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(54) **Title:** MHC PEPTIDE COMPLEXES AND USES THEREOF IN INFECTIOUS DISEASES

(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 are disclosed. The affinity and specificity of the MHC-peptide complexes are surprisingly high. 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 field of therapy, including therapeutic methods and therapeutic compositions. Also comprised by the present invention is the sample-mounted use of MHC complexes and MHC multimers.

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MHC peptide complexes and uses thereof in infectious diseases

All patent and non-patent references cited in US 60/907,217 as well as in this application are hereby incorporated by reference in their entirety. US 60/907,217 is 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 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-tumour 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 cancer and 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, autologous cancer therapy, transplantation, 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-

tumour and anti-virus therapy, including isolation of antigen specific T cells capable of inactivation or elimination of undesirable target cells or isolation of specific T cells capable of regulation of other immune cells.

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 peptide P,

wherein (a-b-P) is the MHC-peptide complex formed when the 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.

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 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 peptide P is provided herein below. In one embodiment, the peptide P can be selected from the group consisting of sequences disclosed in the electronically enclosed "Sequence Listing" and annotated consecutively (using integers) starting with SEQ ID NO:1 and ending with SEQ ID NO:52252.

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.

In yet another aspect there is provided a kit comprising 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, or the 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 antigen specific of T cells specific for the peptide P of thesaid MHC monomer or MHC multimer, 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.

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 and MHC multimers according to the present invention. The immune monitoring methods include e.g. flow cytometry, ELISPOT, LDA, Quantaferon and Quantaferon-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 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 Quantaferon-like detection assays, 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. Cancer diagnostic methods and/or cancer monitoring methods also fall within the scope of the present invention.

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

administering said 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 in accordance with the present invention a method for immune monitoring one or more cancer diseases comprising the step of monitoring one or more cancer antigen specific T-cells, said method comprising the steps of

providing a MHC monomer or MHC multimer, or individual components thereof, according to any of the claims 1 to 797,
providing a population of cancer antigen specific T cells, or individual cancer antigen specific T cells, and

measuring the number and/or presence of cancer antigen specific T cells specific for the peptide P of the MHC monomer or MHC multimer, thereby immune monitoring said one or more cancer diseases.

In a still further aspect there is provided a method for diagnosing one or more cancer diseases in an individual, said method comprising the step of performing an immune monitoration of one or more cancer antigen specific T cell(s), said method comprising the further steps of

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

providing a population of cancer antigen specific T cells, or individual cancer antigen specific T cells, and

measuring the number and/or presence of T cells specific for the peptide P of the MHC monomer or MHC multimer, thereby diagnosing said one or more cancer diseases.

In yet another aspect of the present invention there is provided a method for performing a cancer vaccination of an individual in need thereof, said method comprising the steps of

providing a MHC monomer or MHC multimer according to any of the present invention, and

administering said MHC monomer or said MHC multimer to said individual, thereby performing a cancer vaccination of the said individual.

In a still further aspect of the present invention there is provided a method for performing a cancer therapeutic treatment of an individual comprising the steps of

Providing the MHC multimer according to the present invention, and

Isolation of T cells specific for said MHC multimer, and

Optionally manipulation of said T cell and

Introduction of said T cells into the same or a different individual to obtain a cancer therapeutic treatment.

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 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 one or more functional MHC proteins to generate a MHC-peptide complex (a-b-P); subsequently 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.

DEFINITIONS

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

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.

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

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 monoclonal, preferably but not limited to human or humanized, antibodies that have

binding specificities for at least two different antigens. The antibody 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: 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

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.

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.

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).

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.

A "MHC Class I molecule" as used everywhere herein is defined as a molecule which comprises 1-3 subunits, including a heavy chain, a heavy chain combined with a light chain (beta$_2$m), a heavy chain combined with a light chain (beta$_2$m) through a flexible linker, a heavy chain combined with a peptide, a heavy chain combined with a peptide through a flexible linker, a heavy chain/beta$_2$m dimer combined with a peptide, and a heavy chain/beta$_2$m dimer with a peptide through a flexible linker to the heavy or light chain. The MHC molecule chain 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. By example, it has been shown that substitution of XX with YY in position nn of human beta$_2$m enhance the biochemical stability of MHC Class I molecule complexes and thus can lead to more efficient antigen presentation of subdominant peptide epitopes.

MHC complex: MHC complex is herein used interchangeably with MHC-peptide complex, unless it is specified that the MHC complex is empty, i.e. is not complexed with 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 defined as a molecule which comprises 2-3 subunits including an alpha-chain and a beta-chain (alpha/beta-dimer), an alpha/beta dimer with a peptide, and an alpha/beta dimer combined with a peptide through a flexible linker to the alpha or beta chain, an alpha/beta dimer combined through an interaction by affinity tags e.g. jun-fos, an alpha/beta dimer combined through an interaction by affinity tags e.g. jun-fos and further combined with a peptide through a flexible linker to the alpha or beta chain. The MHC 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 alpha-chain and beta-chain have been fused, to form one subunit, the "MHC Class II molecule" can comprise only 1 subunit.

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" 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.

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 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 interest, and in the mouse system, H-2 alleles are of interest. 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 interest.

"MHC complexes" and "MHC constructs" are used interchangably herein.

"MHC protein" and "MHC molecule" are used interchangably herein. Accordingly, a functional MHC peptide complex comprises a MHC protein or MHC molecule associated with a peptide to be presented for cells or binding partners having an affinity for said peptide.

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.

The MHC molecule can 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.

MHC multimer: The terms 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.
"A plurality" as used everywhere herein should be interpreted as two or more.
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

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 protects 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 abereviation for Bind level.

Aff. is an abereviation for affinity.

DETAILED DESCRIPTION OF THE 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 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

The product of the present invention is 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 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.

In the following it is described how to generate the product 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, SA with two MHC's, coiled-coil dimerization e.g. Fos.Jun dimerization

c) n=3, Trimers, multimerization can be based on SA 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 SA with all four binding sites occupied by MHC molecules or 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 could 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 make use of DC, 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 olace on beads, and surfaces e.g. microtiterplate, tubes, microarray devices, micro-fluidic systems

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.

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. 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 folding of MHC I complexes is very dependent on binding of peptide in the peptide-binding cleft and the peptide binding stabilises correct conformation.

Addition of molar excess of peptide will force the equilibrium against correct 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 β2m are included as stabilizing soluble additives.

Other additives of special interest for stabilization of MHC I 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 could be added to any solution containing MHC I molecules in order to increase the stability of the molecule. That could be during the refolding process, to the soluble monomer or to a solutions containing MHC I bound to a carrier.

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.

Stabilization strategies forf MHC II complexes

- *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.

o *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.

o *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.

- *Stabilization with soluble additives.*

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 complex. Examples are sucrose, mannose, glycine, betaine, alanine, glutamine, glutamic acid and ammonium sulfate. 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 increases surface tension of the MHC complex and simultaneously can interact with charged groups in the protein. Examples are $MgSO_4$, NaCl, polyethylenglycol, 2-methyl-2,4-pentanediol and guanidiniumsulphate.

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, excess β2m is also expected to drive the folding process in direction of correctly folded MHC complexes. Therefore peptide identical to the peptide bound in the peptide-binding cleft and β2m can be included as stabilizing soluble additives.

Other additives of special interest for stabilization of MHC complexes are BSA, fetal and bovine calf serum, and other protein components in serum with a protein stabilizing effect.

All of the above mentioned soluble additives could 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 or to a solution of MHC multimers comprising several MHC complexesThat could be to the soluble monomer, to a solution containing MHC II bound to a carrier or to solutions used during analysis of MHC II specific T cells with MHC II multimers.

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 could be added to any solution containing MHC II molecules in order to increase the stability of the molecule. That could be to the soluble monomer, to a solution containing MHC II bound to a carrier or to solutions used during analysis of MHC II specific T cells with MHC II multimers.

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-biding 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:

<u>Non-classical MHC complexes and other MHC-like molecules:</u>
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..

Generation of antigenic peptide

Approaches and methods for the identification and design of appropriate peptides

MHC class 1 molecules normally 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 molecules bind peptides most often with a total length of 13-18 amino acids around a

9-mer core motif containing the important amino acid anchor residues. However the total length is not strictly defined as for most MHC class 1 molecules.

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

To identify 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 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.

A measure for binding affinity of the peptide to the MHC molecules can for some MHC molecules be found 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

a) from genomic DNA sequences without introns

When only the genomic DNA sequences are known and thereby reading frame and direction of transcription of the genes are 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.

b) from genomic DNA sequences with introns

In organisms having intron/exon gene structure the present approach will not be able to identify peptide sequence motifs that are derived by combination of amino acid sequences derived partly from two separate introns.

c) from cDNA sequences

cDNA sequences can be translated into the actual amino acid sequences to allow peptide identification.

d) from known amino acid sequences

In the case of known protein sequences these can directly be applied to software analysis for prediction of 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 using software that specifically can predict the binding peptide sequences for a subset of MHC alleles for which the binding characteristics of the peptide is known.

Design of MHC class 1 binding peptide sequence

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. All peptides carrying one or more stop codons are omitted for further consideration. 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

Using a directed approach is only possible when working on prediction of peptide sequences binding to MHC class I alleles with known binding preferences. Examples of such programs are www.syfpeithi.de; www.imtech.res.in/raghava/propred1/index.html; www.cbs.dtu.dk/services/NetMHC/. Identified peptides can then be tested for biological relevance in functional assays such as Cytokine release assays, ELISPOT and CTL killing assays.

Prediction of good HLA class 1 peptide binders can be done at the HLA superfamily level even taking the combioned action of endocolic and membrane bound protease

activities as well as the TAP1 and TAP2 transporter specificities into consideration using the program www.cbs.dtu.dk/services/NetCTL/.

Design of MHC class 2 binding peptide sequence.

a) Total approach and b) directed approach

The approach to predict putative peptide binders for MHC class 2 is similar as given above for MHC class 1 binding peptide prediction. The only change is the different size of the peptides, which is preferably 13-16 amino acids long for MHC class 2. The putative binding peptide sequences only describe the central part of of the peptide including the 9-mer core peptide; 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.

Choice of MHC allele

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 human group that one wish to study.

Peptide modifications

Homologous peptides

Predictions of the primary amino acid sequence for the binding peptides of MHC class I and class II molecules can be done as described above on the basis of the genetic information. Peptides homologous to the predicted peptide sequences may also be bound if they are sufficiently homologous i.e. are having an amino acid sequence identity greater than e.g. more than 90%, more than 80% or more than 70%. Identity being most important for the anchor residues.

Homologues MHC peptide sequences may arise from the existence of multiple strongly homologous alleles, from small insertions, deletions, inversions or substitutions.

Uncommon amino acids

Peptides having un-common amino acids may be bound in the MHC groove as well. Two un-common amino acids found in nature are selenocysteine and pyrrolysine.

Artificial amino acids

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.

Chemically modified amino acids

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.

Split or combinatorial peptide

A MHC binding peptide may also 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 part of the peptide bound in the groove.

Position in peptide of amino acid change

Any of the mentioned changes of the bound peptide amino acid sequence, 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, n being the final amino acid of the peptide.

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 MHC bound 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, devided into three main types

a) involving addition include:

acylation, 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 (e.g. of thyroid hormones)

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) involving addition of other proteins or peptides

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) involving changing the chemical nature of 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 peptides

a) From natural sources

Peptides can be obtained from natural sources by enzymatic digestion or proteolysis of natural proteins or proteins derived by *in vitro* translation of mRNA. 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 (contatemeric) antigenic peptides.

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 □-chain, full length or truncated;
Peptide-linker-MHC class 2 □-chain, full length or truncated;
Peptide-linker-MHC class 2 □-chain-linker-MHC class 2 □-chain, both chains can be full length or truncated, truncation may involve, omission of □- and/or □-chain intermembrane domain, or omission of □- and/or □-chain intermembrane plus cytoplasmic domains. MHC class 2 part of the construction may consist of fused

domains from NH2-terminal, MHC class 2 □1domain-MHC class 2 □1domain-constant □3 of MHC class 1, or alternatively of fused domains from NH2-terminal, MHC class 2 □1domain-MHC class 2 □1domain-constant □3 of MHC class 1. In both cases □2m will be associated non-covalently in the folded MHC complex. □2m can also be covalently associated in the folded MHC class 2 complex if the following constructs are used from NH2 terminal, MHC class 2 □1domain-MHC class 2 □1domain-constant-□3 of MHC class 1-linker-□2m, or alternatively of fused domains from NH2-terminal, MHC class 2 □1domain-MHC class 2 □1domain-constant □3 of MHC class 1-linker-□2m; 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.

Loading of the peptide into the MHCmer

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. 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 □ chain-flexible linker-□ chain-flexible linker-peptide

a) during MHC complex folding

a1) 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 □ with the purified recombinant □2 microglobulin and a peptide or a peptide mix.

a2) as part of a recombinant protein construct

Alternatively the peptide to be folded into the binding groove can be encoded together with e.g. the □ 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) by exchange reaction

b1) 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) "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) by aided exchange

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) 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.

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.

Molecular weight of multimerization domain.

- 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 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, chemi-luminescent 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.

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. Generation of a usefull product includes the following basic steps:

1. Design of antigenic peptides
2. Choise of MHC allele
3. Generation of product
4. Validation and optimization of product

In the following strategies for generation of products are given:

How to make a MHC multimer diagnostic or immune monitoring reagent

1. Identify disease of interest. Most relevant diseases in this regard are infectious-, cancer-, auto immune-, transplantation-, or immuno-suppression- related diseases.
2. Identify relevant protein targets. This may be individual proteins, a group of proteins from a given tissue or all or subgroups of proteins from a complete 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 DNA sequence is translated into amino acid sequence in all reading frames.
4. Choose MHC allele. Decide on needed MHC allele population coverage. If a broad coverage of a given population is needed (i.e. when a generally applicable reagent is 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 and/or 11'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, select the best peptide epitopes (the epitopes with highest binding score) 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. In general, favour unique peptide sequences only present in the selected protein.
8. Make selected peptides as described elsewhere herein, 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 of peptide binding to MHC I or II molecules.
9. Generate desired MHC multimer as described elsewhere herein and test efficacy in detecting specific T-cells using 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.

How to make a MHC multimer therapeutic reagent

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

Thus, the present invention relates to methods for detecting the presence of MHC recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC multimer as defined above, and
(c) determining any binding of the MHC multimer, which binding indicates the presence of MHC recognising cells.

Such methods are a powerful tool in diagnosing 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 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 recognising cells in the sample, and accordingly the presence of MHC multimeres displaying the peptide.

The present invention also relates to methods for monitoring MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex as defined above, and
(c) determining any binding of the MHC multimer, thereby monitoring MHC 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 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 recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC 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 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 recognising cells in the sample, and accordingly the presence of MHC complexs displaying the peptide.

The present invention also relates to methods for determining the status of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex as defined above, and
(c) determining any binding of the MHC complex, thereby determining the status of a disease involving MHC 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 complex makes possible these options, since the binding is indicative for the presence of the MHC recognising cells in the sample, and accordingly the presence of MHC complexs displaying the peptide.

The present invention also relates to methods for the diagnosis of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC 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 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 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 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 recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC 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 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 multimeres 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 recognising cells comprising the steps of

(a) providing a sample from a subject receiving treatment with a medicament,
(b) contacting the sample with a as defined herein, and
(c) determining any binding of the MHC multimer, 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 recognising cells in the sample, and accordingly the presence of MHC multimeres displaying the peptide.

The present invention also relates to methods for manipulating MHC recognising cells populations comprising the steps of

(a) providing a sample comprising MHC recognising cells,
(b) contacting the sample with a MHC multimer immobilised onto a solid support as defined above,
(c) isolating the relevant MHC 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 recognising cells" are intended to mean such which are able to recognise and bind to MHC multimeres. The intended meaning of "MHC multimeres" is given above. Such MHC recognising cells may also be called MHC recognising cell clones, target cells, target MHC recognising cells, target MHC molecule recognising cells, MHC molecule receptors, MHC receptors, MHC peptide specific receptors, or peptide-specific cells. The term "MHC 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 recognising cell that binds to the MHC molecule.

As described above, in diseases and various conditions, peptides are displayed by means of MHC multimeres, which are recognised by the immune system, and cells targeting such MHC multimeres are produced (MHC recognising cells). Thus, the presence of such MHC protein recognising cells is a direct indication of the presence of

MHC multimeres 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 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 multimeres of the present invention have numerous uses and are a valuable and powerful tool e.g. in the fields of therapy, diagnosis, prognosis, monitoring, stratification, and determining the status of diseases or conditions. Thus, the MHC multimeres may be applied in the various methods involving the detection of MHC recognising cells.

Furthermore, the present invention relates to compositions comprising the MHC multimeres in a solubilising medium. The present invention also relates to compositions comprising the MHC multimeres immobilised onto a solid or semi-solid support.

The MHC multimers 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 multimeres are very suitable as detection systems. Thus, the present invention relates to the use of the MHC multimeres as defined herein as detection systems.

In another aspect, the present invention relates to the general use of 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 multimeres 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 multimeres to MHC recognising cells and establishing the effectiveness of the medicament or the treatment in question based on the specificity of the MHC 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 MHC multimer as defined herein for use as medicaments, and to the MHC multimeres for use in in vivo and ex vivo therapy.

The present invention relates to therapeutic compositions comprising as active ingredients the MHC multimeres as defined herein.

An important aspect of the present invention is therapeutic compositions comprising as active ingredients effective amounts of MHC recognising cells obtained using the MHC multimeres as defined herein to isolate relevant MHC 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 recognising cells by using the MHC multimeres 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 multimeres for detecting and analysing receptors on MHC 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 multimeres 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.

For all of those applications, it is important to choose the right MHC allele as well as a peptide that binds well to the MHC protein. It is also important that the chosen MHC allele and peptide forms a MHC- peptide complex that is efficiently and specifically recognized by the TCR. For applications that involve binding as well as activation of cells, further restrictions on the choice of MHC and peptide can apply.

Application of MHC multimers in immune monitoring, diagnostics, therapy, vaccine

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.

Developing vaccines that should give rise to lifelong protection is another case where the cellular immune system needs to be activated. Commonly, various childhood vaccines are expected to give lifelong protection but will only come to trial many years after the vaccination has been performed and then there is only to hope that it actually have created effective immunity.

Therapeutically cancer vaccines generally rely on cytotoxic effector T cells and have short duration of function. Therefore, continuous monitoring is important.

MHC multimers are therefore very important for immune monitoring of vaccine responses both during vaccine development, as a means to verify the obtained immunity for lifelong vaccines and to follow cancer patients under treatment with therapeutically cancer vaccines.

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.

In relation to transplantation, the presence of specific T cells directed against minor histocompatibility antigens (mHAgs) are important as they can cause graft versus host reaction/disease that can develop to a fatal situation for the patient. Again, a well-adjusted immune suppressive treatment is important. A similar reaction denoted graft versus cancer is sometimes employed in the treatment of malignancies of the lymphoid system. It is evident that such treatment is balancing on the edge of a knife and will benefit of specific measurement of relevant effector T cells.

Due to lack of organs, transplantations across greater mismatches are increasingly making harsher immune suppressive treatment more common. This calls for more efficient methods to monitor the immune status of the patient so that corrective measures in the treatment can be applied in due cause.

MHC multimers 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. Likewise, cancers can also be diagnosed early in its development if increased numbers of cancer specific T cells can be measured in circulation, even though the tumor is not yet localized.

Antigen specific tumor infiltrating lymphocytes can be used to identify tumor lesions and metastases as the antigen specific T cells will migrate/home to the tumor site to exert their help or immuno modulatory action (CD4+ T helper cells) or cytotoxic killing of tumor cells expressing the tumor specific/tumor associated peptide MHC multimer (CD8+ T-cells). Likewise identification of sites of infection tumor lesions can be identified as they typically attract antigen specific T-cells.
Localization of tumors and sites of infection can be carried out using antigen specific T-cells labelled with a paramagnetic isotope in conjunction with magnetic resonance imaging (MRI) or electron spin resonance (ESR). 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.

For peripheral cancer lesion in skin (e.g. melanoma) fluorescently labeled antigen specific T-cells can be used likewise.
MHC multimers may be used to label the tumor infiltration lymphocytes, e.g. MHC multimers may be labeled with a paramagnetic isotope are injected into the patient, the labeled MHC multimer binds specific T cells and are then internalized thereby introducing the paragmagnetic isotope to the T cell in this way labelleing the T cell.

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.

Therapeutically use of MHC multimers can be possible, either directly or as part of therapeutically vaccines. When performing autologous cancer therapy it is often recognized that the *in vitro* amplified cancer-specific effector T cells do not home effectively to the correct target sites but ends up in the lungs. 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 these cells.

When it become possible to identify and pinpoint the exact function of regulatory T cells it may be possible to directly block, regulate or kill these cells by means of MHCmers bound other functional molecules. The MHC multimeres specifically recognize the target T cells and direct the action of the other molecules to the target.

Derivatives of MHC multimers can be useful as vaccines, as vaccine components or as engineered intelligent adjuvant. The possibility of combining MHC multimeres that specifically bind certain T cells with molecules that trigger, e.g. the humoral response

or the innate immune response, can accelerate vaccine development and improve the efficiency of vaccines.

Diseases

In relation to the use and application of MHCmers in immune monitoring, diagnostics, prognostics, therapy and vaccines in relation to diseases several organisms and human proteins are of relevance, comprising but not limited to the following;

Infectious diseases

a) 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) 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, 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) 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

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, Leishmania tropica giving rise to clinical manifestations such as

Allergic diseases caused by allergens such as,
Birch, Hazel, Elm, Ragweed, Wormwood, Grass, Mould, Dust Mite giving rise to clinical manifestations such as Asthma

Transplantation related disease 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.

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, in relation to clinical manifestations such as 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

Autoimmune and inflammatory diseases, associated with antigens such as GAD64, Collagen, human cartilage glycoprotein 39, □-amyloid, A□42, APP, Presenilin 1, in relation to clinical manifestations such as 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, 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 (e.g. decide on a peptide to be complexed with MHC)
F. MHC (e.g. use a MHC allele that does not interfere with the patient's immune system in an undesired way).

A number of diseases A_1-A_n, relevant in connection with MHC multimeres, have been described herein; a number of applications B_1-B_n, relevant in connection with MHC multimeres, have been described herein; a number of Labels C_1-C_n, relevant in connection with MHC multimeres, have been described herein; a number of biologically active molecules D_1-D_n, relevant in connection with MHC multimeres, have been described herein; a number of peptides E_1-E_n, relevant in connection with MHC multimeres, have been described herein; and a number of MHC molecules F_1-F_n, relevant in connection with MHC multimeres, 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 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 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 T cell receptors/ T cells in a sample, detection of and isolation of cells or entities with antigen specific T cell receptor from a sample and detection and enrichment of cells or entities with antigen specific T cell receptor in a sample.

The sample may be a biologic sample including solid tissue, solid tissue section or a fluid 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, 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 are particularly useful for assaying T-cells in blood samples. Blood samples are 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.

In order to be able to measure detection of 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 multimeres.

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 multimeres 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 multimeres can be differently labelled (i.e. by labelling with different labelling compounds) enabling visualisation of different target MHC recognising cells. Thus, if several different MHC multimeres with different labelling compounds are present, it is possible simultaneously to identify more than one specific receptor, if each of the MHC multimeres present 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 derivated 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

Detection of TCRs with 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. Direct detection includes detection of TCR when TCR is attached to lipid bilayer, 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 is 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 support.

Direct detection of T cells in fluid sample.

T cells can be detected in fluid samples as described elsewhere herein and in suspension of disrupted tissue, in culture media, in buffers or in other liquids.T cells in fluid samples can be detected individually or deteced as populations of T cells. In the following different methods for direct detction of T cells in fluid samples are shown.

Direct detection of individual T cells

- *Direct detection of individual T cells using flow cytometry.*
  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 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 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 synovial fluid or blood.
  When analyzing blood samples whole blood can be used with or without lysis of red blood cells. Alternatively lymphocytes can be purified before flow cytometry analysis using standard procedures like a Ficoll-Hypaque gradient. Another possibility is to isolate T cells from the blood sample for example by binding to

antibody coated plastic surfaces, followed by elution of bound cells. This purified T cell population can then be used for flow cytometry analysis together with MHC multimers. Instead of actively isolating T cells unwanted cells like B cells and NK cells can be removed prior to the analysis. One way to do this is by affinity chromatography using columns coated with antibodies specific for the unwanted cells. Alternatively, specific antibodies can be added to the blood sample together with complement, 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 markers identifying subsets of cells by binding to unique surface proteins. Preferred gating reagents when using MHC multimers are antibodies directed against CD3, CD4, and CD8 identifying major subsets of T cells. Other preferred gating reagents are antibodies against CD14, CD15, CD19, CD25, CD56, CD27, CD28, CD45, CD45RA, CD45RO, CCR7, CCR5, CD62L, Foxp3 recognizing specific proteins 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 like 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 expanded *in vitro*. This can be useful in autologous cancer therapy.

Direct determination of the concentration of MHC-peptide specific T cells in a sample can be obtained by staining blood cells or other cell samples with MHC multimers and relevant gating reagents followed by addition of an exact amount

of counting beads of known concentration. Counting beads is here to be understood as any fluorescent bead with a size that can be visualized by flow cytometry in a sample containing T cells. The beads could 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 m. 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 determined using a predefined gating strategy and then correlating this number to the number of counted counting beads in the same sample using the following equation: Amounts of MHC-peptide specific T cells in a blood sample can be determined by flow cytometry by calculating the amount of MHC'mer 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 staining with MHC'mers together with an exact amount of counting beads followed by flow cytometry analysis. The amount of T cells 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:
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

- *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 measured 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 individual T cells in fluid sample by capture on solid support followed by elution.*
  MHC multimers are immobilized to a support e.g. beads, immunotubes, wells of a microtiterplate, CD, mircrochip or similar and as decribed elsewhere herein, then a suspension of T cells 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 a competitor molecules) and counted.

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 immobilise 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 be 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-specifically 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 labeled cells, e.g. cells are immobilized in a monolayer on a cell culture well or a glass slide. Following staining with labeled multimer a digital picture is taken and labeled cells identified and counted. Alternatively a population of T cells is detected by measurement of total signal from all labeled T cells, e.g. cells are plated to wells of a microtiter plate, stained with labeled MHC multimer and total signal from each well are measured.

- *Direct detection of T cells immobilized on solid support through linker molecule*
  T cell can also be immobilized to solid support through a linker molecule. The linker molecule can be an antibody specific for the T cell, the linker can be MHC multimer or the linker can be any molecule able to bind the T cells. In any case

the linker may be attached directly to the solid support, the linker may be attached to the solid support through another linker or the linker is 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 labeled cells, e.g. a digital picture is taken and labeled cells identified and counted.

Alternatively a population of T cells is detected by measurement of total signal from all labeled T cells.

- *Phenotyping T cell sample using MHC multimer beads.*

Different MHC multimers are immobilized to different beads with different characteristics (e.g. different size, different fluorescence's 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 populations of beads can be analyzed, thereby, phenotyping the sample. The TCR on the T cell is defined by the bead to which it binds.

- *Direct detection of T cells immobilized to solid support in a defined pattern.*

Different MHC multimers are immobilized to a support to form a spatial array in a defined pattern, where the position specifies the identity of the MHC multimer immobilized at this position. 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 and specific T cells will bind the immobilized MHC multimer molecules. The label will thus be located at specific regions of the array, which will allow identification of the MHC multimers that bind the cells, and thus, allows the identification of T cells with recognition specificity for the immobilized MHC multimers. Alternatively, the cells can be labelled after they have been bound to the MHC multimers. The label can be specific for the type of cell that is expected to bind the MHC multimer (e.g. anti-CD4 for the labelling of T-helper cells in general, where some of the T-helper

cells can be specific for a Class II MHC complex), or the label can stain cells in general (e.g. a label that binds DNA).

In this way T cells bound to the 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 multimer molecules immobilized at defined positions on the solid support.

Direct detection of immobilized T cells followed by sorting

T cells immobilized to solid support in either of the ways described above can following washing be eluted from the solid support and treated further. This is a method to sort out specific T cells from a population of different T cells. 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. After the cells have been isolated they can be manipulated in many different ways. 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, 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 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, 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 and bead; or alternatively, release the cells by a change in pH, salt-concentration addition of competitive binder or the like. Preferably, the cells are released under conditions that do not disrupt the integrity of the cells.

Manipulate the isolated cells (induce apoptosis, proliferation or differentiation)

Direct detection of T cells in solid tissue.

- *Direct detection of T cells in solid tissue in vitro.*

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. 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 secretion of specific soluble factor from the stimulated T cell, e.g. secretion 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) To a sample of T cells, preferably a suspension of cells, is added MHC multimer to induce either secretion of soluble factor, up- or down-regulation of surface receptor or other changes in the T cell.
   Alternatively, a sample of T cells containing antigen presenting cells is added antigenic peptide or protein/protein fragments that can be processed into antigenic peptides by the antigen presenting cell and that are able to bind MHC I or MHC II

molecules expressed by the antigen presenting cells thereby generating a cell based MHC multimer in the sample. Several different peptides and proteins be added to the sample. The peptide-loaded antigen presenting cells can then stimulate specific T cells, and thereby induce the secretion of soluble factor, up- or down-regulation of surface receptors, or mediate other changes in the T cell, e.g. enhancing effector functions.

Optionally a second soluble factor, e.g. cytokine and/or growth factor(s) may be added to facilitate continued activation and expansion of T cell population.

b) Detect the presence of soluble factor, the presence/ absence of surface receptor or detect effector function

c) Correlate the measured result with presence of T cells. The measured signal/response indicate 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. 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:

a) Sample of T cells in suspension are plated into culture wells at increasing dilutions

b) MHC multimers are added to stimulate specific T cells . Alternatively antigen presenting cells are provided in the sample and then antigenic peptide I added to the sample as descrinbed above.

Optionally growth factors, cytokines or other factors helping T cells to proliferate are added.

c) 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.

d) Wells are tested for a specific response e.g. secretion of soluble factors, cell proliferation, cytotoxicity or other effector function.

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.

In the following various methods to measure secretion of specific soluble factor, expression of surface receptors, effector functions or proliferation is described.

Indirect detection of T cells by measurement of secretion of soluble factors.

Indirect detection of T cells by measurement of extracellular secreted soluble factors. Secreted soluble factors can be measured directly in fluid suspension, captured by immobilization on solid support and then detected or an effect of the secreted soluble factor can be detected.

- *Indirect detection of T cells by measurement of extracellular secreted soluble factor directly in fluid sample.*
  A sample of T cells are added MHC multimer or antigenic peptide as described above to induce 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 extracellular secreted soluble factor on solid support.*
  A sample of T cells are added MHC multimer or antigenic peptide as described above to induce 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 by capturing of the secreted soluble factors locally by marker molecules, e.g antibodies specific for the soluble factor. Soluble factor recognising marker molecules are then 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 be measured using labelled marker molecule

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 may be stimulated with particular MHC multimer.

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 as where the T cells are or transferred to another solid support with marker molecules for capture and detection e.g. beads or wells of ELISA plate.

- *Indirect detection of T cells immobilized to solid support in a defined pattern.* Different MHC multimers og 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.

- *Indirect detection of T cells by measurement of effect of extracellular 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 peptide 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 intracellular secreted soluble factors

Soluble factor production by stimulated T cells can be 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 by binding specific MHC multimers, e.g. antigen presenting cells loaded with antigenic peptide. An reagent able to block extracellular secretion of cytokine is added, e.g. monensin that interrupt intracellular transport processes leading to accumulation of produced soluble factor, e.g. cytokine in the Golgi complex. During stimulation other soluble factors may be added to the T cell sample during stimulation to enhance activation and/or expansionn .This other soluble factor can be cytokine and or growth factors. 2) addition of one or more labelled marker able to detect special surface receptors (e.g. CD8, CD4, CD3, CD27, CD28, CD2). 3) Fixation of cell membrane using mild fixator followed by permeabilization of cell membrane by. e.g. 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 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 or antigenic peptide as described above to 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 label using flow cytometry, microscopy, immobilization of activated T cell on solid support or any other method like those decribed for direct detection of TCR in lipid bilayer.

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 or antigenic peptide as described above to induce the T cell to be able to do effector function. The effector function is then measured. E.g. activation of antigen specific CD8 positive T cells can be measured in a cytotoxicity assay.

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 peptide 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 cancer vaccines or other types of 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
  - Vaccine administered more than once may change composition from 1st administration to the 2nd, 3rd, etc.
  - Vaccine administered more than once can be administered by alternating routes
  - Vaccine components can be administered alone or in combinations by the same route or by alternating/mixed routes
  - 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

Personalized medicine takes advantage of the large diversity of peptide epitopes that may be generated from a given antigen.

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), 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}. MHC allele diversity combined with large 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.

This is important when designing a MHC multimer-based immune monitoring reagent or immunotherapeutic agent. If an agent is sought that should be as generally applicable as possible, one should try to identify peptide epitopes and MHC alleles that are common for the majority of individuals of a population. As described elsewhere in this application, such peptide epitopes can be identified through computerized search algorithms developed for that same purpose, and may be further strengthened by experimental testing of a large set of individuals.

This approach will be advantageous in many cases, but because of the variability among immune responses of different individuals, is likely to be inefficient or inactive 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 may provide MHC multimers with efficiency for a given individual.

Thus, personalized medicine takes advantage of the wealth of peptide epitopes that may be generated from a given antigen. A large number of the e.g. 8-, 9-, 10-, and 11-mer epitopes that may be generated from a given antigen to be included in a class 1 MHC multimer reagent, for use in immune monitoring or immunotherapy, are therefore of relevance in personalized medicine. 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 only those identified by computerized search algorithms and experimental testing be said to be 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.

Antigenic peptides

The present invention relates to one or more MHC multimers and/or one or more MHC complexes comprising one or more antigenic peptides such as the antigenic peptides listed in table A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, X and Y.

The one or more antigenic peptides can in one embodiment comprise a fragment of one or more cancer antigens.

The one or more cancer antigens can be selected from Table A.

Table A: Protein designation and accession numbers for the four selected cancer antigens Bcl-2, BclX(L), Survivin and Mcl-1. The amino acid sequence of each protein is displayed.

Protein and accession number	Cancer antigen
AAH27258.1 B-cell CLL/lymphoma 2, Bcl-2 [Homo sapiens]	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAP GIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPV VHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRH LHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACI TLGAYLGHK
NP_612815.1 Bcl-X(L) (BCL2-like 1 isoform 1) [Homo sapiens]	MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEME TPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALRE AGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWG RIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLF SRK
AAC51660.1 apoptosis inhibitor survivin [Homo sapiens]	MGAPTLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHC PTENEPDLAQCFFCFKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQ FEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQL AAMD
AAF64255.1 Mcl-1 [Homo sapiens]	MFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARR EIGGGEAGAVIGGSAGASPPSTLTPDSRRVARPPPIGAEVPDVTAT PARLLFFAPTRRAAPLEEMEAPAADAIMSPEEELDGYEPEPLGKRP AVLPLLELVGESGNNTSTDGSLPSTPPPAEEEEDDLYRQSLEIISR YLREQATGAKDTKPMGRSGATSRKALETLRRVGDGVQRNHETAFQG MLRKLDIKNEDDVKSLSRVMIHVFSDGVTNWGRIVTLISFGAFVAK HLKTINQESCIEPLAESITDVLVRTKRDWLVKQRGWDGFVEFFHVE DLEGGIRNVLLAFAGVAGVGAGLAYLIR

The one or more antigenic peptides can in one embodiment comprise one or more fragments from one or more cancer 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 cancer antigens capable of interacting with one or more MHC class 2 molecules.

The one or more antigenic peptides can in one embodiment comprise one or more fragments from BclX(L).

The one or more antigenic peptides can in one embodiment comprise one or more fragments from Bcl-2.

The one or more antigenic peptides can in one embodiment comprise one or more fragments from Survivin.

The one or more antigenic peptides can in one embodiment comprise one or more fragments from Mcl-1.

Preferred fragments of BclX(L) capable of interacting with one or more MHC class 1 molecules are listed in table B.

Table B: Prediction of cancer antigen BclX(L) specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed

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	SEMETPSA	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
	9.mers					
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	QLHITPGTA	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	TPSAINGNPS	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

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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

Preferred fragments of Bcl-2 capable of interacting with one or more MHC class 1 molecules are listed in table C below.

Table C: Prediction of cancer antigen Bcl-2 specific MHC class1, 8- , 9- ,10- ,11- mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mer					
84	ALSPVPPV	0.783	10	SB	Sequence	A0201
218	TLLSLALV	0.723	20	SB	Sequence	A0201
173	ALWMTEYL	0.682	31	SB	Sequence	A0201
154	GVMCVESV	0.630	54	WB	Sequence	A0201
207	PLFDFSWL	0.488	253	WB	Sequence	A0201
215	SLKTLLSL	0.449	387	WB	Sequence	A0201
84	ALSPVPPV	0.710	23	SB	Sequence	A0202
213	WLSLKTLL	0.709	23	SB	Sequence	A0202
215	SLKTLLSL	0.661	39	SB	Sequence	A0202
207	PLFDFSWL	0.653	42	SB	Sequence	A0202
173	ALWMTEYL	0.631	54	WB	Sequence	A0202
154	GVMCVESV	0.630	55	WB	Sequence	A0202
218	TLLSLALV	0.610	68	WB	Sequence	A0202
113	EMSSQLHL	0.570	105	WB	Sequence	A0202
224	LVGACITL	0.534	154	WB	Sequence	A0202
129	FATVVEEL	0.512	195	WB	Sequence	A0202
167	PLVDNIAL	0.508	204	WB	Sequence	A0202
179	YLNRHLHT	0.435	453	WB	Sequence	A0202
209	FDFSWLSL	0.432	464	WB	Sequence	A0202
84	ALSPVPPV	0.909	2	SB	Sequence	A0203
215	SLKTLLSL	0.853	4	SB	Sequence	A0203
154	GVMCVESV	0.754	14	SB	Sequence	A0203
179	YLNRHLHT	0.682	31	SB	Sequence	A0203
218	TLLSLALV	0.673	34	SB	Sequence	A0203
213	WLSLKTLL	0.665	37	SB	Sequence	A0203
140	GVNWGRIV	0.581	92	WB	Sequence	A0203
123	FTARGRFA	0.523	174	WB	Sequence	A0203
173	ALWMTEYL	0.497	229	WB	Sequence	A0203
207	PLFDFSWL	0.478	284	WB	Sequence	A0203
84	ALSPVPPV	0.763	13	SB	Sequence	A0204
173	ALWMTEYL	0.541	144	WB	Sequence	A0204
218	TLLSLALV	0.526	168	WB	Sequence	A0204
154	GVMCVESV	0.478	283	WB	Sequence	A0204
224	LVGACITL	0.451	381	WB	Sequence	A0204
84	ALSPVPPV	0.764	12	SB	Sequence	A0206
154	GVMCVESV	0.743	16	SB	Sequence	A0206
116	SQLHLTPF	0.737	17	SB	Sequence	A0206
218	TLLSLALV	0.714	21	SB	Sequence	A0206
145	RIVAFFEF	0.623	58	WB	Sequence	A0206
217	KTLLSLAL	0.574	100	WB	Sequence	A0206
173	ALWMTEYL	0.538	148	WB	Sequence	A0206
224	LVGACITL	0.463	334	WB	Sequence	A0206
123	FTARGRFA	0.462	335	WB	Sequence	A0206

213	WLSLKTLL	0.451	378	WB	Sequence	A0206
129	FATVVEEL	0.450	383	WB	Sequence	A0206
97	RQAGDDFS	0.436	445	WB	Sequence	A0206
84	ALSPVPPV	0.956	1	SB	Sequence	A0211
218	TLLSLALV	0.954	1	SB	Sequence	A0211
173	ALWMTEYL	0.935	2	SB	Sequence	A0211
207	PLFDFSWL	0.934	2	SB	Sequence	A0211
167	PLVDNIAL	0.888	3	SB	Sequence	A0211
215	SLKTLLSL	0.819	7	SB	Sequence	A0211
213	WLSLKTLL	0.780	10	SB	Sequence	A0211
179	YLNRHLHT	0.716	21	SB	Sequence	A0211
113	EMSSQLHL	0.686	29	SB	Sequence	A0211
140	GVNWGRIV	0.668	36	SB	Sequence	A0211
154	GVMCVESV	0.578	95	WB	Sequence	A0211
148	AFFEFGGV	0.534	154	WB	Sequence	A0211
87	PVPPVVHL	0.512	197	WB	Sequence	A0211
228	CITLGAYL	0.500	223	WB	Sequence	A0211
224	LVGACITL	0.500	223	WB	Sequence	A0211
223	ALVGACIT	0.479	281	WB	Sequence	A0211
27	YEWDAGDV	0.472	303	WB	Sequence	A0211
151	EFGGVMCV	0.452	377	WB	Sequence	A0211
221	SLALVGAC	0.445	405	WB	Sequence	A0211
84	ALSPVPPV	0.874	3	SB	Sequence	A0212
173	ALWMTEYL	0.860	4	SB	Sequence	A0212
218	TLLSLALV	0.857	4	SB	Sequence	A0212
207	PLFDFSWL	0.836	5	SB	Sequence	A0212
167	PLVDNIAL	0.787	9	SB	Sequence	A0212
215	SLKTLLSL	0.756	13	SB	Sequence	A0212
179	YLNRHLHT	0.720	20	SB	Sequence	A0212
113	EMSSQLHL	0.594	80	WB	Sequence	A0212
213	WLSLKTLL	0.564	112	WB	Sequence	A0212
27	YEWDAGDV	0.477	288	WB	Sequence	A0212
154	GVMCVESV	0.460	344	WB	Sequence	A0212
84	ALSPVPPV	0.926	2	SB	Sequence	A0216
173	ALWMTEYL	0.916	2	SB	Sequence	A0216
218	TLLSLALV	0.902	2	SB	Sequence	A0216
207	PLFDFSWL	0.889	3	SB	Sequence	A0216
167	PLVDNIAL	0.767	12	SB	Sequence	A0216
215	SLKTLLSL	0.723	20	SB	Sequence	A0216
213	WLSLKTLL	0.718	21	SB	Sequence	A0216
113	EMSSQLHL	0.665	37	SB	Sequence	A0216
154	GVMCVESV	0.646	46	SB	Sequence	A0216
179	YLNRHLHT	0.631	53	WB	Sequence	A0216
223	ALVGACIT	0.591	83	WB	Sequence	A0216
224	LVGACITL	0.531	159	WB	Sequence	A0216
87	PVPPVVHL	0.526	168	WB	Sequence	A0216
151	EFGGVMCV	0.524	173	WB	Sequence	A0216
228	CITLGAYL	0.522	176	WB	Sequence	A0216
140	GVNWGRIV	0.470	308	WB	Sequence	A0216
84	ALSPVPPV	0.898	3	SB	Sequence	A0219
173	ALWMTEYL	0.871	4	SB	Sequence	A0219
218	TLLSLALV	0.847	5	SB	Sequence	A0219
207	PLFDFSWL	0.785	10	SB	Sequence	A0219
167	PLVDNIAL	0.713	22	SB	Sequence	A0219
113	EMSSQLHL	0.613	65	WB	Sequence	A0219
213	WLSLKTLL	0.599	76	WB	Sequence	A0219
154	GVMCVESV	0.468	317	WB	Sequence	A0219
215	SLKTLLSL	0.466	322	WB	Sequence	A0219

27	YEWDAGDV	0.437	440	WB	Sequence	A0219
179	YLNRHLHT	0.436	447	WB	Sequence	A0219
14	VMKYIHYK	0.629	55	WB	Sequence	A0301
13	IVMKYIHY	0.514	193	WB	Sequence	A0301
119	HLTPFTAR	0.467	319	WB	Sequence	A0301
199	ELYGPSMR	0.456	360	WB	Sequence	A0301
14	VMKYIHYK	0.645	46	SB	Sequence	A1101
131	TVVEELFR	0.616	63	WB	Sequence	A1101
13	IVMKYIHY	0.577	97	WB	Sequence	A1101
142	NWGRIVAF	0.600	75	WB	Sequence	A2301
145	RIVAFFEF	0.518	184	WB	Sequence	A2301
204	SMRPLFDF	0.469	312	WB	Sequence	A2301
122	PFTARGRF	0.441	424	WB	Sequence	A2301
142	NWGRIVAF	0.617	62	WB	Sequence	A2402
212	SWLSLKTL	0.459	349	WB	Sequence	A2402
204	SMRPLFDF	0.547	135	WB	Sequence	A2403
145	RIVAFFEF	0.437	441	WB	Sequence	A2403
13	IVMKYIHY	0.638	50	WB	Sequence	A2602
113	EMSSQLHL	0.445	406	WB	Sequence	A2602
145	RIVAFFEF	0.436	445	WB	Sequence	A2602
12	EIVMKYIH	0.430	478	WB	Sequence	A2602
130	ATVVEELF	0.428	489	WB	Sequence	A2602
13	IVMKYIHY	0.603	73	WB	Sequence	A2902
227	ACITLGAY	0.449	387	WB	Sequence	A2902
14	VMKYIHYK	0.593	81	WB	Sequence	A3001
60	ASRDPVAR	0.498	229	WB	Sequence	A3001
126	RGRFATVV	0.480	276	WB	Sequence	A3001
113	EMSSQLHL	0.446	401	WB	Sequence	A3002
204	SMRPLFDF	0.444	410	WB	Sequence	A3002
14	VMKYIHYK	0.842	5	SB	Sequence	A3101
119	HLTPFTAR	0.709	23	SB	Sequence	A3101
60	ASRDPVAR	0.692	28	SB	Sequence	A3101
102	DFSRRYRR	0.622	59	WB	Sequence	A3101
175	WMTEYLNR	0.564	112	WB	Sequence	A3101
131	TVVEELFR	0.458	351	WB	Sequence	A3101
102	DFSRRYRR	0.883	3	SB	Sequence	A3301
119	HLTPFTAR	0.746	15	SB	Sequence	A3301
210	DFSWLSLK	0.672	34	SB	Sequence	A3301
101	DDFSRRYR	0.622	60	WB	Sequence	A3301
199	ELYGPSMR	0.615	64	WB	Sequence	A3301
131	TVVEELFR	0.546	136	WB	Sequence	A3301
14	VMKYIHYK	0.510	199	WB	Sequence	A3301
131	TVVEELFR	0.843	5	SB	Sequence	A6801
199	ELYGPSMR	0.792	9	SB	Sequence	A6801
119	HLTPFTAR	0.733	18	SB	Sequence	A6801
210	DFSWLSLK	0.637	50	WB	Sequence	A6801
121	TPFTARGR	0.625	58	WB	Sequence	A6801
55	TPHPAASR	0.581	93	WB	Sequence	A6801
101	DDFSRRYR	0.526	168	WB	Sequence	A6801
14	VMKYIHYK	0.524	171	WB	Sequence	A6801
98	QAGDDFSR	0.522	176	WB	Sequence	A6801

175	WMTEYLNR	0.505	211	WB	Sequence	A6801
156	MCVESVNR	0.502	219	WB	Sequence	A6801
102	DFSRRYRR	0.491	247	WB	Sequence	A6801
90	PVVHLTLR	0.456	358	WB	Sequence	A6801
154	GVMCVESV	0.630	54	WB	Sequence	A6802
165	MSPLVDNI	0.606	70	WB	Sequence	A6802
123	FTARGRFA	0.594	80	WB	Sequence	A6802
129	FATVVEEL	0.501	220	WB	Sequence	A6802
72	QTPAAPGA	0.474	297	WB	Sequence	A6802
218	TLLSLALV	0.607	70	WB	Sequence	A6901
123	FTARGRFA	0.486	261	WB	Sequence	A6901
113	EMSSQLHL	0.470	309	WB	Sequence	A6901
84	ALSPVPPV	0.444	409	WB	Sequence	A6901
202	GPSMRPLF	0.599	76	WB	Sequence	B0702
73	TPAAPGAA	0.598	77	WB	Sequence	B0702
69	SPLQTPAA	0.539	146	WB	Sequence	B0702
89	PPVVHLTL	0.503	216	WB	Sequence	B0702
206	RPLFDFSW	0.445	403	WB	Sequence	B0702
116	SQLHLTPF	0.583	91	WB	Sequence	B1501
204	SMRPLFDF	0.523	173	WB	Sequence	B1501
13	IVMKYIHY	0.492	243	WB	Sequence	B1501
145	RIVAFFEF	0.447	397	WB	Sequence	B1501
198	VELYGPSM	0.595	80	WB	Sequence	B1801
177	TEYLNRHL	0.498	228	WB	Sequence	B1801
172	IALWMTEY	0.475	292	WB	Sequence	B1801
116	SQLHLTPF	0.464	328	WB	Sequence	B1801
150	FEFGGVMC	0.452	375	WB	Sequence	B1801
172	IALWMTEY	0.767	12	SB	Sequence	B3501
149	FFEFGGVM	0.548	132	WB	Sequence	B3501
69	SPLQTPAA	0.503	215	WB	Sequence	B3501
111	FAEMSSQL	0.488	253	WB	Sequence	B3501
86	SPVPPVVH	0.443	413	WB	Sequence	B3501
73	TPAAPGAA	0.435	452	WB	Sequence	B3501
129	FATVVEEL	0.430	475	WB	Sequence	B3501
177	TEYLNRHL	0.547	133	WB	Sequence	B4001
11	REIVMKYI	0.513	194	WB	Sequence	B4001
150	FEFGGVMC	0.466	324	WB	Sequence	B4001
11	REIVMKYI	0.497	231	WB	Sequence	B4002
112	AEMSSQLH	0.471	305	WB	Sequence	B4501
134	EELFRDGV	0.465	326	WB	Sequence	B4501
11	REIVMKYI	0.435	450	WB	Sequence	B4501
222	LALVGACI	0.470	308	WB	Sequence	B5101
89	PPVVHLTL	0.448	391	WB	Sequence	B5101
206	RPLFDFSW	0.768	12	SB	Sequence	B5301
202	GPSMRPLF	0.430	474	WB	Sequence	B5301
73	TPAAPGAA	0.677	32	SB	Sequence	B5401
69	SPLQTPAA	0.605	71	WB	Sequence	B5401
37	APPGAAPA	0.557	120	WB	Sequence	B5401
166	SPLVDNIA	0.470	309	WB	Sequence	B5401
88	VPPVVHLT	0.450	382	WB	Sequence	B5401

22	LSQRGYEW	0.648	45	SB	Sequence	B5801
145	RIVAFFEF	0.512	196	WB	Sequence	B5801
168	LVDNIALW	0.475	292	WB	Sequence	B5801
172	IALWMTEY	0.460	345	WB	Sequence	B5801
	9-mer					
171	NIALWMTEY	0.497	230	WB	Sequence	A0101
84	ALSPVPPVV	0.676	33	SB	Sequence	A0201
223	ALVGACITL	0.631	54	WB	Sequence	A0201
217	KTLLSLALV	0.613	65	WB	Sequence	A0201
219	LLSLALVGA	0.542	141	WB	Sequence	A0201
172	IALWMTEYL	0.487	258	WB	Sequence	A0201
219	LLSLALVGA	0.824	6	SB	Sequence	A0202
14	VMKYIHYKL	0.705	24	SB	Sequence	A0202
223	ALVGACITL	0.654	42	SB	Sequence	A0202
215	SLKTLLSLA	0.635	52	WB	Sequence	A0202
160	SVNREMSPL	0.619	61	WB	Sequence	A0202
80	AAGPALSPV	0.617	62	WB	Sequence	A0202
84	ALSPVPPVV	0.593	81	WB	Sequence	A0202
164	EMSPLVDNI	0.582	91	WB	Sequence	A0202
221	SLALVGACI	0.579	94	WB	Sequence	A0202
67	RTSPLQTPA	0.554	124	WB	Sequence	A0202
204	SMRPLFDFS	0.495	234	WB	Sequence	A0202
179	YLNRHLHTW	0.479	280	WB	Sequence	A0202
172	IALWMTEYL	0.459	346	WB	Sequence	A0202
217	KTLLSLALV	0.443	414	WB	Sequence	A0202
113	EMSSQLHLT	0.432	464	WB	Sequence	A0202
215	SLKTLLSLA	0.875	3	SB	Sequence	A0203
84	ALSPVPPVV	0.842	5	SB	Sequence	A0203
219	LLSLALVGA	0.839	5	SB	Sequence	A0203
80	AAGPALSPV	0.770	11	SB	Sequence	A0203
160	SVNREMSPL	0.699	26	SB	Sequence	A0203
124	TARGRFATV	0.666	37	SB	Sequence	A0203
14	VMKYIHYKL	0.642	48	SB	Sequence	A0203
223	ALVGACITL	0.629	55	WB	Sequence	A0203
221	SLALVGACI	0.605	71	WB	Sequence	A0203
217	KTLLSLALV	0.584	90	WB	Sequence	A0203
67	RTSPLQTPA	0.539	146	WB	Sequence	A0203
147	VAFFEFGGV	0.520	180	WB	Sequence	A0203
164	EMSPLVDNI	0.516	187	WB	Sequence	A0203
117	QLHLTPFTA	0.490	249	WB	Sequence	A0203
204	SMRPLFDFS	0.441	425	WB	Sequence	A0203
179	YLNRHLHTW	0.432	468	WB	Sequence	A0203
84	ALSPVPPVV	0.766	12	SB	Sequence	A0204
223	ALVGACITL	0.571	103	WB	Sequence	A0204
80	AAGPALSPV	0.454	366	WB	Sequence	A0204
217	KTLLSLALV	0.742	16	SB	Sequence	A0206
80	AAGPALSPV	0.729	18	SB	Sequence	A0206
116	SQLHLTPFT	0.684	30	SB	Sequence	A0206
71	LQTPAAPGA	0.676	33	SB	Sequence	A0206
150	FEFGGVMCV	0.650	44	SB	Sequence	A0206
223	ALVGACITL	0.635	52	WB	Sequence	A0206
219	LLSLALVGA	0.624	58	WB	Sequence	A0206
84	ALSPVPPVV	0.621	60	WB	Sequence	A0206
123	FTARGRFAT	0.598	77	WB	Sequence	A0206

188	IQDNGGWDA	0.594	80	WB	Sequence	A0206
172	IALWMTEYL	0.589	85	WB	Sequence	A0206
36	AAPPGAAPA	0.569	106	WB	Sequence	A0206
124	TARGRFATV	0.543	140	WB	Sequence	A0206
147	VAFFEFGGV	0.511	198	WB	Sequence	A0206
67	RTSPLQTPA	0.462	336	WB	Sequence	A0206
84	ALSPVPPVV	0.951	1	SB	Sequence	A0211
223	ALVGACITL	0.929	2	SB	Sequence	A0211
207	PLFDFSWLS	0.902	2	SB	Sequence	A0211
150	FEFGGVMCV	0.812	7	SB	Sequence	A0211
179	YLNRHLHTW	0.742	16	SB	Sequence	A0211
221	SLALVGACI	0.715	21	SB	Sequence	A0211
219	LLSLALVGA	0.627	56	WB	Sequence	A0211
164	EMSPLVDNI	0.626	57	WB	Sequence	A0211
117	QLHLTPFTA	0.626	57	WB	Sequence	A0211
215	SLKTLLSLA	0.620	61	WB	Sequence	A0211
168	LVDNIALWM	0.592	82	WB	Sequence	A0211
217	KTLLSLALV	0.581	93	WB	Sequence	A0211
140	GVNWGRIVA	0.575	99	WB	Sequence	A0211
14	VMKYIHYKL	0.561	115	WB	Sequence	A0211
80	AAGPALSPV	0.551	128	WB	Sequence	A0211
113	EMSSQLHLT	0.531	159	WB	Sequence	A0211
6	TGYDNREIV	0.513	194	WB	Sequence	A0211
119	HLTPFTARG	0.505	211	WB	Sequence	A0211
199	ELYGPSMRP	0.504	213	WB	Sequence	A0211
192	GGWDAFVEL	0.503	216	WB	Sequence	A0211
172	IALWMTEYL	0.462	337	WB	Sequence	A0211
173	ALWMTEYLN	0.459	347	WB	Sequence	A0211
36	AAPPGAAPA	0.432	467	WB	Sequence	A0211
84	ALSPVPPVV	0.914	2	SB	Sequence	A0212
223	ALVGACITL	0.760	13	SB	Sequence	A0212
179	YLNRHLHTW	0.739	16	SB	Sequence	A0212
150	FEFGGVMCV	0.735	17	SB	Sequence	A0212
207	PLFDFSWLS	0.676	33	SB	Sequence	A0212
14	VMKYIHYKL	0.596	79	WB	Sequence	A0212
219	LLSLALVGA	0.587	87	WB	Sequence	A0212
221	SLALVGACI	0.529	162	WB	Sequence	A0212
164	EMSPLVDNI	0.520	180	WB	Sequence	A0212
117	QLHLTPFTA	0.476	290	WB	Sequence	A0212
123	FTARGRFAT	0.464	328	WB	Sequence	A0212
84	ALSPVPPVV	0.915	2	SB	Sequence	A0216
223	ALVGACITL	0.909	2	SB	Sequence	A0216
80	AAGPALSPV	0.699	25	SB	Sequence	A0216
150	FEFGGVMCV	0.640	49	SB	Sequence	A0216
221	SLALVGACI	0.630	54	WB	Sequence	A0216
14	VMKYIHYKL	0.570	104	WB	Sequence	A0216
207	PLFDFSWLS	0.530	162	WB	Sequence	A0216
117	QLHLTPFTA	0.490	250	WB	Sequence	A0216
215	SLKTLLSLA	0.489	251	WB	Sequence	A0216
179	YLNRHLHTW	0.461	340	WB	Sequence	A0216
124	TARGRFATV	0.448	393	WB	Sequence	A0216
84	ALSPVPPVV	0.899	2	SB	Sequence	A0219
150	FEFGGVMCV	0.686	29	SB	Sequence	A0219
223	ALVGACITL	0.683	30	SB	Sequence	A0219
80	AAGPALSPV	0.557	120	WB	Sequence	A0219
219	LLSLALVGA	0.542	142	WB	Sequence	A0219
83	PALSPVPPV	0.498	229	WB	Sequence	A0219
164	EMSPLVDNI	0.460	345	WB	Sequence	A0219

113	EMSSQLHLT	0.437	443	WB	Sequence	A0219
179	YLNRHLHTW	0.428	485	WB	Sequence	A0219
13	IVMKYIHYK	0.758	13	SB	Sequence	A0301
230	TLGAYLGHK	0.655	41	SB	Sequence	A0301
209	FDFSWLSLK	0.457	357	WB	Sequence	A0301
13	IVMKYIHYK	0.834	6	SB	Sequence	A1101
230	TLGAYLGHK	0.708	23	SB	Sequence	A1101
130	ATVVEELFR	0.574	100	WB	Sequence	A1101
142	NWGRIVAFF	0.644	47	SB	Sequence	A2301
203	PSMRPLFDF	0.530	161	WB	Sequence	A2301
144	GRIVAFFEF	0.530	162	WB	Sequence	A2301
13	IVMKYIHYK	0.499	226	WB	Sequence	A2301
106	RYRRDFAEM	0.467	321	WB	Sequence	A2301
128	RFATVVEEL	0.454	366	WB	Sequence	A2301
142	NWGRIVAFF	0.739	16	SB	Sequence	A2402
128	RFATVVEEL	0.568	107	WB	Sequence	A2402
212	SWLSLKTLL	0.536	151	WB	Sequence	A2402
106	RYRRDFAEM	0.669	35	SB	Sequence	A2403
128	RFATVVEEL	0.626	57	WB	Sequence	A2403
200	LYGPSMRPL	0.553	125	WB	Sequence	A2403
12	EIVMKYIHY	0.628	55	WB	Sequence	A2601
171	NIALWMTEY	0.622	60	WB	Sequence	A2601
12	EIVMKYIHY	0.935	2	SB	Sequence	A2602
171	NIALWMTEY	0.866	4	SB	Sequence	A2602
160	SVNREMSPL	0.849	5	SB	Sequence	A2602
179	YLNRHLHTW	0.538	148	WB	Sequence	A2602
197	FVELYGPSM	0.520	180	WB	Sequence	A2602
168	LVDNIALWM	0.432	464	WB	Sequence	A2602
171	NIALWMTEY	0.586	88	WB	Sequence	A2902
12	EIVMKYIHY	0.516	188	WB	Sequence	A2902
13	IVMKYIHYK	0.758	13	SB	Sequence	A3001
0	MAHAGRTGY	0.487	258	WB	Sequence	A3001
230	TLGAYLGHK	0.475	293	WB	Sequence	A3001
171	NIALWMTEY	0.427	491	WB	Sequence	A3002
13	IVMKYIHYK	0.797	8	SB	Sequence	A3101
17	YIHYKLSQR	0.715	21	SB	Sequence	A3101
155	VMCVESVNR	0.631	54	WB	Sequence	A3101
97	RQAGDDFSR	0.588	85	WB	Sequence	A3101
14	VMKYIHYKL	0.497	230	WB	Sequence	A3101
130	ATVVEELFR	0.471	307	WB	Sequence	A3101
101	DDFSRRYRR	0.698	26	SB	Sequence	A3301
17	YIHYKLSQR	0.649	44	SB	Sequence	A3301
54	HTPHPAASR	0.476	290	WB	Sequence	A3301
13	IVMKYIHYK	0.427	493	WB	Sequence	A3301
13	IVMKYIHYK	0.790	9	SB	Sequence	A6801
17	YIHYKLSQR	0.747	15	SB	Sequence	A6801
54	HTPHPAASR	0.729	18	SB	Sequence	A6801
120	LTPFTARGR	0.703	24	SB	Sequence	A6801
130	ATVVEELFR	0.655	41	SB	Sequence	A6801

101	DDFSRRYRR	0.571	103	WB	Sequence	A6801
209	FDFSWLSLK	0.540	145	WB	Sequence	A6801
98	QAGDDFSRR	0.529	163	WB	Sequence	A6801
171	NIALWMTEY	0.477	288	WB	Sequence	A6801
230	TLGAYLGHK	0.449	388	WB	Sequence	A6801
0	MAHAGRTGY	0.447	398	WB	Sequence	A6801
123	FTARGRFAT	0.692	27	SB	Sequence	A6802
147	VAFFEFGGV	0.641	48	SB	Sequence	A6802
57	HPAASRDPV	0.627	56	WB	Sequence	A6802
72	QTPAAPGAA	0.604	72	WB	Sequence	A6802
160	SVNREMSPL	0.570	104	WB	Sequence	A6802
124	TARGRFATV	0.531	160	WB	Sequence	A6802
6	TGYDNREIV	0.513	193	WB	Sequence	A6802
164	EMSPLVDNI	0.512	196	WB	Sequence	A6802
67	RTSPLQTPA	0.488	254	WB	Sequence	A6802
225	VGACITLGA	0.472	303	WB	Sequence	A6802
165	MSPLVDNIA	0.466	322	WB	Sequence	A6802
150	FEFGGVMCV	0.449	388	WB	Sequence	A6802
83	PALSPVPPV	0.726	19	SB	Sequence	A6901
33	DVGAAPPGA	0.535	152	WB	Sequence	A6901
57	HPAASRDPV	0.495	235	WB	Sequence	A6901
164	EMSPLVDNI	0.485	262	WB	Sequence	A6901
123	FTARGRFAT	0.483	267	WB	Sequence	A6901
217	KTLLSLALV	0.460	344	WB	Sequence	A6901
73	TPAAPGAAA	0.460	344	WB	Sequence	A6901
172	IALWMTEYL	0.426	497	WB	Sequence	A6901
57	HPAASRDPV	0.770	12	SB	Sequence	B0702
63	DPVARTSPL	0.750	14	SB	Sequence	B0702
166	SPLVDNIAL	0.674	33	SB	Sequence	B0702
73	TPAAPGAAA	0.652	43	SB	Sequence	B0702
206	RPLFDFSWL	0.627	56	WB	Sequence	B0702
86	SPVPPVVHL	0.606	71	WB	Sequence	B0702
76	APGAAAGPA	0.573	101	WB	Sequence	B0702
88	VPPVVHLTL	0.542	142	WB	Sequence	B0702
121	TPFTARGRF	0.505	210	WB	Sequence	B0702
124	TARGRFATV	0.449	389	WB	Sequence	B0702
0	MAHAGRTGY	0.532	158	WB	Sequence	B1501
115	SSQLHLTPF	0.427	490	WB	Sequence	B1501
150	FEFGGVMCV	0.633	53	WB	Sequence	B1801
9	DNREIVMKY	0.541	143	WB	Sequence	B1801
172	IALWMTEYL	0.505	211	WB	Sequence	B1801
144	GRIVAFFEF	0.456	360	WB	Sequence	B2705
105	RRYRRDFAE	0.456	361	WB	Sequence	B2705
166	SPLVDNIAL	0.680	31	SB	Sequence	B3501
0	MAHAGRTGY	0.658	40	SB	Sequence	B3501
197	FVELYGPSM	0.628	55	WB	Sequence	B3501
121	TPFTARGRF	0.610	67	WB	Sequence	B3501
172	IALWMTEYL	0.584	90	WB	Sequence	B3501
63	DPVARTSPL	0.584	90	WB	Sequence	B3501
129	FATVVEELF	0.562	113	WB	Sequence	B3501
73	TPAAPGAAA	0.551	128	WB	Sequence	B3501
171	NIALWMTEY	0.523	174	WB	Sequence	B3501
111	FAEMSSQLH	0.460	343	WB	Sequence	B3501
112	AEMSSQLHL	0.740	16	SB	Sequence	B4001

150	FEFGGVMCV	0.588	86	WB	Sequence	B4001
112	AEMSSQLHL	0.554	124	WB	Sequence	B4002
150	FEFGGVMCV	0.466	323	WB	Sequence	B4002
112	AEMSSQLHL	0.454	368	WB	Sequence	B4402
112	AEMSSQLHL	0.533	157	WB	Sequence	B4403
112	AEMSSQLHL	0.587	87	WB	Sequence	B4501
88	VPPVVHLTL	0.548	132	WB	Sequence	B5101
206	RPLFDFSWL	0.470	307	WB	Sequence	B5301
166	SPLVDNIAL	0.459	348	WB	Sequence	B5301
172	IALWMTEYL	0.450	382	WB	Sequence	B5301
73	TPAAPGAAA	0.715	21	SB	Sequence	B5401
57	HPAASRDPV	0.684	30	SB	Sequence	B5401
76	APGAAAGPA	0.625	57	WB	Sequence	B5401
51	QPGHTPHPA	0.515	189	WB	Sequence	B5401
179	YLNRHLHTW	0.682	31	SB	Sequence	B5801
21	KLSQRGYEW	0.649	44	SB	Sequence	B5801
129	FATVVEELF	0.547	134	WB	Sequence	B5801
40	GAAPAPGIF	0.483	268	WB	Sequence	B5801
	10-mer					
179	YLNRHLHTWI	0.735	17	SB	Sequence	A0201
13	IVMKYIHYKL	0.638	50	WB	Sequence	A0201
218	TLLSLALVGA	0.571	103	WB	Sequence	A0201
207	PLFDFSWLSL	0.536	151	WB	Sequence	A0201
213	WLSLKTLLSL	0.530	161	WB	Sequence	A0201
123	FTARGRFATV	0.522	175	WB	Sequence	A0201
171	NIALWMTEYL	0.521	178	WB	Sequence	A0201
175	WMTEYLNRHL	0.486	260	WB	Sequence	A0201
218	TLLSLALVGA	0.731	18	SB	Sequence	A0202
171	NIALWMTEYL	0.727	19	SB	Sequence	A0202
213	WLSLKTLLSL	0.700	25	SB	Sequence	A0202
215	SLKTLLSLAL	0.646	46	SB	Sequence	A0202
175	WMTEYLNRHL	0.642	47	SB	Sequence	A0202
207	PLFDFSWLSL	0.637	50	WB	Sequence	A0202
79	AAAGPALSPV	0.588	86	WB	Sequence	A0202
13	IVMKYIHYKL	0.569	106	WB	Sequence	A0202
123	FTARGRFATV	0.568	106	WB	Sequence	A0202
199	ELYGPSMRPL	0.541	143	WB	Sequence	A0202
179	YLNRHLHTWI	0.540	145	WB	Sequence	A0202
224	LVGACITLGA	0.483	267	WB	Sequence	A0202
146	IVAFFEFGGV	0.439	431	WB	Sequence	A0202
179	YLNRHLHTWI	0.933	2	SB	Sequence	A0203
123	FTARGRFATV	0.821	6	SB	Sequence	A0203
213	WLSLKTLLSL	0.782	10	SB	Sequence	A0203
215	SLKTLLSLAL	0.773	11	SB	Sequence	A0203
171	NIALWMTEYL	0.682	31	SB	Sequence	A0203
160	SVNREMSPLV	0.680	31	SB	Sequence	A0203
146	IVAFFEFGGV	0.667	36	SB	Sequence	A0203
79	AAAGPALSPV	0.606	71	WB	Sequence	A0203
175	WMTEYLNRHL	0.569	106	WB	Sequence	A0203
218	TLLSLALVGA	0.545	137	WB	Sequence	A0203
13	IVMKYIHYKL	0.532	157	WB	Sequence	A0203
224	LVGACITLGA	0.532	158	WB	Sequence	A0203

