGLIL;ALNDTNTT;LIACKQNV;EIAKSGEV
;KEDGKTLV;EVLKNFTL;GLILALIA;GIGLILAL;TKQDTITV;ATVDKIEL;KLTIADDL;VANDKVT
L
A0212
YLLGIGLI;DLPGEMKV;SLDEKNSA;LLGIGLIL;TLDELKNA;LIACKQNV;ALNDTNTT;FT
LEGKVA
A0216
DLPGEMKV;YLLGIGLI;LLGIGLIL;SLDEKNSA;EIAKSGEV;ALNDTNTT;LIACKQNV;GTGKAKEV
;TLDELKNA;EVLKNFTL;GIGLILAL;ATVDKIEL;GLILALIA
A0219 YLLGIGLI;DLPGEMKV;LLGIGLIL;SLDEKNSA;LIACKQNV;ALNDTNTT;TKQDTITV
A0301
ILALIACK;KTTFELFK;VSRKVSSK;LTISVNSK;TTQLVFTK;TLSKEIAK;KTGAWDSK;KVLVSKEK
;TISVNSKK;MTRENGTK;SLKATVDK;TIADDLSK;KLEYTEMK
A1101
TTQLVFTK;KTTFELFK;LTISVNSK;TIADDLSK;KTGAWDSK;TISVNSKK;TVDKIELK;KVLVSKEK
;TLSKEIAK;ILALIACK;NVSSLDEK;SLKATVDK;NTTQATKK;VSRKVSSK;MTRENGTK;KLEYTEM
K;GTKDDKSK
A2301 KYLLGIGL;KTSTDEMF
A2402
A2403 KYLLGIGL
A2601 DTITVQKY
A2602 DTITVQKY;EIKTLDEL;EVLKNFTL;KTSTDEMF;SVDLPGEM;EIAKSGEV
A2902 DTITVQKY
A3001
MTRENGTK;KVLVSKEK;VSRKVSSK;KTTFELFK;TTQLVFTK;SLKATVDK;KTGAWDSK;GTKDDKSK
;KLEYTEMK;LTISVNSK
A3002
A3101 TTQLVFTK;LSAKTMTR;KTTFELFK;MTRENGTK;KVLVSKEK
A3301 EMKVLVSK;TTQLVFTK
A6801
LTISVNSK;NTTQATKK;TTQLVFTK;NVSSLDEK;LSAKTMTR;KTTFELFK;TISVNSKK;MTRENGTK
;ILALIACK;TIADDLSK;TVDKIELK;DTITVQKY;ELFKEDGK;EMKVLVSK;ELKGTSDK;EGTAVEI
K;TTFELFKE;TLSKEIA
A6802 EIAKSGEV;TSTLTISV;LIACKQNV;EVLKNFTL
A6901 EVLKNFTL;EIAKSGEV;FTLEGKVA;YLLGIGLI;LIACKQNV
B0702 LPGEMKVL
B0801
B0802
B1501
B1801
B2705
B3501 LPGEMKVL;TAVEIKTL
B3901 FKEDGKTL;TRENGTKL;VKEGTVTL
B4001 GELSAKTM

B4002
B4402
B4403
B4501
B5101 LPGEMKVL
B5301 LPGEMKVL
B5401
B5701 ATKKTGAW
B5801 KTSTDEMF

Allele 9-mer
A0101
A0201 YLLGIGLIL;KTSTLTISV;ALIACKQNV;LLGIGLILA;FTKQDTITV
A0202
LIACKQNV;TLDELKNAL;YLLGIGLIL;KTSTLTISV;GIGLILALI;LLGIGLILA;KSGEVTVAL;SL
KATVDKI;FTKQDTITV;DLSKTTFEL;ALNDTNTTQ
A0203
FTKQDTITV;ALIACKQNV;SLKATVDKI;YLLGIGLIL;KTSTLTISV;LLGIGLILA;GIGLILALI;G
TNLEGTAV;TIADDLSKT
A0204 ALIACKQNV;YLLGIGLIL;FTKQDTITV
A0206
FTKQDTITV;KTSTLTISV;YLLGIGLIL;ALIACKQNV;LLGIGLILA;KEVLKNFTL;KVANDKVTL;F
KEDGKTLV
A0211
YLLGIGLIL;TLDELKNAL;ALIACKQNV;LLGIGLILA;DLSKTTFEL;NLEGTAVEI;ALNDTNTTQ;K
TSTLTISV;FTKQDTITV;KVANDKVTL;EVKEGTVTL;EMFNEKGEL;FKEDGKTLV;DLPGEMKVL;SL
DEKNSAS;TLEVKEGTV;SLKATVDKI;VDLPGEMKV;IAKSGEVTV;ANDKVTLEV;GKYSLKATV
A0212
YLLGIGLIL;TLDELKNAL;ALIACKQNV;ALNDTNTTQ;VDLPGEMKV;LLGIGLILA;SLDEKNSAS;F
KEDGKTLV;DLSKTTFEL;FTKQDTITV;IAKSGEVTV;NLEGTAVEI;EVKEGTVTL;TLEVKEGTV
A0216
YLLGIGLIL;DLSKTTFEL;TLDELKNAL;ALIACKQNV;NLEGTAVEI;LLGIGLILA;ALNDTNTTQ;T
LEVKEGTV;EMFNEKGEL;FTKQDTITV;FKEDGKTLV;IAKSGEVTV;GKYSLKATV;EVKEGTVTL;KV
ANDKVTL;KTSTLTISV;SLKATVDKI;DLPGEMKVL
A0219
YLLGIGLIL;DLSKTTFEL;TLDELKNAL;ALIACKQNV;ALNDTNTTQ;NLEGTAVEI;FKEDGKTLV;L
LGIGLILA
A0301
LVSRKVSSK;KTTQLVFTK;LTISVNSKK;LILALIACK;TLTISVNSK;KQDTITVQK;VTLSK
EIAK
A1101
KTTQLVFTK;STDEMFNEK;LTISVNSKK;ATVDKIELK;LTIADDLSK;LILALIACK;VTLSKEIAK;L
VSRKVSSK;SVDLPGEMK;TLTISVNSK;KQDTITVQK;TMTRENGTK;YSLKATVDK;SKTTFELFK;GS
GVLEGTK;DTNTTQATK
A2301 KYDSAGTNL;KYLLGIGLI
A2402 KYLLGIGLI
A2403 KYLLGIGLI;KYDSAGTNL
A2601 EVKEGTVTL
A2602 EVKEGTVTL;DLPGEMKVL
A2902
A3001
KTTQLVFTK;YSLKATVDK;ATVDKIELK;SRKVSSKDK;TGKAKEVLK;KSDGTGKAK;KKTGA
WDSK
A3002
A3101 KTTQLVFTK;LTISVNSKK;LILALIACK;KQDTITVQK;VTLSKEIAK
A3301 ELSAKTMTR;DTNTTQATK

A6801
LTISVNSKK;DTNTTQATK;ELSAKTMTR;KTTQLVFTK;EIKTLDELK;LTIADDLSK;TLTISVNSK;S
TDEMFNEK;ATVDKIELK;LVSRKVSSK;YSLKATVDK
A6802 KTSTLTISV;FTKQDTITV;DLSKTTFEL;TVALNDTNT
A6901 FTKQDTITV;EVKEGTVTL;LPGEMKVLV;DLSKTTFEL
B0702 MTRENGTKL;KVANDKVTL
B0801
B0802
B1501 YLLGIGLIL
B1801 RENGTKLEY
B2705
B3501
B3901
B4001 KEVLKNFTL;VEIKTLDEL
B4002 KEIAKSGEV;KEVLKNFTL
B4402 RENGTKLEY
B4403
B4501
B5101 LPGEMKVLV
B5301 LPGEMKVLV
B5401 LPGEMKVLV
B5701
B5801

Allele 10-mer
A0101
A0201 YLLGIGLILA;SLDEKNSASV;ALNDTNTTQA;LLGIGLILAL
A0202 YLLGIGLILA;LLGIGLILAL;SLDEKNSASV;ALNDTNTTQA
A0203 ALNDTNTTQA;SLDEKNSASV;YLLGIGLILA;LLGIGLILAL;VANDKVTLEV;SVNSKKTTQL
A0204 SLDEKNSASV;ALNDTNTTQA;VTLEVKEGTV;VANDKVTLEV;LLGIGLILAL;SVDLPGEMKV
A0206
SLDEKNSASV;YLLGIGLILA;LLGIGLILAL;KTLDELKNAL;GAWDSKTSTL;VANDKVTLEV;ALNDT
NTTQA
A0211
SLDEKNSASV;YLLGIGLILA;DLPGEMKVLV;LLGIGLILAL;ALNDTNTTQA;SVDLPGEMKV;VANDK
VTLEV;EIAKSGEVTV;ELFKEDGKTL;VTLEVKEGTV;TMTRENGTKL;TLDELKNALK;GAWDSKTSTL
;KTLDELKNAL;TIADDLSKTT;SKTSTLTISV;QLVFTKQDTI;SVNSKKTTQL
A0212
SLDEKNSASV;YLLGIGLILA;LLGIGLILAL;DLPGEMKVLV;ALNDTNTTQA;VTLEVKEGTV;VANDK
VTLEV;SVDLPGEMKV;EIAKSGEVTV;ELFKEDGKTL;TMTRENGTKL;KTLDELKNAL;GAWDSKTSTL
;QLVFTKQDTI
A0216
SLDEKNSASV;YLLGIGLILA;LLGIGLILAL;ALNDTNTTQA;DLPGEMKVLV;EIAKSGEVTV;SVDLP
GEMKV;VANDKVTLEV;GAWDSKTSTL;TMTRENGTKL;ELFKEDGKTL;SVNSKKTTQL;VTLEVKEGTV
;QLVFTKQDTI
A0219
SLDEKNSASV;LLGIGLILAL;YLLGIGLILA;ALNDTNTTQA;VANDKVTLEV;GAWDSKTSTL;DLPGE
MKVLV;SVDLPGEMKV;EIAKSGEVTV
A0301
KTMTRENGTK;VLKNFTLEGK;TLVSRKVSSK;STLTISVNSK;TLTISVNSKK;GLILALIACK;LSKTT
FELFK;KYSLKATVDK;TLDELKNALK;KLTIADDLSK;KIELKGTSDK;ASVDLPGEMK;GTGKAKEVLK
A1101
STLTISVNSK;KTMTRENGTK;TSTDEMFNEK;TVTLSKEIAK;GLILALIACK;KQNVSSLDEK;LSKTT
FELFK;ASVDLPGEMK;TLVSRKVSSK;TLTISVNSKK;GTGKAKEVLK;KATVDKIELK;TLDELKNALK
;GTKLEYTEMK;KLTIADDLSK;KVLVSKEKDK;VLKNFTLEGK;GVLEGTKDDK;KIELKGTSDK;GTKD
DKSKAK

A2301 KYLLGIGLIL;KYSLKATVDK;DLSKTTFELF
A2402 KYLLGIGLIL
A2403 KYLLGIGLIL
A2601
A2602 EIAKSGEVTV
A2902
A3001
KTMTRENGTK;VSRKVSSKDK;LSKTTFELFK;GTKLEYTEMK;KQNVSSLDEK;GTKDDKSKAK;KVLVS
KEKDK;KDKDGKYSLK;VLKNFTLEGK;STLTISVNSK;KATVDKIELK;KYSLKATVDK;EMKVLVSKEK
A3002
A3101 KYSLKATVDK;KKTTQLVFTK
A3301
A6801
DTNTTQATKK;TSTDEMFNEK;TVTLSKEIAK;STLTISVNSK;TLTISVNSKK;TLVSRKVSSK;LSKTT
FELFK;EMKVLVSKEK;GTKLEYTEMK;KTMTRENGTK
A6802 EIAKSGEVTV;TVALNDTNTT;LGIGLILALI
A6901 EIAKSGEVTV;SVDLPGEMKV;VTLEVKEGTV;YLLGIGLILA;SLDEKNSASV
B0702 GAWDSKTSTL;SVNSKKTTQL
B0801
B0802
B1501
B1801 LEVKEGTVTL
B2705
B3501 IADDLSKTTF;SASVDLPGEM
B3901 AKSGEVTVAL
B4001 LEVKEGTVTL;DEMFNEKGEL
B4002
B4402
B4403
B4501
B5101
B5301
B5401 LPGEMKVLVS
B5701
B5801

Allele 11-mer

A0101 MTRENGTKLEY
A0201 YLLGIGLILAL;LVFTKQDTITV;KVANDKVTLEV;LLGIGLILALI;ILALIACKQNV
A0202
ILALIACKQNV;YLLGIGLILAL;LIACKQNVSSL;LLGIGLILALI;ALNDTNTTQAT;GTSDKDNGSGV
;SLKATVDKIEL;SVNSKKTTQLV;LVFTKQDTITV;TLEGKVANDKV;KVANDKVTLEV;ELFKEDGKTL
V;KTMTRENGTKL;VLKNFTLEGKV
A0203
VLKNFTLEGKV;LIACKQNVSSL;YLLGIGLILAL;ILALIACKQNV;LLGIGLILALI;SVNSKKTTQLV
;ALNDTNTTQAT;LVFTKQDTITV;SLKATVDKIEL;GTSDKDNGSGV;KVANDKVTLEV;TLEGKVANDK
V
A0204
KVANDKVTLEV;KTMTRENGTKL;LVFTKQDTITV;YLLGIGLILAL;ILALIACKQNV;SVNSKKTTQLV
;SLKATVDKIEL;VLKNFTLEGKV
A0206
YLLGIGLILAL;KVANDKVTLEV;LVFTKQDTITV;TQLVFTKQDTI;KEIAKSGEVTV;TAVEIKTLDEL
;SAGTNLEGTAV;LLGIGLILALI;ILALIACKQNV;LIACKQNVSSL
A0211
YLLGIGLILAL;ILALIACKQNV;ELFKEDGKTLV;KVANDKVTLEV;LLGIGLILALI;LVFTKQDTITV
;TLEGKVANDKV;SVNSKKTTQLV;VLKNFTLEGKV;SLKATVDKIEL;ALNDTNTTQAT;EMFNEKGELS

A;SSLDEKNSASV;TLEVKEGTVTL;GTSDKDNGSGV;VDLPGEMKVLV;SVDLPGEMKVL;KVTLEVKEG
TV
A0212
YLLGIGLILAL;ELFKEDGKTLV;VLKNFTLEGKV;ILALIACKQNV;LVFTKQDTITV;ALNDTNTTQAT
;TLEGKVANDKV;LLGIGLILALI;EMFNEKGELSA;GTSDKDNGSGV;KVANDKVTLEV;SLKATVDKIE
L;SVNSKKTTQLV;SSLDEKNSASV;VDLPGEMKVLV;TLEVKEGTVTL
A0216
YLLGIGLILAL;ELFKEDGKTLV;TLEGKVANDKV;ILALIACKQNV;VLKNFTLEGKV;LVFTKQDTITV
;KVANDKVTLEV;SLKATVDKIEL;SVNSKKTTQLV;LLGIGLILALI;TLEVKEGTVTL;ALNDTNTTQA
T;EMFNEKGELSA;GTSDKDNGSGV;SSLDEKNSASV;NLEGTAVEIKT;LIACKQNVSSL
A0219
YLLGIGLILAL;ILALIACKQNV;TLEGKVANDKV;ALNDTNTTQAT;LLGIGLILALI;LVFTKQDTITV
;ELFKEDGKTLV;SVNSKKTTQLV;LIACKQNVSSL
A0301 KTLVSRKVSSK;STLTISVNSKK;KTLDELKNALK;KTSTDEMFNEK;FTKQDTITVQK
A1101
STLTISVNSKK;TTFELFKEDGK;KTSTDEMFNEK;KTLDELKNALK;KTLVSRKVSSK;TSTLTISVNSK
;GTVTLSKEIAK;SASVDLPGEMK;ATKKTGAWDSK;AVEIKTLDELK;VANDKVTLEVK;DLSKTTFELF
K;FTKQDTITVQK;LVSRKVSSKDK;EVLKNFTLEGK;YTEMKSDGTGK;FTLEGKVANDK
A2301 KYSLKATVDKI
A2402 KYSLKATVDKI;AWDSKTSTLTI
A2403 KYSLKATVDKI
A2601
A2602 TIADDLSKTTF;MTRENGTKLEY
A2902 MTRENGTKLEY
A3001
ATKKTGAWDSK;KTLVSRKVSSK;KTLDELKNALK;MTRENGTKLEY;EVKEGTVTLSK;KTSTDEMFNEK
;FTKQDTITVQK;STLTISVNSKK;SKKTTQLVFTK
A3002
A3101 KTLVSRKVSSK;KTLDELKNALK;MFNEKGELSAK;STLTISVNSKK;KTSTDEMFNEK
A3301 EVKEGTVTLSK;DLSKTTFELFK
A6801
TTFELFKEDGK;STLTISVNSKK;FTKQDTITVQK;TSTLTISVNSK;EVKEGTVTLSK;EVLKNFTLEGK
;DLSKTTFELFK;FTLEGKVANDK;KTSTDEMFNEK;YTEMKSDGTGK;LVSKEKDKDGK;SASVDLPGEM
K;GTVTLSKEIAK
A6802
TAVEIKTLDEL;DTITVQKYDSA;LVFTKQDTITV;ELFKEDGKTLV;SVNSKKTTQLV;ILALIACKQNV
;LIACKQNVSSL;EIAKSGEVTVA;NVSSLDEKNSA
A6901 LVFTKQDTITV;YLLGIGLILAL;ELFKEDGKTLV
B0702 IAKSGEVTVAL
B0801
B0802
B1501 MTRENGTKLEY;YLLGIGLILAL;VQKYDSAGTNL
B1801 FELFKEDGKTL;MTRENGTKLEY
B2705
B3501 TAVEIKTLDEL;IAKSGEVTVAL;TIADDLSKTTF;MTRENGTKLEY
B3901
B4001 FELFKEDGKTL;LEGTAVEIKTL
B4002 KEIAKSGEVTV
B4402
B4403
B4501 KEIAKSGEVTV
B5101
B5301
B5401 LPGEMKVLVSK
B5701 TTQATKKTGAW

B5801

Allele 15-mer plus 9-mer core

DRB1_0101

KKYLLGIGLILALIA-LLGIGLILA;KYLLGIGLILALIAC-LLGIGLILA;MKKYLLGIGLILALI-
LLGIGLILA;KTGAWDSKTSTLTIS-WDSKTSTLT;TGAWDSKTSTLTISV-
WDSKTSTLT;TKKTGAWDSKTSTLT-KTGAWDSKT;GAWDSKTSTLTISVN-
WDSKTSTLT;KKTGAWDSKTSTLTI-WDSKTSTLT;YLLGIGLILALIACK-
IGLILALIA;LLGIGLILALIACKQ-IGLILALIA;LGIGLILALIACKQN-
IGLILALIA;QLVFTKQDTITVQKY-FTKQDTITV;TQLVFTKQDTITVQK-
FTKQDTITV;TTQLVFTKQDTITVQ-FTKQDTITV;KTTQLVFTKQDTITV-
VFTKQDTIT;LVFTKQDTITVQKYD-FTKQDTITV;VTLEVKEGTVTLSKE-
VKEGTVTLS;KVTLEVKEGTVTLSK-VKEGTVTLS;KLEYTEMKSDGTGKA-
YTEMKSDGT;DKVTLEVKEGTVTLS-LEVKEGTVT;LEVKEGTVTLSKEIA-
VKEGTVTLS;LEYTEMKSDGTGKAK-YTEMKSDGT;TISVNSKKTTQLVFT-
VNSKKTTQL;ISVNSKKTTQLVFTK-VNSKKTTQL;TLTISVNSKKTTQLV-
VNSKKTTQL;TLEVKEGTVTLSKEI-VKEGTVTLS;STLTISVNSKKTTQL-
TISVNSKKT;AWDSKTSTLTISVNS-WDSKTSTLT;LTISVNSKKTTQLVF-
VNSKKTTQL;WDSKTSTLTISVNSK-WDSKTSTLT;ITVQKYDSAGTNLEG-
VQKYDSAGT;TITVQKYDSAGTNLE-VQKYDSAGT;ELFKEDGKTLVSRKV-
FKEDGKTLV;EDGKTLVSRKVSSKD-GKTLVSRKV;GIGLILALIACKQNV-
ILALIACKQ;KEDGKTLVSRKVSSK-GKTLVSRKV;VALNDTNTTQATKKT-
LNDTNTTQA;IGLILALIACKQNVS-ILALIACKQ;YTEMKSDGTGKAKEV-
YTEMKSDGT;LFKEDGKTLVSRKVS-GKTLVSRKV;DTITVQKYDSAGTNL-
VQKYDSAGT;EYTEMKSDGTGKAKE-YTEMKSDGT;QDTITVQKYDSAGTN-
VQKYDSAGT;TKLEYTEMKSDGTGK-YTEMKSDGT;FKEDGKTLVSRKVSS-
GKTLVSRKV;KQDTITVQKYDSAGT-ITVQKYDSA;EVTVALNDTNTTQAT-
VALNDTNTT;GTKLEYTEMKSDGTG-YTEMKSDGT;GEVTVALNDTNTTQA-
VALNDTNTT;NGTKLEYTEMKSDGT-TKLEYTEMK;VTVALNDTNTTQATK-
VALNDTNTT;VFTKQDTITVQKYDS-FTKQDTITV;SVNSKKTTQLVFTKQ-
VNSKKTTQL;QKYDSAGTNLEGTAV-YDSAGTNLE;VNSKKTTQLVFTKQD-
VNSKKTTQL;GLILALIACKQNVSS-ILALIACKQ;FTKQDTITVQKYDSA-
FTKQDTITV;VKEGTVTLSKEIAKS-VKEGTVTLS;EVKEGTVTLSKEIAK-
VKEGTVTLS;KSGEVTVALNDTNTT-EVTVALNDT;DEMFNEKGELSAKTM-
MFNEKGELS;SGEVTVALNDTNTTQ-VALNDTNTT;TDEMFNEKGELSAKT-
MFNEKGELS;TVQKYDSAGTNLEGT-VQKYDSAGT;VQKYDSAGTNLEGTA-
VQKYDSAGT;ALNDTNTTQATKKTG-NTTQATKKT;VDLPGEMKVLVSKEK-
LPGEMKVLV;DGKTLVSRKVSSKDK-GKTLVSRKV;GKTLVSRKVSSKDKT-
GKTLVSRKV;FNEKGELSAKTMTRE-EKGELSAKT;SSLDEKNSASVDLPG-
EKNSASVDL;LNDTNTTQATKKTGA-NTTQATKKT;VSSLDEKNSASVDLP-
EKNSASVDL;NVSSLDEKNSASVDL-LDEKNSASV;TVALNDTNTTQATKK-
LNDTNTTQA;EMFNEKGELSAKTMT-EKGELSAKT

DRB1_0301

DRB1_0401

QLVFTKQDTITVQKY-FTKQDTITV;TQLVFTKQDTITVQK-FTKQDTITV;LVFTKQDTITVQKYD-
FTKQDTITV;TTQLVFTKQDTITVQ-FTKQDTITV;KTTQLVFTKQDTITV-
KTTQLVFTK;LEYTEMKSDGTGKAK-MKSDGTGKA;KLEYTEMKSDGTGKA-
YTEMKSDGT;EYTEMKSDGTGKAKE-MKSDGTGKA;YTEMKSDGTGKAKEV-
MKSDGTGKA;TEMKSDGTGKAKEVL-MKSDGTGKA

DRB1_0404

GEVTVALNDTNTTQA-VALNDTNTT;EVTVALNDTNTTQAT-LNDTNTTQA;VTVALNDTNTTQATK-
LNDTNTTQA;TVALNDTNTTQATKK-LNDTNTTQA;GKAKEVLKNFTLEGK-
VLKNFTLEG;VALNDTNTTQATKKT-LNDTNTTQA;AKEVLKNFTLEGKVA-
VLKNFTLEG;KAKEVLKNFTLEGKV-VLKNFTLEG;TGKAKEVLKNFTLEG-
AKEVLKNFT;KEVLKNFTLEGKVAN-VLKNFTLEG

DRB1_0405

TITVQKYDSAGTNLE-VQKYDSAGT;ITVQKYDSAGTNLEG-YDSAGTNLE;TVQKYDSAGTNLEGT-
YDSAGTNLE;VQKYDSAGTNLEGTA-YDSAGTNLE;QKYDSAGTNLEGTAV-YDSAGTNLE
DRB1_0701
DRB1_0802
DRB1_0901
DRB1_1101
DRB1_1302
STLTISVNSKKTTQL-ISVNSKKTT;TLTISVNSKKTTQLV-ISVNSKKTT;LTISVNSKKTTQLVF-
ISVNSKKTT;EVTVALNDTNTTQAT-VALNDTNTT;GEVTVALNDTNTTQA-
VALNDTNTT;KTSTLTISVNSKKTT-LTISVNSKK;VTVALNDTNTTQATK-
VALNDTNTT;TSTLTISVNSKKTTQ-ISVNSKKTT;KSGEVTVALNDTNTT-
EVTVALNDT;SGEVTVALNDTNTTQ-VALNDTNTT;TISVNSKKTTQLVFT-
ISVNSKKTT;ISVNSKKTTQLVFTK-ISVNSKKTT;VALNDTNTTQATKKT-
VALNDTNTT;TVALNDTNTTQATKK-VALNDTNTT
DRB1_1501
AKEVLKNFTLEGKVA-LKNFTLEGK;KEVLKNFTLEGKVAN-LKNFTLEGK;GKAKEVLKNFTLEGK-
VLKNFTLEG;KAKEVLKNFTLEGKV-LKNFTLEGK;EVLKNFTLEGKVAND-
LKNFTLEGK;VLKNFTLEGKVANDK-LKNFTLEGK;LKNFTLEGKVANDKV-LKNFTLEGK
DRB3_0101
DRB4_0101
DRB5_0101
LPGEMKVLVSKEKDK-MKVLVSKEK;GEMKVLVSKEKDKDG-MKVLVSKEK;VDLPGEMKVLVSKEK-
VDLPGEMKV;PGEMKVLVSKEKDKD-MKVLVSKEK;DLPGEMKVLVSKEKD-MKVLVSKEK

<YP_853838 outer surface protein B;Protein;Borrelia afzelii PKo

Allele 8-mer
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A0202
VLAEENSV;YLLVFALV;LLVFALVL;FLTDGTIT;LVFALVLA;KTKDFVFL;YLNDTTSG;KQYLLVFA
;ATVDTVEL;AMTIADDL;FVFLTDGT;LVGGKTTV
A0203
VLAEENSV;YLLVFALV;LVGGKTTV;FLTDGTIT;KQYLLVFA;LLVFALVL;KTKDFVFL;TLKNGIKL
;VVKKQGSV;ALVLALIA;YLNDTTSG;KTKVAMTI;KLTEGTIT;LTDGTITV;LVFALVLA;ATKAVET
L;ATVDTVEL;
A0204
VLAEENSV;YLLVFALV;LVGGKTTV;ATVDTVEL;LTDGTITV
A0206
YLLVFALV;KQYLLVFA;VLAEENSV;LTDGTITV;ATVDTVEL;FLTDGTIT;FALVLALI;LVGGKTTV
;LLVFALVL;IADDLNTI;FVFLTDGT;KTKDFVFL;LVFALVLA
A0211
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;PLFNGNKI;YLNDTTSG;KLTEGTIT;EMTDSSNA;LVFALVLA;ATVDTVEL;IADDLNTI;KTKDFVF
L;ALVLALIA;TLTREIEQ;DLAALKAA;EIKDLAAL;IKLEGSLV;KLDSKKIT
A0212
YLLVFALV;VLAEENSV;LTDGTITV;LVGGKTTV;FLTDGTIT;LLVFALVL;YLNDTTSG;TLKNGIKL
;PLFNGNKI;SLVGGKTT;EIKDLAAL
A0216
YLLVFALV;VLAEENSV;LVGGKTTV;LTDGTITV;TLKNGIKL;FLTDGTIT;LLVFALVL;PLFNGNKI
;SLVGGKTT;ALVLALIA;ATVDTVEL;TLTREIEQ;KLTEGTIT;VVKKQGSV
A0219
YLLVFALV;VLAEENSV;LTDGTITV;LVGGKTTV;FLTDGTIT;LLVFALVL;YLNDTTSG;IADDLNTI
A0301
ALIACSQK;KIFVSKEK;TTSGSTKK;KTGSEVVK;SVIKESYK;AALKAALK;ETYDASNK;TISADSKK

A1101
SVIKESYK;TTSGSTKK;ALIACSQK;TVDTVELK;AALKAALK;TISADSKK;KIFVSKEK;LTISADSK
;ETYDASNK;KTGSEVVK;KANKLDSK;SQKGTEPK;GTITVQAY;GTKADKTK;SADSKKTK
A2301
QYLLVFAL;TYDASNKK;AYDTAGTK;LFNGNKIF
A2402 QYLLVFAL;VFLTDGTI;VFALVLAL
A2403 QYLLVFAL
A2601 NTITVETY;EIKDLAAL;GTITVQAY;DTVELKGV
A2602 EIKDLAAL;NTITVETY;GTITVQAY;TTLEYSEM;KTKDFVFL;ETTNTLTI
A2902 GTITVQAY
A3001
KIFVSKEK;SQKGTEPK;KTKVAMTI;AALKAALK;GTKADKTK;KTKDFVFL;TTSGSTKK;KEKNSAGK
;KANKLDSK;KTGSEVVK;SGKLEGTK;KKQGSVIK;SVIKESYK
A3002
A3101 KTKDFVFL;SAGKYELR;KIFVSKEK;KANKLDSK
A3301 DTTSGSTK
A6801
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;ETLKNGIK;NTPKDSKK;SAGKYELR;EGTITLTR;ELKGVSDK
A6802 NSAGKYEL;DTVELKGV;ETTNTLTI;LVFALVLA;FVFLTDGT;ATVDTVEL
A6901
LTDGTITV;YLLVFALV;ETTNTLTI;TTLEYSEM;DTVELKGV;FALVLALI;ATVDTVEL;LVFALVLA
B0702 LAALKAAL
B0801
B0802
B1501 GTITVQAY
B1801
B2705
B3501 LAALKAAL;NTITVETY
B3901 TRENETTLB4001 AEENSVPL
B4002 EENSVPLF;AEENSVPL
B4402 EENSVPLF
B4403 EENSVPLF;SEIKDLAA
B4501 AEENSVPL;EENSVPLF
B5101 FALVLALI
B5301 FALVLALI
B5401 FALVLALI
B5701 STKKTATW
B5801 STKKTATW

Allele 9-mer
A0101 MTDSSNATK
A0201
FLTDGTITV;KLTEGTITL;YLLVFALVL;KQYLLVFAL;LVFALVLAL;LLVFALVLA;YLNDTTSGS;T
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A0202
FLTDGTITV;LLVFALVLA;YLNDTTSGS;KLTEGTITL;TIADDLNTI;KQYLLVFAL;LVFALVLAL;K
LEGNSSEI;FVSKEKNSA;SLVGGKTTV;YLLVFALVL
A0203
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IKLEGSLV;ELRATVDTV;KTKVAMTIA;LVFALVLAL;YLLVFALVL;TTNTLTISA
A0204 FLTDGTITV;SLVGGKTTV;KLTEGTITL;KLEGNSSEI;TVLAEENSV;YLLVFALVL
A0206
FLTDGTITV;KLTEGTITL;KQYLLVFAL;TIADDLNTI;SLVGGKTTV;VQAYDTAGT;SEIKDLAAL;L
LVFALVLA;SQDHNDQEI;TVLAEENSV;YLLVFALVL;LVFALVLAL;ITVQAYDTA;FVFLTDGTI;YL
NDTTSGS

A0211
FLTDGTITV;KLTEGTITL;SLVGGKTTV;YLLVFALVL;KLEGNSSEI;TIADDLNTI;DLAALKAAL;E
LRATVDTV;YLNDTTSGS;LVFALVLAL;LLVFALVLA;GKYELRATV;LFNGNKIFV;TVLAEENSV;VL
ALIACSQ;KQYLLVFAL;EMTDSSNAT;KLDSKKITR
A0212
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VFALVLA
A0216
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FALVLAL;YLNDTTSGS
A0219
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A0301
LVGGKTTVK;IINSDNTPK;KTGSEVVKK;LAALKAALK;MTDSSNATK;ATKAVETLK;KANKLDSKK;
A1101
ATVDTVELK;ATKAVETLK;SVPLFNGNK;MTDSSNATK;IINSDNTPK;KTGSEVVKK;QAYDTAGTK;L
TISADSKK;ETYDASNKK;KANKLDSKK;TLTISADSK;LAALKAALK;CSQKGTEPK;GSVIKESYK;LV
GGKTTVK;ISADSKKTK;LALIACSQK;
A2301 AYDTAGTKL;TWNETTNTL;ETYDASNKK
A2402 VFALVLALI;QYLLVFALV;TWNETTNTL
A2403 AYDTAGTKL
A2601 ETTLEYSEM;ETLKNGIKL
A2602 ETTLEYSEM;EVVKKQGSV;ETLKNGIKL
A2902
A3001
ATKAVETLK;ATVDTVELK;KTKDFVFLT;CSQKGTEPK;QAYDTAGTK;ETYDASNKK;KTGSEVVKK;K
TKVAMTIA;KANKLDSKK;MTDSSNATK;IINSDNTPK;SVPLFNGNK
A3002
A3101 KLDSKKITR;ATKAVETLK;MTDSSNATK;KANKLDSKK;KTKDFVFLT
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A6801
ETYDASNKK;EIKDLAALK;LTISADSKK;DTTSGSTKK;NSAGKYELR;MTDSSNATK;QAYDTAGTK;A
TVDTVELK;LAALKAALK;SVPLFNGNK;TLTISADSK;ATKAVETLK;LALIACSQK;IINSDNTPK
A6802
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TTLEYSEM;TVLAEENSV;NSSEIKDLA;FLTDGTITV;SVIKESYKA
A6901
FLTDGTITV;ETLKNGIKL;TTLEYSEMT;TIADDLNTI;EVVKKQGSV;LVFALVLAL;TVLAEENSV;T
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B0702 VPLFNGNKI;TPKDSKKDL;KADKTKVAM;RATVDTVEL;LAEENSVPL
B0801
B0802
B1501 KQYLLVFAL;LVFALVLAL;RENETTLEY
B1801 RENETTLEY;SEIKDLAAL;NETTNTLTI;IEQDGKVKI
B2705 KQYLLVFAL;
B35 01 LAEENSVPL;
B3901
B4001 SEIKDLAAL;AEENSVPLF
B4002 AEENSVPLF;REIEQDGKV;RENETTLEY
B4402 RENETTLEY
B4403 RENETTLEY;EENSVPLFN;AEENSVPLF;REIEQDGKV;
B4501 RENETTLEY;AEENSVPLF;REIEQDGKV
B5101 VPLFNGNKI

B5301 VPLFNGNKI
B5401 FALVLALIA;VPLFNGNKI
B5701
B5801 GSTKKTATW

Allele 10-mer
A0101
A0201
YLLVFALVLA;KQYLLVFALV;VLAEENSVPL;LLVFALVLAL;KLTEGTITLT;YLNDTTSGST;LVFAL
VLALI;FLTDGTITVQ;IADDLNTITV;
A0202
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TITVQ;MTIADDLNTI;KLTEGTITLT;IADDLNTITV
A0203
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A0204 VLAEENSVPL;LLVFALVLAL
A0206
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NTITV;YLLVFALVLA;YELRATVDTV;FLTDGTITVQ;KAVETLKNGI;YLNDTTSGST;LVFALVLALI
;SQDHNDQEII;LTVLAEENSV
A0211
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;LTDGTITVQA;SLVGGKTTVK;ATWNETTNTL;YELRATVDTV
A0212
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NTITV;TVDTVELKGV;KLTEGTITLT;VFLTDGTITV;KITRENETTL;YELRATVDTV
A0216
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TITLT;YLNDTTSGST;KITRENETTL;LVGGKTTVKL;ATWNETTNTL;TVDTVELKGV;VFLTDGTITV
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ELKGV;YLLVFALVLA;ATWNETTNTL;KLTEGTITLT;YELRATVDTV;
A0301
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SSEIK;VQAYDTAGTK
A1101
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GVSDK;NSVPLFNGNK;TLTISADSKK;SLVGGKTTVK;VQAYDTAGTK;KLEGSLVGGK;VIKESYKANK
;EIINSDNTPK;VVKKQGSVIK;VSKEKNSAGK;VSDKNNGSGK
A2301 QYLLVFALVL;SYKANKLDSK
A2402 QYLLVFALVL
A2403 QYLLVFALVL
A2601
A2602 EVVKKQGSVI
A2902
A3001
RATVDTVELK;KLEGNSSEIK;LTREIEQDGK;VVKKQGSVIK;SYKANKLDSK;VSKEKNSAGK;VIKES
YKANK;ACSQKGTEPK;KLEGSLVGGK
A3002
A3101 KNSAGKYELR
A3301
A6801
NATKAVETLK;NTLTISADSK;TVETYDASNK;LTEGTITLTR;EIINSDNTPK;DLAALKAALK;NSVPL

FNGNK;EMTDSSNATK;TLTISADSKK;VLALIACSQK;TISADSKKTK;LTREIEQDGK;RATVDTVELK
;TVELKGVSDK
A6802
MTIADDLNTI;LVFALVLALI;ETTNTLTISA;TTVKLTEGTI;NTITVETYDA;LTVLAEENSV;EVVKK
QGSVI;SVPLFNGNKI;ETTLEYSEMT
A6901
ETTNTLTISA;MTIADDLNTI;ATWNETTNTL;ETYDASNKKT;LVFALVLALI;IADDLNTITV;MTDSS
NATKA;QAYDTAGTKL
B0702 VPLFNGNKIF
B0801
B0802
B1501 KQGSVIKESY;VLAEENSVPL
B1801 IEQDGKVKIY;YELRATVDTV;VKLTEGTITL;
B2705
B3501 VPLFNGNKIF;LAEENSVPLF;DLNTITVETY;
B3901
B4001 VETLKNGIKL
B4002
B4402
B4403
B4501
B5101
B5301 VPLFNGNKIF
B5401
B5701
B5801 SGSTKKTATW

Allele 11-mer
A0101 LTDGTITVQAY;MTDSSNATKAV
A0201
FLTDGTITVQA;YLLVFALVLAL;TIADDLNTITV;FVFLTDGTITV;LLVFALVLALI;SLVGGKTTVKL
;KQYLLVFALVL;AMTIADDLNTI;
A0202
FLTDGTITVQA;LLVFALVLALI;TIADDLNTITV;SLVGGKTTVKL;YLLVFALVLAL;FVFLTDGTITV
;AMTIADDLNTI;MTDSSNATKAV;VQAYDTAGTKL;NSSEIKDLAAL;KQYLLVFALVL
A0203
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;AMTIADDLNTI;YLLVFALVLAL;MTDSSNATKAV;VQAYDTAGTKL;TLKNGIKLEGS;VIKESYKANK
L;MKQYLLVFALV;
A0204
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;VQAYDTAGTKL;LLVFALVLALI;MKQYLLVFALV;MTDSSNATKAV;SLVGGKTTVKL;TVLAEENSVP
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;LLVFALVLALI;MTDSSNATKAV;SAGKYELRATV;YLNDTTSGSTK;KLTEGTITLTR;EMTDSSNATK
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PL;KADKTKVAMTI
A0212
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;SADSKKTKDFV;DLTVLAEENSV;ELRATVDTVEL;LLVFALVLALI;AMTIADDLNTI;MTDSSNATKA
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A0219
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A0301
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;GSLVGGKTTVK
A1101
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;TVETYDASNKK;IACSQKGTEPK;NTLTISADSKK;KQGSVIKESYK;LTISADSKKTK;YLNDTTSGST
K;GSLVGGKTTVK;KAVETLKNGIK;ESYKANKLDSK;FVSKEKNSAGK
A2301 SYKANKLDSKK
A2402 TWNETTNTLTI
A2403
A2601 EIEQDGKVKIY
A2602 EIEQDGKVKIY;LTDGTITVQAY;SVPLFNGNKIF;ITRENETTLEY
A2902 ITRENETTLEY
A3001
ITRENETTLEY;TVQAYDTAGTK;SYKANKLDSKK;YLNDTTSGSTK;KLEGTKADKTK;IACSQKGTEPK
;LTISADSKKTK;LFNGNKIFVSK;SVIKESYKANK;GSLVGGKTTVK;KAVETLKNGIK
A3002
A3101
KLTEGTITLTR;KQGSVIKESYK;LFNGNKIFVSK;SVIKESYKANK;SYKANKLDSKK;LVLALIACSQK
A3301
A6801
NTLTISADSKK;ITVETYDASNK;ESYKANKLDSK;DTVELKGVSDK;TVQAYDTAGTK;SVIKESYKANK
;TVETYDASNKK;LTISADSKKTK;FVSKEKNSAGK;EVVKKQGSVIK;LVLALIACSQK;YLNDTTSGST
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A6802
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;TVLAEENSVPL;STSQDHNDQEI;EGSLVGGKTTV;MTIADDLNTIT;ATVDTVELKGV
A6901
TIADDLNTITV;MTDSSNATKAV;FVFLTDGTITV;TVLAEENSVPL;ATVDTVELKGV;VPLFNGNKIFV
B0702 VPLFNGNKIFV
B0801 YLLVFALVLAL
B0802
B1501 ITRENETTLEY;KQYLLVFALVL;VLAEENSVPLF;VSKEKNSAGKY;YLLVFALVLAL
B1801 IEQDGKVKIYL
B2705 KQYLLVFALVL
B3501 TATWNETTNTL;LTDGTITVQAY;TVLAEENSVPL
B3901 KQYLLVFALVL
B4001 IEQDGKVKIYL;REIEQDGKVKI;KEKNSAGKYEL;LEGNSSEIKDL
B4002 REIEQDGKVKI;KEKNSAGKYEL
B4402
B4403
B4501
B5101 VPLFNGNKIFV
B5301
B5401 VPLFNGNKIFV
B5701 TSGSTKKTATW
B5801 TSGSTKKTATW

Allele 15-mer plus 9-mer core
DRB1_0101

SSEIKDLAALKAALK-IKDLAALKA;GNSSEIKDLAALKAA-IKDLAALKA;NSSEIKDLAALKAAL-
IKDLAALKA;EGNSSEIKDLAALKA-EGNSSEIKD;KQYLLVFALVLALIA-
VFALVLALI;YLLVFALVLALIACS-FALVLALIA;EGSLVGGKTTVKLTE-
VGGKTTVKL;KLEGSLVGGKTTVKL-LVGGKTTVK;LEGSLVGGKTTVKLT-
VGGKTTVKL;LLVFALVLALIACSQ-FALVLALIA;GSLVGGKTTVKLTEG-
VGGKTTVKL;QYLLVFALVLALIAC-FALVLALIA;LVFALVLALIACSQK-
FALVLALIA;SLVGGKTTVKLTEGT-VGGKTTVKL;MKQYLLVFALVLALI-
LVFALVLAL;VFALVLALIACSQKG-LVLALIACS;FALVLALIACSQKGT-
LVLALIACS;ETLKNGIKLEGSLVG-LKNGIKLEG;KNGIKLEGSLVGGKT-
IKLEGSLVG;TITVQAYDTAGTKLE-VQAYDTAGT;TLKNGIKLEGSLVGG-
IKLEGSLVG;LKNGIKLEGSLVGGK-IKLEGSLVG;NGIKLEGSLVGGKTT-
IKLEGSLVG;ITVQAYDTAGTKLEG-VQAYDTAGT;VGGKTTVKLTEGTIT-
VGGKTTVKL;DGTITVQAYDTAGTK-VQAYDTAGT;GTITVQAYDTAGTKL-
VQAYDTAGT;TDGTITVQAYDTAGT-TITVQAYDT;IKLEGSLVGGKTTVK-
IKLEGSLVG;LVGGKTTVKLTEGTI-VGGKTTVKL;TTVKLTEGTITLTRE-
LTEGTITLT;GKTTVKLTEGTITLT-VKLTEGTIT;KTTVKLTEGTITLTR-
LTEGTITLT;ALVLALIACSQKGTE-VLALIACSQ;KIYLNDTTSGSTKKT-
YLNDTTSGS;KDFVFLTDGTITVQA-FLTDGTITV;KVKIYLNDTTSGSTK-
IYLNDTTSG;GKVKIYLNDTTSGST-IYLNDTTSG;TVKLTEGTITLTREI-
LTEGTITLT;VKIYLNDTTSGSTKK-YLNDTTSGS;DFVFLTDGTITVQAY-
FLTDGTITV;FVFLTDGTITVQAYD-FLTDGTITV;VKLTEGTITLTREIE-
LTEGTITLT;DGKVKIYLNDTTSGS-IYLNDTTSG;AGKYELRATVDTVEL-
YELRATVDT;TVQAYDTAGTKLEGN-VQAYDTAGT;TKDFVFLTDGTITVQ-
FLTDGTITV;VQAYDTAGTKLEGNS-VQAYDTAGT;IYLNDTTSGSTKKTA-
TTSGSTKKT;NSAGKYELRATVDTV-YELRATVDT;GKYELRATVDTVELK-
YELRATVDT;KNSAGKYELRATVDT-AGKYELRAT;SAGKYELRATVDTVE-
YELRATVDT;LVLALIACSQKGTEP-LVLALIACS;GIKLEGSLVGGKTTV-
IKLEGSLVG;KTKDFVFLTDGTITV-FVFLTDGTI;GSEVVKKQGSVIKES-
VKKQGSVIK;SEVVKKQGSVIKESY-VKKQGSVIK;TGSEVVKKQGSVIKE-
VKKQGSVIK;KTGSEVVKKQGSVIK-VVKKQGSVI;VFLTDGTITVQAYDT-
FLTDGTITV;EVVKKQGSVIKESYK-VKKQGSVIK;YLNDTTSGSTKKTAT-
TTSGSTKKT;GGKTTVKLTEGTITL-VKLTEGTIT;KTATWNETTNTLTIS-
WNETTNTLT;KKTATWNETTNTLTI-WNETTNTLT;TKKTATWNETTNTLT-
ATWNETTNT;FLTDGTITVQAYDTA-FLTDGTITV;TATWNETTNTLTISA-
WNETTNTLT;LNDTTSGSTKKTATW-TTSGSTKKT;YELRATVDTVELKGV-
YELRATVDT;ATWNETTNTLTISAD-WNETTNTLT;QDGKVKIYLNDTTSG-
KVKIYLNDT;VLALIACSQKGTEPK-VLALIACSQ;QAYDTAGTKLEGNSS-
YDTAGTKLE;DKTKVAMTIADDLNT-VAMTIADDL;KYELRATVDTVELKG-YELRATVDT
DRB1_0301
DRB1_0401
KDSKKDLTVLAEENS-SKKDLTVLA;PKDSKKDLTVLAEEN-SKKDLTVLA;NTPKDSKKDLTVLAE-
SKKDLTVLA;TPKDSKKDLTVLAEE-SKKDLTVLA;DNTPKDSKKDLTVLA-
DNTPKDSKK;FNGNKIFVSKEKNSA-FNGNKIFVS;NKIFVSKEKNSAGKY-
FVSKEKNSA;GNKIFVSKEKNSAGK-FVSKEKNSA;KIFVSKEKNSAGKYE-
FVSKEKNSA;NGNKIFVSKEKNSAG-FVSKEKNSA;VKIYLNDTTSGSTKK-
YLNDTTSGS;GKVKIYLNDTTSGST-YLNDTTSGS;KVKIYLNDTTSGSTK-
YLNDTTSGS;DGKVKIYLNDTTSGS-IYLNDTTSG;KIYLNDTTSGSTKKT-
YLNDTTSGS;DSKKDLTVLAEENSV-SKKDLTVLA;SKKDLTVLAEENSVP-SKKDLTVLA
DRB1_0404
GKVKIYLNDTTSGST-YLNDTTSGS;KVKIYLNDTTSGSTK-YLNDTTSGS;VKIYLNDTTSGSTKK-
YLNDTTSGS
DRB1_0405 HNDQEIINSDNTPKD-IINSDNTPK;DQEIINSDNTPKDSK-
INSDNTPKD;NDQEIINSDNTPKDS-INSDNTPKD;QEIINSDNTPKDSKK-
INSDNTPKD;EIINSDNTPKDSKKD-INSDNTPKD;IINSDNTPKDSKKDL-
INSDNTPKD;INSDNTPKDSKKDLT-INSDNTPKD;TKKTATWNETTNTLT-TKKTATWNE
DRB1_0701

ETYDASNKKTGSEVV-SNKKTGSEV;TYDASNKKTGSEVVK-NKKTGSEVV;YDASNKKTGSEVVKK-
NKKTGSEVV;DASNKKTGSEVVKKQ-NKKTGSEVV
DRB1_0802
DRB1_0901 KQYLLVFALVLALIA-LVFALVLAL;YLLVFALVLALIACS-
LVFALVLAL;MKQYLLVFALVLALI-LVFALVLAL;QYLLVFALVLALIAC-LVFALVLAL
DRB1_1101
DRB1_1302
NSVPLFNGNKIFVSK-VPLFNGNKI;ENSVPLFNGNKIFVS-VPLFNGNKI;DGKVKIYLNDTTSGS-
VKIYLNDTT;GKVKIYLNDTTSGST-YLNDTTSGS;ETLKNGIKLEGSLVG-
LKNGIKLEG;VPLFNGNKIFVSKEK-VPLFNGNKI;SVPLFNGNKIFVSKE-
VPLFNGNKI;KAVETLKNGIKLEGS-LKNGIKLEG;TKAVETLKNGIKLEG-
VETLKNGIK;KVKIYLNDTTSGSTK-YLNDTTSGS;VKIYLNDTTSGSTKK-
YLNDTTSGS;EENSVPLFNGNKIFV-VPLFNGNKI;AVETLKNGIKLEGSL-
LKNGIKLEG;VETLKNGIKLEGSLV-LKNGIKLEG;YLLVFALVLALIACS-
LLVFALVLA;LLVFALVLALIACSQ-LLVFALVLA;QDGKVKIYLNDTTSG-
VKIYLNDTT;KQYLLVFALVLALIA-LLVFALVLA;QYLLVFALVLALIAC-
LLVFALVLA;SEVVKKQGSVIKESY-VKKQGSVIK;TGSEVVKKQGSVIKE-
VKKQGSVIK;MKQYLLVFALVLALI-LLVFALVLA;TLKNGIKLEGSLVGG-
LKNGIKLEG;KTGSEVVKKQGSVIK-VVKKQGSVI;LAEENSVPLFNGNKI-
ENSVPLFNG;GSEVVKKQGSVIKES-VKKQGSVIK;AEENSVPLFNGNKIF-
VPLFNGNKI;LKNGIKLEGSLVGGK-LKNGIKLEG;NGIKLEGSLVGGKTT-
IKLEGSLVG;EVVKKQGSVIKESYK-VKKQGSVIK;KNGIKLEGSLVGGKT-IKLEGSLVG
DRB1_1501 IKLEGSLVGGKTTVK-IKLEGSLVG;KQYLLVFALVLALIA-
LLVFALVLA;MKQYLLVFALVLALI-LLVFALVLA;QYLLVFALVLALIAC-
LLVFALVLA;YLLVFALVLALIACS-LLVFALVLA;LLVFALVLALIACSQ-LLVFALVLA;
DRB3_0101
DRB4_0101
DRB5_0101

<CAF34027 outer surface protein VlsE;Protein;Borrelia afzelii PKo>

Allele 8-mer
A0101
A0201 KLDELVSA;KISSAIFL;KIAAAIVL;ILKAIVEA;
A0202
KISSAIFL;KLDELVSA;KIAAAIVL;ILKAIVEA;LTALLVFI;ALGEKGAL;FINCKNNA;SAIFLTAL
;FLTALLVF;AIFLTALL;AAGAVTAV;AVSGEQIL;GLVADTFF
A0203
ILKAIVEA;KLDELVSA;ALKDVKAA;FINCKNNA;ALGEKGAL;KISSAIFL;AAGAVTAV;KIAAAIVL
;SISSTLKA;MIKAAEEA;SAIFLTAL;LTALLVFI;AAIVLRGV;GIKGIVDA;IAKAAGAV
A0204 ALGEKGAL;AAGAVTAV;KIAAAIVL;KLDELVSA;
A0206
KLDELVSA;KISSAIFL;SAIFLTAL;AAGAVTAV;KIAAAIVL;FIDVFNAF;FAGNANAA;AAIVLRGV
;KAAGAVTA;FLTALLVF;FESISSTL;WLEEMIKA;KASVESAV;AIFLTALL;
A0211
KLDELVSA;KISSAIFL;WLEEMIKA;ALGEKGAL;KIAAAIVL;AIFLTALL;ALKDVKAA;ILKAIVEA
;FLTALLVF;AKDGKFAV;AVSGEQIL;ALLVFINC;IFLTALLV;SISSTLKA;AAGAVTAV
A0212 KLDELVSA;ALGEKGAL;ALKDVKAA;WLEEMIKA;FLTALLVF;AKDGKFAV;AVSGEQIL
A0216
ALGEKGAL;KLDELVSA;KISSAIFL;AAGAVTAV;AIFLTALL;ILKAIVEA;WLEEMIKA;ALKDVKAA
;KIAAAIVL;AVSGEQIL
A0219 KLDELVSA;KISSAIFL;AKDGKFAV
A0301 LVADTFFK;IVLRGVAK;LLVFINCK;VSGEQILK;ESISSTLK;TLKATKGK
A1101
LVADTFFK;SAANHGAK;SSTLKATK;IVLRGVAK;VSGEQILK;ESISSTLK;GAAADIAK;AAFKDEMK
;SAVDEVSK;TFFKSDPK;GIVDAAGK;KAAEEAAK;IAAAIVLR;LLVFINCK;TLKATKGK

A2301 FYESIINL;KWLEEMIK;GLVADTFF
A2402 FYESIINL;IFLTALLV;
A2403 FYESIINL
A2601
A2602 FIDVFNAF
A2902
A3001
TLKATKGK;AGKALGEK;TFFKSDPK;AFKDEMKK;KGIAKGIK;IVLRGVAK;LVADTFFK;KWLEEMIK
A3002
A3101 IAAAIVLR;LVADTFFK
A3301 IAAAIVLR
A6801
ESISSTLK;IAAAIVLR;LVADTFFK;EANADAGK;LLVFINCK;SAVDEVSK;SAANHGAK;SSTLKATK
;TFFKSDPK;DSVKGIAK;AAFKDEMK;DDNGAAFK;DPANQAGK
A6802 LTALLVFI;SAIFLTAL;DSAANHGA;FNAFSGLV;NAAVGAAA
A6901 LTALLVFI
B0702 SAIFLTAL
B0801
B0802
B1501 FLTALLVF;IINLGNGF
B1801 FESISSTL
B2705
B3501 FIDVFNAF;SAIFLTAL;FAGNANAA;NAAVGAAA
B3901 FESISSTL
B4001 FESISSTL
B4002
B4402
B4403
B4501 AEEAKNPI
B5101
B5301
B5401 FAGNANAA
B5701
B5801 KSDVKTYF

Allele 9-mer

A0101
A0201
FLTALLVFI;KLFAGNANA;KISSAIFLT;FINCKNNAV;AIFLTALLV;QILKAIVEA;FAGNANAAV;K
AAGAVTAV
A0202
FLTALLVFI;FINCKNNAV;ILKAIVEAA;KAAGAVTAV;KLFAGNANA;FAGNANAAV;SSAIFLTAL;S
AIFLTALL;KISSAIFLT;SVESAVDEV;KAAEEAAKV;GIKGIVDAA;ALKDVKAAA;GLVADTFFK;
A0203
FINCKNNAV;FLTALLVFI;ILKAIVEAA;KAAGAVTAV;KLFAGNANA;ALKDVKAAA;GIAKGIKGI;N
LGNGFIDV;SVKTFYESI;SVKASVESA;AAAIVLRGV;IINLGNGFI;FAGNANAAV;GIKGIVDAA;SA
IFLTALL;MIKAAEEAA;ATKGKLDEL;SVKGIAKGI;AIFLTALLV;KAAEEAAKV
A0204
FLTALLVFI;KAAGAVTAV;KAAEEAAKV;FINCKNNAV;FAGNANAAV;SVESAVDEV;KLFAGNANA
A0206
FAGNANAAV;FINCKNNAV;FLTALLVFI;KAAGAVTAV;NLGNGFIDV;AIFLTALLV;KAAEEAAKV;K
LFAGNANA;SVESAVDEV;SAIFLTALL;AAAIVLRGV;QILKAIVEA;LVADTFFKS;KISSAIFLT;SS
AIFLTAL
A0211
FLTALLVFI;NLGNGFIDV;AIFLTALLV;KLFAGNANA;AVDEVSKWL;VAKDGKFAV;ALKDVKAAA;K
LDELVSAK;WLEEMIKAA;KAAGAVTAV;KAAEEAAKV;SVESAVDEV;FINCKNNAV;FAGNANAAV;IL
KAIVEAA;QILKAIVEA;GIAKGIKGI;GLVADTFFK;NADAGKLFA;

A0212
FLTALLVFI;NLGNGFIDV;VAKDGKFAV;ALKDVKAAA;KLFAGNANA;FINCKNNAV;FAGNANAAV;A
VDEVSKWL;AIFLTALLV;WLEEMIKAA;KLDELVSAK;GIAKGIKGI;KAAGAVTAV
A0216
NLGNGFIDV;FLTALLVFI;AIFLTALLV;ALKDVKAAA;KLFAGNANA;SVESAVDEV;FAGNANAAV;V
AKDGKFAV;AVDEVSKWL;FINCKNNAV;KAAGAVTAV;EMIKAAEEA;TLKATKGKL;QILKAIVEA;DI
AKAAGAV;WLEEMIKAA
A0219
FLTALLVFI;NLGNGFIDV;VAKDGKFAV;KAAGAVTAV;FAGNANAAV;FINCKNNAV;SVESAVDEV;A
IFLTALLV
A0301
GLVADTFFK;KLDELVSAK;KIAAAIVLR;ALGEKGALK;AVSGEQILK;ISSTLKATK;AAFKDEMKK;A
LLVFINCK
A1101
GLVADTFFK;AVSGEQILK;AAFKDEMKK;ALLVFINCK;STLKATKGK;AIVLRGVAK;KIAAAIVLR;D
TFFKSDPK;ISSTLKATK;KLDELVSAK;AAGKALGEK;ALGEKGALK;TFFKSDPKK;AVGKGNDDK;
A2301 IFLTALLVF;GFIDVFNAF;TFYESIINL;TFFKSDPKK;
A2402 IFLTALLVF;GFIDVFNAF;YFESISSTL
A2403 IFLTALLVF;GFIDVFNAF;YFESISSTL
A2601 SIINLGNGF;EVSKWLEEM;DVFNAFSGL
A2602 EVSKWLEEM;DVFNAFSGL;SIINLGNGF
A2902
A3001
STLKATKGK;AGKKAEEAK;TFFKSDPKK;GLVADTFFK;ALLVFINCK;ANHGAKADK;AAFKDEMKK;D
TFFKSDPK;AAGKALGEK;AVSGEQILK
A3002
A3101 KIAAAIVLR;ISSTLKATK
A3301 DTFFKSDPK
A6801
DTFFKSDPK;ESAVDEVSK;DSAANHGAK;KIAAAIVLR;TFFKSDPKK;GLVADTFFK;ISSTLKATK;S
TLKATKGK;AAFKDEMKK;GAAFKDEMK
A6802
DVFNAFSGL;SAIFLTALL;FINCKNNAV;SSAIFLTAL;DIAKAAGAV;DVKTYFESI;FLTALLVFI;L
VADTFFKS;FAGNANAAV;SVKTFYESI;EGGSVKASV;KAAGAVTAV;NANAAVGAA;AAAIVLRGV;IS
SAIFLTA
A6901
FAGNANAAV;FINCKNNAV;EVSKWLEEM;DIAKAAGAV;DVFNAFSGL;NLGNGFIDV;QILKAIVEA
B0702 KAAGAVTAV;IVDAAGKAL
B0801
B0802
B1501 SIINLGNGF;GFIDVFNAF
B1801
B2705
B3501 FAGNANAAV;TAVSGEQIL;IFLTALLVF;TDDDNGAAF;FSGLVADTF;GFIDVFNAF
B3901 YFESISSTL
B4001
B4002 EEAKNPIAA
B4402
B4403 EEAKNPIAA
B4501 EEAKNPIAA;AEEAKNPIA
B5101
B5301
B5401 NPIAAAIGT
B5701
B5801 SAVDEVSKW

Allele 10-mer

A0101
A0201 KISSAIFLTA;KLFAGNANAA;KTFYESIINL
A0202 KLFAGNANAA;KTFYESIINL;KISSAIFLTA;SSAIFLTALL;SIINLGNGFI;IAAAIVLRGV
A0203
SVKASVESAV;KISSAIFLTA;KLFAGNANAA;IAAAIVLRGV;GIAKGIKGIV;SIINLGNGFI;ATKGK
LDELV;SVKTFYESII;SAIFLTALLV;KTYFESISST;SAKKGEGGSV
A0204 KLFAGNANAA
A0206
KISSAIFLTA;SAIFLTALLV;KLFAGNANAA;AIVEAAGDPA;GVAKDGKFAV;AKAAGAVTAV;ASVES
AVDEV;QILKAIVEAA;SIINLGNGFI;KTFYESIINL;IAAAIVLRGV;GLVADTFFKS
A0211
KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;KLDELVSAKK;KISSAIFLTA;SAIFLTALLV;DVFNA
FSGLV;SVKASVESAV;SAVDEVSKWL;IAAAIVLRGV;LFAGNANAAV;SIINLGNGFI;AVSGEQILKA
;GIVDAAGKAL;FLTALLVFIN
A0212 KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;LFAGNANAAV;KLDELVSAKK
A0216
KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;SVKASVESAV;DVFNAFSGLV;LFAGNANAAV;
A0219 IAAAIVLRGV;LFAGNANAAV
A0301
KALGEKGALK;KLDELVSAKK;AAIVLRGVAK;VLRGVAKDGK;SISSTLKATK;KVGGTGGDGK;SVKGI
AKGIK;ADTFFKSDPK;TAVSGEQILK;VAKDGKFAVK;SSTLKATKGK;
A1101
TALLVFINCK;SISSTLKATK;AAIVLRGVAK;AVGAAADIAK;TAVSGEQILK;KALGEKGALK;SSTLK
ATKGK;SGLVADTFFK;SVKGIAKGIK;DTFFKSDPKK;VSKWLEEMIK;KVGGTGGDGK;KLDELVSAKK
;GAAFKDEMKK;MIKAAEEAAK;AANHGAKADK;VAKDGKFAVK
A2301 TYFESISSTL;IFLTALLVFI;AFSGLVADTF;AIFLTALLVF;FSGLVADTFF
A2402 IFLTALLVFI;TYFESISSTL;AFSGLVADTF
A2403 TYFESISSTL;AFSGLVADTF;IFLTALLVFI
A2601 ESIINLGNGF;SIINLGNGFI
A2602 ESIINLGNGF;GTDDDNGAAF;AIFLTALLVF;EVSKWLEEMI
A2902
A3001
SGLVADTFFK;SVKGIAKGIK;KALGEKGALK;MIKAAEEAAK;AAIVLRGVAK;VAKDGKFAVK;VLRGV
AKDGK;AVGAAADIAK;AANHGAKADK;SSTLKATKGK;KVGGTGGDGK;
A3002
A3101 AAIVLRGVAK;
A3301
A6801
DTFFKSDPKK;TAVSGEQILK;MIKAAEEAAK;DAAGKALGEK;TALLVFINCK;DKIAAAIVLR;YFESI
SSTLK;SISSTLKATK;SVKGIAKGIK;NGAAFKDEMK;GAAFKDEMKK;SSTLKATKGK;
A6802
DVFNAFSGLV;IAAAIVLRGV;SSAIFLTALL;SAIFLTALLV;EAAGDPANQA;DSVKTFYESI;EVSKW
LEEMI;EAKNPIAAAI;SVKASVESAV;ISSAIFLTAL;NANAAVGAAA;HGAKADKDSV;SIINLGNGFI
A6901 DVFNAFSGLV;EVSKWLEEMI;EAAGDPANQA;SAIFLTALLV
B0702
B0801
B0802
B1501 AIFLTALLVF
B1801
B2705
B3501 EANADAGKLF;DPKKSDVKTY;NGFIDVFNAF;FSGLVADTFF;NANAAVGAAA
B3901
B4001
B4002
B4402

B4403
B4501 AEEAKNPIAA;EEMIKAAEEA;AEEAAKVGGT;EEAKNPIAAA
B5101
B5301
B5401
B5701 ESAVDEVSKW
B5801 ESAVDEVSKW;ISSAIFLTAL

Allele 11-mer
A0101
A0201 KLFAGNANAAV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV;AIFLTALLVFI;
A0202
KISSAIFLTAL;KLFAGNANAAV;FIDVFNAFSGL;KIAAAIVLRGV;LLVFINCKNNA;FLTALLVFINC
;ISSAIFLTALL;MIKAAEEAAKV;KTYFESISSTL;LVFINCKNNAV;AIFLTALLVFI;KIGDSAANHG
A;KASVESAVDEV;ALGEKGALKDV;AVSGEQILKAI
A0203
KIAAAIVLRGV;KLFAGNANAAV;MIKAAEEAAKV;ALGEKGALKDV;KISSAIFLTAL;FIDVFNAFSGL
;IAKAAGAVTAV;LLVFINCKNNA;IINLGNGFIDV;KTYFESISSTL;LVFINCKNNAV;FLTALLVFIN
C;KIGDSAANHGA;AAADIAKAAGA
A0204 KLFAGNANAAV;KIAAAIVLRGV;ALGEKGALKDV
A0206
KLFAGNANAAV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV;FAGNANAAVGA;KIGDSAANHGA
;KTYFESISSTL;FLTALLVFINC;KASVESAVDEV;LVFINCKNNAV;KKISSAIFLTA;AIFLTALLVF
I;SSAIFLTALLV;ALGEKGALKDV
A0211
KLFAGNANAAV;ALGEKGALKDV;KIAAAIVLRGV;FIDVFNAFSGL;KISSAIFLTAL;AIFLTALLVFI
;FLTALLVFINC;IINLGNGFIDV;KIGDSAANHGA;KATKGKLDELV;LVFINCKNNAV;MIKAAEEAAK
V;SSAIFLTALLV;AVSGEQILKAI;AVTAVSGEQIL;KTYFESISSTL
A0212
KLFAGNANAAV;ALGEKGALKDV;FIDVFNAFSGL;KIAAAIVLRGV;FLTALLVFINC;MIKAAEEAAKV
;LVFINCKNNAV;KISSAIFLTAL;IINLGNGFIDV
A0216
KLFAGNANAAV;ALGEKGALKDV;MIKAAEEAAKV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV
;AIFLTALLVFI;LVFINCKNNAV;IINLGNGFIDV;KIGDSAANHGA;KATKGKLDELV;LLVFINCKNN
A
A0219 KLFAGNANAAV;FIDVFNAFSGL;KIAAAIVLRGV;KISSAIFLTAL;ALGEKGALKDV
A0301
FSGLVADTFFK;VTAVSGEQILK;GVAKDGKFAVK;FINCKNNAVGK;TYFESISSTLK;LTALLVFINCK
A1101
LTALLVFINCK;VTAVSGEQILK;SVESAVDEVSK;GTDDDNGAAFK;FSGLVADTFFK;TYFESISSTLK
;AAAIVLRGVAK;GVAKDGKFAVK;SAANHGAKADK;VADTFFKSDPK;AAVGAAADIAK;IVLRGVAKDG
K;AAGDPANQAGK;ESISSTLKATK;ISSTLKATKGK;FINCKNNAVGK;EVSKWLEEMIK;GIKGIVDAA
GK
A2301 TYFESISSTLK;AFSGLVADTFF;SAIFLTALLVF
A2402 AFSGLVADTFF
A2403 AFSGLVADTFF
A2601
A2602 KISSAIFLTAL;FIDVFNAFSGL
A2902
A3001 KGKLDELVSAK;TYFESISSTLK;SAKKGEGGSVK;AFKDEMKKSDK;IVLRGVAKDGK
A3002 AFSGLVADTFF
A3101 TYFESISSTLK
A3301
A6801
ESISSTLKATK;LTALLVFINCK;EVSKWLEEMIK;TYFESISSTLK;FSGLVADTFFK;EMIKAAEEAAK

;FINCKNNAVGK;VTAVSGEQILK;SVESAVDEVSK;DSVKGIAKGIK;SAANHGAKADK;NGAAFKDEMK
K;ISSTLKATKGK
A6802
ESIINLGNGFI;ISSAIFLTALL;SSAIFLTALLV;LVFINCKNNAV;FIDVFNAFSGL;KIAAAIVLRGV
;ESAVDEVSKWL;EEAKNPIAAAI;IAAAIVLRGVA;DVFNAFSGLVA;MIKAAEEAAKV
A6901 LVFINCKNNAV;FIDVFNAFSGL;
B0702
B0801
B0802
B1501 VLRGVAKDGKF;KLFAGNANAAV
B1801 YESIINLGNGF;DEANADAGKLF
B2705
B3501 NAFSGLVADTF;SAIFLTALLVF;IGTDDDNGAAF;DPKKSDVKTYF
B3901
B4001 YESIINLGNGF
B4002 EEAKNPIAAAI
B4402
B4403 EEAKNPIAAAI
B4501 EEMIKAAEEAA;AEEAKNPIAAA;EEAKNPIAAAI
B5101
B5301
B5401
B5701
B5801 SAIFLTALLVF;KTYFESISSTL;KSDKIAAAIVL;ISSAIFLTALL

Allele 15-mer plus 9-mer core

DRB1_0101
GKLFAGNANAAVGAA-FAGNANAAV;AGKLFAGNANAAVGA-FAGNANAAV;ADIAKAAGAVTAVSG-
IAKAAGAVT;AADIAKAAGAVTAVS-IAKAAGAVT;GAAADIAKAAGAVTA-
IAKAAGAVT;AAADIAKAAGAVTAV-IAKAAGAVT;DAGKLFAGNANAAVG-
FAGNANAAV;ADAGKLFAGNANAAV-LFAGNANAA;KLFAGNANAAVGAAA-
FAGNANAAV;KSDKIAAAIVLRGVA-IAAAIVLRG;SDKIAAAIVLRGVAK-
IAAAIVLRG;KKSDKIAAAIVLRGV-IAAAIVLRG;DKIAAAIVLRGVAKD-
IAAAIVLRG;MKKSDKIAAAIVLRG-DKIAAAIVL;IDVFNAFSGLVADTF-
VFNAFSGLV;DIAKAAGAVTAVSGE-AKAAGAVTA;FIDVFNAFSGLVADT-
VFNAFSGLV;NGFIDVFNAFSGLVA-VFNAFSGLV;GFIDVFNAFSGLVAD-
VFNAFSGLV;LFAGNANAAVGAAAD-FAGNANAAV;ISSAIFLTALLVFIN-
FLTALLVFI;SSAIFLTALLVFINC-FLTALLVFI;KISSAIFLTALLVFI-
AIFLTALLV;SAIFLTALLVFINCK-FLTALLVFI;AIFLTALLVFINCKN-
FLTALLVFI;IAKAAGAVTAVSGEQ-IAKAAGAVT;VGAAADIAKAAGAVT-
DIAKAAGAV;DVFNAFSGLVADTFF-FNAFSGLVA;GNGFIDVFNAFSGLV-
FIDVFNAFS;FAGNANAAVGAAADI-FAGNANAAV;KIAAAIVLRGVAKDG-
IAAAIVLRG;IAAAIVLRGVAKDGK-IAAAIVLRG;VFNAFSGLVADTFFK-
VFNAFSGLV;AKAAGAVTAVSGEQI-AKAAGAVTA;NADAGKLFAGNANAA-
AGKLFAGNA;TYFESISSTLKATKG-FESISSTLK;KTYFESISSTLKATK-
FESISSTLK;VKTYFESISSTLKAT-FESISSTLK;DVKTYFESISSTLKA-
FESISSTLK;SDVKTYFESISSTLK-YFESISSTL;KGIVDAAGKALGEKG-
IVDAAGKAL;KGIKGIVDAAGKALG-IVDAAGKAL;IFLTALLVFINCKNN-
FLTALLVFI;IKGIVDAAGKALGEK-IVDAAGKAL;GIKGIVDAAGKALGE-
IVDAAGKAL;AKGIKGIVDAAGKAL-IKGIVDAAG;FLTALLVFINCKNNA-
FLTALLVFI;MKKISSAIFLTALLV-MKKISSAIF;FNAFSGLVADTFFKS-
FNAFSGLVA;GKIGDSAANHGAKAD-IGDSAANHG;DGKIGDSAANHGAKA-
IGDSAANHG;GDGKIGDSAANHGAK-IGDSAANHG;KAAGAVTAVSGEQIL-
VTAVSGEQI;GGDGKIGDSAANHGA-IGDSAANHG;GNANAAVGAAADIAK-
AVGAAADIA;YFESISSTLKATKGK-FESISSTLK;AGAVTAVSGEQILKA-
VTAVSGEQI;ANAAVGAAADIAKAA-AVGAAADIA;AAGAVTAVSGEQILK-

VTAVSGEQI;TGGDGKIGDSAANHG-GKIGDSAAN;EEAKNPIAAAIGTDD-
AKNPIAAAI;FESISSTLKATKGKL-FESISSTLK;NANAAVGAAADIAKA-
AVGAAADIA;GIVDAAGKALGEKGA-IVDAAGKAL;GAVTAVSGEQILKAI-
VTAVSGEQI;NAAVGAAADIAKAAG-AVGAAADIA;EQILKAIVEAAGDPA-
LKAIVEAAG;VSGEQILKAIVEAAG-ILKAIVEAA;KKISSAIFLTALLVF-
ISSAIFLTA;IVDAAGKALGEKGAL-IVDAAGKAL;SGEQILKAIVEAAGD-
LKAIVEAAG;IAKGIKGIVDAAGKA-IKGIVDAAG;GEQILKAIVEAAGDP-
LKAIVEAAG;AAAIVLRGVAKDGKF-VLRGVAKDG;LKAIVEAAGDPANQA-
LKAIVEAAG;KGIAKGIKGIVDAAG-IAKGIKGIV;GIAKGIKGIVDAAGK-
IKGIVDAAG;EAKNPIAAAIGTDDD-IAAAIGTDD;AEEAKNPIAAAIGTD-
AKNPIAAAI;KAEEAKNPIAAAIGT-AKNPIAAAI;AAIVLRGVAKDGKFA-
VLRGVAKDG;AGNANAAVGAAADIA-ANAAVGAAA;KAIVEAAGDPANQAG-AAGDPANQA
DRB1_0301
DRB1_0401 DSVKTFYESIINLGN-FYESIINLG;SVKTFYESIINLGNG-
FYESIINLG;KTFYESIINLGNGFI-FYESIINLG;VKTFYESIINLGNGF-
FYESIINLG;KDSVKTFYESIINLG-KTFYESIIN;TFYESIINLGNGFID-
FYESIINLG;FYESIINLGNGFIDV-FYESIINLG;KTYFESISSTLKATK-
FESISSTLK;DVKTYFESISSTLKA-FESISSTLK;VKTYFESISSTLKAT-
FESISSTLK;SDVKTYFESISSTLK-YFESISSTL;TYFESISSTLKATKG-FESISSTLK
DRB1_0404
NGFIDVFNAFSGLVA-VFNAFSGLV;GNGFIDVFNAFSGLV-FIDVFNAFS;GFIDVFNAFSGLVAD-
VFNAFSGLV;FIDVFNAFSGLVADT-VFNAFSGLV;IDVFNAFSGLVADTF-
VFNAFSGLV;DVFNAFSGLVADTFF-VFNAFSGLV;VFNAFSGLVADTFFK-VFNAFSGLV
DRB1_0405
LVADTFFKSDPKKSD-DTFFKSDPK;VADTFFKSDPKKSDV-FKSDPKKSD;DSVKTFYESIINLGN-
VKTFYESII;ADTFFKSDPKKSDVK-FKSDPKKSD;DTFFKSDPKKSDVKT-
FKSDPKKSD;NGFIDVFNAFSGLVA-FIDVFNAFS;SVKTFYESIINLGNG-
YESIINLGN;VKTFYESIINLGNGF-YESIINLGN;TFFKSDPKKSDVKTY-
FKSDPKKSD;KTFYESIINLGNGFI-YESIINLGN;TFYESIINLGNGFID-
YESIINLGN;GFIDVFNAFSGLVAD-FNAFSGLVA;FIDVFNAFSGLVADT-
FNAFSGLVA;IDVFNAFSGLVADTF-FNAFSGLVA;FKSDPKKSDVKTYFE-FKSDPKKSD
DRB1_0701
KTYFESISSTLKATK-YFESISSTL;VKTYFESISSTLKAT-YFESISSTL;DVKTYFESISSTLKA-
YFESISSTL;KSDVKTYFESISSTL-KSDVKTYFE;SDVKTYFESISSTLK-
YFESISSTL;IDVFNAFSGLVADTF-VFNAFSGLV;TYFESISSTLKATKG-
YFESISSTL;LVFINCKNNAVGKGN-FINCKNNAV;TALLVFINCKNNAVG-
FINCKNNAV;NGFIDVFNAFSGLVA-VFNAFSGLV;ALLVFINCKNNAVGK-
FINCKNNAV;LLVFINCKNNAVGKG-FINCKNNAV;GFIDVFNAFSGLVAD-VFNAFSGLV
DRB1_0802
LVADTFFKSDPKKSD-FFKSDPKKS;VADTFFKSDPKKSDV-FFKSDPKKS;DTFFKSDPKKSDVKT-
FFKSDPKKS;ADTFFKSDPKKSDVK-FFKSDPKKS;GLVADTFFKSDPKKS-DTFFKSDPKDRB1_0901
KTYFESISSTLKATK-YFESISSTL;AAADIAKAAGAVTAV-IAKAAGAVT;GAAADIAKAAGAVTA-
IAKAAGAVT;VKTYFESISSTLKAT-YFESISSTL;AADIAKAAGAVTAVS-
IAKAAGAVT;DVKTYFESISSTLKA-YFESISSTL;KTFYESIINLGNGFI-
FYESIINLGDRB1_1101DRB1_1302
TFYESIINLGNGFID-IINLGNGFI;FYESIINLGNGFIDV-IINLGNGFI;LLVFINCKNNAVGKG-
VFINCKNNA;YESIINLGNGFIDVF-IINLGNGFI;ESIINLGNGFIDVFN-
IINLGNGFI;KTFYESIINLGNGFI-FYESIINLG;LVFINCKNNAVGKGN-
CKNNAVGKG;VFINCKNNAVGKGND-CKNNAVGKG;ALLVFINCKNNAVGK-
VFINCKNNA;SIINLGNGFIDVFNA-IINLGNGFI;TALLVFINCKNNAVG-
VFINCKNNA;LTALLVFINCKNNAV-VFINCKNNA
DRB1_1501
IAAAIVLRGVAKDGK-AIVLRGVAK;AAAIVLRGVAKDGKF-LRGVAKDGK;GFIDVFNAFSGLVAD-
VFNAFSGLV;NGFIDVFNAFSGLVA-VFNAFSGLV;AIVLRGVAKDGKFAV-
LRGVAKDGK;AAIVLRGVAKDGKFA-LRGVAKDGK;IDVFNAFSGLVADTF-
VFNAFSGLV;FIDVFNAFSGLVADT-VFNAFSGLV

DRB3_0101
DRB4_0101
DRB5_0101

<ABX71745 CRASP-2;Protein;Borrelia burgdorferi>

Allele 8-mer
A0101 YSEYTGAY
A0201 YMLISISL;KLIDDFAI;FLSIYMLI;MLISISLL;FLGAAVEL;SIYMLISI
A0202
FLSIYMLI;MLISISLL;FLGAAVEL;KLIDDFAI;YMLISISL;KLRKSVAL;FVEENDLI;ALAYIESF
;SIYMLISI;FAIELDQA;KAIKQTLL;LIALKCIV;KVNQAISI
A0203
FLSIYMLI;MLISISLL;FLGAAVEL;YMLISISL;KLIDDFAI;SIYMLISI;KLRKSVAL;LIALKCIV
;KVNQAISI;ALKCIVKT;MKKSFLSI
A0204 FLGAAVEL;KLIDDFAI;YMLISISL;FLSIYMLI;MLISISLL
A0206
KLIDDFAI;YMLISISL;FLGAAVEL;MLISISLL;FAIELDQA;FLSIYMLI;KVNQAISI;FVEENDLI
;AAVELEGA;KAIKQTLL;KSVALAYI;SIYMLISI;KEADFLGA;YSIKLDAI;YIESFDVI
A0211
KLIDDFAI;YMLISISL;FLGAAVEL;MLISISLL;FLSIYMLI;SIYMLISI;KLRKSVAL;ELEGAYKA
;LIALKCIV;KLDAIYSE;AIELDQAV;KFVDSKFV;PMFLSKLI;KVNQAISI;SFLSIYML;DLIALKC
I;YIESFDVI;DVISSKFV
A0212
YMLISISL;FLGAAVEL;KLIDDFAI;FLSIYMLI;MLISISLL;SIYMLISI;KLRKSVAL;AIELDQAV
;LIALKCIV
A0216
FLGAAVEL;MLISISLL;YMLISISL;FLSIYMLI;KLIDDFAI;LIALKCIV;KLRKSVAL;SIYMLISI
;ELEGAYKA;AIELDQAV;DVISSKFV;KFVDSKFV;DVSNARHV
A0219 FLGAAVEL;YMLISISL;MLISISLL;FLSIYMLI;KLIDDFAI
A0301 KIFVEKAK;IMTYIMTY;KAKYYSIK;HVADSYEK;IALKCIVK;RSRYNNFY;ASKKFVNK;
A1101
HVADSYEK;ASKKFVNK;SSKFVDSK;SILKKDNK;QAISILKK;GTSSDKSK;KIFVEKAK;NQAISILK
;IALKCIVK;SRYNNFYK;KAKYYSIK;RYNNFYKK;DSYEKLRK
A2301 FYKKEADF;RYNNFYKK;SFLSIYML;KFVEASKK
A2402 SFLSIYML;FYKKEADF;AYIESFDV
A2403 FYKKEADF;SFLSIYML;AYIESFDV;FVNKAKEF
A2601 EINSRSRY;
A2602 EINSRSRY;SIKLDAIY;FVEKAKYY;AVELEGAY;DVISSKFV;YSEYTGAY;NIDELKIF
A2902 IMTYIMTY;AYNDIMTY;IFVEKAKY;YSEYTGAY;FVEKAKYY
A3001
KAKYYSIK;RYNNFYKK;RSRYNNFY;ASKKFVNK;KIFVEKAK;SSKFVDSK;KFVEASKK;KKFVNKAK
;KLRKSVAL;KSKVNQAI
A3002 AYNDIMTY;IMTYIMTY;RSRYNNFY
A3101 RYNNFYKK;KAKYYSIK;ASKKFVNK;MTYIMTYS;REINSRSR
A3301 DVSRLNQR
A6801
HVADSYEK;DVSRLNQR;QAISILKK;ELKIFVEK;SSKFVDSK;DSYEKLRK;MTYIMTYS;LLSCDVSR
;EGAYKAIK;NQAISILK;EINSRSRY;SRYNNFYK
A6802
DVISSKFV;MLISISLL;EKAKYYSI;MTYIMTYS;ESFDVISS;TSSDKSKV;FLSIYMLI;YSIKLDAI
A6901 DVISSKFV;YMLISISL;EADFLGAA
B0702 KPMFLSKL;KLRKSVAL
B0801 KLRKSVAL
B0802
B1501 YSEYTGAY;IMTYIMTY;RSRYNNFY;YMLISISL;ALAYIESF

B1801 EEYKPMFL;EENDLIAL
B2705 SRYNNFYK
B3501 YSEYTGAY;FVNKAKEF;AVELEGAY;FVEKAKYY;
B3901 YKAIKQTL;YMLISISL
B4001 EEYKPMFL;EENDLIAL
B4002 EEYKPMFL;EENDLIAL
B4402
B4403 EENDLIAL
B4501 EENDLIAL
B5101
B5301
B5401 FAIELDQA
B5701
B5801 KSFLSIYM;KSVALAYI;KAIKQTLL