199	ELYGPSMRPL	0.519	182	WB	Sequence A0203
50	SQPGHTPHPA	0.447	398	WB	Sequence A0203
219	LLSLALVGAC	0.444	410	WB	Sequence A0203
124	TARGRFATVV	0.428	489	WB	Sequence A0203
179	YLNRHLHTWI	0.655	41	SB	Sequence A0204
123	FTARGRFATV	0.613	66	WB	Sequence A0204
13	IVMKYIHYKL	0.509	203	WB	Sequence A0204
79	AAAGPALSPV	0.474	296	WB	Sequence A0204
160	SVNREMSPLV	0.450	384	WB	Sequence A0204
123	FTARGRFATV	0.867	4	SB	Sequence A0206
116	SQLHLTPFTA	0.776	11	SB	Sequence A0206
188	IQDNGGWDAF	0.673	34	SB	Sequence A0206
213	WLSLKTLLSL	0.667	36	SB	Sequence A0206
50	SQPGHTPHPA	0.621	60	WB	Sequence A0206
179	YLNRHLHTWI	0.619	61	WB	Sequence A0206
79	AAAGPALSPV	0.602	74	WB	Sequence A0206
175	WMTEYLNRHL	0.600	75	WB	Sequence A0206
160	SVNREMSPLV	0.567	108	WB	Sequence A0206
171	NIALWMTEYL	0.562	114	WB	Sequence A0206
218	TLLSLALVGA	0.560	116	WB	Sequence A0206
146	IVAFFEFGGV	0.553	125	WB	Sequence A0206
71	LQTPAAPGAA	0.546	135	WB	Sequence A0206
13	IVMKYIHYKL	0.525	171	WB	Sequence A0206
27	YEWDAGDVGA	0.511	199	WB	Sequence A0206
207	PLFDFSWLSL	0.486	260	WB	Sequence A0206
67	RTSPLQTPAA	0.477	286	WB	Sequence A0206
224	LVGACITLGA	0.471	304	WB	Sequence A0206
207	PLFDFSWLSL	0.935	2	SB	Sequence A0211
179	YLNRHLHTWI	0.925	2	SB	Sequence A0211
199	ELYGPSMRPL	0.888	3	SB	Sequence A0211
213	WLSLKTLLSL	0.835	5	SB	Sequence A0211
218	TLLSLALVGA	0.829	6	SB	Sequence A0211
123	FTARGRFATV	0.823	6	SB	Sequence A0211
167	PLVDNIALWM	0.802	8	SB	Sequence A0211
215	SLKTLLSLAL	0.799	8	SB	Sequence A0211
175	WMTEYLNRHL	0.796	9	SB	Sequence A0211
160	SVNREMSPLV	0.788	9	SB	Sequence A0211
87	PVPPVVHLTL	0.705	24	SB	Sequence A0211
79	AAAGPALSPV	0.635	51	WB	Sequence A0211
13	IVMKYIHYKL	0.601	74	WB	Sequence A0211
146	IVAFFEFGGV	0.568	107	WB	Sequence A0211
132	VVEELFRDGV	0.549	131	WB	Sequence A0211
171	NIALWMTEYL	0.547	133	WB	Sequence A0211
164	EMSPLVDNIA	0.488	254	WB	Sequence A0211
168	LVDNIALWMT	0.484	266	WB	Sequence A0211
149	FFEFGGVMCV	0.475	292	WB	Sequence A0211
221	SLALVGACIT	0.462	336	WB	Sequence A0211
187	WIQDNGGWDA	0.453	370	WB	Sequence A0211
179	YLNRHLHTWI	0.878	3	SB	Sequence A0212
207	PLFDFSWLSL	0.859	4	SB	Sequence A0212
123	FTARGRFATV	0.849	5	SB	Sequence A0212
215	SLKTLLSLAL	0.730	18	SB	Sequence A0212
199	ELYGPSMRPL	0.726	19	SB	Sequence A0212
175	WMTEYLNRHL	0.716	21	SB	Sequence A0212
213	WLSLKTLLSL	0.697	26	SB	Sequence A0212
218	TLLSLALVGA	0.692	27	SB	Sequence A0212
132	VVEELFRDGV	0.601	74	WB	Sequence A0212
167	PLVDNIALWM	0.560	116	WB	Sequence A0212

13	IVMKYIHYKL	0.533	156	WB	Sequence A0212
160	SVNREMSPLV	0.509	202	WB	Sequence A0212
187	WIQDNGGWDA	0.479	280	WB	Sequence A0212
146	IVAFFEFGGV	0.476	288	WB	Sequence A0212
87	PVPPVVHLTL	0.475	294	WB	Sequence A0212
27	YEWDAGDVGA	0.467	321	WB	Sequence A0212
179	YLNRHLHTWI	0.854	4	SB	Sequence A0216
207	PLFDFSWLSL	0.849	5	SB	Sequence A0216
123	FTARGRFATV	0.812	7	SB	Sequence A0216
199	ELYGPSMRPL	0.767	12	SB	Sequence A0216
213	WLSLKTLLSL	0.745	15	SB	Sequence A0216
167	PLVDNIALWM	0.702	25	SB	Sequence A0216
160	SVNREMSPLV	0.685	30	SB	Sequence A0216
13	IVMKYIHYKL	0.676	33	SB	Sequence A0216
175	WMTEYLNRHL	0.675	33	SB	Sequence A0216
79	AAAGPALSPV	0.661	39	SB	Sequence A0216
87	PVPPVVHLTL	0.638	50	WB	Sequence A0216
215	SLKTLLSLAL	0.634	52	WB	Sequence A0216
218	TLLSLALVGA	0.574	100	WB	Sequence A0216
171	NIALWMTEYL	0.557	120	WB	Sequence A0216
221	SLALVGACIT	0.472	301	WB	Sequence A0216
146	IVAFFEFGGV	0.429	483	WB	Sequence A0216
207	PLFDFSWLSL	0.805	8	SB	Sequence A0219
179	YLNRHLHTWI	0.789	9	SB	Sequence A0219
213	WLSLKTLLSL	0.766	12	SB	Sequence A0219
123	FTARGRFATV	0.703	24	SB	Sequence A0219
199	ELYGPSMRPL	0.585	88	WB	Sequence A0219
167	PLVDNIALWM	0.574	100	WB	Sequence A0219
79	AAAGPALSPV	0.563	112	WB	Sequence A0219
218	TLLSLALVGA	0.551	129	WB	Sequence A0219
175	WMTEYLNRHL	0.521	178	WB	Sequence A0219
83	PALSPVPPVV	0.486	259	WB	Sequence A0219
13	IVMKYIHYKL	0.461	341	WB	Sequence A0219
171	NIALWMTEYL	0.446	401	WB	Sequence A0219
229	ITLGAYLGHK	0.760	13	SB	Sequence A0301
208	LFDFSWLSLK	0.497	232	WB	Sequence A0301
12	EIVMKYIHYK	0.475	292	WB	Sequence A0301
154	GVMCVESVNR	0.444	411	WB	Sequence A0301
173	ALWMTEYLNR	0.429	480	WB	Sequence A0301
229	ITLGAYLGHK	0.752	14	SB	Sequence A1101
154	GVMCVESVNR	0.637	50	WB	Sequence A1101
12	EIVMKYIHYK	0.540	145	WB	Sequence A1101
173	ALWMTEYLNR	0.455	363	WB	Sequence A1101
208	LFDFSWLSLK	0.435	453	WB	Sequence A1101
178	EYLNRHLHTW	0.686	29	SB	Sequence A2301
200	LYGPSMRPLF	0.686	29	SB	Sequence A2301
128	RFATVVEELF	0.620	60	WB	Sequence A2301
7	GYDNREIVMK	0.595	80	WB	Sequence A2301
102	DFSRRYRRDF	0.499	226	WB	Sequence A2301
13	IVMKYIHYKL	0.451	381	WB	Sequence A2301
94	LTLRQAGDDF	0.437	441	WB	Sequence A2301
128	RFATVVEELF	0.764	12	SB	Sequence A2402
200	LYGPSMRPLF	0.733	17	SB	Sequence A2402
178	EYLNRHLHTW	0.715	21	SB	Sequence A2402
178	EYLNRHLHTW	0.718	21	SB	Sequence A2403

128	RFATVVEELF	0.657	41	SB	Sequence A2403
200	LYGPSMRPLF	0.636	51	WB	Sequence A2403
170	DNIALWMTEY	0.478	283	WB	Sequence A2601
159	ESVNREMSPL	0.621	60	WB	Sequence A2602
199	ELYGPSMRPL	0.595	79	WB	Sequence A2602
171	NIALWMTEYL	0.549	131	WB	Sequence A2602
170	DNIALWMTEY	0.487	258	WB	Sequence A2602
229	ITLGAYLGHK	0.718	21	SB	Sequence A3001
16	KYIHYKLSQR	0.837	5	SB	Sequence A3101
136	LFRDGVNWGR	0.667	36	SB	Sequence A3101
154	GVMCVESVNR	0.576	98	WB	Sequence A3101
119	HLTPFTARGR	0.573	101	WB	Sequence A3101
173	ALWMTEYLNR	0.509	203	WB	Sequence A3101
99	AGDDFSRRYR	0.507	207	WB	Sequence A3101
129	FATVVEELFR	0.493	241	WB	Sequence A3101
117	QLHLTPFTAR	0.431	471	WB	Sequence A3101
136	LFRDGVNWGR	0.553	126	WB	Sequence A3301
16	KYIHYKLSQR	0.520	180	WB	Sequence A3301
129	FATVVEELFR	0.516	188	WB	Sequence A3301
173	ALWMTEYLNR	0.441	423	WB	Sequence A3301
129	FATVVEELFR	0.829	6	SB	Sequence A6801
12	EIVMKYIHYK	0.780	10	SB	Sequence A6801
119	HLTPFTARGR	0.721	20	SB	Sequence A6801
197	FVELYGPSMR	0.688	29	SB	Sequence A6801
154	GVMCVESVNR	0.646	46	SB	Sequence A6801
229	ITLGAYLGHK	0.568	106	WB	Sequence A6801
176	MTEYLNRHLH	0.485	262	WB	Sequence A6801
117	QLHLTPFTAR	0.466	322	WB	Sequence A6801
2	HAGRTGYDNR	0.446	399	WB	Sequence A6801
123	FTARGRFATV	0.861	4	SB	Sequence A6802
146	IVAFFEFGGV	0.809	7	SB	Sequence A6802
171	NIALWMTEYL	0.728	18	SB	Sequence A6802
13	IVMKYIHYKL	0.680	31	SB	Sequence A6802
79	AAAGPALSPV	0.644	47	SB	Sequence A6802
72	QTPAAPGAAA	0.617	63	WB	Sequence A6802
165	MSPLVDNIAL	0.591	83	WB	Sequence A6802
199	ELYGPSMRPL	0.582	92	WB	Sequence A6802
159	ESVNREMSPL	0.550	129	WB	Sequence A6802
205	MRPLFDFSWL	0.522	175	WB	Sequence A6802
160	SVNREMSPLV	0.471	306	WB	Sequence A6802
124	TARGRFATVV	0.441	421	WB	Sequence A6802
123	FTARGRFATV	0.792	9	SB	Sequence A6901
199	ELYGPSMRPL	0.714	22	SB	Sequence A6901
83	PALSPVPPVV	0.580	94	WB	Sequence A6901
171	NIALWMTEYL	0.558	119	WB	Sequence A6901
160	SVNREMSPLV	0.537	149	WB	Sequence A6901
79	AAAGPALSPV	0.502	219	WB	Sequence A6901
33	DVGAAPPGAA	0.489	251	WB	Sequence A6901
146	IVAFFEFGGV	0.464	330	WB	Sequence A6901
13	IVMKYIHYKL	0.441	422	WB	Sequence A6901
76	APGAAAGPAL	0.708	23	SB	Sequence B0702
82	GPALSPVPPV	0.604	72	WB	Sequence B0702
57	HPAASRDPVA	0.536	152	WB	Sequence B0702

202	GPSMRPLFDF	0.468	317	WB	Sequence	B0702
124	TARGRFATVV	0.465	327	WB	Sequence	B0702
42	APAPGIFSSQ	0.451	378	WB	Sequence	B0702
140	GVNWGRIVAF	0.548	132	WB	Sequence	B1501
114	MSSQLHLTPF	0.504	214	WB	Sequence	B1501
188	IQDNGGWDAF	0.490	249	WB	Sequence	B1501
11	REIVMKYIHY	0.603	73	WB	Sequence	B1801
105	RRYRRDFAEM	0.622	59	WB	Sequence	B2705
127	GRFATVVEEL	0.493	241	WB	Sequence	B2705
114	MSSQLHLTPF	0.582	91	WB	Sequence	B3501
147	VAFFEFGGVM	0.561	115	WB	Sequence	B3501
76	APGAAAGPAL	0.526	168	WB	Sequence	B3501
222	LALVGACITL	0.473	297	WB	Sequence	B3501
156	MCVESVNREM	0.473	299	WB	Sequence	B3501
98	QAGDDFSRRY	0.461	340	WB	Sequence	B3501
73	TPAAPGAAAG	0.459	346	WB	Sequence	B3501
140	GVNWGRIVAF	0.455	362	WB	Sequence	B3501
166	SPLVDNIALW	0.453	371	WB	Sequence	B3501
11	REIVMKYIHY	0.502	218	WB	Sequence	B4002
112	AEMSSQLHLT	0.472	303	WB	Sequence	B4002
11	REIVMKYIHY	0.476	289	WB	Sequence	B4402
11	REIVMKYIHY	0.481	273	WB	Sequence	B4403
134	EELFRDGVNW	0.473	300	WB	Sequence	B4403
112	AEMSSQLHLT	0.523	175	WB	Sequence	B4501
11	REIVMKYIHY	0.438	437	WB	Sequence	B4501
134	EELFRDGVNW	0.367	946		Sequence	B4501
222	LALVGACITL	0.480	277	WB	Sequence	B5101
38	PPGAAPAPGI	0.427	490	WB	Sequence	B5101
166	SPLVDNIALW	0.744	15	SB	Sequence	B5301
57	HPAASRDPVA	0.665	37	SB	Sequence	B5401
121	TPFTARGRFA	0.661	39	SB	Sequence	B5401
51	QPGHTPHPAA	0.476	289	WB	Sequence	B5401
82	GPALSPVPPV	0.461	340	WB	Sequence	B5401
86	SPVPPVVHLT	0.434	456	WB	Sequence	B5401
185	HTWIQDNGGW	0.427	491	WB	Sequence	B5701
114	MSSQLHLTPF	0.611	67	WB	Sequence	B5801
185	HTWIQDNGGW	0.580	94	WB	Sequence	B5801
204	SMRPLFDFSW	0.474	294	WB	Sequence	B5801
	11-mer					
223	ALVGACITLGA	0.632	53	WB	Sequence	A0201
84	ALSPVPPVVHL	0.586	88	WB	Sequence	A0201
215	SLKTLLSLALV	0.543	141	WB	Sequence	A0201
188	IQDNGGWDAFV	0.504	215	WB	Sequence	A0201
219	LLSLALVGACI	0.481	275	WB	Sequence	A0201
221	SLALVGACITL	0.473	299	WB	Sequence	A0201
145	RIVAFFEFGGV	0.453	373	WB	Sequence	A0201
21	KLSQRGYEWDA	0.449	388	WB	Sequence	A0201

204 SMRPLFDFSWL	0.772	11	SB	Sequence	A0202
215 SLKTLLSLALV	0.763	12	SB	Sequence	A0202
221 SLALVGACITL	0.710	23	SB	Sequence	A0202
84 ALSPVPPVVHL	0.708	23	SB	Sequence	A0202
219 LLSLALVGACI	0.692	28	SB	Sequence	A0202
164 EMSPLVDNIAL	0.657	41	SB	Sequence	A0202
223 ALVGACITLGA	0.630	54	WB	Sequence	A0202
213 WLSLKTLLSLA	0.616	63	WB	Sequence	A0202
123 FTARGRFATVV	0.602	74	WB	Sequence	A0202
78 GAAAGPALSPV	0.597	78	WB	Sequence	A0202
145 RIVAFFEFGGV	0.569	105	WB	Sequence	A0202
179 YLNRHLHTWIQ	0.529	163	WB	Sequence	A0202
21 KLSQRGYEWDA	0.499	226	WB	Sequence	A0202
131 TVVEELFRDGV	0.478	284	WB	Sequence	A0202
225 VGACITLGAYL	0.469	312	WB	Sequence	A0202
215 SLKTLLSLALV	0.899	2	SB	Sequence	A0203
204 SMRPLFDFSWL	0.853	4	SB	Sequence	A0203
145 RIVAFFEFGGV	0.813	7	SB	Sequence	A0203
78 GAAAGPALSPV	0.774	11	SB	Sequence	A0203
213 WLSLKTLLSLA	0.765	12	SB	Sequence	A0203
84 ALSPVPPVVHL	0.765	12	SB	Sequence	A0203
223 ALVGACITLGA	0.751	14	SB	Sequence	A0203
219 LLSLALVGACI	0.707	23	SB	Sequence	A0203
123 FTARGRFATVV	0.672	34	SB	Sequence	A0203
221 SLALVGACITL	0.617	63	WB	Sequence	A0203
179 YLNRHLHTWIQ	0.565	110	WB	Sequence	A0203
131 TVVEELFRDGV	0.507	206	WB	Sequence	A0203
21 KLSQRGYEWDA	0.476	291	WB	Sequence	A0203
84 ALSPVPPVVHL	0.633	53	WB	Sequence	A0204
221 SLALVGACITL	0.593	82	WB	Sequence	A0204
123 FTARGRFATVV	0.587	87	WB	Sequence	A0204
78 GAAAGPALSPV	0.495	235	WB	Sequence	A0204
21 KLSQRGYEWDA	0.488	255	WB	Sequence	A0204
179 YLNRHLHTWIQ	0.461	340	WB	Sequence	A0204
145 RIVAFFEFGGV	0.868	4	SB	Sequence	A0206
188 IQDNGGWDAFV	0.822	6	SB	Sequence	A0206
123 FTARGRFATVV	0.729	18	SB	Sequence	A0206
131 TVVEELFRDGV	0.725	19	SB	Sequence	A0206
223 ALVGACITLGA	0.670	35	SB	Sequence	A0206
50 SQPGHTPHPAA	0.659	40	SB	Sequence	A0206
71 LQTPAAPGAAA	0.657	40	SB	Sequence	A0206
78 GAAAGPALSPV	0.598	77	WB	Sequence	A0206
217 KTLLSLALVGA	0.537	149	WB	Sequence	A0206
84 ALSPVPPVVHL	0.533	157	WB	Sequence	A0206
204 SMRPLFDFSWL	0.494	239	WB	Sequence	A0206
215 SLKTLLSLALV	0.477	286	WB	Sequence	A0206
213 WLSLKTLLSLA	0.475	293	WB	Sequence	A0206
27 YEWDAGDVGAA	0.474	295	WB	Sequence	A0206
21 KLSQRGYEWDA	0.453	373	WB	Sequence	A0206
84 ALSPVPPVVHL	0.906	2	SB	Sequence	A0211
215 SLKTLLSLALV	0.896	3	SB	Sequence	A0211
221 SLALVGACITL	0.892	3	SB	Sequence	A0211
179 YLNRHLHTWIQ	0.853	4	SB	Sequence	A0211
164 EMSPLVDNIAL	0.832	6	SB	Sequence	A0211
204 SMRPLFDFSWL	0.813	7	SB	Sequence	A0211
223 ALVGACITLGA	0.803	8	SB	Sequence	A0211
123 FTARGRFATVV	0.782	10	SB	Sequence	A0211
188 IQDNGGWDAFV	0.746	15	SB	Sequence	A0211

148 AFFEFGGVMCV	0.730	18	SB	Sequence	A0211
207 PLFDFSWLSLK	0.720	20	SB	Sequence	A0211
131 TVVEELFRDGV	0.717	21	SB	Sequence	A0211
167 PLVDNIALWMT	0.706	24	SB	Sequence	A0211
21 KLSQRGYEWDA	0.702	25	SB	Sequence	A0211
213 WLSLKTLLSLA	0.655	41	SB	Sequence	A0211
145 RIVAFFEFGGV	0.634	52	WB	Sequence	A0211
199 ELYGPSMRPLF	0.626	56	WB	Sequence	A0211
219 LLSLALVGACI	0.581	92	WB	Sequence	A0211
78 GAAAGPALSPV	0.533	156	WB	Sequence	A0211
137 FRDGVNWGRIV	0.516	187	WB	Sequence	A0211
218 TLLSLALVGAC	0.500	223	WB	Sequence	A0211
119 HLTPFTARGRF	0.462	335	WB	Sequence	A0211
175 WMTEYLNRHLH	0.458	352	WB	Sequence	A0211
84 ALSPVPPVVHL	0.817	7	SB	Sequence	A0212
179 YLNRHLHTWIQ	0.794	9	SB	Sequence	A0212
123 FTARGRFATVV	0.784	10	SB	Sequence	A0212
204 SMRPLFDFSWL	0.781	10	SB	Sequence	A0212
215 SLKTLLSLALV	0.719	20	SB	Sequence	A0212
221 SLALVGACITL	0.719	20	SB	Sequence	A0212
164 EMSPLVDNIAL	0.714	22	SB	Sequence	A0212
21 KLSQRGYEWDA	0.616	63	WB	Sequence	A0212
223 ALVGACITLGA	0.604	72	WB	Sequence	A0212
131 TVVEELFRDGV	0.602	74	WB	Sequence	A0212
188 IQDNGGWDAFV	0.569	106	WB	Sequence	A0212
148 AFFEFGGVMCV	0.548	133	WB	Sequence	A0212
145 RIVAFFEFGGV	0.511	198	WB	Sequence	A0212
219 LLSLALVGACI	0.504	213	WB	Sequence	A0212
167 PLVDNIALWMT	0.483	269	WB	Sequence	A0212
207 PLFDFSWLSLK	0.472	301	WB	Sequence	A0212
137 FRDGVNWGRIV	0.431	473	WB	Sequence	A0212
84 ALSPVPPVVHL	0.878	3	SB	Sequence	A0216
221 SLALVGACITL	0.855	4	SB	Sequence	A0216
215 SLKTLLSLALV	0.806	8	SB	Sequence	A0216
204 SMRPLFDFSWL	0.753	14	SB	Sequence	A0216
123 FTARGRFATVV	0.739	16	SB	Sequence	A0216
223 ALVGACITLGA	0.697	26	SB	Sequence	A0216
188 IQDNGGWDAFV	0.637	50	WB	Sequence	A0216
164 EMSPLVDNIAL	0.625	57	WB	Sequence	A0216
179 YLNRHLHTWIQ	0.613	65	WB	Sequence	A0216
131 TVVEELFRDGV	0.586	88	WB	Sequence	A0216
78 GAAAGPALSPV	0.571	103	WB	Sequence	A0216
148 AFFEFGGVMCV	0.563	112	WB	Sequence	A0216
167 PLVDNIALWMT	0.535	153	WB	Sequence	A0216
145 RIVAFFEFGGV	0.503	216	WB	Sequence	A0216
151 EFGGVMCVESV	0.502	217	WB	Sequence	A0216
213 WLSLKTLLSLA	0.493	241	WB	Sequence	A0216
21 KLSQRGYEWDA	0.490	248	WB	Sequence	A0216
219 LLSLALVGACI	0.478	285	WB	Sequence	A0216
207 PLFDFSWLSLK	0.436	445	WB	Sequence	A0216
84 ALSPVPPVVHL	0.786	10	SB	Sequence	A0219
188 IQDNGGWDAFV	0.605	71	WB	Sequence	A0219
123 FTARGRFATVV	0.594	81	WB	Sequence	A0219
164 EMSPLVDNIAL	0.584	89	WB	Sequence	A0219
179 YLNRHLHTWIQ	0.574	100	WB	Sequence	A0219
221 SLALVGACITL	0.561	115	WB	Sequence	A0219
219 LLSLALVGACI	0.551	128	WB	Sequence	A0219
167 PLVDNIALWMT	0.537	149	WB	Sequence	A0219
78 GAAAGPALSPV	0.496	233	WB	Sequence	A0219

215 SLKTLLSLALV	0.490	248	WB	Sequence	A0219
204 SMRPLFDFSWL	0.486	259	WB	Sequence	A0219
223 ALVGACITLGA	0.467	320	WB	Sequence	A0219
207 PLFDFSWLSLK	0.604	72	WB	Sequence	A0301
228 CITLGAYLGHK	0.462	339	WB	Sequence	A0301
207 PLFDFSWLSLK	0.626	57	WB	Sequence	A1101
116 SQLHLTPFTAR	0.586	88	WB	Sequence	A1101
228 CITLGAYLGHK	0.580	94	WB	Sequence	A1101
172 IALWMTEYLNR	0.524	172	WB	Sequence	A1101
6 TGYDNREIVMK	0.437	439	WB	Sequence	A1101
142 NWGRIVAFFEF	0.733	18	SB	Sequence	A2301
178 EYLNRHLHTWI	0.592	82	WB	Sequence	A2301
19 HYKLSQRGYEW	0.563	112	WB	Sequence	A2301
174 LWMTEYLNRHL	0.457	355	WB	Sequence	A2301
212 SWLSLKTLLSL	0.439	431	WB	Sequence	A2301
178 EYLNRHLHTWI	0.794	9	SB	Sequence	A2402
142 NWGRIVAFFEF	0.744	15	SB	Sequence	A2402
212 SWLSLKTLLSL	0.514	192	WB	Sequence	A2402
174 LWMTEYLNRHL	0.497	230	WB	Sequence	A2402
178 EYLNRHLHTWI	0.599	76	WB	Sequence	A2403
19 HYKLSQRGYEW	0.573	101	WB	Sequence	A2403
142 NWGRIVAFFEF	0.486	260	WB	Sequence	A2403
17 YIHYKLSQRGY	0.524	172	WB	Sequence	A2601
113 EMSSQLHLTPF	0.866	4	SB	Sequence	A2602
17 YIHYKLSQRGY	0.817	7	SB	Sequence	A2602
12 EIVMKYIHYKL	0.760	13	SB	Sequence	A2602
187 WIQDNGGWDAF	0.631	54	WB	Sequence	A2602
199 ELYGPSMRPLF	0.568	106	WB	Sequence	A2602
224 LVGACITLGAY	0.545	137	WB	Sequence	A2602
139 DGVNWGRIVAF	0.462	336	WB	Sequence	A2602
207 PLFDFSWLSLK	0.456	359	WB	Sequence	A3001
11 REIVMKYIHYK	0.439	434	WB	Sequence	A3001
113 EMSSQLHLTPF	0.533	156	WB	Sequence	A3002
128 RFATVVEELFR	0.765	12	SB	Sequence	A3101
116 SQLHLTPFTAR	0.741	16	SB	Sequence	A3101
196 AFVELYGPSMR	0.640	48	SB	Sequence	A3101
172 IALWMTEYLNR	0.614	64	WB	Sequence	A3101
11 REIVMKYIHYK	0.571	104	WB	Sequence	A3101
15 MKYIHYKLSQR	0.500	224	WB	Sequence	A3101
98 QAGDDFSRRYR	0.483	269	WB	Sequence	A3101
135 ELFRDGVNWGR	0.634	52	WB	Sequence	A3301
128 RFATVVEELFR	0.492	244	WB	Sequence	A3301
172 IALWMTEYLNR	0.481	273	WB	Sequence	A3301
196 AFVELYGPSMR	0.467	318	WB	Sequence	A3301
135 ELFRDGVNWGR	0.739	16	SB	Sequence	A6801
228 CITLGAYLGHK	0.618	62	WB	Sequence	A6801
172 IALWMTEYLNR	0.593	81	WB	Sequence	A6801
57 HPAASRDPVAR	0.579	95	WB	Sequence	A6801
15 MKYIHYKLSQR	0.540	145	WB	Sequence	A6801
98 QAGDDFSRRYR	0.525	170	WB	Sequence	A6801
6 TGYDNREIVMK	0.515	190	WB	Sequence	A6801

128	RFATVVEELFR	0.507	207	WB	Sequence	A6801
95	TLRQAGDDFSR	0.490	249	WB	Sequence	A6801
207	PLFDFSWLSLK	0.470	308	WB	Sequence	A6801
123	FTARGRFATVV	0.809	7	SB	Sequence	A6802
131	TVVEELFRDGV	0.784	10	SB	Sequence	A6802
145	RIVAFFEFGGV	0.727	19	SB	Sequence	A6802
12	EIVMKYIHYKL	0.592	83	WB	Sequence	A6802
78	GAAAGPALSPV	0.560	116	WB	Sequence	A6802
164	EMSPLVDNIAL	0.520	179	WB	Sequence	A6802
159	ESVNREMSPLV	0.488	254	WB	Sequence	A6802
225	VGACITLGAYL	0.459	349	WB	Sequence	A6802
55	TPHPAASRDPV	0.435	453	WB	Sequence	A6802
123	FTARGRFATVV	0.710	23	SB	Sequence	A6901
164	EMSPLVDNIAL	0.541	144	WB	Sequence	A6901
131	TVVEELFRDGV	0.510	201	WB	Sequence	A6901
159	ESVNREMSPLV	0.485	263	WB	Sequence	A6901
206	RPLFDFSWLSL	0.747	15	SB	Sequence	B0702
86	SPVPPVVHLTL	0.717	21	SB	Sequence	B0702
55	TPHPAASRDPV	0.567	108	WB	Sequence	B0702
82	GPALSPVPPVV	0.559	118	WB	Sequence	B0702
166	SPLVDNIALWM	0.469	312	WB	Sequence	B0702
126	RGRFATVVEEL	0.463	332	WB	Sequence	B0702
121	TPFTARGRFAT	0.443	416	WB	Sequence	B0702
97	RQAGDDFSRRY	0.600	75	WB	Sequence	B1501
187	WIQDNGGWDAF	0.499	226	WB	Sequence	B1501
224	LVGACITLGAY	0.491	245	WB	Sequence	B1501
17	YIHYKLSQRGY	0.476	290	WB	Sequence	B1501
113	EMSSQLHLTPF	0.433	461	WB	Sequence	B1501
140	GVNWGRIVAFF	0.433	463	WB	Sequence	B1501
177	TEYLNRHLHTW	0.585	89	WB	Sequence	B1801
198	VELYGPSMRPL	0.558	119	WB	Sequence	B1801
158	VESVNREMSPL	0.514	191	WB	Sequence	B1801
133	VEELFRDGVNW	0.459	348	WB	Sequence	B1801
127	GRFATVVEELF	0.512	196	WB	Sequence	B2705
108	RRDFAEMSSQL	0.481	273	WB	Sequence	B2705
97	RQAGDDFSRRY	0.445	405	WB	Sequence	B2705
166	SPLVDNIALWM	0.573	101	WB	Sequence	B3501
187	WIQDNGGWDAF	0.544	139	WB	Sequence	B3501
195	DAFVELYGPSM	0.543	140	WB	Sequence	B3501
113	EMSSQLHLTPF	0.543	140	WB	Sequence	B3501
121	TPFTARGRFAT	0.503	217	WB	Sequence	B3501
224	LVGACITLGAY	0.502	218	WB	Sequence	B3501
146	IVAFFEFGGVM	0.500	222	WB	Sequence	B3501
86	SPVPPVVHLTL	0.443	416	WB	Sequence	B3501
139	DGVNWGRIVAF	0.442	419	WB	Sequence	B3501
61	SRDPVARTSPL	0.500	223	WB	Sequence	B3901
198	VELYGPSMRPL	0.547	134	WB	Sequence	B4001
158	VESVNREMSPL	0.471	306	WB	Sequence	B4001
177	TEYLNRHLHTW	0.520	180	WB	Sequence	B4402
112	AEMSSQLHLTP	0.529	163	WB	Sequence	B4501

37	APPGAAPAPGI	0.507	207	WB	Sequence	B5101
82	GPALSPVPPVV	0.465	326	WB	Sequence	B5101
86	SPVPPVVHLTL	0.433	461	WB	Sequence	B5101
166	SPLVDNIALWM	0.453	373	WB	Sequence	B5301
206	RPLFDFSWLSL	0.436	448	WB	Sequence	B5301
121	TPFTARGRFAT	0.638	50	WB	Sequence	B5401
69	SPLQTPAAPGA	0.557	121	WB	Sequence	B5401
89	PPVVHLTLRQA	0.501	220	WB	Sequence	B5401
55	TPHPAASRDPV	0.428	489	WB	Sequence	B5401
165	MSPLVDNIALW	0.462	335	WB	Sequence	B5701
203	PSMRPLFDFSW	0.635	51	WB	Sequence	B5801

Preferred fragments of BclX(L) capable of interacting with one or more MHC class 2 molecules are listed in table D.

Table D: Prediction of cancer antigen BclX(L) specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed

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)

Preferred fragments of Bcl-2 capable of interacting with one or more MHC class 2 molecules are listed in table E.

Table E: Prediction of cancer antigen Bcl-2 specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	Identity
DRB1_0101	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.8912	3	SB	Bcl-2
DRB1_0101	212	FSWLSLKTLLSLALV	LKTLLSLAL	0.8917	3	SB	Bcl-2
DRB1_0101	214	WLSLKTLLSLALVGA	LKTLLSLAL	0.8933	3	SB	Bcl-2
DRB1_0101	215	LSLKTLLSLALVGAC	LKTLLSLAL	0.8867	3	SB	Bcl-2
DRB1_0101	213	SWLSLKTLLSLALVG	LKTLLSLAL	0.8776	4	SB	Bcl-2
DRB1_0101	216	SLKTLLSLALVGACI	LKTLLSLAL	0.8024	8	SB	Bcl-2
DRB1_0101	217	LKTLLSLALVGACIT	LKTLLSLAL	0.8038	8	SB	Bcl-2
DRB1_0101	68	RTSPLQTPAAPGAAA	LQTPAAPGA	0.7623	13	SB	Bcl-2
DRB1_0101	69	TSPLQTPAAPGAAAG	LQTPAAPGA	0.7650	13	SB	Bcl-2
DRB1_0101	70	SPLQTPAAPGAAAGP	LQTPAAPGA	0.7631	13	SB	Bcl-2
DRB1_0101	66	VARTSPLQTPAAPGA	TSPLQTPAA	0.7565	14	SB	Bcl-2
DRB1_0101	67	ARTSPLQTPAAPGAA	LQTPAAPGA	0.7584	14	SB	Bcl-2
DRB1_0101	209	LFDFSWLSLKTLLSL	WLSLKTLLS	0.7419	16	SB	Bcl-2
DRB1_0101	208	PLFDFSWLSLKTLLS	FSWLSLKTL	0.7389	17	SB	Bcl-2
DRB1_0101	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.7403	17	SB	Bcl-2
DRB1_0101	219	TLLSLALVGACITLG	LLSLALVGA	0.7270	19	SB	Bcl-2
DRB1_0101	220	LLSLALVGACITLGA	LVGACITLG	0.7299	19	SB	Bcl-2
DRB1_0101	223	LALVGACITLGAYLG	LVGACITLG	0.7079	24	SB	Bcl-2
DRB1_0101	221	LSLALVGACITLGAY	LVGACITLG	0.7021	25	SB	Bcl-2
DRB1_0101	222	SLALVGACITLGAYL	LVGACITLG	0.7016	25	SB	Bcl-2
DRB1_0101	106	RRYRRDFAEMSSQLH	YRRDFAEMS	0.6774	33	SB	Bcl-2
DRB1_0101	72	LQTPAAPGAAAGPAL	LQTPAAPGA	0.6778	33	SB	Bcl-2
DRB1_0101	71	PLQTPAAPGAAAGPA	LQTPAAPGA	0.6750	34	SB	Bcl-2
DRB1_0101	108	YRRDFAEMSSQLHLT	FAEMSSQLH	0.6686	36	SB	Bcl-2
DRB1_0101	107	RYRRDFAEMSSQLHL	FAEMSSQLH	0.6670	37	SB	Bcl-2
DRB1_0101	218	KTLLSLALVGACITL	LLSLALVGA	0.6642	38	SB	Bcl-2
DRB1_0101	109	RRDFAEMSSQLHLTP	FAEMSSQLH	0.6615	39	SB	Bcl-2
DRB1_0101	110	RDFAEMSSQLHLTPF	FAEMSSQLH	0.6572	41	SB	Bcl-2
DRB1_0101	31	DAGDVGAAPPGAAPA	VGAAPPGAA	0.6561	41	SB	Bcl-2
DRB1_0101	32	AGDVGAAPPGAAPAP	VGAAPPGAA	0.6565	41	SB	Bcl-2
DRB1_0101	29	EWDAGDVGAAPPGAA	DVGAAPPGA	0.6512	44	SB	Bcl-2
DRB1_0101	30	WDAGDVGAAPPGAAP	VGAAPPGAA	0.6504	44	SB	Bcl-2
DRB1_0101	33	GDVGAAPPGAAPAPG	VGAAPPGAA	0.6438	47	SB	Bcl-2
DRB1_0101	207	RPLFDFSWLSLKTLL	FSWLSLKTL	0.6332	53	WB	Bcl-2
DRB1_0101	224	ALVGACITLGAYLGH	LVGACITLG	0.6316	54	WB	Bcl-2
DRB1_0101	206	MRPLFDFSWLSLKTL	DFSWLSLKT	0.6303	55	WB	Bcl-2
DRB1_0101	225	LVGACITLGAYLGHK	LVGACITLG	0.6212	60	WB	Bcl-2
DRB1_0101	13	EIVMKYIHYKLSQRG	MKYIHYKLS	0.6124	66	WB	Bcl-2
DRB1_0101	14	IVMKYIHYKLSQRGY	IHYKLSQRG	0.6114	67	WB	Bcl-2
DRB1_0101	15	VMKYIHYKLSQRGYE	IHYKLSQRG	0.6087	69	WB	Bcl-2
DRB1_0101	16	MKYIHYKLSQRGYEW	IHYKLSQRG	0.6059	71	WB	Bcl-2
DRB1_0101	17	KYIHYKLSQRGYEWD	IHYKLSQRG	0.6042	72	WB	Bcl-2
DRB1_0101	164	REMSPLVDNIALWMT	LVDNIALWM	0.5967	79	WB	Bcl-2
DRB1_0101	165	EMSPLVDNIALWMTE	VDNIALWMT	0.5914	83	WB	Bcl-2
DRB1_0101	167	SPLVDNIALWMTEYL	VDNIALWMT	0.5912	83	WB	Bcl-2
DRB1_0101	166	MSPLVDNIALWMTEY	VDNIALWMT	0.5908	84	WB	Bcl-2
DRB1_0101	63	RDPVARTSPLQTPAA	VARTSPLQT	0.5908	84	WB	Bcl-2
DRB1_0101	64	DPVARTSPLQTPAAP	VARTSPLQT	0.5876	87	WB	Bcl-2
DRB1_0101	168	PLVDNIALWMTEYLN	VDNIALWMT	0.5794	95	WB	Bcl-2
DRB1_0101	196	DAFVELYGPSMRPLF	FVELYGPSM	0.5684	107	WB	Bcl-2
DRB1_0101	34	DVGAAPPGAAPAPGI	VGAAPPGAA	0.5672	108	WB	Bcl-2
DRB1_0101	62	SRDPVARTSPLQTPA	VARTSPLQT	0.5669	108	WB	Bcl-2
DRB1_0101	195	WDAFVELYGPSMRPL	FVELYGPSM	0.5666	109	WB	Bcl-2
DRB1_0101	61	ASRDPVARTSPLQTP	VARTSPLQT	0.5637	112	WB	Bcl-2
DRB1_0101	86	LSPVPPVVHLTLRQA	LSPVPPVVH	0.5639	112	WB	Bcl-2

DRB1_0101	111	DFAEMSSQLHLTPFT	FAEMSSQLH	0.5615	115	WB	Bcl-2
DRB1_0101	89	VPPVVHLTLRQAGDD	VVHLTLRQA	0.5593	118	WB	Bcl-2
DRB1_0101	87	SPVPPVVHLTLRQAG	VVHLTLRQA	0.5579	119	WB	Bcl-2
DRB1_0101	88	PVPPVVHLTLRQAGD	VVHLTLRQA	0.5581	119	WB	Bcl-2
DRB1_0101	112	FAEMSSQLHLTPFTA	FAEMSSQLH	0.5577	120	WB	Bcl-2
DRB1_0101	35	VGAAPPGAAPAPGIF	VGAAPPGAA	0.5569	121	WB	Bcl-2
DRB1_0101	90	PPVVHLTLRQAGDDF	VVHLTLRQA	0.5563	122	WB	Bcl-2
DRB1_0101	80	AAAGPALSPVPPVVH	AAAGPALSP	0.5545	124	WB	Bcl-2
DRB1_0101	160	ESVNREMSPLVDNIA	VNREMSPLV	0.5523	127	WB	Bcl-2
DRB1_0101	60	AASRDPVARTSPLQT	SRDPVARTS	0.5524	127	WB	Bcl-2
DRB1_0101	117	SQLHLTPFTARGRFA	LTPFTARGR	0.5480	133	WB	Bcl-2
DRB1_0101	115	MSSQLHLTPFTARGR	LHLTPFTAR	0.5456	137	WB	Bcl-2
DRB1_0101	116	SSQLHLTPFTARGRF	LTPFTARGR	0.5418	142	WB	Bcl-2
DRB1_0101	81	AAGPALSPVPPVVHL	LSPVPPVVH	0.5390	147	WB	Bcl-2
DRB1_0101	118	QLHLTPFTARGRFAT	LTPFTARGR	0.5379	148	WB	Bcl-2
DRB1_0101	197	AFVELYGPSMRPLFD	LYGPSMRPL	0.5381	148	WB	Bcl-2
DRB1_0101	156	VMCVESVNREMSPLV	VMCVESVNR	0.5366	151	WB	Bcl-2
DRB1_0101	158	CVESVNREMSPLVDN	VNREMSPLV	0.5360	151	WB	Bcl-2
DRB1_0101	159	VESVNREMSPLVDNI	VNREMSPLV	0.5364	151	WB	Bcl-2
DRB1_0101	198	FVELYGPSMRPLFDF	LYGPSMRPL	0.5345	154	WB	Bcl-2
DRB1_0101	157	MCVESVNREMSPLVD	VNREMSPLV	0.5315	159	WB	Bcl-2
DRB1_0101	119	LHLTPFTARGRFATV	LTPFTARGR	0.5307	160	WB	Bcl-2
DRB1_0101	82	AGPALSPVPPVVHLT	LSPVPPVVH	0.5312	160	WB	Bcl-2
DRB1_0101	83	GPALSPVPPVVHLTL	LSPVPPVVH	0.5307	160	WB	Bcl-2
DRB1_0101	148	VAFFEFGGVMCVESV	FEFGGVMCV	0.5291	163	WB	Bcl-2
DRB1_0101	149	AFFEFGGVMCVESVN	FEFGGVMCV	0.5288	164	WB	Bcl-2
DRB1_0101	46	PGIFSSQPGHTPHPA	FSSQPGHTP	0.5270	167	WB	Bcl-2
DRB1_0101	170	VDNIALWMTEYLNRH	VDNIALWMT	0.5265	168	WB	Bcl-2
DRB1_0101	43	APAPGIFSSQPGHTP	IFSSQPGHT	0.5223	176	WB	Bcl-2
DRB1_0101	84	PALSPVPPVVHLTLR	LSPVPPVVH	0.5195	181	WB	Bcl-2
DRB1_0101	147	IVAFFEFGGVMCVES	FEFGGVMCV	0.5190	182	WB	Bcl-2
DRB1_0101	65	PVARTSPLQTPAAPG	VARTSPLQT	0.5190	182	WB	Bcl-2
DRB1_0101	45	APGIFSSQPGHTPHP	FSSQPGHTP	0.5186	183	WB	Bcl-2
DRB1_0101	120	HLTPFTARGRFATVV	LTPFTARGR	0.5178	184	WB	Bcl-2
DRB1_0101	121	LTPFTARGRFATVVE	ARGRFATVV	0.5182	184	WB	Bcl-2
DRB1_0101	136	ELFRDGVNWGRIVAF	FRDGVNWGR	0.5154	189	WB	Bcl-2
DRB1_0101	44	PAPGIFSSQPGHTPH	FSSQPGHTP	0.5142	192	WB	Bcl-2
DRB1_0101	138	FRDGVNWGRIVAFFE	VNWGRIVAF	0.5122	196	WB	Bcl-2
DRB1_0101	169	LVDNIALWMTEYLNR	VDNIALWMT	0.5062	209	WB	Bcl-2
DRB1_0101	18	YIHYKLSQRGYEWDA	IHYKLSQRG	0.5057	210	WB	Bcl-2
DRB1_0101	137	LFRDGVNWGRIVAFF	VNWGRIVAF	0.5023	218	WB	Bcl-2
DRB1_0101	19	IHYKLSQRGYEWDAG	IHYKLSQRG	0.5022	218	WB	Bcl-2
DRB1_0101	47	GIFSSQPGHTPHPAA	FSSQPGHTP	0.5023	218	WB	Bcl-2
DRB1_0101	76	AAPGAAAGPALSPVP	AAAGPALSP	0.5005	222	WB	Bcl-2
DRB1_0101	139	RDGVNWGRIVAFFEF	VNWGRIVAF	0.4998	224	WB	Bcl-2
DRB1_0101	74	TPAAPGAAAGPALSP	GAAAGPALS	0.4991	226	WB	Bcl-2
DRB1_0101	194	GWDAFVELYGPSMRP	FVELYGPSM	0.4987	227	WB	Bcl-2
DRB1_0101	75	PAAPGAAAGPALSPV	AAAGPALSP	0.4981	228	WB	Bcl-2
DRB1_0101	77	APGAAAGPALSPVPP	AAAGPALSP	0.4980	229	WB	Bcl-2
DRB1_0101	140	DGVNWGRIVAFFEFG	VNWGRIVAF	0.4959	234	WB	Bcl-2
DRB1_0101	105	SRRYRRDFAEMSSQL	YRRDFAEMS	0.4945	237	WB	Bcl-2
DRB1_0101	91	PVVHLTLRQAGDDFS	VVHLTLRQA	0.4935	240	WB	Bcl-2
DRB1_0101	199	VELYGPSMRPLFDFS	LYGPSMRPL	0.4895	251	WB	Bcl-2
DRB1_0101	92	VVHLTLRQAGDDFSR	VVHLTLRQA	0.4870	257	WB	Bcl-2
DRB1_0101	104	FSRRYRRDFAEMSSQ	YRRDFAEMS	0.4851	263	WB	Bcl-2
DRB1_0101	103	DFSRRYRRDFAEMSS	YRRDFAEMS	0.4834	268	WB	Bcl-2
DRB1_0101	102	DDFSRRYRRDFAEMS	RYRRDFAEM	0.4800	278	WB	Bcl-2
DRB1_0101	145	GRIVAFFEFGGVMCV	FFEFGGVMC	0.4796	279	WB	Bcl-2
DRB1_0101	146	RIVAFFEFGGVMCVE	FEFGGVMCV	0.4791	280	WB	Bcl-2
DRB1_0101	78	PGAAAGPALSPVPPV	AAAGPALSP	0.4771	286	WB	Bcl-2
DRB1_0101	161	SVNREMSPLVDNIAL	VNREMSPLV	0.4763	289	WB	Bcl-2
DRB1_0101	150	FFEFGGVMCVESVNR	FEFGGVMCV	0.4737	297	WB	Bcl-2
DRB1_0101	162	VNREMSPLVDNIALW	VNREMSPLV	0.4734	298	WB	Bcl-2
DRB1_0101	151	FEFGGVMCVESVNRE	FEFGGVMCV	0.4731	299	WB	Bcl-2
DRB1_0101	114	EMSSQLHLTPFTARG	LHLTPFTAR	0.4711	306	WB	Bcl-2
DRB1_0101	122	TPFTARGRFATVVEE	ARGRFATVV	0.4638	331	WB	Bcl-2
DRB1_0101	73	QTPAAPGAAAGPALS	APGAAAGPA	0.4635	332	WB	Bcl-2
DRB1_0101	49	FSSQPGHTPHPAASR	FSSQPGHTP	0.4615	339	WB	Bcl-2
DRB1_0101	48	IFSSQPGHTPHPAAS	FSSQPGHTP	0.4531	371	WB	Bcl-2
DRB1_0101	36	GAAPPGAAPAPGIFS	PGAAPAPGI	0.4518	376	WB	Bcl-2

DRB1_0101	123	PFTARGRFATVVEEL	ARGRFATVV	0.4516	377	WB	Bcl-2
DRB1_0101	124	FTARGRFATVVEELF	ARGRFATVV	0.4490	388	WB	Bcl-2
DRB1_0101	174	ALWMTEYLNRHLHTW	WMTEYLNRH	0.4444	408	WB	Bcl-2
DRB1_0101	85	ALSPVPPVVHLTLRQ	LSPVPPVVH	0.4436	411	WB	Bcl-2
DRB1_0101	113	AEMSSQLHLTPFTAR	SQLHLTPFT	0.4430	414	WB	Bcl-2
DRB1_0101	171	DNIALWMTEYLNRHL	WMTEYLNRH	0.4414	421	WB	Bcl-2
DRB1_0101	193	GGWDAFVELYGPSMR	FVELYGPSM	0.4396	430	WB	Bcl-2
DRB1_0101	200	ELYGPSMRPLFDFSW	LYGPSMRPL	0.4395	430	WB	Bcl-2
DRB1_0101	37	AAPPGAAPAPGIFSS	AAPAPGIFS	0.4393	431	WB	Bcl-2
DRB1_0101	79	GAAAGPALSPVPPVV	AAAGPALSP	0.4394	431	WB	Bcl-2
DRB1_0101	172	NIALWMTEYLNRHLH	WMTEYLNRH	0.4279	488	WB	Bcl-2
DRB1_0101	28	YEWDAGDVGAAPPGA	WDAGDVGAA	0.4274	490	WB	Bcl-2
DRB1_0101	42	AAPAPGIFSSQPGHT	AAPAPGIFS	0.4268	494	WB	Bcl-2
DRB1_0101	163	NREMSPLVDNIALWM	MSPLVDNIA	0.4266	495	WB	Bcl-2
DRB1_0401	208	PLFDFSWLSLKTLLS	DFSWLSLKT	0.5448	138	WB	Bcl-2
DRB1_0401	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.5436	139	WB	Bcl-2
DRB1_0401	212	FSWLSLKTLLSLALV	WLSLKTLLS	0.5395	146	WB	Bcl-2
DRB1_0401	209	LFDFSWLSLKTLLSL	WLSLKTLLS	0.5358	152	WB	Bcl-2
DRB1_0401	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.5305	161	WB	Bcl-2
DRB1_0401	156	VMCVESVNREMSPLV	MCVESVNRE	0.4924	243	WB	Bcl-2
DRB1_0401	158	CVESVNREMSPLVDN	VNREMSPLV	0.4915	245	WB	Bcl-2
DRB1_0401	157	MCVESVNREMSPLVD	VNREMSPLV	0.4907	247	WB	Bcl-2
DRB1_0401	160	ESVNREMSPLVDNIA	VNREMSPLV	0.4909	247	WB	Bcl-2
DRB1_0401	159	VESVNREMSPLVDNI	VNREMSPLV	0.4870	257	WB	Bcl-2
DRB1_0401	214	WLSLKTLLSLALVGA	WLSLKTLLS	0.4662	322	WB	Bcl-2
DRB1_0401	213	SWLSLKTLLSLALVG	WLSLKTLLS	0.4661	323	WB	Bcl-2
DRB1_0401	106	RRYRRDFAEMSSQLH	YRRDFAEMS	0.4563	359	WB	Bcl-2
DRB1_0401	170	VDNIALWMTEYLNRH	NIALWMTEY	0.4319	467	WB	Bcl-2
DRB1_0404	174	ALWMTEYLNRHLHTW	WMTEYLNRH	0.5813	93	WB	Bcl-2
DRB1_0404	170	VDNIALWMTEYLNRH	IALWMTEYL	0.5418	142	WB	Bcl-2
DRB1_0404	171	DNIALWMTEYLNRHL	WMTEYLNRH	0.5422	142	WB	Bcl-2
DRB1_0404	172	NIALWMTEYLNRHLH	WMTEYLNRH	0.5371	150	WB	Bcl-2
DRB1_0404	173	IALWMTEYLNRHLHT	WMTEYLNRH	0.5341	155	WB	Bcl-2
DRB1_0404	175	LWMTEYLNRHLHTWI	WMTEYLNRH	0.5171	186	WB	Bcl-2
DRB1_0404	115	MSSQLHLTPFTARGR	HLTPFTARG	0.5121	196	WB	Bcl-2
DRB1_0404	114	EMSSQLHLTPFTARG	LHLTPFTAR	0.5118	197	WB	Bcl-2
DRB1_0404	176	WMTEYLNRHLHTWIQ	WMTEYLNRH	0.5110	199	WB	Bcl-2
DRB1_0404	116	SSQLHLTPFTARGRF	HLTPFTARG	0.5043	213	WB	Bcl-2
DRB1_0404	117	SQLHLTPFTARGRFA	HLTPFTARG	0.5004	223	WB	Bcl-2
DRB1_0404	118	QLHLTPFTARGRFAT	HLTPFTARG	0.4918	244	WB	Bcl-2
DRB1_0404	45	APGIFSSQPGHTPHP	FSSQPGHTP	0.4688	313	WB	Bcl-2
DRB1_0404	46	PGIFSSQPGHTPHPA	FSSQPGHTP	0.4665	321	WB	Bcl-2
DRB1_0404	47	GIFSSQPGHTPHPAA	SQPGHTPHP	0.4485	390	WB	Bcl-2
DRB1_0404	109	RRDFAEMSSQLHLTP	FAEMSSQLH	0.4422	418	WB	Bcl-2
DRB1_0404	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.4405	426	WB	Bcl-2
DRB1_0404	110	RDFAEMSSQLHLTPF	FAEMSSQLH	0.4393	431	WB	Bcl-2
DRB1_0404	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.4316	469	WB	Bcl-2
DRB1_0404	212	FSWLSLKTLLSLALV	WLSLKTLLS	0.4313	470	WB	Bcl-2
DRB1_0405	208	PLFDFSWLSLKTLLS	FSWLSLKTL	0.6517	43	SB	Bcl-2
DRB1_0405	209	LFDFSWLSLKTLLSL	WLSLKTLLS	0.6415	48	SB	Bcl-2
DRB1_0405	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.6398	49	SB	Bcl-2
DRB1_0405	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.6392	50	WB	Bcl-2
DRB1_0405	212	FSWLSLKTLLSLALV	WLSLKTLLS	0.6381	50	WB	Bcl-2
DRB1_0405	213	SWLSLKTLLSLALVG	WLSLKTLLS	0.5584	119	WB	Bcl-2
DRB1_0405	214	WLSLKTLLSLALVGA	WLSLKTLLS	0.5575	120	WB	Bcl-2
DRB1_0405	160	ESVNREMSPLVDNIA	NREMSPLVD	0.5021	219	WB	Bcl-2
DRB1_0405	158	CVESVNREMSPLVDN	NREMSPLVD	0.4974	230	WB	Bcl-2
DRB1_0405	159	VESVNREMSPLVDNI	NREMSPLVD	0.4930	241	WB	Bcl-2
DRB1_0405	170	VDNIALWMTEYLNRH	IALWMTEYL	0.4903	248	WB	Bcl-2
DRB1_0405	168	PLVDNIALWMTEYLN	IALWMTEYL	0.4841	266	WB	Bcl-2
DRB1_0405	171	DNIALWMTEYLNRHL	IALWMTEYL	0.4841	266	WB	Bcl-2
DRB1_0405	169	LVDNIALWMTEYLNR	IALWMTEYL	0.4812	274	WB	Bcl-2
DRB1_0405	157	MCVESVNREMSPLVD	VNREMSPLV	0.4756	291	WB	Bcl-2
DRB1_0405	167	SPLVDNIALWMTEYL	NIALWMTEY	0.4744	295	WB	Bcl-2
DRB1_0405	161	SVNREMSPLVDNIAL	NREMSPLVD	0.4718	303	WB	Bcl-2
DRB1_0405	106	RRYRRDFAEMSSQLH	YRRDFAEMS	0.4486	390	WB	Bcl-2
DRB1_0405	162	VNREMSPLVDNIALW	NREMSPLVD	0.4294	480	WB	Bcl-2

DRB1_0701	83	GPALSPVPPVVHLTL	LSPVPPVVH	0.5316	159	WB	Bcl-2
DRB1_0701	82	AGPALSPVPPVVHLT	LSPVPPVVH	0.5286	164	WB	Bcl-2
DRB1_0701	81	AAGPALSPVPPVVHL	LSPVPPVVH	0.5256	169	WB	Bcl-2
DRB1_0701	84	PALSPVPPVVHLTLR	LSPVPPVVH	0.5210	178	WB	Bcl-2
DRB1_0701	80	AAAGPALSPVPPVVH	ALSPVPPVV	0.5179	184	WB	Bcl-2
DRB1_0701	85	ALSPVPPVVHLTLRQ	LSPVPPVVH	0.4370	442	WB	Bcl-2
DRB1_0701	86	LSPVPPVVHLTLRQA	LSPVPPVVH	0.4291	482	WB	Bcl-2
DRB1_0901	196	DAFVELYGPSMRPLF	VELYGPSMR	0.4599	345	WB	Bcl-2
DRB1_0901	197	AFVELYGPSMRPLFD	YGPSMRPLF	0.4582	352	WB	Bcl-2
DRB1_0901	198	FVELYGPSMRPLFDF	YGPSMRPLF	0.4429	415	WB	Bcl-2
DRB1_0901	199	VELYGPSMRPLFDFS	YGPSMRPLF	0.4428	415	WB	Bcl-2
DRB1_1302	212	FSWLSLKTLLSLALV	WLSLKTLLS	0.5351	153	WB	Bcl-2
DRB1_1302	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.5323	158	WB	Bcl-2
DRB1_1302	209	LFDFSWLSLKTLLSL	WLSLKTLLS	0.4963	233	WB	Bcl-2
DRB1_1302	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.4951	236	WB	Bcl-2
DRB1_1302	208	PLFDFSWLSLKTLLS	FSWLSLKTL	0.4783	283	WB	Bcl-2
DRB1_1302	213	SWLSLKTLLSLALVG	WLSLKTLLS	0.4770	287	WB	Bcl-2
DRB1_1302	214	WLSLKTLLSLALVGA	WLSLKTLLS	0.4769	287	WB	Bcl-2
DRB1_1302	196	DAFVELYGPSMRPLF	VELYGPSMR	0.4640	330	WB	Bcl-2
DRB1_1302	197	AFVELYGPSMRPLFD	VELYGPSMR	0.4607	342	WB	Bcl-2
DRB1_1302	167	SPLVDNIALWMTEYL	VDNIALWMT	0.4494	387	WB	Bcl-2
DRB1_1302	168	PLVDNIALWMTEYLN	VDNIALWMT	0.4385	435	WB	Bcl-2
DRB1_1501	13	EIVMKYIHYKLSQRG	YIHYKLSQR	0.6338	53	WB	Bcl-2
DRB1_1501	14	IVMKYIHYKLSQRGY	YIHYKLSQR	0.6318	54	WB	Bcl-2
DRB1_1501	15	VMKYIHYKLSQRGYE	YIHYKLSQR	0.6170	63	WB	Bcl-2
DRB1_1501	16	MKYIHYKLSQRGYEW	YIHYKLSQR	0.6121	66	WB	Bcl-2
DRB1_1501	12	REIVMKYIHYKLSQR	IVMKYIHYK	0.6057	71	WB	Bcl-2
DRB1_1501	17	KYIHYKLSQRGYEWD	YIHYKLSQR	0.5372	150	WB	Bcl-2
DRB1_1501	115	MSSQLHLTPFTARGR	LHLTPFTAR	0.5174	185	WB	Bcl-2
DRB1_1501	116	SSQLHLTPFTARGRF	LHLTPFTAR	0.5162	188	WB	Bcl-2
DRB1_1501	18	YIHYKLSQRGYEWDA	YIHYKLSQR	0.5136	193	WB	Bcl-2
DRB1_1501	117	SQLHLTPFTARGRFA	LHLTPFTAR	0.5054	211	WB	Bcl-2
DRB1_1501	119	LHLTPFTARGRFATV	LTPFTARGR	0.4756	291	WB	Bcl-2
DRB1_1501	135	EELFRDGVNWGRIVA	LFRDGVNWG	0.4694	311	WB	Bcl-2
DRB1_1501	212	FSWLSLKTLLSLALV	WLSLKTLLS	0.4694	312	WB	Bcl-2
DRB1_1501	211	DFSWLSLKTLLSLAL	WLSLKTLLS	0.4655	325	WB	Bcl-2
DRB1_1501	118	QLHLTPFTARGRFAT	LHLTPFTAR	0.4592	348	WB	Bcl-2
DRB1_1501	87	SPVPPVVHLTLRQAG	VVHLTLRQA	0.4553	363	WB	Bcl-2
DRB1_1501	88	PVPPVVHLTLRQAGD	VVHLTLRQA	0.4528	373	WB	Bcl-2
DRB1_1501	214	WLSLKTLLSLALVGA	LKTLLSLAL	0.4517	377	WB	Bcl-2
DRB1_1501	209	LFDFSWLSLKTLLSL	WLSLKTLLS	0.4495	386	WB	Bcl-2
DRB1_1501	156	VMCVESVNREMSPLV	VMCVESVNR	0.4490	388	WB	Bcl-2
DRB1_1501	193	GGWDAFVELYGPSMR	FVELYGPSM	0.4489	389	WB	Bcl-2
DRB1_1501	195	WDAFVELYGPSMRPL	VELYGPSMR	0.4483	391	WB	Bcl-2
DRB1_1501	196	DAFVELYGPSMRPLF	FVELYGPSM	0.4482	392	WB	Bcl-2
DRB1_1501	132	TVVEELFRDGVNWGR	LFRDGVNWG	0.4470	397	WB	Bcl-2
DRB1_1501	133	VVEELFRDGVNWGRI	LFRDGVNWG	0.4467	398	WB	Bcl-2
DRB1_1501	194	GWDAFVELYGPSMRP	VELYGPSMR	0.4467	398	WB	Bcl-2
DRB1_1501	174	ALWMTEYLNRHLHTW	WMTEYLNRH	0.4463	400	WB	Bcl-2
DRB1_1501	208	PLFDFSWLSLKTLLS	LFDFSWLSL	0.4459	401	WB	Bcl-2
DRB1_1501	172	NIALWMTEYLNRHLH	WMTEYLNRH	0.4448	406	WB	Bcl-2
DRB1_1501	173	IALWMTEYLNRHLHT	WMTEYLNRH	0.4448	407	WB	Bcl-2
DRB1_1501	134	VEELFRDGVNWGRIV	LFRDGVNWG	0.4431	414	WB	Bcl-2
DRB1_1501	171	DNIALWMTEYLNRHL	WMTEYLNRH	0.4431	414	WB	Bcl-2
DRB1_1501	89	VPPVVHLTLRQAGDD	VVHLTLRQA	0.4422	418	WB	Bcl-2
DRB1_1501	210	FDFSWLSLKTLLSLA	WLSLKTLLS	0.4399	429	WB	Bcl-2
DRB1_1501	136	ELFRDGVNWGRIVAF	LFRDGVNWG	0.4390	433	WB	Bcl-2
DRB1_1501	86	LSPVPPVVHLTLRQA	PPVVHLTLR	0.4378	438	WB	Bcl-2
DRB1_1501	213	SWLSLKTLLSLALVG	LKTLLSLAL	0.4330	461	WB	Bcl-2
DRB1_1501	90	PPVVHLTLRQAGDDF	VVHLTLRQA	0.4313	470	WB	Bcl-2
DRB4_0101	196	DAFVELYGPSMRPLF	VELYGPSMR	0.5364	151	WB	Bcl-2
DRB4_0101	197	AFVELYGPSMRPLFD	VELYGPSMR	0.5361	151	WB	Bcl-2
DRB4_0101	195	WDAFVELYGPSMRPL	VELYGPSMR	0.5323	158	WB	Bcl-2
DRB4_0101	193	GGWDAFVELYGPSMR	FVELYGPSM	0.4796	279	WB	Bcl-2
DRB4_0101	194	GWDAFVELYGPSMRP	VELYGPSMR	0.4785	282	WB	Bcl-2

DRB4_0101	198	FVELYGPSMRPLFDF	VELYGPSMR	0.4761	289	WB	Bcl-2
DRB4_0101	199	VELYGPSMRPLFDFS	VELYGPSMR	0.4763	289	WB	Bcl-2
DRB4_0101	81	AAGPALSPVPPVVHL	LSPVPPVVH	0.4638	331	WB	Bcl-2
DRB4_0101	80	AAAGPALSPVPPVVH	ALSPVPPVV	0.4614	339	WB	Bcl-2
DRB4_0101	170	VDNIALWMTEYLNRH	IALWMTEYL	0.4593	347	WB	Bcl-2
DRB4_0101	83	GPALSPVPPVVHLTL	LSPVPPVVH	0.4589	349	WB	Bcl-2
DRB4_0101	82	AGPALSPVPPVVHLT	LSPVPPVVH	0.4574	354	WB	Bcl-2
DRB4_0101	84	PALSPVPPVVHLTLR	LSPVPPVVH	0.4565	358	WB	Bcl-2
DRB4_0101	171	DNIALWMTEYLNRHL	WMTEYLNRH	0.4552	363	WB	Bcl-2
DRB4_0101	172	NIALWMTEYLNRHLH	LWMTEYLNR	0.4326	464	WB	Bcl-2
DRB4_0101	173	IALWMTEYLNRHLHT	WMTEYLNRH	0.4273	491	WB	Bcl-2
DRB5_0101	16	MKYIHYKLSQRGYEW	YIHYKLSQR	0.4394	431	WB	Bcl-2
DRB5_0101	15	VMKYIHYKLSQRGYE	YIHYKLSQR	0.4386	435	WB	Bcl-2

Preferred fragments of Survivin capable of interacting with one or more MHC class 1 molecules are listed in table F.

Table F: Prediction of cancer antigen Survivin specific MHC class 1 peptide sequences. Prediction of 8-, 9-, 10-, 11-mers using the program displayed in figure 2.

8 mers: MGAPTLPP; GAPTLPPA; APTLPPAW; PTLPPAWQ; TLPPAWQP; LPPAWQPF; PPAWQPFL; PAWQPFLK; AWQPFLKD; WQPFLKDH; QPFLKDHR; PFLKDHRI; FLKDHRIS; LKDHRIST; KDHRISTF; DHRISTFK; HRISTFKN; RISTFKNW; ISTFKNWP; STFKNWPF; TFKNWPFL; FKNWPFLE; KNWPFLEG; NWPFLEGC; WPFLEGCA; PFLEGCAC; FLEGCACT; LEGCACTP; EGCACTPE; GCACTPER; CACTPERM; ACTPERMA; CTPERMAE; TPERMAEA; PERMAEAG; ERMAEAGF; RMAEAGFI; MAEAGFIH; AEAGFIHC; EAGFIHCP; AGFIHCPT; GFIHCPTE; FIHCPTEN; IHCPTENE; HCPTENEP; CPTENEPD; PTENEPDL; TENEPDLA; ENEPDLAQ; NEPDLAQC; EPDLAQCF; PDLAQCFF; DLAQCFFC; LAQCFFCF; AQCFFCFK; QCFFCFKE; CFFCFKEL; FFCFKELE; FCFKELEG; CFKELEGW; FKELEGWE; KELEGWEP; ELEGWEPD; LEGWEPDD; EGWEPDDD; GWEPDDDP; WEPDDDPI; EPDDDPIE; PDDDPIEE; DDDPIEEH; DDPIEEHK; DPIEEHKK; PIEEHKKH; IEEHKKHS; EEHKKHSS; EHKKHSSG; HKKHSSGC; KKHSSGCA; KHSSGCAF; HSSGCAFL; SSGCAFLS; SGCAFLSV; GCAFLSVK; CAFLSVKK; AFLSVKKQ; FLSVKKQF; LSVKKQFE; SVKKQFEE; VKKQFEEL; KKQFEELT; KQFEELTL; QFEELTLG; FEELTLGE; EELTLGEF; ELTLGEFL; LTLGEFLK; TLGEFLKL; LGEFLKLD; GEFLKLDR; EFLKLDRE; FLKLDRER; LKLDRERA; KLDRERAK; LDRERAKN; DRERAKNK; RERAKNKI; ERAKNKIA; RAKNKIAK; AKNKIAKE; KNKIAKET; NKIAKETN; KIAKETNN; IAKETNNK; AKETNNKK; KETNNKKK; ETNNKKKE; TNNKKKEF; NNKKKEFE; NKKKEFEE; KKKEFEET; KKEFEETA; KEFEETAK; EFEETAKK; FEETAKKV; EETAKKVR; ETAKKVRR; TAKKVRRA; AKKVRRAI; KKVRRAIE; KVRRAIEQ; VRRAIEQL; RRAIEQLA; RAIEQLAA; AIEQLAAM; IEQLAAMD; EQLAAMD1
9 mers: MGAPTLPPA; GAPTLPPAW; APTLPPAWQ; PTLPPAWQP; TLPPAWQPF; LPPAWQPFL; PPAWQPFLK; PAWQPFLKD; AWQPFLKDH; WQPFLKDHR; QPFLKDHRI; PFLKDHRIS; FLKDHRIST; LKDHRISTF; KDHRISTFK; DHRISTFKN; HRISTFKNW; RISTFKNWP; ISTFKNWPF; STFKNWPFL; TFKNWPFLE; FKNWPFLEG; KNWPFLEGC; NWPFLEGCA; WPFLEGCAC; PFLEGCACT; FLEGCACTP; LEGCACTPE; EGCACTPER; GCACTPERM; CACTPERMA; ACTPERMAE; CTPERMAEA; TPERMAEAG; PERMAEAGF; ERMAEAGFI; RMAEAGFIH; MAEAGFIHC; AEAGFIHCP; EAGFIHCPT; AGFIHCPTE; GFIHCPTEN; FIHCPTENE; IHCPTENEP; HCPTENEPD; CPTENEPDL; PTENEPDLA; TENEPDLAQ; ENEPDLAQC; NEPDLAQCF; EPDLAQCFF; PDLAQCFFC; DLAQCFFCF; LAQCFFCFK; AQCFFCFKE; QCFFCFKEL; CFFCFKELE; FFCFKELEG; FCFKELEGW; CFKELEGWE; FKELEGWEP; KELEGWEPD; ELEGWEPDD; LEGWEPDDD; EGWEPDDDP; GWEPDDDPI; WEPDDDPIE; EPDDDPIEE; PDDDPIEEH; DDDPIEEHK; DDPIEEHKK; DPIEEHKKH; PIEEHKKHS; IEEHKKHSS; EEHKKHSSG; EHKKHSSGC; HKKHSSGCA; KKHSSGCAF; KHSSGCAFL; HSSGCAFLS; SSGCAFLSV; SGCAFLSVK; GCAFLSVKK; CAFLSVKKQ; AFLSVKKQF; FLSVKKQFE; LSVKKQFEE; SVKKQFEEL; VKKQFEELT; KKQFEELTL; KQFEELTLG; QFEELTLGE; FEELTLGEF; EELTLGEFL; ELTLGEFLK; LTLGEFLKL; TLGEFLKLD; LGEFLKLDR; GEFLKLDRE; EFLKLDRER; FLKLDRERA; LKLDRERAK; KLDRERAKN; LDRERAKNK; DRERAKNKI; RERAKNKIA; ERAKNKIAK; RAKNKIAKE; AKNKIAKET; KNKIAKETN; NKIAKETNN; KIAKETNNK; IAKETNNKK; AKETNNKKK; KETNNKKKE; ETNNKKKEF; TNNKKKEFE; NNKKKEFEE; NKKKEFEET; KKKEFEETA; KKEFEETAK; KEFEETAKK; EFEETAKKV; FEETAKKVR; EETAKKVRR; ETAKKVRRA; TAKKVRRAI; AKKVRRAIE; KKVRRAIEQ; KVRRAIEQL; VRRAIEQLA; RRAIEQLAA; RAIEQLAAM; AIEQLAAMD;1
10 mers: MGAPTLPPAW; GAPTLPPAWQ; APTLPPAWQP; PTLPPAWQPF; TLPPAWQPFL; LPPAWQPFLK; PPAWQPFLKD; PAWQPFLKDH; AWQPFLKDHR; WQPFLKDHRI; QPFLKDHRIS; PFLKDHRIST; FLKDHRISTF; LKDHRISTFK; KDHRISTFKN;

DHRISTFKNW; HRISTFKNWP; RISTFKNWPF; ISTFKNWPFL; STFKNWPFLE;
TFKNWPFLEG; FKNWPFLEGC; KNWPFLEGCA; NWPFLEGCAC; WPFLEGCACT;
PFLEGCACTP; FLEGCACTPE; LEGCACTPER; EGCACTPERM; GCACTPERMA;
CACTPERMAE; ACTPERMAEA; CTPERMAEAG; TPERMAEAGF; PERMAEAGFI;
ERMAEAGFIH; RMAEAGFIHC; MAEAGFIHCP; AEAGFIHCPT; EAGFIHCPTE;
AGFIHCPTEN; GFIHCPTENE; FIHCPTENEP; IHCPTENEPD; HCPTENEPDL;
CPTENEPDLA; PTENEPDLAQ; TENEPDLAQC; ENEPDLAQCF; NEPDLAQCFF;
EPDLAQCFFC; PDLAQCFFCF; DLAQCFFCFK; LAQCFFCFKE; AQCFFCFKEL;
QCFFCFKELE; CFFCFKELEG; FFCFKELEGW; FCFKELEGWE; CFKELEGWEP;
FKELEGWEPD; KELEGWEPDD; ELEGWEPDDD; LEGWEPDDDP; EGWEPDDDPI;
GWEPDDDPIE; WEPDDDPIEE; EPDDDPIEEH; PDDDPIEEHK; DDDPIEEHKK;
DDPIEEHKKH; DPIEEHKKHS; PIEEHKKHSS; IEEHKKHSSG; EEHKKHSSGC;
EHKKHSSGCA; HKKHSSGCAF; KKHSSGCAFL; KHSSGCAFLS; HSSGCAFLSV;
SSGCAFLSVK; SGCAFLSVKK; GCAFLSVKKQ; CAFLSVKKQF; AFLSVKKQFE;
FLSVKKQFEE; LSVKKQFEEL; SVKKQFEELT; VKKQFEELTL; KKQFEELTLG;
KQFEELTLGE; QFEELTLGEF; FEELTLGEFL; EELTLGEFLK; ELTLGEFLKL;
LTLGEFLKLD; TLGEFLKLDR; LGEFLKLDRE; GEFLKLDRER; EFLKLDRERA;
FLKLDRERAK; LKLDRERAKN; KLDRERAKNK; LDRERAKNKI; DRERAKNKIA;
RERAKNKIAK; ERAKNKIAKE; RAKNKIAKET; AKNKIAKETN; KNKIAKETNN;
NKIAKETNNK; KIAKETNNKK; IAKETNNKKK; AKETNNKKKE; KETNNKKKEF;
ETNNKKKEFE; TNNKKKEFEE; NNKKKEFEET; NKKKEFEETA; KKKEFEETAK;
KKEFEETAKK; KEFEETAKKV; EFEETAKKVR; FEETAKKVRR; EETAKKVRRA;
ETAKKVRRAI; TAKKVRRAIE; AKKVRRAIEQ; KKVRRAIEQL; KVRRAIEQLA;
VRRAIEQLAA; RRAIEQLAAM; RAIEQLAAMD;

11 mers:
MGAPTLPPAWQ; GAPTLPPAWQP; APTLPPAWQPF; PTLPPAWQPFL; TLPPAWQPFLK;
LPPAWQPFLKD; PPAWQPFLKDH; PAWQPFLKDHR; AWQPFLKDHRI; WQPFLKDHRIS;
QPFLKDHRIST; PFLKDHRISTF; FLKDHRISTFK; LKDHRISTFKN; KDHRISTFKNW;
DHRISTFKNWP; HRISTFKNWPF; RISTFKNWPFL; ISTFKNWPFLE; STFKNWPFLEG;
TFKNWPFLEGC; FKNWPFLEGCA; KNWPFLEGCAC; NWPFLEGCACT; WPFLEGCACTP;
PFLEGCACTPE; FLEGCACTPER; LEGCACTPERM; EGCACTPERMA; GCACTPERMAE;
CACTPERMAEA; ACTPERMAEAG; CTPERMAEAGF; TPERMAEAGFI; PERMAEAGFIH;
ERMAEAGFIHC; RMAEAGFIHCP; MAEAGFIHCPT; AEAGFIHCPTE; EAGFIHCPTEN;
AGFIHCPTENE; GFIHCPTENEP; FIHCPTENEPD; IHCPTENEPDL; HCPTENEPDLA;
CPTENEPDLAQ; PTENEPDLAQC; TENEPDLAQCF; ENEPDLAQCFF; NEPDLAQCFFC;
EPDLAQCFFCF; PDLAQCFFCFK; DLAQCFFCFKE; LAQCFFCFKEL; AQCFFCFKELE;
QCFFCFKELEG; CFFCFKELEGW; FFCFKELEGWE; FCFKELEGWEP; CFKELEGWEPD;
FKELEGWEPDD; KELEGWEPDDD; ELEGWEPDDDP; LEGWEPDDDPI; EGWEPDDDPIE;
GWEPDDDPIEE; WEPDDDPIEEH; EPDDDPIEEHK; PDDDPIEEHKK; DDDPIEEHKKH;
DDPIEEHKKHS; DPIEEHKKHSS; PIEEHKKHSSG; IEEHKKHSSGC; EEHKKHSSGCA;
EHKKHSSGCAF; HKKHSSGCAFL; KKHSSGCAFLS; KHSSGCAFLSV; HSSGCAFLSVK;
SSGCAFLSVKK; SGCAFLSVKKQ; GCAFLSVKKQF; CAFLSVKKQFE; AFLSVKKQFEE;
FLSVKKQFEEL; LSVKKQFEELT; SVKKQFEELTL; VKKQFEELTLG; KKQFEELTLGE;
KQFEELTLGEF; QFEELTLGEFL; FEELTLGEFLK; EELTLGEFLKL; ELTLGEFLKLD;
LTLGEFLKLDR; TLGEFLKLDRE; LGEFLKLDRER; GEFLKLDRERA; EFLKLDRERAK;
FLKLDRERAKN; LKLDRERAKNK; KLDRERAKNKI; LDRERAKNKIA; DRERAKNKIAK;
RERAKNKIAKE; ERAKNKIAKET; RAKNKIAKETN; AKNKIAKETNN; KNKIAKETNNK;
NKIAKETNNKK; KIAKETNNKKK; IAKETNNKKKE; AKETNNKKKEF; KETNNKKKEFE;
ETNNKKKEFEE; TNNKKKEFEET; NNKKKEFEETA; NKKKEFEETAK; KKKEFEETAKK;
KKEFEETAKKV; KEFEETAKKVR; EFEETAKKVRR; FEETAKKVRRA; EETAKKVRRAI;
ETAKKVRRAIE; TAKKVRRAIEQ; AKKVRRAIEQL; KKVRRAIEQLA; KVRRAIEQLAA;
VRRAIEQLAAM; RRAIEQLAAMD

Preferred fragments of Mcl-1 capable of interacting with one or more MHC class 2 molecules are listed in table G.

Table G: Prediction of cancer antigen Mcl-1 specific MHC class 2 peptide sequences. Prediction of 13-, 14-, 15-, 16-mers using the program displayed in figure 2.

13 mers:

MFGLKRNAVIGLN; FGLKRNAVIGLNL; GLKRNAVIGLNLY; LKRNAVIGLNLYC;
KRNAVIGLNLYCG; RNAVIGLNLYCGG; NAVIGLNLYCGGA; AVIGLNLYCGGAG;
VIGLNLYCGGAGL; IGLNLYCGGAGLG; GLNLYCGGAGLGA; LNLYCGGAGLGAG;
NLYCGGAGLGAGS; LYCGGAGLGAGSG; YCGGAGLGAGSGG; CGGAGLGAGSGGA;
GGAGLGAGSGGAT; GAGLGAGSGGATR; AGLGAGSGGATRP; GLGAGSGGATRPG;
LGAGSGGATRPGG; GAGSGGATRPGGR; AGSGGATRPGGRL; GSGGATRPGGRLL;
SGGATRPGGRLLA; GGATRPGGRLLAT; GATRPGGRLLATE; ATRPGGRLLATEK;
TRPGGRLLATEKE; RPGGRLLATEKEA; PGGRLLATEKEAS; GGRLLATEKEASA;
GRLLATEKEASAR; RLLATEKEASARR; LLATEKEASARRE; LATEKEASARREI;
ATEKEASARREIG; TEKEASARREIGG; EKEASARREIGGG; KEASARREIGGGE;
EASARREIGGGEA; ASARREIGGGEAG; SARREIGGGEAGA; ARREIGGGEAGAV;
RREIGGGEAGAVI; REIGGGEAGAVIG; EIGGGEAGAVIGG; IGGGEAGAVIGGS;
GGGEAGAVIGGSA; GGEAGAVIGGSAG; GEAGAVIGGSAGA; EAGAVIGGSAGAS;
AGAVIGGSAGASP; GAVIGGSAGASPP; AVIGGSAGASPPS; VIGGSAGASPPST;
IGGSAGASPPSTL; GGSAGASPPSTLT; GSAGASPPSTLTP; SAGASPPSTLTPD;
AGASPPSTLTPDS; GASPPSTLTPDSR; ASPPSTLTPDSRR; SPPSTLTPDSRRV;
PPSTLTPDSRRVA; PSTLTPDSRRVAR; STLTPDSRRVARP; TLTPDSRRVARPP;
LTPDSRRVARPPP; TPDSRRVARPPPI; PDSRRVARPPPIG; DSRRVARPPPIGA;
SRRVARPPPIGAE; RRVARPPPIGAEV; RVARPPPIGAEVP; VARPPPIGAEVPD;
ARPPPIGAEVPDV; RPPPIGAEVPDVT; PPPIGAEVPDVTA; PPIGAEVPDVTAT;
PIGAEVPDVTATP; IGAEVPDVTATPA; GAEVPDVTATPAR; AEVPDVTATPARL;
EVPDVTATPARLL; VPDVTATPARLLF; PDVTATPARLLFF; DVTATPARLLFFA;
VTATPARLLFFAP; TATPARLLFFAPT; ATPARLLFFAPTR; TPARLLFFAPTRR;
PARLLFFAPTRRA; ARLLFFAPTRRAA; RLLFFAPTRRAAP; LLFFAPTRRAAPL;
LFFAPTRRAAPLE; FFAPTRRAAPLEE; FAPTRRAAPLEEM; APTRRAAPLEEME;
PTRRAAPLEEMEA; TRRAAPLEEMEAP; RRAAPLEEMEAPA; RAAPLEEMEAPAA;
AAPLEEMEAPAAD; APLEEMEAPAADA; PLEEMEAPAADAI; LEEMEAPAADAIM;
EEMEAPAADAIMS; EMEAPAADAIMSP; MEAPAADAIMSPE; EAPAADAIMSPEE;
APAADAIMSPEEE; PAADAIMSPEEEL; AADAIMSPEEELD; ADAIMSPEEELDG;
DAIMSPEEELDGY; AIMSPEEELDGYE; IMSPEEELDGYEP; MSPEEELDGYEPE;
SPEEELDGYEPEP; PEEELDGYEPEPL; EEELDGYEPEPLG; EELDGYEPEPLGK;
ELDGYEPEPLGKR; LDGYEPEPLGKRP; DGYEPEPLGKRPA; GYEPEPLGKRPAV;
YEPEPLGKRPAVL; EPEPLGKRPAVLP; PEPLGKRPAVLPL; EPLGKRPAVLPLL;
PLGKRPAVLPLLE; LGKRPAVLPLLEL; GKRPAVLPLLELV; KRPAVLPLLELVG;
RPAVLPLLELVGE; PAVLPLLELVGES; AVLPLLELVGESG; VLPLLELVGESGN;
LPLLELVGESGNN; PLLELVGESGNNT; LLELVGESGNNTS; LELVGESGNNTST;
ELVGESGNNTSTD; LVGESGNNTSTDG; VGESGNNTSTDGS; GESGNNTSTDGSL;
ESGNNTSTDGSLP; SGNNTSTDGSLPS; GNNTSTDGSLPST; NNTSTDGSLPSTP;
NTSTDGSLPSTPP; TSTDGSLPSTPPP; STDGSLPSTPPPA; TDGSLPSTPPPAE;
DGSLPSTPPPAEE; GSLPSTPPPAEEE; SLPSTPPPAEEEE; LPSTPPPAEEEED;
PSTPPPAEEEEDD; STPPPAEEEEDDL; TPPPAEEEEDDLY; PPPAEEEEDDLYR;
PPAEEEEDDLYRQ; PAEEEEDDLYRQS; AEEEEDDLYRQSL; EEEEDDLYRQSLE;
EEEDDLYRQSLEI; EEDDLYRQSLEII; EDDLYRQSLEIIS; DDLYRQSLEIISR;
DLYRQSLEIISRY; LYRQSLEIISRYL; YRQSLEIISRYLR; RQSLEIISRYLRE;
QSLEIISRYLREQ; SLEIISRYLREQA; LEIISRYLREQAT; EIISRYLREQATG;
IISRYLREQATGA; ISRYLREQATGAK; SRYLREQATGAKD; RYLREQATGAKDT;
YLREQATGAKDTK; LREQATGAKDTKP; REQATGAKDTKPM; EQATGAKDTKPMG;
QATGAKDTKPMGR; ATGAKDTKPMGRS; TGAKDTKPMGRSG; GAKDTKPMGRSGA;
AKDTKPMGRSGAT; KDTKPMGRSGATS; DTKPMGRSGATSR; TKPMGRSGATSRK;

KPMGRSGATSRKA; PMGRSGATSRKAL; MGRSGATSRKALE; GRSGATSRKALET;
RSGATSRKALETL; SGATSRKALETLR; GATSRKALETLRR; ATSRKALETLRRV;
TSRKALETLRRVG; SRKALETLRRVGD; RKALETLRRVGDG; KALETLRRVGDGV;
ALETLRRVGDGVQ; LETLRRVGDGVQR; ETLRRVGDGVQRN; TLRRVGDGVQRNH;
LRRVGDGVQRNHE; RRVGDGVQRNHET; RVGDGVQRNHETA; VGDGVQRNHETAF;
GDGVQRNHETAFQ; DGVQRNHETAFQG; GVQRNHETAFQGM; VQRNHETAFQGML;
QRNHETAFQGMLR; RNHETAFQGMLRK; NHETAFQGMLRKL; HETAFQGMLRKLD;
ETAFQGMLRKLDI; TAFQGMLRKLDIK; AFQGMLRKLDIKN; FQGMLRKLDIKNE;
QGMLRKLDIKNED; GMLRKLDIKNEDD; MLRKLDIKNEDDV; LRKLDIKNEDDVK;
RKLDIKNEDDVKS; KLDIKNEDDVKSL; LDIKNEDDVKSLS; DIKNEDDVKSLSR;
IKNEDDVKSLSRV; KNEDDVKSLSRVM; NEDDVKSLSRVMI; EDDVKSLSRVMIH;
DDVKSLSRVMIHV; DVKSLSRVMIHVF; VKSLSRVMIHVFS; KSLSRVMIHVFSD;
SLSRVMIHVFSDG; LSRVMIHVFSDGV; SRVMIHVFSDGVT; RVMIHVFSDGVTN;
VMIHVFSDGVTNW; MIHVFSDGVTNWG; IHVFSDGVTNWGR; HVFSDGVTNWGRI;
VFSDGVTNWGRIV; FSDGVTNWGRIVT; SDGVTNWGRIVTL; DGVTNWGRIVTLI;
GVTNWGRIVTLIS; VTNWGRIVTLISF; TNWGRIVTLISFG; NWGRIVTLISFGA;
WGRIVTLISFGAF; GRIVTLISFGAFV; RIVTLISFGAFVA; IVTLISFGAFVAK;
VTLISFGAFVAKH; TLISFGAFVAKHL; LISFGAFVAKHLK; ISFGAFVAKHLKT;
SFGAFVAKHLKTI; FGAFVAKHLKTIN; GAFVAKHLKTINQ; AFVAKHLKTINQE;
FVAKHLKTINQES; VAKHLKTINQESC; AKHLKTINQESCI; KHLKTINQESCIE;
HLKTINQESCIEP; LKTINQESCIEPL; KTINQESCIEPLA; TINQESCIEPLAE;
INQESCIEPLAES; NQESCIEPLAESI; QESCIEPLAESIT; ESCIEPLAESITD;
SCIEPLAESITDV; CIEPLAESITDVL; IEPLAESITDVLV; EPLAESITDVLVR;
PLAESITDVLVRT; LAESITDVLVRTK; AESITDVLVRTKR; ESITDVLVRTKRD;
SITDVLVRTKRDW; ITDVLVRTKRDWL; TDVLVRTKRDWLV; DVLVRTKRDWLVK;
VLVRTKRDWLVKQ; LVRTKRDWLVKQR; VRTKRDWLVKQRG; RTKRDWLVKQRGW;
TKRDWLVKQRGWD; KRDWLVKQRGWDG; RDWLVKQRGWDGF; DWLVKQRGWDGFV;
WLVKQRGWDGFVE; LVKQRGWDGFVEF; VKQRGWDGFVEFF; KQRGWDGFVEFFH;
QRGWDGFVEFFHV; RGWDGFVEFFHVE; GWDGFVEFFHVED; WDGFVEFFHVEDL;
DGFVEFFHVEDLE; GFVEFFHVEDLEG; FVEFFHVEDLEGG; VEFFHVEDLEGGI;
EFFHVEDLEGGIR; FFHVEDLEGGIRN; FHVEDLEGGIRNV; HVEDLEGGIRNVL;
VEDLEGGIRNVLL; EDLEGGIRNVLLA; DLEGGIRNVLLAF; LEGGIRNVLLAFA;
EGGIRNVLLAFAG; GGIRNVLLAFAGV; GIRNVLLAFAGVA; IRNVLLAFAGVAG;
RNVLLAFAGVAGV; NVLLAFAGVAGVG; VLLAFAGVAGVGA; LLAFAGVAGVGAG;
LAFAGVAGVGAGL; AFAGVAGVGAGLA; FAGVAGVGAGLAY; AGVAGVGAGLAYL;
GVAGVGAGLAYLI; VAGVGAGLAYLIR

14 mers:
MFGLKRNAVIGLNL; FGLKRNAVIGLNLY; GLKRNAVIGLNLYC; LKRNAVIGLNLYCG;
KRNAVIGLNLYCGG; RNAVIGLNLYCGGA; NAVIGLNLYCGGAG; AVIGLNLYCGGAGL;
VIGLNLYCGGAGLG; IGLNLYCGGAGLGA; GLNLYCGGAGLGAG; LNLYCGGAGLGAGS;
NLYCGGAGLGAGSG; LYCGGAGLGAGSGG; YCGGAGLGAGSGGA; CGGAGLGAGSGGAT;
GGAGLGAGSGGATR; GAGLGAGSGGATRP; AGLGAGSGGATRPG; GLGAGSGGATRPGG;
LGAGSGGATRPGGR; GAGSGGATRPGGRL; AGSGGATRPGGRLL; GSGGATRPGGRLLA;
SGGATRPGGRLLAT; GGATRPGGRLLATE; GATRPGGRLLATEK; ATRPGGRLLATEKE;
TRPGGRLLATEKEA; RPGGRLLATEKEAS; PGGRLLATEKEASA; GGRLLATEKEASAR;
GRLLATEKEASARR; RLLATEKEASARRE; LLATEKEASARREI; LATEKEASARREIG;
ATEKEASARREIGG; TEKEASARREIGGG; EKEASARREIGGGE; KEASARREIGGGEA;
EASARREIGGGEAG; ASARREIGGGEAGA; SARREIGGGEAGAV; ARREIGGGEAGAVI;
RREIGGGEAGAVIG; REIGGGEAGAVIGG; EIGGGEAGAVIGGS; IGGGEAGAVIGGSA;
GGGEAGAVIGGSAG; GGEAGAVIGGSAGA; GEAGAVIGGSAGAS; EAGAVIGGSAGASP;
AGAVIGGSAGASPP; GAVIGGSAGASPPS; AVIGGSAGASPPST; VIGGSAGASPPSTL;
IGGSAGASPPSTLT; GGSAGASPPSTLTP; GSAGASPPSTLTPD; SAGASPPSTLTPDS;
AGASPPSTLTPDSR; GASPPSTLTPDSRR; ASPPSTLTPDSRRV; SPPSTLTPDSRRVA;
PPSTLTPDSRRVAR; PSTLTPDSRRVARP; STLTPDSRRVARPP; TLTPDSRRVARPPP;
LTPDSRRVARPPPI; TPDSRRVARPPPIG; PDSRRVARPPPIGA; DSRRVARPPPIGAE;
SRRVARPPPIGAEV; RRVARPPPIGAEVP; RVARPPPIGAEVPD; VARPPPIGAEVPDV;
ARPPPIGAEVPDVT; RPPPIGAEVPDVTA; PPPIGAEVPDVTAT; PPIGAEVPDVTATP;
PIGAEVPDVTATPA; IGAEVPDVTATPAR; GAEVPDVTATPARL; AEVPDVTATPARLL;
EVPDVTATPARLLF; VPDVTATPARLLFF; PDVTATPARLLFFA; DVTATPARLLFFAP;

VTATPARLLFFAPT; TATPARLLFFAPTR; ATPARLLFFAPTRR; TPARLLFFAPTRRA;
PARLLFFAPTRRAA; ARLLFFAPTRRAAP; RLLFFAPTRRAAPL; LLFFAPTRRAAPLE;
LFFAPTRRAAPLEE; FFAPTRRAAPLEEM; FAPTRRAAPLEEME; APTRRAAPLEEMEA;
PTRRAAPLEEMEAP; TRRAAPLEEMEAPA; RRAAPLEEMEAPAA; RAAPLEEMEAPAAD;
AAPLEEMEAPAADA; APLEEMEAPAADAI; PLEEMEAPAADAIM; LEEMEAPAADAIMS;
EEMEAPAADAIMSP; EMEAPAADAIMSPE; MEAPAADAIMSPEE; EAPAADAIMSPEEE;
APAADAIMSPEEEL; PAADAIMSPEEELD; AADAIMSPEEELDG; ADAIMSPEEELDGY;
DAIMSPEEELDGYE; AIMSPEEELDGYEP; IMSPEEELDGYEPE; MSPEEELDGYEPEP;
SPEEELDGYEPEPL; PEEELDGYEPEPLG; EEELDGYEPEPLGK; EELDGYEPEPLGKR;
ELDGYEPEPLGKRP; LDGYEPEPLGKRPA; DGYEPEPLGKRPAV; GYEPEPLGKRPAVL;
YEPEPLGKRPAVLP; EPEPLGKRPAVLPL; PEPLGKRPAVLPLL; EPLGKRPAVLPLLE;
PLGKRPAVLPLLEL; LGKRPAVLPLLELV; GKRPAVLPLLELVG; KRPAVLPLLELVGE;
RPAVLPLLELVGES; PAVLPLLELVGESG; AVLPLLELVGESGN; VLPLLELVGESGNN;
LPLLELVGESGNNT; PLLELVGESGNNTS; LLELVGESGNNTST; LELVGESGNNTSTD;
ELVGESGNNTSTDG; LVGESGNNTSTDGS; VGESGNNTSTDGSL; GESGNNTSTDGSLP;
ESGNNTSTDGSLPS; SGNNTSTDGSLPST; GNNTSTDGSLPSTP; NNTSTDGSLPSTPP;
NTSTDGSLPSTPPP; TSTDGSLPSTPPPA; STDGSLPSTPPPAE; TDGSLPSTPPPAEE;
DGSLPSTPPPAEEE; GSLPSTPPPAEEEE; SLPSTPPPAEEEED; LPSTPPPAEEEEDD;
PSTPPPAEEEEDDL; STPPPAEEEEDDLY; TPPPAEEEEDDLYR; PPPAEEEEDDLYRQ;
PPAEEEEDDLYRQS; PAEEEEDDLYRQSL; AEEEEDDLYRQSLE; EEEEDDLYRQSLEI;
EEEDDLYRQSLEII; EEDDLYRQSLEIIS; EDDLYRQSLEIISR; DDLYRQSLEIISRY;
DLYRQSLEIISRYL; LYRQSLEIISRYLR; YRQSLEIISRYLRE; RQSLEIISRYLREQ;
QSLEIISRYLREQA; SLEIISRYLREQAT; LEIISRYLREQATG; EIISRYLREQATGA;
IISRYLREQATGAK; ISRYLREQATGAKD; SRYLREQATGAKDT; RYLREQATGAKDTK;
YLREQATGAKDTKP; LREQATGAKDTKPM; REQATGAKDTKPMG; EQATGAKDTKPMGR;
QATGAKDTKPMGRS; ATGAKDTKPMGRSG; TGAKDTKPMGRSGA; GAKDTKPMGRSGAT;
AKDTKPMGRSGATS; KDTKPMGRSGATSR; DTKPMGRSGATSRK; TKPMGRSGATSRKA;
KPMGRSGATSRKAL; PMGRSGATSRKALE; MGRSGATSRKALET; GRSGATSRKALETL;
RSGATSRKALETLR; SGATSRKALETLRR; GATSRKALETLRRV; ATSRKALETLRRVG;
TSRKALETLRRVGD; SRKALETLRRVGDG; RKALETLRRVGDGV; KALETLRRVGDGVQ;
ALETLRRVGDGVQR; LETLRRVGDGVQRN; ETLRRVGDGVQRNH; TLRRVGDGVQRNHE;
LRRVGDGVQRNHET; RRVGDGVQRNHETA; RVGDGVQRNHETAF; VGDGVQRNHETAFQ;
GDGVQRNHETAFQG; DGVQRNHETAFQGM; GVQRNHETAFQGML; VQRNHETAFQGMLR;
QRNHETAFQGMLRK; RNHETAFQGMLRKL; NHETAFQGMLRKLD; HETAFQGMLRKLDI;
ETAFQGMLRKLDIK; TAFQGMLRKLDIKN; AFQGMLRKLDIKNE; FQGMLRKLDIKNED;
QGMLRKLDIKNEDD; GMLRKLDIKNEDDV; MLRKLDIKNEDDVK; LRKLDIKNEDDVKS;
RKLDIKNEDDVKSL; KLDIKNEDDVKSLS; LDIKNEDDVKSLSR; DIKNEDDVKSLSRV;
IKNEDDVKSLSRVM; KNEDDVKSLSRVMI; NEDDVKSLSRVMIH; EDDVKSLSRVMIHV;
DDVKSLSRVMIHVF; DVKSLSRVMIHVFS; VKSLSRVMIHVFSD; KSLSRVMIHVFSDG;
SLSRVMIHVFSDGV; LSRVMIHVFSDGVT; SRVMIHVFSDGVTN; RVMIHVFSDGVTNW;
VMIHVFSDGVTNWG; MIHVFSDGVTNWGR; IHVFSDGVTNWGRI; HVFSDGVTNWGRIV;
VFSDGVTNWGRIVT; FSDGVTNWGRIVTL; SDGVTNWGRIVTLI; DGVTNWGRIVTLIS;
GVTNWGRIVTLISF; VTNWGRIVTLISFG; TNWGRIVTLISFGA; NWGRIVTLISFGAF;
WGRIVTLISFGAFV; GRIVTLISFGAFVA; RIVTLISFGAFVAK; IVTLISFGAFVAKH;
VTLISFGAFVAKHL; TLISFGAFVAKHLK; LISFGAFVAKHLKT; ISFGAFVAKHLKTI;
SFGAFVAKHLKTIN; FGAFVAKHLKTINQ; GAFVAKHLKTINQE; AFVAKHLKTINQES;
FVAKHLKTINQESC; VAKHLKTINQESCI; AKHLKTINQESCIE; KHLKTINQESCIEP;
HLKTINQESCIEPL; LKTINQESCIEPLA; KTINQESCIEPLAE; TINQESCIEPLAES;
INQESCIEPLAESI; NQESCIEPLAESIT; QESCIEPLAESITD; ESCIEPLAESITDV;
SCIEPLAESITDVL; CIEPLAESITDVLV; IEPLAESITDVLVR; EPLAESITDVLVRT;
PLAESITDVLVRTK; LAESITDVLVRTKR; AESITDVLVRTKRD; ESITDVLVRTKRDW;
SITDVLVRTKRDWL; ITDVLVRTKRDWLV; TDVLVRTKRDWLVK; DVLVRTKRDWLVKQ;
VLVRTKRDWLVKQR; LVRTKRDWLVKQRG; VRTKRDWLVKQRGW; RTKRDWLVKQRGWD;
TKRDWLVKQRGWDG; KRDWLVKQRGWDGF; RDWLVKQRGWDGFV; DWLVKQRGWDGFVE;
WLVKQRGWDGFVEF; LVKQRGWDGFVEFF; VKQRGWDGFVEFFH; KQRGWDGFVEFFHV;
QRGWDGFVEFFHVE; RGWDGFVEFFHVED; GWDGFVEFFHVEDL; WDGFVEFFHVEDLE;
DGFVEFFHVEDLEG; GFVEFFHVEDLEGG; FVEFFHVEDLEGGI; VEFFHVEDLEGGIR;
EFFHVEDLEGGIRN; FFHVEDLEGGIRNV; FHVEDLEGGIRNVL; HVEDLEGGIRNVLL;
VEDLEGGIRNVLLA; EDLEGGIRNVLLAF; DLEGGIRNVLLAFA; LEGGIRNVLLAFAG;

EGGIRNVLLAFAGV; GGIRNVLLAFAGVA; GIRNVLLAFAGVAG; IRNVLLAFAGVAGV; RNVLLAFAGVAGVG; NVLLAFAGVAGVGA; VLLAFAGVAGVGAG; LLAFAGVAGVGAGL; LAFAGVAGVGAGLA; AFAGVAGVGAGLAY; FAGVAGVGAGLAYL; AGVAGVGAGLAYLI; GVAGVGAGLAYLIR

15 mers:

MFGLKRNAVIGLNLY; FGLKRNAVIGLNLYC; GLKRNAVIGLNLYCG;
LKRNAVIGLNLYCGG; KRNAVIGLNLYCGGA; RNAVIGLNLYCGGAG;
NAVIGLNLYCGGAGL; AVIGLNLYCGGAGLG; VIGLNLYCGGAGLGA;
IGLNLYCGGAGLGAG; GLNLYCGGAGLGAGS; LNLYCGGAGLGAGSG;
NLYCGGAGLGAGSGG; LYCGGAGLGAGSGGA; YCGGAGLGAGSGGAT;
CGGAGLGAGSGGATR; GGAGLGAGSGGATRP; GAGLGAGSGGATRPG;
AGLGAGSGGATRPGG; GLGAGSGGATRPGGR; LGAGSGGATRPGGRL;
GAGSGGATRPGGRLL; AGSGGATRPGGRLLA; GSGGATRPGGRLLAT;
SGGATRPGGRLLATE; GGATRPGGRLLATEK; GATRPGGRLLATEKE;
ATRPGGRLLATEKEA; TRPGGRLLATEKEAS; RPGGRLLATEKEASA;
PGGRLLATEKEASAR; GGRLLATEKEASARR; GRLLATEKEASARRE;
RLLATEKEASARREI; LLATEKEASARREIG; LATEKEASARREIGG;
ATEKEASARREIGGG; TEKEASARREIGGGE; EKEASARREIGGGEA;
KEASARREIGGGEAG; EASARREIGGGEAGA; ASARREIGGGEAGAV;
SARREIGGGEAGAVI; ARREIGGGEAGAVIG; RREIGGGEAGAVIGG;
REIGGGEAGAVIGGS; EIGGGEAGAVIGGSA; IGGGEAGAVIGGSAG;
GGGEAGAVIGGSAGA; GGEAGAVIGGSAGAS; GEAGAVIGGSAGASP;
EAGAVIGGSAGASPP; AGAVIGGSAGASPPS; GAVIGGSAGASPPST;
AVIGGSAGASPPSTL; VIGGSAGASPPSTLT; IGGSAGASPPSTLTP;
GGSAGASPPSTLTPD; GSAGASPPSTLTPDS; SAGASPPSTLTPDSR;
AGASPPSTLTPDSRR; GASPPSTLTPDSRRV; ASPPSTLTPDSRRVA;
SPPSTLTPDSRRVAR; PPSTLTPDSRRVARP; PSTLTPDSRRVARPP;
STLTPDSRRVARPPP; TLTPDSRRVARPPPI; LTPDSRRVARPPPIG;
TPDSRRVARPPPIGA; PDSRRVARPPPIGAE; DSRRVARPPPIGAEV;
SRRVARPPPIGAEVP; RRVARPPPIGAEVPD; RVARPPPIGAEVPDV;
VARPPPIGAEVPDVT; ARPPPIGAEVPDVTA; RPPPIGAEVPDVTAT;
PPPIGAEVPDVTATP; PPIGAEVPDVTATPA; PIGAEVPDVTATPAR;
IGAEVPDVTATPARL; GAEVPDVTATPARLL; AEVPDVTATPARLLF;
EVPDVTATPARLLFF; VPDVTATPARLLFFA; PDVTATPARLLFFAP;
DVTATPARLLFFAPT; VTATPARLLFFAPTR; TATPARLLFFAPTRR;
ATPARLLFFAPTRRA; TPARLLFFAPTRRAA; PARLLFFAPTRRAAP;
ARLLFFAPTRRAAPL; RLLFFAPTRRAAPLE; LLFFAPTRRAAPLEE;
LFFAPTRRAAPLEEM; FFAPTRRAAPLEEME; FAPTRRAAPLEEMEA;
APTRRAAPLEEMEAP; PTRRAAPLEEMEAPA; TRRAAPLEEMEAPAA;
RRAAPLEEMEAPAAD; RAAPLEEMEAPAADA; AAPLEEMEAPAADAI;
APLEEMEAPAADAIM; PLEEMEAPAADAIMS; LEEMEAPAADAIMSP;
EEMEAPAADAIMSPE; EMEAPAADAIMSPEE; MEAPAADAIMSPEEE;
EAPAADAIMSPEEEL; APAADAIMSPEEELD; PAADAIMSPEEELDG;
AADAIMSPEEELDGY; ADAIMSPEEELDGYE; DAIMSPEEELDGYEP;
AIMSPEEELDGYEPE; IMSPEEELDGYEPEP; MSPEEELDGYEPEPL;
SPEEELDGYEPEPLG; PEEELDGYEPEPLGK; EEELDGYEPEPLGKR;
EELDGYEPEPLGKRP; ELDGYEPEPLGKRPA; LDGYEPEPLGKRPAV;
DGYEPEPLGKRPAVL; GYEPEPLGKRPAVLP; YEPEPLGKRPAVLPL;
EPEPLGKRPAVLPLL; PEPLGKRPAVLPLLE; EPLGKRPAVLPLLEL;
PLGKRPAVLPLLELV; LGKRPAVLPLLELVG; GKRPAVLPLLELVGE;
KRPAVLPLLELVGES; RPAVLPLLELVGESG; PAVLPLLELVGESGN;
AVLPLLELVGESGNN; VLPLLELVGESGNNT; LPLLELVGESGNNTS;
PLLELVGESGNNTST; LLELVGESGNNTSTD; LELVGESGNNTSTDG;
ELVGESGNNTSTDGS; LVGESGNNTSTDGSL; VGESGNNTSTDGSLP;
GESGNNTSTDGSLPS; ESGNNTSTDGSLPST; SGNNTSTDGSLPSTP;
GNNTSTDGSLPSTPP; NNTSTDGSLPSTPPP; NTSTDGSLPSTPPPA;
TSTDGSLPSTPPPAE; STDGSLPSTPPPAEE; TDGSLPSTPPPAEEE;
DGSLPSTPPPAEEEE; GSLPSTPPPAEEEED; SLPSTPPPAEEEEDD;
LPSTPPPAEEEEDDL; PSTPPPAEEEEDDLY; STPPPAEEEEDDLYR;

TPPPAEEEEDDLYRQ;	PPPAEEEEDDLYRQS;	PPAEEEEDDLYRQSL;
PAEEEEDDLYRQSLE;	AEEEEDDLYRQSLEI;	EEEEDDLYRQSLEII;
EEEDDLYRQSLEIIS;	EEDDLYRQSLEIISR;	EDDLYRQSLEIISRY;
DDLYRQSLEIISRYL;	DLYRQSLEIISRYLR;	LYRQSLEIISRYLRE;
YRQSLEIISRYLREQ;	RQSLEIISRYLREQA;	QSLEIISRYLREQAT;
SLEIISRYLREQATG;	LEIISRYLREQATGA;	EIISRYLREQATGAK;
IISRYLREQATGAKD;	ISRYLREQATGAKDT;	SRYLREQATGAKDTK;
RYLREQATGAKDTKP;	YLREQATGAKDTKPM;	LREQATGAKDTKPMG;
REQATGAKDTKPMGR;	EQATGAKDTKPMGRS;	QATGAKDTKPMGRSG;
ATGAKDTKPMGRSGA;	TGAKDTKPMGRSGAT;	GAKDTKPMGRSGATS;
AKDTKPMGRSGATSR;	KDTKPMGRSGATSRK;	DTKPMGRSGATSRKA;
TKPMGRSGATSRKAL;	KPMGRSGATSRKALE;	PMGRSGATSRKALET;
MGRSGATSRKALETL;	GRSGATSRKALETLR;	RSGATSRKALETLRR;
SGATSRKALETLRRV;	GATSRKALETLRRVG;	ATSRKALETLRRVGD;
TSRKALETLRRVGDG;	SRKALETLRRVGDGV;	RKALETLRRVGDGVQ;
KALETLRRVGDGVQR;	ALETLRRVGDGVQRN;	LETLRRVGDGVQRNH;
ETLRRVGDGVQRNHE;	TLRRVGDGVQRNHET;	LRRVGDGVQRNHETA;
RRVGDGVQRNHETAF;	RVGDGVQRNHETAFQ;	VGDGVQRNHETAFQG;
GDGVQRNHETAFQGM;	DGVQRNHETAFQGML;	GVQRNHETAFQGMLR;
VQRNHETAFQGMLRK;	QRNHETAFQGMLRKL;	RNHETAFQGMLRKLD;
NHETAFQGMLRKLDI;	HETAFQGMLRKLDIK;	ETAFQGMLRKLDIKN;
TAFQGMLRKLDIKNE;	AFQGMLRKLDIKNED;	FQGMLRKLDIKNEDD;
QGMLRKLDIKNEDDV;	GMLRKLDIKNEDDVK;	MLRKLDIKNEDDVKS;
LRKLDIKNEDDVKSL;	RKLDIKNEDDVKSLS;	KLDIKNEDDVKSLSR;
LDIKNEDDVKSLSRV;	DIKNEDDVKSLSRVM;	IKNEDDVKSLSRVMI;
KNEDDVKSLSRVMIH;	NEDDVKSLSRVMIHV;	EDDVKSLSRVMIHVF;
DDVKSLSRVMIHVFS;	DVKSLSRVMIHVFSD;	VKSLSRVMIHVFSDG;
KSLSRVMIHVFSDGV;	SLSRVMIHVFSDGVT;	LSRVMIHVFSDGVTN;
SRVMIHVFSDGVTNW;	RVMIHVFSDGVTNWG;	VMIHVFSDGVTNWGR;
MIHVFSDGVTNWGRI;	IHVFSDGVTNWGRIV;	HVFSDGVTNWGRIVT;
VFSDGVTNWGRIVTL;	FSDGVTNWGRIVTLI;	SDGVTNWGRIVTLIS;
DGVTNWGRIVTLISF;	GVTNWGRIVTLISFG;	VTNWGRIVTLISFGA;
TNWGRIVTLISFGAF;	NWGRIVTLISFGAFV;	WGRIVTLISFGAFVA;
GRIVTLISFGAFVAK;	RIVTLISFGAFVAKH;	IVTLISFGAFVAKHL;
VTLISFGAFVAKHLK;	TLISFGAFVAKHLKT;	LISFGAFVAKHLKTI;
ISFGAFVAKHLKTIN;	SFGAFVAKHLKTINQ;	FGAFVAKHLKTINQE;
GAFVAKHLKTINQES;	AFVAKHLKTINQESC;	FVAKHLKTINQESCI;
VAKHLKTINQESCIE;	AKHLKTINQESCIEP;	KHLKTINQESCIEPL;
HLKTINQESCIEPLA;	LKTINQESCIEPLAE;	KTINQESCIEPLAES;
TINQESCIEPLAESI;	INQESCIEPLAESIT;	NQESCIEPLAESITD;
QESCIEPLAESITDV;	ESCIEPLAESITDVL;	SCIEPLAESITDVLV;
CIEPLAESITDVLVR;	IEPLAESITDVLVRT;	EPLAESITDVLVRTK;
PLAESITDVLVRTKR;	LAESITDVLVRTKRD;	AESITDVLVRTKRDW;
ESITDVLVRTKRDWL;	SITDVLVRTKRDWLV;	ITDVLVRTKRDWLVK;
TDVLVRTKRDWLVKQ;	DVLVRTKRDWLVKQR;	VLVRTKRDWLVKQRG;
LVRTKRDWLVKQRGW;	VRTKRDWLVKQRGWD;	RTKRDWLVKQRGWDG;
TKRDWLVKQRGWDGF;	KRDWLVKQRGWDGFV;	RDWLVKQRGWDGFVE;
DWLVKQRGWDGFVEF;	WLVKQRGWDGFVEFF;	LVKQRGWDGFVEFFH;
VKQRGWDGFVEFFHV;	KQRGWDGFVEFFHVE;	QRGWDGFVEFFHVED;
RGWDGFVEFFHVEDL;	GWDGFVEFFHVEDLE;	WDGFVEFFHVEDLEG;
DGFVEFFHVEDLEGG;	GFVEFFHVEDLEGGI;	FVEFFHVEDLEGGIR;
VEFFHVEDLEGGIRN;	EFFHVEDLEGGIRNV;	FFHVEDLEGGIRNVL;
FHVEDLEGGIRNVLL;	HVEDLEGGIRNVLLA;	VEDLEGGIRNVLLAF;
EDLEGGIRNVLLAFA;	DLEGGIRNVLLAFAG;	LEGGIRNVLLAFAGV;
EGGIRNVLLAFAGVA;	GGIRNVLLAFAGVAG;	GIRNVLLAFAGVAGV;
IRNVLLAFAGVAGVG;	RNVLLAFAGVAGVGA;	NVLLAFAGVAGVGAG;
VLLAFAGVAGVGAGL;	LLAFAGVAGVGAGLA;	LAFAGVAGVGAGLAY;
AFAGVAGVGAGLAYL;	FAGVAGVGAGLAYLI;	AGVAGVGAGLAYLIR
16 mers:		

MFGLKRNAVIGLNLYC; FGLKRNAVIGLNLYCG; GLKRNAVIGLNLYCGG;
LKRNAVIGLNLYCGGA; KRNAVIGLNLYCGGAG; RNAVIGLNLYCGGAGL;
NAVIGLNLYCGGAGLG; AVIGLNLYCGGAGLGA; VIGLNLYCGGAGLGAG;
IGLNLYCGGAGLGAGS; GLNLYCGGAGLGAGSG; LNLYCGGAGLGAGSGG;
NLYCGGAGLGAGSGGA; LYCGGAGLGAGSGGAT; YCGGAGLGAGSGGATR;
CGGAGLGAGSGGATRP; GGAGLGAGSGGATRPG; GAGLGAGSGGATRPGG;
AGLGAGSGGATRPGGR; GLGAGSGGATRPGGRL; LGAGSGGATRPGGRLL;
GAGSGGATRPGGRLLA; AGSGGATRPGGRLLAT; GSGGATRPGGRLLATE;
SGGATRPGGRLLATEK; GGATRPGGRLLATEKE; GATRPGGRLLATEKEA;
ATRPGGRLLATEKEAS; TRPGGRLLATEKEASA; RPGGRLLATEKEASAR;
PGGRLLATEKEASARR; GGRLLATEKEASARRE; GRLLATEKEASARREI;
RLLATEKEASARREIG; LLATEKEASARREIGG; LATEKEASARREIGGG;
ATEKEASARREIGGGE; TEKEASARREIGGGEA; EKEASARREIGGGEAG;
KEASARREIGGGEAGA; EASARREIGGGEAGAV; ASARREIGGGEAGAVI;
SARREIGGGEAGAVIG; ARREIGGGEAGAVIGG; RREIGGGEAGAVIGGS;
REIGGGEAGAVIGGSA; EIGGGEAGAVIGGSAG; IGGGEAGAVIGGSAGA;
GGGEAGAVIGGSAGAS; GGEAGAVIGGSAGASP; GEAGAVIGGSAGASPP;
EAGAVIGGSAGASPPS; AGAVIGGSAGASPPST; GAVIGGSAGASPPSTL;
AVIGGSAGASPPSTLT; VIGGSAGASPPSTLTP; IGGSAGASPPSTLTPD;
GGSAGASPPSTLTPDS; GSAGASPPSTLTPDSR; SAGASPPSTLTPDSRR;
AGASPPSTLTPDSRRV; GASPPSTLTPDSRRVA; ASPPSTLTPDSRRVAR;
SPPSTLTPDSRRVARP; PPSTLTPDSRRVARPP; PSTLTPDSRRVARPPP;
STLTPDSRRVARPPPI; TLTPDSRRVARPPPIG; LTPDSRRVARPPPIGA;
TPDSRRVARPPPIGAE; PDSRRVARPPPIGAEV; DSRRVARPPPIGAEVP;
SRRVARPPPIGAEVPD; RRVARPPPIGAEVPDV; RVARPPPIGAEVPDVT;
VARPPPIGAEVPDVTA; ARPPPIGAEVPDVTAT; RPPPIGAEVPDVTATP;
PPPIGAEVPDVTATPA; PPIGAEVPDVTATPAR; PIGAEVPDVTATPARL;
IGAEVPDVTATPARLL; GAEVPDVTATPARLLF; AEVPDVTATPARLLFF;
EVPDVTATPARLLFFA; VPDVTATPARLLFFAP; PDVTATPARLLFFAPT;
DVTATPARLLFFAPTR; VTATPARLLFFAPTRR; TATPARLLFFAPTRRA;
ATPARLLFFAPTRRAA; TPARLLFFAPTRRAAP; PARLLFFAPTRRAAPL;
ARLLFFAPTRRAAPLE; RLLFFAPTRRAAPLEE; LLFFAPTRRAAPLEEM;
LFFAPTRRAAPLEEME; FFAPTRRAAPLEEMEA; FAPTRRAAPLEEMEAP;
APTRRAAPLEEMEAPA; PTRRAAPLEEMEAPAA; TRRAAPLEEMEAPAAD;
RRAAPLEEMEAPAADA; RAAPLEEMEAPAADAI; AAPLEEMEAPAADAIM;
APLEEMEAPAADAIMS; PLEEMEAPAADAIMSP; LEEMEAPAADAIMSPE;
EEMEAPAADAIMSPEE; EMEAPAADAIMSPEEE; MEAPAADAIMSPEEEL;
EAPAADAIMSPEEELD; APAADAIMSPEEELDG; PAADAIMSPEEELDGY;
AADAIMSPEEELDGYE; ADAIMSPEEELDGYEP; DAIMSPEEELDGYEPE;
AIMSPEEELDGYEPEP; IMSPEEELDGYEPEPL; MSPEEELDGYEPEPLG;
SPEEELDGYEPEPLGK; PEEELDGYEPEPLGKR; EEELDGYEPEPLGKRP;
EELDGYEPEPLGKRPA; ELDGYEPEPLGKRPAV; LDGYEPEPLGKRPAVL;
DGYEPEPLGKRPAVLP; GYEPEPLGKRPAVLPL; YEPEPLGKRPAVLPLL;
EPEPLGKRPAVLPLLE; PEPLGKRPAVLPLLEL; EPLGKRPAVLPLLELV;
PLGKRPAVLPLLELVG; LGKRPAVLPLLELVGE; GKRPAVLPLLELVGES;
KRPAVLPLLELVGESG; RPAVLPLLELVGESGN; PAVLPLLELVGESGNN;
AVLPLLELVGESGNNT; VLPLLELVGESGNNTS; LPLLELVGESGNNTST;
PLLELVGESGNNTSTD; LLELVGESGNNTSTDG; LELVGESGNNTSTDGS;
ELVGESGNNTSTDGSL; LVGESGNNTSTDGSLP; VGESGNNTSTDGSLPS;
GESGNNTSTDGSLPST; ESGNNTSTDGSLPSTP; SGNNTSTDGSLPSTPP;
GNNTSTDGSLPSTPPP; NNTSTDGSLPSTPPPA; NTSTDGSLPSTPPPAE;
TSTDGSLPSTPPPAEE; STDGSLPSTPPPAEEE; TDGSLPSTPPPAEEEE;
DGSLPSTPPPAEEEED; GSLPSTPPPAEEEEDD; SLPSTPPPAEEEEDDL;
LPSTPPPAEEEEDDLY; PSTPPPAEEEEDDLYR; STPPPAEEEEDDLYRQ;
TPPPAEEEEDDLYRQS; PPPAEEEEDDLYRQSL; PPAEEEEDDLYRQSLE;
PAEEEEDDLYRQSLEI; AEEEEDDLYRQSLEII; EEEEDDLYRQSLEIIS;
EEEDDLYRQSLEIISR; EEDDLYRQSLEIISRY; EDDLYRQSLEIISRYL;
DDLYRQSLEIISRYLR; DLYRQSLEIISRYLRE; LYRQSLEIISRYLREQ;
YRQSLEIISRYLREQA; RQSLEIISRYLREQAT; QSLEIISRYLREQATG;

SLEIISRYLREQATGA; LEIISRYLREQATGAK; EIISRYLREQATGAKD;
IISRYLREQATGAKDT; ISRYLREQATGAKDTK; SRYLREQATGAKDTKP;
RYLREQATGAKDTKPM; YLREQATGAKDTKPMG; LREQATGAKDTKPMGR;
REQATGAKDTKPMGRS; EQATGAKDTKPMGRSG; QATGAKDTKPMGRSGA;
ATGAKDTKPMGRSGAT; TGAKDTKPMGRSGATS; GAKDTKPMGRSGATSR;
AKDTKPMGRSGATSRK; KDTKPMGRSGATSRKA; DTKPMGRSGATSRKAL;
TKPMGRSGATSRKALE; KPMGRSGATSRKALET; PMGRSGATSRKALETL;
MGRSGATSRKALETLR; GRSGATSRKALETLRR; RSGATSRKALETLRRV;
SGATSRKALETLRRVG; GATSRKALETLRRVGD; ATSRKALETLRRVGDG;
TSRKALETLRRVGDGV; SRKALETLRRVGDGVQ; RKALETLRRVGDGVQR;
KALETLRRVGDGVQRN; ALETLRRVGDGVQRNH; LETLRRVGDGVQRNHE;
ETLRRVGDGVQRNHET; TLRRVGDGVQRNHETA; LRRVGDGVQRNHETAF;
RRVGDGVQRNHETAFQ; RVGDGVQRNHETAFQG; VGDGVQRNHETAFQGM;
GDGVQRNHETAFQGML; DGVQRNHETAFQGMLR; GVQRNHETAFQGMLRK;
VQRNHETAFQGMLRKL; QRNHETAFQGMLRKLD; RNHETAFQGMLRKLDI;
NHETAFQGMLRKLDIK; HETAFQGMLRKLDIKN; ETAFQGMLRKLDIKNE;
TAFQGMLRKLDIKNED; AFQGMLRKLDIKNEDD; FQGMLRKLDIKNEDDV;
QGMLRKLDIKNEDDVK; GMLRKLDIKNEDDVKS; MLRKLDIKNEDDVKSL;
LRKLDIKNEDDVKSLS; RKLDIKNEDDVKSLSR; KLDIKNEDDVKSLSRV;
LDIKNEDDVKSLSRVM; DIKNEDDVKSLSRVMI; IKNEDDVKSLSRVMIH;
KNEDDVKSLSRVMIHV; NEDDVKSLSRVMIHVF; EDDVKSLSRVMIHVFS;
DDVKSLSRVMIHVFSD; DVKSLSRVMIHVFSDG; VKSLSRVMIHVFSDGV;
KSLSRVMIHVFSDGVT; SLSRVMIHVFSDGVTN; LSRVMIHVFSDGVTNW;
SRVMIHVFSDGVTNWG; RVMIHVFSDGVTNWGR; VMIHVFSDGVTNWGRI;
MIHVFSDGVTNWGRIV; IHVFSDGVTNWGRIVT; HVFSDGVTNWGRIVTL;
VFSDGVTNWGRIVTLI; FSDGVTNWGRIVTLIS; SDGVTNWGRIVTLISF;
DGVTNWGRIVTLISFG; GVTNWGRIVTLISFGA; VTNWGRIVTLISFGAF;
TNWGRIVTLISFGAFV; NWGRIVTLISFGAFVA; WGRIVTLISFGAFVAK;
GRIVTLISFGAFVAKH; RIVTLISFGAFVAKHL; IVTLISFGAFVAKHLK;
VTLISFGAFVAKHLKT; TLISFGAFVAKHLKTI; LISFGAFVAKHLKTIN;
ISFGAFVAKHLKTINQ; SFGAFVAKHLKTINQE; FGAFVAKHLKTINQES;
GAFVAKHLKTINQESC; AFVAKHLKTINQESCI; FVAKHLKTINQESCIE;
VAKHLKTINQESCIEP; AKHLKTINQESCIEPL; KHLKTINQESCIEPLA;
HLKTINQESCIEPLAE; LKTINQESCIEPLAES; KTINQESCIEPLAESI;
TINQESCIEPLAESIT; INQESCIEPLAESITD; NQESCIEPLAESITDV;
QESCIEPLAESITDVL; ESCIEPLAESITDVLV; SCIEPLAESITDVLVR;
CIEPLAESITDVLVRT; IEPLAESITDVLVRTK; EPLAESITDVLVRTKR;
PLAESITDVLVRTKRD; LAESITDVLVRTKRDW; AESITDVLVRTKRDWL;
ESITDVLVRTKRDWLV; SITDVLVRTKRDWLVK; ITDVLVRTKRDWLVKQ;
TDVLVRTKRDWLVKQR; DVLVRTKRDWLVKQRG; VLVRTKRDWLVKQRGW;
LVRTKRDWLVKQRGWD; VRTKRDWLVKQRGWDG; RTKRDWLVKQRGWDGF;
TKRDWLVKQRGWDGFV; KRDWLVKQRGWDGFVE; RDWLVKQRGWDGFVEF;
DWLVKQRGWDGFVEFF; WLVKQRGWDGFVEFFH; LVKQRGWDGFVEFFHV;
VKQRGWDGFVEFFHVE; KQRGWDGFVEFFHVED; QRGWDGFVEFFHVEDL;
RGWDGFVEFFHVEDLE; GWDGFVEFFHVEDLEG; WDGFVEFFHVEDLEGG;
DGFVEFFHVEDLEGGI; GFVEFFHVEDLEGGIR; FVEFFHVEDLEGGIRN;
VEFFHVEDLEGGIRNV; EFFHVEDLEGGIRNVL; FFHVEDLEGGIRNVLL;
FHVEDLEGGIRNVLLA; HVEDLEGGIRNVLLAF; VEDLEGGIRNVLLAFA;
EDLEGGIRNVLLAFAG; DLEGGIRNVLLAFAGV; LEGGIRNVLLAFAGVA;
EGGIRNVLLAFAGVAG; GGIRNVLLAFAGVAGV; GIRNVLLAFAGVAGVG;
IRNVLLAFAGVAGVGA; RNVLLAFAGVAGVGAG; NVLLAFAGVAGVGAGL;
VLLAFAGVAGVGAGLA; LLAFAGVAGVGAGLAY; LAFAGVAGVGAGLAYL;
AFAGVAGVGAGLAYLI; FAGVAGVGAGLAYLIR

The one or more antigenic peptides can in one embodiment comprise a fragment of one or more BK virus antigens.

The one or more BK virus antigens can be selected from Table H.

Table H: Protein designation and accession numbers for the proteins encoded by the BK virus genome. The amino acid sequence of each protein is displayed.

BK virus protein accession data	Amino acid sequence
>gi|118752|sp|P14998|DNBI_POVBA DNA-binding protein (Agnoprotein)	MFCEPKNLVVLRQLSRQASVKVGKTWTGTKKRAQRIFIFILELLLEFCR GEDSVDGKNKSTTALPAVKDSVKDS
>gi|135313|sp|P15000|TASM_POVBA Small T antigen	MDKVLNREESMELMDLLGLERAAWGNLPLMRKAYLKKCKEFHPDKGGDE DKMKRMNTLYKKMEQDVKVAHQPDFGTWNSSEVCADFPLCPDTLYCKEW PICSKKPSVHCPCMLCQLRLRHLNRKFLRKEPLVWIDCYCIDCFTQWFG LDLTEETLQWWVQIIGETPFRDLKL
>gi|135279|sp|P14999|TALA_POVBA Large T antigen	MDKVLNREESMELMDLLGLERAAWGNLPLMRKAYLKKCKEFHPDKGGDE DKMKRMNTLYKKMEQDVKVAHQPDFGTWNSSEVPTYGTEEWESWWSSFN EKWDEDLFCHEDMFASDEEATADSQHSTPPKKKRKVEDPKDFPSDLHQF LSQAVFSNRTLACFAVYTTKEKAQILYKKLMEKYSVTFISRHMCAGHNI IFFLTPHRHRVSAINNFCQKLCTFSFLICKGVNKEYLLYSALTRDPYHI IEESIQGGLKEHDFNPEEPEETKQVSWKLITEYAVETKCEDVFLLLGMY LEFQYNVEECKKCQKKDQPYHFKYHEKHFANAIIFAESKNQKSICQQAV DTVLAKKRVDTLHMTREEMLTERFNHILDKMDLIFGAHGNAVLEQYMAG VAWLHCLLPKMDSVIFDFLHCVVFNVPKRRYWLFKGPIDSGKTTLAAGL LDLCGGKALNVNLPMERLTFELGVAIDQYMVVFEDVKGTGAESKDLPSG HGINNLDSLRDYLDGSVKVNLEKKHLNKRTQIFPPGLVTMNEYPVPKTL QARFVRQIDFRPKIYLRKSLQNSEFLLEKRILQSGMTLLLLLIWFRPVA DFSKDIQSRIVEWKERLDSEISMYTFSRMKYNICMGKCILDITREEDSE TEDSGHGSSTESQSQCSSQVSDTSAPDSENPHSQELHLCKGFQCFKRPK TPPPK
>gi|116622|sp|P14996|COA1_POVBA Coat protein VP1	MAPTKRKGECPGAAPKKPKEPVQVPKLLIKGGVEVLEVKTGVDAITEVE CFLNPEMGDPDDNLRGYSQHLSAENAFESDSPDRKMLPCYSTARIPLPN LNEDLTCGNLLMWEAVTVKTEVIGITSMLNLHAGSQKVHENGGGKPVQG SNFHFFAVGGDPLEMQGVLMNYRTKYPQGTITPKNPTAQSQVMNTDHKA YLDKNNAYPVECWIPDPSRNENTRYFGTYTGGENVPPVLHVTNTATTVL LDEQGVGPLCKADSLYVSAADICGLFTNSSGTQQWRGLARYFKIRLRKR SVKNPYPISFLLSDLINRRTQKVDGQPMYGMESQVEEVRVFDGTEQLPG DPDMIRYIDRQGQLQTKMV
>gi|116641|sp|P14997|COA2_POVBA Coat protein VP2/VP3	MGAALALLGDLVASVSEAAAATGFSVAEIAAGEAAAAIEVQIASLATVE GITTTSEAIAAIGLTPQTYAVIAGAPGAIAGFAALIQTVTGISSLAQVG YRFFSDWDHKVSTVGLYQQSGMALELFNPDEYYDILFPGVNTFVNNIQY LDPRHWGPSLFATISQALWHVIRDDIPAITSQELQRRTERFFRDSLARF LEETTWTIVNAPINFYNYIQDYYSNLSPIRPSMVRQVAEREGTHVNFGH TYSIDNADSIEEVTQRMDLRNKESVHSGEFIEKTIAPGGANQRTAPQWM LPLLLGLYGTVTPALEAYEDGPNQKKRRVSRGSSQKAKGTRASAKTTNK RRSRSSRS
	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIF SSQPGHTPHPAASRDPVARTS PLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQL

	HLTPFTARGRFATVVEELFRD GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI QDNGGWDAFVELYGPSMRPLF DFSWLSLKTLLSLALVGACITLGAYLGHK

Preferred BK virus fragments capable of interacting with one or more MHC class 1 molecules are listed in Table I.

Table I:

Predicted MHC class 1 BK virus peptide sequences. Prediction of 8-, 9-, 10-, 11-mers from all 6 reading frames of the genome (access no #V01108) obtained using the program displayed in figure 2.