Allele 9-mer

A0101 KLDAIYSEY;YSIKLDAIY
A0201
YMLISISLL;LIDDFAIEL;YIMTYSEGT;LLSCDVSRL;FVDSKFVEA;NIDELKIFV;FVNKAKEFV;F
LSIYMLIS;FAIELDQAV;MLISISLLS;AIYSEYTGA
A0202
LLSCDVSRL;YMLISISLL;FVNKAKEFV;HVADSYEKL;FAIELDQAV;MLISISLLS;AIYSEYTGA;F
LSIYMLIS;FLSKLIDDF;FVDSKFVEA;IMTYIMTYS;LIDDFAIEL;YIMTYSEGT;KVNQAISIL;AY
NDIMTYI;FLGAAVELE;KLRKSVALA;KSFLSIYML;YKAIKQTLL
A0203
LLSCDVSRL;KLRKSVALA;ALKCIVKTI;AIYSEYTGA;YMLISISLL;FVNKAKEFV;KVNQAISIL;S
ISLLSCDV;FLSIYMLIS;YIMTYSEGT;AYNDIMTYI;FAIELDQAV;IMTYIMTYS;MLISISLLS;FV
DSKFVEA;IVKTIGDMV;ILKKDNKIV
A0204 FAIELDQAV;LIDDFAIEL;YMLISISLL
A0206
FAIELDQAV;FVDSKFVEA;FVNKAKEFV;YIMTYSEGT;LIDDFAIEL;YMLISISLL;AIYSEYTGA;N
IDELKIFV;KLIDDFAIE;KEADFLGAA;LSIYMLISI;KIVNKFKEL
A0211
LIDDFAIEL;NIDELKIFV;YMLISISLL;DLIALKCIV;FVNKAKEFV;FAIELDQAV;LLSCDVSRL;K
LDAIYSEY;SISLLSCDV;FVDSKFVEA;ILKKDNKIV;HVADSYEKL;FVEASKKFV;MLISISLLS;KL
RKSVALA;ELEGAYKAI;FLSIYMLIS;ALKCIVKTI;EADFLGAAV;SFLSIYMLI
A0212
LIDDFAIEL;NIDELKIFV;FAIELDQAV;YMLISISLL;FVNKAKEFV;DLIALKCIV;SISLLSCDV;Y
IMTYSEGT;AIYSEYTGA;FVDSKFVEA;ILKKDNKIV;FLSIYMLIS;LLSCDVSRL;LAYIESFDV;
A0216
NIDELKIFV;LIDDFAIEL;FVNKAKEFV;DLIALKCIV;YMLISISLL;LLSCDVSRL;FVEASKKFV;I
LKKDNKIV;FAIELDQAV;SISLLSCDV;HVADSYEKL;KLRKSVALA;FVDSKFVEA
A0219 LIDDFAIEL;YMLISISLL;NIDELKIFV;FVNKAKEFV;LLSCDVSRL;HVADSYEKL
A0301 RSRYNNFYK;ESFDVISSK;LIALKCIVK;NQAISILKK;KLDAIYSEY
A1101
ESFDVISSK;RSRYNNFYK;ISSKFVDSK;AVELEGAYK;ISILKKDNK;VNQAISILK;NQAISILKK;L
IALKCIVK;GAYNDIMTY;SRYNNFYKK;EASKKFVNK;SLLSCDVSR
A2301
IYMLISISL;KFVEASKKF;FYKKEADFL;EYKPMFLSK;NFYKKEADF;SFDVISSKF;AYIESFDVI;E
YTGAYNDI;KFVNKAKEF;AYNDIMTYI;AYKAIKQTL;SFLSIYMLI;DFLGAAVEL;KSFLSIYML;FL
SKLIDDF
A2402
IYMLISISL;SFLSIYMLI;AYIESFDVI;YYSIKLDAI;EYTGAYNDI;AYNDIMTYI;SFDVISSKF;F
YKKEADFL;AYKAIKQTL;

A2403
FYKKEADFL;YYSIKLDAI;KFVNKAKEF;AYIESFDVI;AYKAIKQTL;IYMLISISL;KFVEASKKF;A
YNDIMTYI;SFLSIYMLI;NFYKKEADF;SFDVISSKF;EYTGAYNDI
A2601 YSIKLDAIY;DIMTYIMTY;ELEKIIEEY
A2602
DIMTYIMTY;KIIEEYKPM;YSIKLDAIY;YTGAYNDIM;ELEKIIEEY;KIFVEKAKY;HVADSYEKL;K
VNQAISIL;KIVNKFKEL
A2902 YSIKLDAIY;IYSEYTGAY;KIFVEKAKY
A3001 RSRYNNFYK;KLRKSVALA;EYKPMFLSK
A3002 KIFVEKAKY;AYNDIMTYI
A3101 RSRYNNFYK;SLLSCDVSR;MTYIMTYSE;KSFLSIYML
A3301 DSKFVEASK;ESFDVISSK;EYKPMFLSK
A6801
ESFDVISSK;DSKFVEASK;MTYIMTYSE;EASKKFVNK;ISSKFVDSK;TIGDMVNDR;DIMTYIMTY;R
SRYNNFYK;EENDLIALK;YSEGTSSDK;SLLSCDVSR;ISILKKDNK;EKAKYYSIK;EYKPMFLSK
A6802
HVADSYEKL;FAIELDQAV;FVNKAKEFV;EADFLGAAV;LSIYMLISI;DVSNARHVA;YIMTYSEGT
A6901
EADFLGAAV;NIDELKIFV;FAIELDQAV;FVNKAKEFV;HVADSYEKL;LIDDFAIEL;FVDSKFVEA
B0702 KPMFLSKLI;KVNQAISIL
B0801 YEKLRKSVA
B0802
B1501 YSIKLDAIY;AAVELEGAY;YMLISISLL;GAYNDIMTY
B1801 VEENDLIAL;REINSRSRY;VELEGAYKA
B2705 SRYNNFYKK
B3501
AAVELEGAY;FAIELDQAV;YSIKLDAIY;DIMTYIMTY;IYSEYTGAY;NARHVADSY;GAYNDIMTY;Y
TGAYNDIM;VALAYIESF
B3901 YNDIMTYIM
B4001 KEFVEENDL;VEENDLIAL;IEEYKPMFL
B4002 KEFVEENDL
B4402
B4403
B4501 REINSRSRY
B5101 KPMFLSKLI
B5301
B5401 FAIELDQAV
B5701
B5801 VALAYIESF;YSIKLDAIY

Allele 10-mer
A0101
A0201
FLSIYMLISI;KLIDDFAIEL;FLSKLIDDFA;ALAYIESFDV;SLLSCDVSRL;KLDAIYSEYT;SIYML
ISISL;YMLISISLLS;RLNQRNIDEL;MLISISLLSC;GAYNDIMTYI
A0202
FLSIYMLISI;SLLSCDVSRL;FLSKLIDDFA;KLIDDFAIEL;KLDAIYSEYT;GAYNDIMTYI;SIYML
ISISL;ALAYIESFDV;MLISISLLSC;RLNQRNIDEL;KSFLSIYMLI;FVEENDLIAL;IYMLISISLL
;FLGAAVELEG;YMLISISLLS;KYYSIKLDAI
A0203
FLSIYMLISI;KLIDDFAIEL;FLSKLIDDFA;ALAYIESFDV;RLNQRNIDEL;SIYMLISISL;GAYND
IMTYI;MLISISLLSC;SLLSCDVSRL;CIVKTIGDMV;
A0204 KLIDDFAIEL;SLLSCDVSRL;ALAYIESFDV;RLNQRNIDEL;FLSIYMLISI
A0206
KLIDDFAIEL;FLSIYMLISI;FVEENDLIAL;ALAYIESFDV;MLISISLLSC;FLSKLIDDFA;GAYND
IMTYI;FVEKAKYYSI;KEADFLGAAV;SIYMLISISL;KLDAIYSEYT;CIVKTIGDMV;RLNQRNIDEL

A0211
KLIDDFAIEL;FLSIYMLISI;SLLSCDVSRL;SIYMLISISL;ALAYIESFDV;ELDQAVDNDV;RLNQR
NIDEL;KLDAIYSEYT;FLSKLIDDFA;MLISISLLSC;FVEENDLIAL;SILKKDNKIV;IIEEYKPMFL
;YMLISISLLS;SFDVISSKFV;KEADFLGAAV;GAYNDIMTYI
A0212
KLIDDFAIEL;FLSIYMLISI;ALAYIESFDV;ELDQAVDNDV;SIYMLISISL;FLSKLIDDFA;RLNQR
NIDEL;FVEENDLIAL;SLLSCDVSRL;MLISISLLSC;SILKKDNKIV;KLDAIYSEYT;IIEEYKPMFL
A0216
KLIDDFAIEL;SLLSCDVSRL;FLSIYMLISI;ALAYIESFDV;RLNQRNIDEL;SIYMLISISL;ELDQA
VDNDV;FLSKLIDDFA;IIEEYKPMFL;KLDAIYSEYT;SILKKDNKIV;CIVKTIGDMV;FVEKAKYYSI
;GAYKAIKQTL;MLISISLLSC;FVEENDLIAL;
A0219
ELDQAVDNDV;KLIDDFAIEL;SLLSCDVSRL;FLSIYMLISI;RLNQRNIDEL;FLSKLIDDFA;ALAYI
ESFDV
A0301
KVNQAISILK;RSRYNNFYKK;IVNKFKELEK;KLRKSVALAY;DLIALKCIVK;AIYSEYTGAY;AAVEL
EGAYK;VISSKFVDSK;AISILKKDNK
A1101
KVNQAISILK;IVNKFKELEK;VISSKFVDSK;RSRYNNFYKK;AAVELEGAYK;MVNDREINSR;AISIL
KKDNK;AIYSEYTGAY;ASKKFVNKAK;KTIGDMVNDR;VADSYEKLRK;VNQAISILKK;AVDNDVSNAR
A2301
IYMLISISLL;MFLSKLIDDF;TYSEGTSSDK;EYKPMFLSKL;KYYSIKLDAI;AYKAIKQTLL;ESFDV
ISSKF;ISSKFVDSKF;AYNDIMTYIM;SVALAYIESF
A2402 IYMLISISLL;KYYSIKLDAI;EYKPMFLSKL;AYKAIKQTLL
A2403
MFLSKLIDDF;KYYSIKLDAI;IYMLISISLL;AYKAIKQTLL;EYKPMFLSKL;AYNDIMTYIM;YYSIK
LDAIY
A2601 ESFDVISSKF;
A2602 KIIEEYKPMF;AIYSEYTGAY;KIFVEKAKYY;SVALAYIESF;FVEENDLIAL
A2902 YYSIKLDAIY;AIYSEYTGAY;KIFVEKAKYY
A3001
RSRYNNFYKK;KVNQAISILK;ASKKFVNKAK;KLRKSVALAY;IVNKFKELEK;ARHVADSYEK;KDNKI
VNKFK;KSFLSIYMLI
A3002 KIFVEKAKYY;NSRSRYNNFY
A3101
KTIGDMVNDR;RSRYNNFYKK;ISLLSCDVSR;MVNDREINSR;KVNQAISILK;ASKKFVNKAK;AVDND
VSNAR
A3301
A6801
HVADSYEKLR;MVNDREINSR;DSKFVEASKK;ELEKIIEEYK;KTIGDMVNDR;IVNKFKELEK;KVNQA
ISILK;ISLLSCDVSR;DLIALKCIVK;ELKIFVEKAK;EEYKPMFLSK;TYSEGTSSDK;ESFDVISSKF
;ELEGAYKAIK
A6802 FVEKAKYYSI;SIYMLISISL;EASKKFVNKA;DIMTYIMTYS
A6901
B0702
B0801 YEKLRKSVAL
B0802
B1501 KLRKSVALAY;SVALAYIESF;AIYSEYTGAY;KIIEEYKPMF;KIFVEKAKYY
B1801 VELEGAYKAI;KELEKIIEEY
B2705
B3501 FVEENDLIAL;TGAYNDIMTY;GAAVELEGAY;YYSIKLDAIY;SVALAYIESF
B3901 FVEENDLIAL
B4001 SEYTGAYNDI;KEFVEENDLI;VELEGAYKAI;YEKLRKSVAL
B4002 KEFVEENDLI
B4402 KELEKIIEEY
B4403

B4501 EENDLIALKC
B5101 LAYIESFDVI
B5301
B5401
B5701
B5801 ISSKFVDSKF;KIIEEYKPMF;

Allele 11-mer
A0101 YTGAYNDIMTY;YNDIMTYIMTY;VSNARHVADSY
A0201
FLSKLIDDFAI;FLGAAVELEGA;KLRKSVALAYI;ALAYIESFDVI;KIIEEYKPMFL;VALAYIESFDV
;SIYMLISISLL;YMLISISLLSC;FLSIYMLISIS
A0202
FLSKLIDDFAI;FLGAAVELEGA;ALAYIESFDVI;FLSIYMLISIS;SIYMLISISLL;KLRKSVALAYI
;KIIEEYKPMFL;GAYKAIKQTLL
A0203
FLGAAVELEGA;KLRKSVALAYI;FLSKLIDDFAI;SIYMLISISLL;ALAYIESFDVI;KIIEEYKPMFL
;LISISLLSCDV;FLSIYMLISIS;LIALKCIVKTI;MTYIMTYSEGT;YMLISISLLSC
A0204 FLGAAVELEGA;KIIEEYKPMFL;VALAYIESFDV
A0206
FLSKLIDDFAI;FLGAAVELEGA;KIIEEYKPMFL;ALAYIESFDVI;VALAYIESFDV;YIMTYSEGTSS
;LSIYMLISISL;YMLISISLLSC;LISISLLSCDV
A0211
FLSKLIDDFAI;SIYMLISISLL;FLGAAVELEGA;YMLISISLLSC;KLRKSVALAYI;KIIEEYKPMFL
;ALAYIESFDVI;ESFDVISSKFV;LIDDFAIELDQ;LISISLLSCDV;VALAYIESFDV;KLDAIYSEYT
G;TIGDMVNDREI
A0212
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;LIDDFAIELDQ;KIIEEYKPMFL
A0216
FLSKLIDDFAI;SIYMLISISLL;KLRKSVALAYI;FLGAAVELEGA;ALAYIESFDVI;KIIEEYKPMFL
;ESFDVISSKFV;LISISLLSCDV
A0219 FLGAAVELEGA;FLSKLIDDFAI;VALAYIESFDV;YMLISISLLSC;
A0301
MTYSEGTSSDK;KVNQAISILKK;RLNQRNIDELK;ILKKDNKIVNK;HVADSYEKLRK;KIVNKFKELEK
;NSRSRYNNFYK;FVDSKFVEASK
A1101
MTYSEGTSSDK;KVNQAISILKK;HVADSYEKLRK;KIVNKFKELEK;RLNQRNIDELK;FVEASKKFVNK
;GAAVELEGAYK;SISLLSCDVSR;DVISSKFVDSK;NSRSRYNNFYK;FVDSKFVEASK;YIESFDVISS
K;QAISILKKDNK;NIDELKIFVEK;FVEENDLIALK;VSNARHVADSY
A2301 EYKPMFLSKLI;SYEKLRKSVAL;PMFLSKLIDDF
A2402 EYKPMFLSKLI;SFLSIYMLISI;IYMLISISLLS
A2403 SYEKLRKSVAL;SFLSIYMLISI
A2601 ELKIFVEKAKY;YTGAYNDIMTY;DAIYSEYTGAY;ESFDVISSKFV;
A2602
EINSRSRYNNF;YTGAYNDIMTY;KIIEEYKPMFL;SIKLDAIYSEY;DAIYSEYTGAY;ELKIFVEKAKY
;EFVEENDLIAL;SIYMLISISLL
A2902 KYYSIKLDAIY;YTGAYNDIMTY
A3001
KVNQAISILKK;NSRSRYNNFYK;KLRKSVALAYI;RLNQRNIDELK;NARHVADSYEK;MTYSEGTSSDK
;KIVNKFKELEK
A3002 KYYSIKLDAIY
A3101
NSRSRYNNFYK;LSCDVSRLNQR;KVNQAISILKK;RLNQRNIDELK;SISLLSCDVSR;KYYSIKLDAIY
A3301 DMVNDREINSR;NSRSRYNNFYK;LSCDVSRLNQR

A6801
MTYSEGTSSDK;DVISSKFVDSK;HVADSYEKLRK;LSCDVSRLNQR;SISLLSCDVSR;QAVDNDVSNAR
;YIESFDVISSK;NSRSRYNNFYK;FVEENDLIALK;DMVNDREINSR;NARHVADSYEK;EASKKFVNKA
K;QAISILKKDNK;FVEKAKYYSIK;FVEASKKFVNK;DAIYSEYTGAY;FVDSKFVEASK;MTYIMTYSE
GT;NIDELKIFVEK;YTGAYNDIMTY
A6802
ESFDVISSKFV;TGAYNDIMTYI;MTYIMTYSEGT;LSIYMLISISL;EGAYKAIKQTL;FLSKLIDDFAI
A6901 ESFDVISSKFV;EADFLGAAVEL
B0702
B0801
B0802
B1501
VSNARHVADSY;KSVALAYIESF;YTGAYNDIMTY;NQRNIDELKIF;SIKLDAIYSEY;LGAAVELEGAY
B1801 EEYKPMFLSKL;IESFDVISSKF;SEYTGAYNDIM
B2705
B3501
DAIYSEYTGAY;YTGAYNDIMTY;EADFLGAAVEL;EFVEENDLIAL;YNDIMTYIMTY;GAYNDIMTYIM
B3901
B4001 SEYTGAYNDIM;EEYKPMFLSKL;VEKAKYYSIKL
B4002 KEFVEENDLIA;EENDLIALKCI
B4402
B4403 EENDLIALKCI;SEYTGAYNDIM;KEFVEENDLIA
B4501 EENDLIALKCI
B5101
B5301
B5401
B5701
B5801 KSVALAYIESF;VSNARHVADSY

Allele 15-mer plus 9-mer core
DRB1_0101
SFLSIYMLISISLLS-IYMLISISL;FLSIYMLISISLLSC-IYMLISISL;KSFLSIYMLISISLL-
IYMLISISL;LSIYMLISISLLSCD-IYMLISISL;KKSFLSIYMLISISL-
FLSIYMLIS;EEYKPMFLSKLIDDF-YKPMFLSKL;EKIIEEYKPMFLSKL-
IEEYKPMFL;IEEYKPMFLSKLIDD-YKPMFLSKL;IIEEYKPMFLSKLID-
YKPMFLSKL;KIIEEYKPMFLSKLI-YKPMFLSKL;YNDIMTYIMTYSEGT-
IMTYIMTYS;NDIMTYIMTYSEGTS-YIMTYSEGT;IMTYIMTYSEGTSSD-
YIMTYSEGT;SIYMLISISLLSCDV-IYMLISISL;DIMTYIMTYSEGTSS-
YIMTYSEGT;MTYIMTYSEGTSSDK-YIMTYSEGT;IYMLISISLLSCDVS-
IYMLISISL;EYKPMFLSKLIDDFA-YKPMFLSKL;YKPMFLSKLIDDFAI-
YKPMFLSKL;GAYNDIMTYIMTYSE-YNDIMTYIM;TGAYNDIMTYIMTYS-
YNDIMTYIM;TYIMTYSEGTSSDKS-YIMTYSEGT;YIMTYSEGTSSDKSK-
YIMTYSEGT;SEYTGAYNDIMTYIM-YTGAYNDIM;EYTGAYNDIMTYIMT-
YNDIMTYIM;YTGAYNDIMTYIMTY-YNDIMTYIM;KYYSIKLDAIYSEYT-
YSIKLDAIY;IESFDVISSKFVDSK-FDVISSKFV;ESFDVISSKFVDSKF-
FDVISSKFV;YIESFDVISSKFVDS-FDVISSKFV;YYSIKLDAIYSEYTG-
LDAIYSEYT;IKLDAIYSEYTGAYN-LDAIYSEYT;SIKLDAIYSEYTGAY-
LDAIYSEYT;VELEGAYKAIKQTLL-VELEGAYKA;AYNDIMTYIMTYSEG-
YNDIMTYIM;YSIKLDAIYSEYTGA-LDAIYSEYT;LAYIESFDVISSKFV-
YIESFDVIS;AYIESFDVISSKFVD-FDVISSKFV;DSYEKLRKSVALAYI-
LRKSVALAY;YEKLRKSVALAYIES-LRKSVALAY;SYEKLRKSVALAYIE-
LRKSVALAY;EKLRKSVALAYIESF-LRKSVALAY;DKSKVNQAISILKKD-
VNQAISILK;SDKSKVNQAISILKK-VNQAISILK;SSDKSKVNQAISILK-
KVNQAISIL;KSKVNQAISILKKDN-VNQAISILK;ADSYEKLRKSVALAY-
EKLRKSVAL;YMLISISLLSCDVSR-MLISISLLS;KEADFLGAAVELEGA-
FLGAAVELE;EADFLGAAVELEGAY-FLGAAVELE;SKVNQAISILKKDNK-

VNQAISILK;ADFLGAAVELEGAYK-FLGAAVELE;KKEADFLGAAVELEG-
FLGAAVELE;DFLGAAVELEGAYKA-FLGAAVELE;YKKEADFLGAAVELE-
YKKEADFLG;FLGAAVELEGAYKAI-VELEGAYKA;MLISISLLSCDVSRL-
MLISISLLS;VEENDLIALKCIVKT-ENDLIALKC;NDLIALKCIVKTIGD-
IALKCIVKT;ENDLIALKCIVKTIG-IALKCIVKT;LIDDFAIELDQAVDN-
FAIELDQAV;SKLIDDFAIELDQAV-LIDDFAIEL;DLIALKCIVKTIGDM-
IALKCIVKT;IDDFAIELDQAVDND-FAIELDQAV;SFDVISSKFVDSKFV-
FDVISSKFV;FDVISSKFVDSKFVE-FDVISSKFV;EENDLIALKCIVKTI-
IALKCIVKT;DDFAIELDQAVDNDV-FAIELDQAV;IALKCIVKTIGDMVN-
IALKCIVKT;KLIDDFAIELDQAVD-FAIELDQAV;MKKSFLSIYMLISIS-
FLSIYMLIS;LRKSVALAYIESFDV-LRKSVALAY;KLDAIYSEYTGAYND-
LDAIYSEYT;LDAIYSEYTGAYNDI-LDAIYSEYT;KLRKSVALAYIESFD-LRKSVALAY
DRB1_0301
DRB1_0401 SFLSIYMLISISLLS-IYMLISISL;FLSIYMLISISLLSC-
MLISISLLS;LSIYMLISISLLSCD-MLISISLLS;IYMLISISLLSCDVS-
MLISISLLS;SIYMLISISLLSCDV-MLISISLLS;YMLISISLLSCDVSR-
MLISISLLS;MLISISLLSCDVSRL-MLISISLLS;KKSFLSIYMLISISL-
FLSIYMLIS;KSFLSIYMLISISLL-FLSIYMLIS;IELDQAVDNDVSNAR-
IELDQAVDN;ELDQAVDNDVSNARH-VDNDVSNAR;QAVDNDVSNARHVAD-
VDNDVSNAR;LDQAVDNDVSNARHV-VDNDVSNAR;MKKSFLSIYMLISIS-
FLSIYMLIS;DQAVDNDVSNARHVA-VDNDVSNAR;DIMTYIMTYSEGTSS-
YIMTYSEGT;YNDIMTYIMTYSEGT-DIMTYIMTY;DAIYSEYTGAYNDIM-
IYSEYTGAY;IKLDAIYSEYTGAYN-IYSEYTGAY;MTYIMTYSEGTSSDK-
YIMTYSEGT;IMTYIMTYSEGTSSD-YIMTYSEGT;SIKLDAIYSEYTGAY-
LDAIYSEYT;KLDAIYSEYTGAYND-IYSEYTGAY;NDIMTYIMTYSEGTS-
YIMTYSEGT;LDAIYSEYTGAYNDI-IYSEYTGAY;ADSYEKLRKSVALAY-
YEKLRKSVA;DSYEKLRKSVALAYI-LRKSVALAY
DRB1_0404 FLSIYMLISISLLSC-MLISISLLS;LSIYMLISISLLSCD-
MLISISLLS;SIYMLISISLLSCDV-MLISISLLS;SFLSIYMLISISLLS-
YMLISISLL;NDIMTYIMTYSEGTS-IMTYIMTYS;IYMLISISLLSCDVS-
MLISISLLS;DIMTYIMTYSEGTSS-IMTYSEGTS;YNDIMTYIMTYSEGT-
IMTYIMTYS;IMTYIMTYSEGTSSD-IMTYSEGTS;
DRB1_0405 FLSIYMLISISLLSC-FLSIYMLIS
DRB1_0701 DSYEKLRKSVALAYI-LRKSVALAY;ADSYEKLRKSVALAY-
YEKLRKSVA;SYEKLRKSVALAYIE-LRKSVALAY;YEKLRKSVALAYIES-
LRKSVALAY;EKLRKSVALAYIESF-LRKSVALAY;LAYIESFDVISSKFV-
SFDVISSKF;AYIESFDVISSKFVD-FDVISSKFV;YIESFDVISSKFVDS-
FDVISSKFV;IESFDVISSKFVDSK-FDVISSKFV;ESFDVISSKFVDSKF-FDVISSKFV
DRB1_0802
DRB1_0901 SFLSIYMLISISLLS-YMLISISLL;FLSIYMLISISLLSC-
MLISISLLS;LSIYMLISISLLSCD-MLISISLLS;SIYMLISISLLSCDV-
YMLISISLL;FVDSKFVEASKKFVN-FVEASKKFV;VDSKFVEASKKFVNK-
FVEASKKFV;SKFVEASKKFVNKAK-FVEASKKFV;DSKFVEASKKFVNKA-
FVEASKKFV;KFVDSKFVEASKKFV-FVDSKFVEA;
DRB1_1101 DSYEKLRKSVALAYI-YEKLRKSVA;ADSYEKLRKSVALAY-YEKLRKSVA
DRB1_1302 LSIYMLISISLLSCD-IYMLISISL;FLSIYMLISISLLSC-
IYMLISISL;SFLSIYMLISISLLS-IYMLISISL;TGAYNDIMTYIMTYS-
YNDIMTYIM;GAYNDIMTYIMTYSE-YNDIMTYIM;SIYMLISISLLSCDV-
MLISISLLS;IYMLISISLLSCDVS-MLISISLLS;KSFLSIYMLISISLL-
IYMLISISL;AYNDIMTYIMTYSEG-YNDIMTYIM;EYTGAYNDIMTYIMT-
YNDIMTYIM;YTGAYNDIMTYIMTY-YNDIMTYIM;YNDIMTYIMTYSEGT-
YNDIMTYIM;SEYTGAYNDIMTYIM-AYNDIMTYI;SKVNQAISILKKDNK-
VNQAISILK;SDKSKVNQAISILKK-VNQAISILK;SSDKSKVNQAISILK-
KVNQAISIL;DKSKVNQAISILKKD-VNQAISILK;KSKVNQAISILKKDN-
VNQAISILK;YMLISISLLSCDVSR-MLISISLLS;KKSFLSIYMLISISL-
LSIYMLISI;NDLIALKCIVKTIGD-IALKCIVKT;KVNQAISILKKDNKI-

VNQAISILK;QAISILKKDNKIVNK-ISILKKDNK;IALKCIVKTIGDMVN-
LKCIVKTIG;NQAISILKKDNKIVN-ISILKKDNK;ENDLIALKCIVKTIG-
IALKCIVKT;DLIALKCIVKTIGDM-IALKCIVKT;LIALKCIVKTIGDMV-
LKCIVKTIG;AISILKKDNKIVNKF-LKKDNKIVN;ISILKKDNKIVNKFK-
LKKDNKIVN;VNQAISILKKDNKIV-ISILKKDNK;MVNDREINSRSRYNN-
REINSRSRY;MLISISLLSCDVSRL-MLISISLLS;VNDREINSRSRYNNF-
REINSRSRY;NDREINSRSRYNNFY-REINSRSRY
DRB1_1501 FLSIYMLISISLLSC-MLISISLLS;LSIYMLISISLLSCD-
MLISISLLS;SFLSIYMLISISLLS-IYMLISISL;SIYMLISISLLSCDV-
MLISISLLS;IYMLISISLLSCDVS-MLISISLLS
DRB3_0101
DRB4_0101 EKIIEEYKPMFLSKL-IEEYKPMFL;KELEKIIEEYKPMFL-
IIEEYKPMF;LEKIIEEYKPMFLSK-IEEYKPMFL;ELEKIIEEYKPMFLS-
IEEYKPMFL;IYMLISISLLSCDVS-LISISLLSC;KIIEEYKPMFLSKLI-
IEEYKPMFL;YMLISISLLSCDVSR-ISLLSCDVS;MLISISLLSCDVSRL-ISLLSCDVS
DRB5_0101

<NP_045689 outer surface protein B;Protein;Borrelia burgdorferi B31>

Allele 8-mer
A0101
A0201 FLTDGTIT;LLIGFALA;RLLIGFAL;FALALALI;LTDGTITV;SLFNGNKI;FLNDTAGS
A0202
FLNDTAGS;FLTDGTIT;ALALIGCA;LLIGFALA;SLFNGNKI;KTKDLVFL;RLLIGFAL;ATIDQVEL
;LIGFALAL;KLTVSADL;VSADLNTV;NLSELKNA;FALALALI;LVGGKTTV;
A0203
LLIGFALA;ALALIGCA;LVGGKTTV;FLTDGTIT;SLFNGNKI;KTKDLVFL;FLNDTAGS;RLLIGFAL
;NLSELKNA;TLKNSIKL;KVKLTVSA;LIGFALAL;FALALALI;SIKLEGSL;KLTVSADL;LTDGTIT
V;NQKISSKV;ATKAVETL;VSADLNTV;AQKGAESI
A0204 SLFNGNKI;ATIDQVEL;LVGGKTTV;RLLIGFAL;LTDGTITV
A0206
RLLIGFAL;FALALALI;LTDGTITV;LLIGFALA;FLTDGTIT;ATIDQVEL;LVGGKTTV;QQYNTAGT
;FLNDTAGS;LIGFALAL;AQKGAESI;KTKDLVFL
A0211
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;NLSELKNA;KLDSKKLT;FLNDTAGS;KLTVSADL;VSADLNTV;ALALIGCA;KTKDLVFL;ATIDQVE
L;IKLEGSLV;TTLEYSQI;LIGFALAL;ALIGCAQK
A0212
RLLIGFAL;LTDGTITV;SLFNGNKI;LLIGFALA;LVGGKTTV;FLTDGTIT;FLNDTAGS;SLVGGKTT
;VSADLNTV;LIGFALAL;NLSELKNA
A0216
LVGGKTTV;RLLIGFAL;LTDGTITV;SLFNGNKI;LLIGFALA;TLKNSIKL;FLTDGTIT;SLVGGKTT
;LIGFALAL;ALALIGCA;ATIDQVEL
A0219 LTDGTITV;LVGGKTTV;FLTDGTIT;RLLIGFAL;LLIGFALA;FLNDTAGS
A0301
KISSKVTK;ISSKVTKK;KIFVSKEK;ALIGCAQK;GSNKKTGK;VSLFNGNK;SITXETLK;TISADSKK
A1101
SITXETLK;VSLFNGNK;TISADSKK;KIFVSKEK;LTISADSK;KISSKVTK;ALIGCAQK;TIDQVELK
;KANKLDSK;ISSKVTKK;GSNKKTGK;TLKREIEK;ETLKNSIK;SADSKKTK
A2301 LFNGNKIF;KYDLRATI
A2402 KYDLRATI;VFLTDGTI
A2403 KYDLRATI
A2601 GTITVQQY;EIKNLSEL
A2602 NTVTLEAF;EIKNLSEL;ATIDQVEL;KTKDLVFL;GTITVQQY;ETLKANKL
A2902

A3001
KIFVSKEK;KANKLDSK;KEKNSSGK;TLKREIEK;GSKPDKSK;KISSKVTK;GSNKKTGK;KVKLTVSA
;
A3002
A3101 KISSKVTK;SSGKYDLR;KTKDLVFL;KIFVSKEK;KANKLDSK
A3301
A6801
DTAGSNKK;LTISADSK;ETLKNSIK;TISADSKK;SITXETLK;TIDQVELK;SSGKYDLR;ISSKVTKK
;ELKGTSDK;EGTVTLKR;NTAGTSLE;EAFDASNQ
A6802 TTLEYSQI;ATIDQVEL;VSADLNTV;TSTLTISA
A6901 LTDGTITV;FALALALI;TTLEYSQI;ETLKANKL
B0702
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B0802
B1501
B1801 WEDSTSTL;
B2705
B3501 NTVTLEAF;
B3901 TRSNGTTL;IKEGTVTL
B4001 WEDSTSTL;
B4002
B4402
B4403
B4501
B5101
B5301 FALALALI;
B5401 FALALALI;LPAVTEDS
B5701
B5801

Allele 9-mer
A0101 RSNGTTLEY;VTEDSVSLF
A0201 FLTDGTITV;LLIGFALAL;RLLIGFALA;SLVGGKTTV
A0202
FLTDGTITV;NLSELKNAL;LLIGFALAL;TVSADLNTV;LIGFALALA;SLVGGKTTV;AVTEDSVSL;A
LALALIGC;SLEGSASEI
A0203
FLTDGTITV;SLVGGKTTV;TVSADLNTV;LLIGFALAL;LIGFALALA;RLLIGFALA;SIKLEGSLV;S
TSTLTISA;NLSELKNAL;ALALALIGC
A0204 FLTDGTITV;SLVGGKTTV;LLIGFALAL
A0206
FLTDGTITV;TVSADLNTV;SLVGGKTTV;LLIGFALAL;RLLIGFALA;AVTEDSVSL;SQITDADNA;K
QGSITXET;VQQYNTAGT;ALALALIGC;SEIKNLSEL;VTLEAFDAS
A0211
FLTDGTITV;SLVGGKTTV;LLIGFALAL;NLSELKNAL;RLLIGFALA;AVTEDSVSL;SLEGSASEI;E
IKEGTVTL;TVSADLNTV;DLRATIDQV;DLNTVTLEA;LFNGNKIFV;SADLNTVTL;SLFNGNKIF;SI
TXETLKA;ALALALIGC
A0212
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VTEDSVSL;TVSADLNTV;SLEGSASEI;LFNGNKIFV
A0216
FLTDGTITV;SLVGGKTTV;LLIGFALAL;DLRATIDQV;SLEGSASEI;NLSELKNAL;LFNGNKIFV;R
LLIGFALA;EIKEGTVTL;TVSADLNTV;DLNTVTLEA;AVTEDSVSL
A0219 FLTDGTITV;SLVGGKTTV;LLIGFALAL;DLRATIDQV;TVSADLNTV;NLSELKNAL

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VSLFNGNK;KLDSKKLTR
A1101
SVSLFNGNK;ATIDQVELK;ATKAVETLK;ASNQKISSK;VTLKREIEK;GSITXETLK;KISSKVTKK;L
TISADSKK;ITDADNATK;KANKLDSKK;TLTISADSK;RSNGTTLEY;GSGTLEGSK;LSELKNALK;GA
ESIGSQK;EAFDASNQK;ISADSKKTK;LALIGCAQK
A2301 QYNTAGTSL
A2402 QYNTAGTSL
A2403 QYNTAGTSL
A2601
A2602 EIKEGTVTL;VTEDSVSLF;ETLKNSIKL
A2902
A3001
ATKAVETLK;RSNGTTLEY;ATIDQVELK;KANKLDSKK;KTKDLVFLT;SKKSHQNAK;SVSLFNGNK
A3002
A3101 KLDSKKLTR;ATKAVETLK;KISSKVTKK;KANKLDSKK;ASNQKISSK
A3301
A6801
EAFDASNQK;LTISADSKK;SVSLFNGNK;EIKNLSELK;NSSGKYDLR;ATIDQVELK;TLTISADSK;A
TKAVETLK;GSITXETLK;ITDADNATK
A6802 TVSADLNTV;STSTLTISA;TTVEIKEGT;FLTDGTITV;ETLKNSIKL
A6901 ETLKNSIKL;FLTDGTITV;TVSADLNTV;DADNATKAV;EIKEGTVTL;TTLEYSQIT
B0702 KPDKSKVKL;LTRSNGTTL;LPAVTEDSV;AVTEDSVSL
B0801
B0802
B1501 RSNGTTLEY;SLFNGNKIF;LLIGFALAL;SQKENDLNL
B1801
B2705 MRLLIGFAL
B3501
B3901 SADLNTVTL
B4001 SEIKNLSEL
B4002 SEIKNLSEL
B4402
B4403
B4501
B5101 LPAVTEDSV
B5301 LPAVTEDSV
B5401 LPAVTEDSV;LALALIGCA
B5701
B5801 RSNGTTLEY;GSNKKTGKW

Allele 10-mer
A0101
A0201 SLFNGNKIFV;LLIGFALALA;RLLIGFALAL;FLTDGTITVQ;ALALALIGCA
A0202
LLIGFALALA;SLFNGNKIFV;RLLIGFALAL;KQGSITXETL;ALIGCAQKGA;ALALALIGCA;LTVSA
DLNTV;FLTDGTITVQ;QQYNTAGTSL;FALALALIGC;KLTRSNGTTL;IGFALALALI;DLPAVTEDSV
A0203
LLIGFALALA;ALALALIGCA;SLFNGNKIFV;ALIGCAQKGA;LTVSADLNTV;RLLIGFALAL;KLTRS
NGTTL;FLTDGTITVQ;LIGFALALAL;QQYNTAGTSL;LVGGKTTVEI
A0204 SLFNGNKIFV;LTVSADLNTV;KLTRSNGTTL
A0206
RLLIGFALAL;KQGSITXETL;LTVSADLNTV;QQYNTAGTSL;LLIGFALALA;SLFNGNKIFV;SQITD
ADNAT;FLTDGTITVQ;KAVETLKNSI;LIGFALALAL;TTVEIKEGTV;ALIGCAQKGA;FALALALIGC

A0211
SLFNGNKIFV;RLLIGFALAL;FLTDGTITVQ;LLIGFALALA;DLPAVTEDSV;KLTRSNGTTL;ALIGC
AQKGA;ALALALIGCA;VFLTDGTITV;EIEKDGKVKV;TTVEIKEGTV;LIGFALALAL;SLVGGKTTVE
;KLDSKKLTRS
A0212
SLFNGNKIFV;RLLIGFALAL;FLTDGTITVQ;DLPAVTEDSV;LLIGFALALA;KLTRSNGTTL;VFLTD
GTITV;LIGFALALAL
A0216
SLFNGNKIFV;RLLIGFALAL;DLPAVTEDSV;FLTDGTITVQ;KLTRSNGTTL;LLIGFALALA;EIEKD
GKVKV;ALIGCAQKGA;LTVSADLNTV;LVGGKTTVEI;TTVEIKEGTV;ALALALIGCA;LIGFALALAL
;VFLTDGTITV
A0219 FLTDGTITVQ;SLFNGNKIFV;DLPAVTEDSV;RLLIGFALAL;LLIGFALALA;LTVSADLNTV
A0301
ALALIGCAQK;FLNDTAGSNK;STLTISADSK;NLSELKNALK;TLKANKLDSK;KLEGSLVGGK;TVTLK
REIEK;ITXETLKANK
A1101
STLTISADSK;TVTLKREIEK;ITXETLKANK;TISADSKKTK;SSKKSHQNAK;GTLEGSKPDK;ALALI
GCAQK;AVETLKNSIK;RATIDQVELK;TLKANKLDSK;TLTISADSKK;KLEGSLVGGK;FLNDTAGSNK
;SLEGSASEIK;NLSELKNALK;VSKEKNSSGK;TAGSNKKTGK;QITDADNATK
A2301 VSLFNGNKIF
A2402
A2403
A2601
A2602 AVTEDSVSLF
A2902
A3001
SSKKSHQNAK;GTLEGSKPDK;GSKPDKSKVK;TLKANKLDSK;VSKEKNSSGK;KLEGSLVGGK;RATID
QVELK
A3002
A3101
A3301
A6801
NATKAVETLK;TVTLKREIEK;DSVSLFNGNK;STLTISADSK;EIKEGTVTLK;TLTISADSKK;DASNQ
KISSK;NLSELKNALK;ITXETLKANK;QITDADNATK;TISADSKKTK;FLNDTAGSNK;RATIDQVELK
;DLNLEDSSKK
A6802
EAFDASNQKI;TTVEIKEGTV;LTVSADLNTV;SVSLFNGNKI;NTAGTSLEGS;DLPAVTEDSV;NSIKL
EGSLV
A6901 EAFDASNQKI;TTVEIKEGTV;LTVSADLNTV;SLFNGNKIFV
B0702
B0801
B0802
B1501 QQYNTAGTSL
B1801 VEIKEGTVTL;IEKDGKVKVF;WEDSTSTLTI
B2705
B3501 LPAVTEDSVS;DLNTVTLEAF
B3901
B4001 VEIKEGTVTL;WEDSTSTLTI;VETLKNSIKL
B4002 VEIKEGTVTL
B4402
B4403
B4501
B5101
B5301
B5401 LPAVTEDSVS
B5701

B5801

Allele 11-mer

A0101 LTDGTITVQQY;LTRSNGTTLEY
A0201
LLIGFALALAL;FLTDGTITVQQ;KLTVSADLNTV;RLLIGFALALA;SLVGGKTTVEI;LVFLTDGTITV
A0202
FLTDGTITVQQ;LLIGFALALAL;KLTVSADLNTV;SASEIKNLSEL;LIGFALALALI;SLVGGKTTVEI
;TVSADLNTVTL;RLLIGFALALA;FLNDTAGSNKK;HQNAKQDLPAV;LVFLTDGTITV;ALALALIGCA
Q
A0203
LLIGFALALAL;SLVGGKTTVEI;RLLIGFALALA;LIGFALALALI;KLTVSADLNTV;LVFLTDGTITV
;HQNAKQDLPAV;FLTDGTITVQQ;TVSADLNTVTL
A0204 SLVGGKTTVEI;LLIGFALALAL;KLTVSADLNTV;LVFLTDGTITV
A0206
LLIGFALALAL;HQNAKQDLPAV;KLTVSADLNTV;RLLIGFALALA;VQQYNTAGTSL;LVFLTDGTITV
;SLVGGKTTVEI;FLTDGTITVQQ;TVSADLNTVTL;FALALALIGCA;LIGFALALALI
A0211
LLIGFALALAL;SLVGGKTTVEI;FLTDGTITVQQ;KLTVSADLNTV;RLLIGFALALA;LVFLTDGTITV
;SLFNGNKIFVS;ITDADNATKAV;SADSKKTKDLV;TVSADLNTVTL;DLRATIDQVEL;FLNDTAGSNK
K;SASEIKNLSEL;ALALALIGCAQ
A0212
LLIGFALALAL;SLVGGKTTVEI;FLTDGTITVQQ;LVFLTDGTITV;KLTVSADLNTV;RLLIGFALALA
;FLNDTAGSNKK;SLFNGNKIFVS;DLRATIDQVEL;ITDADNATKAV
A0216
SLVGGKTTVEI;LLIGFALALAL;FLTDGTITVQQ;KLTVSADLNTV;LVFLTDGTITV;RLLIGFALALA
;DLRATIDQVEL;SADSKKTKDLV;SLFNGNKIFVS
A0219
FLTDGTITVQQ;LLIGFALALAL;SLVGGKTTVEI;KLTVSADLNTV;LVFLTDGTITV;ITDADNATKAV
;DLRATIDQVEL
A0301
FLNDTAGSNKK;KQGSITXETLK;TLKANKLDSKK;STLTISADSKK;LFNGNKIFVSK;SITXETLKANK
A1101
STLTISADSKK;SITXETLKANK;TSTLTISADSK;TSLEGSASEIK;SQITDADNATK;ASEIKNLSELK
;GTVTLKREIEK;LALALIGCAQK;KQGSITXETLK;TLEAFDASNQK;LTISADSKKTK;KAVETLKNSI
K;TLKANKLDSKK;FVSKEKNSSGK;LVGGKTTVEIK;FLNDTAGSNKK
A2301 VFLNDTAGSNK
A2402 KWEDSTSTLTI
A2403
A2601
A2602 EIEKDGKVKVF;LTDGTITVQQY
A2902
A3001
LTRSNGTTLEY;TLKANKLDSKK;TSLEGSASEIK;LTISADSKKTK;LFNGNKIFVSK;STLTISADSKK
;KQGSITXETLK
A3002
A3101 LFNGNKIFVSK;KQGSITXETLK;STLTISADSKK
A3301 EIKEGTVTLKR
A6801
TSTLTISADSK;EIKEGTVTLKR;DTAGSNKKTGK;STLTISADSKK;LTISADSKKTK;FVSKEKNSSGK
;ETLKANKLDSK;TLEAFDASNQK;SITXETLKANK;GTVTLKREIEK;DSSKKSHQNAK;FLNDTAGSNK
K;TSLEGSASEIK;TLKANKLDSKK;DNATKAVETLK;LALALIGCAQK
A6802
NTAGTSLEGSA;TVSADLNTVTL;LVFLTDGTITV;SASEIKNLSEL;DASNQKISSKV;EGSLVGGKTTV
;DSVSLFNGNKI
A6901 ITDADNATKAV;FALALALIGCA;TTLEYSQITDA;LVFLTDGTITV;NTAGTSLEGSA

B0702 LPAVTEDSVSL;KPDKSKVKLTV
B0801
B0802
B1501 LTRSNGTTLEY;LLIGFALALAL;VQQYNTAGTSL;VSKEKNSSGKY;SVSLFNGNKIF
B1801 IEKDGKVKVFL;MRLLIGFALAL
B2705 MRLLIGFALAL
B3501 LPAVTEDSVSL;TVSADLNTVTL
B3901
B4001 LEGSASEIKNL;IEKDGKVKVFL;KEKNSSGKYDL
B4002
B4402
B4403
B4501
B5101 LPAVTEDSVSL
B5301 LPAVTEDSVSL
B5401 FALALALIGCA
B5701
B5801

Allele 15-mer plus 9-mer core

DRB1_0101 MRLLIGFALALALIG-IGFALALAL;RLLIGFALALALIGC-
FALALALIG;LLIGFALALALIGCA-FALALALIG;LIGFALALALIGCAQ-
FALALALIG;IGFALALALIGCAQK-FALALALIG;GFALALALIGCAQKG-
FALALALIG;KNSIKLEGSLVGGKT-IKLEGSLVG;NSIKLEGSLVGGKTT-
IKLEGSLVG;LKNSIKLEGSLVGGK-IKLEGSLVG;ETLKNSIKLEGSLVG-
KNSIKLEGS;TLKNSIKLEGSLVGG-IKLEGSLVG;ITVQQYNTAGTSLEG-
VQQYNTAGT;TITVQQYNTAGTSLE-VQQYNTAGT;FALALALIGCAQKGA-
FALALALIG;KTGKWEDSTSTLTIS-WEDSTSTLT;KKTGKWEDSTSTLTI-
WEDSTSTLT;NKKTGKWEDSTSTLT-GKWEDSTST;KLEGSLVGGKTTVEI-
LVGGKTTVE;LEGSLVGGKTTVEIK-VGGKTTVEI;EGSLVGGKTTVEIKE-
VGGKTTVEI;GSLVGGKTTVEIKEG-VGGKTTVEI;IKLEGSLVGGKTTVE-
IKLEGSLVG;TGKWEDSTSTLTISA-WEDSTSTLT;VQQYNTAGTSLEGSA-
YNTAGTSLE;GKWEDSTSTLTISAD-WEDSTSTLT;TVQQYNTAGTSLEGS-
YNTAGTSLE;QQYNTAGTSLEGSAS-YNTAGTSLE;SLVGGKTTVEIKEGT-
VGGKTTVEI;GTITVQQYNTAGTSL-VQQYNTAGT;DGTITVQQYNTAGTS-
VQQYNTAGT;KDLVFLTDGTITVQQ-FLTDGTITV;DLVFLTDGTITVQQY-
FLTDGTITV;TDGTITVQQYNTAGT-ITVQQYNTA;TKDLVFLTDGTITVQ-
FLTDGTITV;LVFLTDGTITVQQYN-FLTDGTITV;SIKLEGSLVGGKTTV-
IKLEGSLVG;SKVKLTVSADLNTVT-VKLTVSADL;KSKVKLTVSADLNTV-
VKLTVSADL;KTKDLVFLTDGTITV-VFLTDGTIT;DKSKVKLTVSADLNT-
VKLTVSADL;QYNTAGTSLEGSASE-YNTAGTSLE;KVKLTVSADLNTVTL-
LTVSADLNT;VKLTVSADLNTVTLE-LTVSADLNT;YNTAGTSLEGSASEI-
YNTAGTSLE;VGGKTTVEIKEGTVT-VGGKTTVEI;PDKSKVKLTVSADLN-
VKLTVSADL;ANKLDSKKLTRSNGT-LDSKKLTRS;LVGGKTTVEIKEGTV-
VGGKTTVEI;KPDKSKVKLTVSADL-SKVKLTVSA;LKANKLDSKKLTRSN-
LDSKKLTRS;QGSITXETLKANKLD-XETLKANKL;KQGSITXETLKANKL-
ITXETLKAN;GSITXETLKANKLDS-XETLKANKL;TLKANKLDSKKLTRS-
ANKLDSKKL;NKLDSKKLTRSNGTT-LDSKKLTRS;KWEDSTSTLTISADS-
WEDSTSTLT;VFLTDGTITVQQYNT-FLTDGTITV;KANKLDSKKLTRSNG-
LDSKKLTRS;NTAGTSLEGSASEIK-GTSLEGSAS;WEDSTSTLTISADSK-
WEDSTSTLT;DASNQKISSKVTKKQ-NQKISSKVT;FLTDGTITVQQYNTA-
FLTDGTITV;LDSKKLTRSNGTTLE-LTRSNGTTL;ASNQKISSKVTKKQG-
ISSKVTKKQ;TAGTSLEGSASEIKN-LEGSASEIK;SKVTKKQGSITXETL-
VTKKQGSIT;LTVSADLNTVTLEAF-VSADLNTVT;SSKVTKKQGSITXET-
VTKKQGSIT;KLTVSADLNTVTLEA-VSADLNTVT;ALIGCAQKGAESIGS-LIGCAQKGA
DRB1_0301

DRB1_0401 FNGNKIFVSKEKNSS-FNGNKIFVS;NKIFVSKEKNSSGKY-
FVSKEKNSS;GNKIFVSKEKNSSGK-FVSKEKNSS;KIFVSKEKNSSGKYD-
FVSKEKNSS;NGNKIFVSKEKNSSG-FVSKEKNSS;ETLKNSIKLEGSLVG-LKNSIKLEG
DRB1_0404 GKVKVFLNDTAGSNK-VKVFLNDTA;DGKVKVFLNDTAGSN-
VKVFLNDTA;KVKVFLNDTAGSNKK-FLNDTAGSN;VKVFLNDTAGSNKKT-FLNDTAGSN;
DRB1_0405 TITVQQYNTAGTSLE-VQQYNTAGT;ITVQQYNTAGTSLEG-
YNTAGTSLE;TVQQYNTAGTSLEGS-YNTAGTSLE;VQQYNTAGTSLEGSA-
YNTAGTSLE;QQYNTAGTSLEGSAS-YNTAGTSLE
DRB1_0701
DRB1_0802
DRB1_0901 MRLLIGFALALALIG-IGFALALAL;RLLIGFALALALIGC-
IGFALALAL;LLIGFALALALIGCA-IGFALALAL;ITVQQYNTAGTSLEG-
VQQYNTAGT;TITVQQYNTAGTSLE-VQQYNTAGT;LIGFALALALIGCAQ-
FALALALIG;TGKWEDSTSTLTISA-WEDSTSTLT;KTGKWEDSTSTLTIS-
WEDSTSTLT;KKTGKWEDSTSTLTI-WEDSTSTLT;
DRB1_1101
DRB1_1302 ETLKNSIKLEGSLVG-LKNSIKLEG;KAVETLKNSIKLEGS-
LKNSIKLEG;TKAVETLKNSIKLEG-VETLKNSIK;AVETLKNSIKLEGSL-
LKNSIKLEG;VETLKNSIKLEGSLV-LKNSIKLEG;TLKNSIKLEGSLVGG-
LKNSIKLEG;LKNSIKLEGSLVGGK-LKNSIKLEG;DSVSLFNGNKIFVSK-
VSLFNGNKI;EDSVSLFNGNKIFVS-VSLFNGNKI;TITVQQYNTAGTSLE-
VQQYNTAGT;ITVQQYNTAGTSLEG-YNTAGTSLE;VSLFNGNKIFVSKEK-
VSLFNGNKI;SVSLFNGNKIFVSKE-VSLFNGNKI;TEDSVSLFNGNKIFV-
VSLFNGNKI;VQQYNTAGTSLEGSA-YNTAGTSLE;TVQQYNTAGTSLEGS-
YNTAGTSLE;EGSASEIKNLSELKN-SASEIKNLS;ASEIKNLSELKNALK-
IKNLSELKN;SASEIKNLSELKNAL-IKNLSELKN;GSASEIKNLSELKNA-
IKNLSELKN;QQYNTAGTSLEGSAS-YNTAGTSLE;LDSKKLTRSNGTTLE-
LTRSNGTTL;NSIKLEGSLVGGKTT-IKLEGSLVG;VTEDSVSLFNGNKIF-
VSLFNGNKI;KNSIKLEGSLVGGKT-IKLEGSLVG
DRB1_1501 MRLLIGFALALALIG-LIGFALALA;RLLIGFALALALIGC-
LIGFALALA;LKNSIKLEGSLVGGK-IKLEGSLVG;KDGKVKVFLNDTAGS-
VKVFLNDTA;DGKVKVFLNDTAGSN-VKVFLNDTA;KNSIKLEGSLVGGKT-IKLEGSLVG
DRB3_0101
DRB4_0101
DRB5_0101

<NP_047005 outer surface protein C;Protein;Borrelia burgdorferi B31>

Allele 8-mer
A0101
A0201
KLFESVEV;LLSSIDEI;LMTLFLFI;LLAGAYAI;VLLAVKEV;SLLAGAYA;AILMTLFL;KITDSNAV
;TLSAILMT
A0202
KLFESVEV;LLSSIDEI;LLAGAYAI;LMTLFLFI;KITDSNAV;KIHQNNGL;TLSAILMT;GAYAISTL
;ILMTLFLF;SLLAGAYA;VLLAVKEV;LSAILMTL
A0203
KLFESVEV;LLAGAYAI;LLSSIDEI;LMTLFLFI;VLLAVKEV;KITDSNAV;SLLAGAYA;TLSAILMT
;GAYAISTL;GLKEKIDA;AVKEVEAL;KIHQNNGL;AILMTLFL
A0204 KLFESVEV;VLLAVKEV;SLLAGAYA;LLAGAYAI;
A0206
KLFESVEV;KITDSNAV;LLAGAYAI;AILMTLFL;KEMLANSV;VLLAVKEV;LMTLFLFI;SLLAGAYA
;ILMTLFLF;LLSSIDEI;GAYAISTL
A0211
KLFESVEV;VLLAVKEV;LLAGAYAI;SLLAGAYA;KITDSNAV;LMTLFLFI;AILMTLFL;LLSSIDEI
;TLFLFISC;TLSAILMT;ELTSPVVA;ILMTLFLF;KIHQNNGL;SIDEIAAK;KLDGLKNE

A0212
KLFESVEV;VLLAVKEV;LLAGAYAI;SLLAGAYA;KITDSNAV;LMTLFLFI;LLSSIDEI;AILMTLFL
;TLFLFISC
A0216
KLFESVEV;VLLAVKEV;SLLAGAYA;LLAGAYAI;AILMTLFL;KITDSNAV;LLSSIDEI;LMTLFLFI
;TLFLFISC;TLSAILMT;GAYAISTL
A0219
LLAGAYAI;VLLAVKEV;KLFESVEV;LLSSIDEI;SLLAGAYA;KITDSNAV;LMTLFLFI;AILMTLFL
A0301 KTNGTKTK;ILKTNGTK;VVAESPKK;GLKNEGLK;IAAKAIGK;NLTEISKK
A1101
KTNGTKTK;VVAESPKK;ISCNNSGK;YAISTLIK;SIDEIAAK;GVTDADAK;ETFTNKLK;CSETFTNK
;IAAKAIGK;AAKAIGKK;FTNKLKEK;ISTLIKQK;PVVAESPK;EVLSKAAK;NSADESVK;ESVEVLS
K;KQKLDGLK;EMLANSVK;NAVLLAVK
A2301 ILMTLFLF;AYAISTLI
A2402 AYAISTLI;ILMTLFLF
A2403 AYAISTLI
A2601
A2602
A2902 ILMTLFLF
A3001 KTNGTKTK;KQKLDGLK;AAKAIGKK;ILKTNGTK
A3002
A3101 KTNGTKTK
A3301 DAKEAILK;EVLSKAAK
A6801
ETFTNKLK;ESVEVLSK;YAISTLIK;NAVLLAVK;EVLSKAAK;FTNKLKEK;NSADESVK;NLTEISKK
;ISCNNSGK;DAKEAILK;IAAKAIGK;ISTLIKQK;EMLANSVK;CSETFTNK;VVAESPKK;GVTDADA
K;EKIDAAKK
A6802 LLAGAYAI
A6901 NTLSAILM
B0702
B0801
B0802
B1501 ILMTLFLF;GSLLAGAY;
B1801
B2705
B3501 SAILMTLF
B3901
B4001 SETFTNKL;AEELGKLF;KEMLANSV
B4002 KELTSPVV;KEMLANSV;
B4402
B4403 AEELGKLF;KEVEALLS;
B4501 AEELGKLF
B5101
B5301 SAILMTLF
B5401
B5701
B5801

Allele 9-mer
A0101
A0201
ILMTLFLFI;ALLSSIDEI;KLFESVEVL;TLSAILMTL;SLLAGAYAI;MLANSVKEL;LLSSIDEIA;K
ITDSNAVL
A0202
TLSAILMTL;ILMTLFLFI;KLFESVEVL;LLSSIDEIA;MLANSVKEL;ALLSSIDEI;SVKELTSPV;F
LFISCNNS;LLAVKEVEA;GLKEKIDAA;GAYAISTLI;SLLAGAYAI;LIKQKLDGL;ELGKLFESV;LL

AGAYAIS;KITDSNAVL;KLKEKHTDL;SANSADESV;NLTEISKKI;SAILMTLFL;LAVKEVEAL;AVK
EVEALL
A0203
SVKELTSPV;MLANSVKEL;TLSAILMTL;GLKEKIDAA;LIKQKLDGL;ILMTLFLFI;KLFESVEVL;K
LKEKHTDL;ALLSSIDEI;SLLAGAYAI;LLAVKEVEA;LLSSIDEIA;ELGKLFESV;GAYAISTLI;MK
KNTLSAI;AVKEVEALL;AVLLAVKEV;LLAGAYAIS;FLFISCNNS
A0204
SLLAGAYAI;TLSAILMTL;KLFESVEVL;MLANSVKEL;ALLSSIDEI;LLAVKEVEA;KLKEKHTDL;I
LMTLFLFI
A0206
SLLAGAYAI;ILMTLFLFI;ALLSSIDEI;KLFESVEVL;TLSAILMTL;SVKELTSPV;SAILMTLFL;G
AYAISTLI;KITDSNAVL;HQNNGLDTE;AVLLAVKEV;KKITDSNAV;AILMTLFLF;SIDEIAAKA;EL
GKLFESV
A0211
SLLAGAYAI;KLFESVEVL;TLSAILMTL;ELGKLFESV;MLANSVKEL;ILMTLFLFI;SIDEIAAKA;A
LLSSIDEI;KITDSNAVL;SVKELTSPV;NLTEISKKI;HTDLGKEGV;AVLLAVKEV;LLAVKEVEA;IT
DSNAVLL;KLDGLKNEG;LLSSIDEIA;GLKEKIDAA;KLKEKHTDL;VLSKAAKEM;AVKEVEALL;SAN
SADESV
A0212
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LANSVKEL;GLKEKIDAA;HTDLGKEGV;LLAVKEVEA;SVKELTSPV;SIDEIAAKA
A0216
ELGKLFESV;TLSAILMTL;SLLAGAYAI;ALLSSIDEI;MLANSVKEL;KLFESVEVL;ILMTLFLFI;S
VKELTSPV;LLAVKEVEA;AVLLAVKEV;SIDEIAAKA;AVKEVEALL;KITDSNAVL;VLSKAAKEM;SA
NSADESV;LLSSIDEIA;NLTEISKKI;HTDLGKEGV
A0219
SLLAGAYAI;TLSAILMTL;ALLSSIDEI;ILMTLFLFI;ELGKLFESV;HTDLGKEGV;MLANSVKEL;K
LFESVEVL;SANSADESV;ITDSNAVLL
A0301 IAAKAIGKK;AILKTNGTK;AISTLIKQK;FISCNNSGK
A1101
SSIDEIAAK;AILKTNGTK;AISTLIKQK;AYAISTLIK;IAAKAIGKK;EIAAKAIGK;FISCNNSGK;P
VVAESPKK
A2301 AILMTLFLF;AYAISTLIK
A2402 AILMTLFLF;
A2403
A2601
A2602 EVEALLSSI
A2902
A3001 AILKTNGTK;AYAISTLIK;KEKHTDLGK
A3002
A3101
A3301
A6801 FISCNNSGK;EIAAKAIGK;SSIDEIAAK;IAAKAIGKK;ETFTNKLKE;
A6802
SVKELTSPV;ELGKLFESV;TLSAILMTL;EVEALLSSI;DSNAVLLAV;ESVEVLSKA;SANSADESV;S
AILMTLFL;ILMTLFLFI;HTDLGKEGV;LTSPVVAES
A6901 ELGKLFESV;HTDLGKEGV;SLLAGAYAI;NTLSAILMT;DSNAVLLAV;
B0702
B0801
B0802
B1501 KLFESVEVL
B1801 DESVKGPNL
B2705
B3501 LAVKEVEAL;NGSLLAGAY
B3901
B4001 TENNHNGSL

B4002 TENNHNGSL
B4402
B4403
B4501
B5101
B5301
B5401
B5701
B5801 LSAILMTLF

Allele 10-mer
A0101
A0201
ALLSSIDEIA;AILMTLFLFI;LLAGAYAIST;LLSSIDEIAA;NTLSAILMTL;KITDSNAVLL;ILMTL
FLFIS;VLLAVKEVEA;LLAVKEVEAL;KLDGLKNEGL;KLFESVEVLS
A0202
LLAVKEVEAL;LLSSIDEIAA;KLDGLKNEGL;ALLSSIDEIA;LLAGAYAIST;NTLSAILMTL;FLFIS
CNNSG;LAGAYAISTL;ILMTLFLFIS;MLANSVKELT;LSAILMTLFL;VLSKAAKEML;KITDSNAVLL
;KLFESVEVLS;AILMTLFLFI;TSANSADESV;TLIKQKLDGL;VLLAVKEVEA;LMTLFLFISC
A0203
AAKEMLANSV;LLAVKEVEAL;LLAGAYAIST;SVKELTSPVV;TLIKQKLDGL;MLANSVKELT;LLSSI
DEIAA;SVKGPNLTEI;VLSKAAKEML;ALLSSIDEIA;NTLSAILMTL;NSVKELTSPV
A0204 VLLAVKEVEA;LLAVKEVEAL;EMLANSVKEL
A0206
KEVEALLSSI;AILMTLFLFI;NTLSAILMTL;KITDSNAVLL;LLAGAYAIST;TLIKQKLDGL;SVKEL
TSPVV;AAKEMLANSV;ALLSSIDEIA;KLDGLKNEGL;NSVKELTSPV
A0211
KLDGLKNEGL;KITDSNAVLL;VLLAVKEVEA;EMLANSVKEL;SIDEIAAKAI;LLAGAYAIST;VLSKA
AKEML;SVKELTSPVV;AILMTLFLFI;LLAVKEVEAL;LLSSIDEIAA;KLFESVEVLS;TLIKQKLDGL
;ALLSSIDEIA;SLLAGAYAIS;MLANSVKELT;LMTLFLFISC;AISTLIKQKL;TLSAILMTLF;NTLS
AILMTL;SVKGPNLTEI
A0212
KLDGLKNEGL;VLLAVKEVEA;LLAVKEVEAL;TLIKQKLDGL;VLSKAAKEML;LLSSIDEIAA;LLAGA
YAIST;EMLANSVKEL;SVKELTSPVV;SIDEIAAKAI;ALLSSIDEIA;SLLAGAYAIS;AILMTLFLFI
A0216
KLDGLKNEGL;VLSKAAKEML;VLLAVKEVEA;LLAGAYAIST;TLIKQKLDGL;LLAVKEVEAL;EMLAN
SVKEL;SVKELTSPVV;KITDSNAVLL;ALLSSIDEIA;LLSSIDEIAA;AILMTLFLFI;MLANSVKELT
;AISTLIKQKL;SVKGPNLTEI;
A0219
KLDGLKNEGL;VLSKAAKEML;LLAGAYAIST;LLAVKEVEAL;EMLANSVKEL;NTLSAILMTL;TLIKQ
KLDGL;VLLAVKEVEA
A0301 GAYAISTLIK;ILKTNGTKTK;KTKGAEELGK;GLKNEGLKEK
A1101
GAYAISTLIK;SANSADESVK;SVEVLSKAAK;TSPVVAESPK;KTKGAEELGK;DSNAVLLAVK;YAIST
LIKQK;LSSIDEIAAK;ETFTNKLKEK;CSETFTNKLK;EIAAKAIGKK
A2301 SAILMTLFLF;LFISCNNSGK
A2402 SAILMTLFLF
A2403
A2601
A2602 EVLSKAAKEM;DTENNHNGSL
A2902
A3001
KTKGAEELGK;ILKTNGTKTK;GAYAISTLIK;SVEVLSKAAK;TSPVVAESPK;KGPNLTEISK;
A3002 TLSAILMTLF;
A3101
A3301

A6801
ETFTNKLKEK;EIAAKAIGKK;YAISTLIKQK;EAILKTNGTK;DSNAVLLAVK;TSPVVAESPK;SANSA
DESVK;GAYAISTLIK;CSETFTNKLK;LFISCNNSGK;LSSIDEIAAK;SVEVLSKAAK
A6802
TSANSADESV;NSVKELTSPV;LSAILMTLFL;NTLSAILMTL;NAVLLAVKEV;ESVEVLSKAA;AGAYA
ISTLI;SSIDEIAAKA
A6901 NTLSAILMTL;EMLANSVKEL;EALLSSIDEI;EVLSKAAKEM
B0702
B0801
B0802
B1501
B1801 KEVEALLSSI;
B2705
B3501 SAILMTLFLF;
B3901
B4001 KEVEALLSSI;TENNHNGSLL
B4002 TENNHNGSLL
B4402
B4403
B4501
B5101
B5301 SAILMTLFLF
B5401
B5701B5801 SAILMTLFLF

Allele 11-mer
A0101
A0201
TLSAILMTLFL;LLAGAYAISTL;ALLSSIDEIAA;VLLAVKEVEAL;KITDSNAVLLA;LLAVKEVEALL
;SLLAGAYAIST;ITDSNAVLLAV
A0202
TLSAILMTLFL;LLAGAYAISTL;LLAVKEVEALL;VLLAVKEVEAL;FLFISCNNSGK;KAAKEMLANSV
;ELGKLFESVEV;LLSSIDEIAAK;ALLSSIDEIAA;VLSKAAKEMLA;LAGAYAISTLI;NTSANSADES
V;ILMTLFLFISC
A0203
LLAGAYAISTL;TLSAILMTLFL;LLAVKEVEALL;KAAKEMLANSV;VLSKAAKEMLA;SVKELTSPVVA
;ALLSSIDEIAA;VLLAVKEVEAL;MLANSVKELTS;ELGKLFESVEV;ILMTLFLFISCA0204
LLAGAYAISTL;VLLAVKEVEAL;LLAVKEVEALL;TLSAILMTLFL;SLLAGAYAISTA0206
KAAKEMLANSV;TLSAILMTLFL;LLAGAYAISTL;ALLSSIDEIAA;SAILMTLFLFI;ITDSNAVLLAV
;SLLAGAYAIST;ILMTLFLFISC;YAISTLIKQKL;KITDSNAVLLA;VLLAVKEVEAL
A0211
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;ALLSSIDEIAA;LLAVKEVEALL;KITDSNAVLLA;VLSKAAKEMLA;KLFESVEVLSK;ILMTLFLFIS
C;KLDGLKNEGLK;KAAKEMLANSV;GVTDADAKEAI;YAISTLIKQKL
A0212
VLLAVKEVEAL;LLAGAYAISTL;ELGKLFESVEV;TLSAILMTLFL;SLLAGAYAIST;ITDSNAVLLAV
;LLAVKEVEALL;ALLSSIDEIAA;VLSKAAKEMLA;ILMTLFLFISC
A0216
LLAGAYAISTL;ELGKLFESVEV;TLSAILMTLFL;SLLAGAYAIST;LLAVKEVEALL;VLLAVKEVEAL
;ALLSSIDEIAA;VLSKAAKEMLA;ITDSNAVLLAV
A0219
LLAGAYAISTL;TLSAILMTLFL;VLLAVKEVEAL;ITDSNAVLLAV;ELGKLFESVEV;SLLAGAYAIST
;NTSANSADESV;ALLSSIDEIAA;LLAVKEVEALL
A0301
KLFESVEVLSK;FLFISCNNSGK;TLIKQKLDGLK;KLDGLKNEGLK;KLKEKHTDLGK;AILKTNGTKTK
;GLKEKIDAAKK;LTSPVVAESPK;LLSSIDEIAAK

A1101
KLFESVEVLSK;TSANSADESVK;LTSPVVAESPK;TLIKQKLDGLK;TSPVVAESPKK;AILKTNGTKTK
;AAKEMLANSVK;KLDGLKNEGLK;FLFISCNNSGK;LLSSIDEIAAK
A2301 AYAISTLIKQK;NTLSAILMTLF
A2402
A2403
A2601
A2602 EVLSKAAKEML;DTENNHNGSLL;NTLSAILMTLF
A2902
A3001
KLFESVEVLSK;KLKEKHTDLGK;LTSPVVAESPK;AILKTNGTKTK;AAKEMLANSVK;TSPVVAESPKK
;KCSETFTNKLK
A3002
A3101
A3301
A6801
ESVEVLSKAAK;LTSPVVAESPK;TSANSADESVK;FLFISCNNSGK;TSPVVAESPKK;TLIKQKLDGLK
;ETFTNKLKEKH;LLSSIDEIAAK
A6802
NTSANSADESV;TLSAILMTLFL;SAILMTLFLFI;EIAAKAIGKKI;ESVKGPNLTEI;ELGKLFESVEV
;NGSLLAGAYAI;
A6901 ITDSNAVLLAV;EVLSKAAKEML;ELGKLFESVEV;NTSANSADESV;EIAAKAIGKKI
B0702
B0801
B0802
B1501
B1801 VEVLSKAAKEM
B2705
B3501 NHNGSLLAGAY
B3901
B4001 KEMLANSVKEL;AEELGKLFESV;
B4002 KEMLANSVKEL
B4402
B4403
B4501 AEELGKLFESV
B5101
B5301 SAILMTLFLFI
B5401
B5701
B5801 LSAILMTLFLF

Allele 15-mer plus 9-mer core
DRB1_0101
GSLLAGAYAISTLIK-LAGAYAIST;HNGSLLAGAYAISTL-LAGAYAIST;NGSLLAGAYAISTLI-
LAGAYAIST;NHNGSLLAGAYAIST-LLAGAYAIS;SLLAGAYAISTLIKQ-
LAGAYAIST;LLAGAYAISTLIKQK-LAGAYAIST;LAGAYAISTLIKQKL-
LAGAYAIST;ANSVKELTSPVVAES-VKELTSPVV;NSVKELTSPVVAESP-
VKELTSPVV;LANSVKELTSPVVAE-VKELTSPVV;MLANSVKELTSPVVA-
VKELTSPVV;EMLANSVKELTSPVV-MLANSVKEL;SVKELTSPVVAESPK-
VKELTSPVV;VKELTSPVVAESPKK-VKELTSPVV;SVEVLSKAAKEMLAN-
VLSKAAKEM;ESVEVLSKAAKEMLA-VLSKAAKEM;VEVLSKAAKEMLANS-
VLSKAAKEM;FESVEVLSKAAKEML-VLSKAAKEM;EVLSKAAKEMLANSV-
VLSKAAKEM;LFESVEVLSKAAKEM-SVEVLSKAA;VLSKAAKEMLANSVK-
VLSKAAKEM;LAVKEVEALLSSIDE-VKEVEALLS;LLAVKEVEALLSSID-
VKEVEALLS;AVLLAVKEVEALLSS-VKEVEALLS;VLLAVKEVEALLSSI-
VKEVEALLS;NAVLLAVKEVEALLS-LAVKEVEAL;SKKITDSNAVLLAVK-

ITDSNAVLL;ISKKITDSNAVLLAV-ITDSNAVLL;KKITDSNAVLLAVKE-
ITDSNAVLL;MKKNTLSAILMTLFL-KNTLSAILM;NTLSAILMTLFLFIS-
LSAILMTLF;AKEAILKTNGTKTKG-LKTNGTKTK;DAKEAILKTNGTKTK-
EAILKTNGT;EISKKITDSNAVLLA-ITDSNAVLL;KNTLSAILMTLFLFI-
LSAILMTLF;KAAKEMLANSVKELT-AKEMLANSV;TLSAILMTLFLFISC-
LMTLFLFIS;TEISKKITDSNAVLL-KKITDSNAV;EAILKTNGTKTKGAE-
LKTNGTKTK;KEAILKTNGTKTKGA-LKTNGTKTK;KELTSPVVAESPKKP-
LTSPVVAES;LSAILMTLFLFISCN-LMTLFLFIS;SKAAKEMLANSVKEL-
AKEMLANSV;SAILMTLFLFISCNN-LMTLFLFIS;KKNTLSAILMTLFLF-
LSAILMTLF;NNHNGSLLAGAYAIS-SLLAGAYAI;AILKTNGTKTKGAEE-
LKTNGTKTK;AAKEMLANSVKELTS-MLANSVKEL;VKEVEALLSSIDEIA-
VKEVEALLS;AKEMLANSVKELTSP-MLANSVKEL;AILMTLFLFISCNNS-
LMTLFLFIS;AVKEVEALLSSIDEI-VKEVEALLS;KITDSNAVLLAVKEV-
ITDSNAVLL;ITDSNAVLLAVKEVE-ITDSNAVLL;EGVTDADAKEAILKT-
VTDADAKEA;KEGVTDADAKEAILK-VTDADAKEA;ADESVKGPNLTEISK-
VKGPNLTEI;LGKEGVTDADAKEAI-VTDADAKEA;DLGKEGVTDADAKEA-
LGKEGVTDA;GKEGVTDADAKEAIL-VTDADAKEA;SADESVKGPNLTEIS-
VKGPNLTEI;DESVKGPNLTEISKK-VKGPNLTEI;ESVKGPNLTEISKKI-
VKGPNLTEI;ILKTNGTKTKGAEEL-LKTNGTKTK;NSADESVKGPNLTEI-
ESVKGPNLT;LKTNGTKTKGAEELG-LKTNGTKTK;SSIDEIAAKAIGKKI-
IDEIAAKAI;LSKAAKEMLANSVKE-AKEMLANSV;KEMLANSVKELTSPV-
MLANSVKEL;LSSIDEIAAKAIGKK-IDEIAAKAI;AGAYAISTLIKQKLD-YAISTLIKQ
DRB1_0301
DRB1_0401
DRB1_0404 ILMTLFLFISCNNSG-FLFISCNNS;LMTLFLFISCNNSGK-
LFISCNNSG;MTLFLFISCNNSGKD-LFISCNNSG;TLFLFISCNNSGKDG-
LFISCNNSG;LFLFISCNNSGKDGN-LFISCNNSG;KEAILKTNGTKTKGA-
ILKTNGTKT;AKEAILKTNGTKTKG-ILKTNGTKT;EAILKTNGTKTKGAE-ILKTNGTKT
DRB1_0405 LAVKEVEALLSSIDE-VKEVEALLS;ANSVKELTSPVVAES-
VKELTSPVV;LANSVKELTSPVVAE-VKELTSPVV;NSVKELTSPVVAESP-
VKELTSPVV;LLAVKEVEALLSSID-VKEVEALLS;
DRB1_0701 MLANSVKELTSPVVA-VKELTSPVV;ANSVKELTSPVVAES-
VKELTSPVV;LANSVKELTSPVVAE-VKELTSPVV;EMLANSVKELTSPVV-
SVKELTSPV;NSVKELTSPVVAESP-VKELTSPVV;SVKELTSPVVAESPK-
VKELTSPVV;VKELTSPVVAESPKK-VKELTSPVV
DRB1_0802
DRB1_0901 FESVEVLSKAAKEML-EVLSKAAKE;ESVEVLSKAAKEMLA-
LSKAAKEML;SVEVLSKAAKEMLAN-LSKAAKEML
DRB1_1101 KCSETFTNKLKEKHT-FTNKLKEKH;SETFTNKLKEKHTDL-
FTNKLKEKH;ETFTNKLKEKHTDLG-FTNKLKEKH;KKCSETFTNKLKEKH-
KKCSETFTN;CSETFTNKLKEKHTD-FTNKLKEKH;
DRB1_1302 AKEAILKTNGTKTKG-LKTNGTKTK;DAKEAILKTNGTKTK-
EAILKTNGT;KEAILKTNGTKTKGA-LKTNGTKTK;EAILKTNGTKTKGAE-
LKTNGTKTK;AILKTNGTKTKGAEE-LKTNGTKTK;EMLANSVKELTSPVV-
LANSVKELT;KEMLANSVKELTSPV-LANSVKELT;KAAKEMLANSVKELT-
MLANSVKEL;AAKEMLANSVKELTS-LANSVKELT;AKEMLANSVKELTSP-
LANSVKELT;ILKTNGTKTKGAEEL-LKTNGTKTK;MLANSVKELTSPVVA-
LANSVKELT;MKKNTLSAILMTLFL-MKKNTLSAI;LANSVKELTSPVVAE-
LANSVKELT;LAGAYAISTLIKQKL-YAISTLIKQ;AGAYAISTLIKQKLD-
ISTLIKQKL;LKTNGTKTKGAEELG-LKTNGTKTK;GAYAISTLIKQKLDG-
ISTLIKQKL;ADAKEAILKTNGTKT-EAILKTNGT;AYAISTLIKQKLDGL-
ISTLIKQKL;YAISTLIKQKLDGLK-ISTLIKQKL
DRB1_1501 MLANSVKELTSPVVA-VKELTSPVV;EMLANSVKELTSPVV-
NSVKELTSP;LANSVKELTSPVVAE-VKELTSPVV;ANSVKELTSPVVAES-
VKELTSPVV;NSVKELTSPVVAESP-VKELTSPVV;VKELTSPVVAESPKK-VKELTSPVV
DRB3_0101

DRB4_0101
DRB5_0101 KQKLDGLKNEGLKEK-KQKLDGLKN;DGLKNEGLKEKIDAA-
LKNEGLKEK;QKLDGLKNEGLKEKI-LKNEGLKEK;KLDGLKNEGLKEKID-
LKNEGLKEK;LDGLKNEGLKEKIDA-LKNEGLKEK

<CAH10086 CRASP-1;Protein;Borrelia garinii>

Allele 8-mer
A0101
A0201 ILTTILTL;KLNILTTI;ILNETIKA;TILTLICI;TLICISCA;ILNISIKI
A0202 KLNILTTI;ILTTILTL;ILNETIKA;TLICISCA;ILNISIKI
A0203
KLNILTTI;ILNETIKA;TLICISCA;ILTTILTL;ILNISIKI;LICISCAV;KINTLKEI;SIKIQFQI
;NIIKLNIL
A0204 KLNILTTI;ILTTILTL
A0206 FQIENALE;IQFQIENA;ILTTILTL;KLNILTTI;TLICISCA;LICISCAV
A0211
ILTTILTL;ILNETIKA;KLNILTTI;ILNISIKI;KLYKNHKY;TILTLICI;LICISCAV;TLICISCA
;TISEDIEM;KINTLKEI
A0212 ILTTILTL;ILNETIKA;KLNILTTI;KLYKNHKY;LICISCAV;HMDENYKE
A0216
ILTTILTL;KLNILTTI;ILNETIKA;LICISCAV;TLICISCA;QIENALEL;KLYKNHKY;ILNISIKI
;EIEKINTL
A0219 ILTTILTL;ILNETIKA
A0301
IIYSSLNY;KLYKNHKY;FILNISIK;KILNETIK;KTKLNIIK;TIISKLEK;SLNYEIEK;TLKEILDK
;
A1101
TIISKLEK;SLNYEIEK;KTKLNIIK;IIYSSLNY;KILNETIK;EILDKLYK;FILNISIK;NTKDFENK
;ISEDIEMK;CISCAVDK;TLKEILDK
A2301 LYKNHKYK;NYKEFDPL
A2402 NFILNISI
A2403 QFQIENAL
A2601 EILNQERY
A2602 EILNQERY;IIYSSLNY;TTARNFIL;EIEKINTL;NIIKLNIL;TISEDIEM;QIDFLENF
A2902 KLYKNHKY;IIYSSLNY
A3001 KTKLNIIK;LYKNHKYK;KILNETIK;
A3002 IIYSSLNY
A3101 LYKNHKYK;KTKLNIIK;KIKRIIYS;
A3301 DIEMKIKR
A6801
NTKDFENK;TIISKLEK;FILNISIK;EILDKLYK;CISCAVDK;ETIKAYNQ;DIEMKIKR;SLNYEIEK
;ISEDIEMK;ENALELMK;HKYKTTAR;ERYEILLK;NLKQKFEK;EPSNTKNK
A6802 TTARNFIL;YSSLNYEI;EIAKITNT;TLICISCA;LTTILTLI
A6901 TILTLICI;TTARNFIL
B0702
B0801
B0802
B1501 KLYKNHKY;IIYSSLNY
B1801 QERYEILL;KEFDPLNL;YEILLKHV
B2705 KRIIYSSL;ERYEILLK
B3501 LAHMDENY;TISEDIEM
B3901 TTARNFIL;NQERYEIL
B4001 KEFDPLNL;QERYEILL;IEDASEIL;FENKSQDL;KETIISKL;YEILLKHV;LEKMIKDL
B4002 KEFDPLNL;QERYEILL;FENKSQDL
B4402 KEILDKLY;

B4403 KEILDKLY;KEFDPLNL
B4501
B5101
B5301
B5401
B5701
B5801 ITNTQIDF

Allele 9-mer
A0101
A0201
FILNISIKI;ILTTILTLI;TLICISCAV;FQIENALEL;SLNYEIEKI;KLNILTTIL;NILTTILTL;K
ILNETIKA;KLNIIKLNI
A0202
ILTTILTLI;KLNILTTIL;TLKEILDKL;SLNYEIEKI;TLICISCAV;IQFQIENAL;ILNQERYEI;F
QIENALEL;ITNTQIDFL;FILNISIKI;KLNIIKLNI;CISCAVDKI;LLKHVEPSL
A0203
ILTTILTLI;TLICISCAV;KLNILTTIL;TLKEILDKL;SLNYEIEKI;LMKEEIEDA;LLKHVEPSL;I
LNQERYEI;NLKQKFEKI;KLNIIKLNI;FILNISIKI;FQIENALEL;CISCAVDKI;KIQFQIENA
A0204 FQIENALEL;ILNQERYEI
A0206
FQIENALEL;TLICISCAV;TQIDFLENF;FILNISIKI;YEIEKINTL;ILTTILTLI;IQFQIENAL;N
ILTTILTL;KILNETIKA;IKLNILTTI;
A0211
TLICISCAV;ILNQERYEI;ILTTILTLI;FILNISIKI;TLKEILDKL;KLNILTTIL;NILTTILTL;K
LNIIKLNI;LLKHVEPSL;SLNYEIEKI;HMDENYKEF;KILNETIKA;FQIENALEL;ILNETIKAY;IL
TLICISC;ALELMKEEI
A0212
LLKHVEPSL;TLICISCAV;TLKEILDKL;FILNISIKI;NILTTILTL;FQIENALEL;ILNQERYEI;L
MKEEIEDA;ILTTILTLI;KLNILTTIL;SLNYEIEKI;HMDENYKEF;KLNIIKLNI
A0216
TLICISCAV;LLKHVEPSL;ILNQERYEI;TLKEILDKL;ILTTILTLI;NILTTILTL;FILNISIKI;K
LNILTTIL;ALELMKEEI;KLNIIKLNI;
A0219 NILTTILTL;TLICISCAV;ILTTILTLI;ILNQERYEI;LLKHVEPSL;
A0301 KLYKNHKYK;RIIYSSLNY;HVEPSLNLK
A1101
SSLNYEIEK;RIIYSSLNY;KLYKNHKYK;TISEDIEMK;HVEPSLNLK;QIDFLENFK;ETIISKLEK;N
TLKEILDK;NSKETIISK;MIKDLEDQK;LAHMDENYK;ISKLEKMIK
A2301 KYKTTARNF;IYSSLNYEI;NFILNISIK;TQIDFLENF
A2402 IYSSLNYEI;KYKTTARNF
A2403 KYKTTARNF;AYNQDLDNI;HMDENYKEF;IYSSLNYEI;
A2601 TIISKLEKM;DTISEDIEM
A2602
TIISKLEKM;QIENALELM;DTISEDIEM;RIIYSSLNY;EIEDASEIL;ITNTQIDFL;EMKIKRIIY;T
TILTLICI
A2902 EFDPLNLDY;RIIYSSLNY;QLAHMDENY
A3001 KLYKNHKYK;ISKLEKMIK;ESKSKTNTK;SSLNYEIEK;LAHMDENYK;LDKLYKNHK
A3002 IYSSLNYEI;RIIYSSLNY;EFDPLNLDY;QLAHMDENY;KITNTQIDF;KYKTTARNF
A3101 KLYKNHKYK;ASEILNQER;KIKRIIYSS;KTTARNFIL;
A3301 NHKYKTTAR
A6801
ETIISKLEK;EIEKINTLK;TISEDIEMK;HVEPSLNLK;MIKDLEDQK;LAHMDENYK;QIDFLENFK;E
SKSKTNTK;NFILNISIK;SSLNYEIEK;EDIEMKIKR;EIAKITNTQ;NSKETIISK;NTLKEILDK;EP
SLNLKQK
A6802
TLICISCAV;TTILTLICI;ISIKIQFQI;ITNTQIDFL;CISCAVDKI;FILNISIKI;EIAKITNTQ

A6901 FILNISIKI;TLICISCAV;NILTTILTL;TTILTLICI;
B0702
B0801
B0802
B1501
ILNETIKAY;FQIENALEL;IQFQIENAL;RIIYSSLNY;TQIDFLENF;EMKIKRIIY;QLAHMDENY
B1801 YEIEKINTL;FQIENALEL
B2705
B3501 ILNETIKAY;DTISEDIEM
B3901 FQIENALEL;YKEFDPLNL;YEIEKINTL;KHVEPSLNL
B4001 YEIEKINTL;FQIENALEL;IQFQIENAL;
B4002 EEIEDASEI;YEIEKINTL
B4402 SEILNQERY
B4403 SEILNQERY;EEIEDASEI
B4501 EEIEDASEI
B5101
B5301
B5401
B5701
B5801 ISIKIQFQI;RIIYSSLNY