BK virus reading frame 1

8 mers:

FCKNCKRI; CKNCKRIG; KNCKRIGI; NCKRIGIS; CKRIGISP; KRIGISPN; RIGISPNS;
IGISPNSF; GISPNSFA; ISPNSFAR; SPNSFARP; PNSFARPQ; NSFARPQK; SFARPQKK;
FARPQKKP; ARPQKKPP; RPQKKPPH; PQKKPPHP; QKKPPHPY; KKPPHPYY; KPPHPYYL;
PPHPYYLR; PHPYYLRE; HPYYLRER; PYYLRERV; YYLRERVE; YLRERVEA; LRERVEAE;
RERVEAEA; ERVEAEAA; RVEAEAAS; VEAEAASA; EAEAASAS; AEAASASY; EAASASYI;
AASASYIL; KKRPQGGA; KRPQGGAA; RPQGGAAY; PQGGAAYP; QGGAAYPW; GGAAYPWN;
GAAYPWNA; AAYPWNAA; AYPWNAAK; YPWNAAKP; PQEGKCMT; QEGKCMTH; EGKCMTHR;
GKCMTHRG; KCMTHRGM; CMTHRGMQ; MTHRGMQP; THRGMQPN; HRGMQPNH; RGMQPNHD;
GMQPNHDL; MQPNHDLR; QPNHDLRK; PNHDLRKE; NHDLRKES; HDLRKESA; LTGRSCLP;
TGRSCLPM; GRSCLPME; RSCLPMEC; SCLPMECS; CLPMECSQ; LPMECSQT; PMECSQTM;
MECSQTMT; ECSQTMTS; CSQTMTSG; SQTMTSGR; QTMTSGRK; TMTSGRKV; MTSGRKVH;
TSGRKVHD; SGRKVHDR; GRKVHDRH; RKVHDRHV; KVHDRHVL; VHDRHVLR; HDRHVLRA;
ESWPCPQL; SWPCPQLN; WPCPQLNW; PCPQLNWT; CPQLNWTK; PQLNWTKA; QLNWTKAM;
LNWTKAMV; NWTKAMVL; WTKAMVLR; TKAMVLRQ; KAMVLRQL; AMVLRQLS; MVLRQLSR;
VLRQLSRQ; LRQLSRQA; RQLSRQAS; QLSRQASV; LSRQASVK; SRQASVKV; RQASVKVG;
QASVKVGK; ASVKVGKT; SVKVGKTW; VKVGKTWT; KVGKTWTG; VGKTWTGT; GKTWTGTK;
KTWTGTKK; TWTGTKKR; WTGTKKRA; TGTKKRAQ; GTKKRAQR; TKKRAQRI; KKRAQRIF;
KRAQRIFI; RAQRIFIF; AQRIFIFI; QRIFIFIL; RIFIFILE; IFIFILEL; FIFILELL;
IFILELLL; FILELLLE; ILELLLEF; LELLLEFC; ELLLEFCR; LLLEFCRG; LLEFCRGE;
LEFCRGED; EFCRGEDS; FCRGEDSV; CRGEDSVD; RGEDSVDG; GEDSVDGK; EDSVDGKN;
DSVDGKNK; SVDGKNKS; VDGKNKST; DGKNKSTT; GKNKSTTA; KNKSTTAL; NKSTTALP;
KSTTALPA; STTALPAV; TTALPAVK; TALPAVKD; ALPAVKDS; LPAVKDSV; PAVKDSVK;
AVKDSVKD; VKDSVKDS; VSNPFFFV; SNPFFFVF; NPFFFVFP; PFFFVFPG; FFFVFPGS;
FFVFPGSW; FVFPGSWV; VFPGSWVL; FPGSWVLL; LPVYLRLL; PVYLRLLL; VYLRLLLP;
YLRLLLPQ; LRLLLPQD; RLLLPQDF; LLLPQDFQ; LLPQDFQW; LPQDFQWL; PQDFQWLK;
QDFQWLKL; DFQWLKLL; FQWLKLLL; QWLKLLLG; WLKLLLGR; LKLLLGRL; KLLLGRLL;
LLLGRLLL; LLGRLLLL; KFKLHPLL; FKLHPLLL; LLVLLGLL; LVLLGLLL; VLLGLLLG;
LLGLLLGL; LGLLLGLL; GLLLGLLL; FKLLVVLV; KLLVVLVP; GISSLMIG; ISSLMIGI;
SSLMIGIT; SLMIGITK; LMIGITKF; MIGITKFP; IGITKFPL; ASISNQAW; SISNQAWL;
ISNQAWLW; SNQAWLWN; NQAWLWNC; QAWLWNCL; AWLWNCLT; WLWNCLTQ; LWNCLTQM;
WNCLTQMS; NCLTQMST; CLTQMSTM; LTQMSTMI; TQMSTMIF; QMSTMIFC; MSTMIFCF;
STMIFCFL; TMIFCFLV; ILLLIIFN; LLLIIFNT; LLIIFNTL; LIIFNTLI; IIFNTLIL;
IFNTLILG; FNTLILGI; NTLILGIG; TLILGIGV; LILGIGVL; ILGIGVLL; LGIGVLLC;
GIGVLLCL; IGVLLCLL; GVLLCLLL; VLLCLLLF; LLCLLLFP; LCLLLFPR; CLLLFPRL;
LLLFPRLC; LLFPRLCG; LFPRLCGM; FPRLCGML; PRLCGMLL; RLCGMLLG; LCGMLLGM;
CGMLLGMI; GMLLGMIY; MLLGMIYL; LLGMIYLL; PHRNCREE; HRNCREEQ; RNCREEQK;
NCREEQKD; CREEQKDF; REEQKDFL; EEQKDFLE; EQKDFLET; QKDFLETP; KDFLETPW;
DFLETPWL; FLETPWLD; LETPWLDF; ETPWLDFW; TPWLDFWR; PWLDFWRK; WLDFWRKL;
LDFWRKLP; DFWRKLPG; FWRKLPGQ; WRKLPGQL; TFIIIFNN; FIIIFNNI; IIIFNNII;
IIFNNIIL; IFNNIILI; FNNIILIF; NNIILIFP; NIILIFPL; IILIFPLL; ILIFPLLG;
LIFPLLGP; IFPLLGPQ; FPLLGPQW; PLLGPQWL; LLGPQWLD; LGPQWLDK; LKGKVPVY;
KGKVPVYI; GKVPVYIL; KVPVYILA; VPVYILAI; PVYILAIL; VYILAILI; YILAILIV;
KKLHKEWT; EINKVYIQ; INKVYIQE; NKVYIQES; KVYIQESL; KKLLPQEV; KLLPQEVL;
LLPQEVLI; LPQEVLIK; PQEVLIKE; QEVLIKEL; EVLIKELL; VLIKELLL; LIKELLLN;
IKELLLNG; KELLLNGC; ELLLNGCC; LLLNGCCL; LLNGCCLY; LNGCCLYF; HLLLKHMK;
LLLKHMKM; LLKHMKMA; LKHMKMAP; KHMKMAPT; HMKMAPTK; MKMAPTKR; KMAPTKRK;
MAPTKRKG; APTKRKGE; PTKRKGEC; TKRKGECP; KRKGECPG; RKGECPGA; KGECPGAA;
GECPGAAP; ECPGAAPK; CPGAAPKK; PGAAPKKP; GAAPKKPK; AAPKKPKE; APKKPKEP;
PKKPKEPV; KKPKEPVQ; KPKEPVQV; PKEPVQVP; KEPVQVPK; EPVQVPKL; PVQVPKLL;
VQVPKLLI; QVPKLLIK; VPKLLIKG; PKLLIKGG; KLLIKGGV; LLIKGGVE; LIKGGVEV;
IKGGVEVL; KGGVEVLE; GGVEVLEV; GVEVLEVK; VEVLEVKT; EVLEVKTG; VLEVKTGV;
LEVKTGVD; EVKTGVDA; VKTGVDAI; KTGVDAIT; TGVDAITE; GVDAITEV; VDAITEVE;
DAITEVEC; AITEVECF; ITEVECFL; TEVECFLN; EVECFLNP; VECFLNPE; ECFLNPEM;

CFLNPEMG; FLNPEMGD; LNPEMGDP; NPEMGDPD; PEMGDPDE; EMGDPDEN; MGDPDENL;
GDPDENLR; DPDENLRG; PDENLRGF; DENLRGFS; ENLRGFSL; NLRGFSLK; LRGFSLKL;
RGFSLKLS; GFSLKLSA; FSLKLSAE; SLKLSAEN; LKLSAEND; KLSAENDF; LSAENDFS;
SAENDFSS; AENDFSSD; ENDFSSDS; NDFSSDSP; DFSSDSPE; FSSDSPER; SSDSPERK;
SDSPERKM; DSPERKML; SPERKMLP; PERKMLPC; ERKMLPCY; RKMLPCYS; KMLPCYST;
MLPCYSTA; LPCYSTAR; PCYSTARI; CYSTARIP; YSTARIPL; STARIPLP; TARIPLPN;
ARIPLPNL; RIPLPNLN; IPLPNLNE; PLPNLNED; LPNLNEDL; PNLNEDLT; NLNEDLTC;
LNEDLTCG; NEDLTCGN; EDLTCGNL; DLTCGNLL; LTCGNLLM; TCGNLLMW; CGNLLMWE;
GNLLMWEA; NLLMWEAV; LLMWEAVT; LMWEAVTV; MWEAVTVQ; WEAVTVQT; EAVTVQTE;
AVTVQTEV; VTVQTEVI; TVQTEVIG; VQTEVIGI; QTEVIGIT; TEVIGITS; EVIGITSM;
VIGITSML; IGITSMLN; GITSMLNL; ITSMLNLH; TSMLNLHA; SMLNLHAG; MLNLHAGS;
LNLHAGSQ; NLHAGSQK; LHAGSQKV; HAGSQKVH; AGSQKVHE; GSQKVHEH; SQKVHEHG;
QKVHEHGG; KVHEHGGG; VHEHGGGK; HEHGGGKP; EHGGGKPI; HGGGKPIQ; GGGKPIQG;
GGKPIQGS; GKPIQGSN; KPIQGSNF; PIQGSNFH; IQGSNFHF; QGSNFHFF; GSNFHFFA;
SNFHFFAV; NFHFFAVG; FHFFAVGG; HFFAVGGE; FFAVGGEP; FAVGGEPL; AVGGEPLE;
VGGEPLEM; GGEPLEMQ; GEPLEMQG; EPLEMQGV; PLEMQGVL; LEMQGVLM; EMQGVLMN;
MQGVLMNY; QGVLMNYR; GVLMNYRS; VLMNYRSK; LMNYRSKY; MNYRSKYP; NYRSKYPD;
YRSKYPDG; RSKYPDGT; SKYPDGTI; KYPDGTIT; YPDGTITP; PDGTITPK; DGTITPKN;
GTITPKNP; TITPKNPT; ITPKNPTA; TPKNPTAQ; PKNPTAQS; KNPTAQSQ; NPTAQSQV;
PTAQSQVM; TAQSQVMN; AQSQVMNT; QSQVMNTD; SQVMNTDH; QVMNTDHK; VMNTDHKA;
MNTDHKAY; NTDHKAYL; TDHKAYLD; DHKAYLDK; HKAYLDKN; KAYLDKNN; AYLDKNNA;
YLDKNNAY; LDKNNAYP; DKNNAYPV; KNNAYPVE; NNAYPVEC; NAYPVECW; AYPVECWV;
YPVECWVP; PVECWVPD; VECWVPDP; ECWVPDPS; CWVPDPSR; WVPDPSRN; VPDPSRNE;
PDPSRNEN; DPSRNENA; PSRNENAR; SRNENARY; RNENARYF; NENARYFG; ENARYFGT;
NARYFGTF; ARYFGTFT; RYFGTFTG; YFGTFTGG; FGTFTGGE; GTFTGGEN; TFTGGENV;
FTGGENVP; TGGENVPP; GGENVPPV; GENVPPVL; ENVPPVLH; NVPPVLHV; VPPVLHVT;
PPVLHVTN; PVLHVTNT; VLHVTNTA; LHVTNTAT; HVTNTATT; VTNTATTV; TNTATTVL;
NTATTVLL; TATTVLLD; ATTVLLDE; TTVLLDEQ; TVLLDEQG; VLLDEQGV; LLDEQGVG;
LDEQGVGP; DEQGVGPL; EQGVGPLC; QGVGPLCK; GVGPLCKA; VGPLCKAD; GPLCKADS;
PLCKADSL; LCKADSLY; CKADSLYV; KADSLYVS; ADSLYVSA; DSLYVSAA; SLYVSAAD;
LYVSAADI; YVSAADIC; VSAADICG; SAADICGL; AADICGLF; ADICGLFT; DICGLFTN;
ICGLFTNS; CGLFTNSS; GLFTNSSG; LFTNSSGT; FTNSSGTQ; TNSSGTQQ; NSSGTQQW;
SSGTQQWR; SGTQQWRG; GTQQWRGL; TQQWRGLA; QQWRGLAR; QWRGLARY; WRGLARYF;
RGLARYFK; GLARYFKI; LARYFKIR; ARYFKIRL; RYFKIRLR; YFKIRLRK; FKIRLRKR;
KIRLRKRS; IRLRKRSV; RLRKRSVK; LRKRSVKN; RKRSVKNP; KRSVKNPY; RSVKNPYP;
SVKNPYPI; VKNPYPIS; KNPYPISF; NPYPISFL; PYPISFLL; YPISFLLS; PISFLLSD;
ISFLLSDL; SFLLSDLI; FLLSDLIN; LLSDLINR; LSDLINRR; SDLINRRT; DLINRRTQ;
LINRRTQR; INRRTQRV; NRRTQRVD; RRTQRVDG; RTQRVDGQ; TQRVDGQP; QRVDGQPM;
RVDGQPMY; VDGQPMYG; DGQPMYGM; GQPMYGME; QPMYGMES; PMYGMESQ; MYGMESQV;
YGMESQVE; GMESQVEE; MESQVEEV; ESQVEEVR; SQVEEVRV; QVEEVRVF; VEEVRVFD;
EEVRVFDG; EVRVFDGT; VRVFDGTE; RVFDGTER; VFDGTERL; FDGTERLP; DGTERLPG;
GTERLPGD; TERLPGDP; ERLPGDPD; RLPGDPDM; LPGDPDMI; PGDPDMIR; GDPDMIRY;
DPDMIRYI; PDMIRYID; DMIRYIDK; MIRYIDKQ; IRYIDKQG; RYIDKQGQ; YIDKQGQL;
IDKQGQLQ; DKQGQLQT; KQGQLQTK; QGQLQTKM; GQLQTKML; TGAFIVHI; GAFIVHIH;
AFIVHIHL; FIVHIHLI; IVHIHLIN; VHIHLINA; HIHLINAA; IHLINAAF; HLINAAFV;
ATFKLVLF; TFKLVLFW; FKLVLFWG; KLVLFWGW; LVLFWGWC; VLFWGWCF; LFWGWCFR;
FWGWCFRP; WGWCFRPF; GWCFRPFK; WCFRPFKT; CFRPFKTL; FRPFKTLK; RPFKTLKA;
PFKTLKAF; FKTLKAFT; KTLKAFTQ; TLKAFTQM; LKAFTQMQ; KAFTQMQL; AFTQMQLL;
FTQMQLLT; TQMQLLTM; QMQLLTMG; MQLLTMGV; PLGIFSRG; SMSRVFSF; ILFSCNIK;
LFSCNIKN; FSCNIKNT; SCNIKNTF; CNIKNTFP; NIKNTFPH; IKNTFPHA; KNTFPHAY;
NTFPHAYI; TFPHAYII; FPHAYIIF; PHAYIIFH; HAYIIFHP; KSIHTYLR; SIHTYLRI;
IHTYLRIQ; HTYLRIQP; TYLRIQPF; YLRIQPFL; LRIQPFLP; RIQPFLPF; IQPFLPFN;
QPFLPFNN; PFLPFNNS; FLPFNNSR; LPFNNSRL; PFNNSRLY; FNNSRLYI; NNSRLYIS;
NSRLYISC; SRLYISCK; RLYISCKI; LYISCKIS; YISCKISY; ISCKISYR; SCKISYRP;
CKISYRPK; KISYRPKP; ISYRPKPN; IYFGPKIY; YFGPKIYL; FGPKIYLS; GPKIYLSY;
PKIYLSYK; KIYLSYKS; IYLSYKSS; YLSYKSSL; LSYKSSLQ; SYKSSLQG; YKSSLQGF;
KSSLQGFR; SSLQGFRD; SLQGFRDR; LQGFRDRI; QGFRDRIL; GFRDRILI; FRDRILIH;
RDRILIHC; DRILIHCN; RILIHCNQ; ILIHCNQA; LIHCNQAW; IHCNQAWW; HCNQAWWK;
CNQAWWKY; NQAWWKYL; QAWWKYLG; AWWKYLGS; WWKYLGSF; WKYLGSFV; FSSCPFYI;
SSCPFYIF; SCPFYIFK; CPFYIFKN; PFYIFKNN; FYIFKNNH; YIFKNNHV; IFKNNHVL;
FKNNHVLI; KNNHVLIY; NNHVLIYS; NHVLIYSY; HVLIYSYT; CCFSTING; CFSTINGT;
FSTINGTF; STINGTFK; PVSSFRYI; VSSFRYIE; SSFRYIEN; SFRYIENN; FRYIENNT;
RYIENNTV; YIENNTVQ; IENNTVQK; ENNTVQKI; NNTVQKIK; NTVQKIKY; TVQKIKYY;
VQKIKYYR; QKIKYYRI; KIKYYRIH; IKYYRIHF; KYYRIHFR; QTVQPSNT; TVQPSNTC;
VQPSNTCH; QPSNTCHI; PSNTCHIL; SNTCHILF; YSISMSSK; SISMSSKY; HFFPGHMK;

FFPGHMKG; FPGHMKGI; PGHMKGIY; GHMKGIYS; HMKGIYSF; MKGIYSFF; KGIYSFFS;
NCIYCLLT; CIYCLLTN; IYCLLTNT; YCLLTNTF; CLLTNTFL; LLTNTFLI; LTNTFLIF;
TNTFLIFT; NTFLIFTF; TFLIFTFC; FLIFTFCK; LIFTFCKN; IFTFCKNN; FTFCKNNS;
TFCKNNSI; FCKNNSIC; CKNNSICK; KNNSICKV; NNSICKVL; NSICKVLF; SICKVLFM;
ICKVLFMI; CKVLFMIL; KVLFMILK; VLFMILKV; LFMILKVI; FMILKVIR; MILKVIRL;
ILKVIRLV; LKVIRLVF; KVIRLVFF; VIRLVFFL; IRLVFFLT; RLVFFLTL; LVFFLTLF;
VFFLTLFT; FFLTLFTL; FLTLFTLL; LTLFTLLY; TLFTLLYI; LFTLLYIV; FTLLYIVL;
TLLYIVLK; LLYIVLKF; KHILTLCL; HILTLCLY; ILTLCLYC; LTLCLYCI; TLCLYCIL;
LCLYCILS; CLYCILSN; FPRHLLCF; PRHLLCFF; RHLLCFFR; HLLCFFRL; LLCFFRLF;
LCFFRLFW; CFFRLFWA; FFRLFWAK; FRLFWAKI; RLFWAKIM; LFWAKIML; FWAKIMLL;
APLNAFFY; PLNAFFYS; LNAFFYSM; NAFFYSMV; AFFYSMVW; FFYSMVWI; FYSMVWIS;
YSMVWISS; VFLINTLT; FLINTLTN; KTKGTQLL; TKGTQLLT; KGTQLLTE; GTQLLTEI;
TQLLTEII; QLLTEIIN; LLTEIINC; LTEIINCR; TEIINCRN; EIINCRNS; IINCRNSM;
INCRNSMS; NCRNSMSM; CRNSMSMW; RNSMSMWS; KEYNIMPS; EYNIMPST; YNIMPSTH;
NIMPSTHV; IMPSTHVS; MPSTHVST; PSTHVSTN; STHVSTNK; THVSTNKS; HVSTNKSY;
VSTNKSYR; STNKSYRI; TNKSYRIF; NKSYRIFF; KSYRIFFH; SYRIFFHK; YRIFFHKF;
RIFFHKFF; IFFHKFFI; FFHKFFIQ; FHKFFIQN; HKFFIQNL; KFFIQNLS; FFIQNLSF;
FIQNLSFF; IQNLSFFF; QNLSFFFS; NLSFFFSS; LSFFFSSI; SFFFSSIH; FFFSSIHS;
FFSSIHSK; FSSIHSKA; SSIHSKAG; SIHSKAGK; IHSKAGKG; HSKAGKGS; SKAGKGSI;
KAGKGSIT; AGKGSITK; GKGSITKY; KGSITKYS; GSITKYSL; SITKYSLT; ITKYSLTK;
TKYSLTKK; KYSLTKKL; YSLTKKLV; IRGKVFRV; RGKVFRVF; GKVFRVFY; KVFRVFYL;
VFRVFYLS; FRVFYLSF; RVFYLSFF; VFYLSFFF; FYLSFFFG; YLSFFFGW; LSFFFGWC;
VLRICCCF; LRICCCFF; RICCCFFI; ICCCFFIT; CCCFFITG; CCFFITGK; CFFITGKH;
FFITGKHI; FITGKHIF; ITGKHIFM; TGKHIFMA; GKHIFMAK; IFIPFFIK; FIPFFIKG;
IPFFIKGT; PFFIKGTP; FFIKGTPP; FIKGTPPG; IKGTPPGL; KGTPPGLP; GTPPGLPL;
TPPGLPLF; PPGLPLFC; PGLPLFCS; GLPLFCSI; LPLFCSIG; PLFCSIGW; LFCSIGWH;
FCSIGWHL; YFIIYLNI; FIIYLNIS; SFRSLKGV; FRSLKGVS; RSLKGVSP; SLKGVSPI;
LKGVSPII; KGVSPIIW; GVSPIIWT; VSPIIWTH; SPIIWTHH; PIIWTHHC; IIWTHHCR;
IWTHHCRV; WTHHCRVS; THHCRVSS; HHCRVSSV; HCRVSSVR; CRVSSVRS; RVSSVRSK;
VSSVRSKP; SSVRSKPN; SVRSKPNH; VRSKPNHC; RSKPNHCV; SKPNHCVK; KPNHCVKQ;
PNHCVKQS; NHCVKQSM; HCVKQSMQ; QSIQTKGS; SIQTKGSF; IQTKGSFL; QTKGSFLK;
TKGSFLKN; KGSFLKNF; GSFLKNFL; SFLKNFLF; FLKNFLFK; LKNFLFKC; KNFLFKCL;
NFLFKCLN; FLFKCLNL; LFKCLNLS; HSMQGQCT; SMQGQCTE; MQGQCTEG; QGQCTEGF;
GQCTEGFL; QCTEGFLE; CTEGFLEQ; TEGFLEQI; EGFLEQIG; GFLEQIGH; FLEQIGHS;
LEQIGHSL; EQIGHSLQ; QIGHSLQY; IGHSLQYR; GHSLQYRV; HSLQYRVS; SLQYRVSG;
LQYRVSGQ; QYRVSGQR; YRVSGQRG; RVSGQRGK; VSGQRGKS; SGQRGKSA; GQRGKSAQ;
QRGKSAQT; RGKSAQTS; GKSAQTSE; KSAQTSEL; SAQTSELL; AQTSELLQ; QTSELLQV;
TSELLQVP; SELLQVPK; ELLQVPKS; LLQVPKSG; ATFTSCSI; TFTSCSIF; FTSCSIFL;
TSCSIFLY; SCSIFLYK; CSIFLYKV; SIFLYKVF; IFLYKVFI; FLYKVFIL; LYKVFILF;
YKVFILFI; KVFILFIL; VFILFILS; FILFILSS; ILFILSSS; LFILSSSP; FILSSSPP;
ILSSSPPL; LSSSPPLS; SSSPPLSG; AFLIKGRF; FLIKGRFP; LIKGRFPQ; IKGRFPQA;
KGRFPQAA; GRFPQAAL; RFPQAALS; FPQAALSR; PQAALSRP; QAALSRPK; AALSRPKR;
ALSRPKRS; LSRPKRSM; SRPKRSMS; RPKRSMSS; PKRSMSSM; KRSMSSMD; RSMSSMDS;
SMSSMDSS; MSSMDSSL; SSMDSSLL; SMDSSLLR; MDSSLLRT; DSSLLRTL; SSLLRTLS

9 mers:
FCKNCKRIG; CKNCKRIGI; KNCKRIGIS; NCKRIGISP; CKRIGISPN; KRIGISPNS; RIGISPNSF;
IGISPNSFA; GISPNSFAR; ISPNSFARP; SPNSFARPQ; PNSFARPQK; NSFARPQKK; SFARPQKKP;
FARPQKKPP; ARPQKKPPH; RPQKKPPHP; PQKKPPHPY; QKKPPHPYY; KKPPHPYYL; KPPHPYYLR;
PPHPYYLRE; PHPYYLRER; HPYYLRERV; PYYLRERVE; YYLRERVEA; YLRERVEAE; LRERVEAEA;
RERVEAEAA; ERVEAEAAS; RVEAEAASA; VEAEAASAS; EAEAASASY; AEAASASYI; EAASASYIL;
KKRPQGGAA; KRPQGGAAY; RPQGGAAYP; PQGGAAYPW; QGGAAYPWN; GGAAYPWNA; GAAYPWNAA;
AAYPWNAAK; AYPWNAAKP; PQEGKCMTH; QEGKCMTHR; EGKCMTHRG; GKCMTHRGM; KCMTHRGMQ;
CMTHRGMQP; MTHRGMQPN; THRGMQPNH; HRGMQPNHD; RGMQPNHDL; GMQPNHDLR; MQPNHDLRK;
QPNHDLRKE; PNHDLRKES; NHDLRKESA; LTGRSCLPM; TGRSCLPME; GRSCLPMEC; RSCLPMECS;
SCLPMECSQ; CLPMECSQT; LPMECSQTM; PMECSQTMT; MECSQTMTS; ECSQTMTSG; CSQTMTSGR;
SQTMTSGRK; QTMTSGRKV; TMTSGRKVH; MTSGRKVHD; TSGRKVHDR; SGRKVHDRH; GRKVHDRHV;
RKVHDRHVL; KVHDRHVLR; VHDRHVLRA; ESWPCPQLN; SWPCPQLNW; WPCPQLNWT; PCPQLNWTK;
CPQLNWTKA; PQLNWTKAM; QLNWTKAMV; LNWTKAMVL; NWTKAMVLR; WTKAMVLRQ; TKAMVLRQL;
KAMVLRQLS; AMVLRQLSR; MVLRQLSRQ; VLRQLSRQA; LRQLSRQAS; RQLSRQASV; QLSRQASVK;
LSRQASVKV; SRQASVKVG; RQASVKVGK; QASVKVGKT; ASVKVGKTW; SVKVGKTWT; VKVGKTWTG;
KVGKTWTGT; VGKTWTGTK; GKTWTGTKK; KTWTGTKKR; TWTGTKKRA; WTGTKKRAQ; TGTKKRAQR;
GTKKRAQRI; TKKRAQRIF; KKRAQRIFI; KRAQRIFIF; RAQRIFIFI; AQRIFIFIL; QRIFIFILE;
RIFIFILEL; IFIFILELL; FIFILELLL; IFILELLLE; FILELLLEF; ILELLLEFC; LELLLEFCR;
ELLLEFCRG; LLLEFCRGE; LLEFCRGED; LEFCRGEDS; EFCRGEDSV; FCRGEDSVD; CRGEDSVDG;
RGEDSVDGK; GEDSVDGKN; EDSVDGKNK; DSVDGKNKS; SVDGKNKST; VDGKNKSTT; DGKNKSTTA;

GKNKSTTAL; KNKSTTALP; NKSTTALPA; KSTTALPAV; STTALPAVK; TTALPAVKD; TALPAVKDS;
ALPAVKDSV; LPAVKDSVK; PAVKDSVKD; AVKDSVKDS; VSNPFFFVF; SNPFFFVFP; NPFFFVFPG;
PFFFVFPGS; FFFVFPGSW; FFVFPGSWV; FVFPGSWVL; VFPGSWVLL; LPVYLRLLL; PVYLRLLLP;
VYLRLLLPQ; YLRLLLPQD; LRLLLPQDF; RLLLPQDFQ; LLLPQDFQW; LLPQDFQWL; LPQDFQWLK;
PQDFQWLKL; QDFQWLKLL; DFQWLKLLL; FQWLKLLLG; QWLKLLLGR; WLKLLLGRL; LKLLLGRLL;
KLLLGRLLL; LLLGRLLLL; KFKLHPLLL; LLVLLGLLL; LVLLGLLLG; VLLGLLLGL; LLGLLLGLL;
LGLLLGLLL; FKLLVVLVP; GISSLMIGI; ISSLMIGIT; SSLMIGITK; SLMIGITKF; LMIGITKFP;
MIGITKFPL; ASISNQAWL; SISNQAWLW; ISNQAWLWN; SNQAWLWNC; NQAWLWNCL; QAWLWNCLT;
AWLWNCLTQ; WLWNCLTQM; LWNCLTQMS; WNCLTQMST; NCLTQMSTM; CLTQMSTMI; LTQMSTMIF;
TQMSTMIFC; QMSTMIFCF; MSTMIFCFL; STMIFCFLV; ILLLIIFNT; LLLIIFNTL; LLIIFNTLI;
LIIFNTLIL; IIFNTLILG; IFNTLILGI; FNTLILGIG; NTLILGIGV; TLILGIGVL; LILGIGVLL;
ILGIGVLLC; LGIGVLLCL; GIGVLLCLL; IGVLLCLLL; GVLLCLLLF; VLLCLLLFP; LLCLLLFPR;
LCLLLFPRL; CLLLFPRLC; LLLFPRLCG; LLFPRLCGM; LFPRLCGML; FPRLCGMLL; PRLCGMLLG;
RLCGMLLGM; LCGMLLGMI; CGMLLGMIY; GMLLGMIYL; MLLGMIYLL; PHRNCREEQ; HRNCREEQK;
RNCREEQKD; NCREEQKDF; CREEQKDFL; REEQKDFLE; EEQKDFLET; EQKDFLETP; QKDFLETPW;
KDFLETPWL; DFLETPWLD; FLETPWLDF; LETPWLDFW; ETPWLDFWR; TPWLDFWRK; PWLDFWRKL;
WLDFWRKLP; LDFWRKLPG; DFWRKLPGQ; FWRKLPGQL; TFIIIFNNI; FIIIFNNII; IIIFNNIIL;
IIFNNIILI; IFNNIILIF; FNNIILIFP; NNIILIFPL; NIILIFPLL; IILIFPLLG; ILIFPLLGP;
LIFPLLGPQ; IFPLLGPQW; FPLLGPQWL; PLLGPQWLD; LLGPQWLDK; LKGKVPVYI; KGKVPVYIL;
GKVPVYILA; KVPVYILAI; VPVYILAIL; PVYILAILI; VYILAILIV; EINKVYIQE; INKVYIQES;
NKVYIQESL; KKLLPQEVL; KLLPQEVLI; LLPQEVLIK; LPQEVLIKE; PQEVLIKEL; QEVLIKELL;
EVLIKELLL; VLIKELLLN; LIKELLLNG; IKELLLNGC; KELLLNGCC; ELLLNGCCL; LLLNGCCLY;
LLNGCCLYF; HLLLKHMKM; LLLKHMKMA; LLKHMKMAP; LKHMKMAPT; KHMKMAPTK; HMKMAPTKR;
MKMAPTKRK; KMAPTKRKG; MAPTKRKGE; APTKRKGEC; PTKRKGECP; TKRKGECPG; KRKGECPGA;
RKGECPGAA; KGECPGAAP; GECPGAAPK; ECPGAAPKK; CPGAAPKKP; PGAAPKKPK; GAAPKKPKE;
AAPKKPKEP; APKKPKEPV; PKKPKEPVQ; KKPKEPVQV; KPKEPVQVP; PKEPVQVPK; KEPVQVPKL;
EPVQVPKLL; PVQVPKLLI; VQVPKLLIK; QVPKLLIKG; VPKLLIKGG; PKLLIKGGV; KLLIKGGVE;
LLIKGGVEV; LIKGGVEVL; IKGGVEVLE; KGGVEVLEV; GGVEVLEVK; GVEVLEVKT; VEVLEVKTG;
EVLEVKTGV; VLEVKTGVD; LEVKTGVDA; EVKTGVDAI; VKTGVDAIT; KTGVDAITE; TGVDAITEV;
GVDAITEVE; VDAITEVEC; DAITEVECF; AITEVECFL; ITEVECFLN; TEVECFLNP; EVECFLNPE;
VECFLNPEM; ECFLNPEMG; CFLNPEMGD; FLNPEMGDP; LNPEMGDPD; NPEMGDPDE; PEMGDPDEN;
EMGDPDENL; MGDPDENLR; GDPDENLRG; DPDENLRGF; PDENLRGFS; DENLRGFSL; ENLRGFSLK;
NLRGFSLKL; LRGFSLKLS; RGFSLKLSA; GFSLKLSAE; FSLKLSAEN; SLKLSAEND; LKLSAENDF;
KLSAENDFS; LSAENDFSS; SAENDFSSD; AENDFSSDS; ENDFSSDSP; NDFSSDSPE; DFSSDSPER;
FSSDSPERK; SSDSPERKM; SDSPERKML; DSPERKMLP; SPERKMLPC; PERKMLPCY; ERKMLPCYS;
RKMLPCYST; KMLPCYSTA; MLPCYSTAR; LPCYSTARI; PCYSTARIP; CYSTARIPL; YSTARIPLP;
STARIPLPN; TARIPLPNL; ARIPLPNLN; RIPLPNLNE; IPLPNLNED; PLPNLNEDL; LPNLNEDLT;
PNLNEDLTC; NLNEDLTCG; LNEDLTCGN; NEDLTCGNL; EDLTCGNLL; DLTCGNLLM; LTCGNLLMW;
TCGNLLMWE; CGNLLMWEA; GNLLMWEAV; NLLMWEAVT; LLMWEAVTV; LMWEAVTVQ; MWEAVTVQT;
WEAVTVQTE; EAVTVQTEV; AVTVQTEVI; VTVQTEVIG; TVQTEVIGI; VQTEVIGIT; QTEVIGITS;
TEVIGITSM; EVIGITSML; VIGITSMLN; IGITSMLNL; GITSMLNLH; ITSMLNLHA; TSMLNLHAG;
SMLNLHAGS; MLNLHAGSQ; LNLHAGSQK; NLHAGSQKV; LHAGSQKVH; HAGSQKVHE; AGSQKVHEH;
GSQKVHEHG; SQKVHEHGG; QKVHEHGGG; KVHEHGGGK; VHEHGGGKP; HEHGGGKPI; EHGGGKPIQ;
HGGGKPIQG; GGGKPIQGS; GGKPIQGSN; GKPIQGSNF; KPIQGSNFH; PIQGSNFHF; IQGSNFHFF;
QGSNFHFFA; GSNFHFFAV; SNFHFFAVG; NFHFFAVGG; FHFFAVGGE; HFFAVGGEP; FFAVGGEPL;
FAVGGEPLE; AVGGEPLEM; VGGEPLEMQ; GGEPLEMQG; GEPLEMQGV; EPLEMQGVL; PLEMQGVLM;
LEMQGVLMN; EMQGVLMNY; MQGVLMNYR; QGVLMNYRS; GVLMNYRSK; VLMNYRSKY; LMNYRSKYP;
MNYRSKYPD; NYRSKYPDG; YRSKYPDGT; RSKYPDGTI; SKYPDGTIT; KYPDGTITP; YPDGTITPK;
PDGTITPKN; DGTITPKNP; GTITPKNPT; TITPKNPTA; ITPKNPTAQ; TPKNPTAQS; PKNPTAQSQ;
KNPTAQSQV; NPTAQSQVM; PTAQSQVMN; TAQSQVMNT; AQSQVMNTD; QSQVMNTDH; SQVMNTDHK;
QVMNTDHKA; VMNTDHKAY; MNTDHKAYL; NTDHKAYLD; TDHKAYLDK; DHKAYLDKN; HKAYLDKNN;
KAYLDKNNA; AYLDKNNAY; YLDKNNAYP; LDKNNAYPV; DKNNAYPVE; KNNAYPVEC; NNAYPVECW;
NAYPVECWV; AYPVECWVP; YPVECWVPD; PVECWVPDP; VECWVPDPS; ECWVPDPSR; CWVPDPSRN;
WVPDPSRNE; VPDPSRNEN; PDPSRNENA; DPSRNENAR; PSRNENARY; SRNENARYF; RNENARYFG;
NENARYFGT; ENARYFGTF; NARYFGTFT; ARYFGTFTG; RYFGTFTGG; YFGTFTGGE; FGTFTGGEN;
GTFTGGENV; TFTGGENVP; FTGGENVPP; TGGENVPPV; GGENVPPVL; GENVPPVLH; ENVPPVLHV;
NVPPVLHVT; VPPVLHVTN; PPVLHVTNT; PVLHVTNTA; VLHVTNTAT; LHVTNTATT; HVTNTATTV;
VTNTATTVL; TNTATTVLL; NTATTVLLD; TATTVLLDE; ATTVLLDEQ; TTVLLDEQG; TVLLDEQGV;
VLLDEQGVG; LLDEQGVGP; LDEQGVGPL; DEQGVGPLC; EQGVGPLCK; QGVGPLCKA; GVGPLCKAD;
VGPLCKADS; GPLCKADSL; PLCKADSLY; LCKADSLYV; CKADSLYVS; KADSLYVSA; ADSLYVSAA;
DSLYVSAAD; SLYVSAADI; LYVSAADIC; YVSAADICG; VSAADICGL; SAADICGLF; AADICGLFT;
ADICGLFTN; DICGLFTNS; ICGLFTNSS; CGLFTNSSG; GLFTNSSGT; LFTNSSGTQ; FTNSSGTQQ;
TNSSGTQQW; NSSGTQQWR; SSGTQQWRG; SGTQQWRGL; GTQQWRGLA; TQQWRGLAR; QQWRGLARY;
QWRGLARYF; WRGLARYFK; RGLARYFKI; GLARYFKIR; LARYFKIRL; ARYFKIRLR; RYFKIRLRK;
YFKIRLRKR; FKIRLRKRS; KIRLRKRSV; IRLRKRSVK; RLRKRSVKN; LRKRSVKNP; RKRSVKNPY;

KRSVKNPYP; RSVKNPYPI; SVKNPYPIS; VKNPYPISF; KNPYPISFL; NPYPISFLL; PYPISFLLS;
YPISFLLSD; PISFLLSDL; ISFLLSDLI; SFLLSDLIN; FLLSDLINR; LLSDLINRR; LSDLINRRT;
SDLINRRTQ; DLINRRTQR; LINRRTQRV; INRRTQRVD; NRRTQRVDG; RRTQRVDGQ; RTQRVDGQP;
TQRVDGQPM; QRVDGQPMY; RVDGQPMYG; VDGQPMYGM; DGQPMYGME; GQPMYGMES; QPMYGMESQ;
PMYGMESQV; MYGMESQVE; YGMESQVEE; GMESQVEEV; MESQVEEVR; ESQVEEVRV; SQVEEVRVF;
QVEEVRVFD; VEEVRVFDG; EEVRVFDGT; EVRVFDGTE; VRVFDGTER; RVFDGTERL; VFDGTERLP;
FDGTERLPG; DGTERLPGD; GTERLPGDP; TERLPGDPD; ERLPGDPDM; RLPGDPDMI; LPGDPDMIR;
PGDPDMIRY; GDPDMIRYI; DPDMIRYID; PDMIRYIDK; DMIRYIDKQ; MIRYIDKQG; IRYIDKQGQ;
RYIDKQGQL; YIDKQGQLQ; IDKQGQLQT; DKQGQLQTK; KQGQLQTKM; QGQLQTKML; TGAFIVHIH;
GAFIVHIHL; AFIVHIHLI; FIVHIHLIN; IVHIHLINA; VHIHLINAA; HIHLINAAF; IHLINAAFV;
ATFKLVLFW; TFKLVLFWG; FKLVLFWGW; KLVLFWGWC; LVLFWGWCF; VLFWGWCFR; LFWGWCFRP;
FWGWCFRPF; WGWCFRPFK; GWCFRPFKT; WCFRPFKTL; CFRPFKTLK; FRPFKTLKA; RPFKTLKAF;
PFKTLKAFT; FKTLKAFTQ; KTLKAFTQM; TLKAFTQMQ; LKAFTQMQL; KAFTQMQLL; AFTQMQLLT;
FTQMQLLTM; TQMQLLTMG; QMQLLTMGV; ILFSCNIKN; LFSCNIKNT; FSCNIKNTF; SCNIKNTFP;
CNIKNTFPH; NIKNTFPHA; IKNTFPHAY; KNTFPHAYI; NTFPHAYII; TFPHAYIIF; FPHAYIIFH;
PHAYIIFHP; KSIHTYLRI; SIHTYLRIQ; IHTYLRIQP; HTYLRIQPF; TYLRIQPFL; YLRIQPFLP;
LRIQPFLPF; RIQPFLPFN; IQPFLPFNN; QPFLPFNNS; PFLPFNNSR; FLPFNNSRL; LPFNNSRLY;
PFNNSRLYI; FNNSRLYIS; NNSRLYISC; NSRLYISCK; SRLYISCKI; RLYISCKIS; LYISCKISY;
YISCKISYR; ISCKISYRP; SCKISYRPK; CKISYRPKP; KISYRPKPN; IYFGPKIYL; YFGPKIYLS;
FGPKIYLSY; GPKIYLSYK; PKIYLSYKS; KIYLSYKSS; IYLSYKSSL; YLSYKSSLQ; LSYKSSLQG;
SYKSSLQGF; YKSSLQGFR; KSSLQGFRD; SSLQGFRDR; SLQGFRDRI; LQGFRDRIL; QGFRDRILI;
GFRDRILIH; FRDRILIHC; RDRILIHCN; DRILIHCNQ; RILIHCNQA; ILIHCNQAW; LIHCNQAWW;
IHCNQAWWK; HCNQAWWKY; CNQAWWKYL; NQAWWKYLG; QAWWKYLGS; AWWKYLGSF; WWKYLGSFV;
FSSCPFYIF; SSCPFYIFK; SCPFYIFKN; CPFYIFKNN; PFYIFKNNH; FYIFKNNHV; YIFKNNHVL;
IFKNNHVLI; FKNNHVLIY; KNNHVLIYS; NNHVLIYSY; NHVLIYSYT; CCFSTINGT; CFSTINGTF;
FSTINGTFK; PVSSFRYIE; VSSFRYIEN; SSFRYIENN; SFRYIENNT; FRYIENNTV; RYIENNTVQ;
YIENNTVQK; IENNTVQKI; ENNTVQKIK; NNTVQKIKY; NTVQKIKYY; TVQKIKYYR; VQKIKYYRI;
QKIKYYRIH; KIKYYRIHF; IKYYRIHFR; QTVQPSNTC; TVQPSNTCH; VQPSNTCHI; QPSNTCHIL;
PSNTCHILF; YSISMSSKY; HFFPGHMKG; FFPGHMKGI; FPGHMKGIY; PGHMKGIYS; GHMKGIYSF;
HMKGIYSFF; MKGIYSFFS; NCIYCLLTN; CIYCLLTNT; IYCLLTNTF; YCLLTNTFL; CLLTNTFLI;
LLTNTFLIF; LTNTFLIFT; TNTFLIFTF; NTFLIFTFC; TFLIFTFCK; FLIFTFCKN; LIFTFCKNN;
IFTFCKNNS; FTFCKNNSI; TFCKNNSIC; FCKNNSICK; CKNNSICKV; KNNSICKVL; NNSICKVLF;
NSICKVLFM; SICKVLFMI; ICKVLFMIL; CKVLFMILK; KVLFMILKV; VLFMILKVI; LFMILKVIR;
FMILKVIRL; MILKVIRLV; ILKVIRLVF; LKVIRLVFF; KVIRLVFFL; VIRLVFFLT; IRLVFFLTL;
RLVFFLTLF; LVFFLTLFT; VFFLTLFTL; FFLTLFTLL; FLTLFTLLY; LTLFTLLYI; TLFTLLYIV;
LFTLLYIVL; FTLLYIVLK; TLLYIVLKF; KHILTLCLY; HILTLCLYC; ILTLCLYCI; LTLCLYCIL;
TLCLYCILS; LCLYCILSN; FPRHLLCFF; PRHLLCFFR; RHLLCFFRL; HLLCFFRLF; LLCFFRLFW;
LCFFRLFWA; CFFRLFWAK; FFRLFWAKI; FRLFWAKIM; RLFWAKIML; LFWAKIMLL; APLNAFFYS;
PLNAFFYSM; LNAFFYSMV; NAFFYSMVW; AFFYSMVWI; FFYSMVWIS; FYSMVWISS; VFLINTLTN;
KTKGTQLLT; TKGTQLLTE; KGTQLLTEI; GTQLLTEII; TQLLTEIIN; QLLTEIINC; LLTEIINCR;
LTEIINCRN; TEIINCRNS; EIINCRNSM; IINCRNSMS; INCRNSMSM; NCRNSMSMW; CRNSMSMWS;
KEYNIMPST; EYNIMPSTH; YNIMPSTHV; NIMPSTHVS; IMPSTHVST; MPSTHVSTN; PSTHVSTNK;
STHVSTNKS; THVSTNKSY; HVSTNKSYR; VSTNKSYRI; STNKSYRIF; TNKSYRIFF; NKSYRIFFH;
KSYRIFFHK; SYRIFFHKF; YRIFFHKFF; RIFFHKFFI; IFFHKFFIQ; FFHKFFIQN; FHKFFIQNL;
HKFFIQNLS; KFFIQNLSF; FFIQNLSFF; FIQNLSFFF; IQNLSFFFS; QNLSFFFSS; NLSFFFSSI;
LSFFFSSIH; SFFFSSIHS; FFFSSIHSK; FFSSIHSKA; FSSIHSKAG; SSIHSKAGK; SIHSKAGKG;
IHSKAGKGS; HSKAGKGSI; SKAGKGSIT; KAGKGSITK; AGKGSITKY; GKGSITKYS; KGSITKYSL;
GSITKYSLT; SITKYSLTK; ITKYSLTKK; TKYSLTKKL; KYSLTKKLV; IRGKVFRVF; RGKVFRVFY;
GKVFRVFYL; KVFRVFYLS; VFRVFYLSF; FRVFYLSFF; RVFYLSFFF; VFYLSFFFG; FYLSFFFGW;
YLSFFFGWC; VLRICCCFF; LRICCCFFI; RICCCFFIT; ICCCFFITG; CCCFFITGK; CCFFITGKH;
CFFITGKHI; FFITGKHIF; FITGKHIFM; ITGKHIFMA; TGKHIFMAK; IFIPFFIKG; FIPFFIKGT;
IPFFIKGTP; PFFIKGTPP; FFIKGTPPG; FIKGTPPGL; IKGTPPGLP; KGTPPGLPL; GTPPGLPLF;
TPPGLPLFC; PPGLPLFCS; PGLPLFCSI; GLPLFCSIG; LPLFCSIGW; PLFCSIGWH; LFCSIGWHL;
YFIIYLNIS; SFRSLKGVS; FRSLKGVSP; RSLKGVSPI; SLKGVSPII; LKGVSPIIW; KGVSPIIWT;
GVSPIIWTH; VSPIIWTHH; SPIIWTHHC; PIIWTHHCR; IIWTHHCRV; IWTHHCRVS; WTHHCRVSS;
THHCRVSSV; HHCRVSSVR; HCRVSSVRS; CRVSSVRSK; RVSSVRSKP; VSSVRSKPN; SSVRSKPNH;
SVRSKPNHC; VRSKPNHCV; RSKPNHCVK; SKPNHCVKQ; KPNHCVKQS; PNHCVKQSM; NHCVKQSMQ;
QSIQTKGSF; SIQTKGSFL; IQTKGSFLK; QTKGSFLKN; TKGSFLKNF; KGSFLKNFL; GSFLKNFLF;
SFLKNFLFK; FLKNFLFKC; LKNFLFKCL; KNFLFKCLN; NFLFKCLNL; FLFKCLNLS; HSMQGQCTE;
SMQGQCTEG; MQGQCTEGF; QGQCTEGFL; GQCTEGFLE; QCTEGFLEQ; CTEGFLEQI; TEGFLEQIG;
EGFLEQIGH; GFLEQIGHS; FLEQIGHSL; LEQIGHSLQ; EQIGHSLQY; QIGHSLQYR; IGHSLQYRV;
GHSLQYRVS; HSLQYRVSG; SLQYRVSGQ; LQYRVSGQR; QYRVSGQRG; YRVSGQRGK; RVSGQRGKS;
VSGQRGKSA; SGQRGKSAQ; GQRGKSAQT; QRGKSAQTS; RGKSAQTSE; GKSAQTSEL; KSAQTSELL;
SAQTSELLQ; AQTSELLQV; QTSELLQVP; TSELLQVPK; SELLQVPKS; ELLQVPKSG; ATFTSCSIF;
TFTSCSIFL; FTSCSIFLY; TSCSIFLYK; SCSIFLYKV; CSIFLYKVF; SIFLYKVFI; IFLYKVFIL;

FLYKVFILF; LYKVFILFI; YKVFILFIL; KVFILFILS; VFILFILSS; FILFILSSS; ILFILSSSP; LFILSSSPP; FILSSSPPL; ILSSSPPLS; LSSSPPLSG; AFLIKGRFP; FLIKGRFPQ; LIKGRFPQA; IKGRFPQAA; KGRFPQAAL; GRFPQAALS; RFPQAALSR; FPQAALSRP; PQAALSRPK; QAALSRPKR; AALSRPKRS; ALSRPKRSM; LSRPKRSMS; SRPKRSMSS; RPKRSMSSM; PKRSMSSMD; KRSMSSMDS; RSMSSMDSS; SMSSMDSSL; MSSMDSSLL; SSMDSSLLR; SMDSSLLRT; MDSSLLRTL; DSSLLRTLS

10 mers:

FCKNCKRIGI; CKNCKRIGIS; KNCKRIGISP; NCKRIGISPN; CKRIGISPNS; KRIGISPNSF; RIGISPNSFA; IGISPNSFAR; GISPNSFARP; ISPNSFARPQ; SPNSFARPQK; PNSFARPQKK; NSFARPQKKP; SFARPQKKPP; FARPQKKPPH; ARPQKKPPHP; RPQKKPPHPY; PQKKPPHPYY; QKKPPHPYYL; KKPPHPYYLR; KPPHPYYLRE; PPHPYYLRER; PHPYYLRERV; HPYYLRERVE; PYYLRERVEA; YYLRERVEAE; YLRERVEAEA; LRERVEAEAA; RERVEAEAAS; ERVEAEAASA; RVEAEAASAS; VEAEAASASY; EAEAASASYI; AEAASASYIL; KKRPQGGAAY; KRPQGGAAYP; RPQGGAAYPW; PQGGAAYPWN; QGGAAYPWNA; GGAAYPWNAA; GAAYPWNAAK; AAYPWNAAKP; PQEGKCMTHR; QEGKCMTHRG; EGKCMTHRGM; GKCMTHRGMQ; KCMTHRGMQP; CMTHRGMQPN; MTHRGMQPNH; THRGMQPNHD; HRGMQPNHDL; RGMQPNHDLR; GMQPNHDLRK; MQPNHDLRKE; QPNHDLRKES; PNHDLRKESA; LTGRSCLPME; TGRSCLPMEC; GRSCLPMECS; RSCLPMECSQ; SCLPMECSQT; CLPMECSQTM; LPMECSQTMT; PMECSQTMTS; MECSQTMTSG; ECSQTMTSGR; CSQTMTSGRK; SQTMTSGRKV; QTMTSGRKVH; TMTSGRKVHD; MTSGRKVHDR; TSGRKVHDRH; SGRKVHDRHV; GRKVHDRHVL; RKVHDRHVLR; KVHDRHVLRA; ESWPCPQLNW; SWPCPQLNWT; WPCPQLNWTK; PCPQLNWTKA; CPQLNWTKAM; PQLNWTKAMV; QLNWTKAMVL; LNWTKAMVLR; NWTKAMVLRQ; WTKAMVLRQL; TKAMVLRQLS; KAMVLRQLSR; AMVLRQLSRQ; MVLRQLSRQA; VLRQLSRQAS; LRQLSRQASV; RQLSRQASVK; QLSRQASVKV; LSRQASVKVG; SRQASVKVGK; RQASVKVGKT; QASVKVGKTW; ASVKVGKTWT; SVKVGKTWTG; VKVGKTWTGT; KVGKTWTGTK; VGKTWTGTKK; GKTWTGTKKR; KTWTGTKKRA; TWTGTKKRAQ; WTGTKKRAQR; TGTKKRAQRI; GTKKRAQRIF; TKKRAQRIFI; KKRAQRIFIF; KRAQRIFIFI; RAQRIFIFIL; AQRIFIFILE; QRIFIFILEL; RIFIFILELL; IFIFILELLL; FIFILELLLE; IFILELLLEF; FILELLLEFC; ILELLLEFCR; LELLLEFCRG; ELLLEFCRGE; LLLEFCRGED; LLEFCRGEDS; LEFCRGEDSV; EFCRGEDSVD; FCRGEDSVDG; CRGEDSVDGK; RGEDSVDGKN; GEDSVDGKNK; EDSVDGKNKS; DSVDGKNKST; SVDGKNKSTT; VDGKNKSTTA; DGKNKSTTAL; GKNKSTTALP; KNKSTTALPA; NKSTTALPAV; KSTTALPAVK; STTALPAVKD; TTALPAVKDS; TALPAVKDSV; ALPAVKDSVK; LPAVKDSVKD; PAVKDSVKDS; VSNPFFFVFP; SNPFFFVFPG; NPFFFVFPGS; PFFFVFPGSW; FFFVFPGSWV; FFVFPGSWVL; FVFPGSWVLL; LPVYLRLLLP; PVYLRLLLPQ; VYLRLLLPQD; YLRLLLPQDF; LRLLLPQDFQ; RLLLPQDFQW; LLLPQDFQWL; LLPQDFQWLK; LPQDFQWLKL; PQDFQWLKLL; QDFQWLKLLL; DFQWLKLLLG; FQWLKLLLGR; QWLKLLLGRL; WLKLLLGRLL; LKLLLGRLLL; KLLLGRLLLL; LLVLLGLLLG; LVLLGLLLGL; VLLGLLLGLL; LLGLLLGLLL; GISSLMIGIT; ISSLMIGITK; SSLMIGITKF; SLMIGITKFP; LMIGITKFPL; ASISNQAWLW; SISNQAWLWN; ISNQAWLWNC; SNQAWLWNCL; NQAWLWNCLT; QAWLWNCLTQ; AWLWNCLTQM; WLWNCLTQMS; LWNCLTQMST; WNCLTQMSTM; NCLTQMSTMI; CLTQMSTMIF; LTQMSTMIFC; TQMSTMIFCF; QMSTMIFCFL; MSTMIFCFLV; ILLLIIFNTL; LLLIIFNTLI; LLIIFNTLIL; LIIFNTLILG; IIFNTLILGI; IFNTLILGIG; FNTLILGIGV; NTLILGIGVL; TLILGIGVLL; LILGIGVLLC; ILGIGVLLCL; LGIGVLLCLL; GIGVLLCLLL; IGVLLCLLLF; GVLLCLLLFP; VLLCLLLFPR; LLCLLLFPRL; LCLLLFPRLC; CLLLFPRLCG; LLLFPRLCGM; LLFPRLCGML; LFPRLCGMLL; FPRLCGMLLG; PRLCGMLLGM; RLCGMLLGMI; LCGMLLGMIY; CGMLLGMIYL; GMLLGMIYLL; PHRNCREEQK; HRNCREEQKD; RNCREEQKDF; NCREEQKDFL; CREEQKDFLE; REEQKDFLET; EEQKDFLETP; EQKDFLETPW; QKDFLETPWL; KDFLETPWLD; DFLETPWLDF; FLETPWLDFW; LETPWLDFWR; ETPWLDFWRK; TPWLDFWRKL; PWLDFWRKLP; WLDFWRKLPG; LDFWRKLPGQ; DFWRKLPGQL; TFIIIFNNII; FIIIFNNIIL; IIIFNNIILI; IIFNNIILIF; IFNNIILIFP; FNNIILIFPL; NNIILIFPLL; NIILIFPLLG; IILIFPLLGP; ILIFPLLGPQ; LIFPLLGPQW; IFPLLGPQWL; FPLLGPQWLD; PLLGPQWLDK; LKGKVPVYIL; KGKVPVYILA; GKVPVYILAI; KVPVYILAIL; VPVYILAILI; PVYILAILIV; EINKVYIQES; INKVYIQESL; KKLLPQEVLI; KLLPQEVLIK; LLPQEVLIKE; LPQEVLIKEL; PQEVLIKELL; QEVLIKELLL; EVLIKELLLN; VLIKELLLNG; LIKELLLNGC; IKELLLNGCC; KELLLNGCCL; ELLLNGCCLY; LLLNGCCLYF; HLLLKHMKMA; LLLKHMKMAP; LLKHMKMAPT; LKHMKMAPTK; KHMKMAPTKR; HMKMAPTKRK; MKMAPTKRKG; KMAPTKRKGE; MAPTKRKGEC; APTKRKGECP; PTKRKGECPG; TKRKGECPGA; KRKGECPGAA; RKGECPGAAP; KGECPGAAPK; GECPGAAPKK; ECPGAAPKKP; CPGAAPKKPK; PGAAPKKPKE; GAAPKKPKEP; AAPKKPKEPV; APKKPKEPVQ; PKKPKEPVQV; KKPKEPVQVP; KPKEPVQVPK; PKEPVQVPKL; KEPVQVPKLL; EPVQVPKLLI; PVQVPKLLIK; VQVPKLLIKG; QVPKLLIKGG; VPKLLIKGGV; PKLLIKGGVE; KLLIKGGVEV; LLIKGGVEVL; LIKGGVEVLE; IKGGVEVLEV; KGGVEVLEVK; GGVEVLEVKT; GVEVLEVKTG; VEVLEVKTGV; EVLEVKTGVD; VLEVKTGVDA; LEVKTGVDAI; EVKTGVDAIT; VKTGVDAITE; KTGVDAITEV; TGVDAITEVE; GVDAITEVEC; VDAITEVECF; DAITEVECFL; AITEVECFLN; ITEVECFLNP; TEVECFLNPE; EVECFLNPEM; VECFLNPEMG; ECFLNPEMGD; CFLNPEMGDP; FLNPEMGDPD; LNPEMGDPDE; NPEMGDPDEN; PEMGDPDENL; EMGDPDENLR; MGDPDENLRG; GDPDENLRGF; DPDENLRGFS; PDENLRGFSL; DENLRGFSLK; ENLRGFSLKL; NLRGFSLKLS; LRGFSLKLSA; RGFSLKLSAE; GFSLKLSAEN; FSLKLSAEND; SLKLSAENDF; LKLSAENDFS; KLSAENDFSS;

LSAENDFSSD; SAENDFSSDS; AENDFSSDSP; ENDFSSDSPE; NDFSSDSPER; DFSSDSPERK;
FSSDSPERKM; SSDSPERKML; SDSPERKMLP; DSPERKMLPC; SPERKMLPCY; PERKMLPCYS;
ERKMLPCYST; RKMLPCYSTA; KMLPCYSTAR; MLPCYSTARI; LPCYSTARIP; PCYSTARIPL;
CYSTARIPLP; YSTARIPLPN; STARIPLPNL; TARIPLPNLN; ARIPLPNLNE; RIPLPNLNED;
IPLPNLNEDL; PLPNLNEDLT; LPNLNEDLTC; PNLNEDLTCG; NLNEDLTCGN; LNEDLTCGNL;
NEDLTCGNLL; EDLTCGNLLM; DLTCGNLLMW; LTCGNLLMWE; TCGNLLMWEA; CGNLLMWEAV;
GNLLMWEAVT; NLLMWEAVTV; LLMWEAVTVQ; LMWEAVTVQT; MWEAVTVQTE; WEAVTVQTEV;
EAVTVQTEVI; AVTVQTEVIG; VTVQTEVIGI; TVQTEVIGIT; VQTEVIGITS; QTEVIGITSM;
TEVIGITSML; EVIGITSMLN; VIGITSMLNL; IGITSMLNLH; GITSMLNLHA; ITSMLNLHAG;
TSMLNLHAGS; SMLNLHAGSQ; MLNLHAGSQK; LNLHAGSQKV; NLHAGSQKVH; LHAGSQKVHE;
HAGSQKVHEH; AGSQKVHEHG; GSQKVHEHGG; SQKVHEHGGG; QKVHEHGGGK; KVHEHGGGKP;
VHEHGGGKPI; HEHGGGKPIQ; EHGGGKPIQG; HGGGKPIQGS; GGGKPIQGSN; GGKPIQGSNF;
GKPIQGSNFH; KPIQGSNFHF; PIQGSNFHFF; IQGSNFHFFA; QGSNFHFFAV; GSNFHFFAVG;
SNFHFFAVGG; NFHFFAVGGE; FHFFAVGGEP; HFFAVGGEPL; FFAVGGEPLE; FAVGGEPLEM;
AVGGEPLEMQ; VGGEPLEMQG; GGEPLEMQGV; GEPLEMQGVL; EPLEMQGVLM; PLEMQGVLMN;
LEMQGVLMNY; EMQGVLMNYR; MQGVLMNYRS; QGVLMNYRSK; GVLMNYRSKY; VLMNYRSKYP;
LMNYRSKYPD; MNYRSKYPDG; NYRSKYPDGT; YRSKYPDGTI; RSKYPDGTIT; SKYPDGTITP;
KYPDGTITPK; YPDGTITPKN; PDGTITPKNP; DGTITPKNPT; GTITPKNPTA; TITPKNPTAQ;
ITPKNPTAQS; TPKNPTAQSQ; PKNPTAQSQV; KNPTAQSQVM; NPTAQSQVMN; PTAQSQVMNT;
TAQSQVMNTD; AQSQVMNTDH; QSQVMNTDHK; SQVMNTDHKA; QVMNTDHKAY; VMNTDHKAYL;
MNTDHKAYLD; NTDHKAYLDK; TDHKAYLDKN; DHKAYLDKNN; HKAYLDKNNA; KAYLDKNNAY;
AYLDKNNAYP; YLDKNNAYPV; LDKNNAYPVE; DKNNAYPVEC; KNNAYPVECW; NNAYPVECWV;
NAYPVECWVP; AYPVECWVPD; YPVECWVPDP; PVECWVPDPS; VECWVPDPSR; ECWVPDPSRN;
CWVPDPSRNE; WVPDPSRNEN; VPDPSRNENA; PDPSRNENAR; DPSRNENARY; PSRNENARYF;
SRNENARYFG; RNENARYFGT; NENARYFGTF; ENARYFGTFT; NARYFGTFTG; ARYFGTFTGG;
RYFGTFTGGE; YFGTFTGGEN; FGTFTGGENV; GTFTGGENVP; TFTGGENVPP; FTGGENVPPV;
TGGENVPPVL; GGENVPPVLH; GENVPPVLHV; ENVPPVLHVT; NVPPVLHVTN; VPPVLHVTNT;
PPVLHVTNTA; PVLHVTNTAT; VLHVTNTATT; LHVTNTATTV; HVTNTATTVL; VTNTATTVLL;
TNTATTVLLD; NTATTVLLDE; TATTVLLDEQ; ATTVLLDEQG; TTVLLDEQGV; TVLLDEQGVG;
VLLDEQGVGP; LLDEQGVGPL; LDEQGVGPLC; DEQGVGPLCK; EQGVGPLCKA; QGVGPLCKAD;
GVGPLCKADS; VGPLCKADSL; GPLCKADSLY; PLCKADSLYV; LCKADSLYVS; CKADSLYVSA;
KADSLYVSAA; ADSLYVSAAD; DSLYVSAADI; SLYVSAADIC; LYVSAADICG; YVSAADICGL;
VSAADICGLF; SAADICGLFT; AADICGLFTN; ADICGLFTNS; DICGLFTNSS; ICGLFTNSSG;
CGLFTNSSGT; GLFTNSSGTQ; LFTNSSGTQQ; FTNSSGTQQW; TNSSGTQQWR; NSSGTQQWRG;
SSGTQQWRGL; SGTQQWRGLA; GTQQWRGLAR; TQQWRGLARY; QQWRGLARYF; QWRGLARYFK;
WRGLARYFKI; RGLARYFKIR; GLARYFKIRL; LARYFKIRLR; ARYFKIRLRK; RYFKIRLRKR;
YFKIRLRKRS; FKIRLRKRSV; KIRLRKRSVK; IRLRKRSVKN; RLRKRSVKNP; LRKRSVKNPY;
RKRSVKNPYP; KRSVKNPYPI; RSVKNPYPIS; SVKNPYPISF; VKNPYPISFL; KNPYPISFLL;
NPYPISFLLS; PYPISFLLSD; YPISFLLSDL; PISFLLSDLI; ISFLLSDLIN; SFLLSDLINR;
FLLSDLINRR; LLSDLINRRT; LSDLINRRTQ; SDLINRRTQR; DLINRRTQRV; LINRRTQRVD;
INRRTQRVDG; NRRTQRVDGQ; RRTQRVDGQP; RTQRVDGQPM; TQRVDGQPMY; QRVDGQPMYG;
RVDGQPMYGM; VDGQPMYGME; DGQPMYGMES; GQPMYGMESQ; QPMYGMESQV; PMYGMESQVE;
MYGMESQVEE; YGMESQVEEV; GMESQVEEVR; MESQVEEVRV; ESQVEEVRVF; SQVEEVRVFD;
QVEEVRVFDG; VEEVRVFDGT; EEVRVFDGTE; EVRVFDGTER; VRVFDGTERL; RVFDGTERLP;
VFDGTERLPG; FDGTERLPGD; DGTERLPGDP; GTERLPGDPD; TERLPGDPDM; ERLPGDPDMI;
RLPGDPDMIR; LPGDPDMIRY; PGDPDMIRYI; GDPDMIRYID; DPDMIRYIDK; PDMIRYIDKQ;
DMIRYIDKQG; MIRYIDKQGQ; IRYIDKQGQL; RYIDKQGQLQ; YIDKQGQLQT; IDKQGQLQTK;
DKQGQLQTKM; KQGQLQTKML; TGAFIVHIHL; GAFIVHIHLI; AFIVHIHLIN; FIVHIHLINA;
IVHIHLINAA; VHIHLINAAF; HIHLINAAFV; ATFKLVLFWG; TFKLVLFWGW; FKLVLFWGWC;
KLVLFWGWCF; LVLFWGWCFR; VLFWGWCFRP; LFWGWCFRPF; FWGWCFRPFK; WGWCFRPFKT;
GWCFRPFKTL; WCFRPFKTLK; CFRPFKTLKA; FRPFKTLKAF; RPFKTLKAFT; PFKTLKAFTQ;
FKTLKAFTQM; KTLKAFTQMQ; TLKAFTQMQL; LKAFTQMQLL; KAFTQMQLLT; AFTQMQLLTM;
FTQMQLLTMG; TQMQLLTMGV; ILFSCNIKNT; LFSCNIKNTF; FSCNIKNTFP; SCNIKNTFPH;
CNIKNTFPHA; NIKNTFPHAY; IKNTFPHAYI; KNTFPHAYII; NTFPHAYIIF; TFPHAYIIFH;
FPHAYIIFHP; KSIHTYLRIQ; SIHTYLRIQP; IHTYLRIQPF; HTYLRIQPFL; TYLRIQPFLP;
YLRIQPFLPF; LRIQPFLPFN; RIQPFLPFNN; IQPFLPFNNS; QPFLPFNNSR; PFLPFNNSRL;
FLPFNNSRLY; LPFNNSRLYI; PFNNSRLYIS; FNNSRLYISC; NNSRLYISCK; NSRLYISCKI;
SRLYISCKIS; RLYISCKISY; LYISCKISYR; YISCKISYRP; ISCKISYRPK; SCKISYRPKP;
CKISYRPKPN; IYFGPKIYLS; YFGPKIYLSY; FGPKIYLSYK; GPKIYLSYKS; PKIYLSYKSS;
KIYLSYKSSL; IYLSYKSSLQ; YLSYKSSLQG; LSYKSSLQGF; SYKSSLQGFR; YKSSLQGFRD;
KSSLQGFRDR; SSLQGFRDRI; SLQGFRDRIL; LQGFRDRILI; QGFRDRILIH; GFRDRILIHC;
FRDRILIHCN; RDRILIHCNQ; DRILIHCNQA; RILIHCNQAW; ILIHCNQAWW; LIHCNQAWWK;
IHCNQAWWKY; HCNQAWWKYL; CNQAWWKYLG; NQAWWKYLGS; QAWWKYLGSF; AWWKYLGSFV;
FSSCPFYIFK; SSCPFYIFKN; SCPFYIFKNN; CPFYIFKNNH; PFYIFKNNHV; FYIFKNNHVL;
YIFKNNHVLI; IFKNNHVLIY; FKNNHVLIYS; KNNHVLIYSY; NNHVLIYSYT; CCFSTINGTF;