Allele 10-mer

A0101 ASEILNQERY
A0201
ILLKHVEPSL;IIYSSLNYEI;FQIENALELM;NILTTILTLI;LTLICISCAV;ILTLICISCA;KLNIL
TTILT
A0202
IIYSSLNYEI;FQIENALELM;LTLICISCAV;ILNQERYEIL;ILLKHVEPSL;TISEDIEMKI;KLNII
KLNIL;NILTTILTLI;KITNTQIDFL;ILTLICISCA;KIKRIIYSSL;KAYNQDLDNI;KLNILTTILT
A0203
KIKRIIYSSL;IIYSSLNYEI;KLNIIKLNIL;IIKLNILTTI;ILNQERYEIL;KLNILTTILT;ILLKH
VEPSL;ILTLICISCA;NILTTILTLI;LTLICISCAV;TIISKLEKMI
A0204 ILLKHVEPSL
A0206 FQIENALELM;IIYSSLNYEI;ILLKHVEPSL;LTLICISCAV;NILTTILTLI;KITNTQIDFL
A0211
ILLKHVEPSL;ILNQERYEIL;IIYSSLNYEI;TISEDIEMKI;KLYKNHKYKT;KLNIIKLNIL;KITNT
QIDFL;ILTLICISCA;NILTTILTLI;KLNILTTILT;LTLICISCAV;EILNQERYEI;NISIKIQFQI
;KIKRIIYSSL;ILTTILTLIC
A0212 ILLKHVEPSL;KLYKNHKYKT;ILNQERYEIL;IIYSSLNYEI;TISEDIEMKI;KLNIIKLNIL
A0216
ILLKHVEPSL;KLYKNHKYKT;ILNQERYEIL;IIYSSLNYEI;KITNTQIDFL;KLNIIKLNIL;KIKRI
IYSSL;PLEKNSKETI;EIAKITNTQI;NLKQKFEKIL;ILTLICISCA
A0219 ILLKHVEPSL;ILNQERYEIL;IIYSSLNYEI
A0301 SLNLKQKFEK;IISKLEKMIK;LICISCAVDK;ILDKLYKNHK;TQIDFLENFK
A1101
TQIDFLENFK;KTNTKDFENK;SLNLKQKFEK;AVDKIDPESK;KMIKDLEDQK;YSSLNYEIEK;IISKL
EKMIK;LICISCAVDK;SQDLEPSNTK;QIENALELMK;QLAHMDENYK;NQERYEILLK
A2301
KYKTTARNFI;NYKEFDPLNL;NYEIEKINTL;AYNQDLDNIK;NFILNISIKI;AHMDENYKEF;NTQID
FLENF
A2402 KYKTTARNFI;NFILNISIKI
A2403 AHMDENYKEF;QFQIENALEL;KYKTTARNFI
A2601 ETIISKLEKM;ETIKAYNQDL
A2602 ETIISKLEKM;ETIKAYNQDL;KILNETIKAY;NTQIDFLENF;KIKRIIYSSL
A2902
A3001 KNKDLEPLEK;SLNLKQKFEK;KTNTKDFENK;KNHKYKTTAR;KYKTTARNFI

A3002
A3101 KNHKYKTTAR
A3301
A6801 DASEILNQER;DTISEDIEMK;YSSLNYEIEK;TQIDFLENFK;QLAHMDENYK;LICISCAVDK
A6802 TTARNFILNI;EIAKITNTQI;ETIKAYNQDL;LTLICISCAV;TISEDIEMKI;NISIKIQFQI
A6901
LTLICISCAV;TTARNFILNI;EIAKITNTQI;NALELMKEEI;NILTTILTLI;EILNQERYEI;ETIKA
YNQDL;ETIISKLEKM;IIYSSLNYEI
B0702
B0801
B0802
B1501 FQIENALELM;KILNETIKAY
B1801 IEMKIKRIIY;KEFDPLNLDY;EEIEDASEIL;
B2705 KRIIYSSLNY
B3501 EPSLNLKQKF
B3901 YKTTARNFIL
B4001 EEIEDASEIL
B4002 EEIEDASEIL;KEFDPLNLDY;
B4402 KEFDPLNLDY
B4403 KEFDPLNLDY;EEIEDASEIL;
B4501 EEIEDASEIL
B5101
B5301 EPSLNLKQKF
B5401
B5701
B5801 KSNEDQLAHM

Allele 11-mer
A0101 ILDKLYKNHKY
A0201
ILTTILTLICI;KLNILTTILTL;ILTLICISCAV;RIIYSSLNYEI;ILNQERYEILL;NIIKLNILTTI
A0202
ILNQERYEILL;ILTLICISCAV;KLNILTTILTL;ILTTILTLICI;SLNLKQKFEKI;IQFQIENALEL
;KLNIIKLNILT;LLKHVEPSLNL
A0203
KLNILTTILTL;ILTLICISCAV;LLKHVEPSLNL;ILTTILTLICI;SLNLKQKFEKI;NIIKLNILTTI
;ILNQERYEILL;SIKIQFQIENA;RIIYSSLNYEI;IIKLNILTTIL;MKIKRIIYSSL;ILNISIKIQF
Q;KLYKNHKYKTT
A0204 KLNILTTILTL;ILNQERYEILL
A0206
RIIYSSLNYEI;IQFQIENALEL;NIIKLNILTTI;ILTLICISCAV;TQIDFLENFKS;FILNISIKIQF
;ILTTILTLICI;MKIKRIIYSSL
A0211
ILTLICISCAV;ILNQERYEILL;KLNILTTILTL;ILTTILTLICI;LLKHVEPSLNL;SLNLKQKFEKI
;KLNIIKLNILT;KLYKNHKYKTT;ILDKLYKNHKY;ILNETIKAYNQ;NIIKLNILTTI;FILNISIKIQ
F;EILLKHVEPSL
A0212
ILTLICISCAV;ILNQERYEILL;LLKHVEPSLNL;KLNILTTILTL;ILTTILTLICI;KLYKNHKYKTT
;ILNETIKAYNQ
A0216
ILTLICISCAV;ILNQERYEILL;KLNILTTILTL;LLKHVEPSLNL;ILTTILTLICI;KLYKNHKYKTT
;NIIKLNILTTI;EILLKHVEPSL
A0219 ILTLICISCAV;ILTTILTLICI;ILNQERYEILL;KLNILTTILTL
A0301 KINTLKEILDK;TLICISCAVDK;TLKEILDKLYK;TIISKLEKMIK;KAYNQDLDNIK
A1101
TIISKLEKMIK;KSQDLEPSNTK;NTQIDFLENFK;TLICISCAVDK;KINTLKEILDK;KAYNQDLDNIK

;TLKEILDKLYK;TISEDIEMKIK;FQIENALELMK;HVEPSLNLKQK;PSLNLKQKFEK;IYSSLNYEIE
K;EILDKLYKNHK
A2301 IYSSLNYEIEK;KYKTTARNFIL;NYEIEKINTLK;FILNISIKIQF;KFEKILNETIK
A2402 KYKTTARNFIL
A2403 KYKTTARNFIL;FILNISIKIQF
A2601 EKILNETIKAY;NTLKEILDKLY
A2602 DIEMKIKRIIY;EILNQERYEIL;EKILNETIKAY;ETIISKLEKMI;EILLKHVEPSL
A2902 ILDKLYKNHKY
A3001 KSQDLEPSNTK;TLKEILDKLYK;KINTLKEILDK
A3002
A3101 IYSSLNYEIEK;ISEDIEMKIKR
A3301 EILDKLYKNHK
A6801
NTQIDFLENFK;TLICISCAVDK;TIISKLEKMIK;EILDKLYKNHK;ISEDIEMKIKR;HVEPSLNLKQK
;EDASEILNQER;CAVDKIDPESK;IYSSLNYEIEK;TLKEILDKLYK;TISEDIEMKIK
A6802
DTISEDIEMKI;TTARNFILNIS;NIIKLNILTTI;RIIYSSLNYEI;ILTLICISCAV;MKIKRIIYSSL
A6901 EPLEKNSKETI;ETIISKLEKMI;EILLKHVEPSL;NIIKLNILTTI
B0702
B0801
B0802
B1501 IQFQIENALEL
B1801 VEPSLNLKQKF
B2705
B3501 DASEILNQERY;LAHMDENYKEF
B3901
B4001 KEEIEDASEIL;SEILNQERYEI;IEKINTLKEIL;NETIKAYNQDL
B4002 SEILNQERYEI
B4402
B4403 SEILNQERYEI;EEIEDASEILN
B4501
B5101 EPLEKNSKETI
B5301 EPLEKNSKETI
B5401
B5701
B5801

Allele 15-mer plus 9-mer core
DRB1_0101 LNIIKLNILTTILTL-LNILTTILT;NIIKLNILTTILTLI-
LNILTTILT;IIKLNILTTILTLIC-LNILTTILT;IKLNILTTILTLICI-
LNILTTILT;KLNIIKLNILTTILT-KLNILTTIL;KLNILTTILTLICIS-
LNILTTILT;LNILTTILTLICISC-LNILTTILT;NILTTILTLICISCA-
LTTILTLIC;DKLYKNHKYKTTARN-YKNHKYKTT;KLYKNHKYKTTARNF-
YKNHKYKTT;LDKLYKNHKYKTTAR-YKNHKYKTT;ILDKLYKNHKYKTTA-
YKNHKYKTT;EILDKLYKNHKYKTT-LYKNHKYKT;TKLNIIKLNILTTIL-
IIKLNILTT;DIEMKIKRIIYSSLN-MKIKRIIYS;IEMKIKRIIYSSLNY-
MKIKRIIYS;EDIEMKIKRIIYSSL-MKIKRIIYS;ILTTILTLICISCAV-
LTLICISCA;KIQFQIENALELMKE-FQIENALEL;KTKLNIIKLNILTTI-
IIKLNILTT;IQFQIENALELMKEE-FQIENALEL;NQDLDNIKSNEDQLA-
LDNIKSNED;QDLDNIKSNEDQLAH-IKSNEDQLA;IKIQFQIENALELMK-
FQIENALEL;SIKIQFQIENALELM-FQIENALEL;ISIKIQFQIENALEL-
IQFQIENAL;TTARNFILNISIKIQ-FILNISIKI;SEDIEMKIKRIIYSS-
MKIKRIIYS;ISEDIEMKIKRIIYS-IEMKIKRII;YKNHKYKTTARNFIL-
YKNHKYKTT;LTTILTLICISCAVD-LTLICISCA;ARNFILNISIKIQFQ-
FILNISIKI;LYKNHKYKTTARNFI-YKNHKYKTT;TARNFILNISIKIQF-
FILNISIKI;LDNIKSNEDQLAHMD-IKSNEDQLA;DLDNIKSNEDQLAHM-

IKSNEDQLA;RNFILNISIKIQFQI-FILNISIKI;YEILLKHVEPSLNLK-
LKHVEPSLN;EILLKHVEPSLNLKQ-LKHVEPSLN;MKIKRIIYSSLNYEI-
MKIKRIIYS;RYEILLKHVEPSLNL-LKHVEPSLN;ILLKHVEPSLNLKQK-
LKHVEPSLN;KKTKLNIIKLNILTT-LNIIKLNIL;TTILTLICISCAVDK-
LTLICISCA;KTTARNFILNISIKI-ARNFILNIS
DRB1_0301
DRB1_0401 IIKLNILTTILTLIC-LNILTTILT;KLNIIKLNILTTILT-
IIKLNILTT;IKLNILTTILTLICI-LNILTTILT;LNIIKLNILTTILTL-
LNILTTILT;NIIKLNILTTILTLI-LNILTTILT
DRB1_0404 IIKLNILTTILTLIC-ILTTILTLI;NTQIDFLENFKSEPH-FLENFKSEP
DRB1_0405 YEIEKINTLKEILDK-IEKINTLKE;NYEIEKINTLKEILD-
IEKINTLKE;IEKINTLKEILDKLY-INTLKEILD;EIEKINTLKEILDKL-
INTLKEILD;SSLNYEIEKINTLKE-YEIEKINTL;IIKLNILTTILTLIC-
LNILTTILT;IKLNILTTILTLICI-LNILTTILT;SLNYEIEKINTLKEI-
IEKINTLKE;LNYEIEKINTLKEIL-IEKINTLKE;KAYNQDLDNIKSNED-
YNQDLDNIK;AYNQDLDNIKSNEDQ-LDNIKSNED;HMDENYKEFDPLNLD-
YKEFDPLNL;MKIKRIIYSSLNYEI-KRIIYSSLN;MDENYKEFDPLNLDY-
KEFDPLNLD;YNQDLDNIKSNEDQL-LDNIKSNED;ISIKIQFQIENALEL-
IKIQFQIEN;ETIKAYNQDLDNIKS-IKAYNQDLD
DRB1_0701 YKNHKYKTTARNFIL-YKTTARNFI;NHKYKTTARNFILNI-
YKTTARNFI;KNHKYKTTARNFILN-YKTTARNFI;LYKNHKYKTTARNFI-
KYKTTARNF;HKYKTTARNFILNIS-YKTTARNFI;KYKTTARNFILNISI-
YKTTARNFI;KLYKNHKYKTTARNF-YKNHKYKTT
DRB1_0802
DRB1_0901 YKNHKYKTTARNFIL-YKTTARNFI;LYKNHKYKTTARNFI-
NHKYKTTAR;NHKYKTTARNFILNI-YKTTARNFI;KNHKYKTTARNFILN-
YKTTARNFI;HKYKTTARNFILNIS-YKTTARNFI
DRB1_1101
DRB1_1302 LNIIKLNILTTILTL-LNILTTILT;NIIKLNILTTILTLI-
LNILTTILT;IIKLNILTTILTLIC-LNILTTILT;KLNIIKLNILTTILT-
IKLNILTTI;IKLNILTTILTLICI-LNILTTILT;KLNILTTILTLICIS-
LNILTTILT;LNILTTILTLICISC-LNILTTILT;KTKLNIIKLNILTTI-
LNIIKLNIL;TKLNIIKLNILTTIL-IKLNILTTI;RNFILNISIKIQFQI-
FILNISIKI;TARNFILNISIKIQF-FILNISIKI;KKTKLNIIKLNILTT-
LNIIKLNIL;ARNFILNISIKIQFQ-FILNISIKI;NFILNISIKIQFQIE-
LNISIKIQF;TTARNFILNISIKIQ-FILNISIKI;MKKTKLNIIKLNILT-
LNIIKLNIL;FILNISIKIQFQIEN-LNISIKIQF;KTTARNFILNISIKI-
ARNFILNIS;EILDKLYKNHKYKTT-LYKNHKYKT;ILDKLYKNHKYKTTA-
YKNHKYKTT;LYKNHKYKTTARNFI-YKNHKYKTT;LDKLYKNHKYKTTAR-
YKNHKYKTT;EDIEMKIKRIIYSSL-MKIKRIIYS;DKLYKNHKYKTTARN-
YKNHKYKTT;ILNISIKIQFQIENA-LNISIKIQF;IEMKIKRIIYSSLNY-
MKIKRIIYS;DIEMKIKRIIYSSLN-MKIKRIIYS;HKYKTTARNFILNIS-
YKTTARNFI;SEDIEMKIKRIIYSS-MKIKRIIYS;ISEDIEMKIKRIIYS-
IEMKIKRII;KLYKNHKYKTTARNF-YKNHKYKTT;YKTTARNFILNISIK-
ARNFILNIS;YKNHKYKTTARNFIL-YKNHKYKTT;KYKTTARNFILNISI-
ARNFILNIS;EMKIKRIIYSSLNYE-MKIKRIIYS;MKIKRIIYSSLNYEI-
MKIKRIIYS;LNISIKIQFQIENAL-LNISIKIQF;ERYEILLKHVEPSLN-
YEILLKHVE;NYEIEKINTLKEILD-EKINTLKEI;YEIEKINTLKEILDK-
INTLKEILD;NILTTILTLICISCA-ILTTILTLI;LNYEIEKINTLKEIL-
YEIEKINTL;RYEILLKHVEPSLNL-LKHVEPSLN;SLNYEIEKINTLKEI-
YEIEKINTL;YEILLKHVEPSLNLK-LKHVEPSLN;ILTTILTLICISCAV-
ILTTILTLI;KEILDKLYKNHKYKT-LDKLYKNHK
DRB1_1501 NTQIDFLENFKSEPH-IDFLENFKS;TQIDFLENFKSEPHD-
LENFKSEPH;IDFLENFKSEPHDTI-LENFKSEPH;QIDFLENFKSEPHDT-
LENFKSEPH;DFLENFKSEPHDTIS-LENFKSEPH;IEMKIKRIIYSSLNY-
MKIKRIIYS;EDIEMKIKRIIYSSL-MKIKRIIYS;DIEMKIKRIIYSSLN-MKIKRIIYS

DRB3_0101
DRB4_0101
DRB5_0101 YKNHKYKTTARNFIL-YKTTARNFI;LYKNHKYKTTARNFI-
YKNHKYKTT;DKLYKNHKYKTTARN-YKNHKYKTT;KLYKNHKYKTTARNF-
YKNHKYKTT;EILDKLYKNHKYKTT-LDKLYKNHK;LDKLYKNHKYKTTAR-
YKNHKYKTT;ENKSQDLEPSNTKNK-QDLEPSNTK;NKSQDLEPSNTKNKD-
LEPSNTKNK;KSQDLEPSNTKNKDL-LEPSNTKNK;ILDKLYKNHKYKTTA-
YKNHKYKTT;SQDLEPSNTKNKDLE-LEPSNTKNK;QDLEPSNTKNKDLEP-LEPSNTKNK

<AAU07022 4-alpha-glucanotransferase;Protein;Borrelia garinii PBi>

Allele 8-mer
A0101
A0201
QMFAYSPI;LLDFASFV;ILLNISSL;FIDSDLNL;YIFDYLNT;YAFNGLWV;ILSKEIKV;VMNLPLFI
;FAGNVYYI;VLFDRGIL;GISPDYFL;ILRKYIDV;SLPSKYGI
A0202
LLDFASFV;GISPDYFL;ILSKEIKV;QMFAYSPI;FVNSLDDL;FIDSDLNL;ILLNISSL;ALNFINRA
;FLFASSQS;SLPSKYGI;NISFITRL;FAGNVYYI;ILNEIKDL;VLFDRGIL;FDSDNQNL;FSAFAGN
V;YIFDYLNT;VAFKEYFL;FFSQFQAL;ILRKYIDV;SVSDSVII;VMNLPLFI;YAFNGLWV;FIDFLF
AS;MSSVSDSV;KKSSYWLL;YYIDLEAL
A0203
ALNFINRA;LLDFASFV;ILRKYIDV;QMFAYSPI;ILLNISSL;ILSKEIKV;VMNLPLFI;SLPSKYGI
;VLFDRGIL;YAFNGLWV;FLKDSRDA;ILNEIKDL;NLKRKSGI;GMRIMKLA;YIFDYLNT;NISFITR
L;FAGNVYYI;FQALKRYA;GISPDYFL;SVSDSVII;FIDSDLNL;FVNSLDDL;IAYDSADV;KIRINL
NL;GIGDNSTI;FLFASSQS;ELVMNLPL
A0204
LLDFASFV;YAFNGLWV;ILSKEIKV;VMNLPLFI;ILLNISSL;VLFDRGIL;FAGNVYYI;QMFAYSPI
A0206
YAFNGLWV;LLDFASFV;WLLDFASF;FIDSDLNL;FQALKRYA;QMFAYSPI;FAGNVYYI;ILLNISSL
;WQMFAYSP;YIFDYLNT;LQYFFFSQ;SQSYWQMF;GISPDYFL;NTNEDFVV;KEIKVQEV;KEAALNF
I;KFIDFLFA;ILSKEIKV;YYIDLEAL;YSIFSAFA;FIDFLFAS;FVNSLDDL;SVSDSVII
A0211
LLDFASFV;YAFNGLWV;ILLNISSL;ILSKEIKV;VLFDRGIL;SLDDLHKK;GISPDYFL;SLPSKYGI
;FIDSDLNL;PMQDYINL;WLLDFASF;QMFAYSPI;YIFDYLNT;ELVMNLPL;ILRKYIDV;VMNLPLF
I;DLEDVSRL;ILNEIKDL;SVSDSVII;GIGDNSTI;NLGNEFRA;ALNFINRA;NTNEDFVV;YYIDLE
AL;IAYDSADV;FLFASSQS;GFVSTWEV;DLFKLRNI;FLKDSRDA;RLRDFFNF;NLPLFIAY;KFIDF
LFA;NISFITRL;IKDLKIWV;FAGNVYYI
A0212
LLDFASFV;YAFNGLWV;ILSKEIKV;ILRKYIDV;ILLNISSL;VLFDRGIL;PMQDYINL;FIDSDLNL
;YIFDYLNT;SLPSKYGI;SLDDLHKK;QMFAYSPI;ILNEIKDL;WLLDFASF;YYIDLEAL;GISPDYF
L;VMNLPLFI;FLKDSRDA;ELVMNLPL;GIGDNSTI;IAYDSADV;DLEDVSRL;FFSQFQAL;FLFASS
QS;RLRDFFNF;FENDLEDV;VAFKEYFL
A0216
LLDFASFV;ILSKEIKV;ILLNISSL;YAFNGLWV;ILRKYIDV;VLFDRGIL;GISPDYFL;PMQDYINL
;DLEDVSRL;ELVMNLPL;QMFAYSPI;SLPSKYGI;NLGNEFRA;GIGDNSTI;FIDSDLNL;ALNFINR
A;VMNLPLFI;YIFDYLNT;SLDDLHKK;GFVSTWEV;FAGNVYYI;WLLDFASF;FLFASSQS;ILNEIK
DL;IAYDSADV;VAFKEYFL;NISFITRL
A0219
LLDFASFV;ILLNISSL;YAFNGLWV;ILSKEIKV;FIDSDLNL;PMQDYINL;DLEDVSRL;VMNLPLFI
;WLLDFASF;VLFDRGIL;SLPSKYGI;GISPDYFL;SLDDLHKK;ILRKYIDV;IAYDSADV;ELVMNLP
L
A0301
KLRNILSK;RSFEKFKK;KLRFDASK;TLNNWIFR;FSQFQALK;FASFVAFK;NISSLPSK;RINLNLKR
;KVQEVLQY;ISFITRLY

A1101
RSFEKFKK;TLNNWIFR;FASFVAFK;NISSLPSK;FSQFQALK;AALNFINR;GILIRNEK;SLDDLHKK
;AYSWNVLK;KVQEVLQY;NSLDDLHK;AFNGLWVK;SQFQALKR;SFKDKFLK;AFKEYFLK;KLRNILS
K;WAHQKYFK;SAFAGNVY;RINLNLKR;ISFITRLY
A2301
QYFFFSQF;PYSIFSAF;KYIDVIKI;AYKFIDFL;AYSWNVLK;NTLNNWIF;VWAHQKYF;YYIDLEAL
;EVLQYFFF;AYAFNGLW;RYSDLKKL;DVIKIDHF;RLRDFFNF;IMKLAFDF;RYANDKGI;DFASFVA
F;GAYKFIDF;AYDSADVW;WLLDFASF;TLSKNISF;NFILNEIK;AFKEYFLK;SFKDKFLK;FAYSPI
DF
A2402
KYIDVIKI;PYSIFSAF;QYFFFSQF;YYIDLEAL;DFASFVAF;VWAHQKYF;AYAFNGLW;AYKFIDFL
;RYANDKGI;AYSWNVLK;EVLQYFFF;WWAKRIGI;LVMNLPLF
A2403
QYFFFSQF;YYIDLEAL;AYDSADVW;AYKFIDFL;AYAFNGLW;RSPPYSIF;KYIDVIKI;KFLKEAAL
;RYANDKGI;VWAHQKYF;PYSIFSAF;RYSDLKKL;EVLQYFFF;SYWQMFAY;FVAFKEYF;DFASFVA
F;FFSQFQAL
A2601 YIKNCIVY;DVIKIDHF;EVLQYFFF;DVWAHQKY;EVGVGEAY;NVLKNVKY
A2602
EVLQYFFF;DVIKIDHF;EVGVGEAY;VIIPMQDY;YIKNCIVY;DVWAHQKY;EVRSFEKF;FVAFKEYF
;EIKVQEVL;DVSRLRDF;EIKDLKIW;ELVMNLPL;KVQEVLQY;DFASFVAF;NLPLFIAY;YINLGNE
F;NTLNNWIF;FIDSDLNL;NVLKNVKY;SVDEVRSF;LVMNLPLF
A2902
SYWQMFAY;VIIPMQDY;AFAGNVYY;YIKNCIVY;KVQEVLQY;SAFAGNVY;LFASSQSY;EVGVGEAY
;NVLKNVKY;QYFFFSQF;NLPLFIAY
A3001
KLRFDASK;KLRNILSK;AFKEYFLK;RSFEKFKK;EFRANIPK;SFKDKFLK;ETRYSDLK;WAHQKYFK
;AFNGLWVK
A3002 RYSDLKKL;VIIPMQDY
A3101
TLNNWIFR;HQKYFKLR;VIKIDHFR;AFNVLFDR;AALNFINR;KYEWWAKR;SFKDKFLK;AFKEYFLK
;RSFEKFKK;RINLNLKR;KNISFITR;FFNFPGMR;KLRNILSK;FITRLYGR;AFNGLWVK;SQFQALK
R;LLKENETR;RASVDEVR;YSPIDFTR;WAHQKYFK;RLRDFFNF
A3301
EYFLKDSR;TLNNWIFR;DLKKLSFK;VIKIDHFR;HQKYFKLR;FFNFPGMR;EFRANIPK;FITRLYGR
;AFNVLFDR;KYEWWAKR;SFKDKFLK
A6801
FASFVAFK;FVVWDMIR;ETRYSDLK;TLNNWIFR;FITRLYGR;FSQFQALK;YSPIDFTR;EYFLKDSR
;NISSLPSK;WAHQKYFK;VIKIDHFR;FFNFPGMR;DLKKLSFK;RSFEKFKK;NVYYIDLE;NFILNEI
K;SQFQALKR;HQKYFKLR;ISFITRLY;RINLNLKR;RASVDEVR;AALNFINR;NSLDDLHK
A6802
EAYAFNGL;FSAFAGNV;NTNEDFVV;MSSVSDSV;NISFITRL;QMFAYSPI;YSIFSAFA;NRASVDEV
;NSTIREFV;NCIVYTGI;FAGNVYYI;SPAYSWNV;QSYWQMFA;TRSPPYSI;YAFNGLWV;SVSDSVI
I;DSRDAFNV
A6901
YAFNGLWV;EAYAFNGL;NTNEDFVV;FSAFAGNV;SPAYSWNV;QMFAYSPI;FAGNVYYI;QSYWQMFA
;ELVMNLPL
B0702 SPAYSWNV
B0801 WAKRIGIL
B0802
B1501
SAFAGNVY;SQSYWQMF;YINLGNEF;YIKNCIVY;WLLDFASF;IMKLAFDF;RLRDFFNF;NQNLPHNY
;ISFITRLY;KVQEVLQY;VQEVLQYF;YLNTNEDF;QMFAYSPI;TLSKNISF;QAWDSPAY;LFASSQS
Y;LVMNLPLF
B1801 QEVLQYFF;YEWWAKRI;WEVGVGEA
B2705 KRIGILRK;MRIMKLAF

B3501
QAWDSPAY;SAFAGNVY;EVGVGEAY;SYWQMFAY;YINLGNEF;DFASFVAF;EVLQYFFF;FFSQFQAL
;DVWAHQKY;WLLDFASF;LVMNLPLF;FAYSPIDF;LFASSQSY;FVAFKEYF;YIKNCIVY;FASSQSY
W;
B3901 SRDAFNVL;IREFVNSL
B4001 VEDFENDL;QEVLQYFF;NETRYSDL;RDFFNFIL;NEKDLFKL
B4002 QEVLQYFF;KEIKVQEV
B4402 QEVLQYFF
B4403 QEVLQYFF
B4501
B5101
B5301 FASSQSYW;FAGNVYYI
B5401 PPYSIFSA;LPLFIAYD
B5701
B5801 FASSQSYW;SSYWLLDF;FAYSPIDF

Allele 9-mer
A0101 FSAFAGNVY;YSDLKKLSF;SLDDLHKKY
A0201
TLNNWIFRL;WLLDFASFV;YLNTNEDFV;VLFDRGILI;FVSTWEVGV;FIDSDLNLL;AMSSVSDSV;F
IAYDSADV;LVMNLPLFI;TLSKNISFI;LLDFASFVA;FVAFKEYFL;RLLESDLDA;SQSYWQMFA;NI
LSKEIKV;VIIPMQDYI;FILNEIKDL;YIKNCIVYT;VVWDMIRSA;VMNLPLFIA;WQMFAYSPI
A0202
YLNTNEDFV;FIDSDLNLL;FVAFKEYFL;AMSSVSDSV;TLSKNISFI;FVSTWEVGV;MIRSAMSSV;W
LLDFASFV;TLNNWIFRL;KLSFKDKFL;FIAYDSADV;VLFDRGILI;GAYKFIDFL;VIIPMQDYI;FF
NFILNEI;ILRKYIDVI;WQMFAYSPI;LLDFASFVA;FFFSQFQAL;LVMNLPLFI;FLFASSQSY;TIR
EFVNSL;LLESDLDAT;FLKDSRDAF;FIDFLFASS;SSYWLLDFA;YANDKGIEL;FASSQSYWQ
A0203
MIRSAMSSV;AMSSVSDSV;YLNTNEDFV;TLNNWIFRL;FVSTWEVGV;WLLDFASFV;TLSKNISFI;F
IAYDSADV;TIREFVNSL;FIDSDLNLL;WQMFAYSPI;FVAFKEYFL;VLFDRGILI;ILRKYIDVI;FT
RSPPYSI;SQSYWQMFA;VMNLPLFIA;LVMNLPLFI;YIKNCIVYT;VVWDMIRSA;FFNFILNEI;VII
PMQDYI;GILLNISSL;KIDHFRGFV;KLSFKDKFL;LLDFASFVA;RLRDFFNFP;SSYWLLDFA;ASKD
KVAGI;NLKRKSGIL
A0204
WLLDFASFV;TLNNWIFRL;FVSTWEVGV;YLNTNEDFV;VLFDRGILI;AMSSVSDSV;LVMNLPLFI;F
TRSPPYSI;FVAFKEYFL;VMNLPLFIA;YANDKGIEL
A0206
WLLDFASFV;WQMFAYSPI;FIDSDLNLL;SQSYWQMFA;FVSTWEVGV;AMSSVSDSV;FIAYDSADV;M
IRSAMSSV;TLNNWIFRL;YLNTNEDFV;VIIPMQDYI;FVAFKEYFL;VLFDRGILI;LQYFFFSQF;LL
DFASFVA;VVWDMIRSA;KIDHFRGFV;RGFVSTWEV;LVMNLPLFI;RLLESDLDA;FVVWDMIRS;KVQ
EVLQYF;YKFIDFLFA;GEAYAFNGL;FFFSQFQAL;AALNFINRA;SSYWLLDFA;FAYSPIDFT;GILL
NISSL;YIFDYLNTN;FIDFLFASS;GAYKFIDFL;
A0211
WLLDFASFV;YLNTNEDFV;VLFDRGILI;AMSSVSDSV;TLNNWIFRL;KIDHFRGFV;EIKDLKIWV;L
LDFASFVA;SLDDLHKKY;FIDSDLNLL;FVSTWEVGV;TLSKNISFI;VVWDMIRSA;FLFASSQSY;NI
LSKEIKV;YANDKGIEL;RLLESDLDA;MIRSAMSSV;YIFDYLNTN;FVAFKEYFL;VIIPMQDYI;TIR
EFVNSL;VMNLPLFIA;DLFKLRNIL;GILRKYIDV;YSWNVLKNV;KLSFKDKFL;FIAYDSADV;VLQY
FFFSQ;RGFVSTWEV;GILLNISSL;ILRKYIDVI;PLFIAYDSA;ANDKGIELV;AFAGNVYYI;YAFNG
LWVK;GAYKFIDFL;LVMNLPLFI
A0212
WLLDFASFV;YLNTNEDFV;VLFDRGILI;AMSSVSDSV;FVSTWEVGV;TLNNWIFRL;FLFASSQSY;M
IRSAMSSV;FIDSDLNLL;EIKDLKIWV;LLDFASFVA;VVWDMIRSA;GILRKYIDV;VLQYFFFSQ;SL
DDLHKKY;YIFDYLNTN;RLLESDLDA;NILSKEIKV;ILIRNEKDL;FVAFKEYFL;ILRKYIDVI;FIA
YDSADV;VIIPMQDYI;FFFSQFQAL;TLSKNISFI;TIREFVNSL;FILNEIKDL;KIDHFRGFV;WVED
FENDL;YANDKGIEL;VMNLPLFIA;GILLNISSL;YSWNVLKNV;LLKENETRY;DLFKLRNIL;FLKDS
RDAF

A0216
WLLDFASFV;YLNTNEDFV;AMSSVSDSV;TLNNWIFRL;EIKDLKIWV;TLSKNISFI;VLFDRGILI;K
IDHFRGFV;MIRSAMSSV;NILSKEIKV;FVSTWEVGV;FVAFKEYFL;DLFKLRNIL;GAYKFIDFL;FI
DSDLNLL;LLDFASFVA;VIIPMQDYI;ILRKYIDVI;GILRKYIDV;TIREFVNSL;KLSFKDKFL;GIL
LNISSL;PLFIAYDSA;YANDKGIEL;VVWDMIRSA;YSWNVLKNV;FLFASSQSY;
A0219
WLLDFASFV;YLNTNEDFV;AMSSVSDSV;TLNNWIFRL;FIDSDLNLL;FVSTWEVGV;TLSKNISFI;M
IRSAMSSV;LLDFASFVA;VLFDRGILI;VVWDMIRSA;FLFASSQSY;NILSKEIKV;YANDKGIEL;FV
AFKEYFL;YSWNVLKNV
A0301
RSFEKFKKK;LSFKDKFLK;VAFKEYFLK;FLFASSQSY;RINLNLKRK;KIRINLNLK;QSYWQMFAY;I
LNEIKDLK;KVAGISPDY;PAYSWNVLK;ALKRYANDK
A1101
VAFKEYFLK;LSFKDKFLK;SADVWAHQK;RSFEKFKKK;QSYWQMFAY;NTLNNWIFR;PAYSWNVLK;S
AFAGNVYY;YAFNGLWVK;RINLNLKRK;NSLDDLHKK;ILNEIKDLK;KIRINLNLK;SVIIPMQDY;NV
KYEWWAK;ASFVAFKEY;KVAGISPDY;
A2301
AYKFIDFLF;DYLNTNEDF;DYINLGNEF;KYKKIRINL;YWLLDFASF;SFVAFKEYF;MFAYSPIDF;V
YYIDLEAL;VWAHQKYFK;KYGIGDLGK;KFIDSDLNL;RIMKLAFDF;SRLRDFFNF;AYSPIDFTR;FL
KEAALNF;KVQEVLQYF;NYIKNCIVY;AFAGNVYYI;LQYFFFSQF;ELVMNLPLF;DLGKGAYKF;FFN
FILNEI;EFVNSLDDL
A2402
AYKFIDFLF;DYINLGNEF;YWLLDFASF;AFAGNVYYI;DYLNTNEDF;AYAFNGLWV;MFAYSPIDF;K
YEWWAKRI;VYYIDLEAL;KYKKIRINL;WWAKRIGIL
A2403
YWLLDFASF;AYKFIDFLF;VYYIDLEAL;YFLEQEQAW;KVQEVLQYF;DYINLGNEF;DYLNTNEDF;S
FVAFKEYF;KYKKIRINL;RIMKLAFDF;KFKKKSSYW;FFFSQFQAL;AFAGNVYYI;MFAYSPIDF;AT
LSKNISF;KYEWWAKRI;AYAFNGLWV;FFNFILNEI;AWDSPAYSW
A2601 ELVMNLPLF;SVIIPMQDY
A2602
SVIIPMQDY;DVWAHQKYF;ELVMNLPLF;DVSRLRDFF;QSYWQMFAY;KVQEVLQYF;FIDSDLNLL;F
VAFKEYFL;KVAGISPDY;EFVNSLDDL;NISFITRLY;NISSLPSKY
A2902
SAFAGNVYY;NYIKNCIVY;FLFASSQSY;QSYWQMFAY;SVIIPMQDY;MNLPLFIAY;AYKFIDFLF;F
SAFAGNVY;DYINLGNEF;NISSLPSKY
A3001
KIRINLNLK;RSFEKFKKK;EVRSFEKFK;RGILIRNEK;ALKRYANDK;ETRYSDLKK;RLRDFFNFP;R
INLNLKRK;NVKYEWWAK;LSFKDKFLK;VAFKEYFLK;SDLDATLSK;AKRIGILRK;SWNVLKNVK;RN
ILSKEIK;RGFVSTWEV
A3002
KVAGISPDY;NISSLPSKY;DVSRLRDFF;KSSYWLLDF;AYKFIDFLF;KYKKIRINL;VQEVLQYFF
A3101
SFITRLYGR;AYSPIDFTR;NTLNNWIFR;YINLGNEFR;WAKRIGILR;RSFEKFKKK;DVIKIDHFR;K
YKKIRINL;GLWVKSPGR;LSFKDKFLK;DFFNFPGMR;KIRINLNLK;VWAHQKYFK;DAFNVLFDR;KE
YFLKDSR;VAFKEYFLK;YAFNGLWVK;SYWQMFAYS
A3301
DVIKIDHFR;DFFNFPGMR;DAFNVLFDR;DFVVWDMIR;DFASFVAFK;SFITRLYGR;YINLGNEFR;N
TLNNWIFR;DLEDVSRLR;EVRSFEKFK;NVKYEWWAK;AYSPIDFTR;EAALNFINR;FFSQFQALK
A6801
DVIKIDHFR;DAFNVLFDR;DFASFVAFK;EAALNFINR;YINLGNEFR;NTLNNWIFR;LSFKDKFLK;Y
AFNGLWVK;EVRSFEKFK;ETRYSDLKK;DFFNFPGMR;VAFKEYFLK;FSQFQALKR;QSYWQMFAY;FF
SQFQALK;NISFITRLY;NVKYEWWAK;SAFAGNVYY;DFVVWDMIR;DLEDVSRLR;ILNEIKDLK;WAK
RIGILR;PAYSWNVLK;AYSPIDFTR;SFITRLYGR;FASFVAFKE;SADVWAHQK;NFPGMRIMK;NSLD
DLHKK;EAYAFNGLW;FNFILNEIK
A6802
FVAFKEYFL;FTRSPPYSI;DSPAYSWNV;FIAYDSADV;WQMFAYSPI;NVYYIDLEA;MIRSAMSSV;F

VSTWEVGV;DNSTIREFV;EVLQYFFFS;WLLDFASFV;LVMNLPLFI;RGFVSTWEV;TLSKNISFI;TL
NNWIFRL;EDFVVWDMI;MSSVSDSVI;HKKYIFDYL;EIKDLKIWV;TGIGDNSTI
A6901
FVSTWEVGV;YSWNVLKNV;WLLDFASFV;LVMNLPLFI;FIAYDSADV;TLNNWIFRL;FTRSPPYSI;D
SPAYSWNV;FIDSDLNLL;EVLQYFFFS;QAWDSPAYS;NILSKEIKV;FAYSPIDFT;EVGVGEAYA;EI
KDLKIWV;
B0702
SPAYSWNVL;FPGMRIMKL;PPYSIFSAF;MIRSAMSSV;SPPYSIFSA;IPMQDYINL;RANIPKNTL;T
IREFVNSL
B0801 NLKRKSGIL
B0802
B1501
FLFASSQSY;EQAWDSPAY;FSAFAGNVY;SAFAGNVYY;FLKEAALNF;FLKDSRDAF;SQFQALKRY;G
MRIMKLAF;KVAGISPDY;WVKSPGRDF;LQYFFFSQF;QSYWQMFAY;HQKYFKLRF;KVQEVLQYF;WQ
MFAYSPI;SVIIPMQDY;ASVDEVRSF;ASFVAFKEY;LLKENETRY;WEVGVGEAY
B1801
WEVGVGEAY;IELVMNLPL;MNLPLFIAY;QEVLQYFFF;IKVQEVLQY;DEVRSFEKF;LESDLDATL;Q
SYWQMFAY
B2705 KRIGILRKY;IRINLNLKR
B3501
EQAWDSPAY;FSAFAGNVY;PPYSIFSAF;QSYWQMFAY;SPAYSWNVL;FFFSQFQAL;WEVGVGEAY;M
NLPLFIAY;SAFAGNVYY;YANDKGIEL;YFLEQEQAW;FLFASSQSY;IAYDSADVW;IPMQDYINL;LD
FASFVAF;FLKDSRDAF;VGVGEAYAF;SPGRDFFNF
B3901 GRDFFNFIL
B4001 GEAYAFNGL;IELVMNLPL;KEIKVQEVL;QEVLQYFFF;LESDLDATL
B4002 QEVLQYFFF;KEIKVQEVL
B4402 QEVLQYFFF
B4403 QEVLQYFFF
B4501
B5101 IPMQDYINL
B5301 SPGRDFFNF;IPKNTLNNW;FPGMRIMKL;PPYSIFSAF;IPMQDYINL
B5401 LPLFIAYDS;SPPYSIFSA
B5701 NTNEDFVVW;IAYDSADVW
B5801
IAYDSADVW;KSSYWLLDF;LFASSQSYW;EAYAFNGLW;NTNEDFVVW;QSYWQMFAY;RIMKLAFDF;F
SAFAGNVY;KVAGISPDY;ASSQSYWQM;VAGISPDYF

Allele 10-mer

A0101 SADVWAHQKY;FSAFAGNVYY
A0201
YLNTNEDFVV;FLKEAALNFI;WLLDFASFVA;FINRASVDEV;TLNNWIFRLL;ALNFINRASV;SIFSA
FAGNV;YANDKGIELV;ALDKFIDSDL;SAMSSVSDSV;ILNEIKDLKI;SAFAGNVYYI;LVMNLPLFIA
;FVVWDMIRSA;AMSSVSDSVI;SLDDLHKKYI;RLLESDLDAT;LLESDLDATL;SVSDSVIIPM;ATLS
KNISFI
A0202
FLKEAALNFI;WLLDFASFVA;YLNTNEDFVV;SAFAGNVYYI;LLESDLDATL;AMSSVSDSVI;LVMNL
PLFIA;FLFASSQSYW;TLNNWIFRLL;FAGNVYYIDL;SAMSSVSDSV;ALDKFIDSDL;NVYYIDLEAL
;SLDDLHKKYI;SVSDSVIIPM;WIFRLLESDL;ALNFINRASV;NLGNEFRANI;FINRASVDEV;ILNE
IKDLKI;RLLESDLDAT;SIFSAFAGNV;YANDKGIELV;SVIIPMQDYI;ILLNISSLPS;ATLSKNISF
I;FASSQSYWQM;RLRDFFNFPG;NTLNNWIFRL
A0203
FLKEAALNFI;ALNFINRASV;FINRASVDEV;YLNTNEDFVV;FVVWDMIRSA;TLNNWIFRLL;SIFSA
FAGNV;YANDKGIELV;KLRNILSKEI;SAMSSVSDSV;AMSSVSDSVI;DMIRSAMSSV;ILNEIKDLKI
;NLNLKRKSGI;STIREFVNSL;NLGNEFRANI;YINLGNEFRA;WLLDFASFVA;NLKRKSGILL;NVYY
IDLEAL;LLESDLDATL;LVMNLPLFIA;SLDDLHKKYI;SAFAGNVYYI