CFSTINGTFK; PVSSFRYIEN; VSSFRYIENN; SSFRYIENNT; SFRYIENNTV; FRYIENNTVQ; RYIENNTVQK; YIENNTVQKI; IENNTVQKIK; ENNTVQKIKY; NNTVQKIKYY; NTVQKIKYYR; TVQKIKYYRI; VQKIKYYRIH; QKIKYYRIHF; KIKYYRIHFR; QTVQPSNTCH; TVQPSNTCHI; VQPSNTCHIL; QPSNTCHILF; HFFPGHMKGI; FFPGHMKGIY; FPGHMKGIYS; PGHMKGIYSF; GHMKGIYSFF; HMKGIYSFFS; NCIYCLLTNT; CIYCLLTNTF; IYCLLTNTFL; YCLLTNTFLI; CLLTNTFLIF; LLTNTFLIFT; LTNTFLIFTF; TNTFLIFTFC; NTFLIFTFCK; TFLIFTFCKN; FLIFTFCKNN; LIFTFCKNNS; IFTFCKNNSI; FTFCKNNSIC; TFCKNNSICK; FCKNNSICKV; CKNNSICKVL; KNNSICKVLF; NNSICKVLFM; NSICKVLFMI; SICKVLFMIL; ICKVLFMILK; CKVLFMILKV; KVLFMILKVI; VLFMILKVIR; LFMILKVIRL; FMILKVIRLV; MILKVIRLVF; ILKVIRLVFF; LKVIRLVFFL; KVIRLVFFLT; VIRLVFFLTL; IRLVFFLTLF; RLVFFLTLFT; LVFFLTLFTL; VFFLTLFTLL; FFLTLFTLLY; FLTLFTLLYI; LTLFTLLYIV; TLFTLLYIVL; LFTLLYIVLK; FTLLYIVLKF; KHILTLCLYC; HILTLCLYCI; ILTLCLYCIL; LTLCLYCILS; TLCLYCILSN; FPRHLLCFFR; PRHLLCFFRL; RHLLCFFRLF; HLLCFFRLFW; LLCFFRLFWA; LCFFRLFWAK; CFFRLFWAKI; FFRLFWAKIM; FRLFWAKIML; RLFWAKIMLL; APLNAFFYSM; PLNAFFYSMV; LNAFFYSMVW; NAFFYSMVWI; AFFYSMVWIS; FFYSMVWISS; KTKGTQLLTE; TKGTQLLTEI; KGTQLLTEII; GTQLLTEIIN; TQLLTEIINC; QLLTEIINCR; LLTEIINCRN; LTEIINCRNS; TEIINCRNSM; EIINCRNSMS; IINCRNSMSM; INCRNSMSMW; NCRNSMSMWS; KEYNIMPSTH; EYNIMPSTHV; YNIMPSTHVS; NIMPSTHVST; IMPSTHVSTN; MPSTHVSTNK; PSTHVSTNKS; STHVSTNKSY; THVSTNKSYR; HVSTNKSYRI; VSTNKSYRIF; STNKSYRIFF; TNKSYRIFFH; NKSYRIFFHK; KSYRIFFHKF; SYRIFFHKFF; YRIFFHKFFI; RIFFHKFFIQ; IFFHKFFIQN; FFHKFFIQNL; FHKFFIQNLS; HKFFIQNLSF; KFFIQNLSFF; FFIQNLSFFF; FIQNLSFFFS; IQNLSFFFSS; QNLSFFFSSI; NLSFFFSSIH; LSFFFSSIHS; SFFFSSIHSK; FFFSSIHSKA; FFSSIHSKAG; FSSIHSKAGK; SSIHSKAGKG; SIHSKAGKGS; IHSKAGKGSI; HSKAGKGSIT; SKAGKGSITK; KAGKGSITKY; AGKGSITKYS; GKGSITKYSL; KGSITKYSLT; GSITKYSLTK; SITKYSLTKK; ITKYSLTKKL; TKYSLTKKLV; IRGKVFRVFY; RGKVFRVFYL; GKVFRVFYLS; KVFRVFYLSF; VFRVFYLSFF; FRVFYLSFFF; RVFYLSFFFG; VFYLSFFFGW; FYLSFFFGWC; VLRICCCFFI; LRICCCFFIT; RICCCFFITG; ICCCFFITGK; CCCFFITGKH; CCFFITGKHI; CFFITGKHIF; FFITGKHIFM; FITGKHIFMA; ITGKHIFMAK; IFIPFFIKGT; FIPFFIKGTP; IPFFIKGTPP; PFFIKGTPPG; FFIKGTPPGL; FIKGTPPGLP; IKGTPPGLPL; KGTPPGLPLF; GTPPGLPLFC; TPPGLPLFCS; PPGLPLFCSI; PGLPLFCSIG; GLPLFCSIGW; LPLFCSIGWH; PLFCSIGWHL; SFRSLKGVSP; FRSLKGVSPI; RSLKGVSPII; SLKGVSPIIW; LKGVSPIIWT; KGVSPIIWTH; GVSPIIWTHH; VSPIIWTHHC; SPIIWTHHCR; PIIWTHHCRV; IIWTHHCRVS; IWTHHCRVSS; WTHHCRVSSV; THHCRVSSVR; HHCRVSSVRS; HCRVSSVRSK; CRVSSVRSKP; RVSSVRSKPN; VSSVRSKPNH; SSVRSKPNHC; SVRSKPNHCV; VRSKPNHCVK; RSKPNHCVKQ; SKPNHCVKQS; KPNHCVKQSM; PNHCVKQSMQ; QSIQTKGSFL; SIQTKGSFLK; IQTKGSFLKN; QTKGSFLKNF; TKGSFLKNFL; KGSFLKNFLF; GSFLKNFLFK; SFLKNFLFKC; FLKNFLFKCL; LKNFLFKCLN; KNFLFKCLNL; NFLFKCLNLS; HSMQGQCTEG; SMQGQCTEGF; MQGQCTEGFL; QGQCTEGFLE; GQCTEGFLEQ; QCTEGFLEQI; CTEGFLEQIG; TEGFLEQIGH; EGFLEQIGHS; GFLEQIGHSL; FLEQIGHSLQ; LEQIGHSLQY; EQIGHSLQYR; QIGHSLQYRV; IGHSLQYRVS; GHSLQYRVSG; HSLQYRVSGQ; SLQYRVSGQR; LQYRVSGQRG; QYRVSGQRGK; YRVSGQRGKS; RVSGQRGKSA; VSGQRGKSAQ; SGQRGKSAQT; GQRGKSAQTS; QRGKSAQTSE; RGKSAQTSEL; GKSAQTSELL; KSAQTSELLQ; SAQTSELLQV; AQTSELLQVP; QTSELLQVPK; TSELLQVPKS; SELLQVPKSG; ATFTSCSIFL; TFTSCSIFLY; FTSCSIFLYK; TSCSIFLYKV; SCSIFLYKVF; CSIFLYKVFI; SIFLYKVFIL; IFLYKVFILF; FLYKVFILFI; LYKVFILFIL; YKVFILFILS; KVFILFILSS; VFILFILSSS; FILFILSSSP; ILFILSSSPP; LFILSSSPPL; FILSSSPPLS; ILSSSPPLSG; AFLIKGRFPQ; FLIKGRFPQA; LIKGRFPQAA; IKGRFPQAAL; KGRFPQAALS; GRFPQAALSR; RFPQAALSRP; FPQAALSRPK; PQAALSRPKR; QAALSRPKRS; AALSRPKRSM; ALSRPKRSMS; LSRPKRSMSS; SRPKRSMSSM; RPKRSMSSMD; PKRSMSSMDS; KRSMSSMDSS; RSMSSMDSSL; SMSSMDSSLL; MSSMDSSLLR; SSMDSSLLRT; SMDSSLLRTL; MDSSLLRTLS

11 mers:

FCKNCKRIGIS; CKNCKRIGISP; KNCKRIGISPN; NCKRIGISPNS; CKRIGISPNSF; KRIGISPNSFA; RIGISPNSFAR; IGISPNSFARP; GISPNSFARPQ; ISPNSFARPQK; SPNSFARPQKK; PNSFARPQKKP; NSFARPQKKPP; SFARPQKKPPH; FARPQKKPPHP; ARPQKKPPHPY; RPQKKPPHPYY; PQKKPPHPYYL; QKKPPHPYYLR; KKPPHPYYLRE; KPPHPYYLRER; PPHPYYLRERV; PHPYYLRERVE; HPYYLRERVEA; PYYLRERVEAE; YYLRERVEAEA; YLRERVEAEAA; LRERVEAEAAS; RERVEAEAASA; ERVEAEAASAS; RVEAEAASASY; VEAEAASASYI; EAEAASASYIL; KKRPQGGAAYP; KRPQGGAAYPW; RPQGGAAYPWN; PQGGAAYPWNA; QGGAAYPWNAA; GGAAYPWNAAK; GAAYPWNAAKP; PQEGKCMTHRG; QEGKCMTHRGM; EGKCMTHRGMQ; GKCMTHRGMQP; KCMTHRGMQPN; CMTHRGMQPNH; MTHRGMQPNHD; THRGMQPNHDL; HRGMQPNHDLR; RGMQPNHDLRK; GMQPNHDLRKE; MQPNHDLRKES; QPNHDLRKESA; LTGRSCLPMEC; TGRSCLPMECS; GRSCLPMECSQ; RSCLPMECSQT; SCLPMECSQTM; CLPMECSQTMT; LPMECSQTMTS; PMECSQTMTSG; MECSQTMTSGR; ECSQTMTSGRK; CSQTMTSGRKV; SQTMTSGRKVH; QTMTSGRKVHD; TMTSGRKVHDR; MTSGRKVHDRH; TSGRKVHDRHV; SGRKVHDRHVL; GRKVHDRHVLR; RKVHDRHVLRA; ESWPCPQLNWT; SWPCPQLNWTK; WPCPQLNWTKA; PCPQLNWTKAM; CPQLNWTKAMV; PQLNWTKAMVL; QLNWTKAMVLR; LNWTKAMVLRQ; NWTKAMVLRQL; WTKAMVLRQLS; TKAMVLRQLSR; KAMVLRQLSRQ;

AMVLRQLSRQA; MVLRQLSRQAS; VLRQLSRQASV; LRQLSRQASVK; RQLSRQASVKV; QLSRQASVKVG;
LSRQASVKVGK; SRQASVKVGKT; RQASVKVGKTW; QASVKVGKTWT; ASVKVGKTWTG; SVKVGKTWTGT;
VKVGKTWTGTK; KVGKTWTGTKK; VGKTWTGTKKR; GKTWTGTKKRA; KTWTGTKKRAQ; TWTGTKKRAQR;
WTGTKKRAQRI; TGTKKRAQRIF; GTKKRAQRIFI; TKKRAQRIFIF; KKRAQRIFIFI; KRAQRIFIFIL;
RAQRIFIFILE; AQRIFIFILEL; QRIFIFILELL; RIFIFILELLL; IFIFILELLLE; FIFILELLLEF;
IFILELLLEFC; FILELLLEFCR; ILELLLEFCRG; LELLLEFCRGE; ELLLEFCRGED; LLLEFCRGEDS;
LLEFCRGEDSV; LEFCRGEDSVD; EFCRGEDSVDG; FCRGEDSVDGK; CRGEDSVDGKN; RGEDSVDGKNK;
GEDSVDGKNKS; EDSVDGKNKST; DSVDGKNKSTT; SVDGKNKSTTA; VDGKNKSTTAL; DGKNKSTTALP;
GKNKSTTALPA; KNKSTTALPAV; NKSTTALPAVK; KSTTALPAVKD; STTALPAVKDS; TTALPAVKDSV;
TALPAVKDSVK; ALPAVKDSVKD; LPAVKDSVKDS; VSNPFFFVFPG; SNPFFFVFPGS; NPFFFVFPGSW;
PFFFVFPGSWV; FFFVFPGSWVL; FFVFPGSWVLL; LPVYLRLLLPQ; PVYLRLLLPQD; VYLRLLLPQDF;
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LKLLLGRLLLL; LLVLLGLLLGL; LVLLGLLLGLL; VLLGLLLGLLL; GISSLMIGITK; ISSLMIGITKF;
SSLMIGITKFP; SLMIGITKFPL; ASISNQAWLWN; SISNQAWLWNC; ISNQAWLWNCL; SNQAWLWNCLT;
NQAWLWNCLTQ; QAWLWNCLTQM; AWLWNCLTQMS; WLWNCLTQMST; LWNCLTQMSTM; WNCLTQMSTMI;
NCLTQMSTMIF; CLTQMSTMIFC; LTQMSTMIFCF; TQMSTMIFCFL; QMSTMIFCFLV; ILLLIIFNTLI;
LLLIIFNTLIL; LLIIFNTLILG; LIIFNTLILGI; IIFNTLILGIG; IFNTLILGIGV; FNTLILGIGVL;
NTLILGIGVLL; TLILGIGVLLC; LILGIGVLLCL; ILGIGVLLCLL; LGIGVLLCLLL; GIGVLLCLLLF;
IGVLLCLLLFP; GVLLCLLLFPR; VLLCLLLFPRL; LLCLLLFPRLC; LCLLLFPRLCG; CLLLFPRLCGM;
LLLFPRLCGML; LLFPRLCGMLL; LFPRLCGMLLG; FPRLCGMLLGM; PRLCGMLLGMI; RLCGMLLGMIY;
LCGMLLGMIYL; CGMLLGMIYLL; PHRNCREEQKD; HRNCREEQKDF; RNCREEQKDFL; NCREEQKDFLE;
CREEQKDFLET; REEQKDFLETP; EEQKDFLETPW; EQKDFLETPWL; QKDFLETPWLD; KDFLETPWLDF;
DFLETPWLDFW; FLETPWLDFWR; LETPWLDFWRK; ETPWLDFWRKL; TPWLDFWRKLP; PWLDFWRKLPG;
WLDFWRKLPGQ; LDFWRKLPGQL; TFIIIFNNIIL; FIIIFNNIILI; IIIFNNIILIF; IIFNNIILIFP;
IFNNIILIFPL; FNNIILIFPLL; NNIILIFPLLG; NIILIFPLLGP; IILIFPLLGPQ; ILIFPLLGPQW;
LIFPLLGPQWL; IFPLLGPQWLD; FPLLGPQWLDK; LKGKVPVYILA; KGKVPVYILAI; GKVPVYILAIL;
KVPVYILAILI; VPVYILAILIV; EINKVYIQESL; KKLLPQEVLIK; KLLPQEVLIKE; LLPQEVLIKEL;
LPQEVLIKELL; PQEVLIKELLL; QEVLIKELLLN; EVLIKELLLNG; VLIKELLLNGC; LIKELLLNGCC;
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APTKRKGECPG; PTKRKGECPGA; TKRKGECPGAA; KRKGECPGAAP; RKGECPGAAPK; KGECPGAAPKK;
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KLLIKGGVEVL; LLIKGGVEVLE; LIKGGVEVLEV; IKGGVEVLEVK; KGGVEVLEVKT; GGVEVLEVKTG;
GVEVLEVKTGV; VEVLEVKTGVD; EVLEVKTGVDA; VLEVKTGVDAI; LEVKTGVDAIT; EVKTGVDAITE;
VKTGVDAITEV; KTGVDAITEVE; TGVDAITEVEC; GVDAITEVECF; VDAITEVECFL; DAITEVECFLN;
AITEVECFLNP; ITEVECFLNPE; TEVECFLNPEM; EVECFLNPEMG; VECFLNPEMGD; ECFLNPEMGDP;
CFLNPEMGDPD; FLNPEMGDPDE; LNPEMGDPDEN; NPEMGDPDENL; PEMGDPDENLR; EMGDPDENLRG;
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NLRGFSLKLSA; LRGFSLKLSAE; RGFSLKLSAEN; GFSLKLSAEND; FSLKLSAENDF; SLKLSAENDFS;
LKLSAENDFSS; KLSAENDFSSD; LSAENDFSSDS; SAENDFSSDSP; AENDFSSDSPE; ENDFSSDSPER;
NDFSSDSPERK; DFSSDSPERKM; FSSDSPERKML; SSDSPERKMLP; SDSPERKMLPC; DSPERKMLPCY;
SPERKMLPCYS; PERKMLPCYST; ERKMLPCYSTA; RKMLPCYSTAR; KMLPCYSTARI; MLPCYSTARIP;
LPCYSTARIPL; PCYSTARIPLP; CYSTARIPLPN; YSTARIPLPNL; STARIPLPNLN; TARIPLPNLNE;
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NLNEDLTCGNL; LNEDLTCGNLL; NEDLTCGNLLM; EDLTCGNLLMW; DLTCGNLLMWE; LTCGNLLMWEA;
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MWEAVTVQTEV; WEAVTVQTEVI; EAVTVQTEVIG; AVTVQTEVIGI; VTVQTEVIGIT; TVQTEVIGITS;
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GITSMLNLHAG; ITSMLNLHAGS; TSMLNLHAGSQ; SMLNLHAGSQK; MLNLHAGSQKV; LNLHAGSQKVH;
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QGSNFHFFAVG; GSNFHFFAVGG; SNFHFFAVGGE; NFHFFAVGGEP; FHFFAVGGEPL; HFFAVGGEPLE;
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HVTNTATTVLL; VTNTATTVLLD; TNTATTVLLDE; NTATTVLLDEQ; TATTVLLDEQG; ATTVLLDEQGV;
TTVLLDEQGVG; TVLLDEQGVGP; VLLDEQGVGPL; LLDEQGVGPLC; LDEQGVGPLCK; DEQGVGPLCKA;
EQGVGPLCKAD; QGVGPLCKADS; GVGPLCKADSL; VGPLCKADSLY; GPLCKADSLYV; PLCKADSLYVS;
LCKADSLYVSA; CKADSLYVSAA; KADSLYVSAAD; ADSLYVSAADI; DSLYVSAADIC; SLYVSAADICG;
LYVSAADICGL; YVSAADICGLF; VSAADICGLFT; SAADICGLFTN; AADICGLFTNS; ADICGLFTNSS;
DICGLFTNSSG; ICGLFTNSSGT; CGLFTNSSGTQ; GLFTNSSGTQQ; LFTNSSGTQQW; FTNSSGTQQWR;
TNSSGTQQWRG; NSSGTQQWRGL; SSGTQQWRGLA; SGTQQWRGLAR; GTQQWRGLARY; TQQWRGLARYF;
QQWRGLARYFK; QWRGLARYFKI; WRGLARYFKIR; RGLARYFKIRL; GLARYFKIRLR; LARYFKIRLRK;
ARYFKIRLRKR; RYFKIRLRKRS; YFKIRLRKRSV; FKIRLRKRSVK; KIRLRKRSVKN; IRLRKRSVKNP;
RLRKRSVKNPY; LRKRSVKNPYP; RKRSVKNPYPI; KRSVKNPYPIS; RSVKNPYPISF; SVKNPYPISFL;
VKNPYPISFLL; KNPYPISFLLS; NPYPISFLLSD; PYPISFLLSDL; YPISFLLSDLI; PISFLLSDLIN;
ISFLLSDLINR; SFLLSDLINRR; FLLSDLINRRT; LLSDLINRRTQ; LSDLINRRTQR; SDLINRRTQRV;
DLINRRTQRVD; LINRRTQRVDG; INRRTQRVDGQ; NRRTQRVDGQP; RRTQRVDGQPM; RTQRVDGQPMY;
TQRVDGQPMYG; QRVDGQPMYGM; RVDGQPMYGME; VDGQPMYGMES; DGQPMYGMESQ; GQPMYGMESQV;
QPMYGMESQVE; PMYGMESQVEE; MYGMESQVEEV; YGMESQVEEVR; GMESQVEEVRV; MESQVEEVRVF;
ESQVEEVRVFD; SQVEEVRVFDG; QVEEVRVFDGT; VEEVRVFDGTE; EEVRVFDGTER; EVRVFDGTERL;
VRVFDGTERLP; RVFDGTERLPG; VFDGTERLPGD; FDGTERLPGDP; DGTERLPGDPD; GTERLPGDPDM;
TERLPGDPDMI; ERLPGDPDMIR; RLPGDPDMIRY; LPGDPDMIRYI; PGDPDMIRYID; GDPDMIRYIDK;
DPDMIRYIDKQ; PDMIRYIDKQG; DMIRYIDKQGQ; MIRYIDKQGQL; IRYIDKQGQLQ; RYIDKQGQLQT;
YIDKQGQLQTK; IDKQGQLQTKM; DKQGQLQTKML; TGAFIVHIHLI; GAFIVHIHLIN; AFIVHIHLINA;
FIVHIHLINAA; IVHIHLINAAF; VHIHLINAAFV; ATFKLVLFWGW; TFKLVLFWGWC; FKLVLFWGWCF;
KLVLFWGWCFR; LVLFWGWCFRP; VLFWGWCFRPF; LFWGWCFRPFK; FWGWCFRPFKT; WGWCFRPFKTL;
GWCFRPFKTLK; WCFRPFKTLKA; CFRPFKTLKAF; FRPFKTLKAFT; RPFKTLKAFTQ; PFKTLKAFTQM;
FKTLKAFTQMQ; KTLKAFTQMQL; TLKAFTQMQLL; LKAFTQMQLLT; KAFTQMQLLTM; AFTQMQLLTMG;
FTQMQLLTMGV; ILFSCNIKNTF; LFSCNIKNTFP; FSCNIKNTFPH; SCNIKNTFPHA; CNIKNTFPHAY;
NIKNTFPHAYI; IKNTFPHAYII; KNTFPHAYIIF; NTFPHAYIIFH; TFPHAYIIFHP; KSIHTYLRIQP;
SIHTYLRIQPF; IHTYLRIQPFL; HTYLRIQPFLP; TYLRIQPFLPF; YLRIQPFLPFN; LRIQPFLPFNN;
RIQPFLPFNNS; IQPFLPFNNSR; QPFLPFNNSRL; PFLPFNNSRLY; FLPFNNSRLYI; LPFNNSRLYIS;
PFNNSRLYISC; FNNSRLYISCK; NNSRLYISCKI; NSRLYISCKIS; SRLYISCKISY; RLYISCKISYR;
LYISCKISYRP; YISCKISYRPK; ISCKISYRPKP; SCKISYRPKPN; IYFGPKIYLSY; YFGPKIYLSYK;
FGPKIYLSYKS; GPKIYLSYKSS; PKIYLSYKSSL; KIYLSYKSSLQ; IYLSYKSSLQG; YLSYKSSLQGF;
LSYKSSLQGFR; SYKSSLQGFRD; YKSSLQGFRDR; KSSLQGFRDRI; SSLQGFRDRIL; SLQGFRDRILI;
LQGFRDRILIH; QGFRDRILIHC; GFRDRILIHCN; FRDRILIHCNQ; RDRILIHCNQA; DRILIHCNQAW;
RILIHCNQAWW; ILIHCNQAWWK; LIHCNQAWWKY; IHCNQAWWKYL; HCNQAWWKYLG; CNQAWWKYLGS;
NQAWWKYLGSF; QAWWKYLGSFV; FSSCPFYIFKN; SSCPFYIFKNN; SCPFYIFKNNH; CPFYIFKNNHV;
PFYIFKNNHVL; FYIFKNNHVLI; YIFKNNHVLIY; IFKNNHVLIYS; FKNNHVLIYSY; KNNHVLIYSYT;
CCFSTINGTFK; PVSSFRYIENN; VSSFRYIENNT; SSFRYIENNTV; SFRYIENNTVQ; FRYIENNTVQK;
RYIENNTVQKI; YIENNTVQKIK; IENNTVQKIKY; ENNTVQKIKYY; NNTVQKIKYYR; NTVQKIKYYRI;
TVQKIKYYRIH; VQKIKYYRIHF; QKIKYYRIHFR; QTVQPSNTCHI; TVQPSNTCHIL; VQPSNTCHILF;
HFFPGHMKGIY; FFPGHMKGIYS; FPGHMKGIYSF; PGHMKGIYSFF; GHMKGIYSFFS; NCIYCLLTNTF;
CIYCLLTNTFL; IYCLLTNTFLI; YCLLTNTFLIF; CLLTNTFLIFT; LLTNTFLIFTF; LTNTFLIFTFC;
TNTFLIFTFCK; NTFLIFTFCKN; TFLIFTFCKNN; FLIFTFCKNNS; LIFTFCKNNSI; IFTFCKNNSIC;
FTFCKNNSICK; TFCKNNSICKV; FCKNNSICKVL; CKNNSICKVLF; KNNSICKVLFM; NNSICKVLFMI;
NSICKVLFMIL; SICKVLFMILK; ICKVLFMILKV; CKVLFMILKVI; KVLFMILKVIR; VLFMILKVIRL;
LFMILKVIRLV; FMILKVIRLVF; MILKVIRLVFF; ILKVIRLVFFL; LKVIRLVFFLT; KVIRLVFFLTL;
VIRLVFFLTLF; IRLVFFLTLFT; RLVFFLTLFTL; LVFFLTLFTLL; VFFLTLFTLLY; FFLTLFTLLYI;
FLTLFTLLYIV; LTLFTLLYIVL; TLFTLLYIVLK; LFTLLYIVLKF; KHILTLCLYCI; HILTLCLYCIL;
ILTLCLYCILS; LTLCLYCILSN; FPRHLLCFFRL; PRHLLCFFRLF; RHLLCFFRLFW; HLLCFFRLFWA;
LLCFFRLFWAK; LCFFRLFWAKI; CFFRLFWAKIM; FFRLFWAKIML; FRLFWAKIMLL; APLNAFFYSMV;
PLNAFFYSMVW; LNAFFYSMVWI; NAFFYSMVWIS; AFFYSMVWISS; KTKGTQLLTEI; TKGTQLLTEII;
KGTQLLTEIIN; GTQLLTEIINC; TQLLTEIINCR; QLLTEIINCRN; LLTEIINCRNS; LTEIINCRNSM;
TEIINCRNSMS; EIINCRNSMSM; IINCRNSMSMW; INCRNSMSMWS; KEYNIMPSTHV; EYNIMPSTHVS;
YNIMPSTHVST; NIMPSTHVSTN; IMPSTHVSTNK; MPSTHVSTNKS; PSTHVSTNKSY; STHVSTNKSYR;
THVSTNKSYRI; HVSTNKSYRIF; VSTNKSYRIFF; STNKSYRIFFH; TNKSYRIFFHK; NKSYRIFFHKF;
KSYRIFFHKFF; SYRIFFHKFFI; YRIFFHKFFIQ; RIFFHKFFIQN; IFFHKFFIQNL; FFHKFFIQNLS;
FHKFFIQNLSF; HKFFIQNLSFF; KFFIQNLSFFF; FFIQNLSFFFS; FIQNLSFFFSS; IQNLSFFFSSI;
QNLSFFFSSIH; NLSFFFSSIHS; LSFFFSSIHSK; SFFFSSIHSKA; FFFSSIHSKAG; FFSSIHSKAGK;
FSSIHSKAGKG; SSIHSKAGKGS; SIHSKAGKGSI; IHSKAGKGSIT; HSKAGKGSITK; SKAGKGSITKY;
KAGKGSITKYS; AGKGSITKYSL; GKGSITKYSLT; KGSITKYSLTK; GSITKYSLTKK; SITKYSLTKKL;
ITKYSLTKKLV; IRGKVFRVFYL; RGKVFRVFYLS; GKVFRVFYLSF; KVFRVFYLSFF; VFRVFYLSFFF;

FRVFYLSFFFG; RVFYLSFFFGW; VFYLSFFFGWC; VLRICCCFFIT; LRICCCFFITG; RICCCFFITGK; ICCCFFITGKH; CCCFFITGKHI; CCFFITGKHIF; CFFITGKHIFM; FFITGKHIFMA; FITGKHIFMAK; IFIPFFIKGTP; FIPFFIKGTPP; IPFFIKGTPPG; PFFIKGTPPGL; FFIKGTPPGLP; FIKGTPPGLPL; IKGTPPGLPLF; KGTPPGLPLFC; GTPPGLPLFCS; TPPGLPLFCSI; PPGLPLFCSIG; PGLPLFCSIGW; GLPLFCSIGWH; LPLFCSIGWHL; SFRSLKGVSPI; FRSLKGVSPII; RSLKGVSPIIW; SLKGVSPIIWT; LKGVSPIIWTH; KGVSPIIWTHH; GVSPIIWTHHC; VSPIIWTHHCR; SPIIWTHHCRV; PIIWTHHCRVS; IIWTHHCRVSS; IWTHHCRVSSV; WTHHCRVSSVR; THHCRVSSVRS; HHCRVSSVRSK; HCRVSSVRSKP; CRVSSVRSKPN; RVSSVRSKPNH; VSSVRSKPNHC; SSVRSKPNHCV; SVRSKPNHCVK; VRSKPNHCVKQ; RSKPNHCVKQS; SKPNHCVKQSM; KPNHCVKQSMQ; QSIQTKGSFLK; SIQTKGSFLKN; IQTKGSFLKNF; QTKGSFLKNFL; TKGSFLKNFLF; KGSFLKNFLFK; GSFLKNFLFKC; SFLKNFLFKCL; FLKNFLFKCLN; LKNFLFKCLNL; KNFLFKCLNLS; HSMQGQCTEGF; SMQGQCTEGFL; MQGQCTEGFLE; QGQCTEGFLEQ; GQCTEGFLEQI; QCTEGFLEQIG; CTEGFLEQIGH; TEGFLEQIGHS; EGFLEQIGHSL; GFLEQIGHSLQ; FLEQIGHSLQY; LEQIGHSLQYR; EQIGHSLQYRV; QIGHSLQYRVS; IGHSLQYRVSG; GHSLQYRVSGQ; HSLQYRVSGQR; SLQYRVSGQRG; LQYRVSGQRGK; QYRVSGQRGKS; YRVSGQRGKSA; RVSGQRGKSAQ; VSGQRGKSAQT; SGQRGKSAQTS; GQRGKSAQTSE; QRGKSAQTSEL; RGKSAQTSELL; GKSAQTSELLQ; KSAQTSELLQV; SAQTSELLQVP; AQTSELLQVPK; QTSELLQVPKS; TSELLQVPKSG; ATFTSCSIFLY; TFTSCSIFLYK; FTSCSIFLYKV; TSCSIFLYKVF; SCSIFLYKVFI; CSIFLYKVFIL; SIFLYKVFILF; IFLYKVFILFI; FLYKVFILFIL; LYKVFILFILS; YKVFILFILSS; KVFILFILSSS; VFILFILSSSP; FILFILSSSPP; ILFILSSSPPL; LFILSSSPPLS; FILSSSPPLSG; AFLIKGRFPQA; FLIKGRFPQAA; LIKGRFPQAAL; IKGRFPQAALS; KGRFPQAALSR; GRFPQAALSRP; RFPQAALSRPK; FPQAALSRPKR; PQAALSRPKRS; QAALSRPKRSM; AALSRPKRSMS; ALSRPKRSMSS; LSRPKRSMSSM; SRPKRSMSSMD; RPKRSMSSMDS; PKRSMSSMDSS; KRSMSSMDSSL; RSMSSMDSSLL; SMSSMDSSLLR; MSSMDSSLLRT; SSMDSSLLRTL; SMDSSLLRTLS

BK virus reading frame 2

8 mers:

GFPQIVLL; FPQIVLLG; PQIVLLGL; QIVLLGLR; IVLLGLRK; VLLGLRKS; LLGLRKSL; LGLRKSLH; GLRKSLHT; LRKSLHTL; RKSLHTLT; KSLHTLTT; EKGWRQRR; KGWRQRRP; GWRQRRPR; WRQRRPRP; RQRRPRPL; QRRPRPLI; RRPRPLIY; RPRPLIYY; PRPLIYYK; RPLIYYKK; PLIYYKKK; LIYYKKKG; IYYKKKGH; YYKKKGHR; YKKKGHRE; KKKGHREE; KKGHREEL; KGHREELL; GHREELLT; HREELLTH; REELLTHG; EELLTHGM; ELLTHGMQ; LLTHGMQP; LTHGMQPN; THGMQPNH; HGMQPNHD; GMQPNHDL; MQPNHDLR; QPNHDLRK; PNHDLRKE; NHDLRKES; HDLRKESA; LTGECSQT; TGECSQTM; GECSQTMT; ECSQTMTS; CSQTMTSG; SQTMTSGR; QTMTSGRK; TMTSGRKV; MTSGRKVH; TSGRKVHD; SGRKVHDS; GRKVHDSQ; RKVHDSQG; KVHDSQGG; VHDSQGGA; HDSQGGAA; DSQGGAAY; SQGGAAYP; QGGAAYPW; GGAAYPWN; GAAYPWNA; AAYPWNAA; AYPWNAAK; YPWNAAKP; PQEGKCMT; QEGKCMTD; EGKCMTDM; GKCMTDMF; KCMTDMFC; CMTDMFCE; MTDMFCEP; TDMFCEPR; DMFCEPRN; MFCEPRNL; FCEPRNLG; CEPRNLGL; EPRNLGLV; PRNLGLVP; RNLGLVPS; TGQRPWFC; GQRPWFCA; QRPWFCAS; RPWFCASC; PWFCASCH; WFCASCHD; FCASCHDK; CASCHDKL; ASCHDKLQ; KLVKPGLE; LVKPGLEQ; VKPGLEQK; KPGLEQKK; PGLEQKKE; GLEQKKEL; LEQKKELR; EQKKELRG; QKKELRGF; KKELRGFL; KELRGFLF; ELRGFLFL; LRGFLFLF; SFCWNFVE; FCWNFVEV; CWNFVEVK; WNFVEVKT; NFVEVKTV; TGKTKVPL; GKTKVPLL; KTKVPLLY; TKVPLLYL; KVPLLYLL; VIPFFLYF; IPFFLYFQ; PFFLYFQV; FFLYFQVH; FLYFQVHG; LYFQVHGC; YFQVHGCC; FQVHGCCS; QVHGCCSS; VHGCCSST; HGCCSSTF; GCCSSTFG; CCSSTFGG; CSSTFGGP; SSTFGGPS; STFGGPSC; TFGGPSCQ; FGGPSCQC; GGPSCQCI; GCCCHRIF; CCCHRIFS; CCHRIFSG; NCCWGGCC; CCWGGCCC; CWGGCCCY; WGGCCCYR; GGCCCYRS; GCCCYRSS; CCCYRSSN; CCYRSSNC; CYRSSNCI; YRSSNCIP; RSSNCIPC; SSNCIPCY; SNCIPCYC; NCIPCYCR; CIPCYCRG; IPCYCRGH; PCYCRGHN; CYCRGHNK; YCRGHNKY; CRGHNKYL; RGHNKYLR; GHNKYLRG; HNKYLRGY; NKYLRGYS; KYLRGYSC; YLRGYSCY; LRGYSCYR; RGYSCYRP; GYSCYRPN; YSCYRPNS; SCYRPNSS; CYRPNSSN; YRPNSSNI; RPNSSNIC; PNSSNICC; NSSNICCN; SSNICCNC; SNICCNCW; NICCNCWC; ICCNCWCS; CCNCWCSW; CNCWCSWG; NCWCSWGY; CWCSWGYC; WCSWGYCW; CSWGYCWV; SWGYCWVC; WGYCWVCC; GYCWVCCF; YCWVCCFN; CWVCCFNS; WVCCFNSN; VCCFNSNC; LGSQSFHC; GSQSFHCR; SQSFHCRP; QSFHCRPL; SFHCRPLS; FHCRPLSA; HCRPLSAI; CRPLSAIR; RPLSAIRH; PLSAIRHG; LSAIRHGF; SAIRHGFG; AIRHGFGI; IRHGFGIV; YSVSWCKY; SVSWCKYF; VSWCKYFC; ALGSFFVC; LGSFFVCY; GSFFVCYY; SFFVCYYF; FFVCYYFP; FVCYYFPG; VCYYFPGF; CYYFPGFV; YYFPGFVA; YFPGFVAC; FPGFVACY; YTFYNLTG; TFYNLTGI; FYNLTGIA; YNLTGIAE; NLTGIAEK; LTGIAEKN; TGIAEKNR; GIAEKNRK; IAEKNRKI; AEKNRKIF; IFGGNYLD; FGGNYLDN; GGNYLDNC; GNYLDNCK; NYLDNCKC; YLDNCKCP; LDNCKCPY; DNCKCPYK; NCKCPYKL; CKCPYKLL; KGRYPCTF; GRYPCTFW; RYPCTFWP; YPCTFWPY; PCTFWPYL; QYRRSYTK; YRRSYTKN; RRSYTKNG; RSYTKNGL; SYTKNGLK; YTKNGLKK; TKNGLKKS; KNGLKKST; NGLKKSTK; GLKKSTKC; LKKSTKCT; KKSTKCTF; KSTKCTFR; STKCTFRR; TKCTFRRV; KCTFRRVY; CTFRRVYR; TFRRVYRK; FRRVYRKN; RRVYRKNY; RVYRKNYC; VYRKNYCP; YRKNYCPR; RKNYCPRR; KNYCPRRC; SKNCSSMD; KNCSSMDV; NCSSMDVA; CSSMDVAF; SSMDVAFT; SMDVAFTS; MDVAFTSR; DVAFTSRP; VAFTSRPV; AFTSRPVR; FTSRPVRD;

TSRPVRDC; SRPVRDCN; RPVRDCNT; PVRDCNTC; VRDCNTCS; RWPQPKEK; WPQPKEKE;
PQPKEKES; QPKEKESV; PKEKESVQ; KEKESVQG; EKESVQGQ; KESVQGQL; ESVQGQLP;
SVQGQLPK; VQGQLPKS; QGQLPKSQ; GQLPKSQR; QLPKSQRN; LPKSQRNP; PKSQRNPC;
KSQRNPCK; SQRNPCKC; QRNPCKCQ; RNPCKCQN; NPCKCQNY; TQKWGIQM; QKWGIQMK;
KWGIQMKT; WGIQMKTL; GIQMKTLG; IQMKTLGA; QMKTLGAL; MKTLGALV; VLKMTLAV;
LKMTLAVI; KMTLAVIA; MTLAVIAQ; TLAVIAQR; LAVIAQRE; AVIAQREK; VIAQREKC;
IAQREKCF; AQREKCFP; QREKCFPV; REKCFPVT; EKCFPVTA; KCFPVTAQ; CFPVTAQQ;
FPVTAQQE; PVTAQQEF; VTAQQEFP; TAQQEFPS; AQQEFPSP; QQEFPSPI; LYKQRLLE;
LACLTFMQ; ACLTFMQG; CLTFMQGH; LTFMQGHK; TFMQGHKK; FMQGHKKC; MQGHKKCM;
QGHKKCMS; GHKKCMSM; HKKCMSMV; KKCMSMVE; KCMSMVEE; CMSMVEEN; MSMVEENL;
SMVEENLF; MVEENLFK; VEENLFKA; EENLFKAV; ENLFKAVI; NLFKAVIS; LFKAVIST;
FKAVISTS; KAVISTSL; AVISTSLL; VENPWKCR; ENPWKCRE; NPWKCREC; ITGQSTLM;
TGQSTLMV; GQSTLMVL; PLKTQQPS; LKTQQPSP; KTQQPSPR; ILTIRPIW; LTIRPIWT;
TIRPIWTK; IRPIWTKT; RPIWTKTM; PIWTKTML; IWTKTMLI; WTKTMLIQ; TKTMLIQL;
KTMLIQLS; TMLIQLSA; MLIQLSAG; LIQLSAGY; IQLSAGYL; QLSAGYLI; LSAGYLIP;
SAGYLIPV; AGYLIPVE; GYLIPVEM; YLIPVEMK; LIPVEMKM; IPVEMKML; PVEMKMLG;
VEMKMLGI; EMKMLGIL; MKMLGILG; KMLGILGL; MLGILGLS; LGILGLSQ; GILGLSQE;
ILGLSQEG; LGLSQEGK; GLSQEGKM; LSQEGKMF; SQEGKMFP; QEGKMFPQ; EGKMFPQY;
GKMFPQYF; KMFPQYFM; PTQLPQCC; MNRVWGLF; NRVWGLFV; RVWGLFVK; VWGLFVKL;
WGLFVKLI; GLFVKLIA; LFVKLIAC; FVKLIACM; VKLIACMF; KLIACMFQ; LIACMFQL;
IACMFQLL; ACMFQLLI; CMFQLLIF; MFQLLIFV; FQLLIFVA; QLLIFVAC; LLIFVACL;
LIFVACLL; IFVACLLT; FVACLLTA; VACLLTAL; ACLLTALE; CLLTALEH; LLTALEHN;
LTALEHNS; TALEHNSG; ALEHNSGE; LEHNSGEA; EHNSGEAL; HNSGEALQ; NSGEALQD;
SGEALQDI; GEALQDIL; EALQDILR; ALQDILRS; LQDILRSA; RILTQFPF; ILTQFPFC;
TGEPREWM; GEPREWMG; EPREWMGS; PREWMGSL; REWMGSLC; EWMGSLCM; WMGSLCMV;
MGSLCMVW; GSLCMVWN; SLCMVWNP; LCMVWNPR; KRLGCLMA; RLGCLMAQ; LGCLMAQK;
GCLMAQKD; CLMAQKDF; LMAQKDFQ; MAQKDFQG; AQKDFQGT; QKDFQGTQ; KDFQGTQI;
DILTNRDN; ILTNRDNC; LTNRDNCK; TNRDNCKP; NRDNCKPK; RDNCKPKC; DNCKPKCF;
NCKPKCFK; CKPKCFKQ; KPKCFKQV; PKCFKQVL; KCFKQVLL; CFKQVLLL; FKQVLLLY;
KQVLLLYI; QVLLLYIY; VLLLYIYI; MLLLYKPL; LLLYKPLL; LLYKPLLS; LYKPLLSL;
YKPLLSLC; KPLLSLCY; PLLSLCYF; LLSLCYFG; LSLCYFGG; SLCYFGGG; LCYFGGGV;
CYFGGGVL; YFGGGVLG; FGGGVLGL; GGGVLGLL; GGVLGLLK; GVLGLLKH; KPLHKCNS;
LWGSDLWE; WGSDLWES; GSDLWESS; SDLWESSA; DLWESSAG; LWESSAGA; WESSAGAE;
ESSAGAEV; SSAGAEVS; SAGAEVSE; AGAEVSET; GAEVSETW; AEVSETWE; EVSETWEE;
VSETWEEH; SETWEEHC; ETWEEHCD; TWEEHCDW; WEEHCDWD; EEHCDWDS; EHCDWDSV;
HCDWDSVL; CDWDSVLD; DWDSVLDP; WDSVLDPC; DSVLDPCP; SVLDPCPE; VLDPCPES;
LDPCPESS; DPCPESSV; PCPESSVS; CPESSVSE; PESSVSES; ESSVSESS; SSVSESSS;
SVSESSSL; VSESSSLV; SESSSLVI; ESSSLVIS; SSSLVISR; SSLVISRI; SLVISRIH;
LVISRIHF; VISRIHFP; ISRIHFPM; SRIHFPMH; RIHFPMHI; IHFPMHIL; HFPMHILY;
FPMHILYF; PMHILYFI; MHILYFIL; HILYFILE; ILYFILEK; LYFILEKV; YFILEKVY;
FILEKVYI; ILEKVYIL; LEKVYILI; EKVYILIS; KVYILISE; VYILISES; YILISESS;
ILISESSL; LISESSLS; ISESSLSF; SESSLSFH; ESSLSFHS; SSLSFHST; SLSFHSTI;
LSFHSTIL; SFHSTILD; FHSTILDC; HSTILDCI; STILDCIS; TILDCISV; ILDCISVA;
LDCISVAK; DCISVAKS; CISVAKSA; ISVAKSAT; SVAKSATG; VAKSATGL; AKSATGLN;
KSATGLNQ; SATGLNQI; ATGLNQIS; TGLNQISS; GLNQISSS; LNQISSSN; NQISSSNK;
QISSSNKV; ISSSNKVI; SSSNKVIP; SSNKVIPL; SNKVIPLC; NKVIPLCK; KVIPLCKI;
VIPLCKIL; IPLCKILF; PLCKILFS; LCKILFSS; CKILFSSK; KILFSSKN; ILFSSKNS;
LFSSKNSE; FSSKNSEF; SSKNSEFC; SKNSEFCK; KNSEFCKD; NSEFCKDF; SEFCKDFL;
EFCKDFLK; FCKDFLKY; CKDFLKYI; KDFLKYIL; DFLKYILG; FLKYILGL; LKYILGLK;
KYILGLKS; YILGLKSI; ILGLKSIC; LGLKSICL; GLKSICLT; LKSICLTN; KSICLTNL;
SICLTNLA; ICLTNLAC; CLTNLACR; LTNLACRV; TNLACRVL; NLACRVLG; LACRVLGT;
ACRVLGTG; CRVLGTGY; RVLGTGYS; VLGTGYSF; LGTGYSFI; GTGYSFIV; TGYSFIVT;
GYSFIVTK; YSFIVTKP; SFIVTKPG; FIVTKPGG; IVTKPGGN; VTKPGGNI; TKPGGNIW;
KPGGNIWV; PGGNIWVL; GGNIWVLL; GNIWVLLF; NIWVLLFK; IWVLLFKC; WVLLFKCF;
VLLFKCFF; LLFKCFFS; LFKCFFSK; FKCFFSKF; KCFFSKFT; CFFSKFTL; FFSKFTLT;
FSKFTLTL; SKFTLTLP; KFTLTLPS; FTLTLPSK; SLKLSKLF; LKLSKLFI; KLSKLFIP;
LSKLFIPC; SKLFIPCP; KLFIPCPE; LFIPCPEG; FIPCPEGK; IPCPEGKS; PCPEGKSF;
CPEGKSFD; PEGKSFDS; EGKSFDSA; GKSFDSAP; KSFDSAPV; SFDSAPVP; FDSAPVPF;
DSAPVPFT; SAPVPFTS; APVPFTSS; PVPFTSSK; VPFTSSKT; PFTSSKTT; FTSSKTTM;
TSSKTTMY; SIATPSSK; IATPSSKV; ATPSSKVS; TPSSKVSL; PSSKVSLS; SSKVSLSM;
SKVSLSMG; KVSLSMGR; VSLSMGRF; SLSMGRFT; LSMGRFTF; SMGRFTFK; MGRFTFKA;
GRFTFKAL; RFTFKALP; FTFKALPP; TFKALPPH; FKALPPHK; KALPPHKS; ALPPHKSN;
LPPHKSNN; PPHKSNNP; PHKSNNPA; HKSNNPAA; KSNNPAAS; SNNPAASV; NNPAASVV;
NPAASVVF; PAASVVFP; AASVVFPL; ASVVFPLS; SVVFPLSM; VVFPLSMG; VFPLSMGP;
FPLSMGPL; PLSMGPLN; LSMGPLNN; SMGPLNNQ; MGPLNNQY; GPLNNQYL; PLNNQYLL;

LNNQYLLL; NNQYLLLG; NQYLLLGT; QYLLLGTL; YLLLGTLK; LLLGTLKT; LLGTLKTI;
LGTLKTIQ; GTLKTIQC; TLKTIQCK; LKTIQCKK; KTIQCKKS; TIQCKKSN; IQCKKSNI;
QCKKSNIT; CKKSNITE; KKSNITES; KSNITESI; SNITESIL; NITESILG; ITESILGS;
TESILGSK; ESILGSKQ; SILGSKQC; ILGSKQCS; LGSKQCSQ; GSKQCSQA; SKQCSQAT;
KQCSQATP; QCSQATPA; CSQATPAI; SQATPAIY; QATPAIYC; ATPAIYCS; TPAIYCSS;
PAIYCSST; AIYCSSTA; IYCSSTAF; YCSSTAFP; APNIKSIL; PNIKSILS; NIKSILSN;
IKSILSNI; LNLSVSIS; NLSVSISS; LSVSISSL; SVSISSLV; VSISSLVI; RVSTLFLA;
VSTLFLAK; STLFLAKT; TLFLAKTV; LFLAKTVS; FLAKTVST; LAKTVSTA; AKTVSTAC;
FLLSAKII; LLSAKIIA; LSAKIIAF; SAKIIAFA; AKIIAFAK; KIIAFAKC; IIAFAKCF;
IAFAKCFS; HFLHSSTL; FLHSSTLY; NSKYIPNN; SKYIPNNK; KYIPNNKN; YIPNNKNT;
IPNNKNTS; PNNKNTSS; NNKNTSSH; NKNTSSHF; KNTSSHFV; NTSSHFVS; TSSHFVST;
SSHFVSTA; SHFVSTAY; HFVSTAYS; FVSTAYSV; VSTAYSVI; STAYSVIN; TAYSVINF;
AYSVINFQ; YSVINFQD; SVINFQDT; VINFQDTC; INFQDTCF; NFQDTCFV; FQDTCFVS;
QDTCFVSS; DTCFVSSG; TCFVSSGS; CFVSSGSS; FVSSGSSG; VSSGSSGL; SSGSSGLK;
SGSSGLKS; GSSGLKSC; SSGLKSCS; SGLKSCSF; GLKSCSFK; LKSCSFKP; KSCSFKPP;
MLSSIVWY; LSSIVWYG; SSIVWYGS; SIVWYGSL; IVWYGSLV; VWYGSLVK; WYGSLVKA;
YGSLVKAL; GSLVKALY; SLVKALYS; LVKALYSK; VKALYSKY; KALYSKYS; ALYSKYSL;
LYSKYSLL; YSKYSLLT; SKYSLLTP; KYSLLTPL; YSLLTPLQ; SLLTPLQI; LLTPLQIK;
LTPLQIKK; TPLQIKKL; PLQIKKLK; LQIKKLKV; QIKKLKVH; IKKLKVHS; KKLKVHSF;
QKLLIAET; KLLIAETL; LLIAETLC; LIAETLCL; IAETLCLC; AETLCLCG; ETLCLCGV;
TLCLCGVK; LCLCGVKK; CLCGVKKN; LCGVKKNI; CGVKKNII; GVKKNIIL; VKKNIILC;
KKNIILCP; KNIILCPA; NIILCPAH; IILCPAHM; ILCPAHMC; LCPAHMCL; CPAHMCLL;
PAHMCLLI; AHMCLLIK; HMCLLIKV; MCLLIKVT; CLLIKVTE; LLIKVTEY; LIKVTEYF;
IKVTEYFS; KVTEYFSI; VTEYFSIS; TEYFSISF; EYFSISFL; YFSISFLY; FSISFLYR;
SISFLYRI; AFSLVVYT; FSLVVYTA; SLVVYTAK; LVVYTAKQ; VVYTAKQA; VYTAKQAR;
YTAKQARV; TAKQARVL; AKQARVLL; KQARVLLL; QARVLLLN; ARVLLLNT; RVLLLNTA;
LRNWCRSE; RNWCRSEG; NWCRSEGK; WCRSEGKS; CRSEGKSL; RSEGKSLG; SEGKSLGS;
EGKSLGSS; GKSLGSST; KSLGSSTF; SLGSSTFL; LGSSTFLF; GSSTFLFF; SSTFLFFL;
STFLFFLG; TFLFFLGG; FLFFLGGV; LFFLGGVE; FFLGGVEC; ESAVASSS; SAVASSSL;
AVASSSLA; VASSSLAN; ASSSLANI; SSSLANIS; SSLANISS; SLANISSW; LANISSWQ;
ANISSWQN; NISSWQNK; ISSWQNKS; SSWQNKSS; SWQNKSSS; WQNKSSSH; QNKSSSHF;
NKSSSHFS; KSSSHFSL; SSSHFSLK; SSHFSLKE; SHFSLKEL; HFSLKELH; FSLKELHQ;
SLKELHQD; LKELHQDS; KELHQDSH; ELHQDSHS; LHQDSHSS; HQDSHSSV; QDSHSSVP;
VGTYKKNN; GTYKKNNY; TYKKNNYL; YKKNNYLG; KKNNYLGP; KNNYLGPF; NNYLGPFN;
NYLGPFNI; YLGPFNIL; LGPFNILL; GPFNILLF; PFNILLFI; VSYLKALD; SYLKALDL;
REFLQLFG; EFLQLFGP; FLQLFGPT; LQLFGPTI; QLFGPTIA; LFGPTIAE; FGPTIAEF;
GPTIAEFL; PTIAEFLQ; TIAEFLQL; IAEFLQLG; AEFLQLGL; EFLQLGLS; FLQLGLSQ;
LQLGLSQT; QLGLSQTT; LGLSQTTV; SSQCSSNL; SQCSSNLS; QCSSNLSK; CSSNLSKP;
SSNLSKPR; SNLSKPRA; NLSKPRAL; LSKPRALF; SKPRALFL; KPRALFLK; PRALFLKI;
RALFLKIF; ALFLKIFY; LFLKIFYL; FLKIFYLN; LKIFYLNA; KIFYLNAL; IFYLNALI;
ADIACKGS; DIACKGSA; IACKGSAQ; ACKGSAQK; CKGSAQKA; KGSAQKAF; GSAQKAFW;
SAQKAFWN; AQKAFWNK; AIPCSTGY; IPCSTGYL; PCSTGYLG; CSTGYLGK; STGYLGKE;
TGYLGKEE; GYLGKEEN; YLGKEENQ; LGKEENQH; GKEENQHK; KEENQHKP; EENQHKPL;
ENQHKPLS; NQHKPLSY; QHKPLSYS; HKPLSYSR; KPLSYSRF; PLSYSRFQ; LSYSRFQN;
SYSRFQNQ; YSRFQNQA; SRFQNQAD; RFQNQADE; FQNQADEL; QNQADELP; NQADELPL;
QADELPLH; ADELPLHP; DELPLHPA; ELPLHPAP; LPLHPAPF; PLHPAPFF; LHPAPFFY;
HPAPFFYT; PAPFFYTK; APFFYTKY; PFFYTKYS; FFYTKYSF; FYTKYSFS; YTKYSFSS;
TKYSFSSF; KYSFSSFY; YSFSSFYP; SFSSFYPR; FSSFYPRR; SSFYPRRP; SFYPRRPL;
FYPRRPLC; YPRRPLCQ; PRRPLCQG; RRPLCQGE; RPLCQGEI; PLCQGEIP; LCQGEIPY;
CQGEIPYT; QGEIPYTS; GEIPYTSL; EIPYTSLN; IPYTSLNK; PYTSLNKL; YTSLNKLF;
TSLNKLFS; SLNKLFSL; LNKLFSLR; NKLFSLRE; KLFSLRED; LFSLREDF; FSLREDFP;
SLREDFPR; LREDFPRQ; REDFPRQL; EDFPRQLF; DFPRQLFQ; FPRQLFQG; PRQLFQGL;
RQLFQGLK; QLFQGLKG; LFQGLKGP

9 mers:
GFPQIVLLG; FPQIVLLGL; PQIVLLGLR; QIVLLGLRK; IVLLGLRKS; VLLGLRKSL; LLGLRKSLH;
LGLRKSLHT; GLRKSLHTL; LRKSLHTLT; RKSLHTLTT; EKGWRQRRP; KGWRQRRPR; GWRQRRPRP;
WRQRRPRPL; RQRRPRPLI; QRRPRPLIY; RRPRPLIYY; RPRPLIYYK; PRPLIYYKK; RPLIYYKKK;
PLIYYKKKG; LIYYKKKGH; IYYKKKGHR; YYKKKGHRE; YKKKGHREE; KKKGHREEL; KKGHREELL;
KGHREELLT; GHREELLTH; HREELLTHG; REELLTHGM; EELLTHGMQ; ELLTHGMQP; LLTHGMQPN;
LTHGMQPNH; THGMQPNHD; HGMQPNHDL; GMQPNHDLR; MQPNHDLRK; QPNHDLRKE; PNHDLRKES;
NHDLRKESA; LTGECSQTM; TGECSQTMT; GECSQTMTS; ECSQTMTSG; CSQTMTSGR; SQTMTSGRK;
QTMTSGRKV; TMTSGRKVH; MTSGRKVHD; TSGRKVHDS; SGRKVHDSQ; GRKVHDSQG; RKVHDSQGG;
KVHDSQGGA; VHDSQGGAA; HDSQGGAAY; DSQGGAAYP; SQGGAAYPW; QGGAAYPWN; GGAAYPWNA;
GAAYPWNAA; AAYPWNAAK; AYPWNAAKP; PQEGKCMTD; QEGKCMTDM; EGKCMTDMF; GKCMTDMFC;
KCMTDMFCE; CMTDMFCEP; MTDMFCEPR; TDMFCEPRN; DMFCEPRNL; MFCEPRNLG; FCEPRNLGL;

CEPRNLGLV; EPRNLGLVP; PRNLGLVPS; TGQRPWFCA; GQRPWFCAS; QRPWFCASC; RPWFCASCH;
PWFCASCHD; WFCASCHDK; FCASCHDKL; CASCHDKLQ; KLVKPGLEQ; LVKPGLEQK; VKPGLEQKK;
KPGLEQKKE; PGLEQKKEL; GLEQKKELR; LEQKKELRG; EQKKELRGF; QKKELRGFL; KKELRGFLF;
KELRGFLFL; ELRGFLFLF; SFCWNFVEV; FCWNFVEVK; CWNFVEVKT; WNFVEVKTV; TGKTKVPLL;
GKTKVPLLY; KTKVPLLYL; TKVPLLYLL; VIPFFLYFQ; IPFFLYFQV; PFFLYFQVH; FFLYFQVHG;
FLYFQVHGC; LYFQVHGCC; YFQVHGCCS; FQVHGCCSS; QVHGCCSST; VHGCCSSTF; HGCCSSTFG;
GCCSSTFGG; CCSSTFGGP; CSSTFGGPS; SSTFGGPSC; STFGGPSCQ; TFGGPSCQC; FGGPSCQCI;
GCCCHRIFS; CCCHRIFSG; NCCWGGCCC; CCWGGCCCY; CWGGCCCYR; WGGCCCYRS; GGCCCYRSS;
GCCCYRSSN; CCCYRSSNC; CCYRSSNCI; CYRSSNCIP; YRSSNCIPC; RSSNCIPCY; SSNCIPCYC;
SNCIPCYCR; NCIPCYCRG; CIPCYCRGH; IPCYCRGHN; PCYCRGHNK; CYCRGHNKY; YCRGHNKYL;
CRGHNKYLR; RGHNKYLRG; GHNKYLRGY; HNKYLRGYS; NKYLRGYSC; KYLRGYSCY; YLRGYSCYR;
LRGYSCYRP; RGYSCYRPN; GYSCYRPNS; YSCYRPNSS; SCYRPNSSN; CYRPNSSNI; YRPNSSNIC;
RPNSSNICC; PNSSNICCN; NSSNICCNC; SSNICCNCW; SNICCNCWC; NICCNCWCS; ICCNCWCSW;
CCNCWCSWG; CNCWCSWGY; NCWCSWGYC; CWCSWGYCW; WCSWGYCWV; CSWGYCWVC; SWGYCWVCC;
WGYCWVCCF; GYCWVCCFN; YCWVCCFNS; CWVCCFNSN; WVCCFNSNC; LGSQSFHCR; GSQSFHCRP;
SQSFHCRPL; QSFHCRPLS; SFHCRPLSA; FHCRPLSAI; HCRPLSAIR; CRPLSAIRH; RPLSAIRHG;
PLSAIRHGF; LSAIRHGFG; SAIRHGFGI; AIRHGFGIV; YSVSWCKYF; SVSWCKYFC; ALGSFFVCY;
LGSFFVCYY; GSFFVCYYF; SFFVCYYFP; FFVCYYFPG; FVCYYFPGF; VCYYFPGFV; CYYFPGFVA;
YYFPGFVAC; YFPGFVACY; YTFYNLTGI; TFYNLTGIA; FYNLTGIAE; YNLTGIAEK; NLTGIAEKN;
LTGIAEKNR; TGIAEKNRK; GIAEKNRKI; IAEKNRKIF; IFGGNYLDN; FGGNYLDNC; GGNYLDNCK;
GNYLDNCKC; NYLDNCKCP; YLDNCKCPY; LDNCKCPYK; DNCKCPYKL; NCKCPYKLL; KGRYPCTFW;
GRYPCTFWP; RYPCTFWPY; YPCTFWPYL; QYRRSYTKN; YRRSYTKNG; RRSYTKNGL; RSYTKNGLK;
SYTKNGLKK; YTKNGLKKS; TKNGLKKST; KNGLKKSTK; NGLKKSTKC; GLKKSTKCT; LKKSTKCTF;
KKSTKCTFR; KSTKCTFRR; STKCTFRRV; TKCTFRRVY; KCTFRRVYR; CTFRRVYRK; TFRRVYRKN;
FRRVYRKNY; RRVYRKNYC; RVYRKNYCP; VYRKNYCPR; YRKNYCPRR; RKNYCPRRC; SKNCSSMDV;
KNCSSMDVA; NCSSMDVAF; CSSMDVAFT; SSMDVAFTS; SMDVAFTSR; MDVAFTSRP; DVAFTSRPV;
VAFTSRPVR; AFTSRPVRD; FTSRPVRDC; TSRPVRDCN; SRPVRDCNT; RPVRDCNTC; PVRDCNTCS;
RWPQPKEKE; WPQPKEKES; PQPKEKESV; QPKEKESVQ; PKEKESVQG; KEKESVQGQ; EKESVQGQL;
KESVQGQLP; ESVQGQLPK; SVQGQLPKS; VQGQLPKSQ; QGQLPKSQR; GQLPKSQRN; QLPKSQRNP;
LPKSQRNPC; PKSQRNPCK; KSQRNPCKC; SQRNPCKCQ; QRNPCKCQN; RNPCKCQNY; TQKWGIQMK;
QKWGIQMKT; KWGIQMKTL; WGIQMKTLG; GIQMKTLGA; IQMKTLGAL; QMKTLGALV; VLKMTLAVI;
LKMTLAVIA; KMTLAVIAQ; MTLAVIAQR; TLAVIAQRE; LAVIAQREK; AVIAQREKC; VIAQREKCF;
IAQREKCFP; AQREKCFPV; QREKCFPVT; REKCFPVTA; EKCFPVTAQ; KCFPVTAQQ; CFPVTAQQE;
FPVTAQQEF; PVTAQQEFP; VTAQQEFPS; TAQQEFPSP; AQQEFPSPI; LACLTFMQG; ACLTFMQGH;
CLTFMQGHK; LTFMQGHKK; TFMQGHKKC; FMQGHKKCM; MQGHKKCMS; QGHKKCMSM; GHKKCMSMV;
HKKCMSMVE; KKCMSMVEE; KCMSMVEEN; CMSMVEENL; MSMVEENLF; SMVEENLFK; MVEENLFKA;
VEENLFKAV; EENLFKAVI; ENLFKAVIS; NLFKAVIST; LFKAVISTS; FKAVISTSL; KAVISTSLL;
VENPWKCRE; ENPWKCREC; ITGQSTLMV; TGQSTLMVL; PLKTQQPSP; LKTQQPSPR; ILTIRPIWT;
LTIRPIWTK; TIRPIWTKT; IRPIWTKTM; RPIWTKTML; PIWTKTMLI; IWTKTMLIQ; WTKTMLIQL;
TKTMLIQLS; KTMLIQLSA; TMLIQLSAG; MLIQLSAGY; LIQLSAGYL; IQLSAGYLI; QLSAGYLIP;
LSAGYLIPV; SAGYLIPVE; AGYLIPVEM; GYLIPVEMK; YLIPVEMKM; LIPVEMKML; IPVEMKMLG;
PVEMKMLGI; VEMKMLGIL; EMKMLGILG; MKMLGILGL; KMLGILGLS; MLGILGLSQ; LGILGLSQE;
GILGLSQEG; ILGLSQEGK; LGLSQEGKM; GLSQEGKMF; LSQEGKMFP; SQEGKMFPQ; QEGKMFPQY;
EGKMFPQYF; GKMFPQYFM; MNRVWGLFV; NRVWGLFVK; RVWGLFVKL; VWGLFVKLI; WGLFVKLIA;
GLFVKLIAC; LFVKLIACM; FVKLIACMF; VKLIACMFQ; KLIACMFQL; LIACMFQLL; IACMFQLLI;
ACMFQLLIF; CMFQLLIFV; MFQLLIFVA; FQLLIFVAC; QLLIFVACL; LLIFVACLL; LIFVACLLT;
IFVACLLTA; FVACLLTAL; VACLLTALE; ACLLTALEH; CLLTALEHN; LLTALEHNS; LTALEHNSG;
TALEHNSGE; ALEHNSGEA; LEHNSGEAL; EHNSGEALQ; HNSGEALQD; NSGEALQDI; SGEALQDIL;
GEALQDILR; EALQDILRS; ALQDILRSA; RILTQFPFC; TGEPREWMG; GEPREWMGS; EPREWMGSL;
PREWMGSLC; REWMGSLCM; EWMGSLCMV; WMGSLCMVW; MGSLCMVWN; GSLCMVWNP; SLCMVWNPR;
KRLGCLMAQ; RLGCLMAQK; LGCLMAQKD; GCLMAQKDF; CLMAQKDFQ; LMAQKDFQG; MAQKDFQGT;
AQKDFQGTQ; QKDFQGTQI; DILTNRDNC; ILTNRDNCK; LTNRDNCKP; TNRDNCKPK; NRDNCKPKC;
RDNCKPKCF; DNCKPKCFK; NCKPKCFKQ; CKPKCFKQV; KPKCFKQVL; PKCFKQVLL; KCFKQVLLL;
CFKQVLLLY; FKQVLLLYI; KQVLLLYIY; QVLLLYIYI; MLLLYKPLL; LLLYKPLLS; LLYKPLLSL;
LYKPLLSLC; YKPLLSLCY; KPLLSLCYF; PLLSLCYFG; LLSLCYFGG; LSLCYFGGG; SLCYFGGGV;
LCYFGGGVL; CYFGGGVLG; YFGGGVLGL; FGGGVLGLL; GGGVLGLLK; GGVLGLLKH; LWGSDLWES;
WGSDLWESS; GSDLWESSA; SDLWESSAG; DLWESSAGA; LWESSAGAE; WESSAGAEV; ESSAGAEVS;
SSAGAEVSE; SAGAEVSET; AGAEVSETW; GAEVSETWE; AEVSETWEE; EVSETWEEH; VSETWEEHC;
SETWEEHCD; ETWEEHCDW; TWEEHCDWD; WEEHCDWDS; EEHCDWDSV; EHCDWDSVL; HCDWDSVLD;
CDWDSVLDP; DWDSVLDPC; WDSVLDPCP; DSVLDPCPE; SVLDPCPES; VLDPCPESS; LDPCPESSV;
DPCPESSVS; PCPESSVSE; CPESSVSES; PESSVSESS; ESSVSESSS; SSVSESSSL; SVSESSSLV;
VSESSSLVI; SESSSLVIS; ESSSLVISR; SSSLVISRI; SSLVISRIH; SLVISRIHF; LVISRIHFP;
VISRIHFPM; ISRIHFPMH; SRIHFPMHI; RIHFPMHIL; IHFPMHILY; HFPMHILYF; FPMHILYFI;
PMHILYFIL; MHILYFILE; HILYFILEK; ILYFILEKV; LYFILEKVY; YFILEKVYI; FILEKVYIL;
ILEKVYILI; LEKVYILIS; EKVYILISE; KVYILISES; VYILISESS; YILISESSL; ILISESSLS;