A0204
YLNTNEDFVV;FINRASVDEV;FLKEAALNFI;STWEVGVGEA;ALNFINRASV;SIFSAFAGNV;YANDK
GIELV;TLNNWIFRLL;LVMNLPLFIA;SAFAGNVYYI
A0206
WLLDFASFVA;FVVWDMIRSA;FINRASVDEV;FLKEAALNFI;SAMSSVSDSV;YLNTNEDFVV;SIFSA
FAGNV;YANDKGIELV;SQFQALKRYA;SAFAGNVYYI;STIREFVNSL;RLLESDLDAT;YWLLDFASFV
;NTLNNWIFRL;YINLGNEFRA;LLDFASFVAF;NVYYIDLEAL;SQSYWQMFAY;STWEVGVGEA;LVMN
LPLFIA;FASSQSYWQM;ATLSKNISFI;TLNNWIFRLL;KSSYWLLDFA;YIFDYLNTNE;SVIIPMQDY
I;ALNFINRASV;YTGIGDNSTI;RSPPYSIFSA
A0211
YLNTNEDFVV;SLDDLHKKYI;WLLDFASFVA;ALNFINRASV;YANDKGIELV;TLNNWIFRLL;FINRA
SVDEV;FLKEAALNFI;SIFSAFAGNV;ALDKFIDSDL;DMIRSAMSSV;LLESDLDATL;ILNEIKDLKI
;ELVMNLPLFI;YINLGNEFRA;SAFAGNVYYI;SVSDSVIIPM;VVWDMIRSAM;DLGKGAYKFI;EAYA
FNGLWV;KLRNILSKEI;DLDATLSKNI;RLLESDLDAT;STWEVGVGEA;AMSSVSDSVI;FVVWDMIRS
A;NLGNEFRANI;GISPDYFLEQ;LLDFASFVAF;VLFDRGILIR;TLSKNISFIT;NTLNNWIFRL;NLK
RKSGILL;FLFASSQSYW;YFFFSQFQAL;FIDFLFASSQ;SAMSSVSDSV;YWLLDFASFV;WIFRLLES
DL;SVDEVRSFEK;IIPMQDYINL;YIFDYLNTNE
A0212
YLNTNEDFVV;SLDDLHKKYI;WLLDFASFVA;ALNFINRASV;ALDKFIDSDL;FLKEAALNFI;YANDK
GIELV;FINRASVDEV;LLESDLDATL;SIFSAFAGNV;ILNEIKDLKI;YINLGNEFRA;VVWDMIRSAM
;DMIRSAMSSV;TLNNWIFRLL;WIFRLLESDL;VLFDRGILIR;YIFDYLNTNE;RLLESDLDAT;YFFF
SQFQAL;ELVMNLPLFI;AMSSVSDSVI;FLFASSQSYW;SAFAGNVYYI
A0216
YLNTNEDFVV;SLDDLHKKYI;ALNFINRASV;DMIRSAMSSV;WLLDFASFVA;FINRASVDEV;FLKEA
ALNFI;SIFSAFAGNV;LLESDLDATL;ALDKFIDSDL;YANDKGIELV;DLGKGAYKFI;TLNNWIFRLL
;ELVMNLPLFI;ILNEIKDLKI;EAYAFNGLWV;SAFAGNVYYI;YINLGNEFRA;NLKRKSGILL;TLSK
NISFIT;AMSSVSDSVI;SAMSSVSDSV;KLRNILSKEI;NLGNEFRANI;FRGFVSTWEV;WIFRLLESD
L
A0219
YLNTNEDFVV;WLLDFASFVA;YANDKGIELV;FINRASVDEV;LLESDLDATL;SLDDLHKKYI;DMIRS
AMSSV;FLKEAALNFI;TLNNWIFRLL;ALNFINRASV;SAMSSVSDSV;ALDKFIDSDL;DLDATLSKNI
;ELVMNLPLFI
A0301
KLSFKDKFLK;FVAFKEYFLK;LLNISSLPSK;AYAFNGLWVK;LIRNEKDLFK;KLRFDASKDK;YSDLK
KLSFK;ILRKYIDVIK;FILNEIKDLK;VMNLPLFIAY;DVWAHQKYFK;FFFSQFQALK;SVDEVRSFEK
;LFKLRNILSK;FSAFAGNVYY;SPAYSWNVLK;VLFDRGILIR;LDFASFVAFK;SQSYWQMFAY;FIDS
DLNLLK
A1101
SVDEVRSFEK;FVAFKEYFLK;KLSFKDKFLK;LLNISSLPSK;ISFITRLYGR;SQSYWQMFAY;FVNSL
DDLHK;YSDLKKLSFK;FIDSDLNLLK;DVWAHQKYFK;VMNLPLFIAY;SPAYSWNVLK;NQNLPHNYIK
;DSADVWAHQK;VLFDRGILIR;AYAFNGLWVK;YSWNVLKNVK;LDFASFVAFK;FFFSQFQALK
A2301
SYWLLDFASF;KFLKEAALNF;AYAFNGLWVK;RYSDLKKLSF;YFLKDSRDAF;YYIDLEALDK;GAYKF
IDFLF;RYANDKGIEL;VSRLRDFFNF;VLQYFFFSQF;VWAHQKYFKL;LWVKSPGRDF;KVQEVLQYFF
;KFIDSDLNLL;DFFNFILNEI;SFVAFKEYFL;ILIRNEKDLF;DYFLEQEQAW;KFKKKSSYWL;IWVE
DFENDL;YFFFSQFQAL;NFILNEIKDL;FFFSQFQALK;KSPGRDFFNF
A2402
SYWLLDFASF;RYSDLKKLSF;YWQMFAYSPI;KFLKEAALNF;VWAHQKYFKL;YFLKDSRDAF;AYSWN
VLKNV;RYANDKGIEL;VQEVLQYFFF;KFIDSDLNLL
A2403
YFLKDSRDAF;KFLKEAALNF;SYWLLDFASF;RYANDKGIEL;RYSDLKKLSF;YFFFSQFQAL;KVQEV
LQYFF;KFKKKSSYWL;FTRSPPYSIF;AYSWNVLKNV;YWQMFAYSPI;AHQKYFKLRF
A2601 EIKVQEVLQY;SVSDSVIIPM;STIREFVNSL
A2602
EIKVQEVLQY;FTRSPPYSIF;EVGVGEAYAF;STIREFVNSL;ETRYSDLKKL;SVSDSVIIPM;YIDLE

ALDKF;WVKSPGRDFF;KVQEVLQYFF;YIDVIKIDHF;KVAGISPDYF;PIDFTRSPPY;SVIIPMQDYI
;VVWDMIRSAM;VIKIDHFRGF;DLHKKYIFDY;DSVIIPMQDY
A2902
VMNLPLFIAY;SWNVLKNVKY;FSAFAGNVYY;SQSYWQMFAY;IFSAFAGNVY;FASFVAFKEY;SYWLL
DFASF;HNYIKNCIVY
A3001
KLRFDASKDK;LLNISSLPSK;ILRKYIDVIK;LFKLRNILSK;EVRSFEKFKK;LIRNEKDLFK;KLSFK
DKFLK;RLRDFFNFPG;KIRINLNLKR;YFKLRFDASK;SVDEVRSFEK;KNVKYEWWAK;WAKRIGILRK
A3002 RYSDLKKLSF;SQSYWQMFAY;KVQEVLQYFF;SWNVLKNVKY
A3101
KIRINLNLKR;ISFITRLYGR;LSKNISFITR;FAYSPIDFTR;KLSFKDKFLK;DYINLGNEFR;FFSQF
QALKR;KNTLNNWIFR;WWAKRIGILR;RDAFNVLFDR;FFFSQFQALK;FVAFKEYFLK;AYAFNGLWVK
;KYKKIRINLN
A3301
DYINLGNEFR;FFSQFQALKR;FAYSPIDFTR;LSKNISFITR;FFFSQFQALK;ISFITRLYGR;DFASF
VAFKE;VLFDRGILIR
A6801
FAYSPIDFTR;FVAFKEYFLK;DSADVWAHQK;ISFITRLYGR;EVRSFEKFKK;NVKYEWWAKR;DVWAH
QKYFK;DYINLGNEFR;FVNSLDDLHK;FFFSQFQALK;FFSQFQALKR;SVDEVRSFEK;LSKNISFITR
;SPAYSWNVLK;FSAFAGNVYY;EDFVVWDMIR;FFNFILNEIK;WAHQKYFKLR;FASFVAFKEY;LDFA
SFVAFK;TGIGDNSTIR;FILNEIKDLK;FNFPGMRIMK;ESDLDATLSK;EVLQYFFFSQ;YYIDLEALD
K;VLFDRGILIR
A6802
EAALNFINRA;SAFAGNVYYI;NVYYIDLEAL;SIFSAFAGNV;STIREFVNSL;EAYAFNGLWV;SAMSS
VSDSV;SVIIPMQDYI;NTLNNWIFRL;FINRASVDEV;DMIRSAMSSV;SVSDSVIIPM;FVVWDMIRSA
;FRGFVSTWEV;YANDKGIELV;LVMNLPLFIA;STWEVGVGEA;WDSPAYSWNV;SGILLNISSL
A6901
EAYAFNGLWV;STWEVGVGEA;NTLNNWIFRL;YANDKGIELV;SIFSAFAGNV;SAFAGNVYYI;FINRA
SVDEV;ELVMNLPLFI;SVSDSVIIPM;NVLFDRGILI;WLLDFASFVA;DMIRSAMSSV;SAMSSVSDSV
;LVMNLPLFIA;FVVWDMIRSA;NVYYIDLEAL;FASSQSYWQM;EVLQYFFFSQ
B0702 SPPYSIFSAF;LPSKYGIGDL;VVWDMIRSAM;SVSDSVIIPM
B0801
B0802
B1501
VMNLPLFIAY;SQSYWQMFAY;QMFAYSPIDF;FSAFAGNVYY;IFSAFAGNVY;QEQAWDSPAY;WVKSP
GRDFF;KVAGISPDYF;FLFASSQSYW;FTRSPPYSIF
B1801
IELVMNLPLF;YEWWAKRIGI;WEVGVGEAYA;IKVQEVLQYF;NEIKDLKIWV;QEQAWDSPAY;
B2705 KRIGILRKYI
B3501
FASFVAFKEY;SPPYSIFSAF;FASSQSYWQM;VVWDMIRSAM;FSAFAGNVYY;EVGVGEAYAF;LLDFA
SFVAF;SVSDSVIIPM;IFSAFAGNVY;DFLFASSQSY;YFLKDSRDAF;YFFFSQFQAL;SADVWAHQKY
;NVYYIDLEAL;VMNLPLFIAY;QAWDSPAYSW;QEQAWDSPAY;SYWLLDFASF;FIAYDSADVW
B3901 FRANIPKNTL
B4001 REFVNSLDDL;YEWWAKRIGI;KENETRYSDL;NEIKDLKIWV;IELVMNLPLF
B4002 REFVNSLDDL;KENETRYSDL;QEVLQYFFFS
B4402 GEAYAFNGLW
B4403 QEVLQYFFFS;GEAYAFNGLW
B4501
B5101 LPLFIAYDSA;IPKNTLNNWI;LPHNYIKNCI;
B5301 SPGRDFFNFI;SPPYSIFSAF;LPHNYIKNCI;IPKNTLNNWI;LPSKYGIGDL
B5401 LPLFIAYDSA;FPGMRIMKLA;LPHNYIKNCI;PPYSIFSAFA;IPKNTLNNWI
B5701
B5801
QAWDSPAYSW;FLFASSQSYW;KVAGISPDYF;RASVDEVRSF;GAYKFIDFLF;FIAYDSADVW;ASSQS
YWQMF;ASFVAFKEYF;FSAFAGNVYY;KSPGRDFFNF;FASSQSYWQM

Allele 11-mer

A0101 DSDNQNLPHNY;SSQSYWQMFAY;DSADVWAHQKY

A0201

RLLESDLDATL;FLKDSRDAFNV;QMFAYSPIDFT;FILNEIKDLKI;AMSSVSDSVII;ILSKEIKVQEV
;FLFASSQSYWQ;KVAGISPDYFL;FIAYDSADVWA;RLRDFFNFPGM;YIKNCIVYTGI;VIIPMQDYIN
L;ILRKYIDVIKI;KIWVEDFENDL

A0202

FLKDSRDAFNV;FLFASSQSYWQ;ILSKEIKVQEV;AMSSVSDSVII;FIAYDSADVWA;KVAGISPDYFL
;FSAFAGNVYYI;GVGEAYAFNGL;YIKNCIVYTGI;FDYLNTNEDFV;VIIPMQDYINL;RLLESDLDAT
L;RLRDFFNFPGM;KLAFDFDSDNQ;KLRFDASKDKV;NISSLPSKYGI;QMFAYSPIDFT;ILRKYIDVI
KI;NLPLFIAYDSA;FENDLEDVSRL;SLPSKYGIGDL;LQYFFFSQFQA;FVVWDMIRSAM;YLNTNEDF
VVW

A0203

FLKDSRDAFNV;YIKNCIVYTGI;ILSKEIKVQEV;RLRDFFNFPGM;AMSSVSDSVII;ILRKYIDVIKI
;FIAYDSADVWA;SLPSKYGIGDL;VIKIDHFRGFV;NLPLFIAYDSA;KLRFDASKDKV;ALKRYANDKG
I;GVGEAYAFNGL;VLKNVKYEWWA;RLLESDLDATL;FLFASSQSYWQ;AALNFINRASV;VIIPMQDYI
NL;LQYFFFSQFQA;FVVWDMIRSAM;NISSLPSKYGI;NLNLKRKSGIL;PLFIAYDSADV

A0204 ILSKEIKVQEV;RLLESDLDATL;FLKDSRDAFNV;KVAGISPDYFL

A0206

FLKDSRDAFNV;WLLDFASFVAF;RLLESDLDATL;LQYFFFSQFQA;FVVWDMIRSAM;AALNFINRASV
;FIAYDSADVWA;MQDYINLGNEF;KVAGISPDYFL;GVGEAYAFNGL;SQSYWQMFAYS;FILNEIKDLK
I;RLRDFFNFPGM;YIKNCIVYTGI;VIIPMQDYINL;WQMFAYSPIDF;ILSKEIKVQEV;KVQEVLQYF
FF;GEAYAFNGLWV;FLFASSQSYWQ;FSAFAGNVYYI;RSAMSSVSDSV;AMSSVSDSVII

A0211

FLKDSRDAFNV;RLLESDLDATL;ILSKEIKVQEV;FLFASSQSYWQ;VLKNVKYEWWA;SLDDLHKKYIF
;WLLDFASFVAF;SYWLLDFASFV;KVAGISPDYFL;PLFIAYDSADV;AMSSVSDSVII;RLRDFFNFPG
M;AALNFINRASV;YIDLEALDKFI;KLRFDASKDKV;VIIPMQDYINL;NLPLFIAYDSA;ELVMNLPLF
IA;ILRKYIDVIKI;SLPSKYGIGDL;NLPHNYIKNCI;VLFDRGILIRN;LLDFASFVAFK;VIKIDHFR
GFV;VLQYFFFSQFQ;QMFAYSPIDFT;DLHKKYIFDYL;KIDHFRGFVST;HFRGFVSTWEV;RIGILRK
YIDV;DVWAHQKYFKL;AWDSPAYSWNV;YIKNCIVYTGI;RYANDKGIELV;TLNNWIFRLLE;FILNEI
KDLKI;KIWVEDFENDL;IGDNSTIREFV;FIAYDSADVWA;SVSDSVIIPMQ;ILLNISSLPSK;YIFDY
LNTNED

A0212

FLKDSRDAFNV;RLLESDLDATL;ILSKEIKVQEV;FLFASSQSYWQ;VLKNVKYEWWA;RLRDFFNFPGM
;PLFIAYDSADV;WLLDFASFVAF;VIIPMQDYINL;AMSSVSDSVII;VLQYFFFSQFQ;SLDDLHKKYI
F;KLRFDASKDKV;FILNEIKDLKI;AALNFINRASV;ILRKYIDVIKI;SYWLLDFASFV;SLPSKYGIG
DL;VLFDRGILIRN;QMFAYSPIDFT;KVAGISPDYFL;KIWVEDFENDL;ALKRYANDKGI;YIDLEALD
KFI;NLPHNYIKNCI

A0216

FLKDSRDAFNV;ILSKEIKVQEV;RLLESDLDATL;VLKNVKYEWWA;FLFASSQSYWQ;SYWLLDFASFV
;DLHKKYIFDYL;AALNFINRASV;KVAGISPDYFL;PLFIAYDSADV;KLRFDASKDKV;ILRKYIDVIK
I;AMSSVSDSVII;VIKIDHFRGFV;NLPLFIAYDSA;QMFAYSPIDFT;VIIPMQDYINL;NLPHNYIKN
CI;DVWAHQKYFKL;HFRGFVSTWEV;RLRDFFNFPGM;SLPSKYGIGDL;RIGILRKYIDV;VLQYFFFS
QFQ;ELVMNLPLFIA;GVGEAYAFNGL

A0219

FLKDSRDAFNV;ILSKEIKVQEV;FLFASSQSYWQ;RLLESDLDATL;AMSSVSDSVII;KVAGISPDYFL
;WLLDFASFVAF

A0301

ILLNISSLPSK;LLDFASFVAFK;KLRNILSKEIK;ILIRNEKDLFK;YFFFSQFQALK;FFNFPGMRIMK
;KIRINLNLKRK;DLFKLRNILSK;LVMNLPLFIAY;TLSKNISFITR;KYFKLRFDASK;LLNISSLPSK
Y;GILRKYIDVIK;FVNSLDDLHKK;GIGDLGKGAYK

A1101

ILLNISSLPSK;SSQSYWQMFAY;ASVDEVRSFEK;LVMNLPLFIAY;SFVAFKEYFLK;FVNSLDDLHKK
;KFIDSDLNLLK;LLDFASFVAFK;EAYAFNGLWVK;SIFSAFAGNVY;ILIRNEKDLFK;YFFFSQFQAL

K;GILRKYIDVIK;GIGDLGKGAYK;KYFKLRFDASK;RYSDLKKLSFK;TLSKNISFITR;DSPAYSWNV
LK;AYSWNVLKNVK
A2301
KYIDVIKIDHF;YYIDLEALDKF;EYFLKDSRDAF;KYFKLRFDASK;VYYIDLEALDK;KYKKIRINLNL
;AYSWNVLKNVK;LWVKSPGRDFF;RYSDLKKLSFK;IFDYLNTNEDF;KVQEVLQYFFF;QYFFFSQFQA
L;SFVAFKEYFLK;EFVNSLDDLHK;KFIDSDLNLLK;VYTGIGDNSTI;WQMFAYSPIDF;YFFFSQFQA
LK;DFTRSPPYSIF;EVLQYFFFSQF;DYLNTNEDFVV;NFILNEIKDLK;WLLDFASFVAF;KFLKEAAL
NFI;SYWQMFAYSPI;FFNFPGMRIMK;DFFNFILNEIK;WWAKRIGILRK;DVIKIDHFRGF;KFKKKSS
YWLL;DVSRLRDFFNF;DFLFASSQSYW;NWIFRLLESDL
A2402
YYIDLEALDKF;KYIDVIKIDHF;SYWQMFAYSPI;VYTGIGDNSTI;QYFFFSQFQAL;KFLKEAALNFI
;KFKKKSSYWLL;LWVKSPGRDFF;KYKKIRINLNL;DFTRSPPYSIF;KVQEVLQYFFF;EYFLKDSRDA
F;DYLNTNEDFVV;KYEWWAKRIGI
A2403
YYIDLEALDKF;KYIDVIKIDHF;KVQEVLQYFFF;RSPPYSIFSAF;QYFFFSQFQAL;KFLKEAALNFI
;KYKKIRINLNL;KYEWWAKRIGI;KFKKKSSYWLL;EYFLKDSRDAF;AFAGNVYYIDL;SYWQMFAYSP
I;IFDYLNTNEDF
A2601
DVIKIDHFRGF;STWEVGVGEAY;DSADVWAHQKY;YGIGDLGKGAY;SIFSAFAGNVY;EVLQYFFFSQF
;FVVWDMIRSAM;YSWNVLKNVKY
A2602
EIKVQEVLQYF;DVIKIDHFRGF;EVLQYFFFSQF;FVVWDMIRSAM;YGIGDLGKGAY;KVQEVLQYFFF
;DVSRLRDFFNF;SIFSAFAGNVY;LVMNLPLFIAY;DVWAHQKYFKL;VIIPMQDYINL;NTNEDFVVWD
M;STWEVGVGEAY;SSQSYWQMFAY;DFTRSPPYSIF;SVDEVRSFEKF;DFFNFPGMRIM;DFASFVAFK
EY;KVAGISPDYFL;DSADVWAHQKY
A2902
LVMNLPLFIAY;IFSAFAGNVYY;YSWNVLKNVKY;YYIDLEALDKF;FFSQFQALKRY;SIFSAFAGNVY
;STWEVGVGEAY;SSQSYWQMFAY
A3001
KLRNILSKEIK;KYFKLRFDASK;KIRINLNLKRK;LGNEFRANIPK;KFIDSDLNLLK;YFFFSQFQALK
;RYSDLKKLSFK;EVRSFEKFKKK;SFVAFKEYFLK;RLRDFFNFPGM;KENETRYSDLK;ASVDEVRSFE
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A3002
RYSDLKKLSFK;KYIDVIKIDHF;DVSRLRDFFNF;KVQEVLQYFFF;IFSAFAGNVYY;KYKKIRINLNL
A3101
KYFKLRFDASK;MFAYSPIDFTR;AFKEYFLKDSR;RYSDLKKLSFK;YFFFSQFQALK;FFFSQFQALKR
;TLSKNISFITR;SFVAFKEYFLK;KNVKYEWWAKR;YIDVIKIDHFR;NISFITRLYGR;KLRNILSKEI
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K;DLFKLRNILSK
A6801
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;DSPAYSWNVLK;FVNSLDDLHKK;TLSKNISFITR;FFFSQFQALKR;SFVAFKEYFLK;NVLFDRGILI
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KK;LLDFASFVAFK;EFVNSLDDLHK;FFNFPGMRIMK;DSADVWAHQKY;QDYINLGNEFR;EWWAKRIG
ILR;FASFVAFKEYF;SIFSAFAGNVY;ILIRNEKDLFK
A6802
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;RSAMSSVSDSV;NISSLPSKYGI;DAFNVLFDRGI;EAALNFINRAS;SAMSSVSDSVI;NTLNNWIFRL
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KL

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B0801
B0802
B1501
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;SIFSAFAGNVY;IFSAFAGNVYY;GMRIMKLAFDF;EQEQAWDSPAY;LLNISSLPSKY;YSWNVLKNVK
Y
B1801
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;WLLDFASFVAF
B2705 KRYANDKGIEL;TRYSDLKKLSF
B3501
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;STWEVGVGEAY;IPKNTLNNWIF;EQEQAWDSPAY;FASFVAFKEYF;WLLDFASFVAF;SIFSAFAGNV
Y;WEVGVGEAYAF;EVLQYFFFSQF;YSWNVLKNVKY;IAYDSADVWAH;YGIGDLGKGAY;FFSQFQALK
RY;WAHQKYFKLRF;SSVSDSVIIPM;DFASFVAFKEY;MQDYINLGNEF;SSQSYWQMFAY
B3901 FKDKFLKEAAL;EKDLFKLRNIL
B4001
WEVGVGEAYAF;GEAYAFNGLWV;YEWWAKRIGIL;FENDLEDVSRL;IELVMNLPLFI;NETRYSDLKKL
B4002 WEVGVGEAYAF
B4402 KEIKVQEVLQY
B4403 KEIKVQEVLQY
B4501
B5101 LPHNYIKNCIV
B5301 FPGMRIMKLAF;IPKNTLNNWIF;SPGRDFFNFIL;FASFVAFKEYF;SPIDFTRSPPY
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B5701
B5801
FASFVAFKEYF;LFIAYDSADVW;FASSQSYWQMF;YLNTNEDFVVW;ILNEIKDLKIW;KGAYKFIDFLF
;SSYWLLDFASF

Allele 15-mer plus 9-mer core

DRB1_0101 GILLNISSLPSKYGI-ISSLPSKYG;LRDFFNFPGMRIMKL-
FFNFPGMRI;RDFFNFPGMRIMKLA-FPGMRIMKL;SGILLNISSLPSKYG-
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IRSAMSSVS;DFFNFPGMRIMKLAF-FPGMRIMKL;FFNFPGMRIMKLAFD-
FPGMRIMKL;ILLNISSLPSKYGIG-ISSLPSKYG;LLNISSLPSKYGIGD-
ISSLPSKYG;VWDMIRSAMSSVSDS-IRSAMSSVS;WDMIRSAMSSVSDSV-
IRSAMSSVS;DKGIELVMNLPLFIA-LVMNLPLFI;GIELVMNLPLFIAYD-
VMNLPLFIA;IELVMNLPLFIAYDS-VMNLPLFIA;KGIELVMNLPLFIAY-
VMNLPLFIA;DMIRSAMSSVSDSVI-IRSAMSSVS;FNFPGMRIMKLAFDF-
FPGMRIMKL;LNISSLPSKYGIGDL-ISSLPSKYG;ELVMNLPLFIAYDSA-
VMNLPLFIA;ASSQSYWQMFAYSPI-YWQMFAYSP;QSYWQMFAYSPIDFT-
YWQMFAYSP;SQSYWQMFAYSPIDF-YWQMFAYSP;SSQSYWQMFAYSPID-
YWQMFAYSP;DFVVWDMIRSAMSSV-WDMIRSAMS;RKSGILLNISSLPSK-
LLNISSLPS;FASSQSYWQMFAYSP-FASSQSYWQ;KSGILLNISSLPSKY-
LLNISSLPS;EDFVVWDMIRSAMSS-WDMIRSAMS;KRKSGILLNISSLPS-
ILLNISSLP;AYSPIDFTRSPPYSI-YSPIDFTRS;IDFTRSPPYSIFSAF-
FTRSPPYSI;NEDFVVWDMIRSAMS-VVWDMIRSA;PIDFTRSPPYSIFSA-
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FTRSPPYSI;KDLFKLRNILSKEIK-LRNILSKEI;DLFKLRNILSKEIKV-
LRNILSKEI;EKDLFKLRNILSKEI-LFKLRNILS;LFKLRNILSKEIKVQ-
LRNILSKEI;FKLRNILSKEIKVQE-LRNILSKEI;YWQMFAYSPIDFTRS-

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FRANIPKNT;LVMNLPLFIAYDSAD-VMNLPLFIA;NEFRANIPKNTLNNW-
FRANIPKNT;MIRSAMSSVSDSVII-IRSAMSSVS;NLGNEFRANIPKNTL-
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FTRSPPYSI;EKFKKKSSYWLLDFA-FKKKSSYWL;VRSFEKFKKKSSYWL-
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FIDFLFASS;DKFLKEAALNFINRA-LKEAALNFI;FKDKFLKEAALNFIN-
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DRB1_0401 MKYKKIRINLNLKRK-YKKIRINLN;KFKKKSSYWLLDFAS-
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YIFDYLNTN;KKYIFDYLNTNEDFV-YIFDYLNTN;HKKYIFDYLNTNEDF-
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LFKLRNILS;RNEKDLFKLRNILSK-LFKLRNILS;VVWDMIRSAMSSVSD-
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DRB1_0802 FNVLFDRGILIRNEK-FDRGILIRN;VLFDRGILIRNEKDL-
RGILIRNEK;LFDRGILIRNEKDLF-RGILIRNEK;LEQEQAWDSPAYSWN-
EQAWDSPAY;ASSQSYWQMFAYSPI-YWQMFAYSP;PLFIAYDSADVWAHQ-
FIAYDSADV;YDSADVWAHQKYFKL-VWAHQKYFK;SSQSYWQMFAYSPID-
WQMFAYSPI;SQFQALKRYANDKGI-FQALKRYAN;FSQFQALKRYANDKG-
FQALKRYAN;YFFFSQFQALKRYAN-FFSQFQALK;DATLSKNISFITRLY-
LSKNISFIT;FFSQFQALKRYANDK-FQALKRYAN;FFFSQFQALKRYAND-FQALKRYAN

DRB1_0901 FDASKDKVAGISPDY-FDASKDKVA;YGIGDLGKGAYKFID-
LGKGAYKFI;IDFLFASSQSYWQMF-FLFASSQSY;FIDFLFASSQSYWQM-
FLFASSQSY;KFIDFLFASSQSYWQ-FLFASSQSY;IVYTGIGDNSTIREF-
IVYTGIGDN;ANIPKNTLNNWIFRL-PKNTLNNWI;KYGIGDLGKGAYKFI-
IGDLGKGAY;QSYWQMFAYSPIDFT-MFAYSPIDF;SYWQMFAYSPIDFTR-
MFAYSPIDF;DFLFASSQSYWQMFA-FASSQSYWQ;SLPSKYGIGDLGKGA-
PSKYGIGDL;FLFASSQSYWQMFAY-FASSQSYWQ;NFILNEIKDLKIWVE-
FILNEIKDL;FKDKFLKEAALNFIN-LKEAALNFI;SFKDKFLKEAALNFI-
FLKEAALNF;DKFLKEAALNFINRA-LKEAALNFI;KDKFLKEAALNFINR-
LKEAALNFI;DVWAHQKYFKLRFDA-WAHQKYFKL;LDDLHKKYIFDYLNT-
HKKYIFDYL;YWQMFAYSPIDFTRS-MFAYSPIDF;WQMFAYSPIDFTRSP-
MFAYSPIDF;YKFIDFLFASSQSYW-FLFASSQSY;KFLKEAALNFINRAS-
LKEAALNFI;NILSKEIKVQEVLQY-EIKVQEVLQ;IREFVNSLDDLHKKY-
FVNSLDDLH;YSWNVLKNVKYEWWA-WNVLKNVKY;SQSYWQMFAYSPIDF-
WQMFAYSPI;AYKFIDFLFASSQSY-IDFLFASSQ;VWAHQKYFKLRFDAS-
WAHQKYFKL;FEKFKKKSSYWLLDF-FKKKSSYWL;EKFKKKSSYWLLDFA-
FKKKSSYWL;SFEKFKKKSSYWLLD-FKKKSSYWL;RIGILRKYIDVIKID-
LRKYIDVIK;NVKYEWWAKRIGILR-WWAKRIGIL;RSFEKFKKKSSYWLL-
FKKKSSYWL;FVVWDMIRSAMSSVS-WDMIRSAMS;AGNVYYIDLEALDKF-
YYIDLEALD;HKKYIFDYLNTNEDF-FDYLNTNED
DRB1_1101 LKNVKYEWWAKRIGI-YEWWAKRIG;KNVKYEWWAKRIGIL-
YEWWAKRIG;VLKNVKYEWWAKRIG-VKYEWWAKR;NVKYEWWAKRIGILR-
YEWWAKRIG;VKYEWWAKRIGILRK-YEWWAKRIG;VYYIDLEALDKFIDS-
YIDLEALDK;QALKRYANDKGIELV-LKRYANDKG;NVYYIDLEALDKFID-
YIDLEALDK;IAYDSADVWAHQKYF-YDSADVWAH;FKLRNILSKEIKVQE-
FKLRNILSK;FDRGILIRNEKDLFK-RGILIRNEK;EVRSFEKFKKKSSYW-
FEKFKKKSS;KYEWWAKRIGILRKY-YEWWAKRIG;HNYIKNCIVYTGIGD-
YIKNCIVYT;YEWWAKRIGILRKYI-YEWWAKRIG;DFLFASSQSYWQMFA-
FASSQSYWQ;SRDAFNVLFDRGILI-FNVLFDRGI;EFRANIPKNTLNNWI-
FRANIPKNT;YFLEQEQAWDSPAYS-EQAWDSPAY;FSQFQALKRYANDKG-
FQALKRYAN;SQFQALKRYANDKGI-FQALKRYAN;LEDVSRLRDFFNFPG-LEDVSRLRD
DRB1_1302 IRINLNLKRKSGILL-INLNLKRKS;RINLNLKRKSGILLN-
LKRKSGILL;INLNLKRKSGILLNI-LKRKSGILL;KSGILLNISSLPSKY-
ILLNISSLP;RKSGILLNISSLPSK-ILLNISSLP;SGILLNISSLPSKYG-
ILLNISSLP;LKRKSGILLNISSLP-LKRKSGILL;EWWAKRIGILRKYID-
WAKRIGILR;KKIRINLNLKRKSGI-INLNLKRKS;KRKSGILLNISSLPS-
ILLNISSLP;YKKIRINLNLKRKSG-INLNLKRKS;KIRINLNLKRKSGIL-
INLNLKRKS;WWAKRIGILRKYIDV-IGILRKYID;WAKRIGILRKYIDVI-
IGILRKYID;KYKKIRINLNLKRKS-IRINLNLKR;AKRIGILRKYIDVIK-
IGILRKYID;KRIGILRKYIDVIKI-IGILRKYID;GILLNISSLPSKYGI-
ILLNISSLP;LPHNYIKNCIVYTGI-IKNCIVYTG;LNLKRKSGILLNISS-
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LKRKSGILL;PHNYIKNCIVYTGIG-IKNCIVYTG;HNYIKNCIVYTGIGD-
IKNCIVYTG;KGIELVMNLPLFIAY-VMNLPLFIA;ILLNISSLPSKYGIG-
ILLNISSLP;PAYSWNVLKNVKYEW-WNVLKNVKY;DKGIELVMNLPLFIA-
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LVMNLPLFI;YSWNVLKNVKYEWWA-WNVLKNVKY;DSPAYSWNVLKNVKY-
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IRINLNLKR;RIGILRKYIDVIKID-IGILRKYID;IGILRKYIDVIKIDH-
IGILRKYID;RDFFNFILNEIKDLK-FFNFILNEI;DLDATLSKNISFITR-
LSKNISFIT;NDKGIELVMNLPLFI-IELVMNLPL;DATLSKNISFITRLY-
LSKNISFIT;LDATLSKNISFITRL-LSKNISFIT;ATLSKNISFITRLYG-
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VAGISPDYF;NIPKNTLNNWIFRLL-IPKNTLNNW;SDLDATLSKNISFIT-
DATLSKNIS;IPKNTLNNWIFRLLE-LNNWIFRLL;ELVMNLPLFIAYDSA-

VMNLPLFIA;FVVWDMIRSAMSSVS-VWDMIRSAM;NLKRKSGILLNISSL-
LKRKSGILL;DFFNFILNEIKDLKI-ILNEIKDLK;WEVGVGEAYAFNGLW-
VGVGEAYAF;CIVYTGIGDNSTIRE-VYTGIGDNS;FFNFILNEIKDLKIW-
ILNEIKDLK;KFIDSDLNLLKENET-FIDSDLNLL;IVYTGIGDNSTIREF-
IGDNSTIRE;VYTGIGDNSTIREFV-IGDNSTIRE;LFDRGILIRNEKDLF-
RGILIRNEK;FIDSDLNLLKENETR-LNLLKENET;SWNVLKNVKYEWWAK-
WNVLKNVKY;KDLFKLRNILSKEIK-LFKLRNILS;SDLNLLKENETRYSD-
LNLLKENET;DSDLNLLKENETRYS-LNLLKENET;PKNTLNNWIFRLLES-
LNNWIFRLL;IKNCIVYTGIGDNST-IKNCIVYTG;FDRGILIRNEKDLFK-
RGILIRNEK;FNVLFDRGILIRNEK-VLFDRGILI;YTGIGDNSTIREFVN-
IGDNSTIRE;TGIGDNSTIREFVNS-IGDNSTIRE;NSLDDLHKKYIFDYL-
LDDLHKKYI;VAFKEYFLKDSRDAF-FKEYFLKDS;KNTLNNWIFRLLESD-
LNNWIFRLL;EDFENDLEDVSRLRD-FENDLEDVS;EKDLFKLRNILSKEI-
LFKLRNILS;VVWDMIRSAMSSVSD-IRSAMSSVS;NEFRANIPKNTLNNW-
FRANIPKNT;VWDMIRSAMSSVSDS-IRSAMSSVS;LVMNLPLFIAYDSAD-
LVMNLPLFI;NTLNNWIFRLLESDL-LNNWIFRLL;DLFKLRNILSKEIKV-
LRNILSKEI;WNVLKNVKYEWWAKR-WNVLKNVKY;DLEALDKFIDSDLNL-
LEALDKFID;NFILNEIKDLKIWVE-ILNEIKDLK;NVLFDRGILIRNEKD-
RGILIRNEK;LGNEFRANIPKNTLN-FRANIPKNT;GRDFFNFILNEIKDL-
FFNFILNEI;NLGNEFRANIPKNTL-FRANIPKNT;FNFILNEIKDLKIWV-
ILNEIKDLK;VLFDRGILIRNEKDL-RGILIRNEK;TLSKNISFITRLYGR-
LSKNISFIT;MQDYINLGNEFRANI-YINLGNEFR;FLFASSQSYWQMFAY-
FLFASSQSY;IDSDLNLLKENETRY-LNLLKENET;EAALNFINRASVDEV-
FINRASVDE;WDMIRSAMSSVSDSV-IRSAMSSVS;LSKNISFITRLYGRT-
LSKNISFIT;LFKLRNILSKEIKVQ-LRNILSKEI;YEWWAKRIGILRKYI-
WAKRIGILR;KYEWWAKRIGILRKY-WAKRIGILR;RGILIRNEKDLFKLR-
LIRNEKDLF;DRGILIRNEKDLFKL-LIRNEKDLF;YKFIDFLFASSQSYW-
FLFASSQSY;VKYEWWAKRIGILRK-WAKRIGILR;QDYINLGNEFRANIP-
YINLGNEFR;AALNFINRASVDEVR-INRASVDEV;IPMQDYINLGNEFRA-
YINLGNEFR;LLNISSLPSKYGIGD-LLNISSLPS;INLGNEFRANIPKNT-
LGNEFRANI;GNEFRANIPKNTLNN-FRANIPKNT;EFRANIPKNTLNNWI-FRANIPKNT
DRB1_1501 KDLFKLRNILSKEIK-LFKLRNILS;EKDLFKLRNILSKEI-
LFKLRNILS;NEKDLFKLRNILSKE-LFKLRNILS;SGILLNISSLPSKYG-
LLNISSLPS;GILLNISSLPSKYGI-LLNISSLPS;RNEKDLFKLRNILSK-
LFKLRNILS;KSGILLNISSLPSKY-LLNISSLPS;RKSGILLNISSLPSK-
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IRINLNLKR;LFKLRNILSKEIKVQ-FKLRNILSK;KYKKIRINLNLKRKS-
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EQAWDSPAY;KRKSGILLNISSLPS-GILLNISSL;WNVLKNVKYEWWAKR-
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SFITRLYGR;AKRIGILRKYIDVIK-ILRKYIDVI;VLKNVKYEWWAKRIG-
VKYEWWAKR;NVLKNVKYEWWAKRI-VKYEWWAKR;LKNVKYEWWAKRIGI-
VKYEWWAKR;FKLRNILSKEIKVQE-LRNILSKEI;KRIGILRKYIDVIKI-
ILRKYIDVI;LLNISSLPSKYGIGD-LLNISSLPS;WAKRIGILRKYIDVI-
WAKRIGILR;VKYEWWAKRIGILRK-WAKRIGILR;VRSFEKFKKKSSYWL-
VRSFEKFKK;NVKYEWWAKRIGILR-VKYEWWAKR;IGILRKYIDVIKIDH-
ILRKYIDVI;KIRINLNLKRKSGIL-IRINLNLKR;KNVKYEWWAKRIGIL-
VKYEWWAKR;RIGILRKYIDVIKID-ILRKYIDVI;IRINLNLKRKSGILL-
IRINLNLKR;DFVVWDMIRSAMSSV-FVVWDMIRS;TLSKNISFITRLYGR-
SKNISFITR;EAALNFINRASVDEV-ALNFINRAS;KEAALNFINRASVDE-
ALNFINRAS;EAYAFNGLWVKSPGR-YAFNGLWVK;VVWDMIRSAMSSVSD-
MIRSAMSSV;LKEAALNFINRASVD-ALNFINRAS;FLKEAALNFINRASV-
ALNFINRAS;AYAFNGLWVKSPGRD-GLWVKSPGR;IDHFRGFVSTWEVGV-
FRGFVSTWE;ISSLPSKYGIGDLGK-ISSLPSKYG;KIDHFRGFVSTWEVG-
FRGFVSTWE;WDMIRSAMSSVSDSV-IRSAMSSVS;DHFRGFVSTWEVGVG-

FRGFVSTWE;VWDMIRSAMSSVSDS-MIRSAMSSV;LLESDLDATLSKNIS-
LDATLSKNI;VGEAYAFNGLWVKSP-AYAFNGLWV;GEAYAFNGLWVKSPG-
AYAFNGLWV;IIPMQDYINLGNEFR-PMQDYINLG;EWWAKRIGILRKYID-
WAKRIGILR;ALDKFIDSDLNLLKE-FIDSDLNLL;NEDFVVWDMIRSAMS-
FVVWDMIRS;EDFVVWDMIRSAMSS-FVVWDMIRS;RSFEKFKKKSSYWLL-
FKKKSSYWL;TLNNWIFRLLESDLD-IFRLLESDL;IPMQDYINLGNEFRA-
YINLGNEFR;GNEFRANIPKNTLNN-FRANIPKNT;PMQDYINLGNEFRAN-
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DRB3_0101 LESDLDATLSKNISF-LESDLDATL;VKSPGRDFFNFILNE-
PGRDFFNFI;LFDRGILIRNEKDLF-ILIRNEKDL;IDLEALDKFIDSDLN-
EALDKFIDS;FDFDSDNQNLPHNYI-FDSDNQNLP;RKSGILLNISSLPSK-
LLNISSLPS;KEYFLKDSRDAFNVL-FLKDSRDAF;AFDFDSDNQNLPHNY-
FDSDNQNLP;EYFLKDSRDAFNVLF-FLKDSRDAF;FKDKFLKEAALNFIN-
FLKEAALNF;FENDLEDVSRLRDFF-FENDLEDVS;VAFKEYFLKDSRDAF-
FKEYFLKDS;FIDSDLNLLKENETR-IDSDLNLLK;AFKEYFLKDSRDAFN-
FLKDSRDAF;FKEYFLKDSRDAFNV-FLKDSRDAF;QDYINLGNEFRANIP-
LGNEFRANI;AFNVLFDRGILIRNE-VLFDRGILI
DRB4_0101 FFNFILNEIKDLKIW-ILNEIKDLK;VGVGEAYAFNGLWVK-
GEAYAFNGL;NVKYEWWAKRIGILR-YEWWAKRIG;VKYEWWAKRIGILRK-
YEWWAKRIG;SDLDATLSKNISFIT-DATLSKNIS;QNLPHNYIKNCIVYT-
LPHNYIKNC;KNVKYEWWAKRIGIL-YEWWAKRIG;LLDFASFVAFKEYFL-
LLDFASFVA;NVLKNVKYEWWAKRI-VKYEWWAKR;VLKNVKYEWWAKRIG-
VKYEWWAKR;LKNVKYEWWAKRIGI-YEWWAKRIG;NQNLPHNYIKNCIVY-
LPHNYIKNC;LPHNYIKNCIVYTGI-LPHNYIKNC;KYEWWAKRIGILRKY-
YEWWAKRIG;YEWWAKRIGILRKYI-YEWWAKRIG
DRB5_0101 KNVKYEWWAKRIGIL-VKYEWWAKR;VLKNVKYEWWAKRIG-
VKYEWWAKR;LKNVKYEWWAKRIGI-VKYEWWAKR;NVLKNVKYEWWAKRI-
VKYEWWAKR;WNVLKNVKYEWWAKR-WNVLKNVKY;AHQKYFKLRFDASKD-
FKLRFDASK;NVKYEWWAKRIGILR-VKYEWWAKR;VKYEWWAKRIGILRK-
VKYEWWAKR;LSKEIKVQEVLQYFF-IKVQEVLQY;NDKGIELVMNLPLFI-
ELVMNLPLF;LPHNYIKNCIVYTGI-YIKNCIVYT;IFDYLNTNEDFVVWD-
YLNTNEDFV;WIFRLLESDLDATLS-FRLLESDLD;AKRIGILRKYIDVIK-
AKRIGILRK;KFLKEAALNFINRAS-FLKEAALNF;IDHFRGFVSTWEVGV-
FRGFVSTWE;FENDLEDVSRLRDFF-DLEDVSRLR