LISESSLSF; ISESSLSFH; SESSLSFHS; ESSLSFHST; SSLSFHSTI; SLSFHSTIL; LSFHSTILD;
SFHSTILDC; FHSTILDCI; HSTILDCIS; STILDCISV; TILDCISVA; ILDCISVAK; LDCISVAKS;
DCISVAKSA; CISVAKSAT; ISVAKSATG; SVAKSATGL; VAKSATGLN; AKSATGLNQ; KSATGLNQI;
SATGLNQIS; ATGLNQISS; TGLNQISSS; GLNQISSSN; LNQISSSNK; NQISSSNKV; QISSSNKVI;
ISSSNKVIP; SSSNKVIPL; SSNKVIPLC; SNKVIPLCK; NKVIPLCKI; KVIPLCKIL; VIPLCKILF;
IPLCKILFS; PLCKILFSS; LCKILFSSK; CKILFSSKN; KILFSSKNS; ILFSSKNSE; LFSSKNSEF;
FSSKNSEFC; SSKNSEFCK; SKNSEFCKD; KNSEFCKDF; NSEFCKDFL; SEFCKDFLK; EFCKDFLKY;
FCKDFLKYI; CKDFLKYIL; KDFLKYILG; DFLKYILGL; FLKYILGLK; LKYILGLKS; KYILGLKSI;
YILGLKSIC; ILGLKSICL; LGLKSICLT; GLKSICLTN; LKSICLTNL; KSICLTNLA; SICLTNLAC;
ICLTNLACR; CLTNLACRV; LTNLACRVL; TNLACRVLG; NLACRVLGT; LACRVLGTG; ACRVLGTGY;
CRVLGTGYS; RVLGTGYSF; VLGTGYSFI; LGTGYSFIV; GTGYSFIVT; TGYSFIVTK; GYSFIVTKP;
YSFIVTKPG; SFIVTKPGG; FIVTKPGGN; IVTKPGGNI; VTKPGGNIW; TKPGGNIWV; KPGGNIWVL;
PGGNIWVLL; GGNIWVLLF; GNIWVLLFK; NIWVLLFKC; IWVLLFKCF; WVLLFKCFF; VLLFKCFFS;
LLFKCFFSK; LFKCFFSKF; FKCFFSKFT; KCFFSKFTL; CFFSKFTLT; FFSKFTLTL; FSKFTLTLP;
SKFTLTLPS; KFTLTLPSK; SLKLSKLFI; LKLSKLFIP; KLSKLFIPC; LSKLFIPCP; SKLFIPCPE;
KLFIPCPEG; LFIPCPEGK; FIPCPEGKS; IPCPEGKSF; PCPEGKSFD; CPEGKSFDS; PEGKSFDSA;
EGKSFDSAP; GKSFDSAPV; KSFDSAPVP; SFDSAPVPF; FDSAPVPFT; DSAPVPFTS; SAPVPFTSS;
APVPFTSSK; PVPFTSSKT; VPFTSSKTT; PFTSSKTTM; FTSSKTTMY; SIATPSSKV; IATPSSKVS;
ATPSSKVSL; TPSSKVSLS; PSSKVSLSM; SSKVSLSMG; SKVSLSMGR; KVSLSMGRF; VSLSMGRFT;
SLSMGRFTF; LSMGRFTFK; SMGRFTFKA; MGRFTFKAL; GRFTFKALP; RFTFKALPP; FTFKALPPH;
TFKALPPHK; FKALPPHKS; KALPPHKSN; ALPPHKSNN; LPPHKSNNP; PPHKSNNPA; PHKSNNPAA;
HKSNNPAAS; KSNNPAASV; SNNPAASVV; NNPAASVVF; NPAASVVFP; PAASVVFPL; AASVVFPLS;
ASVVFPLSM; SVVFPLSMG; VVFPLSMGP; VFPLSMGPL; FPLSMGPLN; PLSMGPLNN; LSMGPLNNQ;
SMGPLNNQY; MGPLNNQYL; GPLNNQYLL; PLNNQYLLL; LNNQYLLLG; NNQYLLLGT; NQYLLLGTL;
QYLLLGTLK; YLLLGTLKT; LLLGTLKTI; LLGTLKTIQ; LGTLKTIQC; GTLKTIQCK; TLKTIQCKK;
LKTIQCKKS; KTIQCKKSN; TIQCKKSNI; IQCKKSNIT; QCKKSNITE; CKKSNITES; KKSNITESI;
KSNITESIL; SNITESILG; NITESILGS; ITESILGSK; TESILGSKQ; ESILGSKQC; SILGSKQCS;
ILGSKQCSQ; LGSKQCSQA; GSKQCSQAT; SKQCSQATP; KQCSQATPA; QCSQATPAI; CSQATPAIY;
SQATPAIYC; QATPAIYCS; ATPAIYCSS; TPAIYCSST; PAIYCSSTA; AIYCSSTAF; IYCSSTAFP;
APNIKSILS; PNIKSILSN; NIKSILSNI; LNLSVSISS; NLSVSISSL; LSVSISSLV; SVSISSLVI;
RVSTLFLAK; VSTLFLAKT; STLFLAKTV; TLFLAKTVS; LFLAKTVST; FLAKTVSTA; LAKTVSTAC;
FLLSAKIIA; LLSAKIIAF; LSAKIIAFA; SAKIIAFAK; AKIIAFAKC; KIIAFAKCF; IIAFAKCFS;
HFLHSSTLY; NSKYIPNNK; SKYIPNNKN; KYIPNNKNT; YIPNNKNTS; IPNNKNTSS; PNNKNTSSH;
NNKNTSSHF; NKNTSSHFV; KNTSSHFVS; NTSSHFVST; TSSHFVSTA; SSHFVSTAY; SHFVSTAYS;
HFVSTAYSV; FVSTAYSVI; VSTAYSVIN; STAYSVINF; TAYSVINFQ; AYSVINFQD; YSVINFQDT;
SVINFQDTC; VINFQDTCF; INFQDTCFV; NFQDTCFVS; FQDTCFVSS; QDTCFVSSG; DTCFVSSGS;
TCFVSSGSS; CFVSSGSSG; FVSSGSSGL; VSSGSSGLK; SSGSSGLKS; SGSSGLKSC; GSSGLKSCS;
SSGLKSCSF; SGLKSCSFK; GLKSCSFKP; LKSCSFKPP; MLSSIVWYG; LSSIVWYGS; SSIVWYGSL;
SIVWYGSLV; IVWYGSLVK; VWYGSLVKA; WYGSLVKAL; YGSLVKALY; GSLVKALYS; SLVKALYSK;
LVKALYSKY; VKALYSKYS; KALYSKYSL; ALYSKYSLL; LYSKYSLLT; YSKYSLLTP; SKYSLLTPL;
KYSLLTPLQ; YSLLTPLQI; SLLTPLQIK; LLTPLQIKK; LTPLQIKKL; TPLQIKKLK; PLQIKKLKV;
LQIKKLKVH; QIKKLKVHS; IKKLKVHSF; QKLLIAETL; KLLIAETLC; LLIAETLCL; LIAETLCLC;
IAETLCLCG; AETLCLCGV; ETLCLCGVK; TLCLCGVKK; LCLCGVKKN; CLCGVKKNI; LCGVKKNII;
CGVKKNIIL; GVKKNIILC; VKKNIILCP; KKNIILCPA; KNIILCPAH; NIILCPAHM; IILCPAHMC;
ILCPAHMCL; LCPAHMCLL; CPAHMCLLI; PAHMCLLIK; AHMCLLIKV; HMCLLIKVT; MCLLIKVTE;
CLLIKVTEY; LLIKVTEYF; LIKVTEYFS; IKVTEYFSI; KVTEYFSIS; VTEYFSISF; TEYFSISFL;
EYFSISFLY; YFSISFLYR; FSISFLYRI; AFSLVVYTA; FSLVVYTAK; SLVVYTAKQ; LVVYTAKQA;
VVYTAKQAR; VYTAKQARV; YTAKQARVL; TAKQARVLL; AKQARVLLL; KQARVLLLN; QARVLLLNT;
ARVLLLNTA; LRNWCRSEG; RNWCRSEGK; NWCRSEGKS; WCRSEGKSL; CRSEGKSLG; RSEGKSLGS;
SEGKSLGSS; EGKSLGSST; GKSLGSSTF; KSLGSSTFL; SLGSSTFLF; LGSSTFLFF; GSSTFLFFL;
SSTFLFFLG; STFLFFLGG; TFLFFLGGV; FLFFLGGVE; LFFLGGVEC; ESAVASSSL; SAVASSSLA;
AVASSSLAN; VASSSLANI; ASSSLANIS; SSSLANISS; SSLANISSW; SLANISSWQ; LANISSWQN;
ANISSWQNK; NISSWQNKS; ISSWQNKSS; SSWQNKSSS; SWQNKSSSH; WQNKSSSHF; QNKSSSHFS;
NKSSSHFSL; KSSSHFSLK; SSSHFSLKE; SSHFSLKEL; SHFSLKELH; HFSLKELHQ; FSLKELHQD;
SLKELHQDS; LKELHQDSH; KELHQDSHS; ELHQDSHSS; LHQDSHSSV; HQDSHSSVP; VGTYKKNNY;
GTYKKNNYL; TYKKNNYLG; YKKNNYLGP; KKNNYLGPF; KNNYLGPFN; NNYLGPFNI; NYLGPFNIL;
YLGPFNILL; LGPFNILLF; GPFNILLFI; VSYLKALDL; REFLQLFGP; EFLQLFGPT; FLQLFGPTI;
LQLFGPTIA; QLFGPTIAE; LFGPTIAEF; FGPTIAEFL; GPTIAEFLQ; PTIAEFLQL; TIAEFLQLG;
IAEFLQLGL; AEFLQLGLS; EFLQLGLSQ; FLQLGLSQT; LQLGLSQTT; QLGLSQTTV; SSQCSSNLS;
SQCSSNLSK; QCSSNLSKP; CSSNLSKPR; SSNLSKPRA; SNLSKPRAL; NLSKPRALF; LSKPRALFL;
SKPRALFLK; KPRALFLKI; PRALFLKIF; RALFLKIFY; ALFLKIFYL; LFLKIFYLN; FLKIFYLNA;
LKIFYLNAL; KIFYLNALI; ADIACKGSA; DIACKGSAQ; IACKGSAQK; ACKGSAQKA; CKGSAQKAF;
KGSAQKAFW; GSAQKAFWN; SAQKAFWNK; AIPCSTGYL; IPCSTGYLG; PCSTGYLGK; CSTGYLGKE;
STGYLGKEE; TGYLGKEEN; GYLGKEENQ; YLGKEENQH; LGKEENQHK; GKEENQHKP; KEENQHKPL;
EENQHKPLS; ENQHKPLSY; NQHKPLSYS; QHKPLSYSR; HKPLSYSRF; KPLSYSRFQ; PLSYSRFQN;

LSYSRFQNQ; SYSRFQNQA; YSRFQNQAD; SRFQNQADE; RFQNQADEL; FQNQADELP; QNQADELPL; NQADELPLH; QADELPLHP; ADELPLHPA; DELPLHPAP; ELPLHPAPF; LPLHPAPFF; PLHPAPFFY; LHPAPFFYT; HPAPFFYTK; PAPFFYTKY; APFFYTKYS; PFFYTKYSF; FFYTKYSFS; FYTKYSFSS; YTKYSFSSF; TKYSFSSFY; KYSFSSFYP; YSFSSFYPR; SFSSFYPRR; FSSFYPRRP; SSFYPRRPL; SFYPRRPLC; FYPRRPLCQ; YPRRPLCQG; PRRPLCQGE; RRPLCQGEI; RPLCQGEIP; PLCQGEIPY; LCQGEIPYT; CQGEIPYTS; QGEIPYTSL; GEIPYTSLN; EIPYTSLNK; IPYTSLNKL; PYTSLNKLF; YTSLNKLFS; TSLNKLFSL; SLNKLFSLR; LNKLFSLRE; NKLFSLRED; KLFSLREDF; LFSLREDFP; FSLREDFPR; SLREDFPRQ; LREDFPRQL; REDFPRQLF; EDFPRQLFQ; DFPRQLFQG; FPRQLFQGL; PRQLFQGLK; RQLFQGLKG; QLFQGLKGP

10 mers:

GFPQIVLLGL; FPQIVLLGLR; PQIVLLGLRK; QIVLLGLRKS; IVLLGLRKSL; VLLGLRKSLH; LLGLRKSLHT; LGLRKSLHTL; GLRKSLHTLT; LRKSLHTLTT; EKGWRQRRPR; KGWRQRRPRP; GWRQRRPRPL; WRQRRPRPLI; RQRRPRPLIY; QRRPRPLIYY; RRPRPLIYYK; RPRPLIYYKK; PRPLIYYKKK; RPLIYYKKKG; PLIYYKKKGH; LIYYKKKGHR; IYYKKKGHRE; YYKKKGHREE; YKKKGHREEL; KKKGHREELL; KKGHREELLT; KGHREELLTH; GHREELLTHG; HREELLTHGM; REELLTHGMQ; EELLTHGMQP; ELLTHGMQPN; LLTHGMQPNH; LTHGMQPNHD; THGMQPNHDL; HGMQPNHDLR; GMQPNHDLRK; MQPNHDLRKE; QPNHDLRKES; PNHDLRKESA; LTGECSQTMT; TGECSQTMTS; GECSQTMTSG; ECSQTMTSGR; CSQTMTSGRK; SQTMTSGRKV; QTMTSGRKVH; TMTSGRKVHD; MTSGRKVHDS; TSGRKVHDSQ; SGRKVHDSQG; GRKVHDSQGG; RKVHDSQGGA; KVHDSQGGAA; VHDSQGGAAY; HDSQGGAAYP; DSQGGAAYPW; SQGGAAYPWN; QGGAAYPWNA; GGAAYPWNAA; GAAYPWNAAK; AAYPWNAAKP; PQEGKCMTDM; QEGKCMTDMF; EGKCMTDMFC; GKCMTDMFCE; KCMTDMFCEP; CMTDMFCEPR; MTDMFCEPRN; TDMFCEPRNL; DMFCEPRNLG; MFCEPRNLGL; FCEPRNLGLV; CEPRNLGLVP; EPRNLGLVPS; TGQRPWFCAS; GQRPWFCASC; QRPWFCASCH; RPWFCASCHD; PWFCASCHDK; WFCASCHDKL; FCASCHDKLQ; KLVKPGLEQK; LVKPGLEQKK; VKPGLEQKKE; KPGLEQKKEL; PGLEQKKELR; GLEQKKELRG; LEQKKELRGF; EQKKELRGFL; QKKELRGFLF; KKELRGFLFL; KELRGFLFLF; SFCWNFVEVK; FCWNFVEVKT; CWNFVEVKTV; TGKTKVPLLY; GKTKVPLLYL; KTKVPLLYLL; VIPFFLYFQV; IPFFLYFQVH; PFFLYFQVHG; FFLYFQVHGC; FLYFQVHGCC; LYFQVHGCCS; YFQVHGCCSS; FQVHGCCSST; QVHGCCSSTF; VHGCCSSTFG; HGCCSSTFGG; GCCSSTFGGP; CCSSTFGGPS; CSSTFGGPSC; SSTFGGPSCQ; STFGGPSCQC; TFGGPSCQCI; GCCCHRIFSG; NCCWGGCCCY; CCWGGCCCYR; CWGGCCCYRS; WGGCCCYRSS; GGCCCYRSSN; GCCCYRSSNC; CCCYRSSNCI; CCYRSSNCIP; CYRSSNCIPC; YRSSNCIPCY; RSSNCIPCYC; SSNCIPCYCR; SNCIPCYCRG; NCIPCYCRGH; CIPCYCRGHN; IPCYCRGHNK; PCYCRGHNKY; CYCRGHNKYL; YCRGHNKYLR; CRGHNKYLRG; RGHNKYLRGY; GHNKYLRGYS; HNKYLRGYSC; NKYLRGYSCY; KYLRGYSCYR; YLRGYSCYRP; LRGYSCYRPN; RGYSCYRPNS; GYSCYRPNSS; YSCYRPNSSN; SCYRPNSSNI; CYRPNSSNIC; YRPNSSNICC; RPNSSNICCN; PNSSNICCNC; NSSNICCNCW; SSNICCNCWC; SNICCNCWCS; NICCNCWCSW; ICCNCWCSWG; CCNCWCSWGY; CNCWCSWGYC; NCWCSWGYCW; CWCSWGYCWV; WCSWGYCWVC; CSWGYCWVCC; SWGYCWVCCF; WGYCWVCCFN; GYCWVCCFNS; YCWVCCFNSN; CWVCCFNSNC; LGSQSFHCRP; GSQSFHCRPL; SQSFHCRPLS; QSFHCRPLSA; SFHCRPLSAI; FHCRPLSAIR; HCRPLSAIRH; CRPLSAIRHG; RPLSAIRHGF; PLSAIRHGFG; LSAIRHGFGI; SAIRHGFGIV; YSVSWCKYFC; ALGSFFVCYY; LGSFFVCYYF; GSFFVCYYFP; SFFVCYYFPG; FFVCYYFPGF; FVCYYFPGFV; VCYYFPGFVA; CYYFPGFVAC; YYFPGFVACY; YTFYNLTGIA; TFYNLTGIAE; FYNLTGIAEK; YNLTGIAEKN; NLTGIAEKNR; LTGIAEKNRK; TGIAEKNRKI; GIAEKNRKIF; IFGGNYLDNC; FGGNYLDNCK; GGNYLDNCKC; GNYLDNCKCP; NYLDNCKCPY; YLDNCKCPYK; LDNCKCPYKL; DNCKCPYKLL; KGRYPCTFWP; GRYPCTFWPY; RYPCTFWPYL; QYRRSYTKNG; YRRSYTKNGL; RRSYTKNGLK; RSYTKNGLKK; SYTKNGLKKS; YTKNGLKKST; TKNGLKKSTK; KNGLKKSTKC; NGLKKSTKCT; GLKKSTKCTF; LKKSTKCTFR; KKSTKCTFRR; KSTKCTFRRV; STKCTFRRVY; TKCTFRRVYR; KCTFRRVYRK; CTFRRVYRKN; TFRRVYRKNY; FRRVYRKNYC; RRVYRKNYCP; RVYRKNYCPR; VYRKNYCPRR; YRKNYCPRRC; SKNCSSMDVA; KNCSSMDVAF; NCSSMDVAFT; CSSMDVAFTS; SSMDVAFTSR; SMDVAFTSRP; MDVAFTSRPV; DVAFTSRPVR; VAFTSRPVRD; AFTSRPVRDC; FTSRPVRDCN; TSRPVRDCNT; SRPVRDCNTC; RPVRDCNTCS; RWPQPKEKES; WPQPKEKESV; PQPKEKESVQ; QPKEKESVQG; PKEKESVQGQ; KEKESVQGQL; EKESVQGQLP; KESVQGQLPK; ESVQGQLPKS; SVQGQLPKSQ; VQGQLPKSQR; QGQLPKSQRN; GQLPKSQRNP; QLPKSQRNPC; LPKSQRNPCK; PKSQRNPCKC; KSQRNPCKCQ; SQRNPCKCQN; QRNPCKCQNY; TQKWGIQMKT; QKWGIQMKTL; KWGIQMKTLG; WGIQMKTLGA; GIQMKTLGAL; IQMKTLGALV; VLKMTLAVIA; LKMTLAVIAQ; KMTLAVIAQR; MTLAVIAQRE; TLAVIAQREK; LAVIAQREKC; AVIAQREKCF; VIAQREKCFP; IAQREKCFPV; AQREKCFPVT; QREKCFPVTA; REKCFPVTAQ; EKCFPVTAQQ; KCFPVTAQQE; CFPVTAQQEF; FPVTAQQEFP; PVTAQQEFPS; VTAQQEFPSP; TAQQEFPSPI; LACLTFMQGH; ACLTFMQGHK; CLTFMQGHKK; LTFMQGHKKC; TFMQGHKKCM; FMQGHKKCMS; MQGHKKCMSM; QGHKKCMSMV; GHKKCMSMVE; HKKCMSMVEE; KKCMSMVEEN; KCMSMVEENL; CMSMVEENLF; MSMVEENLFK; SMVEENLFKA; MVEENLFKAV; VEENLFKAVI; EENLFKAVIS; ENLFKAVIST; NLFKAVISTS; LFKAVISTSL; FKAVISTSLL; VENPWKCREC; ITGQSTLMVL; PLKTQQPSPR; ILTIRPIWTK; LTIRPIWTKT; TIRPIWTKTM; IRPIWTKTML; RPIWTKTMLI; PIWTKTMLIQ; IWTKTMLIQL; WTKTMLIQLS; TKTMLIQLSA; KTMLIQLSAG; TMLIQLSAGY; MLIQLSAGYL; LIQLSAGYLI; IQLSAGYLIP;

QLSAGYLIPV; LSAGYLIPVE; SAGYLIPVEM; AGYLIPVEMK; GYLIPVEMKM; YLIPVEMKML;
LIPVEMKMLG; IPVEMKMLGI; PVEMKMLGIL; VEMKMLGILG; EMKMLGILGL; MKMLGILGLS;
KMLGILGLSQ; MLGILGLSQE; LGILGLSQEG; GILGLSQEGK; ILGLSQEGKM; LGLSQEGKMF;
GLSQEGKMFP; LSQEGKMFPQ; SQEGKMFPQY; QEGKMFPQYF; EGKMFPQYFM; MNRVWGLFVK;
NRVWGLFVKL; RVWGLFVKLI; VWGLFVKLIA; WGLFVKLIAC; GLFVKLIACM; LFVKLIACMF;
FVKLIACMFQ; VKLIACMFQL; KLIACMFQLL; LIACMFQLLI; IACMFQLLIF; ACMFQLLIFV;
CMFQLLIFVA; MFQLLIFVAC; FQLLIFVACL; QLLIFVACLL; LLIFVACLLT; LIFVACLLTA;
IFVACLLTAL; FVACLLTALE; VACLLTALEH; ACLLTALEHN; CLLTALEHNS; LLTALEHNSG;
LTALEHNSGE; TALEHNSGEA; ALEHNSGEAL; LEHNSGEALQ; EHNSGEALQD; HNSGEALQDI;
NSGEALQDIL; SGEALQDILR; GEALQDILRS; EALQDILRSA; TGEPREWMGS; GEPREWMGSL;
EPREWMGSLC; PREWMGSLCM; REWMGSLCMV; EWMGSLCMVW; WMGSLCMVWN; MGSLCMVWNP;
GSLCMVWNPR; KRLGCLMAQK; RLGCLMAQKD; LGCLMAQKDF; GCLMAQKDFQ; CLMAQKDFQG;
LMAQKDFQGT; MAQKDFQGTQ; AQKDFQGTQI; DILTNRDNCK; ILTNRDNCKP; LTNRDNCKPK;
TNRDNCKPKC; NRDNCKPKCF; RDNCKPKCFK; DNCKPKCFKQ; NCKPKCFKQV; CKPKCFKQVL;
KPKCFKQVLL; PKCFKQVLLL; KCFKQVLLLY; CFKQVLLLYI; FKQVLLLYIY; KQVLLLYIYI;
MLLLYKPLLS; LLLYKPLLSL; LLYKPLLSLC; LYKPLLSLCY; YKPLLSLCYF; KPLLSLCYFG;
PLLSLCYFGG; LLSLCYFGGG; LSLCYFGGGV; SLCYFGGGVL; LCYFGGGVLG; CYFGGGVLGL;
YFGGGVLGLL; FGGGVLGLLK; GGGVLGLLKH; LWGSDLWESS; WGSDLWESSA; GSDLWESSAG;
SDLWESSAGA; DLWESSAGAE; LWESSAGAEV; WESSAGAEVS; ESSAGAEVSE; SSAGAEVSET;
SAGAEVSETW; AGAEVSETWE; GAEVSETWEE; AEVSETWEEH; EVSETWEEHC; VSETWEEHCD;
SETWEEHCDW; ETWEEHCDWD; TWEEHCDWDS; WEEHCDWDSV; EEHCDWDSVL; EHCDWDSVLD;
HCDWDSVLDP; CDWDSVLDPC; DWDSVLDPCP; WDSVLDPCPE; DSVLDPCPES; SVLDPCPESS;
VLDPCPESSV; LDPCPESSVS; DPCPESSVSE; PCPESSVSES; CPESSVSESS; PESSVSESSS;
ESSVSESSSL; SSVSESSSLV; SVSESSSLVI; VSESSSLVIS; SESSSLVISR; ESSSLVISRI;
SSSLVISRIH; SSLVISRIHF; SLVISRIHFP; LVISRIHFPM; VISRIHFPMH; ISRIHFPMHI;
SRIHFPMHIL; RIHFPMHILY; IHFPMHILYF; HFPMHILYFI; FPMHILYFIL; PMHILYFILE;
MHILYFILEK; HILYFILEKV; ILYFILEKVY; LYFILEKVYI; YFILEKVYIL; FILEKVYILI;
ILEKVYILIS; LEKVYILISE; EKVYILISES; KVYILISESS; VYILISESSL; YILISESSLS;
ILISESSLSF; LISESSLSFH; ISESSLSFHS; SESSLSFHST; ESSLSFHSTI; SSLSFHSTIL;
SLSFHSTILD; LSFHSTILDC; SFHSTILDCI; FHSTILDCIS; HSTILDCISV; STILDCISVA;
TILDCISVAK; ILDCISVAKS; LDCISVAKSA; DCISVAKSAT; CISVAKSATG; ISVAKSATGL;
SVAKSATGLN; VAKSATGLNQ; AKSATGLNQI; KSATGLNQIS; SATGLNQISS; ATGLNQISSS;
TGLNQISSSN; GLNQISSSNK; LNQISSSNKV; NQISSSNKVI; QISSSNKVIP; ISSSNKVIPL;
SSSNKVIPLC; SSNKVIPLCK; SNKVIPLCKI; NKVIPLCKIL; KVIPLCKILF; VIPLCKILFS;
IPLCKILFSS; PLCKILFSSK; LCKILFSSKN; CKILFSSKNS; KILFSSKNSE; ILFSSKNSEF;
LFSSKNSEFC; FSSKNSEFCK; SSKNSEFCKD; SKNSEFCKDF; KNSEFCKDFL; NSEFCKDFLK;
SEFCKDFLKY; EFCKDFLKYI; FCKDFLKYIL; CKDFLKYILG; KDFLKYILGL; DFLKYILGLK;
FLKYILGLKS; LKYILGLKSI; KYILGLKSIC; YILGLKSICL; ILGLKSICLT; LGLKSICLTN;
GLKSICLTNL; LKSICLTNLA; KSICLTNLAC; SICLTNLACR; ICLTNLACRV; CLTNLACRVL;
LTNLACRVLG; TNLACRVLGT; NLACRVLGTG; LACRVLGTGY; ACRVLGTGYS; CRVLGTGYSF;
RVLGTGYSFI; VLGTGYSFIV; LGTGYSFIVT; GTGYSFIVTK; TGYSFIVTKP; GYSFIVTKPG;
YSFIVTKPGG; SFIVTKPGGN; FIVTKPGGNI; IVTKPGGNIW; VTKPGGNIWV; TKPGGNIWVL;
KPGGNIWVLL; PGGNIWVLLF; GGNIWVLLFK; GNIWVLLFKC; NIWVLLFKCF; IWVLLFKCFF;
WVLLFKCFFS; VLLFKCFFSK; LLFKCFFSKF; LFKCFFSKFT; FKCFFSKFTL; KCFFSKFTLT;
CFFSKFTLTL; FFSKFTLTLP; FSKFTLTLPS; SKFTLTLPSK; SLKLSKLFIP; LKLSKLFIPC;
KLSKLFIPCP; LSKLFIPCPE; SKLFIPCPEG; KLFIPCPEGK; LFIPCPEGKS; FIPCPEGKSF;
IPCPEGKSFD; PCPEGKSFDS; CPEGKSFDSA; PEGKSFDSAP; EGKSFDSAPV; GKSFDSAPVP;
KSFDSAPVPF; SFDSAPVPFT; FDSAPVPFTS; DSAPVPFTSS; SAPVPFTSSK; APVPFTSSKT;
PVPFTSSKTT; VPFTSSKTTM; PFTSSKTTMY; SIATPSSKVS; IATPSSKVSL; ATPSSKVSLS;
TPSSKVSLSM; PSSKVSLSMG; SSKVSLSMGR; SKVSLSMGRF; KVSLSMGRFT; VSLSMGRFTF;
SLSMGRFTFK; LSMGRFTFKA; SMGRFTFKAL; MGRFTFKALP; GRFTFKALPP; RFTFKALPPH;
FTFKALPPHK; TFKALPPHKS; FKALPPHKSN; KALPPHKSNN; ALPPHKSNNP; LPPHKSNNPA;
PPHKSNNPAA; PHKSNNPAAS; HKSNNPAASV; KSNNPAASVV; SNNPAASVVF; NNPAASVVFP;
NPAASVVFPL; PAASVVFPLS; AASVVFPLSM; ASVVFPLSMG; SVVFPLSMGP; VVFPLSMGPL;
VFPLSMGPLN; FPLSMGPLNN; PLSMGPLNNQ; LSMGPLNNQY; SMGPLNNQYL; MGPLNNQYLL;
GPLNNQYLLL; PLNNQYLLLG; LNNQYLLLGT; NNQYLLLGTL; NQYLLLGTLK; QYLLLGTLKT;
YLLLGTLKTI; LLLGTLKTIQ; LLGTLKTIQC; LGTLKTIQCK; GTLKTIQCKK; TLKTIQCKKS;
LKTIQCKKSN; KTIQCKKSNI; TIQCKKSNIT; IQCKKSNITE; QCKKSNITES; CKKSNITESI;
KKSNITESIL; KSNITESILG; SNITESILGS; NITESILGSK; ITESILGSKQ; TESILGSKQC;
ESILGSKQCS; SILGSKQCSQ; ILGSKQCSQA; LGSKQCSQAT; GSKQCSQATP; SKQCSQATPA;
KQCSQATPAI; QCSQATPAIY; CSQATPAIYC; SQATPAIYCS; QATPAIYCSS; ATPAIYCSST;
TPAIYCSSTA; PAIYCSSTAF; AIYCSSTAFP; APNIKSILSN; PNIKSILSNI; LNLSVSISSL;
NLSVSISSLV; LSVSISSLVI; RVSTLFLAKT; VSTLFLAKTV; STLFLAKTVS; TLFLAKTVST;
LFLAKTVSTA; FLAKTVSTAC; FLLSAKIIAF; LLSAKIIAFA; LSAKIIAFAK; SAKIIAFAKC;
AKIIAFAKCF; KIIAFAKCFS; NSKYIPNNKN; SKYIPNNKNT; KYIPNNKNTS; YIPNNKNTSS;

IPNNKNTSSH; PNNKNTSSHF; NNKNTSSHFV; NKNTSSHFVS; KNTSSHFVST; NTSSHFVSTA;
TSSHFVSTAY; SSHFVSTAYS; SHFVSTAYSV; HFVSTAYSVI; FVSTAYSVIN; VSTAYSVINF;
STAYSVINFQ; TAYSVINFQD; AYSVINFQDT; YSVINFQDTC; SVINFQDTCF; VINFQDTCFV;
INFQDTCFVS; NFQDTCFVSS; FQDTCFVSSG; QDTCFVSSGS; DTCFVSSGSS; TCFVSSGSSG;
CFVSSGSSGL; FVSSGSSGLK; VSSGSSGLKS; SSGSSGLKSC; SGSSGLKSCS; GSSGLKSCSF;
SSGLKSCSFK; SGLKSCSFKP; GLKSCSFKPP; MLSSIVWYGS; LSSIVWYGSL; SSIVWYGSLV;
SIVWYGSLVK; IVWYGSLVKA; VWYGSLVKAL; WYGSLVKALY; YGSLVKALYS; GSLVKALYSK;
SLVKALYSKY; LVKALYSKYS; VKALYSKYSL; KALYSKYSLL; ALYSKYSLLT; LYSKYSLLTP;
YSKYSLLTPL; SKYSLLTPLQ; KYSLLTPLQI; YSLLTPLQIK; SLLTPLQIKK; LLTPLQIKKL;
LTPLQIKKLK; TPLQIKKLKV; PLQIKKLKVH; LQIKKLKVHS; QIKKLKVHSF; QKLLIAETLC;
KLLIAETLCL; LLIAETLCLC; LIAETLCLCG; IAETLCLCGV; AETLCLCGVK; ETLCLCGVKK;
TLCLCGVKKN; LCLCGVKKNI; CLCGVKKNII; LCGVKKNIIL; CGVKKNIILC; GVKKNIILCP;
VKKNIILCPA; KKNIILCPAH; KNIILCPAHM; NIILCPAHMC; IILCPAHMCL; ILCPAHMCLL;
LCPAHMCLLI; CPAHMCLLIK; PAHMCLLIKV; AHMCLLIKVT; HMCLLIKVTE; MCLLIKVTEY;
CLLIKVTEYF; LLIKVTEYFS; LIKVTEYFSI; IKVTEYFSIS; KVTEYFSISF; VTEYFSISFL;
TEYFSISFLY; EYFSISFLYR; YFSISFLYRI; AFSLVVYTAK; FSLVVYTAKQ; SLVVYTAKQA;
LVVYTAKQAR; VVYTAKQARV; VYTAKQARVL; YTAKQARVLL; TAKQARVLLL; AKQARVLLLN;
KQARVLLLNT; QARVLLLNTA; LRNWCRSEGK; RNWCRSEGKS; NWCRSEGKSL; WCRSEGKSLG;
CRSEGKSLGS; RSEGKSLGSS; SEGKSLGSST; EGKSLGSSTF; GKSLGSSTFL; KSLGSSTFLF;
SLGSSTFLFF; LGSSTFLFFL; GSSTFLFFLG; SSTFLFFLGG; STFLFFLGGV; TFLFFLGGVE;
FLFFLGGVEC; ESAVASSSLA; SAVASSSLAN; AVASSSLANI; VASSSLANIS; ASSSLANISS;
SSSLANISSW; SSLANISSWQ; SLANISSWQN; LANISSWQNK; ANISSWQNKS; NISSWQNKSS;
ISSWQNKSSS; SSWQNKSSSH; SWQNKSSSHF; WQNKSSSHFS; QNKSSSHFSL; NKSSSHFSLK;
KSSSHFSLKE; SSSHFSLKEL; SSHFSLKELH; SHFSLKELHQ; HFSLKELHQD; FSLKELHQDS;
SLKELHQDSH; LKELHQDSHS; KELHQDSHSS; ELHQDSHSSV; LHQDSHSSVP; VGTYKKNNYL;
GTYKKNNYLG; TYKKNNYLGP; YKKNNYLGPF; KKNNYLGPFN; KNNYLGPFNI; NNYLGPFNIL;
NYLGPFNILL; YLGPFNILLF; LGPFNILLFI; REFLQLFGPT; EFLQLFGPTI; FLQLFGPTIA;
LQLFGPTIAE; QLFGPTIAEF; LFGPTIAEFL; FGPTIAEFLQ; GPTIAEFLQL; PTIAEFLQLG;
TIAEFLQLGL; IAEFLQLGLS; AEFLQLGLSQ; EFLQLGLSQT; FLQLGLSQTT; LQLGLSQTTV;
SSQCSSNLSK; SQCSSNLSKP; QCSSNLSKPR; CSSNLSKPRA; SSNLSKPRAL; SNLSKPRALF;
NLSKPRALFL; LSKPRALFLK; SKPRALFLKI; KPRALFLKIF; PRALFLKIFY; RALFLKIFYL;
ALFLKIFYLN; LFLKIFYLNA; FLKIFYLNAL; LKIFYLNALI; ADIACKGSAQ; DIACKGSAQK;
IACKGSAQKA; ACKGSAQKAF; CKGSAQKAFW; KGSAQKAFWN; GSAQKAFWNK; AIPCSTGYLG;
IPCSTGYLGK; PCSTGYLGKE; CSTGYLGKEE; STGYLGKEEN; TGYLGKEENQ; GYLGKEENQH;
YLGKEENQHK; LGKEENQHKP; GKEENQHKPL; KEENQHKPLS; EENQHKPLSY; ENQHKPLSYS;
NQHKPLSYSR; QHKPLSYSRF; HKPLSYSRFQ; KPLSYSRFQN; PLSYSRFQNQ; LSYSRFQNQA;
SYSRFQNQAD; YSRFQNQADE; SRFQNQADEL; RFQNQADELP; FQNQADELPL; QNQADELPLH;
NQADELPLHP; QADELPLHPA; ADELPLHPAP; DELPLHPAPF; ELPLHPAPFF; LPLHPAPFFY;
PLHPAPFFYT; LHPAPFFYTK; HPAPFFYTKY; PAPFFYTKYS; APFFYTKYSF; PFFYTKYSFS;
FFYTKYSFSS; FYTKYSFSSF; YTKYSFSSFY; TKYSFSSFYP; KYSFSSFYPR; YSFSSFYPRR;
SFSSFYPRRP; FSSFYPRRPL; SSFYPRRPLC; SFYPRRPLCQ; FYPRRPLCQG; YPRRPLCQGE;
PRRPLCQGEI; RRPLCQGEIP; RPLCQGEIPY; PLCQGEIPYT; LCQGEIPYTS; CQGEIPYTSL;
QGEIPYTSLN; GEIPYTSLNK; EIPYTSLNKL; IPYTSLNKLF; PYTSLNKLFS; YTSLNKLFSL;
TSLNKLFSLR; SLNKLFSLRE; LNKLFSLRED; NKLFSLREDF; KLFSLREDFP; LFSLREDFPR;
FSLREDFPRQ; SLREDFPRQL; LREDFPRQLF; REDFPRQLFQ; EDFPRQLFQG; DFPRQLFQGL;
FPRQLFQGLK; PRQLFQGLKG; RQLFQGLKGP

11 mers:

GFPQIVLLGLR; FPQIVLLGLRK; PQIVLLGLRKS; QIVLLGLRKSL; IVLLGLRKSLH; VLLGLRKSLHT;
LLGLRKSLHTL; LGLRKSLHTLT; GLRKSLHTLTT; EKGWRQRRPRP; KGWRQRRPRPL; GWRQRRPRPLI;
WRQRRPRPLIY; RQRRPRPLIYY; QRRPRPLIYYK; RRPRPLIYYKK; RPRPLIYYKKK; PRPLIYYKKKG;
RPLIYYKKKGH; PLIYYKKKGHR; LIYYKKKGHRE; IYYKKKGHREE; YYKKKGHREEL; YKKKGHREELL;
KKKGHREELLT; KKGHREELLTH; KGHREELLTHG; GHREELLTHGM; HREELLTHGMQ; REELLTHGMQP;
EELLTHGMQPN; ELLTHGMQPNH; LLTHGMQPNHD; LTHGMQPNHDL; THGMQPNHDLR; HGMQPNHDLRK;
GMQPNHDLRKE; MQPNHDLRKES; QPNHDLRKESA; LTGECSQTMTS; TGECSQTMTSG; GECSQTMTSGR;
ECSQTMTSGRK; CSQTMTSGRKV; SQTMTSGRKVH; QTMTSGRKVHD; TMTSGRKVHDS; MTSGRKVHDSQ;
TSGRKVHDSQG; SGRKVHDSQGG; GRKVHDSQGGA; RKVHDSQGGAA; KVHDSQGGAAY; VHDSQGGAAYP;
HDSQGGAAYPW; DSQGGAAYPWN; SQGGAAYPWNA; QGGAAYPWNAA; GGAAYPWNAAK; GAAYPWNAAKP;
PQEGKCMTDMF; QEGKCMTDMFC; EGKCMTDMFCE; GKCMTDMFCEP; KCMTDMFCEPR; CMTDMFCEPRN;
MTDMFCEPRNL; TDMFCEPRNLG; DMFCEPRNLGL; MFCEPRNLGLV; FCEPRNLGLVP; CEPRNLGLVPS;
TGQRPWFCASC; GQRPWFCASCH; QRPWFCASCHD; RPWFCASCHDK; PWFCASCHDKL; WFCASCHDKLQ;
KLVKPGLEQKK; LVKPGLEQKKE; VKPGLEQKKEL; KPGLEQKKELR; PGLEQKKELRG; GLEQKKELRGF;
LEQKKELRGFL; EQKKELRGFLF; QKKELRGFLFL; KKELRGFLFLF; SFCWNFVEVKT; FCWNFVEVKTV;
TGKTKVPLLYL; GKTKVPLLYLL; VIPFFLYFQVH; IPFFLYFQVHG; PFFLYFQVHGC; FFLYFQVHGCC;
FLYFQVHGCCS; LYFQVHGCCSS; YFQVHGCCSST; FQVHGCCSSTF; QVHGCCSSTFG; VHGCCSSTFGG;
HGCCSSTFGGP; GCCSSTFGGPS; CCSSTFGGPSC; CSSTFGGPSCQ; SSTFGGPSCQC; STFGGPSCQCI;

NCCWGGCCCYR; CCWGGCCCYRS; CWGGCCCYRSS; WGGCCCYRSSN; GGCCCYRSSNC; GCCCYRSSNCI;
CCCYRSSNCIP; CCYRSSNCIPC; CYRSSNCIPCY; YRSSNCIPCYC; RSSNCIPCYCR; SSNCIPCYCRG;
SNCIPCYCRGH; NCIPCYCRGHN; CIPCYCRGHNK; IPCYCRGHNKY; PCYCRGHNKYL; CYCRGHNKYLR;
YCRGHNKYLRG; CRGHNKYLRGY; RGHNKYLRGYS; GHNKYLRGYSC; HNKYLRGYSCY; NKYLRGYSCYR;
KYLRGYSCYRP; YLRGYSCYRPN; LRGYSCYRPNS; RGYSCYRPNSS; GYSCYRPNSSN; YSCYRPNSSNI;
SCYRPNSSNIC; CYRPNSSNICC; YRPNSSNICCN; RPNSSNICCNC; PNSSNICCNCW; NSSNICCNCWC;
SSNICCNCWCS; SNICCNCWCSW; NICCNCWCSWG; ICCNCWCSWGY; CCNCWCSWGYC; CNCWCSWGYCW;
NCWCSWGYCWV; CWCSWGYCWVC; WCSWGYCWVCC; CSWGYCWVCCF; SWGYCWVCCFN; WGYCWVCCFNS;
GYCWVCCFNSN; YCWVCCFNSNC; LGSQSFHCRPL; GSQSFHCRPLS; SQSFHCRPLSA; QSFHCRPLSAI;
SFHCRPLSAIR; FHCRPLSAIRH; HCRPLSAIRHG; CRPLSAIRHGF; RPLSAIRHGFG; PLSAIRHGFGI;
LSAIRHGFGIV; ALGSFFVCYYF; LGSFFVCYYFP; GSFFVCYYFPG; SFFVCYYFPGF; FFVCYYFPGFV;
FVCYYFPGFVA; VCYYFPGFVAC; CYYFPGFVACY; YTFYNLTGIAE; TFYNLTGIAEK; FYNLTGIAEKN;
YNLTGIAEKNR; NLTGIAEKNRK; LTGIAEKNRKI; TGIAEKNRKIF; IFGGNYLDNCK; FGGNYLDNCKC;
GGNYLDNCKCP; GNYLDNCKCPY; NYLDNCKCPYK; YLDNCKCPYKL; LDNCKCPYKLL; KGRYPCTFWPY;
GRYPCTFWPYL; QYRRSYTKNGL; YRRSYTKNGLK; RRSYTKNGLKK; RSYTKNGLKKS; SYTKNGLKKST;
YTKNGLKKSTK; TKNGLKKSTKC; KNGLKKSTKCT; NGLKKSTKCTF; GLKKSTKCTFR; LKKSTKCTFRR;
KKSTKCTFRRV; KSTKCTFRRVY; STKCTFRRVYR; TKCTFRRVYRK; KCTFRRVYRKN; CTFRRVYRKNY;
TFRRVYRKNYC; FRRVYRKNYCP; RRVYRKNYCPR; RVYRKNYCPRR; VYRKNYCPRRC; SKNCSSMDVAF;
KNCSSMDVAFT; NCSSMDVAFTS; CSSMDVAFTSR; SSMDVAFTSRP; SMDVAFTSRPV; MDVAFTSRPVR;
DVAFTSRPVRD; VAFTSRPVRDC; AFTSRPVRDCN; FTSRPVRDCNT; TSRPVRDCNTC; SRPVRDCNTCS;
RWPQPKEKESV; WPQPKEKESVQ; PQPKEKESVQG; QPKEKESVQGQ; PKEKESVQGQL; KEKESVQGQLP;
EKESVQGQLPK; KESVQGQLPKS; ESVQGQLPKSQ; SVQGQLPKSQR; VQGQLPKSQRN; QGQLPKSQRNP;
GQLPKSQRNPC; QLPKSQRNPCK; LPKSQRNPCKC; PKSQRNPCKCQ; KSQRNPCKCQN; SQRNPCKCQNY;
TQKWGIQMKTL; QKWGIQMKTLG; KWGIQMKTLGA; WGIQMKTLGAL; GIQMKTLGALV; VLKMTLAVIAQ;
LKMTLAVIAQR; KMTLAVIAQRE; MTLAVIAQREK; TLAVIAQREKC; LAVIAQREKCF; AVIAQREKCFP;
VIAQREKCFPV; IAQREKCFPVT; AQREKCFPVTA; QREKCFPVTAQ; REKCFPVTAQQ; EKCFPVTAQQE;
KCFPVTAQQEF; CFPVTAQQEFP; FPVTAQQEFPS; PVTAQQEFPSP; VTAQQEFPSPI; LACLTFMQGHK;
ACLTFMQGHKK; CLTFMQGHKKC; LTFMQGHKKCM; TFMQGHKKCMS; FMQGHKKCMSM; MQGHKKCMSMV;
QGHKKCMSMVE; GHKKCMSMVEE; HKKCMSMVEEN; KKCMSMVEENL; KCMSMVEENLF; CMSMVEENLFK;
MSMVEENLFKA; SMVEENLFKAV; MVEENLFKAVI; VEENLFKAVIS; EENLFKAVIST; ENLFKAVISTS;
NLFKAVISTSL; LFKAVISTSLL; ILTIRPIWTKT; LTIRPIWTKTM; TIRPIWTKTML; IRPIWTKTMLI;
RPIWTKTMLIQ; PIWTKTMLIQL; IWTKTMLIQLS; WTKTMLIQLSA; TKTMLIQLSAG; KTMLIQLSAGY;
TMLIQLSAGYL; MLIQLSAGYLI; LIQLSAGYLIP; IQLSAGYLIPV; QLSAGYLIPVE; LSAGYLIPVEM;
SAGYLIPVEMK; AGYLIPVEMKM; GYLIPVEMKML; YLIPVEMKMLG; LIPVEMKMLGI; IPVEMKMLGIL;
PVEMKMLGILG; VEMKMLGILGL; EMKMLGILGLS; MKMLGILGLSQ; KMLGILGLSQE; MLGILGLSQEG;
LGILGLSQEGK; GILGLSQEGKM; ILGLSQEGKMF; LGLSQEGKMFP; GLSQEGKMFPQ; LSQEGKMFPQY;
SQEGKMFPQYF; QEGKMFPQYFM; MNRVWGLFVKL; NRVWGLFVKLI; RVWGLFVKLIA; VWGLFVKLIAC;
WGLFVKLIACM; GLFVKLIACMF; LFVKLIACMFQ; FVKLIACMFQL; VKLIACMFQLL; KLIACMFQLLI;
LIACMFQLLIF; IACMFQLLIFV; ACMFQLLIFVA; CMFQLLIFVAC; MFQLLIFVACL; FQLLIFVACLL;
QLLIFVACLLT; LLIFVACLLTA; LIFVACLLTAL; IFVACLLTALE; FVACLLTALEH; VACLLTALEHN;
ACLLTALEHNS; CLLTALEHNSG; LLTALEHNSGE; LTALEHNSGEA; TALEHNSGEAL; ALEHNSGEALQ;
LEHNSGEALQD; EHNSGEALQDI; HNSGEALQDIL; NSGEALQDILR; SGEALQDILRS; GEALQDILRSA;
TGEPREWMGSL; GEPREWMGSLC; EPREWMGSLCM; PREWMGSLCMV; REWMGSLCMVW; EWMGSLCMVWN;
WMGSLCMVWNP; MGSLCMVWNPR; KRLGCLMAQKD; RLGCLMAQKDF; LGCLMAQKDFQ; GCLMAQKDFQG;
CLMAQKDFQGT; LMAQKDFQGTQ; MAQKDFQGTQI; DILTNRDNCKP; ILTNRDNCKPK; LTNRDNCKPKC;
TNRDNCKPKCF; NRDNCKPKCFK; RDNCKPKCFKQ; DNCKPKCFKQV; NCKPKCFKQVL; CKPKCFKQVLL;
KPKCFKQVLLL; PKCFKQVLLLY; KCFKQVLLLYI; CFKQVLLLYIY; FKQVLLLYIYI; MLLLYKPLLSL;
LLLYKPLLSLC; LLYKPLLSLCY; LYKPLLSLCYF; YKPLLSLCYFG; KPLLSLCYFGG; PLLSLCYFGGG;
LLSLCYFGGGV; LSLCYFGGGVL; SLCYFGGGVLG; LCYFGGGVLGL; CYFGGGVLGLL; YFGGGVLGLLK;
FGGGVLGLLKH; LWGSDLWESSA; WGSDLWESSAG; GSDLWESSAGA; SDLWESSAGAE; DLWESSAGAEV;
LWESSAGAEVS; WESSAGAEVSE; ESSAGAEVSET; SSAGAEVSETW; SAGAEVSETWE; AGAEVSETWEE;
GAEVSETWEEH; AEVSETWEEHC; EVSETWEEHCD; VSETWEEHCDW; SETWEEHCDWD; ETWEEHCDWDS;
TWEEHCDWDSV; WEEHCDWDSVL; EEHCDWDSVLD; EHCDWDSVLDP; HCDWDSVLDPC; CDWDSVLDPCP;
DWDSVLDPCPE; WDSVLDPCPES; DSVLDPCPESS; SVLDPCPESSV; VLDPCPESSVS; LDPCPESSVSE;
DPCPESSVSES; PCPESSVSESS; CPESSVSESSS; PESSVSESSSL; ESSVSESSSLV; SSVSESSSLVI;
SVSESSSLVIS; VSESSSLVISR; SESSSLVISRI; ESSSLVISRIH; SSSLVISRIHF; SSLVISRIHFP;
SLVISRIHFPM; LVISRIHFPMH; VISRIHFPMHI; ISRIHFPMHIL; SRIHFPMHILY; RIHFPMHILYF;
IHFPMHILYFI; HFPMHILYFIL; FPMHILYFILE; PMHILYFILEK; MHILYFILEKV; HILYFILEKVY;
ILYFILEKVYI; LYFILEKVYIL; YFILEKVYILI; FILEKVYILIS; ILEKVYILISE; LEKVYILISES;
EKVYILISESS; KVYILISESSL; VYILISESSLS; YILISESSLSF; ILISESSLSFH; LISESSLSFHS;
ISESSLSFHST; SESSLSFHSTI; ESSLSFHSTIL; SSLSFHSTILD; SLSFHSTILDC; LSFHSTILDCI;
SFHSTILDCIS; FHSTILDCISV; HSTILDCISVA; STILDCISVAK; TILDCISVAKS; ILDCISVAKSA;
LDCISVAKSAT; DCISVAKSATG; CISVAKSATGL; ISVAKSATGLN; SVAKSATGLNQ; VAKSATGLNQI;
AKSATGLNQIS; KSATGLNQISS; SATGLNQISSS; ATGLNQISSSN; TGLNQISSSNK; GLNQISSSNKV;
LNQISSSNKVI; NQISSSNKVIP; QISSSNKVIPL; ISSSNKVIPLC; SSSNKVIPLCK; SSNKVIPLCKI;

SNKVIPLCKIL; NKVIPLCKILF; KVIPLCKILFS; VIPLCKILFSS; IPLCKILFSSK; PLCKILFSSKN;
LCKILFSSKNS; CKILFSSKNSE; KILFSSKNSEF; ILFSSKNSEFC; LFSSKNSEFCK; FSSKNSEFCKD;
SSKNSEFCKDF; SKNSEFCKDFL; KNSEFCKDFLK; NSEFCKDFLKY; SEFCKDFLKYI; EFCKDFLKYIL;
FCKDFLKYILG; CKDFLKYILGL; KDFLKYILGLK; DFLKYILGLKS; FLKYILGLKSI; LKYILGLKSIC;
KYILGLKSICL; YILGLKSICLT; ILGLKSICLTN; LGLKSICLTNL; GLKSICLTNLA; LKSICLTNLAC;
KSICLTNLACR; SICLTNLACRV; ICLTNLACRVL; CLTNLACRVLG; LTNLACRVLGT; TNLACRVLGTG;
NLACRVLGTGY; LACRVLGTGYS; ACRVLGTGYSF; CRVLGTGYSFI; RVLGTGYSFIV; VLGTGYSFIVT;
LGTGYSFIVTK; GTGYSFIVTKP; TGYSFIVTKPG; GYSFIVTKPGG; YSFIVTKPGGN; SFIVTKPGGNI;
FIVTKPGGNIW; IVTKPGGNIWV; VTKPGGNIWVL; TKPGGNIWVLL; KPGGNIWVLLF; PGGNIWVLLFK;
GGNIWVLLFKC; GNIWVLLFKCF; NIWVLLFKCFF; IWVLLFKCFFS; WVLLFKCFFSK; VLLFKCFFSKF;
LLFKCFFSKFT; LFKCFFSKFTL; FKCFFSKFTLT; KCFFSKFTLTL; CFFSKFTLTLP; FFSKFTLTLPS;
FSKFTLTLPSK; SLKLSKLFIPC; LKLSKLFIPCP; KLSKLFIPCPE; LSKLFIPCPEG; SKLFIPCPEGK;
KLFIPCPEGKS; LFIPCPEGKSF; FIPCPEGKSFD; IPCPEGKSFDS; PCPEGKSFDSA; CPEGKSFDSAP;
PEGKSFDSAPV; EGKSFDSAPVP; GKSFDSAPVPF; KSFDSAPVPFT; SFDSAPVPFTS; FDSAPVPFTSS;
DSAPVPFTSSK; SAPVPFTSSKT; APVPFTSSKTT; PVPFTSSKTTM; VPFTSSKTTMY; SIATPSSKVSL;
IATPSSKVSLS; ATPSSKVSLSM; TPSSKVSLSMG; PSSKVSLSMGR; SSKVSLSMGRF; SKVSLSMGRFT;
KVSLSMGRFTF; VSLSMGRFTFK; SLSMGRFTFKA; LSMGRFTFKAL; SMGRFTFKALP; MGRFTFKALPP;
GRFTFKALPPH; RFTFKALPPHK; FTFKALPPHKS; TFKALPPHKSN; FKALPPHKSNN; KALPPHKSNNP;
ALPPHKSNNPA; LPPHKSNNPAA; PPHKSNNPAAS; PHKSNNPAASV; HKSNNPAASVV; KSNNPAASVVF;
SNNPAASVVFP; NNPAASVVFPL; NPAASVVFPLS; PAASVVFPLSM; AASVVFPLSMG; ASVVFPLSMGP;
SVVFPLSMGPL; VVFPLSMGPLN; VFPLSMGPLNN; FPLSMGPLNNQ; PLSMGPLNNQY; LSMGPLNNQYL;
SMGPLNNQYLL; MGPLNNQYLLL; GPLNNQYLLLG; PLNNQYLLLGT; LNNQYLLLGTL; NNQYLLLGTLK;
NQYLLLGTLKT; QYLLLGTLKTI; YLLLGTLKTIQ; LLLGTLKTIQC; LLGTLKTIQCK; LGTLKTIQCKK;
GTLKTIQCKKS; TLKTIQCKKSN; LKTIQCKKSNI; KTIQCKKSNIT; TIQCKKSNITE; IQCKKSNITES;
QCKKSNITESI; CKKSNITESIL; KKSNITESILG; KSNITESILGS; SNITESILGSK; NITESILGSKQ;
ITESILGSKQC; TESILGSKQCS; ESILGSKQCSQ; SILGSKQCSQA; ILGSKQCSQAT; LGSKQCSQATP;
GSKQCSQATPA; SKQCSQATPAI; KQCSQATPAIY; QCSQATPAIYC; CSQATPAIYCS; SQATPAIYCSS;
QATPAIYCSST; ATPAIYCSSTA; TPAIYCSSTAF; PAIYCSSTAFP; APNIKSILSNI; LNLSVSISSLV;
NLSVSISSLVI; RVSTLFLAKTV; VSTLFLAKTVS; STLFLAKTVST; TLFLAKTVSTA; LFLAKTVSTAC;
FLLSAKIIAFA; LLSAKIIAFAK; LSAKIIAFAKC; SAKIIAFAKCF; AKIIAFAKCFS; NSKYIPNNKNT;
SKYIPNNKNTS; KYIPNNKNTSS; YIPNNKNTSSH; IPNNKNTSSHF; PNNKNTSSHFV; NNKNTSSHFVS;
NKNTSSHFVST; KNTSSHFVSTA; NTSSHFVSTAY; TSSHFVSTAYS; SSHFVSTAYSV; SHFVSTAYSVI;
HFVSTAYSVIN; FVSTAYSVINF; VSTAYSVINFQ; STAYSVINFQD; TAYSVINFQDT; AYSVINFQDTC;
YSVINFQDTCF; SVINFQDTCFV; VINFQDTCFVS; INFQDTCFVSS; NFQDTCFVSSG; FQDTCFVSSGS;
QDTCFVSSGSS; DTCFVSSGSSG; TCFVSSGSSGL; CFVSSGSSGLK; FVSSGSSGLKS; VSSGSSGLKSC;
SSGSSGLKSCS; SGSSGLKSCSF; GSSGLKSCSFK; SSGLKSCSFKP; SGLKSCSFKPP; MLSSIVWYGSL;
LSSIVWYGSLV; SSIVWYGSLVK; SIVWYGSLVKA; IVWYGSLVKAL; VWYGSLVKALY; WYGSLVKALYS;
YGSLVKALYSK; GSLVKALYSKY; SLVKALYSKYS; LVKALYSKYSL; VKALYSKYSLL; KALYSKYSLLT;
ALYSKYSLLTP; LYSKYSLLTPL; YSKYSLLTPLQ; SKYSLLTPLQI; KYSLLTPLQIK; YSLLTPLQIKK;
SLLTPLQIKKL; LLTPLQIKKLK; LTPLQIKKLKV; TPLQIKKLKVH; PLQIKKLKVHS; LQIKKLKVHSF;
QKLLIAETLCL; KLLIAETLCLC; LLIAETLCLCG; LIAETLCLCGV; IAETLCLCGVK; AETLCLCGVKK;
ETLCLCGVKKN; TLCLCGVKKNI; LCLCGVKKNII; CLCGVKKNIIL; LCGVKKNIILC; CGVKKNIILCP;
GVKKNIILCPA; VKKNIILCPAH; KKNIILCPAHM; KNIILCPAHMC; NIILCPAHMCL; IILCPAHMCLL;
ILCPAHMCLLI; LCPAHMCLLIK; CPAHMCLLIKV; PAHMCLLIKVT; AHMCLLIKVTE; HMCLLIKVTEY;
MCLLIKVTEYF; CLLIKVTEYFS; LLIKVTEYFSI; LIKVTEYFSIS; IKVTEYFSISF; KVTEYFSISFL;
VTEYFSISFLY; TEYFSISFLYR; EYFSISFLYRI; AFSLVVYTAKQ; FSLVVYTAKQA; SLVVYTAKQAR;
LVVYTAKQARV; VVYTAKQARVL; VYTAKQARVLL; YTAKQARVLLL; TAKQARVLLLN; AKQARVLLLNT;
KQARVLLLNTA; LRNWCRSEGKS; RNWCRSEGKSL; NWCRSEGKSLG; WCRSEGKSLGS; CRSEGKSLGSS;
RSEGKSLGSST; SEGKSLGSSTF; EGKSLGSSTFL; GKSLGSSTFLF; KSLGSSTFLFF; SLGSSTFLFFL;
LGSSTFLFFLG; GSSTFLFFLGG; SSTFLFFLGGV; STFLFFLGGVE; TFLFFLGGVEC; ESAVASSSLAN;
SAVASSSLANI; AVASSSLANIS; VASSSLANISS; ASSSLANISSW; SSSLANISSWQ; SSLANISSWQN;
SLANISSWQNK; LANISSWQNKS; ANISSWQNKSS; NISSWQNKSSS; ISSWQNKSSSH; SSWQNKSSSHF;
SWQNKSSSHFS; WQNKSSSHFSL; QNKSSSHFSLK; NKSSSHFSLKE; KSSSHFSLKEL; SSSHFSLKELH;
SSHFSLKELHQ; SHFSLKELHQD; HFSLKELHQDS; FSLKELHQDSH; SLKELHQDSHS; LKELHQDSHSS;
KELHQDSHSSV; ELHQDSHSSVP; VGTYKKNNYLG; GTYKKNNYLGP; TYKKNNYLGPF; YKKNNYLGPFN;
KKNNYLGPFNI; KNNYLGPFNIL; NNYLGPFNILL; NYLGPFNILLF; YLGPFNILLFI; REFLQLFGPTI;
EFLQLFGPTIA; FLQLFGPTIAE; LQLFGPTIAEF; QLFGPTIAEFL; LFGPTIAEFLQ; FGPTIAEFLQL;
GPTIAEFLQLG; PTIAEFLQLGL; TIAEFLQLGLS; IAEFLQLGLSQ; AEFLQLGLSQT; EFLQLGLSQTT;
FLQLGLSQTTV; SSQCSSNLSKP; SQCSSNLSKPR; QCSSNLSKPRA; CSSNLSKPRAL; SSNLSKPRALF;
SNLSKPRALFL; NLSKPRALFLK; LSKPRALFLKI; SKPRALFLKIF; KPRALFLKIFY; PRALFLKIFYL;
RALFLKIFYLN; ALFLKIFYLNA; LFLKIFYLNAL; FLKIFYLNALI; ADIACKGSAQK; DIACKGSAQKA;
IACKGSAQKAF; ACKGSAQKAFW; CKGSAQKAFWN; KGSAQKAFWNK; AIPCSTGYLGK; IPCSTGYLGKE;
PCSTGYLGKEE; CSTGYLGKEEN; STGYLGKEENQ; TGYLGKEENQH; GYLGKEENQHK; YLGKEENQHKP;
LGKEENQHKPL; GKEENQHKPLS; KEENQHKPLSY; EENQHKPLSYS; ENQHKPLSYSR; NQHKPLSYSRF;
QHKPLSYSRFQ; HKPLSYSRFQN; KPLSYSRFQNQ; PLSYSRFQNQA; LSYSRFQNQAD; SYSRFQNQADE;

YSRFQNQADEL; SRFQNQADELP; RFQNQADELPL; FQNQADELPLH; QNQADELPLHP; NQADELPLHPA; QADELPLHPAP; ADELPLHPAPF; DELPLHPAPFF; ELPLHPAPFFY; LPLHPAPFFYT; PLHPAPFFYTK; LHPAPFFYTKY; HPAPFFYTKYS; PAPFFYTKYSF; APFFYTKYSFS; PFFYTKYSFSS; FFYTKYSFSSF; FYTKYSFSSFY; YTKYSFSSFYP; TKYSFSSFYPR; KYSFSSFYPRR; YSFSSFYPRRP; SFSSFYPRRPL; FSSFYPRRPLC; SSFYPRRPLCQ; SFYPRRPLCQG; FYPRRPLCQGE; YPRRPLCQGEI; PRRPLCQGEIP; RRPLCQGEIPY; RPLCQGEIPYT; PLCQGEIPYTS; LCQGEIPYTSL; CQGEIPYTSLN; QGEIPYTSLNK; GEIPYTSLNKL; EIPYTSLNKLF; IPYTSLNKLFS; PYTSLNKLFSL; YTSLNKLFSLR; TSLNKLFSLRE; SLNKLFSLRED; LNKLFSLREDF; NKLFSLREDFP; KLFSLREDFPR; LFSLREDFPRQ; FSLREDFPRQL; SLREDFPRQLF; LREDFPRQLFQ; REDFPRQLFQG; EDFPRQLFQGL; DFPRQLFQGLK; FPRQLFQGLKG; PRQLFQGLKGP

BK reading frame 3

8 mers:

LQKLQKNR; QKLQKNRD; KLQKNRDF; LQKNRDFP; QKNRDFPK; ASEKASTP; SEKASTPL; EKASTPLL; KASTPLLL; ASTPLLLE; STPLLLER; TPLLLERK; PLLLERKG; LLLERKGG; LLERKGGG; LERKGGGR; ERKGGGRG; RKGGGRGG; KGGGRGGL; GGGRGGLG; GGRGGLGL; GRGGLGLL; RGGLGLLY; GGLGLLYI; GLGLLYII; LGLLYIIK; GLLYIIKK; LLYIIKKK; LYIIKKKA; YIIKKKAT; IIKKKATG; IKKKATGR; KKKATGRS; KKATGRSC; KATGRSCL; ATGRSCLP; TGRSCLPM; GRSCLPME; RSCLPMEC; SCLPMECS; CLPMECSQ; LPMECSQT; PMECSQTM; MECSQTMT; ECSQTMTS; CSQTMTSG; SQTMTSGR; QTMTSGRK; TMTSGRKV; MTSGRKVH; TSGRKVHD; SGRKVHDS; GRKVHDSQ; RKVHDSQG; KVHDSQGN; VHDSQGNA; HDSQGNAA; DSQGNAAK; SQGNAAKP; PQEGKCMT; QEGKCMTH; EGKCMTHR; GKCMTHRE; KCMTHREE; CMTHREEL; MTHREELL; THREELLT; HREELLTH; REELLTHG; EELLTHGM; ELLTHGMQ; LLTHGMQP; LTHGMQPN; THGMQPNH; HGMQPNHD; GMQPNHDL; MQPNHDLR; QPNHDLRK; PNHDLRKE; NHDLRKES; HDLRKESA; QTCFASLG; TCFASLGI; CFASLGIL; FASLGILA; ASLGILAL; SLGILALS; LGILALSP; GILALSPV; ILALSPVK; LALSPVKL; ALSPVKLD; LSPVKLDK; SPVKLDKG; PVKLDKGH; VKLDKGHG; KLDKGHGS; LDKGHGSA; DKGHGSAP; KGHGSAPA; GHGSAPAV; HGSAPAVT; GSAPAVTT; SAPAVTTS; APAVTTSF; PAVTTSFS; AVTTSFSE; VTTSFSES; TTSFSESW; NLDWNKKK; LDWNKKKS; DWNKKKSS; WNKKKSSE; NKKKSSED; KKKSSEDF; KKSSEDFY; KSSEDFYF; SSEDFYFY; SEDFYFYF; EDFYFYFR; DFYFYFRA; FYFYFRAF; YFYFRAFA; FYFRAFAG; YFRAFAGI; FRAFAGIL; RQCRREKQ; QCRREKQK; CRREKQKY; RREKQKYH; REKQKYHC; EKQKYHCF; KQKYHCFT; QKYHCFTC; KYHCFTCC; YHCFTCCK; HCFTCCKR; CFTCCKRL; FTCCKRLC; TCCKRLCK; CCKRLCKR; CKRLCKRL; KRLCKRLL; RLCKRLLG; LCKRLLGK; SLFFCISR; LFFCISRF; FFCISRFM; FCISRFMG; CISRFMGA; ISRFMGAA; SRFMGAAL; RFMGAALA; FMGAALAL; MGAALALL; GAALALLG; AALALLGD; ALALLGDL; LALLGDLV; ALLGDLVA; LLGDLVAS; LGDLVASV; GDLVASVS; DLVASVSE; LVASVSEA; VASVSEAA; ASVSEAAA; SVSEAAAA; VSEAAAAT; SEAAAATG; EAAAATGF; AAAATGFS; AAATGFSV; AATGFSVA; ATGFSVAE; TGFSVAEI; GFSVAEIA; FSVAEIAA; SVAEIAAG; VAEIAAGE; AEIAAGEA; EIAAGEAA; IAAGEAAA; AAGEAAAA; AGEAAAAI; GEAAAAIE; EAAAAIEV; AAAAIEVQ; AAAIEVQI; AAIEVQIA; AIEVQIAS; IEVQIASL; EVQIASLA; VQIASLAT; QIASLATV; IASLATVE; ASLATVEG; SLATVEGI; LATVEGIT; ATVEGITS; TVEGITST; VEGITSTS; EGITSTSE; GITSTSEA; ITSTSEAI; TSTSEAIA; STSEAIAA; TSEAIAAI; SEAIAAIG; EAIAAIGL; AIAAIGLT; IAAIGLTP; AAIGLTPQ; AIGLTPQT; IGLTPQTY; GLTPQTYA; LTPQTYAV; TPQTYAVI; PQTYAVIA; QTYAVIAG; TYAVIAGA; YAVIAGAP; AVIAGAPG; VIAGAPGA; IAGAPGAI; AGAPGAIA; GAPGAIAG; APGAIAGF; PGAIAGFA; GAIAGFAA; AIAGFAAL; IAGFAALI; AGFAALIQ; GFAALIQT; FAALIQTV; AALIQTVS; ALIQTVSG; LIQTVSGI; IQTVSGIS; QTVSGISS; TVSGISSL; VSGISSLA; SGISSLAQ; GISSLAQV; ISSLAQVG; SSLAQVGY; SLAQVGYK; LAQVGYKF; AQVGYKFF; QVGYKFFD; VGYKFFDD; GYKFFDDW; YKFFDDWD; KFFDDWDH; FFDDWDHK; FDDWDHKV; DDWDHKVS; DWDHKVST; WDHKVSTV; DHKVSTVG; HKVSTVGL; KVSTVGLY; VSTVGLYQ; STVGLYQQ; TVGLYQQS; VGLYQQSG; GLYQQSGM; LYQQSGMA; YQQSGMAL; QQSGMALE; QSGMALEL; SGMALELF; GMALELFN; MALELFNP; ALELFNPD; LELFNPDE; ELFNPDEY; LFNPDEYY; FNPDEYYD; NPDEYYDI; PDEYYDIL; DEYYDILF; EYYDILFP; YYDILFPG; YDILFPGV; DILFPGVN; ILFPGVNT; LFPGVNTF; FPGVNTFV; PGVNTFVN; GVNTFVNN; VNTFVNNI; NTFVNNIQ; TFVNNIQY; FVNNIQYL; VNNIQYLD; NNIQYLDP; NIQYLDPR; IQYLDPRH; QYLDPRHW; YLDPRHWG; LDPRHWGP; DPRHWGPS; PRHWGPSL; RHWGPSLF; HWGPSLFA; WGPSLFAT; GPSLFATI; PSLFATIS; SLFATISQ; LFATISQA; FATISQAL; ATISQALW; TISQALWH; ISQALWHV; SQALWHVI; QALWHVIR; ALWHVIRD; LWHVIRDD; WHVIRDDI; HVIRDDIP; VIRDDIPS; IRDDIPSI; RDDIPSIT; DDIPSITS; DIPSITSQ; IPSITSQE; PSITSQEL; SITSQELQ; ITSQELQR; TSQELQRR; SQELQRRT; QELQRRTE; ELQRRTER; LQRRTERF; QRRTERFF; RRTERFFR; RTERFFRD; TERFFRDS; ERFFRDSL; RFFRDSLA; FFRDSLAR; FRDSLARF; RDSLARFL; DSLARFLE; SLARFLEE; LARFLEET; ARFLEETT; RFLEETTW; FLEETTWT; LEETTWTI; EETTWTIV; ETTWTIVN; TTWTIVNA; TWTIVNAP; WTIVNAPI; TIVNAPIN; IVNAPINF; VNAPINFY; NAPINFYN; APINFYNY; PINFYNYI; INFYNYIQ; NFYNYIQQ; FYNYIQQY; YNYIQQYY; NYIQQYYS; YIQQYYSD; IQQYYSDL; QQYYSDLS; QYYSDLSP;