<CAA59727 outer surface protein A;Protein;Borrelia garinii>

Allele 8-mer
A0101
A0201 YLLGIGLI;SLDEKNSV;FTLEGTLA;LMATVEKL
A0202
LMATVEKL;SLDEKNSV;YLLGIGLI;LIACKQNV;LLGIGLIL;KAVEITTL;KLTIAEDL;GIGLILAL
;LVSKKVTL;SLMATVEK
A0203
YLLGIGLI;LMATVEKL;SLDEKNSV;LIACKQNV;LLGIGLIL;GLILALIA;SQKTKNLV;KVTEGTVV
;FTLEGTLA;TLKDKSST;KAVEITTL;LVSKKVTL
A0204 SLDEKNSV;LMATVEKL;KVTEGTVV;LLGIGLIL;FTLEGTLA;LIACKQNV;
A0206 KAVEITTL;FTLEGTLA;KVTEGTVV;YLLGIGLI;SLDEKNSV;ATVEKLEL;LIACKQNV
A0211
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;EISEKTIV;LIACKQNV;KEDGKTLV;FTLEGTLA;KLTIAEDL;GLILALIA;AADGKTTL;GIGLILA
L;EVLKDFTL;SLMATVEK
A0212
SLDEKNSV;YLLGIGLI;DLPGGMKV;LMATVEKL;LLGIGLIL;ALDDSDTT;TLEGTLAA;KVTEGTVV
;LIACKQNV;EISEKTIV;FTLEGTLA

A0216
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;EISEKTIV;LIACKQNV;AADGKTTL;GIGLILAL;LVSKKVTL;TLKDKSST;EVLKDFTL;GLILALI
A
A0219
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;AADGKTTL
A0301
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;TISVNSQK;KVLVSKEK;TIAEDLSK;KTDKSKVK
A1101
KTTFEIFK;SLMATVEK;SVNSQKTK;TIAEDLSK;TISVNSQK;GTLAADGK;TVEKLELK;KTGKWDSK
;KVLVSKEK;VLSKNILK;VSKKVTLK;ITTLEKLK;ILALIACK;NVSSLDEK;GMKVLVSK;KTDKSKV
K;TKNLVFTK
A2301 KYLLGIGL
A2402 KYSLMATV
A2403 KYLLGIGL
A2601 DTITVQKY
A2602 DTITVQKY;EVLKDFTL;EITTLEKL;SVDLPGGM;EISEKTIV
A2902 DTITVQKY
A3001
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;IVRANGTR;RLEYTDIK
A3002
A3101 IVRANGTR;KTTFEIFK;GMKVLVSK;ISEKTIVR;VSKKVTLK;KVLVSKEK
A3301 IVRANGTR
A6801
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;ITTLEKLK;SLMATVEK;DTITVQKY;TTFEIFKE;SVNSQKTK;IVRANGTR;ELKGTSDK;EDTITVQ
K;EGTVVLSK
A6802 TSTLTISV;LIACKQNV;EISEKTIV;EVLKDFTL;TVVLSKNI
A6901 FTLEGTLA;EVLKDFTL;EISEKTIV;YLLGIGLI;LIACKQNV
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B0801
B0802
B1501
B1801
B2705
B3501 LPGGMKVL
B3901 FKEDGKTL
B4001 GEISEKTI
B4002
B4402
B4403
B4501 AEDLSKTT
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B5301 LPGGMKVL
B5401
B5701
B5801 KSSTEEKF;KAVEITTL

Allele 9-mer
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A0201
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A0202
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A0203
FTKEDTITV;ILKSGEITV;SLMATVEKL;ALIACKQNV;YLLGIGLIL;KTSTLTISV;LLGIGLILA;F
TLEGTLAA;GKYSLMATV;GIGLILALI;TLKVTEGTV;TLVSKKVTL
A0204 SLMATVEKL;ALIACKQNV;ILKSGEITV;FTKEDTITV;YLLGIGLIL;FTLEGTLAA
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A0211
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SLMATV;VDLPGGMKV
A0212
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LPGGMKV;TLKVTEGTV;SSLDEKNSV;VLSKNILKS;VLKDFTLEG
A0216
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EDGKTLV;KVTEGTVVL;GKYSLMATV;KTSTLTISV
A0219
ILKSGEITV;YLLGIGLIL;SLMATVEKL;LAADGKTTL;ALIACKQNV;DLSKTTFEI;ALDDSDTTQ;T
LVSKKVTL;FKEDGKTLV;FTLEGTLAA;LLGIGLILA;DLPGGMKVL
A0301 VVLSKNILK;KTKNLVFTK;LVSKKVTLK;LILALIACK;LTISVNSQK
A1101
VVLSKNILK;KTKNLVFTK;LTISVNSQK;AVEITTLEK;LTIAEDLSK;LILALIACK;STEEKFNEK;A
TVEKLELK;SVDLPGGMK;YSLMATVEK;LVSKKVTLK;AADGKTTLK;SAGTNLEGK;GSGTLEGEK;TQ
ATKKTGK;GGMKVLVSK;RANGTRLEY;ISVNSQKTK;KSDGSGKAK
A2301 KYDSAGTNL;KYLLGIGLI
A2402 KYLLGIGLI
A2403 KYLLGIGLI;KYDSAGTNL
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A2602 DLPGGMKVL
A2902
A3001
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SVNSQKTK;
A3002 RANGTRLEY
A3101 KTKNLVFTK;LTISVNSQK;VVLSKNILK;LILALIACK
A3301 EISEKTIVR
A6801
LTISVNSQK;TIVRANGTR;YSLMATVEK;EISEKTIVR;EITTLEKLK;LTIAEDLSK;KTKNLVFTK;S
TEEKFNEK;LVSKKVTLK;ATVEKLELK
A6802 KTSTLTISV;FTKEDTITV;TTLKVTEGT;DLSKTTFEI
A6901 FTLEGTLAA;FTKEDTITV;DLSKTTFEI
B0702 IVRANGTRL;KVTEGTVVL;LAADGKTTL
B0801
B0802
B1501 SQKTKNLVF;RANGTRLEY;YLLGIGLIL
B1801 VEITTLEKL
B2705
B3501 LAADGKTTL;RANGTRLEY;
B3901

B4001 KEVLKDFTL;AEDLSKTTF;GEISEKTIV
B4002 GEISEKTIV;AEDLSKTTF;KEVLKDFTL
B4402 AEDLSKTTF
B4403 KEVLKDFTL
B4501 AEDLSKTTF
B5101 LPGGMKVLV
B5301 LPGGMKVLV
B5401 LPGGMKVLV
B5701
B5801 RANGTRLEY

Allele 10-mer

A0101
A0201 YLLGIGLILA;SLDEKNSVSV;ALDDSDTTQA;LMATVEKLEL;LLGIGLILAL
A0202
YLLGIGLILA;LLGIGLILAL;LMATVEKLEL;TLAADGKTTL;SLDEKNSVSV;ALDDSDTTQA;VLKDF
TLEGT;ILKSGEITVA;YSLMATVEKL
A0203
SLDEKNSVSV;YLLGIGLILA;LLGIGLILAL;VLKDFTLEGT;ILKSGEITVA;TLAADGKTTL;LMATV
EKLEL;TLKVTEGTVV;ALDDSDTTQA;NILKSGEITV
A0204 SLDEKNSVSV;LMATVEKLEL;TLAADGKTTL;LLGIGLILAL;SVDLPGGMKV
A0206
SLDEKNSVSV;YLLGIGLILA;NILKSGEITV;ALDDSDTTQA;LLGIGLILAL;FTLEGTLAAD;AADGK
TTLKV;TTLKVTEGTV
A0211
SLDEKNSVSV;YLLGIGLILA;DLPGGMKVLV;ALDDSDTTQA;LLGIGLILAL;TLAADGKTTL;LMATV
EKLEL;SVDLPGGMKV;NILKSGEITV;AADGKTTLKV;VLKDFTLEGT;TLKVTEGTVV;ILKSGEITVA
;TTLKVTEGTV;SKTSTLTISV;EISEKTIVRA;VFTKEDTITV
A0212
SLDEKNSVSV;YLLGIGLILA;LLGIGLILAL;DLPGGMKVLV;LMATVEKLEL;ALDDSDTTQA;TLAAD
GKTTL;VLKDFTLEGT;NILKSGEITV;SVDLPGGMKV;ILKSGEITVA;AADGKTTLKV;TLKVTEGTVV
A0216
SLDEKNSVSV;DLPGGMKVLV;YLLGIGLILA;LLGIGLILAL;ALDDSDTTQA;NILKSGEITV;TLAAD
GKTTL;LMATVEKLEL;AADGKTTLKV;SVDLPGGMKV;TLKVTEGTVV;TTLKVTEGTV;TIVRANGTRL
;ILKSGEITVA;NLVFTKEDTI
A0219
SLDEKNSVSV;ALDDSDTTQA;LLGIGLILAL;YLLGIGLILA;DLPGGMKVLV;TLAADGKTTL;AADGK
TTLKV;LMATVEKLEL;NILKSGEITV
A0301
TLVSKKVTLK;TLTISVNSQK;KYSLMATVEK;TVVLSKNILK;KLTIAEDLSK;GLILALIACK;LAADG
KTTLK;VTEGTVVLSK;KLELKGTSDK;GMKVLVSKEK;KAVEITTLEK;LSKTTFEIFK;VSVDLPGGMK
;TTQATKKTGK
A1101
TVVLSKNILK;TTQATKKTGK;VTEGTVVLSK;SSTEEKFNEK;KAVEITTLEK;GLILALIACK;KQNVS
SLDEK;TLTISVNSQK;TLVSKKVTLK;VSVDLPGGMK;LSKTTFEIFK;TISVNSQKTK;MATVEKLELK
;LAADGKTTLK;KTIVRANGTR;KLTIAEDLSK;KVLVSKEKDK;GSGKAKEVLK;GTLEGEKTDK;KYSL
MATVEK;TLEKLKDALK;GMKVLVSKEK
A2301 KYSLMATVEK;KYLLGIGLIL;DLSKTTFEIF;NSQKTKNLVF
A2402 KYLLGIGLIL;
A2403 KYLLGIGLIL;
A2601
A2602 SVSVDLPGGM;EIFKEDGKTL
A2902
A3001
KAVEITTLEK;GTRLEYTDIK;LSKTTFEIFK;KQNVSSLDEK;KYSLMATVEK;GMKVLVSKEK;KVLVS
KEKDK;TTQATKKTGK;VSKKVTLKDK;TVVLSKNILK;KTIVRANGTR;KLELKGTSDK

A3002
A3101 KYSLMATVEK;KTIVRANGTR;LSKTTFEIFK
A3301
A6801
TVVLSKNILK;MATVEKLELK;TLTISVNSQK;DSAGTNLEGK;TTQATKKTGK;LAADGKTTLK;KTIVR
ANGTR;TISVNSQKTK;TLVSKKVTLK;SSTEEKFNEK;KAVEITTLEK;LSKTTFEIFK
A6802 TTLKVTEGTV;EISEKTIVRA;LGIGLILALI
A6901
TTLKVTEGTV;NILKSGEITV;SVDLPGGMKV;EISEKTIVRA;YLLGIGLILA;TTLEKLKDAL;
B0702
B0801
B0802
B1501
B1801 VDLPGGMKVL;
B2705
B3501 IAEDLSKTTF
B3901
B4001
B4002
B4402
B4403
B4501 EEKFNEKGEI
B5101
B5301
B5401 LPGGMKVLVS
B5701
B5801

Allele 11-mer
A0101
A0201
YLLGIGLILAL;SLMATVEKLEL;LVFTKEDTITV;LLGIGLILALI;ILALIACKQNV;ALDDSDTTQAT
A0202
ILALIACKQNV;SLMATVEKLEL;YLLGIGLILAL;LIACKQNVSSL;ILKSGEITVAL;LLGIGLILALI
;KAVEITTLEKL;VLKDFTLEGTL;LVFTKEDTITV;SVNSQKTKNLV;NVSSLDEKNSV;ALDDSDTTQA
T;LAADGKTTLKV
A0203
LIACKQNVSSL;VLKDFTLEGTL;YLLGIGLILAL;ILALIACKQNV;LLGIGLILALI;ILKSGEITVAL
;SLMATVEKLEL;LVFTKEDTITV;LAADGKTTLKV;SVNSQKTKNLV;TLKVTEGTVVL;KTTLKVTEGT
V
A0204
SLMATVEKLEL;YLLGIGLILAL;LVFTKEDTITV;LAADGKTTLKV;ILALIACKQNV;SVNSQKTKNLV
A0206
YLLGIGLILAL;KAVEITTLEKL;LVFTKEDTITV;LAADGKTTLKV;LLGIGLILALI;ALDDSDTTQAT
;ILALIACKQNV;LIACKQNVSSL;SLMATVEKLEL;KTIVRANGTRL;TTLKVTEGTVV
A0211
YLLGIGLILAL;ILALIACKQNV;SLMATVEKLEL;ALDDSDTTQAT;LLGIGLILALI;ILKSGEITVAL
;VLKDFTLEGTL;LAADGKTTLKV;LVFTKEDTITV;EIFKEDGKTLV;SVNSQKTKNLV;SSLDEKNSVS
V;NVSSLDEKNSV;TLKVTEGTVVL;SVDLPGGMKVL;VDLPGGMKVLV;TTLKVTEGTVV;NLEGKAVEI
TT;KTDKSKVKLTI
A0212
YLLGIGLILAL;VLKDFTLEGTL;ILKSGEITVAL;SLMATVEKLEL;ALDDSDTTQAT;ILALIACKQNV
;LVFTKEDTITV;LAADGKTTLKV;LLGIGLILALI;EIFKEDGKTLV;SSLDEKNSVSV;SVNSQKTKNL
V;NVSSLDEKNSV;TLKVTEGTVVL
A0216
YLLGIGLILAL;SLMATVEKLEL;ILALIACKQNV;ILKSGEITVAL;VLKDFTLEGTL;LVFTKEDTITV

;LAADGKTTLKV;LLGIGLILALI;EIFKEDGKTLV;SVNSQKTKNLV;ALDDSDTTQAT;NVSSLDEKNS
V;TLKVTEGTVVL;NLEGKAVEITT;TTLKVTEGTVV;LIACKQNVSSL
A0219
YLLGIGLILAL;LAADGKTTLKV;SLMATVEKLEL;ILALIACKQNV;ALDDSDTTQAT;ILKSGEITVAL
;LLGIGLILALI;NVSSLDEKNSV;LVFTKEDTITV;VLKDFTLEGTL;LIACKQNVSSL
A0301
TLAADGKTTLK;STLTISVNSQK;KTLVSKKVTLK;KVTEGTVVLSK;LMATVEKLELK;LTISVNSQKTK
;GTVVLSKNILK;FTKEDTITVQK;IVRANGTRLEY;TTLEKLKDALK
A1101
STLTISVNSQK;TTFEIFKEDGK;SVSVDLPGGMK;KVTEGTVVLSK;KTLVSKKVTLK;TTLEKLKDALK
;GTVVLSKNILK;TLAADGKTTLK;LTISVNSQKTK;SQKTKNLVFTK;KSSTEEKFNEK;AVEITTLEKL
K;ATKKTGKWDSK;LMATVEKLELK;TLKDKSSTEEK;FTKEDTITVQK;DLSKTTFEIFK;TLEGTLAAD
GK;LVSKKVTLKDK
A2301 KYSLMATVEKL
A2402 KYSLMATVEKL;KWDSKTSTLTI
A2403 KYSLMATVEKL
A2601
A2602 TIAEDLSKTTF;KTIVRANGTRL;SVDLPGGMKVL;
A2902 IVRANGTRLEY
A3001
KTLVSKKVTLK;ATKKTGKWDSK;TLKDKSSTEEK;KVTEGTVVLSK;IVRANGTRLEY;SQKTKNLVFTK
;KFNEKGEISEK;FTKEDTITVQK;GTVVLSKNILK;AVEITTLEKLK;LTISVNSQKTK
A3002
A3101 KTLVSKKVTLK;SQKTKNLVFTK;KFNEKGEISEK;STLTISVNSQK
A3301 DLSKTTFEIFK;EKTIVRANGTR
A6801
TTFEIFKEDGK;STLTISVNSQK;LTISVNSQKTK;DTTQATKKTGK;FTKEDTITVQK;DLSKTTFEIFK
;TTLEKLKDALK;TLAADGKTTLK;LMATVEKLELK;EKTIVRANGTR;GTVVLSKNILK;SVSVDLPGGM
K;LVSKEKDKDGK;TLKDKSSTEEK;YTDIKSDGSGK
A6802
NVSSLDEKNSV;EIFKEDGKTLV;TTLKVTEGTVV;DTITVQKYDSA;SVNSQKTKNLV;ILALIACKQNV
;LIACKQNVSSL;LVFTKEDTITV;LAADGKTTLKV;
A6901
LAADGKTTLKV;TTLKVTEGTVV;EIFKEDGKTLV;YLLGIGLILAL;LVFTKEDTITV;SVNSQKTKNLV
B0702
B0801
B0802
B1501 IVRANGTRLEY;YLLGIGLILAL;VQKYDSAGTNL
B1801
B2705
B3501 TIAEDLSKTTF
B3901
B4001 FEIFKEDGKTL;LEGKAVEITTL;AEDLSKTTFEI;GEKTDKSKVKL
B4002
B4402
B4403
B4501 AEDLSKTTFEI
B5101
B5301
B5401 LPGGMKVLVSK
B5701
B5801

Allele 15-mer plus 9-mer core
DRB1_0101 KKYLLGIGLILALIA-LLGIGLILA;KYLLGIGLILALIAC-
LLGIGLILA;MKKYLLGIGLILALI-LLGIGLILA;KTGKWDSKTSTLTIS-

WDSKTSTLT;TGKWDSKTSTLTISV-WDSKTSTLT;GKWDSKTSTLTISVN-
WDSKTSTLT;KKTGKWDSKTSTLTI-WDSKTSTLT;TKKTGKWDSKTSTLT-
TGKWDSKTS;LKDFTLEGTLAADGK-FTLEGTLAA;VLKDFTLEGTLAADG-
FTLEGTLAA;KDFTLEGTLAADGKT-FTLEGTLAA;YLLGIGLILALIACK-
IGLILALIA;LLGIGLILALIACKQ-IGLILALIA;KEVLKDFTLEGTLAA-
LKDFTLEGT;EVLKDFTLEGTLAAD-FTLEGTLAA;ISEKTIVRANGTRLE-
IVRANGTRL;SEKTIVRANGTRLEY-IVRANGTRL;TTLKVTEGTVVLSKN-
VTEGTVVLS;KTTLKVTEGTVVLSK-VTEGTVVLS;EKTIVRANGTRLEYT-
IVRANGTRL;GKTTLKVTEGTVVLS-LKVTEGTVV;KTIVRANGTRLEYTD-
IVRANGTRL;KNILKSGEITVALDD-LKSGEITVA;LSKNILKSGEITVAL-
LKSGEITVA;SKNILKSGEITVALD-LKSGEITVA;NILKSGEITVALDDS-
LKSGEITVA;DFTLEGTLAADGKTT-FTLEGTLAA;FTLEGTLAADGKTTL-
FTLEGTLAA;TLKVTEGTVVLSKNI-VTEGTVVLS;LGIGLILALIACKQN-
IGLILALIA;VLSKNILKSGEITVA-KNILKSGEI;LKVTEGTVVLSKNIL-
VTEGTVVLS;TIVRANGTRLEYTDI-VRANGTRLE;KEDGKTLVSKKVTLK-
GKTLVSKKV;EDGKTLVSKKVTLKD-GKTLVSKKV;SAGTNLEGKAVEITT-
LEGKAVEIT;DSAGTNLEGKAVEIT-GTNLEGKAV;KWDSKTSTLTISVNS-
WDSKTSTLT;WDSKTSTLTISVNSQ-WDSKTSTLT;AGTNLEGKAVEITTL-
LEGKAVEIT;GTNLEGKAVEITTLE-LEGKAVEIT;VDLPGGMKVLVSKEK-
LPGGMKVLV;DGKTTLKVTEGTVVL-LKVTEGTVV;VSVDLPGGMKVLVSK-
LPGGMKVLV;ITVQKYDSAGTNLEG-VQKYDSAGT;TITVQKYDSAGTNLE-
VQKYDSAGT;SVSVDLPGGMKVLVS-LPGGMKVLV;TNLEGKAVEITTLEK-
LEGKAVEIT;NLVFTKEDTITVQKY-FTKEDTITV;EISEKTIVRANGTRL-
KTIVRANGT;GIGLILALIACKQNV-ILALIACKQ;KNLVFTKEDTITVQK-
FTKEDTITV;IGLILALIACKQNVS-ILALIACKQ;TKNLVFTKEDTITVQ-
FTKEDTITV;KTKNLVFTKEDTITV-VFTKEDTIT;ADGKTTLKVTEGTVV-
ADGKTTLKV;IVRANGTRLEYTDIK-IVRANGTRL;LVFTKEDTITVQKYD-
FTKEDTITV;LKSGEITVALDDSDT-LKSGEITVA;DKDGKYSLMATVEKL-
YSLMATVEK;ILKSGEITVALDDSD-LKSGEITVA;KDKDGKYSLMATVEK-
KDGKYSLMA;KDGKYSLMATVEKLE-YSLMATVEK;DTITVQKYDSAGTNL-
VQKYDSAGT;SVDLPGGMKVLVSKE-LPGGMKVLV;GKTLVSKKVTLKDKS-
LVSKKVTLK;DGKTLVSKKVTLKDK-LVSKKVTLK;DGKYSLMATVEKLEL-
YSLMATVEK;EDTITVQKYDSAGTN-VQKYDSAGT;KEDTITVQKYDSAGT-
ITVQKYDSA;GKYSLMATVEKLELK-YSLMATVEK;EIFKEDGKTLVSKKV-
FKEDGKTLV;NSVSVDLPGGMKVLV-VDLPGGMKV;DLPGGMKVLVSKEKD-
MKVLVSKEK;LEGTLAADGKTTLKV-LEGTLAADG;TISVNSQKTKNLVFT-
VNSQKTKNL;YSLMATVEKLELKGT-YSLMATVEK;LEYTDIKSDGSGKAK-
IKSDGSGKA;RLEYTDIKSDGSGKA-YTDIKSDGS;TLTISVNSQKTKNLV-
VNSQKTKNL;GLILALIACKQNVSS-ILALIACKQ;STLTISVNSQKTKNL-
TISVNSQKT;ISVNSQKTKNLVFTK-VNSQKTKNL;TVQKYDSAGTNLEGK-
VQKYDSAGT;VQKYDSAGTNLEGKA-VQKYDSAGT;IFKEDGKTLVSKKVT-
GKTLVSKKV;VTEGTVVLSKNILKS-VTEGTVVLS;LPGGMKVLVSKEKDK-
MKVLVSKEK;VALDDSDTTQATKKT-LDDSDTTQA;YTDIKSDGSGKAKEV-
IKSDGSGKA;FKEDGKTLVSKKVTL-GKTLVSKKV;QKYDSAGTNLEGKAV-
YDSAGTNLE;TLEGTLAADGKTTLK-LEGTLAADG;LTISVNSQKTKNLVF-
VNSQKTKNL;KVTEGTVVLSKNILK-VTEGTVVLS;EYTDIKSDGSGKAKE-
IKSDGSGKA;SKVKLTIAEDLSKTT-VKLTIAEDL;VRANGTRLEYTDIKS-VRANGTRLE
DRB1_0301
DRB1_0401 KEVLKDFTLEGTLAA-VLKDFTLEG;EVLKDFTLEGTLAAD-
FTLEGTLAA;VLKDFTLEGTLAADG-FTLEGTLAA;LKDFTLEGTLAADGK-
FTLEGTLAA;KDFTLEGTLAADGKT-FTLEGTLAA;KNLVFTKEDTITVQK-
FTKEDTITV;NLVFTKEDTITVQKY-FTKEDTITV;LVFTKEDTITVQKYD-
FTKEDTITV;DFTLEGTLAADGKTT-FTLEGTLAA;LEYTDIKSDGSGKAK-
IKSDGSGKA;TKNLVFTKEDTITVQ-FTKEDTITV;FTLEGTLAADGKTTL-
FTLEGTLAA;RLEYTDIKSDGSGKA-YTDIKSDGS;KTKNLVFTKEDTITV-
KTKNLVFTK;AKEVLKDFTLEGTLA-VLKDFTLEG;EYTDIKSDGSGKAKE-IKSDGSGKA

DRB1_0404 KEVLKDFTLEGTLAA-VLKDFTLEG;GKAKEVLKDFTLEGT-
VLKDFTLEG;AKEVLKDFTLEGTLA-VLKDFTLEG;KAKEVLKDFTLEGTL-
VLKDFTLEG;SGKAKEVLKDFTLEG-AKEVLKDFT
DRB1_0405 TITVQKYDSAGTNLE-VQKYDSAGT;ITVQKYDSAGTNLEG-
YDSAGTNLE;TVQKYDSAGTNLEGK-YDSAGTNLE;VQKYDSAGTNLEGKA-
YDSAGTNLE;QKYDSAGTNLEGKAV-YDSAGTNLE
DRB1_0701 DGKTTLKVTEGTVVL-LKVTEGTVV;GKTTLKVTEGTVVLS-
LKVTEGTVV;KTTLKVTEGTVVLSK-LKVTEGTVV;ADGKTTLKVTEGTVV-
TLKVTEGTV;TTLKVTEGTVVLSKN-LKVTEGTVV
DRB1_0802
DRB1_0901
DRB1_1101
DRB1_1302 TEGTVVLSKNILKSG-TVVLSKNIL;EGTVVLSKNILKSGE-
TVVLSKNIL;GTVVLSKNILKSGEI-VVLSKNILK;VTEGTVVLSKNILKS-
TVVLSKNIL;TVVLSKNILKSGEIT-TVVLSKNIL;ISEKTIVRANGTRLE-
IVRANGTRL;SEKTIVRANGTRLEY-IVRANGTRL;EKTIVRANGTRLEYT-
IVRANGTRL;KTIVRANGTRLEYTD-IVRANGTRL;TLTISVNSQKTKNLV-
VNSQKTKNL;STLTISVNSQKTKNL-ISVNSQKTK;LTISVNSQKTKNLVF-
VNSQKTKNL;KVTEGTVVLSKNILK-TVVLSKNIL;TISVNSQKTKNLVFT-
VNSQKTKNL;LKVTEGTVVLSKNIL-LKVTEGTVV;TIVRANGTRLEYTDI-
VRANGTRLE;ISVNSQKTKNLVFTK-VNSQKTKNL;VVLSKNILKSGEITV-
VVLSKNILK;EISEKTIVRANGTRL-KTIVRANGT;EDGKTLVSKKVTLKD-
LVSKKVTLK;DGKTLVSKKVTLKDK-LVSKKVTLK
DRB1_1501 TEGTVVLSKNILKSG-VLSKNILKS;EGTVVLSKNILKSGE-VLSKNILKS
DRB3_0101
DRB4_0101
DRB5_0101 LPGGMKVLVSKEKDK-MKVLVSKEK;GGMKVLVSKEKDKDG-
MKVLVSKEK;VDLPGGMKVLVSKEK-VDLPGGMKV;PGGMKVLVSKEKDKD-
MKVLVSKEK;DLPGGMKVLVSKEKD-MKVLVSKEK;

<AAN87995 Outer Surface Protein C;Protein;Borrelia garinii>

Allele 8-mer
A0101 ITDSNAFV
A0201 LMTLFLFI;LLAGAYAI;FVLAVKEV;SLLAGAYA;ITDSNAFV;LISSIDEL
A0202
LLAGAYAI;LISSIDEL;LMTLFLFI;KLKNSEEL;GAYAISTL;ILMTLFLF;SLLAGAYA;FVLAVKEV
;ITDSNAFV;VIHQNNGL
A0203
LLAGAYAI;LMTLFLFI;FVLAVKEV;SLLAGAYA;GAYAISTL;KLKNSEEL;LISSIDEL;AVKEVEAL
;GQNGSLLA;VIHQNNGL;HQNNGLNA
A0204 FVLAVKEV;SLLAGAYA;LLAGAYAI
A0206
AQLGVAAA;FVLAVKEV;LLAGAYAI;GQNGSLLA;ITDSNAFV;LMTLFLFI;SLLAGAYA;ILMTLFLF
;HQNNGLNA;GAYAISTL;
A0211
LLAGAYAI;SLLAGAYA;FVLAVKEV;LMTLFLFI;ITDSNAFV;TLFLFISC;KLKNSEEL;ELTNPVVA
;RLKGSHAQ;LISSIDEL;ILMTLFLF;AKGPNLTV
A0212
LLAGAYAI;FVLAVKEV;SLLAGAYA;LMTLFLFI;VIHQNNGL;ITDSNAFV;TLFLFISC;KLKNSEEL
;RLKGSHAQ
A0216
SLLAGAYA;LLAGAYAI;FVLAVKEV;ITDSNAFV;KLKNSEEL;LMTLFLFI;LISSIDEL;TLFLFISC
;GAYAISTL;AKGPNLTV;ELTNPVVA
A0219 LLAGAYAI;ITDSNAFV;FVLAVKEV;SLLAGAYA;LMTLFLFI;LISSIDEL
A0301 ILKSNPTK;LITEKLSK;ISTLITEK;NLTVISKK;KSNPTKDK

A1101
SIDELANK;ISTLITEK;NAFVLAVK;AATDDHAK;LITEKLSK;KSNPTKDK;LANKAIGK;HAKEAILK
;PVVAESPK;EAFTNRLK;ESVESLAK
A2301 ILMTLFLF;AYAISTLI
A2402 AYAISTLI;ILMTLFLF
A2403 AYAISTLI
A2601
A2602 KITDSNAF;
A2902 ILMTLFLF;
A3001 KSNPTKDK;ILKSNPTK;PTKDKGAK;HAKEAILK;LANKAIGK;RLKGSHAQ;TEKLSKLK
A3002
A3101 HSEAFTNR;
A3301 HSEAFTNR;
A6801
EAFTNRLK;HSEAFTNR;NAFVLAVK;ESVESLAK;ISTLITEK;EALANSVK;NLTVISKK;HAKEAILK
;LANKAIGK
A6802 FVLAVKEV;LLAGAYAI;SNAFVLAV;STNPDESA
A6901 FVLAVKEV;ITDSNAFV;ESAKGPNL
B0702
B0801
B0802
B1501 KITDSNAF;ILMTLFLF;GSLLAGAY
B1801 DELANKAI
B2705
B3501
B3901 DHAKEAIL
B4001 SEAFTNRL
B4002 KELTNPVV
B4402
B4403 KEVEALIS
B4501
B5101
B5301
B5401
B5701
B5801

Allele 9-mer
A0101
A0201 ILMTLFLFI;ALISSIDEL;KITDSNAFV;SLLAGAYAI;ALANSVKEL
A0202
ALISSIDEL;ILMTLFLFI;KITDSNAFV;SVKELTNPV;LISSIDELA;SLAKAAQEA;ALANSVKEL;F
LFISCNNS;LITEKLSKL;RLKGSHAQL;KVIHQNNGL;GAYAISTLI;SLLAGAYAI;LLAGAYAIS;EL
KDLSESV;VLAVKEVEA;DLSESVESL;LAVKEVEAL
A0203
SVKELTNPV;ALISSIDEL;ALANSVKEL;ILMTLFLFI;LITEKLSKL;KITDSNAFV;RLKGSHAQL;E
LKDLSESV;SLAKAAQEA;SLLAGAYAI;LANKAIGKV;GAYAISTLI;VLAVKEVEA;AVKEVEALI;LL
AGAYAIS;ELNKKIEEA;FLFISCNNS;
A0204
SLLAGAYAI;SLAKAAQEA;ALANSVKEL;ALISSIDEL;KITDSNAFV;ILMTLFLFI;VLAVKEVEA
A0206
KITDSNAFV;SLLAGAYAI;ALISSIDEL;ILMTLFLFI;AQEALANSV;AQLGVAAAT;SVKELTNPV;G
AYAISTLI;KVIHQNNGL;LITEKLSKL
A0211
KITDSNAFV;SLLAGAYAI;ELKDLSESV;SLAKAAQEA;RLKGSHAQL;ILMTLFLFI;ALANSVKEL;D

LSESVESL;ALISSIDEL;SVKELTNPV;SIDELANKA;SAKGPNLTV;VLAVKEVEA;ITDSNAFVL;EL
NKKIEEA;LITEKLSKL;ATDDHAKEA;NLTVISKKI
A0212
SLLAGAYAI;ELKDLSESV;ILMTLFLFI;KITDSNAFV;SLAKAAQEA;ALISSIDEL;RLKGSHAQL;V
LAVKEVEA;DLSESVESL;SVKELTNPV;SIDELANKA;LITEKLSKL;SAKGPNLTV;ALANSVKEL
A0216
ELKDLSESV;KITDSNAFV;SLLAGAYAI;SLAKAAQEA;ALISSIDEL;RLKGSHAQL;ALANSVKEL;I
LMTLFLFI;SVKELTNPV;DLSESVESL;SAKGPNLTV;ELNKKIEEA;VLAVKEVEA;LITEKLSKL
A0219
SLLAGAYAI;ELKDLSESV;KITDSNAFV;ALISSIDEL;DLSESVESL;ILMTLFLFI;ITDSNAFVL;S
LAKAAQEA;ALANSVKEL
A0301 AILKSNPTK;TLITEKLSK;AISTLITEK;ELANKAIGK;ITEKLSKLK
A1101
SSIDELANK;AISTLITEK;STNPDESAK;AILKSNPTK;TLITEKLSK;AAATDDHAK;ITEKLSKLK;S
NAFVLAVK;
A2301
A2402
A2403
A2601
A2602 EAKNHSEAF;KVIHQNNGL;EVEALISSI
A2902
A3001 AILKSNPTK;ITEKLSKLK;KDKGAKELK;SVKELTNPV;STNPDESAK
A3002
A3101
A3301
A6801 STNPDESAK;ELANKAIGK;SSIDELANK;SNAFVLAVK;ITEKLSKLK
A6802
SVKELTNPV;EVEALISSI;DSNAFVLAV;ELKDLSESV;ILMTLFLFI;HSEAFTNRL;ISTLITEKL;L
ISSIDELA;ESVESLAKA
A6901 SLLAGAYAI;SVKELTNPV;ESVESLAKA;DSNAFVLAV
B0702
B0801
B0802
B1501
B1801
B2705
B3501 EAKNHSEAF;LAVKEVEAL;NGSLLAGAY
B3901 HSEAFTNRL
B4001
B4002
B4402
B4403
B4501 EEAKNHSEA
B5101
B5301
B5401
B5701
B5801 ITDSNAFVL

Allele 10-mer
A0101
A0201
ALISSIDELA;LLAGAYAIST;KITDSNAFVL;SLAKAAQEAL;ILMTLFLFIS;FVLAVKEVEA;VLAVK
EVEAL;TLITEKLSKL;AISTLITEKL

A0202
ALISSIDELA;SLAKAAQEAL;LLAGAYAIST;VLAVKEVEAL;TLITEKLSKL;AISTLITEKL;FLFIS
CNNSG;LAGAYAISTL;ILMTLFLFIS;KITDSNAFVL;ELANKAIGKV;FVLAVKEVEA;LMTLFLFISC
A0203
GQNGSLLAGA;LLAGAYAIST;ALISSIDELA;TLITEKLSKL;SLAKAAQEAL;VLAVKEVEAL;ELANK
AIGKV;AISTLITEKL;SVKELTNPVV;AAQEALANSV;HQNNGLNANA
A0204 SLAKAAQEAL;ELANKAIGKV;VLAVKEVEAL;FVLAVKEVEA;AAQEALANSV
A0206
GQNGSLLAGA;KEVEALISSI;AAQEALANSV;KITDSNAFVL;HQNNGLNANA;FVLAVKEVEA;ALISS
IDELA;KELKDLSESV;KKITDSNAFV;LLAGAYAIST;SLAKAAQEAL;SVKELTNPVV
A0211
SLAKAAQEAL;KITDSNAFVL;ELANKAIGKV;LLAGAYAIST;SIDELANKAI;VLAVKEVEAL;SVKEL
TNPVV;TLITEKLSKL;ALISSIDELA;DLSESVESLA;SLLAGAYAIS;LMTLFLFISC;ATDDHAKEAI
;AISTLITEKL;FVLAVKEVEA;AAQEALANSV;ALANSVKELT
A0212
SLAKAAQEAL;VLAVKEVEAL;LLAGAYAIST;TLITEKLSKL;ELANKAIGKV;SIDELANKAI;FVLAV
KEVEA;SVKELTNPVV;KITDSNAFVL;AAQEALANSV;SLLAGAYAIS
A0216
SLAKAAQEAL;ELANKAIGKV;TLITEKLSKL;LLAGAYAIST;VLAVKEVEAL;KITDSNAFVL;ALISS
IDELA;SVKELTNPVV;AAQEALANSV;AISTLITEKL;FVLAVKEVEA;ALANSVKELT;DLSESVESLA
A0219
SLAKAAQEAL;LLAGAYAIST;ELANKAIGKV;KITDSNAFVL;VLAVKEVEAL;TLITEKLSKL;AAQEA
LANSV
A0301 STLITEKLSK;KLKNSEELNK;LITEKLSKLK;ILKSNPTKDK;HSEAFTNRLK;LSESVESLAK
A1101
STLITEKLSK;YAISTLITEK;ISSIDELANK;HSEAFTNRLK;ASTNPDESAK;DSNAFVLAVK;VAAAT
DDHAK;LSESVESLAK;AQEALANSVK;LITEKLSKLK;KLKNSEELNK
A2301
A2402
A2403
A2601
A2602
A2902
A3001 KLKNSEELNK;KGPNLTVISK;STLITEKLSK;ILKSNPTKDK;HSEAFTNRLK
A3002
A3101
A3301
A6801
YAISTLITEK;DSNAFVLAVK;EAILKSNPTK;HSEAFTNRLK;ELNKKIEEAK;VAAATDDHAK;STLIT
EKLSK;LSESVESLAK
A6802
NSVKELTNPV;ESAKGPNLTV;ELANKAIGKV;NAFVLAVKEV;TASTNPDESA;AGAYAISTLI;NANAG
QNGSL;
A6901 ESAKGPNLTV;EALANSVKEL;ELANKAIGKV;EALISSIDEL;NAFVLAVKEV;FVLAVKEVEA
B0702
B0801
B0802
B1501
B1801 KEVEALISSI
B2705
B3501
B3901 NHSEAFTNRL
B4001 KEVEALISSI
B4002 EEAKNHSEAF
B4402
B4403 EEAKNHSEAF

B4501 EEAKNHSEAF
B5101
B5301 LAVKEVEALI
B5401
B5701
B5801

Allele 11-mer
A0101 ITDSNAFVLAV
A0201
LLAGAYAISTL;FVLAVKEVEAL;KITDSNAFVLA;SLLAGAYAIST;ITDSNAFVLAV;VLAVKEVEALI
;YAISTLITEKL;KLSKLKNSEEL
A0202
LLAGAYAISTL;KLSKLKNSEEL;SLAKAAQEALA;VLAVKEVEALI;RLKGSHAQLGV;FVLAVKEVEAL
;YAISTLITEKL;KITDSNAFVLA;FLFISCNNSGG;KAAQEALANSV;LAGAYAISTLI;ILMTLFLFIS
C
A0203
LLAGAYAISTL;RLKGSHAQLGV;SLAKAAQEALA;VLAVKEVEALI;YAISTLITEKL;KAAQEALANSV
;SVKELTNPVVA;KLSKLKNSEEL;KITDSNAFVLA;ILMTLFLFISC;FVLAVKEVEAL
A0204 LLAGAYAISTL;SLAKAAQEALA;SLLAGAYAIST;FVLAVKEVEAL;VLAVKEVEALI
A0206
FVLAVKEVEAL;KAAQEALANSV;YAISTLITEKL;KITDSNAFVLA;LLAGAYAISTL;SLLAGAYAIST
;ILMTLFLFISC;ITDSNAFVLAV;RLKGSHAQLGV
A0211
RLKGSHAQLGV;LLAGAYAISTL;SLLAGAYAIST;KLSKLKNSEEL;ITDSNAFVLAV;SLAKAAQEALA
;KITDSNAFVLA;VLAVKEVEALI;FVLAVKEVEAL;ILMTLFLFISC;ATDDHAKEAIL;KAAQEALANS
V;ELANKAIGKVI
A0212
RLKGSHAQLGV;LLAGAYAISTL;KLSKLKNSEEL;SLLAGAYAIST;FVLAVKEVEAL;ITDSNAFVLAV
;VLAVKEVEALI;SLAKAAQEALA;ILMTLFLFISC;ATDDHAKEAIL
A0216
LLAGAYAISTL;RLKGSHAQLGV;KLSKLKNSEEL;SLAKAAQEALA;SLLAGAYAIST;VLAVKEVEALI
;ITDSNAFVLAV;FVLAVKEVEAL
A0219
LLAGAYAISTL;ITDSNAFVLAV;RLKGSHAQLGV;FVLAVKEVEAL;SLLAGAYAIST;KLSKLKNSEEL
;YAISTLITEKL;
A0301 TLITEKLSKLK;KLKNSEELNKK;LTNPVVAESPK;ISTLITEKLSK;AILKSNPTKDK
A1101
LTNPVVAESPK;GVAAATDDHAK;AAQEALANSVK;TLITEKLSKLK;ISTLITEKLSK;TASTNPDESAK
;LISSIDELANK;KSNPTKDKGAK;AILKSNPTKDK;AYAISTLITEK
A2301 AYAISTLITEK
A2402
A2403
A2601
A2602 ATDDHAKEAIL
A2902
A3001
KSNPTKDKGAK;LTNPVVAESPK;KLKNSEELNKK;PTKDKGAKELK;AILKSNPTKDK;RLKGSHAQLGV
A3002
A3101 LTNPVVAESPK;KSNPTKDKGAK
A3301
A6801
LTNPVVAESPK;TASTNPDESAK;LISSIDELANK;ISTLITEKLSK;GVAAATDDHAK;TLITEKLSKLK
A6802
DTASTNPDESA;FVLAVKEVEAL;ESAKGPNLTVI;YAISTLITEKL;NGSLLAGAYAI;SNAFVLAVKEV
A6901 ITDSNAFVLAV;FVLAVKEVEAL;YAISTLITEKL;DTASTNPDESA;EALISSIDELA

B0702 NPTKDKGAKEL
B0801
B0802
B1501 GQNGSLLAGAY;ISKKITDSNAF
B1801
B2705
B3501 YAISTLITEKL;FVLAVKEVEAL
B3901
B4001 VEALISSIDEL;QEALANSVKEL
B4002
B4402
B4403
B4501 EEAKNHSEAFT
B5101
B5301
B5401
B5701
B5801

Allele 15-mer plus 9-mer core

DRB1_0101 GSLLAGAYAISTLIT-LAGAYAIST;NGSLLAGAYAISTLI-
LAGAYAIST;QNGSLLAGAYAISTL-LAGAYAIST;SLLAGAYAISTLITE-
LAGAYAIST;GQNGSLLAGAYAIST-LLAGAYAIS;NRLKGSHAQLGVAAA-
LKGSHAQLG;TNRLKGSHAQLGVAA-LKGSHAQLG;AFTNRLKGSHAQLGV-
LKGSHAQLG;EAFTNRLKGSHAQLG-TNRLKGSHA;FTNRLKGSHAQLGVA-
LKGSHAQLG;LAGAYAISTLITEKL-LAGAYAIST;LLAGAYAISTLITEK-
LAGAYAIST;LKGSHAQLGVAAATD-LKGSHAQLG;RLKGSHAQLGVAAAT-
LKGSHAQLG;AGAYAISTLITEKLS-ISTLITEKL;HQNNGLNANAGQNGS-
LNANAGQNG;IHQNNGLNANAGQNG-NNGLNANAG;YAISTLITEKLSKLK-
ISTLITEKL;AYAISTLITEKLSKL-ISTLITEKL;GAYAISTLITEKLSK-
ISTLITEKL;NNGLNANAGQNGSLL-LNANAGQNG;QNNGLNANAGQNGSL-
LNANAGQNG;NGLNANAGQNGSLLA-LNANAGQNG;LNANAGQNGSLLAGA-
LNANAGQNG;AKEAILKSNPTKDKG-LKSNPTKDK;GLNANAGQNGSLLAG-
LNANAGQNG;ANSVKELTNPVVAES-VKELTNPVV;HAKEAILKSNPTKDK-
EAILKSNPT;NSVKELTNPVVAESP-LTNPVVAES;KGSHAQLGVAAATDD-
AQLGVAAAT;GSHAQLGVAAATDDH-LGVAAATDD;AGQNGSLLAGAYAIS-
GQNGSLLAG;EAILKSNPTKDKGAK-LKSNPTKDK;KEAILKSNPTKDKGA-
LKSNPTKDK;SHAQLGVAAATDDHA-LGVAAATDD;AISTLITEKLSKLKN-
ISTLITEKL;ISTLITEKLSKLKNS-ISTLITEKL;SVKELTNPVVAESPK-
LTNPVVAES;VLAVKEVEALISSID-VKEVEALIS;AFVLAVKEVEALISS-
VKEVEALIS;FVLAVKEVEALISSI-VKEVEALIS;LAVKEVEALISSIDE-
VKEVEALIS;NAFVLAVKEVEALIS-LAVKEVEAL;HAQLGVAAATDDHAK-
LGVAAATDD;SSIDELANKAIGKVI-LANKAIGKV;ESLAKAAQEALANSV-
LAKAAQEAL;ISSIDELANKAIGKV-IDELANKAI;EALANSVKELTNPVV-
LANSVKELT;AQLGVAAATDDHAKE-LGVAAATDD;IDELANKAIGKVIHQ-
LANKAIGKV;SIDELANKAIGKVIH-LANKAIGKV;LANSVKELTNPVVAE-
VKELTNPVV;ALANSVKELTNPVVA-VKELTNPVV;VESLAKAAQEALANS-
LAKAAQEAL;ESVESLAKAAQEALA-SLAKAAQEA;AILKSNPTKDKGAKE-
LKSNPTKDK;DELANKAIGKVIHQN-LANKAIGKV;SVESLAKAAQEALAN-
LAKAAQEAL;SLAKAAQEALANSVK-AQEALANSV;SESVESLAKAAQEAL-SLAKAAQEA
DRB1_0301
DRB1_0401 EALANSVKELTNPVV-SVKELTNPV;QEALANSVKELTNPV-
LANSVKELT;LANSVKELTNPVVAE-SVKELTNPV;ALANSVKELTNPVVA-
SVKELTNPV;ANSVKELTNPVVAES-SVKELTNPV

DRB1_0404 LMTLFLFISCNNSGG-LFISCNNSG;MTLFLFISCNNSGGD-
LFISCNNSG;ILMTLFLFISCNNSG-FLFISCNNS;TLFLFISCNNSGGDT-
LFISCNNSG;LFLFISCNNSGGDTA-LFISCNNSG
DRB1_0405 ANSVKELTNPVVAES-VKELTNPVV;LANSVKELTNPVVAE-
VKELTNPVV;EALANSVKELTNPVV-SVKELTNPV;NSVKELTNPVVAESP-
VKELTNPVV;ALANSVKELTNPVVA-VKELTNPVV
DRB1_0701 VISKKITDSNAFVLA-ITDSNAFVL;ISKKITDSNAFVLAV-
ITDSNAFVL;TVISKKITDSNAFVL-SKKITDSNA;SKKITDSNAFVLAVK-
ITDSNAFVL;KKITDSNAFVLAVKE-ITDSNAFVL;ALANSVKELTNPVVA-
VKELTNPVV;LANSVKELTNPVVAE-VKELTNPVV;ANSVKELTNPVVAES-
VKELTNPVV;NSVKELTNPVVAESP-VKELTNPVV;EALANSVKELTNPVV-
SVKELTNPV;KITDSNAFVLAVKEV-ITDSNAFVL;ITDSNAFVLAVKEVE-ITDSNAFVL
DRB1_0802
DRB1_0901
DRB1_1101
DRB1_1302 EALANSVKELTNPVV-LANSVKELT;SAKGPNLTVISKKIT-
KGPNLTVIS;KGPNLTVISKKITDS-LTVISKKIT;AKGPNLTVISKKITD-
LTVISKKIT;QEALANSVKELTNPV-LANSVKELT;GPNLTVISKKITDSN-
LTVISKKIT;PNLTVISKKITDSNA-LTVISKKIT;AAQEALANSVKELTN-
LANSVKELT;KAAQEALANSVKELT-EALANSVKE;AQEALANSVKELTNP-
LANSVKELT;ALANSVKELTNPVVA-LANSVKELT;LANSVKELTNPVVAE-
LANSVKELT;AKEAILKSNPTKDKG-EAILKSNPT;HAKEAILKSNPTKDK-
EAILKSNPT;NLTVISKKITDSNAF-LTVISKKIT;LTVISKKITDSNAFV-
LTVISKKIT;AIGKVIHQNNGLNAN-IHQNNGLNA;IGKVIHQNNGLNANA-
HQNNGLNAN;KEAILKSNPTKDKGA-LKSNPTKDK;EAILKSNPTKDKGAK-
LKSNPTKDK;GKVIHQNNGLNANAG-HQNNGLNAN;LAGAYAISTLITEKL-
YAISTLITE;KVIHQNNGLNANAGQ-HQNNGLNAN;AGAYAISTLITEKLS-
ISTLITEKL;HQNNGLNANAGQNGS-LNANAGQNG;YAISTLITEKLSKLK-
ISTLITEKL;AYAISTLITEKLSKL-ISTLITEKL;NGLNANAGQNGSLLA-LNANAGQNG
DRB1_1501 ALANSVKELTNPVVA-VKELTNPVV;ANSVKELTNPVVAES-
VKELTNPVV;LANSVKELTNPVVAE-VKELTNPVV;EALANSVKELTNPVV-
SVKELTNPV;NSVKELTNPVVAESP-VKELTNPVV
DRB3_0101
DRB4_0101
DRB5_0101

<CAF34024 outer surface protein VlsE;Protein;Borrelia garinii>

Allele 8-mer
A0101
A0201 KLDELVSA;KISSAIFL;KIAAAIVL;ILKAIVEA
A0202
KISSAIFL;KLDELVSA;KIAAAIVL;ILKAIVEA;LTALLVFI;ALGEKGAL;FINCKNNA;SAIFLTAL
;FLTALLVF;AIFLTALL;AAGAVTAV;AVSGEQIL;GLVADTFF
A0203
ILKAIVEA;KLDELVSA;ALKDVKAA;FINCKNNA;ALGEKGAL;KISSAIFL;AAGAVTAV;KIAAAIVL
;SISSTLKA;MIKAAEEA;SAIFLTAL;LTALLVFI;AAIVLRGV;GIKGIVDA;IAKAAGAV
A0204 ALGEKGAL;AAGAVTAV;KIAAAIVL;KLDELVSA
A0206
KLDELVSA;KISSAIFL;SAIFLTAL;AAGAVTAV;KIAAAIVL;FIDVFNAF;FAGNANAA;AAIVLRGV
;KAAGAVTA;FLTALLVF;FESISSTL;WLEEMIKA;KASVESAV;AIFLTALL;
A0211
KLDELVSA;KISSAIFL;WLEEMIKA;ALGEKGAL;KIAAAIVL;AIFLTALL;ALKDVKAA;ILKAIVEA
;FLTALLVF;AKDGKFAV;AVSGEQIL;ALLVFINC;IFLTALLV;SISSTLKA;AAGAVTAV
A0212 KLDELVSA;ALGEKGAL;ALKDVKAA;WLEEMIKA;FLTALLVF;AKDGKFAV;AVSGEQIL

A0216
ALGEKGAL;KLDELVSA;KISSAIFL;AAGAVTAV;AIFLTALL;ILKAIVEA;WLEEMIKA;ALKDVKAA
;KIAAAIVL;AVSGEQIL
A0219 KLDELVSA;KISSAIFL;AKDGKFAV
A0301 LVADTFFK;IVLRGVAK;LLVFINCK;VSGEQILK;ESISSTLK;TLKATKGK
A1101
LVADTFFK;SAANHGAK;SSTLKATK;IVLRGVAK;VSGEQILK;ESISSTLK;GAAADIAK;AAFKDEMK
;SAVDEVSK;TFFKSDPK;GIVDAAGK;KAAEEAAK;IAAAIVLR;LLVFINCK;TLKATKGK
A2301 FYESIINL;KWLEEMIK;GLVADTFF
A2402 FYESIINL;IFLTALLV
A2403 FYESIINL
A2601
A2602 FIDVFNAF
A2902
A3001
TLKATKGK;AGKALGEK;TFFKSDPK;AFKDEMKK;KGIAKGIK;IVLRGVAK;LVADTFFK;KWLEEMIK
A3002
A3101 IAAAIVLR;LVADTFFK
A3301 IAAAIVLR
A6801
ESISSTLK;IAAAIVLR;LVADTFFK;EANADAGK;LLVFINCK;SAVDEVSK;SAANHGAK;SSTLKATK
;TFFKSDPK;DSVKGIAK;AAFKDEMK;DDNGAAFK;DPANQAGK
A6802 LTALLVFI;SAIFLTAL;DSAANHGA;FNAFSGLV;NAAVGAAA
A6901 LTALLVFI
B0702 SAIFLTAL
B0801
B0802
B1501 FLTALLVF;IINLGNGF
B1801 FESISSTL
B2705
B3501 FIDVFNAF;SAIFLTAL;FAGNANAA;NAAVGAAA
B3901 FESISSTL
B4001 FESISSTL
B4002
B4402
B4403
B4501 AEEAKNPI
B5101
B5301
B5401 FAGNANAA
B5701
B5801 KSDVKTYF

Allele 9-mer
A0101
A0201
FLTALLVFI;KLFAGNANA;KISSAIFLT;FINCKNNAV;AIFLTALLV;QILKAIVEA;FAGNANAAV;K
AAGAVTAV
A0202
FLTALLVFI;FINCKNNAV;ILKAIVEAA;KAAGAVTAV;KLFAGNANA;FAGNANAAV;SSAIFLTAL;S
AIFLTALL;KISSAIFLT;SVESAVDEV;KAAEEAAKV;GIKGIVDAA;ALKDVKAAA;GLVADTFFK
A0203
FINCKNNAV;FLTALLVFI;ILKAIVEAA;KAAGAVTAV;KLFAGNANA;ALKDVKAAA;GIAKGIKGI;N
LGNGFIDV;SVKTFYESI;SVKASVESA;AAAIVLRGV;IINLGNGFI;FAGNANAAV;GIKGIVDAA;SA
IFLTALL;MIKAAEEAA;ATKGKLDEL;SVKGIAKGI;AIFLTALLV;KAAEEAAKV

A0204
FLTALLVFI;KAAGAVTAV;KAAEEAAKV;FINCKNNAV;FAGNANAAV;SVESAVDEV;KLFAGNANA
A0206
FAGNANAAV;FINCKNNAV;FLTALLVFI;KAAGAVTAV;NLGNGFIDV;AIFLTALLV;KAAEEAAKV;K
LFAGNANA;SVESAVDEV;SAIFLTALL;AAAIVLRGV;QILKAIVEA;LVADTFFKS;KISSAIFLT;SS
AIFLTAL
A0211
FLTALLVFI;NLGNGFIDV;AIFLTALLV;KLFAGNANA;AVDEVSKWL;VAKDGKFAV;ALKDVKAAA;K
LDELVSAK;WLEEMIKAA;KAAGAVTAV;KAAEEAAKV;SVESAVDEV;FINCKNNAV;FAGNANAAV;IL
KAIVEAA;QILKAIVEA;GIAKGIKGI;GLVADTFFK;NADAGKLFA
A0212
FLTALLVFI;NLGNGFIDV;VAKDGKFAV;ALKDVKAAA;KLFAGNANA;FINCKNNAV;FAGNANAAV;A
VDEVSKWL;AIFLTALLV;WLEEMIKAA;KLDELVSAK;GIAKGIKGI;KAAGAVTAV
A0216
NLGNGFIDV;FLTALLVFI;AIFLTALLV;ALKDVKAAA;KLFAGNANA;SVESAVDEV;FAGNANAAV;V
AKDGKFAV;AVDEVSKWL;FINCKNNAV;KAAGAVTAV;EMIKAAEEA;TLKATKGKL;QILKAIVEA;DI
AKAAGAV;WLEEMIKAA
A0219
FLTALLVFI;NLGNGFIDV;VAKDGKFAV;KAAGAVTAV;FAGNANAAV;FINCKNNAV;SVESAVDEV;A
IFLTALLV
A0301
GLVADTFFK;KLDELVSAK;KIAAAIVLR;ALGEKGALK;AVSGEQILK;ISSTLKATK;AAFKDEMKK;A
LLVFINCK
A1101
GLVADTFFK;AVSGEQILK;AAFKDEMKK;ALLVFINCK;STLKATKGK;AIVLRGVAK;KIAAAIVLR;D
TFFKSDPK;ISSTLKATK;KLDELVSAK;AAGKALGEK;ALGEKGALK;TFFKSDPKK;AVGKGNDDK
A2301 IFLTALLVF;GFIDVFNAF;TFYESIINL;TFFKSDPKK
A2402 IFLTALLVF;GFIDVFNAF;YFESISSTL
A2403 IFLTALLVF;GFIDVFNAF;YFESISSTL
A2601 SIINLGNGF;EVSKWLEEM;DVFNAFSGL
A2602 EVSKWLEEM;DVFNAFSGL;SIINLGNGF
A2902
A3001
STLKATKGK;AGKKAEEAK;TFFKSDPKK;GLVADTFFK;ALLVFINCK;ANHGAKADK;AAFKDEMKK;D
TFFKSDPK;AAGKALGEK;AVSGEQILK
A3002
A3101 KIAAAIVLR;ISSTLKATK
A3301 DTFFKSDPK
A6801
DTFFKSDPK;ESAVDEVSK;DSAANHGAK;KIAAAIVLR;TFFKSDPKK;GLVADTFFK;ISSTLKATK;S
TLKATKGK;AAFKDEMKK;GAAFKDEMK
A6802
DVFNAFSGL;SAIFLTALL;FINCKNNAV;SSAIFLTAL;DIAKAAGAV;DVKTYFESI;FLTALLVFI;L
VADTFFKS;FAGNANAAV;SVKTFYESI;EGGSVKASV;KAAGAVTAV;NANAAVGAA;AAAIVLRGV;IS
SAIFLTA
A6901
FAGNANAAV;FINCKNNAV;EVSKWLEEM;DIAKAAGAV;DVFNAFSGL;NLGNGFIDV;QILKAIVEA
B0702 KAAGAVTAV;IVDAAGKAL
B0801
B0802
B1501 SIINLGNGF;GFIDVFNAF
B1801
B2705
B3501 FAGNANAAV;TAVSGEQIL;IFLTALLVF;TDDDNGAAF;FSGLVADTF;GFIDVFNAF
B3901 YFESISSTL
B4001

B4002 EEAKNPIAA
B4402
B4403 EEAKNPIAA
B4501 EEAKNPIAA;AEEAKNPIA
B5101
B5301
B5401 NPIAAAIGT
B5701
B5801 SAVDEVSKW;

Allele 10-mer
A0101
A0201 KISSAIFLTA;KLFAGNANAA;KTFYESIINL
A0202 KLFAGNANAA;KTFYESIINL;KISSAIFLTA;SSAIFLTALL;SIINLGNGFI;IAAAIVLRGV
A0203
SVKASVESAV;KISSAIFLTA;KLFAGNANAA;IAAAIVLRGV;GIAKGIKGIV;SIINLGNGFI;ATKGK
LDELV;SVKTFYESII;SAIFLTALLV;KTYFESISST;SAKKGEGGSV
A0204 KLFAGNANAA;
A0206
KISSAIFLTA;SAIFLTALLV;KLFAGNANAA;AIVEAAGDPA;GVAKDGKFAV;AKAAGAVTAV;ASVES
AVDEV;QILKAIVEAA;SIINLGNGFI;KTFYESIINL;IAAAIVLRGV;GLVADTFFKS
A0211
KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;KLDELVSAKK;KISSAIFLTA;SAIFLTALLV;DVFNA
FSGLV;SVKASVESAV;SAVDEVSKWL;IAAAIVLRGV;LFAGNANAAV;SIINLGNGFI;AVSGEQILKA
;GIVDAAGKAL;FLTALLVFIN
A0212 KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;LFAGNANAAV;KLDELVSAKK
A0216 KLFAGNANAA;GVAKDGKFAV;GIAKGIKGIV;SVKASVESAV;DVFNAFSGLV;LFAGNANAAV
A0219 IAAAIVLRGV;LFAGNANAAV
A0301
KALGEKGALK;KLDELVSAKK;AAIVLRGVAK;VLRGVAKDGK;SISSTLKATK;KVGGTGGDGK;SVKGI
AKGIK;ADTFFKSDPK;TAVSGEQILK;VAKDGKFAVK;SSTLKATKGK
A1101
TALLVFINCK;SISSTLKATK;AAIVLRGVAK;AVGAAADIAK;TAVSGEQILK;KALGEKGALK;SSTLK
ATKGK;SGLVADTFFK;SVKGIAKGIK;DTFFKSDPKK;VSKWLEEMIK;KVGGTGGDGK;KLDELVSAKK
;GAAFKDEMKK;MIKAAEEAAK;AANHGAKADK;VAKDGKFAVK
A2301 TYFESISSTL;IFLTALLVFI;AFSGLVADTF;AIFLTALLVF;FSGLVADTFF
A2402 IFLTALLVFI;TYFESISSTL;AFSGLVADTF
A2403 TYFESISSTL;AFSGLVADTF;IFLTALLVFI
A2601 ESIINLGNGF;SIINLGNGFI;
A2602 ESIINLGNGF;GTDDDNGAAF;AIFLTALLVF;EVSKWLEEMI
A2902
A3001
SGLVADTFFK;SVKGIAKGIK;KALGEKGALK;MIKAAEEAAK;AAIVLRGVAK;VAKDGKFAVK;VLRGV
AKDGK;AVGAAADIAK;AANHGAKADK;SSTLKATKGK;KVGGTGGDGK
A3002
A3101 AAIVLRGVAK
A3301
A6801
DTFFKSDPKK;TAVSGEQILK;MIKAAEEAAK;DAAGKALGEK;TALLVFINCK;DKIAAAIVLR;YFESI
SSTLK;SISSTLKATK;SVKGIAKGIK;NGAAFKDEMK;GAAFKDEMKK;SSTLKATKGK
A6802
DVFNAFSGLV;IAAAIVLRGV;SSAIFLTALL;SAIFLTALLV;EAAGDPANQA;DSVKTFYESI;EVSKW
LEEMI;EAKNPIAAAI;SVKASVESAV;ISSAIFLTAL;NANAAVGAAA;HGAKADKDSV;SIINLGNGFI
A6901 DVFNAFSGLV;EVSKWLEEMI;EAAGDPANQA;SAIFLTALLV
B0702
B0801

B0802
B1501 AIFLTALLVF
B1801
B2705
B3501 EANADAGKLF;DPKKSDVKTY;NGFIDVFNAF;FSGLVADTFF;NANAAVGAAA
B3901
B4001
B4002
B4402
B4403
B4501 AEEAKNPIAA;EEMIKAAEEA;AEEAAKVGGT;EEAKNPIAAA
B5101
B5301
B5401
B5701 ESAVDEVSKW
B5801 ESAVDEVSKW;ISSAIFLTAL

Allele 11-mer

A0101
A0201 KLFAGNANAAV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV;AIFLTALLVFI
A0202
KISSAIFLTAL;KLFAGNANAAV;FIDVFNAFSGL;KIAAAIVLRGV;LLVFINCKNNA;FLTALLVFINC
;ISSAIFLTALL;MIKAAEEAAKV;KTYFESISSTL;LVFINCKNNAV;AIFLTALLVFI;KIGDSAANHG
A;KASVESAVDEV;ALGEKGALKDV;AVSGEQILKAI
A0203
KIAAAIVLRGV;KLFAGNANAAV;MIKAAEEAAKV;ALGEKGALKDV;KISSAIFLTAL;FIDVFNAFSGL
;IAKAAGAVTAV;LLVFINCKNNA;IINLGNGFIDV;KTYFESISSTL;LVFINCKNNAV;FLTALLVFIN
C;KIGDSAANHGA;AAADIAKAAGA
A0204 KLFAGNANAAV;KIAAAIVLRGV;ALGEKGALKDV
A0206
KLFAGNANAAV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV;FAGNANAAVGA;KIGDSAANHGA
;KTYFESISSTL;FLTALLVFINC;KASVESAVDEV;LVFINCKNNAV;KKISSAIFLTA;AIFLTALLVF
I;SSAIFLTALLV;ALGEKGALKDV
A0211
KLFAGNANAAV;ALGEKGALKDV;KIAAAIVLRGV;FIDVFNAFSGL;KISSAIFLTAL;AIFLTALLVFI
;FLTALLVFINC;IINLGNGFIDV;KIGDSAANHGA;KATKGKLDELV;LVFINCKNNAV;MIKAAEEAAK
V;SSAIFLTALLV;AVSGEQILKAI;AVTAVSGEQIL;KTYFESISSTL
A0212
KLFAGNANAAV;ALGEKGALKDV;FIDVFNAFSGL;KIAAAIVLRGV;FLTALLVFINC;MIKAAEEAAKV
;LVFINCKNNAV;KISSAIFLTAL;IINLGNGFIDV
A0216
KLFAGNANAAV;ALGEKGALKDV;MIKAAEEAAKV;FIDVFNAFSGL;KISSAIFLTAL;KIAAAIVLRGV
;AIFLTALLVFI;LVFINCKNNAV;IINLGNGFIDV;KIGDSAANHGA;KATKGKLDELV;LLVFINCKNN
A
A0219 KLFAGNANAAV;FIDVFNAFSGL;KIAAAIVLRGV;KISSAIFLTAL;ALGEKGALKDV
A0301
FSGLVADTFFK;VTAVSGEQILK;GVAKDGKFAVK;FINCKNNAVGK;TYFESISSTLK;LTALLVFINCK
A1101
LTALLVFINCK;VTAVSGEQILK;SVESAVDEVSK;GTDDDNGAAFK;FSGLVADTFFK;TYFESISSTLK
;AAAIVLRGVAK;GVAKDGKFAVK;SAANHGAKADK;VADTFFKSDPK;AAVGAAADIAK;IVLRGVAKDG
K;AAGDPANQAGK;ESISSTLKATK;ISSTLKATKGK;FINCKNNAVGK;EVSKWLEEMIK;GIKGIVDAA
GK
A2301 TYFESISSTLK;AFSGLVADTFF;SAIFLTALLVF
A2402 AFSGLVADTFF
A2403 AFSGLVADTFF
A2601

A2602 KISSAIFLTAL;FIDVFNAFSGL
A2902
A3001 KGKLDELVSAK;TYFESISSTLK;SAKKGEGGSVK;AFKDEMKKSDK;IVLRGVAKDGK
A3002 AFSGLVADTFF
A3101 TYFESISSTLK
A3301
A6801
ESISSTLKATK;LTALLVFINCK;EVSKWLEEMIK;TYFESISSTLK;FSGLVADTFFK;EMIKAAEEAAK
;FINCKNNAVGK;VTAVSGEQILK;SVESAVDEVSK;DSVKGIAKGIK;SAANHGAKADK;NGAAFKDEMK
K;ISSTLKATKGK
A6802
ESIINLGNGFI;ISSAIFLTALL;SSAIFLTALLV;LVFINCKNNAV;FIDVFNAFSGL;KIAAAIVLRGV
;ESAVDEVSKWL;EEAKNPIAAAI;IAAAIVLRGVA;DVFNAFSGLVA;MIKAAEEAAKV
A6901 LVFINCKNNAV;FIDVFNAFSGL
B0702
B0801
B0802
B1501 VLRGVAKDGKF;KLFAGNANAAV
B1801 YESIINLGNGF;DEANADAGKLF
B2705
B3501 NAFSGLVADTF;SAIFLTALLVF;IGTDDDNGAAF;DPKKSDVKTYF
B3901
B4001 YESIINLGNGF
B4002 EEAKNPIAAAI
B4402
B4403 EEAKNPIAAAI
B4501 EEMIKAAEEAA;AEEAKNPIAAA;EEAKNPIAAAI
B5101
B5301
B5401
B5701
B5801 SAIFLTALLVF;KTYFESISSTL;KSDKIAAAIVL;ISSAIFLTALL

Allele 15-mer plus 9-mer core

DRB1_0101 EQILNAIVTAAGQAG-LNAIVTAAG;AGDVKDAAAAVGAVS-
VKDAAAAVG;GDVKDAAAAVGAVSG-VKDAAAAVG;QILNAIVTAAGQAGQ-
IVTAAGQAG;ADAGDVKDAAAAVGA-VKDAAAAVG;DAGDVKDAAAAVGAV-
VKDAAAAVG;ILNAIVTAAGQAGQA-IVTAAGQAG;LNAIVTAAGQAGQAG-
IVTAAGQAG;EGVKFAPKAAADAAA-FAPKAAADA;GADAGDVKDAAAAVG-
AGDVKDAAA;GVKFAPKAAADAAAA-FAPKAAADA;VEGVKFAPKAAADAA-
FAPKAAADA;VKFAPKAAADAAAAD-FAPKAAADA;NAIVTAAGQAGQAGK-
IVTAAGQAG;DQIAAALVLRGVAKD-IAAALVLRG;KKNDQIAAALVLRGV-
IAAALVLRG;KNDQIAAALVLRGVA-IAAALVLRG;KVEGVKFAPKAAADA-
VKFAPKAAA;NDQIAAALVLRGVAK-IAAALVLRG;KKKNDQIAAALVLRG-
DQIAAALVL;SGEQILNAIVTAAGQ-LNAIVTAAG;GEQILNAIVTAAGQA-
LNAIVTAAG;VSGEQILNAIVTAAG-ILNAIVTAA;DVKDAAAAVGAVSGE-
VKDAAAAVG;VKDAAAAVGAVSGEQ-VKDAAAAVG;IEVFNAFSGLVADAF-
VFNAFSGLV;FIEVFNAFSGLVADA-VFNAFSGLV;GFIEVFNAFSGLVAD-
VFNAFSGLV;NGFIEVFNAFSGLVA-VFNAFSGLV;AIVTAAGQAGQAGKK-
IVTAAGQAG;KFAPKAAADAAAADG-FAPKAAADA;IVTAAGQAGQAGKKA-
IVTAAGQAG;FAPKAAADAAAADGN-FAPKAAADA;QIAAALVLRGVAKDG-
IAAALVLRG;AVSGEQILNAIVTAA-EQILNAIVT;GKLFGTAAGADAGDV-
FGTAAGADA;KAGKLFGTAAGADAG-FGTAAGADA;KLFGTAAGADAGDVK-
FGTAAGADA;AGKLFGTAAGADAGD-FGTAAGADA;EVFNAFSGLVADAFS-
FNAFSGLVA;IAAALVLRGVAKDGK-IAAALVLRG;KKAGKLFGTAAGADA-
LFGTAAGAD;AIFIVAFLALIGCKN-IVAFLALIG;ISSAIFIVAFLALIG-

FIVAFLALI;SAIFIVAFLALIGCK-IVAFLALIG;SSAIFIVAFLALIGC-
IVAFLALIG;SDKIGNVAAGGGAGA-IGNVAAGGG;DKIGNVAAGGGAGAD-
IGNVAAGGG;GNGFIEVFNAFSGLV-FIEVFNAFS;IFIVAFLALIGCKNN-
IVAFLALIG;VFNAFSGLVADAFSK-VFNAFSGLV;KIGNVAAGGGAGADK-
VAAGGGAGA;IGNVAAGGGAGADKE-VAAGGGAGA;LFGTAAGADAGDVKD-
FGTAAGADA;FNAFSGLVADAFSKA-FSGLVADAF;FGTAAGADAGDVKDA-
FGTAAGADA;FIVAFLALIGCKNNV-IVAFLALIG;NAFSGLVADAFSKAD-
FSGLVADAF;KISSAIFIVAFLALI-IFIVAFLAL;GLVADAFSKADPKKS-
VADAFSKAD;LVADAFSKADPKKSD-FSKADPKKS;ADAFSKADPKKSDVK-
FSKADPKKS;GSDKIGNVAAGGGAG-IGNVAAGGG;VADAFSKADPKKSDV-
FSKADPKKS;DAFSKADPKKSDVKT-FSKADPKKS;GNVAAGGGAGADKES-
VAAGGGAGA;GGSDKIGNVAAGGGA-IGNVAAGGG;KDAAAAVGAVSGEQI-
AAAVGAVSG;IKKKNDQIAAALVLR-DQIAAALVL;GGGSDKIGNVAAGGG-
KIGNVAAGG;IVAFLALIGCKNNVG-IVAFLALIG;EAKNAIEAAIGAAGD-
IEAAIGAAG;DEAKNAIEAAIGAAG-KNAIEAAIG;SIFYQSIINLGNGFI-
YQSIINLGN;AKNAIEAAIGAAGDA-IEAAIGAAG;DAAAAVGAVSGEQIL-
VGAVSGEQI;KNAIEAAIGAAGDAD-IEAAIGAAG;DIKKKNDQIAAALVL-
IKKKNDQIA;AAALVLRGVAKDGKF-VLRGVAKDG;AFSGLVADAFSKADP-
LVADAFSKA;FSGLVADAFSKADPK-LVADAFSKA;NAIEAAIGAAGDADF-
IEAAIGAAG;AAAVGAVSGEQILNA-VGAVSGEQI;KESVNGIAGAIKGIV-
VNGIAGAIK;AASIFYQSIINLGNG-FYQSIINLG;ASIFYQSIINLGNGF-
FYQSIINLG;TAASIFYQSIINLGN-FYQSIINLG;ESVNGIAGAIKGIVE-
VNGIAGAIK;DKESVNGIAGAIKGI-VNGIAGAIK;MKKISSAIFIVAFLA-
MKKISSAIF;IFYQSIINLGNGFIE-YQSIINLGN;VGAVSGEQILNAIVT-
VSGEQILNA;AAAAVGAVSGEQILN-VGAVSGEQI;AALVLRGVAKDGKFA-
VLRGVAKDG;ADKESVNGIAGAIKG-VNGIAGAIK

DRB1_0301

DRB1_0401 TAASIFYQSIINLGN-FYQSIINLG;AASIFYQSIINLGNG-
FYQSIINLG;SIFYQSIINLGNGFI-FYQSIINLG;ASIFYQSIINLGNGF-
FYQSIINLG;DTAASIFYQSIINLG-SIFYQSIIN;IFYQSIINLGNGFIE-
FYQSIINLG;FYQSIINLGNGFIEV-FYQSIINLG;SGEQILNAIVTAAGQ-
LNAIVTAAG;VSGEQILNAIVTAAG-ILNAIVTAA;GEQILNAIVTAAGQA-
LNAIVTAAG;EQILNAIVTAAGQAG-LNAIVTAAG

DRB1_0404 NGFIEVFNAFSGLVA-VFNAFSGLV;GNGFIEVFNAFSGLV-
FIEVFNAFS;GFIEVFNAFSGLVAD-VFNAFSGLV;FIEVFNAFSGLVADA-
VFNAFSGLV;IEVFNAFSGLVADAF-VFNAFSGLV;EQILNAIVTAAGQAG-
ILNAIVTAA;VSGEQILNAIVTAAG-ILNAIVTAA;GEQILNAIVTAAGQA-
ILNAIVTAA;SGEQILNAIVTAAGQ-ILNAIVTAA;AVSGEQILNAIVTAA-
VSGEQILNA;EVFNAFSGLVADAFS-VFNAFSGLV;VFNAFSGLVADAFSK-
VFNAFSGLV;QILNAIVTAAGQAGQ-ILNAIVTAA;ILNAIVTAAGQAGQA-ILNAIVTAA

DRB1_0405 TAASIFYQSIINLGN-FYQSIINLG;AASIFYQSIINLGNG-
YQSIINLGN;ASIFYQSIINLGNGF-YQSIINLGN;SIFYQSIINLGNGFI-
YQSIINLGN;IFYQSIINLGNGFIE-YQSIINLGN;NGFIEVFNAFSGLVA-
FIEVFNAFS;GFIEVFNAFSGLVAD-FNAFSGLVA;FIEVFNAFSGLVADA-
FNAFSGLVA;FYQSIINLGNGFIEV-YQSIINLGN;YQSIINLGNGFIEVF-
YQSIINLGN;IEVFNAFSGLVADAF-FNAFSGLVA;EVFNAFSGLVADAFS-FNAFSGLVA

DRB1_0701 IEVFNAFSGLVADAF-VFNAFSGLV;NGFIEVFNAFSGLVA-
VFNAFSGLV;GFIEVFNAFSGLVAD-VFNAFSGLV;FIEVFNAFSGLVADA-VFNAFSGLV

DRB1_0802 GLVADAFSKADPKKS-AFSKADPKK;LVADAFSKADPKKSD-
FSKADPKKS;VADAFSKADPKKSDV-FSKADPKKS;ADAFSKADPKKSDVK-
FSKADPKKS;DAFSKADPKKSDVKT-FSKADPKKS;AFSKADPKKSDVKTY-
FSKADPKKS;FSKADPKKSDVKTYF-FSKADPKKS

DRB1_0901 SIFYQSIINLGNGFI-FYQSIINLG;DTAASIFYQSIINLG-
IFYQSIINL;ASIFYQSIINLGNGF-FYQSIINLG;AASIFYQSIINLGNG-
FYQSIINLG;TAASIFYQSIINLGN-FYQSIINLG

DRB1_1101

DRB1_1302 SIFYQSIINLGNGFI-FYQSIINLG;VSGEQILNAIVTAAG-
ILNAIVTAA;SGEQILNAIVTAAGQ-ILNAIVTAA;IFYQSIINLGNGFIE-
IINLGNGFI;FYQSIINLGNGFIEV-IINLGNGFI;GEQILNAIVTAAGQA-
ILNAIVTAA;EQILNAIVTAAGQAG-ILNAIVTAA;AVSGEQILNAIVTAA-
EQILNAIVT;YQSIINLGNGFIEVF-IINLGNGFI;QSIINLGNGFIEVFN-
IINLGNGFI;ASIFYQSIINLGNGF-FYQSIINLG;AASIFYQSIINLGNG-
FYQSIINLG;TAASIFYQSIINLGN-FYQSIINLG;QILNAIVTAAGQAGQ-
ILNAIVTAA;SIINLGNGFIEVFNA-IINLGNGFI;DTAASIFYQSIINLG-IFYQSIINL
DRB1_1501 GFIEVFNAFSGLVAD-VFNAFSGLV;NGFIEVFNAFSGLVA-
VFNAFSGLV;SAIFIVAFLALIGCK-IVAFLALIG;SSAIFIVAFLALIGC-
IVAFLALIG;IAAALVLRGVAKDGK-ALVLRGVAK;IEVFNAFSGLVADAF-
VFNAFSGLV;AAALVLRGVAKDGKF-LRGVAKDGK;FIEVFNAFSGLVADA-
VFNAFSGLV;AIFIVAFLALIGCKN-IVAFLALIG;IVAFLALIGCKNNVG-
IVAFLALIG;ALVLRGVAKDGKFAG-LRGVAKDGK;AALVLRGVAKDGKFA-
LRGVAKDGK;IFIVAFLALIGCKNN-IVAFLALIG;SIFYQSIINLGNGFI-FYQSIINLG
DRB3_0101
DRB4_0101
DRB5_0101

Fig. 42.

A) Special selected HLA-A*0201 binding peptides from Borrelia proteins

<OspA7;Protein;Borrelia species>FTLEGTLAA
<OspA 8;Protein;Borrelia species>TLVSKKVTL
<OspB 8;Protein;Borrelia species>IMLEGNLV
<OspB 9;Protein;Borrelia species>TMSITDDL
<OspC 7;Protein;Borrelia species>LMTLFLFI
<OspC 8;Protein;Borrelia species>LLAGAYAI
<FlaB 6;Protein;Borrelia species>QASWTLRV
<FlaB 7;Protein;Borrelia species>IAVNIYAA
<VlsE 8;Protein;Borrelia species>LSAIVTAA
<VlsE 9;Protein;Borrelia species>ILSAIVTA
<OspG 6;Protein;Borrelia species>IICAVFVL
<FlaA 6;Protein;Borrelia species>IWSNPNYI
<OspE 4;Protein;Borrelia species>IICAVFVL
<OspE 5;Protein;Borrelia species>FSEFTVNI
<BmpA 3;Protein;Borrelia species>MYSDGIDI
<BmpA 4;Protein;Borrelia species>LAPNNVIT
<BmpB 3;Protein;Borrelia species>LIGVVFRI
<BmpB 4;Protein;Borrelia species>VGDALYLI
<BmpC 3;Protein;Borrelia species>MTEDAYEV
<BmpC 4;Protein;Borrelia species>LNQDQSYI
<BmpD 2;Protein;Borrelia species>MYGYEAGA
<BmpD 3;Protein;Borrelia species>LAPNNVLV
<DbpA 3;Protein;Borrelia species>ILKAKIKA
<DbpA 4;Protein;Borrelia species>TADGIIAI
<DbpB 2;Protein;Borrelia species>LAACNFGL
<DbpB 3;Protein;Borrelia species>LVACSIGL
<BapA 4;Protein;Borrelia species>LFILSLSA
<CRASP-1a;Protein;Borrelia species>KLNIIKLNI
<CRASP-1b;Protein;Borrelia species>LNYEIEKI
<CRASP-1c;Protein;Borrelia species>KLNILTTIL
<CRASP-2a;Protein;Borrelia species>MLISISLL
<CRASP-2b;Protein;Borrelia species>LIDDFAIEL
<CRASP-2c;Protein;Borrelia species>LSCDVSRL
<MalQ 4;Protein;Borrelia species>LLDFASFV
<MalQ 5;Protein;Borrelia species>LNTNEDFV
<MalQ 6;Protein;Borrelia species>IAYDSADV

B) Special selected HLA-A*0301 binding peptides from Borrelia proteins

<BmpA 5;Protein;Borrelia species>IVFLSCSGK
<BmpA 6;Protein;Borrelia species>FLTGYIAAK
<BmpB 5;Protein;Borrelia species>EIFIKQILK
<BmpB 6;Protein;Borrelia species>ALYLITGEY
<BmpC 5;Protein;Borrelia species>KEMARFMYK
<BmpC 6;Protein;Borrelia species>YIAAKMSRK
<BmpD 5;Protein;Borrelia species>SLMYSLTKK

<BmpD 6;Protein;Borrelia species>RSTASNMYR
<DbpA 5;Protein;Borrelia species>IIAIVKVMK
<DbpA 6;Protein;Borrelia species>FTNTQTGSK
<DbpB 5;Protein;Borrelia species>FTGLKTGSK
<DbpB 6;Protein;Borrelia species>LFEAFTGLK
<HSP90 6;Protein;Borrelia species>LLTSGMPSK
<OspA 7;Protein;Borrelia species>LILALIACK
<OspA 8;Protein;Borrelia species>KTKNLVFTK
<Osp A 9;Protein;Borrelia species>ISVNSQKTK
<OspB 9;Protein;Borrelia species>VTLKKEIEK
<OspB 10;Protein;Borrelia species>RTNGTTLEY
<OspB 11;Protein;Borrelia species>MTDADNATK
<OspC 9;Protein;Borrelia species>LANKAIGKK
<OspC 10;Protein;Borrelia species>ILMTLFLFI
<OspC 11;Protein;Borrelia species>AISTLITEK
<OspE 6;Protein;Borrelia species>GSFKTSLYY
<OspE 7;Protein;Borrelia species>NLGTLVIRK
<OspG 7;Protein;Borrelia species>VFVLIISCK
<FlaA 7;Protein;Borrelia species>RVSKSHSSK
<FlaB 8;Protein;Borrelia species>SINAANLSK
<FlaB 9;Protein;Borrelia species>KINTPASLS
<FlaB 10;Protein;Borrelia species>SQASRNTSK
<FlaB 11;Protein;Borrelia species>FQNRLESIK
<VlsE 10;Protein;Borrelia species>AVSGEQILK
<VlsE 11;Protein;Borrelia species>AIVLRGLAK
<BapA 5;Protein;Borrelia species>KQILADLPK
<BapA 6;Protein;Borrelia species>QLNSDKIDY
<CRASP-1d;Protein;Borrelia species> RIIYSSLNY
<CRASP-1e;Protein;Borrelia species>SSLNYEIEK
<CRASP-2d;Protein;Borrelia species>RSRYNNFYK
<CRASP-2e;Protein;Borrelia species> ESFDVISSK
<CRASP-2f;Protein;Borrelia species>LIALKCIVK
<MalQ 1;Protein;Borrelia species>RSFEKFKKK
<MalQ 2;Protein;Borrelia species>FLFASSQSY
<MalQ 3;Protein;Borrelia species>RINLNLKRK

<Nonsense 3;Protein;artificial>GLFGAGAFK
<Nonsense 4;Protein;artificial>GVYAGAVMK