YYSDLSPI; YSDLSPIR; SDLSPIRP; DLSPIRPS; LSPIRPSM; SPIRPSMV; PIRPSMVR;
IRPSMVRQ; RPSMVRQV; PSMVRQVA; SMVRQVAE; MVRQVAER; VRQVAERE; RQVAEREG;
QVAEREGT; VAEREGTR; AEREGTRV; EREGTRVH; REGTRVHF; EGTRVHFG; GTRVHFGH;
TRVHFGHT; RVHFGHTY; VHFGHTYS; HFGHTYSI; FGHTYSID; GHTYSIDD; HTYSIDDA;
TYSIDDAD; YSIDDADS; SIDDADSI; IDDADSIE; DDADSIEE; DADSIEEV; ADSIEEVT;
DSIEEVTQ; SIEEVTQR; IEEVTQRM; EEVTQRMD; EVTQRMDL; VTQRMDLR; TQRMDLRN;
QRMDLRNQ; RMDLRNQQ; MDLRNQQS; DLRNQQSV; LRNQQSVH; RNQQSVHS; NQQSVHSG;
QQSVHSGE; QSVHSGEF; SVHSGEFI; VHSGEFIE; HSGEFIEK; SGEFIEKT; GEFIEKTI;
EFIEKTIA; FIEKTIAP; IEKTIAPG; EKTIAPGG; KTIAPGGA; TIAPGGAN; IAPGGANQ;
APGGANQR; PGGANQRT; GGANQRTA; GANQRTAP; ANQRTAPQ; NQRTAPQW; QRTAPQWM;
RTAPQWML; TAPQWMLP; APQWMLPL; PQWMLPLL; QWMLPLLL; WMLPLLLG; MLPLLLGL;
LPLLLGLY; PLLLGLYG; LLLGLYGT; LLGLYGTV; LGLYGTVT; GLYGTVTP; LYGTVTPA;
YGTVTPAL; GTVTPALE; TVTPALEA; VTPALEAY; TPALEAYE; PALEAYED; ALEAYEDG;
LEAYEDGP; EAYEDGPN; AYEDGPNQ; YEDGPNQK; EDGPNQKK; DGPNQKKR; GPNQKKRR;
PNQKKRRV; NQKKRRVS; QKKRRVSR; KKRRVSRG; KRRVSRGS; RRVSRGSS; RVSRGSSQ;
VSRGSSQK; SRGSSQKA; RGSSQKAK; GSSQKAKG; SSQKAKGT; SQKAKGTR; QKAKGTRA;
KAKGTRAS; AKGTRASA; KGTRASAK; GTRASAKT; TRASAKTT; RASAKTTN; ASAKTTNK;
SAKTTNKR; AKTTNKRR; KTTNKRRS; TTNKRRSR; TNKRRSRS; NKRRSRSS; KRRSRSSR;
RRSRSSRS; NWGRCYYR; WGRCYYRG; GRCYYRGR; RCYYRGRM; CYYRGRML; YYRGRMLP;
YRGRMLPK; RGRMLPKP; GRMLPKPR; RMLPKPRN; MLPKPRNG; LPKPRNGG; PKPRNGGS;
KPRNGGSR; PREKNASL; REKNASLL; EKNASLLQ; KNASLLQH; NASLLQHS; ASLLQHSK;
SLLQHSKN; LLQHSKNS; LQHSKNSP; QHSKNSPP; HSKNSPPQ; SKNSPPQF; KNSPPQFK;
GPNLWKST; PNLWKSTD; NLWKSTDV; LWKSTDVG; WKSTDVGG; KSTDVGGC; STDVGGCN;
TDVGGCNC; DVGGCNCT; VGGCNCTN; GGCNCTNR; GCNCTNRG; CNCTNRGY; NCTNRGYW;
CTNRGYWN; TNRGYWNN; PSCRVTKS; SCRVTKSA; AWWRKTYS; WWRKTYSR; WRKTYSRQ;
FPLLCCRW; PLLCCRWR; LLCCRWRT; LCCRWRTL; CCRWRTLG; CRWRTLGN; RWRTLGNA;
WRTLGNAG; RTLGNAGS; TLGNAGSA; LGNAGSAN; GNAGSANE; NAGSANEL; AGSANELQ;
GSANELQV; SANELQVK; ANELQVKV; NELQVKVP; KPNSPVPG; PNSPVPGN; NSPVPGNE;
SPVPGNEY; GLFGQKQC; LFGQKQCL; FGQKQCLS; GQKQCLSS; VFWDFHRR; FWDFHRRG;
WDFHRRGK; DFHRRGKC; FHRRGKCS; HRRGKCSP; RRGKCSPS; RGKCSPST; GKCSPSTS;
KCSPSTSC; CSPSTSCD; SPSTSCDQ; PSTSCDQH; STSCDQHS; TSCDQHSY; SCDQHSYH;
CDQHSYHS; DQHSYHSV; QHSYHSVA; HSYHSVAR; QLWNTTVE; LWNTTVER; WNTTVERP;
NTTVERPC; TTVERPCK; TVERPCKI; VERPCKIF; DPPEKKIC; PPEKKICK; PEKKICKE;
EKKICKES; KKICKESL; KICKESLP; ICKESLPN; CKESLPNF; KESLPNFL; ESLPNFLF;
SLPNFLFA; LPNFLFAK; PYKQENPE; YKQENPES; KQENPESG; QENPESGW; ENPESGWA;
NPESGWAA; PESGWAAY; ESGWAAYV; SGWAAYVW; GWAAYVWY; WAAYVWYG; AAYVWYGI;
AYVWYGIP; YVWYGIPG; VWYGIPGR; WYGIPGRR; YGIPGRRG; WHRKTSRG; HRKTSRGP;
RKTSRGPR; KTSRGPRY; TSRGPRYD; SRGPRYDK; RGPRYDKI; GPRYDKIY; QTGTIANQ;
TGTIANQN; GTIANQNA; TIANQNAL; IANQNALN; ANQNALNR; NQNALNRC; QNALNRCF;
NALNRCFY; ALNRCFYC; LNRCFYCT; NRCFYCTY; RCFYCTYT; CFYCTYTF; FYCTYTFN;
YCTYTFNK; CTYTFNKC; TYTFNKCC; YTFNKCCF; TFNKCCFC; FNKCCFCI; NKCCFCIS;
KCCFCISH; CCFCISHF; ACVILGVV; CVILGVVF; NTESLYTN; TESLYTNA; ESLYTNAT;
SLYTNATL; LYTNATLD; YTNATLDY; TNATLDYG; NATLDYGG; ATLDYGGL; TLDYGGLT;
LDYGGLTF; DYGGLTFG; YGGLTFGN; GGLTFGNL; GLTFGNLQ; LTFGNLQQ; TFGNLQQG;
FGNLQQGL; GNLQQGLK; NLQQGLKY; LQQGLKYL; QQGLKYLR; QGLKYLRL; GLKYLRLG;
LKYLRLGK; KYLRLGKS; YLRLGKSI; LRLGKSIV; RLGKSIVI; LGKSIVIG; GKSIVIGI;
KSIVIGIQ; SIVIGIQC; IVIGIQCL; VIGIQCLI; IGIQCLIH; GIQCLIHV; IQCLIHVQ;
QCLIHVQS; CLIHVQSL; LIHVQSLQ; IHVQSLQF; HVQSLQFL; VQSLQFLN; QSLQFLNP;
SLQFLNPL; LQFLNPLL; QFLNPLLL; YQEYISPC; QEYISPCI; EYISPCIY; YISPCIYY;
ISPCIYYI; SPCIYYIS; PCIYYISS; CIYYISSL; IYYISSLK; YYISSLKK; YISSLKKY;
ISSLKKYT; SSLKKYTY; SLKKYTYL; LKKYTYLS; KKYTYLSQ; KYTYLSQN; YTYLSQNP;
TYLSQNPA; YLSQNPAF; LSQNPAFP; SQNPAFPS; QNPAFPSI; NPAFPSIQ; PAFPSIQQ;
AFPSIQQF; IVYQLQNQ; VYQLQNQL; YQLQNQLQ; QLQNQLQA; TKLAVATR; KLAVATRS;
LAVATRSF; AVATRSFH; VATRSFHF; ATRSFHFV; TRSFHFVK; RSFHFVKF; SFHFVKFF;
FHFVKFFF; HFVKFFFQ; FVKFFFQV; VKFFFQVR; KFFFQVRT; FFFQVRTL; FFQVRTLS;
FQVRTLSF; QVRTLSFV; VRTLSFVR; RTLSFVRI; TLSFVRIF; LSFVRIFL; SFVRIFLN;
FVRIFLNI; VRIFLNIF; RIFLNIFW; IFLNIFWA; PSLVEIFG; SLVEIFGF; LVEIFGFF;
VEIFGFFC; EIFGFFCL; IFGFFCLN; FGFFCLNV; GFFCLNVS; FFCLNVSF; FCLNVSFL;
CLNVSFLN; LNVSFLNL; NVSFLNLP; HFHLNNLS; FHLNNLSN; HLNNLSNC; LNNLSNCL;
NNLSNCLN; NLSNCLNC; LSNCLNCL; SNCLNCLF; NCLNCLFH; CLNCLFHV; LNCLFHVL;
NCLFHVLK; CLFHVLKA; LFHVLKAN; FHVLKANP; HVLKANPL; VLKANPLI; LKANPLIQ;
KANPLIQL; ANPLIQLL; NPLIQLLS; PLIQLLSL; LIQLLSLL; IQLLSLLH; QLLSLLHL;
LLSLLHLQ; LSLLHLQK; SLLHLQKQ; LLHLQKQP; LHLQKQPC; HLQKQPCT; LQKQPCTD;
QKQPCTDL; LHLAQRLA; HLAQRLAF; LAQRLAFP; AQRLAFPW; QRLAFPWV; RLAFPWVG;
LAFPWVGL; AFPWVGLH; FPWVGLHL; PWVGLHLR; WVGLHLRL; VGLHLRLY; GLHLRLYH;

LHLRLYHH; HLRLYHHT; LRLYHHTN; RLYHHTNL; LYHHTNLI; YHHTNLIT; HHTNLITL;
HTNLITLQ; TNLITLQL; NLITLQLV; LITLQLVL; ITLQLVLF; TLQLVLFF; LQLVLFFH;
QLVLFFHY; LVLFFHYQ; VLFFHYQW; LFFHYQWD; FFHYQWDL; KQYSAKNQ; QYSAKNQI;
YSAKNQIL; SAKNQILQ; AKNQILQN; KNQILQNP; NQILQNPF; VANSAAKQ; ANSAAKQH;
NSAAKQHL; SAAKQHLP; AAKQHLPY; AKQHLPYI; KQHLPYIV; QHLPYIVL; HLPYIVLV;
LPYIVLVQ; PYIVLVQH; YIVLVQHF; IVLVQHFH; VLVQHFHE; LVQHFHEL; VQHFHELQ;
QHFHELQI; HFHELQIL; FHELQILN; HELQILNP; ELQILNPF; LQILNPFY; QILNPFYL;
ILNPFYLI; LNPFYLIY; NPFYLIYD; IFLLAFLP; FLLAFLPW; LLAFLPWS; LAFLPWSY;
AFLPWSYE; FLPWSYEG; LPWSYEGY; PWSYEGYL; WSYEGYLL; SYEGYLLF; YEGYLLFF;
LKLYLLLA; KLYLLLAD; LYLLLADK; YLLLADKY; LLLADKYF; LLADKYFF; LADKYFFD;
ADKYFFDF; DKYFFDFY; KYFFDFYF; YFFDFYFL; FFDFYFLQ; FDFYFLQK; HLQSAFHD;
LQSAFHDT; SDKAGLFS; DKAGLFSD; KAGLFSDT; AGLFSDTF; GLFSDTFY; LFSDTFYT;
FSDTFYTP; SDTFYTPL; DTFYTPLH; TFYTPLHC; FYTPLHCI; YTPLHCIE; TPLHCIEI;
PLHCIEIL; LHCIEILN; HCIEILNT; CIEILNTY; IEILNTYL; EILNTYLI; ILNTYLII;
LNTYLIIK; NTYLIIKT; TYLIIKTH; YLIIKTHP; LIIKTHPH; IIKTHPHT; IKTHPHTL;
KTHPHTLS; THPHTLSL; HPHTLSLL; PHTLSLLH; HTLSLLHT; TLSLLHTQ; LISKTPAL;
ISKTPALF; SKTPALFL; KTPALFLQ; TPALFLQA; PALFLQAL; ALFLQALL; LFLQALLG;
NHAPLSPL; HAPLSPLE; APLSPLEC; PLSPLECF; LSPLECFL; SPLECFLL; LRHYIVSI;
RHYIVSIP; HYIVSIPY; RYTAFDRN; YTAFDRNY; LQKLYVYV; QKLYVYVE; KLYVYVEL;
LYVYVELK; YVYVELKR; VYVELKRI; YYAQHTCV; YAQHTCVY; VFYTEFEL; FYTEFELF;
YTEFELFL; YTQQSRQG; TQQSRQGF; QQSRQGFY; QSRQGFYY; ETGVDQRE; TGVDQRES;
GVDQRESL; GLLPFFFF; LLPFFFFW; LPFFFFWV; PFFFFWVV; FFFFWVVL; FFFWVVLS;
FFWVVLSV; FWVVLSVE; WVVLSVEN; VVLSVENL; VLSVENLL; LSVENLLL; SVENLLLL;
VENLLLLL; ENLLLLLH; NLLLLLHH; LLLLLHHW; LLLLHHWQ; LLLHHWQT; LLHHWQTY;
LHHWQTYL; HHWQTYLH; HWQTYLHG; WQTYLHGK; QTYLHGKI; TYLHGKIN; YLHGKINL;
LHGKINLH; HGKINLHP; GKINLHPI; KINLHPIF; INLHPIFH; RNSTRTPT; NSTRTPTL;
STRTPTLL; TRTPTLLF; RTPTLLFH; TPTLLFHR; PTLLFHRL; TLLFHRLA; LLFHRLAP;
LFHRLAPI; FHRLAPIK; HRLAPIKK; RLAPIKKI; LAPIKKII; APIKKIIT; GLLIFYYL;
LLIFYYLS; LIFYYLSK; IFYYLSKY; FYYLSKYK; YYLSKYKL; YLSKYKLV; LSKYKLVT;
SKYKLVTL; KYKLVTLK; YKLVTLKL; ISEGSFSN; SEGSFSNY; EGSFSNYL; GSFSNYLD;
SFSNYLDP; FSNYLDPP; SNYLDPPL; NYLDPPLQ; YLDPPLQS; LDPPLQSF; DPPLQSFF;
PPLQSFFS; AKPLCEAV; KPLCEAVN; PLCEAVNA; LCEAVNAV; CEAVNAVA; EAVNAVAI;
AVNAVAIY; VNAVAIYP; NAVAIYPN; AVAIYPNQ; VAIYPNQG; AIYPNQGL; IYPNQGLF;
YPNQGLFS; HARAVHRR; ARAVHRRL; RAVHRRLF; AVHRRLFG; VHRRLFGT; HRRLFGTN;
RRLFGTNR; RLFGTNRP; LFGTNRPF; FGTNRPFL; GTNRPFLA; TNRPFLAV; NRPFLAVQ;
RPFLAVQG; PFLAVQGI; FLAVQGIW; LAVQGIWA; AVQGIWAK; VQGIWAKR; QGIWAKRK;
GIWAKRKI; IWAKRKIS; WAKRKIST; AKRKISTN; KRKISTNL; ATPGSKIR; TPGSKIRL;
PGSKIRLM; GSKIRLMS; SKIRLMSY; KIRLMSYL; IRLMSYLY; RLMSYLYI; LMSYLYIL;
MSYLYILL; SYLYILLH; YLYILLHF; LYILLHFF; YILLHFFI; ILLHFFIQ; LLHFFIQS;
LHFFIQSI; HFFIQSIH; FFIQSIHS; FIQSIHSL; IQSIHSLH; QSIHSLHF; SIHSLHFI;
IHSLHFIL; HSLHFILV; SLHFILVA; LHFILVAP; HFILVAPF; FILVAPFV; ILVAPFVR;
LVAPFVRV; VAPFVRVK; APFVRVKF; PFVRVKFL; FVRVKFLT; VRVKFLTL; RVKFLTLP;
GKISPGSS; KISPGSSF; ISPGSSFK; SPGSSFKA; KVHELHGF; VHELHGFF; HELHGFFP;
ELHGFFPV; LHGFFPVK; HGFFPVKN; GFFPVKNF; FFPVKNFI; FPVKNFIH

9 mers:
LQKLQKNRD; QKLQKNRDF; KLQKNRDFP; LQKNRDFPK; ASEKASTPL; SEKASTPLL; EKASTPLLL;
KASTPLLLE; ASTPLLLER; STPLLLERK; TPLLLERKG; PLLLERKGG; LLLERKGGG; LLERKGGGR;
LERKGGGRG; ERKGGGRGG; RKGGGRGGL; KGGGRGGLG; GGGRGGLGL; GGRGGLGLL; GRGGLGLLY;
RGGLGLLYI; GGLGLLYII; GLGLLYIIK; LGLLYIIKK; GLLYIIKKK; LLYIIKKKA; LYIIKKKAT;
YIIKKKATG; IIKKKATGR; IKKKATGRS; KKKATGRSC; KKATGRSCL; KATGRSCLP; ATGRSCLPM;
TGRSCLPME; GRSCLPMEC; RSCLPMECS; SCLPMECSQ; CLPMECSQT; LPMECSQTM; PMECSQTMT;
MECSQTMTS; ECSQTMTSG; CSQTMTSGR; SQTMTSGRK; QTMTSGRKV; TMTSGRKVH; MTSGRKVHD;
TSGRKVHDS; SGRKVHDSQ; GRKVHDSQG; RKVHDSQGN; KVHDSQGNA; VHDSQGNAA; HDSQGNAAK;
DSQGNAAKP; PQEGKCMTH; QEGKCMTHR; EGKCMTHRE; GKCMTHREE; KCMTHREEL; CMTHREELL;
MTHREELLT; THREELLTH; HREELLTHG; REELLTHGM; EELLTHGMQ; ELLTHGMQP; LLTHGMQPN;
LTHGMQPNH; THGMQPNHD; HGMQPNHDL; GMQPNHDLR; MQPNHDLRK; QPNHDLRKE; PNHDLRKES;
NHDLRKESA; QTCFASLGI; TCFASLGIL; CFASLGILA; FASLGILAL; ASLGILALS; SLGILALSP;
LGILALSPV; GILALSPVK; ILALSPVKL; LALSPVKLD; ALSPVKLDK; LSPVKLDKG; SPVKLDKGH;
PVKLDKGHG; VKLDKGHGS; KLDKGHGSA; LDKGHGSAP; DKGHGSAPA; KGHGSAPAV; GHGSAPAVT;
HGSAPAVTT; GSAPAVTTS; SAPAVTTSF; APAVTTSFS; PAVTTSFSE; AVTTSFSES; VTTSFSESW;
NLDWNKKKS; LDWNKKKSS; DWNKKKSSE; WNKKKSSED; NKKKSSEDF; KKKSSEDFY; KKSSEDFYF;
KSSEDFYFY; SSEDFYFYF; SEDFYFYFR; EDFYFYFRA; DFYFYFRAF; FYFYFRAFA; YFYFRAFAG;
FYFRAFAGI; YFRAFAGIL; RQCRREKQK; QCRREKQKY; CRREKQKYH; RREKQKYHC; REKQKYHCF;
EKQKYHCFT; KQKYHCFTC; QKYHCFTCC; KYHCFTCCK; YHCFTCCKR; HCFTCCKRL; CFTCCKRLC;
FTCCKRLCK; TCCKRLCKR; CCKRLCKRL; CKRLCKRLL; KRLCKRLLG; RLCKRLLGK; SLFFCISRF;

LFFCISRFM; FFCISRFMG; FCISRFMGA; CISRFMGAA; ISRFMGAAL; SRFMGAALA; RFMGAALAL;
FMGAALALL; MGAALALLG; GAALALLGD; AALALLGDL; ALALLGDLV; LALLGDLVA; ALLGDLVAS;
LLGDLVASV; LGDLVASVS; GDLVASVSE; DLVASVSEA; LVASVSEAA; VASVSEAAA; ASVSEAAAA;
SVSEAAAAT; VSEAAAATG; SEAAAATGF; EAAAATGFS; AAAATGFSV; AAATGFSVA; AATGFSVAE;
ATGFSVAEI; TGFSVAEIA; GFSVAEIAA; FSVAEIAAG; SVAEIAAGE; VAEIAAGEA; AEIAAGEAA;
EIAAGEAAA; IAAGEAAAA; AAGEAAAAI; AGEAAAAIE; GEAAAAIEV; EAAAAIEVQ; AAAAIEVQI;
AAAIEVQIA; AAIEVQIAS; AIEVQIASL; IEVQIASLA; EVQIASLAT; VQIASLATV; QIASLATVE;
IASLATVEG; ASLATVEGI; SLATVEGIT; LATVEGITS; ATVEGITST; TVEGITSTS; VEGITSTSE;
EGITSTSEA; GITSTSEAI; ITSTSEAIA; TSTSEAIAA; STSEAIAAI; TSEAIAAIG; SEAIAAIGL;
EAIAAIGLT; AIAAIGLTP; IAAIGLTPQ; AAIGLTPQT; AIGLTPQTY; IGLTPQTYA; GLTPQTYAV;
LTPQTYAVI; TPQTYAVIA; PQTYAVIAG; QTYAVIAGA; TYAVIAGAP; YAVIAGAPG; AVIAGAPGA;
VIAGAPGAI; IAGAPGAIA; AGAPGAIAG; GAPGAIAGF; APGAIAGFA; PGAIAGFAA; GAIAGFAAL;
AIAGFAALI; IAGFAALIQ; AGFAALIQT; GFAALIQTV; FAALIQTVS; AALIQTVSG; ALIQTVSGI;
LIQTVSGIS; IQTVSGISS; QTVSGISSL; TVSGISSLA; VSGISSLAQ; SGISSLAQV; GISSLAQVG;
ISSLAQVGY; SSLAQVGYK; SLAQVGYKF; LAQVGYKFF; AQVGYKFFD; QVGYKFFDD; VGYKFFDDW;
GYKFFDDWD; YKFFDDWDH; KFFDDWDHK; FFDDWDHKV; FDDWDHKVS; DDWDHKVST; DWDHKVSTV;
WDHKVSTVG; DHKVSTVGL; HKVSTVGLY; KVSTVGLYQ; VSTVGLYQQ; STVGLYQQS; TVGLYQQSG;
VGLYQQSGM; GLYQQSGMA; LYQQSGMAL; YQQSGMALE; QQSGMALEL; QSGMALELF; SGMALELFN;
GMALELFNP; MALELFNPD; ALELFNPDE; LELFNPDEY; ELFNPDEYY; LFNPDEYYD; FNPDEYYDI;
NPDEYYDIL; PDEYYDILF; DEYYDILFP; EYYDILFPG; YYDILFPGV; YDILFPGVN; DILFPGVNT;
ILFPGVNTF; LFPGVNTFV; FPGVNTFVN; PGVNTFVNN; GVNTFVNNI; VNTFVNNIQ; NTFVNNIQY;
TFVNNIQYL; FVNNIQYLD; VNNIQYLDP; NNIQYLDPR; NIQYLDPRH; IQYLDPRHW; QYLDPRHWG;
YLDPRHWGP; LDPRHWGPS; DPRHWGPSL; PRHWGPSLF; RHWGPSLFA; HWGPSLFAT; WGPSLFATI;
GPSLFATIS; PSLFATISQ; SLFATISQA; LFATISQAL; FATISQALW; ATISQALWH; TISQALWHV;
ISQALWHVI; SQALWHVIR; QALWHVIRD; ALWHVIRDD; LWHVIRDDI; WHVIRDDIP; HVIRDDIPS;
VIRDDIPSI; IRDDIPSIT; RDDIPSITS; DDIPSITSQ; DIPSITSQE; IPSITSQEL; PSITSQELQ;
SITSQELQR; ITSQELQRR; TSQELQRRT; SQELQRRTE; QELQRRTER; ELQRRTERF; LQRRTERFF;
QRRTERFFR; RRTERFFRD; RTERFFRDS; TERFFRDSL; ERFFRDSLA; RFFRDSLAR; FFRDSLARF;
FRDSLARFL; RDSLARFLE; DSLARFLEE; SLARFLEET; LARFLEETT; ARFLEETTW; RFLEETTWT;
FLEETTWTI; LEETTWTIV; EETTWTIVN; ETTWTIVNA; TTWTIVNAP; TWTIVNAPI; WTIVNAPIN;
TIVNAPINF; IVNAPINFY; VNAPINFYN; NAPINFYNY; APINFYNYI; PINFYNYIQ; INFYNYIQQ;
NFYNYIQQY; FYNYIQQYY; YNYIQQYYS; NYIQQYYSD; YIQQYYSDL; IQQYYSDLS; QQYYSDLSP;
QYYSDLSPI; YYSDLSPIR; YSDLSPIRP; SDLSPIRPS; DLSPIRPSM; LSPIRPSMV; SPIRPSMVR;
PIRPSMVRQ; IRPSMVRQV; RPSMVRQVA; PSMVRQVAE; SMVRQVAER; MVRQVAERE; VRQVAEREG;
RQVAEREGT; QVAEREGTR; VAEREGTRV; AEREGTRVH; EREGTRVHF; REGTRVHFG; EGTRVHFGH;
GTRVHFGHT; TRVHFGHTY; RVHFGHTYS; VHFGHTYSI; HFGHTYSID; FGHTYSIDD; GHTYSIDDA;
HTYSIDDAD; TYSIDDADS; YSIDDADSI; SIDDADSIE; IDDADSIEE; DDADSIEEV; DADSIEEVT;
ADSIEEVTQ; DSIEEVTQR; SIEEVTQRM; IEEVTQRMD; EEVTQRMDL; EVTQRMDLR; VTQRMDLRN;
TQRMDLRNQ; QRMDLRNQQ; RMDLRNQQS; MDLRNQQSV; DLRNQQSVH; LRNQQSVHS; RNQQSVHSG;
NQQSVHSGE; QQSVHSGEF; QSVHSGEFI; SVHSGEFIE; VHSGEFIEK; HSGEFIEKT; SGEFIEKTI;
GEFIEKTIA; EFIEKTIAP; FIEKTIAPG; IEKTIAPGG; EKTIAPGGA; KTIAPGGAN; TIAPGGANQ;
IAPGGANQR; APGGANQRT; PGGANQRTA; GGANQRTAP; GANQRTAPQ; ANQRTAPQW; NQRTAPQWM;
QRTAPQWML; RTAPQWMLP; TAPQWMLPL; APQWMLPLL; PQWMLPLLL; QWMLPLLLG; WMLPLLLGL;
MLPLLLGLY; LPLLLGLYG; PLLLGLYGT; LLLGLYGTV; LLGLYGTVT; LGLYGTVTP; GLYGTVTPA;
LYGTVTPAL; YGTVTPALE; GTVTPALEA; TVTPALEAY; VTPALEAYE; TPALEAYED; PALEAYEDG;
ALEAYEDGP; LEAYEDGPN; EAYEDGPNQ; AYEDGPNQK; YEDGPNQKK; EDGPNQKKR; DGPNQKKRR;
GPNQKKRRV; PNQKKRRVS; NQKKRRVSR; QKKRRVSRG; KKRRVSRGS; KRRVSRGSS; RRVSRGSSQ;
RVSRGSSQK; VSRGSSQKA; SRGSSQKAK; RGSSQKAKG; GSSQKAKGT; SSQKAKGTR; SQKAKGTRA;
QKAKGTRAS; KAKGTRASA; AKGTRASAK; KGTRASAKT; GTRASAKTT; TRASAKTTN; RASAKTTNK;
ASAKTTNKR; SAKTTNKRR; AKTTNKRRS; KTTNKRRSR; TTNKRRSRS; TNKRRSRSS; NKRRSRSSR;
KRRSRSSRS; NWGRCYYRG; WGRCYYRGR; GRCYYRGRM; RCYYRGRML; CYYRGRMLP; YYRGRMLPK;
YRGRMLPKP; RGRMLPKPR; GRMLPKPRN; RMLPKPRNG; MLPKPRNGG; LPKPRNGGS; PKPRNGGSR;
PREKNASLL; REKNASLLQ; EKNASLLQH; KNASLLQHS; NASLLQHSK; ASLLQHSKN; SLLQHSKNS;
LLQHSKNSP; LQHSKNSPP; QHSKNSPPQ; HSKNSPPQF; SKNSPPQFK; GPNLWKSTD; PNLWKSTDV;
NLWKSTDVG; LWKSTDVGG; WKSTDVGGC; KSTDVGGCN; STDVGGCNC; TDVGGCNCT; DVGGCNCTN;
VGGCNCTNR; GGCNCTNRG; GCNCTNRGY; CNCTNRGYW; NCTNRGYWN; CTNRGYWNN; PSCRVTKSA;
AWWRKTYSR; WWRKTYSRQ; FPLLCCRWR; PLLCCRWRT; LLCCRWRTL; LCCRWRTLG; CCRWRTLGN;
CRWRTLGNA; RWRTLGNAG; WRTLGNAGS; RTLGNAGSA; TLGNAGSAN; LGNAGSANE; GNAGSANEL;
NAGSANELQ; AGSANELQV; GSANELQVK; SANELQVKV; ANELQVKVP; KPNSPVPGN; PNSPVPGNE;
NSPVPGNEY; GLFGQKQCL; LFGQKQCLS; FGQKQCLSS; VFWDFHRRG; FWDFHRRGK; WDFHRRGKC;
DFHRRGKCS; FHRRGKCSP; HRRGKCSPS; RRGKCSPST; RGKCSPSTS; GKCSPSTSC; KCSPSTSCD;
CSPSTSCDQ; SPSTSCDQH; PSTSCDQHS; STSCDQHSY; TSCDQHSYH; SCDQHSYHS; CDQHSYHSV;
DQHSYHSVA; QHSYHSVAR; QLWNTTVER; LWNTTVERP; WNTTVERPC; NTTVERPCK; TTVERPCKI;
TVERPCKIF; DPPEKKICK; PPEKKICKE; PEKKICKES; EKKICKESL; KKICKESLP; KICKESLPN;
ICKESLPNF; CKESLPNFL; KESLPNFLF; ESLPNFLFA; SLPNFLFAK; PYKQENPES; YKQENPESG;

KQENPESGW; QENPESGWA; ENPESGWAA; NPESGWAAY; PESGWAAYV; ESGWAAYVW; SGWAAYVWY;
GWAAYVWYG; WAAYVWYGI; AAYVWYGIP; AYVWYGIPG; YVWYGIPGR; VWYGIPGRR; WYGIPGRRG;
WHRKTSRGP; HRKTSRGPR; RKTSRGPRY; KTSRGPRYD; TSRGPRYDK; SRGPRYDKI; RGPRYDKIY;
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QNALNRCFY; NALNRCFYC; ALNRCFYCT; LNRCFYCTY; NRCFYCTYT; RCFYCTYTF; CFYCTYTFN;
FYCTYTFNK; YCTYTFNKC; CTYTFNKCC; TYTFNKCCF; YTFNKCCFC; TFNKCCFCI; FNKCCFCIS;
NKCCFCISH; KCCFCISHF; ACVILGVVF; NTESLYTNA; TESLYTNAT; ESLYTNATL; SLYTNATLD;
LYTNATLDY; YTNATLDYG; TNATLDYGG; NATLDYGGL; ATLDYGGLT; TLDYGGLTF; LDYGGLTFG;
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GNLQQGLKY; NLQQGLKYL; LQQGLKYLR; QQGLKYLRL; QGLKYLRLG; GLKYLRLGK; LKYLRLGKS;
KYLRLGKSI; YLRLGKSIV; LRLGKSIVI; RLGKSIVIG; LGKSIVIGI; GKSIVIGIQ; KSIVIGIQC;
SIVIGIQCL; IVIGIQCLI; VIGIQCLIH; IGIQCLIHV; GIQCLIHVQ; IQCLIHVQS; QCLIHVQSL;
CLIHVQSLQ; LIHVQSLQF; IHVQSLQFL; HVQSLQFLN; VQSLQFLNP; QSLQFLNPL; SLQFLNPLL;
LQFLNPLLL; YQEYISPCI; QEYISPCIY; EYISPCIYY; YISPCIYYI; ISPCIYYIS; SPCIYYISS;
PCIYYISSL; CIYYISSLK; IYYISSLKK; YYISSLKKY; YISSLKKYT; ISSLKKYTY; SSLKKYTYL;
SLKKYTYLS; LKKYTYLSQ; KKYTYLSQN; KYTYLSQNP; YTYLSQNPA; TYLSQNPAF; YLSQNPAFP;
LSQNPAFPS; SQNPAFPSI; QNPAFPSIQ; NPAFPSIQQ; PAFPSIQQF; IVYQLQNQL; VYQLQNQLQ;
YQLQNQLQA; TKLAVATRS; KLAVATRSF; LAVATRSFH; AVATRSFHF; VATRSFHFV; ATRSFHFVK;
TRSFHFVKF; RSFHFVKFF; SFHFVKFFF; FHFVKFFFQ; HFVKFFFQV; FVKFFFQVR; VKFFFQVRT;
KFFFQVRTL; FFFQVRTLS; FFQVRTLSF; FQVRTLSFV; QVRTLSFVR; VRTLSFVRI; RTLSFVRIF;
TLSFVRIFL; LSFVRIFLN; SFVRIFLNI; FVRIFLNIF; VRIFLNIFW; RIFLNIFWA; PSLVEIFGF;
SLVEIFGFF; LVEIFGFFC; VEIFGFFCL; EIFGFFCLN; IFGFFCLNV; FGFFCLNVS; GFFCLNVSF;
FFCLNVSFL; FCLNVSFLN; CLNVSFLNL; LNVSFLNLP; HFHLNNLSN; FHLNNLSNC; HLNNLSNCL;
LNNLSNCLN; NNLSNCLNC; NLSNCLNCL; LSNCLNCLF; SNCLNCLFH; NCLNCLFHV; CLNCLFHVL;
LNCLFHVLK; NCLFHVLKA; CLFHVLKAN; LFHVLKANP; FHVLKANPL; HVLKANPLI; VLKANPLIQ;
LKANPLIQL; KANPLIQLL; ANPLIQLLS; NPLIQLLSL; PLIQLLSLL; LIQLLSLLH; IQLLSLLHL;
QLLSLLHLQ; LLSLLHLQK; LSLLHLQKQ; SLLHLQKQP; LLHLQKQPC; LHLQKQPCT; HLQKQPCTD;
LQKQPCTDL; LHLAQRLAF; HLAQRLAFP; LAQRLAFPW; AQRLAFPWV; QRLAFPWVG; RLAFPWVGL;
LAFPWVGLH; AFPWVGLHL; FPWVGLHLR; PWVGLHLRL; WVGLHLRLY; VGLHLRLYH; GLHLRLYHH;
LHLRLYHHT; HLRLYHHTN; LRLYHHTNL; RLYHHTNLI; LYHHTNLIT; YHHTNLITL; HHTNLITLQ;
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QLVLFFHYQ; LVLFFHYQW; VLFFHYQWD; LFFHYQWDL; KQYSAKNQI; QYSAKNQIL; YSAKNQILQ;
SAKNQILQN; AKNQILQNP; KNQILQNPF; VANSAAKQH; ANSAAKQHL; NSAAKQHLP; SAAKQHLPY;
AAKQHLPYI; AKQHLPYIV; KQHLPYIVL; QHLPYIVLV; HLPYIVLVQ; LPYIVLVQH; PYIVLVQHF;
YIVLVQHFH; IVLVQHFHE; VLVQHFHEL; LVQHFHELQ; VQHFHELQI; QHFHELQIL; HFHELQILN;
FHELQILNP; HELQILNPF; ELQILNPFY; LQILNPFYL; QILNPFYLI; ILNPFYLIY; LNPFYLIYD;
IFLLAFLPW; FLLAFLPWS; LLAFLPWSY; LAFLPWSYE; AFLPWSYEG; FLPWSYEGY; LPWSYEGYL;
PWSYEGYLL; WSYEGYLLF; SYEGYLLFF; LKLYLLLAD; KLYLLLADK; LYLLLADKY; YLLLADKYF;
LLLADKYFF; LLADKYFFD; LADKYFFDF; ADKYFFDFY; DKYFFDFYF; KYFFDFYFL; YFFDFYFLQ;
FFDFYFLQK; HLQSAFHDT; SDKAGLFSD; DKAGLFSDT; KAGLFSDTF; AGLFSDTFY; GLFSDTFYT;
LFSDTFYTP; FSDTFYTPL; SDTFYTPLH; DTFYTPLHC; TFYTPLHCI; FYTPLHCIE; YTPLHCIEI;
TPLHCIEIL; PLHCIEILN; LHCIEILNT; HCIEILNTY; CIEILNTYL; IEILNTYLI; EILNTYLII;
ILNTYLIIK; LNTYLIIKT; NTYLIIKTH; TYLIIKTHP; YLIIKTHPH; LIIKTHPHT; IIKTHPHTL;
IKTHPHTLS; KTHPHTLSL; THPHTLSLL; HPHTLSLLH; PHTLSLLHT; HTLSLLHTQ; LISKTPALF;
ISKTPALFL; SKTPALFLQ; KTPALFLQA; TPALFLQAL; PALFLQALL; ALFLQALLG; NHAPLSPLE;
HAPLSPLEC; APLSPLECF; PLSPLECFL; LSPLECFLL; LRHYIVSIP; RHYIVSIPY; RYTAFDRNY;
LQKLYVYVE; QKLYVYVEL; KLYVYVELK; LYVYVELKR; YVYVELKRI; YYAQHTCVY; VFYTEFELF;
FYTEFELFL; YTQQSRQGF; TQQSRQGFY; QQSRQGFYY; ETGVDQRES; TGVDQRESL; GLLPFFFFW;
LLPFFFFWV; LPFFFFWVV; PFFFFWVVL; FFFFWVVLS; FFFWVVLSV; FFWVVLSVE; FWVVLSVEN;
WVVLSVENL; VVLSVENLL; VLSVENLLL; LSVENLLLL; SVENLLLLL; VENLLLLLH; ENLLLLLHH;
NLLLLLHHW; LLLLLHHWQ; LLLLHHWQT; LLLHHWQTY; LLHHWQTYL; LHHWQTYLH; HHWQTYLHG;
HWQTYLHGK; WQTYLHGKI; QTYLHGKIN; TYLHGKINL; YLHGKINLH; LHGKINLHP; HGKINLHPI;
GKINLHPIF; KINLHPIFH; RNSTRTPTL; NSTRTPTLL; STRTPTLLF; TRTPTLLFH; RTPTLLFHR;
TPTLLFHRL; PTLLFHRLA; TLLFHRLAP; LLFHRLAPI; LFHRLAPIK; FHRLAPIKK; HRLAPIKKI;
RLAPIKKII; LAPIKKIIT; GLLIFYYLS; LLIFYYLSK; LIFYYLSKY; IFYYLSKYK; FYYLSKYKL;
YYLSKYKLV; YLSKYKLVT; LSKYKLVTL; SKYKLVTLK; KYKLVTLKL; ISEGSFSNY; SEGSFSNYL;
EGSFSNYLD; GSFSNYLDP; SFSNYLDPP; FSNYLDPPL; SNYLDPPLQ; NYLDPPLQS; YLDPPLQSF;
LDPPLQSFF; DPPLQSFFS; AKPLCEAVN; KPLCEAVNA; PLCEAVNAV; LCEAVNAVA; CEAVNAVAI;
EAVNAVAIY; AVNAVAIYP; VNAVAIYPN; NAVAIYPNQ; AVAIYPNQG; VAIYPNQGL; AIYPNQGLF;
IYPNQGLFS; HARAVHRRL; ARAVHRRLF; RAVHRRLFG; AVHRRLFGT; VHRRLFGTN; HRRLFGTNR;
RRLFGTNRP; RLFGTNRPF; LFGTNRPFL; FGTNRPFLA; GTNRPFLAV; TNRPFLAVQ; NRPFLAVQG;
RPFLAVQGI; PFLAVQGIW; FLAVQGIWA; LAVQGIWAK; AVQGIWAKR; VQGIWAKRK; QGIWAKRKI;
GIWAKRKIS; IWAKRKIST; WAKRKISTN; AKRKISTNL; ATPGSKIRL; TPGSKIRLM; PGSKIRLMS;
GSKIRLMSY; SKIRLMSYL; KIRLMSYLY; IRLMSYLYI; RLMSYLYIL; LMSYLYILL; MSYLYILLH;
SYLYILLHF; YLYILLHFF; LYILLHFFI; YILLHFFIQ; ILLHFFIQS; LLHFFIQSI; LHFFIQSIH;

HFFIQSIHS; FFIQSIHSL; FIQSIHSLH; IQSIHSLHF; QSIHSLHFI; SIHSLHFIL; IHSLHFILV; HSLHFILVA; SLHFILVAP; LHFILVAPF; HFILVAPFV; FILVAPFVR; ILVAPFVRV; LVAPFVRVK; VAPFVRVKF; APFVRVKFL; PFVRVKFLT; FVRVKFLTL; VRVKFLTLP; GKISPGSSF; KISPGSSFK; ISPGSSFKA; KVHELHGFF; VHELHGFFP; HELHGFFPV; ELHGFFPVK; LHGFFPVKN; HGFFPVKNF; GFFPVKNFI; FFPVKNFIH

10 mers:

LQKLQKNRDF; QKLQKNRDFP; KLQKNRDFPK; ASEKASTPLL; SEKASTPLLL; EKASTPLLLE; KASTPLLLER; ASTPLLLERK; STPLLLERKG; TPLLLERKGG; PLLLERKGGG; LLLERKGGGR; LLERKGGGRG; LERKGGGRGG; ERKGGGRGGL; RKGGGRGGLG; KGGGRGGLGL; GGGRGGLGLL; GGRGGLGLLY; GRGGLGLLYI; RGGLGLLYII; GGLGLLYIIK; GLGLLYIIKK; LGLLYIIKKK; GLLYIIKKKA; LLYIIKKKAT; LYIIKKKATG; YIIKKKATGR; IIKKKATGRS; IKKKATGRSC; KKKATGRSCL; KKATGRSCLP; KATGRSCLPM; ATGRSCLPME; TGRSCLPMEC; GRSCLPMECS; RSCLPMECSQ; SCLPMECSQT; CLPMECSQTM; LPMECSQTMT; PMECSQTMTS; MECSQTMTSG; ECSQTMTSGR; CSQTMTSGRK; SQTMTSGRKV; QTMTSGRKVH; TMTSGRKVHD; MTSGRKVHDS; TSGRKVHDSQ; SGRKVHDSQG; GRKVHDSQGN; RKVHDSQGNA; KVHDSQGNAA; VHDSQGNAAK; HDSQGNAAKP; PQEGKCMTHR; QEGKCMTHRE; EGKCMTHREE; GKCMTHREEL; KCMTHREELL; CMTHREELLT; MTHREELLTH; THREELLTHG; HREELLTHGM; REELLTHGMQ; EELLTHGMQP; ELLTHGMQPN; LLTHGMQPNH; LTHGMQPNHD; THGMQPNHDL; HGMQPNHDLR; GMQPNHDLRK; MQPNHDLRKE; QPNHDLRKES; PNHDLRKESA; QTCFASLGIL; TCFASLGILA; CFASLGILAL; FASLGILALS; ASLGILALSP; SLGILALSPV; LGILALSPVK; GILALSPVKL; ILALSPVKLD; LALSPVKLDK; ALSPVKLDKG; LSPVKLDKGH; SPVKLDKGHG; PVKLDKGHGS; VKLDKGHGSA; KLDKGHGSAP; LDKGHGSAPA; DKGHGSAPAV; KGHGSAPAVT; GHGSAPAVTT; HGSAPAVTTS; GSAPAVTTSF; SAPAVTTSFS; APAVTTSFSE; PAVTTSFSES; AVTTSFSESW; NLDWNKKKSS; LDWNKKKSSE; DWNKKKSSED; WNKKKSSEDF; NKKKSSEDFY; KKKSSEDFYF; KKSSEDFYFY; KSSEDFYFYF; SSEDFYFYFR; SEDFYFYFRA; EDFYFYFRAF; DFYFYFRAFA; FYFYFRAFAG; YFYFRAFAGI; FYFRAFAGIL; RQCRREKQKY; QCRREKQKYH; CRREKQKYHC; RREKQKYHCF; REKQKYHCFT; EKQKYHCFTC; KQKYHCFTCC; QKYHCFTCCK; KYHCFTCCKR; YHCFTCCKRL; HCFTCCKRLC; CFTCCKRLCK; FTCCKRLCKR; TCCKRLCKRL; CCKRLCKRLL; CKRLCKRLLG; KRLCKRLLGK; SLFFCISRFM; LFFCISRFMG; FFCISRFMGA; FCISRFMGAA; CISRFMGAAL; ISRFMGAALA; SRFMGAALAL; RFMGAALALL; FMGAALALLG; MGAALALLGD; GAALALLGDL; AALALLGDLV; ALALLGDLVA; LALLGDLVAS; ALLGDLVASV; LLGDLVASVS; LGDLVASVSE; GDLVASVSEA; DLVASVSEAA; LVASVSEAAA; VASVSEAAAA; ASVSEAAAAT; SVSEAAAATG; VSEAAAATGF; SEAAAATGFS; EAAAATGFSV; AAAATGFSVA; AAATGFSVAE; AATGFSVAEI; ATGFSVAEIA; TGFSVAEIAA; GFSVAEIAAG; FSVAEIAAGE; SVAEIAAGEA; VAEIAAGEAA; AEIAAGEAAA; EIAAGEAAAA; IAAGEAAAAI; AAGEAAAAIE; AGEAAAAIEV; GEAAAAIEVQ; EAAAAIEVQI; AAAAIEVQIA; AAAIEVQIAS; AAIEVQIASL; AIEVQIASLA; IEVQIASLAT; EVQIASLATV; VQIASLATVE; QIASLATVEG; IASLATVEGI; ASLATVEGIT; SLATVEGITS; LATVEGITST; ATVEGITSTS; TVEGITSTSE; VEGITSTSEA; EGITSTSEAI; GITSTSEAIA; ITSTSEAIAA; TSTSEAIAAI; STSEAIAAIG; TSEAIAAIGL; SEAIAAIGLT; EAIAAIGLTP; AIAAIGLTPQ; IAAIGLTPQT; AAIGLTPQTY; AIGLTPQTYA; IGLTPQTYAV; GLTPQTYAVI; LTPQTYAVIA; TPQTYAVIAG; PQTYAVIAGA; QTYAVIAGAP; TYAVIAGAPG; YAVIAGAPGA; AVIAGAPGAI; VIAGAPGAIA; IAGAPGAIAG; AGAPGAIAGF; GAPGAIAGFA; APGAIAGFAA; PGAIAGFAAL; GAIAGFAALI; AIAGFAALIQ; IAGFAALIQT; AGFAALIQTV; GFAALIQTVS; FAALIQTVSG; AALIQTVSGI; ALIQTVSGIS; LIQTVSGISS; IQTVSGISSL; QTVSGISSLA; TVSGISSLAQ; VSGISSLAQV; SGISSLAQVG; GISSLAQVGY; ISSLAQVGYK; SSLAQVGYKF; SLAQVGYKFF; LAQVGYKFFD; AQVGYKFFDD; QVGYKFFDDW; VGYKFFDDWD; GYKFFDDWDH; YKFFDDWDHK; KFFDDWDHKV; FFDDWDHKVS; FDDWDHKVST; DDWDHKVSTV; DWDHKVSTVG; WDHKVSTVGL; DHKVSTVGLY; HKVSTVGLYQ; KVSTVGLYQQ; VSTVGLYQQS; STVGLYQQSG; TVGLYQQSGM; VGLYQQSGMA; GLYQQSGMAL; LYQQSGMALE; YQQSGMALEL; QQSGMALELF; QSGMALELFN; SGMALELFNP; GMALELFNPD; MALELFNPDE; ALELFNPDEY; LELFNPDEYY; ELFNPDEYYD; LFNPDEYYDI; FNPDEYYDIL; NPDEYYDILF; PDEYYDILFP; DEYYDILFPG; EYYDILFPGV; YYDILFPGVN; YDILFPGVNT; DILFPGVNTF; ILFPGVNTFV; LFPGVNTFVN; FPGVNTFVNN; PGVNTFVNNI; GVNTFVNNIQ; VNTFVNNIQY; NTFVNNIQYL; TFVNNIQYLD; FVNNIQYLDP; VNNIQYLDPR; NNIQYLDPRH; NIQYLDPRHW; IQYLDPRHWG; QYLDPRHWGP; YLDPRHWGPS; LDPRHWGPSL; DPRHWGPSLF; PRHWGPSLFA; RHWGPSLFAT; HWGPSLFATI; WGPSLFATIS; GPSLFATISQ; PSLFATISQA; SLFATISQAL; LFATISQALW; FATISQALWH; ATISQALWHV; TISQALWHVI; ISQALWHVIR; SQALWHVIRD; QALWHVIRDD; ALWHVIRDDI; LWHVIRDDIP; WHVIRDDIPS; HVIRDDIPSI; VIRDDIPSIT; IRDDIPSITS; RDDIPSITSQ; DDIPSITSQE; DIPSITSQEL; IPSITSQELQ; PSITSQELQR; SITSQELQRR; ITSQELQRRT; TSQELQRRTE; SQELQRRTER; QELQRRTERF; ELQRRTERFF; LQRRTERFFR; QRRTERFFRD; RRTERFFRDS; RTERFFRDSL; TERFFRDSLA; ERFFRDSLAR; RFFRDSLARF; FFRDSLARFL; FRDSLARFLE; RDSLARFLEE; DSLARFLEET; SLARFLEETT; LARFLEETTW; ARFLEETTWT; RFLEETTWTI; FLEETTWTIV; LEETTWTIVN; EETTWTIVNA; ETTWTIVNAP; TTWTIVNAPI; TWTIVNAPIN; WTIVNAPINF; TIVNAPINFY; IVNAPINFYN; VNAPINFYNY; NAPINFYNYI; APINFYNYIQ; PINFYNYIQQ; INFYNYIQQY; NFYNYIQQYY; FYNYIQQYYS; YNYIQQYYSD;

NYIQQYYSDL; YIQQYYSDLS; IQQYYSDLSP; QQYYSDLSPI; QYYSDLSPIR; YYSDLSPIRP;
YSDLSPIRPS; SDLSPIRPSM; DLSPIRPSMV; LSPIRPSMVR; SPIRPSMVRQ; PIRPSMVRQV;
IRPSMVRQVA; RPSMVRQVAE; PSMVRQVAER; SMVRQVAERE; MVRQVAEREG; VRQVAEREGT;
RQVAEREGTR; QVAEREGTRV; VAEREGTRVH; AEREGTRVHF; EREGTRVHFG; REGTRVHFGH;
EGTRVHFGHT; GTRVHFGHTY; TRVHFGHTYS; RVHFGHTYSI; VHFGHTYSID; HFGHTYSIDD;
FGHTYSIDDA; GHTYSIDDAD; HTYSIDDADS; TYSIDDADSI; YSIDDADSIE; SIDDADSIEE;
IDDADSIEEV; DDADSIEEVT; DADSIEEVTQ; ADSIEEVTQR; DSIEEVTQRM; SIEEVTQRMD;
IEEVTQRMDL; EEVTQRMDLR; EVTQRMDLRN; VTQRMDLRNQ; TQRMDLRNQQ; QRMDLRNQQS;
RMDLRNQQSV; MDLRNQQSVH; DLRNQQSVHS; LRNQQSVHSG; RNQQSVHSGE; NQQSVHSGEF;
QQSVHSGEFI; QSVHSGEFIE; SVHSGEFIEK; VHSGEFIEKT; HSGEFIEKTI; SGEFIEKTIA;
GEFIEKTIAP; EFIEKTIAPG; FIEKTIAPGG; IEKTIAPGGA; EKTIAPGGAN; KTIAPGGANQ;
TIAPGGANQR; IAPGGANQRT; APGGANQRTA; PGGANQRTAP; GGANQRTAPQ; GANQRTAPQW;
ANQRTAPQWM; NQRTAPQWML; QRTAPQWMLP; RTAPQWMLPL; TAPQWMLPLL; APQWMLPLLL;
PQWMLPLLLG; QWMLPLLLGL; WMLPLLLGLY; MLPLLLGLYG; LPLLLGLYGT; PLLLGLYGTV;
LLLGLYGTVT; LLGLYGTVTP; LGLYGTVTPA; GLYGTVTPAL; LYGTVTPALE; YGTVTPALEA;
GTVTPALEAY; TVTPALEAYE; VTPALEAYED; TPALEAYEDG; PALEAYEDGP; ALEAYEDGPN;
LEAYEDGPNQ; EAYEDGPNQK; AYEDGPNQKK; YEDGPNQKKR; EDGPNQKKRR; DGPNQKKRRV;
GPNQKKRRVS; PNQKKRRVSR; NQKKRRVSRG; QKKRRVSRGS; KKRRVSRGSS; KRRVSRGSSQ;
RRVSRGSSQK; RVSRGSSQKA; VSRGSSQKAK; SRGSSQKAKG; RGSSQKAKGT; GSSQKAKGTR;
SSQKAKGTRA; SQKAKGTRAS; QKAKGTRASA; KAKGTRASAK; AKGTRASAKT; KGTRASAKTT;
GTRASAKTTN; TRASAKTTNK; RASAKTTNKR; ASAKTTNKRR; SAKTTNKRRS; AKTTNKRRSR;
KTTNKRRSRS; TTNKRRSRSS; TNKRRSRSSR; NKRRSRSSRS; NWGRCYYRGR; WGRCYYRGRM;
GRCYYRGRML; RCYYRGRMLP; CYYRGRMLPK; YYRGRMLPKP; YRGRMLPKPR; RGRMLPKPRN;
GRMLPKPRNG; RMLPKPRNGG; MLPKPRNGGS; LPKPRNGGSR; PREKNASLLQ; REKNASLLQH;
EKNASLLQHS; KNASLLQHSK; NASLLQHSKN; ASLLQHSKNS; SLLQHSKNSP; LLQHSKNSPP;
LQHSKNSPPQ; QHSKNSPPQF; HSKNSPPQFK; GPNLWKSTDV; PNLWKSTDVG; NLWKSTDVGG;
LWKSTDVGGC; WKSTDVGGCN; KSTDVGGCNC; STDVGGCNCT; TDVGGCNCTN; DVGGCNCTNR;
VGGCNCTNRG; GGCNCTNRGY; GCNCTNRGYW; CNCTNRGYWN; NCTNRGYWNN; AWWRKTYSRQ;
FPLLCCRWRT; PLLCCRWRTL; LLCCRWRTLG; LCCRWRTLGN; CCRWRTLGNA; CRWRTLGNAG;
RWRTLGNAGS; WRTLGNAGSA; RTLGNAGSAN; TLGNAGSANE; LGNAGSANEL; GNAGSANELQ;
NAGSANELQV; AGSANELQVK; GSANELQVKV; SANELQVKVP; KPNSPVPGNE; PNSPVPGNEY;
GLFGQKQCLS; LFGQKQCLSS; VFWDFHRRGK; FWDFHRRGKC; WDFHRRGKCS; DFHRRGKCSP;
FHRRGKCSPS; HRRGKCSPST; RRGKCSPSTS; RGKCSPSTSC; GKCSPSTSCD; KCSPSTSCDQ;
CSPSTSCDQH; SPSTSCDQHS; PSTSCDQHSY; STSCDQHSYH; TSCDQHSYHS; SCDQHSYHSV;
CDQHSYHSVA; DQHSYHSVAR; QLWNTTVERP; LWNTTVERPC; WNTTVERPCK; NTTVERPCKI;
TTVERPCKIF; DPPEKKICKE; PPEKKICKES; PEKKICKESL; EKKICKESLP; KKICKESLPN;
KICKESLPNF; ICKESLPNFL; CKESLPNFLF; KESLPNFLFA; ESLPNFLFAK; PYKQENPESG;
YKQENPESGW; KQENPESGWA; QENPESGWAA; ENPESGWAAY; NPESGWAAYV; PESGWAAYVW;
ESGWAAYVWY; SGWAAYVWYG; GWAAYVWYGI; WAAYVWYGIP; AAYVWYGIPG; AYVWYGIPGR;
YVWYGIPGRR; VWYGIPGRRG; WHRKTSRGPR; HRKTSRGPRY; RKTSRGPRYD; KTSRGPRYDK;
TSRGPRYDKI; SRGPRYDKIY; QTGTIANQNA; TGTIANQNAL; GTIANQNALN; TIANQNALNR;
IANQNALNRC; ANQNALNRCF; NQNALNRCFY; QNALNRCFYC; NALNRCFYCT; ALNRCFYCTY;
LNRCFYCTYT; NRCFYCTYTF; RCFYCTYTFN; CFYCTYTFNK; FYCTYTFNKC; YCTYTFNKCC;
CTYTFNKCCF; TYTFNKCCFC; YTFNKCCFCI; TFNKCCFCIS; FNKCCFCISH; NKCCFCISHF;
NTESLYTNAT; TESLYTNATL; ESLYTNATLD; SLYTNATLDY; LYTNATLDYG; YTNATLDYGG;
TNATLDYGGL; NATLDYGGLT; ATLDYGGLTF; TLDYGGLTFG; LDYGGLTFGN; DYGGLTFGNL;
YGGLTFGNLQ; GGLTFGNLQQ; GLTFGNLQQG; LTFGNLQQGL; TFGNLQQGLK; FGNLQQGLKY;
GNLQQGLKYL; NLQQGLKYLR; LQQGLKYLRL; QQGLKYLRLG; QGLKYLRLGK; GLKYLRLGKS;
LKYLRLGKSI; KYLRLGKSIV; YLRLGKSIVI; LRLGKSIVIG; RLGKSIVIGI; LGKSIVIGIQ;
GKSIVIGIQC; KSIVIGIQCL; SIVIGIQCLI; IVIGIQCLIH; VIGIQCLIHV; IGIQCLIHVQ;
GIQCLIHVQS; IQCLIHVQSL; QCLIHVQSLQ; CLIHVQSLQF; LIHVQSLQFL; IHVQSLQFLN;
HVQSLQFLNP; VQSLQFLNPL; QSLQFLNPLL; SLQFLNPLLL; YQEYISPCIY; QEYISPCIYY;
EYISPCIYYI; YISPCIYYIS; ISPCIYYISS; SPCIYYISSL; PCIYYISSLK; CIYYISSLKK;
IYYISSLKKY; YYISSLKKYT; YISSLKKYTY; ISSLKKYTYL; SSLKKYTYLS; SLKKYTYLSQ;
LKKYTYLSQN; KKYTYLSQNP; KYTYLSQNPA; YTYLSQNPAF; TYLSQNPAFP; YLSQNPAFPS;
LSQNPAFPSI; SQNPAFPSIQ; QNPAFPSIQQ; NPAFPSIQQF; IVYQLQNQLQ; VYQLQNQLQA;
TKLAVATRSF; KLAVATRSFH; LAVATRSFHF; AVATRSFHFV; VATRSFHFVK; ATRSFHFVKF;
TRSFHFVKFF; RSFHFVKFFF; SFHFVKFFFQ; FHFVKFFFQV; HFVKFFFQVR; FVKFFFQVRT;
VKFFFQVRTL; KFFFQVRTLS; FFFQVRTLSF; FFQVRTLSFV; FQVRTLSFVR; QVRTLSFVRI;
VRTLSFVRIF; RTLSFVRIFL; TLSFVRIFLN; LSFVRIFLNI; SFVRIFLNIF; FVRIFLNIFW;
VRIFLNIFWA; PSLVEIFGFF; SLVEIFGFFC; LVEIFGFFCL; VEIFGFFCLN; EIFGFFCLNV;
IFGFFCLNVS; FGFFCLNVSF; GFFCLNVSFL; FFCLNVSFLN; FCLNVSFLNL; CLNVSFLNLP;
HFHLNNLSNC; FHLNNLSNCL; HLNNLSNCLN; LNNLSNCLNC; NNLSNCLNCL; NLSNCLNCLF;
LSNCLNCLFH; SNCLNCLFHV; NCLNCLFHVL; CLNCLFHVLK; LNCLFHVLKA; NCLFHVLKAN;
CLFHVLKANP; LFHVLKANPL; FHVLKANPLI; HVLKANPLIQ; VLKANPLIQL; LKANPLIQLL;

KANPLIQLLS; ANPLIQLLSL; NPLIQLLSLL; PLIQLLSLLH; LIQLLSLLHL; IQLLSLLHLQ;
QLLSLLHLQK; LLSLLHLQKQ; LSLLHLQKQP; SLLHLQKQPC; LLHLQKQPCT; LHLQKQPCTD;
HLQKQPCTDL; LHLAQRLAFP; HLAQRLAFPW; LAQRLAFPWV; AQRLAFPWVG; QRLAFPWVGL;
RLAFPWVGLH; LAFPWVGLHL; AFPWVGLHLR; FPWVGLHLRL; PWVGLHLRLY; WVGLHLRLYH;
VGLHLRLYHH; GLHLRLYHHT; LHLRLYHHTN; HLRLYHHTNL; LRLYHHTNLI; RLYHHTNLIT;
LYHHTNLITL; YHHTNLITLQ; HHTNLITLQL; HTNLITLQLV; TNLITLQLVL; NLITLQLVLF;
LITLQLVLFF; ITLQLVLFFH; TLQLVLFFHY; LQLVLFFHYQ; QLVLFFHYQW; LVLFFHYQWD;
VLFFHYQWDL; KQYSAKNQIL; QYSAKNQILQ; YSAKNQILQN; SAKNQILQNP; AKNQILQNPF;
VANSAAKQHL; ANSAAKQHLP; NSAAKQHLPY; SAAKQHLPYI; AAKQHLPYIV; AKQHLPYIVL;
KQHLPYIVLV; QHLPYIVLVQ; HLPYIVLVQH; LPYIVLVQHF; PYIVLVQHFH; YIVLVQHFHE;
IVLVQHFHEL; VLVQHFHELQ; LVQHFHELQI; VQHFHELQIL; QHFHELQILN; HFHELQILNP;
FHELQILNPF; HELQILNPFY; ELQILNPFYL; LQILNPFYLI; QILNPFYLIY; ILNPFYLIYD;
IFLLAFLPWS; FLLAFLPWSY; LLAFLPWSYE; LAFLPWSYEG; AFLPWSYEGY; FLPWSYEGYL;
LPWSYEGYLL; PWSYEGYLLF; WSYEGYLLFF; LKLYLLLADK; KLYLLLADKY; LYLLLADKYF;
YLLLADKYFF; LLLADKYFFD; LLADKYFFDF; LADKYFFDFY; ADKYFFDFYF; DKYFFDFYFL;
KYFFDFYFLQ; YFFDFYFLQK; SDKAGLFSDT; DKAGLFSDTF; KAGLFSDTFY; AGLFSDTFYT;
GLFSDTFYTP; LFSDTFYTPL; FSDTFYTPLH; SDTFYTPLHC; DTFYTPLHCI; TFYTPLHCIE;
FYTPLHCIEI; YTPLHCIEIL; TPLHCIEILN; PLHCIEILNT; LHCIEILNTY; HCIEILNTYL;
CIEILNTYLI; IEILNTYLII; EILNTYLIIK; ILNTYLIIKT; LNTYLIIKTH; NTYLIIKTHP;
TYLIIKTHPH; YLIIKTHPHT; LIIKTHPHTL; IIKTHPHTLS; IKTHPHTLSL; KTHPHTLSLL;
THPHTLSLLH; HPHTLSLLHT; PHTLSLLHTQ; LISKTPALFL; ISKTPALFLQ; SKTPALFLQA;
KTPALFLQAL; TPALFLQALL; PALFLQALLG; NHAPLSPLEC; HAPLSPLECF; APLSPLECFL;
PLSPLECFLL; LRHYIVSIPY; LQKLYVYVEL; QKLYVYVELK; KLYVYVELKR; LYVYVELKRI;
VFYTEFELFL; YTQQSRQGFY; TQQSRQGFYY; ETGVDQRESL; GLLPFFFFWV; LLPFFFFWVV;
LPFFFFWVVL; PFFFFWVVLS; FFFFWVVLSV; FFFWVVLSVE; FFWVVLSVEN; FWVVLSVENL;
WVVLSVENLL; VVLSVENLLL; VLSVENLLLL; LSVENLLLLL; SVENLLLLLH; VENLLLLLHH;
ENLLLLLHHW; NLLLLLHHWQ; LLLLLHHWQT; LLLLHHWQTY; LLLHHWQTYL; LLHHWQTYLH;
LHHWQTYLHG; HHWQTYLHGK; HWQTYLHGKI; WQTYLHGKIN; QTYLHGKINL; TYLHGKINLH;
YLHGKINLHP; LHGKINLHPI; HGKINLHPIF; GKINLHPIFH; RNSTRTPTLL; NSTRTPTLLF;
STRTPTLLFH; TRTPTLLFHR; RTPTLLFHRL; TPTLLFHRLA; PTLLFHRLAP; TLLFHRLAPI;
LLFHRLAPIK; LFHRLAPIKK; FHRLAPIKKI; HRLAPIKKII; RLAPIKKIIT; GLLIFYYLSK;
LLIFYYLSKY; LIFYYLSKYK; IFYYLSKYKL; FYYLSKYKLV; YYLSKYKLVT; YLSKYKLVTL;
LSKYKLVTLK; SKYKLVTLKL; ISEGSFSNYL; SEGSFSNYLD; EGSFSNYLDP; GSFSNYLDPP;
SFSNYLDPPL; FSNYLDPPLQ; SNYLDPPLQS; NYLDPPLQSF; YLDPPLQSFF; LDPPLQSFFS;
AKPLCEAVNA; KPLCEAVNAV; PLCEAVNAVA; LCEAVNAVAI; CEAVNAVAIY; EAVNAVAIYP;
AVNAVAIYPN; VNAVAIYPNQ; NAVAIYPNQG; AVAIYPNQGL; VAIYPNQGLF; AIYPNQGLFS;
HARAVHRRLF; ARAVHRRLFG; RAVHRRLFGT; AVHRRLFGTN; VHRRLFGTNR; HRRLFGTNRP;
RRLFGTNRPF; RLFGTNRPFL; LFGTNRPFLA; FGTNRPFLAV; GTNRPFLAVQ; TNRPFLAVQG;
NRPFLAVQGI; RPFLAVQGIW; PFLAVQGIWA; FLAVQGIWAK; LAVQGIWAKR; AVQGIWAKRK;
VQGIWAKRKI; QGIWAKRKIS; GIWAKRKIST; IWAKRKISTN; WAKRKISTNL; ATPGSKIRLM;
TPGSKIRLMS; PGSKIRLMSY; GSKIRLMSYL; SKIRLMSYLY; KIRLMSYLYI; IRLMSYLYIL;
RLMSYLYILL; LMSYLYILLH; MSYLYILLHF; SYLYILLHFF; YLYILLHFFI; LYILLHFFIQ;
YILLHFFIQS; ILLHFFIQSI; LLHFFIQSIH; LHFFIQSIHS; HFFIQSIHSL; FFIQSIHSLH;
FIQSIHSLHF; IQSIHSLHFI; QSIHSLHFIL; SIHSLHFILV; IHSLHFILVA; HSLHFILVAP;
SLHFILVAPF; LHFILVAPFV; HFILVAPFVR; FILVAPFVRV; ILVAPFVRVK; LVAPFVRVKF;
VAPFVRVKFL; APFVRVKFLT; PFVRVKFLTL; FVRVKFLTLP; GKISPGSSFK; KISPGSSFKA;
KVHELHGFFP; VHELHGFFPV; HELHGFFPVK; ELHGFFPVKN; LHGFFPVKNF; HGFFPVKNFI;
GFFPVKNFIH

11 mers:
LQKLQKNRDFP; QKLQKNRDFPK; ASEKASTPLLL; SEKASTPLLLE; EKASTPLLLER; KASTPLLLERK;
ASTPLLLERKG; STPLLLERKGG; TPLLLERKGGG; PLLLERKGGGR; LLLERKGGGRG; LLERKGGGRGG;
LERKGGGRGGL; ERKGGGRGGLG; RKGGGRGGLGL; KGGGRGGLGLL; GGGRGGLGLLY; GGRGGLGLLYI;
GRGGLGLLYII; RGGLGLLYIIK; GGLGLLYIIKK; GLGLLYIIKKK; LGLLYIIKKKA; GLLYIIKKKAT;
LLYIIKKKATG; LYIIKKKATGR; YIIKKKATGRS; IIKKKATGRSC; IKKKATGRSCL; KKKATGRSCLP;
KKATGRSCLPM; KATGRSCLPME; ATGRSCLPMEC; TGRSCLPMECS; GRSCLPMECSQ; RSCLPMECSQT;
SCLPMECSQTM; CLPMECSQTMT; LPMECSQTMTS; PMECSQTMTSG; MECSQTMTSGR; ECSQTMTSGRK;
CSQTMTSGRKV; SQTMTSGRKVH; QTMTSGRKVHD; TMTSGRKVHDS; MTSGRKVHDSQ; TSGRKVHDSQG;
SGRKVHDSQGN; GRKVHDSQGNA; RKVHDSQGNAA; KVHDSQGNAAK; VHDSQGNAAKP; PQEGKCMTHRE;
QEGKCMTHREE; EGKCMTHREEL; GKCMTHREELL; KCMTHREELLT; CMTHREELLTH; MTHREELLTHG;
THREELLTHGM; HREELLTHGMQ; REELLTHGMQP; EELLTHGMQPN; ELLTHGMQPNH; LLTHGMQPNHD;
LTHGMQPNHDL; THGMQPNHDLR; HGMQPNHDLRK; GMQPNHDLRKE; MQPNHDLRKES; QPNHDLRKESA;
QTCFASLGILA; TCFASLGILAL; CFASLGILALS; FASLGILALSP; ASLGILALSPV; SLGILALSPVK;
LGILALSPVKL; GILALSPVKLD; ILALSPVKLDK; LALSPVKLDKG; ALSPVKLDKGH; LSPVKLDKGHG;
SPVKLDKGHGS; PVKLDKGHGSA; VKLDKGHGSAP; KLDKGHGSAPA; LDKGHGSAPAV; DKGHGSAPAVT;

KGHGSAPAVTT; GHGSAPAVTTS; HGSAPAVTTSF; GSAPAVTTSFS; SAPAVTTSFSE; APAVTTSFSES;
PAVTTSFSESW; NLDWNKKKSSE; LDWNKKKSSED; DWNKKKSSEDF; WNKKKSSEDFY; NKKKSSEDFYF;
KKKSSEDFYFY; KKSSEDFYFYF; KSSEDFYFYFR; SSEDFYFYFRA; SEDFYFYFRAF; EDFYFYFRAFA;
DFYFYFRAFAG; FYFYFRAFAGI; YFYFRAFAGIL; RQCRREKQKYH; QCRREKQKYHC; CRREKQKYHCF;
RREKQKYHCFT; REKQKYHCFTC; EKQKYHCFTCC; KQKYHCFTCCK; QKYHCFTCCKR; KYHCFTCCKRL;
YHCFTCCKRLC; HCFTCCKRLCK; CFTCCKRLCKR; FTCCKRLCKRL; TCCKRLCKRLL; CCKRLCKRLLG;
CKRLCKRLLGK; SLFFCISRFMG; LFFCISRFMGA; FFCISRFMGAA; FCISRFMGAAL; CISRFMGAALA;
ISRFMGAALAL; SRFMGAALALL; RFMGAALALLG; FMGAALALLGD; MGAALALLGDL; GAALALLGDLV;
AALALLGDLVA; ALALLGDLVAS; LALLGDLVASV; ALLGDLVASVS; LLGDLVASVSE; LGDLVASVSEA;
GDLVASVSEAA; DLVASVSEAAA; LVASVSEAAAA; VASVSEAAAAT; ASVSEAAAATG; SVSEAAAATGF;
VSEAAAATGFS; SEAAAATGFSV; EAAAATGFSVA; AAAATGFSVAE; AAATGFSVAEI; AATGFSVAEIA;
ATGFSVAEIAA; TGFSVAEIAAG; GFSVAEIAAGE; FSVAEIAAGEA; SVAEIAAGEAA; VAEIAAGEAAA;
AEIAAGEAAAA; EIAAGEAAAAI; IAAGEAAAAIE; AAGEAAAAIEV; AGEAAAAIEVQ; GEAAAAIEVQI;
EAAAAIEVQIA; AAAAIEVQIAS; AAAIEVQIASL; AAIEVQIASLA; AIEVQIASLAT; IEVQIASLATV;
EVQIASLATVE; VQIASLATVEG; QIASLATVEGI; IASLATVEGIT; ASLATVEGITS; SLATVEGITST;
LATVEGITSTS; ATVEGITSTSE; TVEGITSTSEA; VEGITSTSEAI; EGITSTSEAIA; GITSTSEAIAA;
ITSTSEAIAAI; TSTSEAIAAIG; STSEAIAAIGL; TSEAIAAIGLT; SEAIAAIGLTP; EAIAAIGLTPQ;
AIAAIGLTPQT; IAAIGLTPQTY; AAIGLTPQTYA; AIGLTPQTYAV; IGLTPQTYAVI; GLTPQTYAVIA;
LTPQTYAVIAG; TPQTYAVIAGA; PQTYAVIAGAP; QTYAVIAGAPG; TYAVIAGAPGA; YAVIAGAPGAI;
AVIAGAPGAIA; VIAGAPGAIAG; IAGAPGAIAGF; AGAPGAIAGFA; GAPGAIAGFAA; APGAIAGFAAL;
PGAIAGFAALI; GAIAGFAALIQ; AIAGFAALIQT; IAGFAALIQTV; AGFAALIQTVS; GFAALIQTVSG;
FAALIQTVSGI; AALIQTVSGIS; ALIQTVSGISS; LIQTVSGISSL; IQTVSGISSLA; QTVSGISSLAQ;
TVSGISSLAQV; VSGISSLAQVG; SGISSLAQVGY; GISSLAQVGYK; ISSLAQVGYKF; SSLAQVGYKFF;
SLAQVGYKFFD; LAQVGYKFFDD; AQVGYKFFDDW; QVGYKFFDDWD; VGYKFFDDWDH; GYKFFDDWDHK;
YKFFDDWDHKV; KFFDDWDHKVS; FFDDWDHKVST; FDDWDHKVSTV; DDWDHKVSTVG; DWDHKVSTVGL;
WDHKVSTVGLY; DHKVSTVGLYQ; HKVSTVGLYQQ; KVSTVGLYQQS; VSTVGLYQQSG; STVGLYQQSGM;
TVGLYQQSGMA; VGLYQQSGMAL; GLYQQSGMALE; LYQQSGMALEL; YQQSGMALELF; QQSGMALELFN;
QSGMALELFNP; SGMALELFNPD; GMALELFNPDE; MALELFNPDEY; ALELFNPDEYY; LELFNPDEYYD;
ELFNPDEYYDI; LFNPDEYYDIL; FNPDEYYDILF; NPDEYYDILFP; PDEYYDILFPG; DEYYDILFPGV;
EYYDILFPGVN; YYDILFPGVNT; YDILFPGVNTF; DILFPGVNTFV; ILFPGVNTFVN; LFPGVNTFVNN;
FPGVNTFVNNI; PGVNTFVNNIQ; GVNTFVNNIQY; VNTFVNNIQYL; NTFVNNIQYLD; TFVNNIQYLDP;
FVNNIQYLDPR; VNNIQYLDPRH; NNIQYLDPRHW; NIQYLDPRHWG; IQYLDPRHWGP; QYLDPRHWGPS;
YLDPRHWGPSL; LDPRHWGPSLF; DPRHWGPSLFA; PRHWGPSLFAT; RHWGPSLFATI; HWGPSLFATIS;
WGPSLFATISQ; GPSLFATISQA; PSLFATISQAL; SLFATISQALW; LFATISQALWH; FATISQALWHV;
ATISQALWHVI; TISQALWHVIR; ISQALWHVIRD; SQALWHVIRDD; QALWHVIRDDI; ALWHVIRDDIP;
LWHVIRDDIPS; WHVIRDDIPSI; HVIRDDIPSIT; VIRDDIPSITS; IRDDIPSITSQ; RDDIPSITSQE;
DDIPSITSQEL; DIPSITSQELQ; IPSITSQELQR; PSITSQELQRR; SITSQELQRRT; ITSQELQRRTE;
TSQELQRRTER; SQELQRRTERF; QELQRRTERFF; ELQRRTERFFR; LQRRTERFFRD; QRRTERFFRDS;
RRTERFFRDSL; RTERFFRDSLA; TERFFRDSLAR; ERFFRDSLARF; RFFRDSLARFL; FFRDSLARFLE;
FRDSLARFLEE; RDSLARFLEET; DSLARFLEETT; SLARFLEETTW; LARFLEETTWT; ARFLEETTWTI;
RFLEETTWTIV; FLEETTWTIVN; LEETTWTIVNA; EETTWTIVNAP; ETTWTIVNAPI; TTWTIVNAPIN;
TWTIVNAPINF; WTIVNAPINFY; TIVNAPINFYN; IVNAPINFYNY; VNAPINFYNYI; NAPINFYNYIQ;
APINFYNYIQQ; PINFYNYIQQY; INFYNYIQQYY; NFYNYIQQYYS; FYNYIQQYYSD; YNYIQQYYSDL;
NYIQQYYSDLS; YIQQYYSDLSP; IQQYYSDLSPI; QQYYSDLSPIR; QYYSDLSPIRP; YYSDLSPIRPS;
YSDLSPIRPSM; SDLSPIRPSMV; DLSPIRPSMVR; LSPIRPSMVRQ; SPIRPSMVRQV; PIRPSMVRQVA;
IRPSMVRQVAE; RPSMVRQVAER; PSMVRQVAERE; SMVRQVAEREG; MVRQVAEREGT; VRQVAEREGTR;
RQVAEREGTRV; QVAEREGTRVH; VAEREGTRVHF; AEREGTRVHFG; EREGTRVHFGH; REGTRVHFGHT;
EGTRVHFGHTY; GTRVHFGHTYS; TRVHFGHTYSI; RVHFGHTYSID; VHFGHTYSIDD; HFGHTYSIDDA;
FGHTYSIDDAD; GHTYSIDDADS; HTYSIDDADSI; TYSIDDADSIE; YSIDDADSIEE; SIDDADSIEEV;
IDDADSIEEVT; DDADSIEEVTQ; DADSIEEVTQR; ADSIEEVTQRM; DSIEEVTQRMD; SIEEVTQRMDL;
IEEVTQRMDLR; EEVTQRMDLRN; EVTQRMDLRNQ; VTQRMDLRNQQ; TQRMDLRNQQS; QRMDLRNQQSV;
RMDLRNQQSVH; MDLRNQQSVHS; DLRNQQSVHSG; LRNQQSVHSGE; RNQQSVHSGEF; NQQSVHSGEFI;
QQSVHSGEFIE; QSVHSGEFIEK; SVHSGEFIEKT; VHSGEFIEKTI; HSGEFIEKTIA; SGEFIEKTIAP;
GEFIEKTIAPG; EFIEKTIAPGG; FIEKTIAPGGA; IEKTIAPGGAN; EKTIAPGGANQ; KTIAPGGANQR;
TIAPGGANQRT; IAPGGANQRTA; APGGANQRTAP; PGGANQRTAPQ; GGANQRTAPQW; GANQRTAPQWM;
ANQRTAPQWML; NQRTAPQWMLP; QRTAPQWMLPL; RTAPQWMLPLL; TAPQWMLPLLL; APQWMLPLLLG;
PQWMLPLLLGL; QWMLPLLLGLY; WMLPLLLGLYG; MLPLLLGLYGT; LPLLLGLYGTV; PLLLGLYGTVT;
LLLGLYGTVTP; LLGLYGTVTPA; LGLYGTVTPAL; GLYGTVTPALE; LYGTVTPALEA; YGTVTPALEAY;
GTVTPALEAYE; TVTPALEAYED; VTPALEAYEDG; TPALEAYEDGP; PALEAYEDGPN; ALEAYEDGPNQ;
LEAYEDGPNQK; EAYEDGPNQKK; AYEDGPNQKKR; YEDGPNQKKRR; EDGPNQKKRRV; DGPNQKKRRVS;
GPNQKKRRVSR; PNQKKRRVSRG; NQKKRRVSRGS; QKKRRVSRGSS; KKRRVSRGSSQ; KRRVSRGSSQK;
RRVSRGSSQKA; RVSRGSSQKAK; VSRGSSQKAKG; SRGSSQKAKGT; RGSSQKAKGTR; GSSQKAKGTRA;
SSQKAKGTRAS; SQKAKGTRASA; QKAKGTRASAK; KAKGTRASAKT; AKGTRASAKTT; KGTRASAKTTN;
GTRASAKTTNK; TRASAKTTNKR; RASAKTTNKRR; ASAKTTNKRRS; SAKTTNKRRSR; AKTTNKRRSRS;
KTTNKRRSRSS; TTNKRRSRSSR; TNKRRSRSSRS; NWGRCYYRGRM; WGRCYYRGRML; GRCYYRGRMLP;

RCYYRGRMLPK; CYYRGRMLPKP; YYRGRMLPKPR; YRGRMLPKPRN; RGRMLPKPRNG; GRMLPKPRNGG;
RMLPKPRNGGS; MLPKPRNGGSR; PREKNASLLQH; REKNASLLQHS; EKNASLLQHSK; KNASLLQHSKN;
NASLLQHSKNS; ASLLQHSKNSP; SLLQHSKNSPP; LLQHSKNSPPQ; LQHSKNSPPQF; QHSKNSPPQFK;
GPNLWKSTDVG; PNLWKSTDVGG; NLWKSTDVGGC; LWKSTDVGGCN; WKSTDVGGCNC; KSTDVGGCNCT;
STDVGGCNCTN; TDVGGCNCTNR; DVGGCNCTNRG; VGGCNCTNRGY; GGCNCTNRGYW; GCNCTNRGYWN;
CNCTNRGYWNN; FPLLCCRWRTL; PLLCCRWRTLG; LLCCRWRTLGN; LCCRWRTLGNA; CCRWRTLGNAG;
CRWRTLGNAGS; RWRTLGNAGSA; WRTLGNAGSAN; RTLGNAGSANE; TLGNAGSANEL; LGNAGSANELQ;
GNAGSANELQV; NAGSANELQVK; AGSANELQVKV; GSANELQVKVP; KPNSPVPGNEY; GLFGQKQCLSS;
VFWDFHRRGKC; FWDFHRRGKCS; WDFHRRGKCSP; DFHRRGKCSPS; FHRRGKCSPST; HRRGKCSPSTS;
RRGKCSPSTSC; RGKCSPSTSCD; GKCSPSTSCDQ; KCSPSTSCDQH; CSPSTSCDQHS; SPSTSCDQHSY;
PSTSCDQHSYH; STSCDQHSYHS; TSCDQHSYHSV; SCDQHSYHSVA; CDQHSYHSVAR; QLWNTTVERPC;
LWNTTVERPCK; WNTTVERPCKI; NTTVERPCKIF; DPPEKKICKES; PPEKKICKESL; PEKKICKESLP;
EKKICKESLPN; KKICKESLPNF; KICKESLPNFL; ICKESLPNFLF; CKESLPNFLFA; KESLPNFLFAK;
PYKQENPESGW; YKQENPESGWA; KQENPESGWAA; QENPESGWAAY; ENPESGWAAYV; NPESGWAAYVW;
PESGWAAYVWY; ESGWAAYVWYG; SGWAAYVWYGI; GWAAYVWYGIP; WAAYVWYGIPG; AAYVWYGIPGR;
AYVWYGIPGRR; YVWYGIPGRRG; WHRKTSRGPRY; HRKTSRGPRYD; RKTSRGPRYDK; KTSRGPRYDKI;
TSRGPRYDKIY; QTGTIANQNAL; TGTIANQNALN; GTIANQNALNR; TIANQNALNRC; IANQNALNRCF;
ANQNALNRCFY; NQNALNRCFYC; QNALNRCFYCT; NALNRCFYCTY; ALNRCFYCTYT; LNRCFYCTYTF;
NRCFYCTYTFN; RCFYCTYTFNK; CFYCTYTFNKC; FYCTYTFNKCC; YCTYTFNKCCF; CTYTFNKCCFC;
TYTFNKCCFCI; YTFNKCCFCIS; TFNKCCFCISH; FNKCCFCISHF; NTESLYTNATL; TESLYTNATLD;
ESLYTNATLDY; SLYTNATLDYG; LYTNATLDYGG; YTNATLDYGGL; TNATLDYGGLT; NATLDYGGLTF;
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YLRLGKSIVIG; LRLGKSIVIGI; RLGKSIVIGIQ; LGKSIVIGIQC; GKSIVIGIQCL; KSIVIGIQCLI;
SIVIGIQCLIH; IVIGIQCLIHV; VIGIQCLIHVQ; IGIQCLIHVQS; GIQCLIHVQSL; IQCLIHVQSLQ;
QCLIHVQSLQF; CLIHVQSLQFL; LIHVQSLQFLN; IHVQSLQFLNP; HVQSLQFLNPL; VQSLQFLNPLL;
QSLQFLNPLLL; YQEYISPCIYY; QEYISPCIYYI; EYISPCIYYIS; YISPCIYYISS; ISPCIYYISSL;
SPCIYYISSLK; PCIYYISSLKK; CIYYISSLKKY; IYYISSLKKYT; YYISSLKKYTY; YISSLKKYTYL;
ISSLKKYTYLS; SSLKKYTYLSQ; SLKKYTYLSQN; LKKYTYLSQNP; KKYTYLSQNPA; KYTYLSQNPAF;
YTYLSQNPAFP; TYLSQNPAFPS; YLSQNPAFPSI; LSQNPAFPSIQ; SQNPAFPSIQQ; QNPAFPSIQQF;
IVYQLQNQLQA; TKLAVATRSFH; KLAVATRSFHF; LAVATRSFHFV; AVATRSFHFVK; VATRSFHFVKF;
ATRSFHFVKFF; TRSFHFVKFFF; RSFHFVKFFFQ; SFHFVKFFFQV; FHFVKFFFQVR; HFVKFFFQVRT;
FVKFFFQVRTL; VKFFFQVRTLS; KFFFQVRTLSF; FFFQVRTLSFV; FFQVRTLSFVR; FQVRTLSFVRI;
QVRTLSFVRIF; VRTLSFVRIFL; RTLSFVRIFLN; TLSFVRIFLNI; LSFVRIFLNIF; SFVRIFLNIFW;
FVRIFLNIFWA; PSLVEIFGFFC; SLVEIFGFFCL; LVEIFGFFCLN; VEIFGFFCLNV; EIFGFFCLNVS;
IFGFFCLNVSF; FGFFCLNVSFL; GFFCLNVSFLN; FFCLNVSFLNL; FCLNVSFLNLP; HFHLNNLSNCL;
FHLNNLSNCLN; HLNNLSNCLNC; LNNLSNCLNCL; NNLSNCLNCLF; NLSNCLNCLFH; LSNCLNCLFHV;
SNCLNCLFHVL; NCLNCLFHVLK; CLNCLFHVLKA; LNCLFHVLKAN; NCLFHVLKANP; CLFHVLKANPL;
LFHVLKANPLI; FHVLKANPLIQ; HVLKANPLIQL; VLKANPLIQLL; LKANPLIQLLS; KANPLIQLLSL;
ANPLIQLLSLL; NPLIQLLSLLH; PLIQLLSLLHL; LIQLLSLLHLQ; IQLLSLLHLQK; QLLSLLHLQKQ;
LLSLLHLQKQP; LSLLHLQKQPC; SLLHLQKQPCT; LLHLQKQPCTD; LHLQKQPCTDL; LHLAQRLAFPW;
HLAQRLAFPWV; LAQRLAFPWVG; AQRLAFPWVGL; QRLAFPWVGLH; RLAFPWVGLHL; LAFPWVGLHLR;
AFPWVGLHLRL; FPWVGLHLRLY; PWVGLHLRLYH; WVGLHLRLYHH; VGLHLRLYHHT; GLHLRLYHHTN;
LHLRLYHHTNL; HLRLYHHTNLI; LRLYHHTNLIT; RLYHHTNLITL; LYHHTNLITLQ; YHHTNLITLQL;
HHTNLITLQLV; HTNLITLQLVL; TNLITLQLVLF; NLITLQLVLFF; LITLQLVLFFH; ITLQLVLFFHY;
TLQLVLFFHYQ; LQLVLFFHYQW; QLVLFFHYQWD; LVLFFHYQWDL; KQYSAKNQILQ; QYSAKNQILQN;
YSAKNQILQNP; SAKNQILQNPF; VANSAAKQHLP; ANSAAKQHLPY; NSAAKQHLPYI; SAAKQHLPYIV;
AAKQHLPYIVL; AKQHLPYIVLV; KQHLPYIVLVQ; QHLPYIVLVQH; HLPYIVLVQHF; LPYIVLVQHFH;
PYIVLVQHFHE; YIVLVQHFHEL; IVLVQHFHELQ; VLVQHFHELQI; LVQHFHELQIL; VQHFHELQILN;
QHFHELQILNP; HFHELQILNPF; FHELQILNPFY; HELQILNPFYL; ELQILNPFYLI; LQILNPFYLIY;
QILNPFYLIYD; IFLLAFLPWSY; FLLAFLPWSYE; LLAFLPWSYEG; LAFLPWSYEGY; AFLPWSYEGYL;
FLPWSYEGYLL; LPWSYEGYLLF; PWSYEGYLLFF; LKLYLLLADKY; KLYLLLADKYF; LYLLLADKYFF;
YLLLADKYFFD; LLLADKYFFDF; LLADKYFFDFY; LADKYFFDFYF; ADKYFFDFYFL; DKYFFDFYFLQ;
KYFFDFYFLQK; SDKAGLFSDTF; DKAGLFSDTFY; KAGLFSDTFYT; AGLFSDTFYTP; GLFSDTFYTPL;
LFSDTFYTPLH; FSDTFYTPLHC; SDTFYTPLHCI; DTFYTPLHCIE; TFYTPLHCIEI; FYTPLHCIEIL;
YTPLHCIEILN; TPLHCIEILNT; PLHCIEILNTY; LHCIEILNTYL; HCIEILNTYLI; CIEILNTYLII;
IEILNTYLIIK; EILNTYLIIKT; ILNTYLIIKTH; LNTYLIIKTHP; NTYLIIKTHPH; TYLIIKTHPHT;
YLIIKTHPHTL; LIIKTHPHTLS; IIKTHPHTLSL; IKTHPHTLSLL; KTHPHTLSLLH; THPHTLSLLHT;
HPHTLSLLHTQ; LISKTPALFLQ; ISKTPALFLQA; SKTPALFLQAL; KTPALFLQALL; TPALFLQALLG;
NHAPLSPLECF; HAPLSPLECFL; APLSPLECFLL; LQKLYVYVELK; QKLYVYVELKR; KLYVYVELKRI;
YTQQSRQGFYY; GLLPFFFFWVV; LLPFFFFWVVL; LPFFFFWVVLS; PFFFFWVVLSV; FFFFWVVLSVE;
FFFWVVLSVEN; FFWVVLSVENL; FWVVLSVENLL; WVVLSVENLLL; VVLSVENLLLL; VLSVENLLLLL;
LSVENLLLLLH; SVENLLLLLHH; VENLLLLLHHW; ENLLLLLHHWQ; NLLLLLHHWQT; LLLLLHHWQTY;
LLLLHHWQTYL; LLLHHWQTYLH; LLHHWQTYLHG; LHHWQTYLHGK; HHWQTYLHGKI; HWQTYLHGKIN;

WQTYLHGKINL; QTYLHGKINLH; TYLHGKINLHP; YLHGKINLHPI; LHGKINLHPIF; HGKINLHPIFH; RNSTRTPTLLF; NSTRTPTLLFH; STRTPTLLFHR; TRTPTLLFHRL; RTPTLLFHRLA; TPTLLFHRLAP; PTLLFHRLAPI; TLLFHRLAPIK; LLFHRLAPIKK; LFHRLAPIKKI; FHRLAPIKKII; HRLAPIKKIIT; GLLIFYYLSKY; LLIFYYLSKYK; LIFYYLSKYKL; IFYYLSKYKLV; FYYLSKYKLVT; YYLSKYKLVTL; YLSKYKLVTLK; LSKYKLVTLKL; ISEGSFSNYLD; SEGSFSNYLDP; EGSFSNYLDPP; GSFSNYLDPPL; SFSNYLDPPLQ; FSNYLDPPLQS; SNYLDPPLQSF; NYLDPPLQSFF; YLDPPLQSFFS; AKPLCEAVNAV; KPLCEAVNAVA; PLCEAVNAVAI; LCEAVNAVAIY; CEAVNAVAIYP; EAVNAVAIYPN; AVNAVAIYPNQ; VNAVAIYPNQG; NAVAIYPNQGL; AVAIYPNQGLF; VAIYPNQGLFS; HARAVHRRLFG; ARAVHRRLFGT; RAVHRRLFGTN; AVHRRLFGTNR; VHRRLFGTNRP; HRRLFGTNRPF; RRLFGTNRPFL; RLFGTNRPFLA; LFGTNRPFLAV; FGTNRPFLAVQ; GTNRPFLAVQG; TNRPFLAVQGI; NRPFLAVQGIW; RPFLAVQGIWA; PFLAVQGIWAK; FLAVQGIWAKR; LAVQGIWAKRK; AVQGIWAKRKI; VQGIWAKRKIS; QGIWAKRKIST; GIWAKRKISTN; IWAKRKISTNL; ATPGSKIRLMS; TPGSKIRLMSY; PGSKIRLMSYL; GSKIRLMSYLY; SKIRLMSYLYI; KIRLMSYLYIL; IRLMSYLYILL; RLMSYLYILLH; LMSYLYILLHF; MSYLYILLHFF; SYLYILLHFFI; YLYILLHFFIQ; LYILLHFFIQS; YILLHFFIQSI; ILLHFFIQSIH; LLHFFIQSIHS; LHFFIQSIHSL; HFFIQSIHSLH; FFIQSIHSLHF; FIQSIHSLHFI; IQSIHSLHFIL; QSIHSLHFILV; SIHSLHFILVA; IHSLHFILVAP; HSLHFILVAPF; SLHFILVAPFV; LHFILVAPFVR; HFILVAPFVRV; FILVAPFVRVK; ILVAPFVRVKF; LVAPFVRVKFL; VAPFVRVKFLT; APFVRVKFLTL; PFVRVKFLTLP; GKISPGSSFKA; KVHELHGFFPV; VHELHGFFPVK; HELHGFFPVKN; ELHGFFPVKNF; LHGFFPVKNFI; HGFFPVKNFIH

BK virus complementary reading frame 1

8 mers:

MDKVLNRE; DKVLNREE; KVLNREES; VLNREESM; LNREESME; NREESMEL; REESMELM; EESMELMD; ESMELMDL; SMELMDLL; MELMDLLG; ELMDLLGL; LMDLLGLE; MDLLGLER; DLLGLERA; LLGLERAA; LGLERAAW; GLERAAWG; LERAAWGN; ERAAWGNL; RAAWGNLP; AAWGNLPL; AWGNLPLM; WGNLPLMR; GNLPLMRK; NLPLMRKA; LPLMRKAY; PLMRKAYL; LMRKAYLR; MRKAYLRK; RKAYLRKC; KAYLRKCK; AYLRKCKE; YLRKCKEF; LRKCKEFH; RKCKEFHP; KCKEFHPD; CKEFHPDK; KEFHPDKG; EFHPDKGG; FHPDKGGD; HPDKGGDE; PDKGGDED; DKGGDEDK; KGGDEDKM; GGDEDKMK; GDEDKMKR; DEDKMKRM; EDKMKRMN; DKMKRMNT; KMKRMNTL; MKRMNTLY; KRMNTLYK; RMNTLYKK; MNTLYKKM; NTLYKKME; TLYKKMEQ; LYKKMEQD; YKKMEQDV; KKMEQDVK; KMEQDVKV; MEQDVKVA; EQDVKVAH; QDVKVAHQ; DVKVAHQP; VKVAHQPD; KVAHQPDF; VAHQPDFG; AHQPDFGT; HQPDFGTW; QPDFGTWS; PDFGTWSS; DFGTWSSS; FGTWSSSE; GTWSSSEV; TWSSSEVC; WSSSEVCA; SSSEVCAD; SSEVCADF; SEVCADFP; EVCADFPL; VCADFPLC; CADFPLCP; ADFPLCPD; DFPLCPDT; FPLCPDTL; PLCPDTLY; LCPDTLYC; CPDTLYCK; PDTLYCKE; DTLYCKEW; TLYCKEWP; LYCKEWPI; YCKEWPIC; CKEWPICS; KEWPICSK; EWPICSKK; WPICSKKP; PICSKKPS; ICSKKPSV; CSKKPSVH; SKKPSVHC; KKPSVHCP; KPSVHCPC; PSVHCPCM; SVHCPCML; VHCPCMLC; HCPCMLCQ; CPCMLCQL; PCMLCQLR; CMLCQLRL; MLCQLRLR; LCQLRLRH; CQLRLRHL; QLRLRHLN; LRLRHLNR; RLRHLNRK; LRHLNRKF; RHLNRKFL; HLNRKFLR; LNRKFLRK; NRKFLRKE; RKFLRKEP; KFLRKEPL; FLRKEPLV; LRKEPLVW; RKEPLVWI; KEPLVWID; EPLVWIDC; PLVWIDCY; LVWIDCYC; VWIDCYCI; WIDCYCID; IDCYCIDC; DCYCIDCF; CYCIDCFT; YCIDCFTQ; CIDCFTQW; IDCFTQWF; DCFTQWFG; CFTQWFGL; FTQWFGLD; TQWFGLDL; QWFGLDLT; WFGLDLTE; FGLDLTEE; GLDLTEET; LDLTEETL; DLTEETLQ; LTEETLQW; TEETLQWW; EETLQWWV; ETLQWWVQ; TLQWWVQI; LQWWVQII; QWWVQIIG; WWVQIIGE; WVQIIGET; VQIIGETP; QIIGETPF; IIGETPFR; IGETPFRD; GETPFRDL; ETPFRDLK; TPFRDLKL; KALSNYFF; ALSNYFFY; LSNYFFYR; SNYFFYRC; NYFFYRCQ; YFFYRCQP; FFYRCQPM; FYRCQPME; YRCQPMEQ; RCQPMEQK; CQPMEQKS; QPMEQKSG; PMEQKSGS; MEQKSGSP; EQKSGSPG; QKSGSPGG; KSGSPGGV; SGSPGGVP; GSPGGVPL; SPGGVPLM; PGGVPLMK; GGVPLMKN; GVPLMKNG; VPLMKNGM; PLMKNGMK; LMKNGMKI; MKNGMKIY; KNGMKIYF; NGMKIYFA; GMKIYFAM; MKIYFAMK; KIYFAMKI; IYFAMKIC; YFAMKICL; FAMKICLP; AMKICLPV; MKICLPVM; KICLPVMK; ICLPVMKK; CLPVMKKQ; LPVMKKQQ; PVMKKQQQ; VMKKQQQI; MKKQQQIL; KKQQQILN; KQQQILNT; QQQILNTQ; QQILNTQH; QILNTQHH; ILNTQHHP; LNTQHHPK; NTQHHPKK; TQHHPKKK; QHHPKKKE; HHPKKKER; KTLKTFPL; TLKTFPLI; LKTFPLIY; KTFPLIYT; TFPLIYTS; FPLIYTSF; PLIYTSFL; LIYTSFLV; IYTSFLVK; YTSFLVKL; TSFLVKLY; SFLVKLYL; FLVKLYLV; LVKLYLVI; VKLYLVIE; KLYLVIEP; LYLVIEPL; YLVIEPLP; LVIEPLPA; VIEPLPAL; IEPLPALL; EPLPALLC; PLPALLCI; LPALLCIL; PALLCILL; ALLCILLK; LLCILLKK; LCILLKKK; CILLKKKL; ILLKKKLK; LLKKKLKF; LKKKLKFC; KKKLKFCI; KKLKFCIK; KLKFCIKN; LKFCIKNL; KFCIKNLW; FCIKNLWK; CIKNLWKN; IKNLWKNI; KNLWKNIL; LLLVDTCV; LLVDTCVL; LVDTCVLG; VDTCVLGI; DTCVLGII; TCVLGIIL; CVLGIILY; VLGIILYS; LGIILYSF; LHIDIEFL; HIDIEFLQ; IDIEFLQL; DIEFLQLI; IEFLQLII; EFLQLIIS; FLQLIISV; LQLIISVK; QLIISVKS; LIISVKSC; IISVKSCV; ISVKSCVP; SVKSCVPL; VKSCVPLV; KSCVPLVF; FVRVLIRN; VRVLIRNT; RVLIRNTY; VLIRNTYY; LIRNTYYI; IRNTYYIV; RNTYYIVP; RSMILAQK; SMILAQKS; MILAQKSL; ILAQKSLK; LAQKSLKK; AQKSLKKQ; QKSLKKQS; KSLKKQSR; SLKKQSRC; LKKQSRCL; KKQSRCLG; KQSRCLGN; RQSVRMCF; QSVRMCFY; SVRMCFYY; RSVKSVRK;

SVKSVRKK; VKSVRKKT; KSVRKKTS; SVRKKTSL; VRKKTSLI; RKKTSLIT; KKTSLITL;
KTSLITLS; TSLITLSI; SLITLSIM; LITLSIMK; ITLSIMKS; TLSIMKST; LSIMKSTL;
SIMKSTLQ; IMKSTLQM; MKSTLQML; KSTLQMLL; STLQMLLF; TLQMLLFL; LQMLLFLQ;
QMLLFLQK; MLLFLQKV; LLFLQKVK; LFLQKVKI; FLQKVKIK; LQKVKIKK; QKVKIKKV;
KVKIKKVF; VKIKKVFV; KIKKVFVS; IKKVFVSK; KKVFVSKQ; YLELMEML; LELMEMLY;
NNIWQVLL; NIWQVLLG; IWQVLLGC; WQVLLGCT; QVLLGCTV; VLLGCTVC; LLGCTVCY;
LGCTVCYL; GCTVCYLK; CTVCYLKW; TVCYLKWI; VCYLKWIL; YLIFCTVL; LIFCTVLF;
IFCTVLFS; FCTVLFSM; CTVLFSMY; TVLFSMYL; VLFSMYLK; LFSMYLKE; FSMYLKED;
SMYLKEDT; MYLKEDTG; YLKEDTGY; LKEDTGYL; KEDTGYLK; EDTGYLKV; DTGYLKVP;
TGYLKVPL; GYLKVPLI; YLKVPLIV; LKVPLIVE; KVPLIVEK; VPLIVEKQ; PLIVEKQH;
ISTWLFLK; STWLFLKM; KGQELNQR; GQELNQRI; QELNQRIC; ELNQRICL; LNQRICLQ;
NQRICLQD; QRICLQDM; RICLQDME; TKEPKYFH; KEPKYFHQ; EPKYFHQA; PKYFHQAW;
KYFHQAWL; YFHQAWLQ; MSILSLKP; SILSLKPC; ILSLKPCK; LSLKPCKL; SLKPCKLD;
LKPCKLDL; ENPYKTQS; NPYKTQSS; PYKTQSSY; YKTQSSYL; KTQSSYLK; TQSSYLKK;
QSSYLKKE; SSYLKKEF; SYLKKEFY; YLKKEFYK; LKKEFYKV; KKEFYKVE; LILQLIYN;
ILQLIYNL; LQLIYNLE; QLIYNLEL; LIYNLELL; IYNLELLN; YNLELLNG; NLELLNGR;
LELLNGRK; ELLNGRKG; LLNGRKGW; LNGRKGWI; NGRKGWIL; GRKGWILR; NIIYAWGN;
IIYAWGNV; IYAWGNVF; YAWGNVFL; AWGNVFLI; WGNVFLIL; GNVFLILQ; NVFLILQE;
VFLILQEK; FLILQEKR; LILQEKRI; ILQEKRIQ; LQEKRIQK; QEKRIQKL; EKRIQKLK;
KRIQKLKT; RIQKLKTL; IQKLKTLD; QKLKTLDM; KLKTLDMD; LKTLDMDQ; KTLDMDQA;
TLDMDQAL; LDMDQALN; DMDQALNP; MDQALNPN; DQALNPNH; QALNPNHN; ALNPNHNA;
LNPNHNAL; NPNHNALP; PNHNALPK; NHNALPKS; HNALPKSQ; NALPKSQI; ALPKSQIL;
LPKSQILQ; PKSQILQP; KSQILQPL; SQILQPLL; QILQPLLK; ILQPLLKI; LQPLLKIP;
QPLLKIPK; PLLKIPKG; LLKIPKGQ; LKIPKGQT; KIPKGQTP; IPKGQTPI; PKGQTPIV;
KGQTPIVK; GQTPIVKS; QTPIVKSC; TPIVKSCI; PIVKSCIC; IVKSCICV; VKSCICVK;
KSCICVKA; SCICVKAF; CICVKAFS; ICVKAFSV; CVKAFSVL; VKAFSVLK; KAFSVLKG;
AFSVLKGL; FSVLKGLK; SVLKGLKH; VLKGLKHH; LKGLKHHP; KGLKHHPQ; GLKHHPQN;
LKHHPQNN; KHHPQNNT; HHPQNNTS; HPQNNTSL; PQNNTSLK; QNNTSLKV; NNTSLKVA;
NTSLKVAY; TSLKVAYT; SLKVAYTK; LKVAYTKA; KVAYTKAA; VAYTKAAF; AYTKAAFI;
YTKAAFIK; TKAAFIKC; KAAFIKCI; AAFIKCIC; AFIKCICT; FIKCICTI; IKCICTIK;
KCICTIKA; CICTIKAP; ICTIKAPV; SILVCNCP; ILVCNCPC; LVCNCPCL; VCNCPCLS;
CNCPCLSI; NCPCLSIY; CPCLSIYL; PCLSIYLI; CLSIYLII; LSIYLIIS; SIYLIISG;
IYLIISGS; YLIISGSP; LIISGSPG; IISGSPGS; ISGSPGSL; SGSPGSLS; GSPGSLSV;
SPGSLSVP; PGSLSVPS; GSLSVPSN; SLSVPSNT; LSVPSNTL; SVPSNTLT; VPSNTLTS;
PSNTLTSS; SNTLTSST; NTLTSSTW; TLTSSTWD; LTSSTWDS; TSSTWDSI; SSTWDSIP;
STWDSIPY; TWDSIPYI; WDSIPYIG; DSIPYIGC; SIPYIGCP; IPYIGCPS; PYIGCPST;
YIGCPSTL; IGCPSTLW; GCPSTLWV; CPSTLWVL; PSTLWVLL; STLWVLLF; TLWVLLFI;
LWVLLFIR; WVLLFIRS; VLLFIRSL; LLFIRSLS; LFIRSLSK; FIRSLSKK; IRSLSKKE;
RSLSKKEI; SLSKKEIG; GFFTDLFL; FFTDLFLR; FTDLFLRR; TDLFLRRI; DLFLRRIL;
LFLRRILK; FLRRILKY; LRRILKYL; RRILKYLA; RILKYLAR; ILKYLARP; LKYLARPL;
KYLARPLH; YLARPLHC; LARPLHCC; ARPLHCCV; RPLHCCVP; PLHCCVPE; LHCCVPEL;
HCCVPELL; CCVPELLV; CVPELLVN; VPELLVNR; PELLVNRP; ELLVNRPQ; LLVNRPQI;
LVNRPQIS; VNRPQISA; NRPQISAA; RPQISAAE; PQISAAET; QISAAETY; ISAAETYR;
SAAETYRL; AAETYRLS; AETYRLSA; ETYRLSAL; TYRLSALQ; YRLSALQR; RLSALQRG;
LSALQRGP; SALQRGPT; ALQRGPTP; LQRGPTPC; QRGPTPCS; RGPTPCSS; GPTPCSSS;
PTPCSSSN; TPCSSSNT; PCSSSNTV; CSSSNTVV; SSSNTVVA; SSNTVVAV; SNTVVAVL;
NTVVAVLV; TVVAVLVT; STGGTFSP; TGGTFSPP; GGTFSPPV; GTFSPPVK; TFSPPVKV;
FSPPVKVP; SPPVKVPK; PPVKVPKY; PVKVPKYL; VKVPKYLA; KVPKYLAF; VPKYLAFS;
PKYLAFSF; KYLAFSFL; YLAFSFLL; LAFSFLLG; AFSFLLGS; FSFLLGSG; SFLLGSGT;
FLLGSGTQ; LLGSGTQH; LGSGTQHS; GSGTQHST; SGTQHSTG; ALWSVFIT; LWSVFITW;
WSVFITWD; SVFITWDW; VFITWDWA; FITWDWAV; ITWDWAVG; TWDWAVGF; WDWAVGFL;
DWAVGFLG; WAVGFLGV; AVGFLGVI; VGFLGVIV; GFLGVIVP; FLGVIVPS; LGVIVPSG;
GVIVPSGY; VIVPSGYF; IVPSGYFD; VPSGYFDL; FISTPCIS; ISTPCISK; STPCISKG;
TPCISKGS; PCISKGSP; CISKGSPP; ISKGSPPT; SKGSPPTA; KGSPPTAK; GSPPTAKK;
SPPTAKKW; PPTAKKWK; PTAKKWKL; TAKKWKLL; AKKWKLLP; IGFPPPCS; GFPPPCSC;
FPPPCSCT; PPPCSCTF; PPCSCTFC; PCSCTFCD; CSCTFCDP; SCTFCDPA; RLSMLVIP;
LSMLVIPI; SMLVIPIT; MLVIPITS; LVIPITSV; VIPITSVC; IPITSVCT; PITSVCTV;
ITSVCTVT; TSVCTVTA; SVCTVTAS; VCTVTASH; CTVTASHI; TVTASHIS; VTASHISR;
TASHISRF; ASHISRFP; SHISRFPQ; HISRFPQV; ISRFPQVR; SRFPQVRS; RFPQVRSS;
FPQVRSSF; PQVRSSFK; QVRSSFKL; VRSSFKLG; RSSFKLGR; SSFKLGRG; SFKLGRGI;
FKLGRGIL; KLGRGILA; LGRGILAV; GRGILAVL; QGSIFLSG; GSIFLSGL; SIFLSGLS;
IFLSGLSL; FLSGLSLL; LSGLSLLK; SGLSLLKS; GLSLLKSF; LSLLKSFS; SLLKSFSA;
LLKSFSAL; LKSFSALS; KSFSALSF; SFSALSFR; FSALSFRL; SALSFRLK; ALSFRLKP;
LSFRLKPL; SFRLKPLR; FRLKPLRF; RLKPLRFS; LKPLRFSS; KPLRFSSG; PLRFSSGS;
LRFSSGSP; RFSSGSPI; FSSGSPIS; SSGSPISG; SGSPISGF; GSPISGFR; SPISGFRK;

PISGFRKH; ISGFRKHS; SGFRKHST; GFRKHSTS; FRKHSTSV; RKHSTSVI; KHSTSVIA;
HSTSVIAS; STSVIAST; TSVIASTP; SVIASTPV; VIASTPVL; IASTPVLT; ASTPVLTS;
STPVLTSR; TPVLTSRT; PVLTSRTS; VLTSRTST; LTSRTSTP; TSRTSTPP; SRTSTPPF;
RTSTPPFI; TSTPPFIS; STPPFISS; TPPFISSF; PPFISSFG; PFISSFGT; FISSFGTC;
ISSFGTCT; SSFGTCTG; SFGTCTGS; FGTCTGSF; GTCTGSFG; TCTGSFGF; CTGSFGFL;
TGSFGFLG; GSFGFLGA; SFGFLGAA; FGFLGAAP; GFLGAAPG; FLGAAPGH; LGAAPGHS;
GAAPGHSP; AAPGHSPF; APGHSPFL; PGHSPFLL; GHSPFLLV; HSPFLLVG; SPFLLVGA;
PFLLVGAI; FLLVGAIF; LLVGAIFI; LVGAIFIC; VGAIFICF; GAIFICFK; AIFICFKS;
IFICFKSR; FICFKSRC; ICFKSRCY; CFKSRCYS; FKSRCYSP; KSRCYSPV; SRCYSPVQ;
RCYSPVQA; RQHPLRSS; QHPLRSSS; HPLRSSSL; PLRSSSLI; LRSSSLIS; RSSSLIST;
SSSLISTS; SSLISTSW; SLISTSWG; LISTSWGN; ISTSWGNS; STSWGNSF; TSWGNSFF;
SWGNSFFY; WGNSFFYK; GNSFFYKL; NSFFYKLS; VHSLCNFF; HSLCNFFY; SLCNFFYT;
LCNFFYTV; CNFFYTVS; NFFYTVSI; FFYTVSII; FYTVSIIY; YTVSIIYT; TVSIIYTI;
VSIIYTIS; SIIYTISM; IIYTISMA; IYTISMAK; YTISMAKM; TISMAKMY; ISMAKMYT;
SMAKMYTG; MAKMYTGT; AKMYTGTF; KMYTGTFP; MYTGTFPF; YTGTFPFS; TGTFPFSY;
GTFPFSYL; TFPFSYLS; FPFSYLSN; PFSYLSNH; GPNRGKIR; PNRGKIRI; NRGKIRII;
RGKIRIIL; GKIRIILL; KIRIILLN; IRIILLNI; RIILLNII; IILLNIII; ILLNIIIK;
LLNIIIKV; LNIIIKVY; NIIIKVYR; IIIKVYRG; IIKVYRGI; IKVYRGIY; KVYRGIYN;
VYRGIYNC; YRGIYNCP; RGIYNCPG; GIYNCPGS; IYNCPGSF; YNCPGSFL; NCPGSFLQ;
CPGSFLQK; PGSFLQKS; GSFLQKSS; SFLQKSSQ; FLQKSSQG; LQKSSQGV; QKSSQGVS;
KSSQGVSK; SSQGVSKK; SQGVSKKS; QGVSKKSF; GVSKKSFC; VSKKSFCS; SKKSFCSS;
KKSFCSSL; KSFCSSLQ; SFCSSLQF; FCSSLQFL; GYRRYIIP; YRRYIIPN; RRYIIPNN;
RYIIPNNM; YIIPNNMP; IIPNNMPQ; IPNNMPQS; PNNMPQSL; NNMPQSLG; NMPQSLGN;
MPQSLGNS; PQSLGNSS; QSLGNSSK; SLGNSSKQ; LGNSSKQR; GNSSKQRR; NSSKQRRT;
SSKQRRTP; SKQRRTPM; KQRRTPMP; QRRTPMPR; RRTPMPRI; RTPMPRIK; TPMPRIKV;
PMPRIKVL; MPRIKVLN; PRIKVLNI; RIKVLNII; IKVLNIIN; KVLNIINK; VLNIINKS;
LNIINKSI; NIINKSIY; IINKSIYT; INKSIYTR; NKSIYTRK; KSIYTRKQ; SIYTRKQN;
IYTRKQNI; YTRKQNII; TRKQNIIV; RKQNIIVL; KQNIIVLI; QNIIVLIW; NIIVLIWV;
IIVLIWVK; IVLIWVKQ; VLIWVKQF; LIWVKQFQ; IWVKQFQS; WVKQFQSH; VKQFQSHA;
LLIEAYSG; LIEAYSGN; IEAYSGNF; EAYSGNFV; AYSGNFVI; YSGNFVIP; SGNFVIPI;
GNFVIPII; NFVIPIIK; FVIPIIKE; VIPIIKEL; IPIIKELI; PIIKELIP; IIKELIPY;
IKELIPYL; KELIPYLS; GTNTTNSL; TNTTNSLN; SSKPSNSP; SKPSNSPR; KPSNSPRS;
PSNSPRST; SNSPRSTS; NSPRSTSN; SPRSTSNY; PRSTSNYS; RSTSNYSI; STSNYSIC;
TSNYSICL; SNYSICLR; NYSICLRS; GTCYALYS; TCYALYSS; CYALYSSK; YALYSSKG;
ALYSSKGC; LYSSKGCN; YSSKGCNL; SSKGCNLN; SKGCNLNF; KGCNLNFY; GCNLNFYS;
CNLNFYSS; NLNFYSSS; LNFYSSSS; NFYSSSSL; FYSSSSLP; YSSSSLPS; SSSSLPSS;
SSSLPSSN; SSLPSSNF; SLPSSNFS; LPSSNFSH; KSCGSSSL; SCGSSSLR; CGSSSLRY;
GSSSLRYT; SSSLRYTG; SSLRYTGN; SSTHEPGN; STHEPGNT; THEPGNTK; HEPGNTKK;
EPGNTKKK; PGNTKKKG; GNTKKKGL; NTKKKGLL; TKKKGLLT; ESFTESFT; SFTESFTA;
FTESFTAG; TESFTAGK; ESFTAGKA; SFTAGKAV; FTAGKAVV; TAGKAVVL; AGKAVVLL;
GKAVVLLF; KAVVLLFF; AVVLLFFP; VVLLFFPS; VLLFFPST; LLFFPSTL; LFFPSTLS;
FFPSTLSS; FPSTLSSP; PSTLSSPL; STLSSPLQ; TLSSPLQN; LSSPLQNS; SSPLQNSS;
SPLQNSSK; PLQNSSKS; LQNSSKSS; QNSSKSSK; NSSKSSKI; SSKSSKIK; SKSSKIKI;
KSSKIKIK; SSKIKIKI; SKIKIKIL; ALFFVPVQ; LFFVPVQV; FFVPVQVL; FVPVQVLP;
VPVQVLPT; PVQVLPTF; VQVLPTFT; QVLPTFTE; VLPTFTEA; LPTFTEAC; PTFTEACR;
TFTEACRD; FTEACRDS; TEACRDSW; EACRDSWR; ACRDSWRR; CRDSWRRT; RDSWRRTM;
DSWRRTMA; SWRRTMAF; WRRTMAFV; RRTMAFVQ; RTMAFVQF; TMAFVQFN; MAFVQFNW;
AFVQFNWG; FVQFNWGQ; VQFNWGQG; QFNWGQGQ; FNWGQGQD; NWGQGQDS; ARKTCLSC;
RKTCLSCT; KTCLSCTF; TCLSCTFL; CLSCTFLP; LSCTFLPE; SCTFLPEV; CTFLPEVM;
TFLPEVMV; FLPEVMVW; LPEVMVWL; PEVMVWLH; EVMVWLHS; VMVWLHSM; MVWLHSMG;
VWLHSMGK; WLHSMGKQ; LHSMGKQL; HSMGKQLL; SMGKQLLP; MGKQLLPV; GKQLLPVS;
KQLLPVSH; QLLPVSHA; LLPVSHAL; LPVSHALS; PVSHALSF; VSHALSFL; SHALSFLR;
HALSFLRS; ALSFLRSW; LSFLRSWF; SFLRSWFG; FLRSWFGC; LRSWFGCI; RSWFGCIP;
SWFGCIPL; GHGLAAFH; HGLAAFHG; AAPPCGLF; APPCGLFF; PPCGLFFY; PCGLFFYN;
CGLFFYNI; EAEAASAS; AEAASAST; EAASASTL; AASASTLS; ASASTLSL; SASTLSLK;
GLAKLFGE; LAKLFGEI; AKLFGEIP; KLFGEIPI; LFGEIPIL; FGEIPILL; GEIPILLQ;
EIPILLQF; IPILLQFL; PILLQFLQ

9 mers:
MDKVLNREE; DKVLNREES; KVLNREESM; VLNREESME; LNREESMEL; NREESMELM; REESMELMD;
EESMELMDL; ESMELMDLL; SMELMDLLG; MELMDLLGL; ELMDLLGLE; LMDLLGLER; MDLLGLERA;
DLLGLERAA; LLGLERAAW; LGLERAAWG; GLERAAWGN; LERAAWGNL; ERAAWGNLP; RAAWGNLPL;
AAWGNLPLM; AWGNLPLMR; WGNLPLMRK; GNLPLMRKA; NLPLMRKAY; LPLMRKAYL; PLMRKAYLR;
LMRKAYLRK; MRKAYLRKC; RKAYLRKCK; KAYLRKCKE; AYLRKCKEF; YLRKCKEFH; LRKCKEFHP;
RKCKEFHPD; KCKEFHPDK; CKEFHPDKG; KEFHPDKGG; EFHPDKGGD; FHPDKGGDE; HPDKGGDED;
PDKGGDEDK; DKGGDEDKM; KGGDEDKMK; GGDEDKMKR; GDEDKMKRM; DEDKMKRMN; EDKMKRMNT;

DKMKRMNTL; KMKRMNTLY; MKRMNTLYK; KRMNTLYKK; RMNTLYKKM; MNTLYKKME; NTLYKKMEQ;
TLYKKMEQD; LYKKMEQDV; YKKMEQDVK; KKMEQDVKV; KMEQDVKVA; MEQDVKVAH; EQDVKVAHQ;
QDVKVAHQP; DVKVAHQPD; VKVAHQPDF; KVAHQPDFG; VAHQPDFGT; AHQPDFGTW; HQPDFGTWS;
QPDFGTWSS; PDFGTWSSS; DFGTWSSSE; FGTWSSSEV; GTWSSSEVC; TWSSSEVCA; WSSSEVCAD;
SSSEVCADF; SSEVCADFP; SEVCADFPL; EVCADFPLC; VCADFPLCP; CADFPLCPD; ADFPLCPDT;
DFPLCPDTL; FPLCPDTLY; PLCPDTLYC; LCPDTLYCK; CPDTLYCKE; PDTLYCKEW; DTLYCKEWP;
TLYCKEWPI; LYCKEWPIC; YCKEWPICS; CKEWPICSK; KEWPICSKK; EWPICSKKP; WPICSKKPS;
PICSKKPSV; ICSKKPSVH; CSKKPSVHC; SKKPSVHCP; KKPSVHCPC; KPSVHCPCM; PSVHCPCML;
SVHCPCMLC; VHCPCMLCQ; HCPCMLCQL; CPCMLCQLR; PCMLCQLRL; CMLCQLRLR; MLCQLRLRH;
LCQLRLRHL; CQLRLRHLN; QLRLRHLNR; LRLRHLNRK; RLRHLNRKF; LRHLNRKFL; RHLNRKFLR;
HLNRKFLRK; LNRKFLRKE; NRKFLRKEP; RKFLRKEPL; KFLRKEPLV; FLRKEPLVW; LRKEPLVWI;
RKEPLVWID; KEPLVWIDC; EPLVWIDCY; PLVWIDCYC; LVWIDCYCI; VWIDCYCID; WIDCYCIDC;
IDCYCIDCF; DCYCIDCFT; CYCIDCFTQ; YCIDCFTQW; CIDCFTQWF; IDCFTQWFG; DCFTQWFGL;
CFTQWFGLD; FTQWFGLDL; TQWFGLDLT; QWFGLDLTE; WFGLDLTEE; FGLDLTEET; GLDLTEETL;
LDLTEETLQ; DLTEETLQW; LTEETLQWW; TEETLQWWV; EETLQWWVQ; ETLQWWVQI; TLQWWVQII;
LQWWVQIIG; QWWVQIIGE; WWVQIIGET; WVQIIGETP; VQIIGETPF; QIIGETPFR; IIGETPFRD;
IGETPFRDL; GETPFRDLK; ETPFRDLKL; KALSNYFFY; ALSNYFFYR; LSNYFFYRC; SNYFFYRCQ;
NYFFYRCQP; YFFYRCQPM; FFYRCQPME; FYRCQPMEQ; YRCQPMEQK; RCQPMEQKS; CQPMEQKSG;
QPMEQKSGS; PMEQKSGSP; MEQKSGSPG; EQKSGSPGG; QKSGSPGGV; KSGSPGGVP; SGSPGGVPL;
GSPGGVPLM; SPGGVPLMK; PGGVPLMKN; GGVPLMKNG; GVPLMKNGM; VPLMKNGMK; PLMKNGMKI;
LMKNGMKIY; MKNGMKIYF; KNGMKIYFA; NGMKIYFAM; GMKIYFAMK; MKIYFAMKI; KIYFAMKIC;
IYFAMKICL; YFAMKICLP; FAMKICLPV; AMKICLPVM; MKICLPVMK; KICLPVMKK; ICLPVMKKQ;
CLPVMKKQQ; LPVMKKQQQ; PVMKKQQQI; VMKKQQQIL; MKKQQQILN; KKQQQILNT; KQQQILNTQ;
QQQILNTQH; QQILNTQHH; QILNTQHHP; ILNTQHHPK; LNTQHHPKK; NTQHHPKKK; TQHHPKKKE;
QHHPKKKER; KTLKTFPLI; TLKTFPLIY; LKTFPLIYT; KTFPLIYTS; TFPLIYTSF; FPLIYTSFL;
PLIYTSFLV; LIYTSFLVK; IYTSFLVKL; YTSFLVKLY; TSFLVKLYL; SFLVKLYLV; FLVKLYLVI;
LVKLYLVIE; VKLYLVIEP; KLYLVIEPL; LYLVIEPLP; YLVIEPLPA; LVIEPLPAL; VIEPLPALL;
IEPLPALLC; EPLPALLCI; PLPALLCIL; LPALLCILL; PALLCILLK; ALLCILLKK; LLCILLKKK;
LCILLKKKL; CILLKKKLK; ILLKKKLKF; LLKKKLKFC; LKKKLKFCI; KKKLKFCIK; KKLKFCIKN;
KLKFCIKNL; LKFCIKNLW; KFCIKNLWK; FCIKNLWKN; CIKNLWKNI; IKNLWKNIL; LLLVDTCVL;
LLVDTCVLG; LVDTCVLGI; VDTCVLGII; DTCVLGIIL; TCVLGIILY; CVLGIILYS; VLGIILYSF;
LHIDIEFLQ; HIDIEFLQL; IDIEFLQLI; DIEFLQLII; IEFLQLIIS; EFLQLIISV; FLQLIISVK;
LQLIISVKS; QLIISVKSC; LIISVKSCV; IISVKSCVP; ISVKSCVPL; SVKSCVPLV; VKSCVPLVF;
FVRVLIRNT; VRVLIRNTY; RVLIRNTYY; VLIRNTYYI; LIRNTYYIV; IRNTYYIVP; RSMILAQKS;
SMILAQKSL; MILAQKSLK; ILAQKSLKK; LAQKSLKKQ; AQKSLKKQS; QKSLKKQSR; KSLKKQSRC;
SLKKQSRCL; LKKQSRCLG; KKQSRCLGN; RQSVRMCFY; QSVRMCFYY; RSVKSVRKK; SVKSVRKKT;
VKSVRKKTS; KSVRKKTSL; SVRKKTSLI; VRKKTSLIT; RKKTSLITL; KKTSLITLS; KTSLITLSI;
TSLITLSIM; SLITLSIMK; LITLSIMKS; ITLSIMKST; TLSIMKSTL; LSIMKSTLQ; SIMKSTLQM;
IMKSTLQML; MKSTLQMLL; KSTLQMLLF; STLQMLLFL; TLQMLLFLQ; LQMLLFLQK; QMLLFLQKV;
MLLFLQKVK; LLFLQKVKI; LFLQKVKIK; FLQKVKIKK; LQKVKIKKV; QKVKIKKVF; KVKIKKVFV;
VKIKKVFVS; KIKKVFVSK; IKKVFVSKQ; YLELMEMLY; NNIWQVLLG; NIWQVLLGC; IWQVLLGCT;
WQVLLGCTV; QVLLGCTVC; VLLGCTVCY; LLGCTVCYL; LGCTVCYLK; GCTVCYLKW; CTVCYLKWI;
TVCYLKWIL; YLIFCTVLF; LIFCTVLFS; IFCTVLFSM; FCTVLFSMY; CTVLFSMYL; TVLFSMYLK;
VLFSMYLKE; LFSMYLKED; FSMYLKEDT; SMYLKEDTG; MYLKEDTGY; YLKEDTGYL; LKEDTGYLK;
KEDTGYLKV; EDTGYLKVP; DTGYLKVPL; TGYLKVPLI; GYLKVPLIV; YLKVPLIVE; LKVPLIVEK;
KVPLIVEKQ; VPLIVEKQH; ISTWLFLKM; KGQELNQRI; GQELNQRIC; QELNQRICL; ELNQRICLQ;
LNQRICLQD; NQRICLQDM; QRICLQDME; TKEPKYFHQ; KEPKYFHQA; EPKYFHQAW; PKYFHQAWL;
KYFHQAWLQ; MSILSLKPC; SILSLKPCK; ILSLKPCKL; LSLKPCKLD; SLKPCKLDL; ENPYKTQSS;
NPYKTQSSY; PYKTQSSYL; YKTQSSYLK; KTQSSYLKK; TQSSYLKKE; QSSYLKKEF; SSYLKKEFY;
SYLKKEFYK; YLKKEFYKV; LKKEFYKVE; LILQLIYNL; ILQLIYNLE; LQLIYNLEL; QLIYNLELL;
LIYNLELLN; IYNLELLNG; YNLELLNGR; NLELLNGRK; LELLNGRKG; ELLNGRKGW; LLNGRKGWI;
LNGRKGWIL; NGRKGWILR; NIIYAWGNV; IIYAWGNVF; IYAWGNVFL; YAWGNVFLI; AWGNVFLIL;
WGNVFLILQ; GNVFLILQE; NVFLILQEK; VFLILQEKR; FLILQEKRI; LILQEKRIQ; ILQEKRIQK;
LQEKRIQKL; QEKRIQKLK; EKRIQKLKT; KRIQKLKTL; RIQKLKTLD; IQKLKTLDM; QKLKTLDMD;
KLKTLDMDQ; LKTLDMDQA; KTLDMDQAL; TLDMDQALN; LDMDQALNP; DMDQALNPN; MDQALNPNH;
DQALNPNHN; QALNPNHNA; ALNPNHNAL; LNPNHNALP; NPNHNALPK; PNHNALPKS; NHNALPKSQ;
HNALPKSQI; NALPKSQIL; ALPKSQILQ; LPKSQILQP; PKSQILQPL; KSQILQPLL; SQILQPLLK;
QILQPLLKI; ILQPLLKIP; LQPLLKIPK; QPLLKIPKG; PLLKIPKGQ; LLKIPKGQT; LKIPKGQTP;
KIPKGQTPI; IPKGQTPIV; PKGQTPIVK; KGQTPIVKS; GQTPIVKSC; QTPIVKSCI; TPIVKSCIC;
PIVKSCICV; IVKSCICVK; VKSCICVKA; KSCICVKAF; SCICVKAFS; CICVKAFSV; ICVKAFSVL;
CVKAFSVLK; VKAFSVLKG; KAFSVLKGL; AFSVLKGLK; FSVLKGLKH; SVLKGLKHH; VLKGLKHHP;
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PQNNTSLKV; QNNTSLKVA; NNTSLKVAY; NTSLKVAYT; TSLKVAYTK; SLKVAYTKA; LKVAYTKAA;
KVAYTKAAF; VAYTKAAFI; AYTKAAFIK; YTKAAFIKC; TKAAFIKCI; KAAFIKCIC; AAFIKCICT;
AFIKCICTI; FIKCICTIK; IKCICTIKA; KCICTIKAP; CICTIKAPV; SILVCNCPC; ILVCNCPCL;

LVCNCPCLS; VCNCPCLSI; CNCPCLSIY; NCPCLSIYL; CPCLSIYLI; PCLSIYLII; CLSIYLIIS;
LSIYLIISG; SIYLIISGS; IYLIISGSP; YLIISGSPG; LIISGSPGS; IISGSPGSL; ISGSPGSLS;
SGSPGSLSV; GSPGSLSVP; SPGSLSVPS; PGSLSVPSN; GSLSVPSNT; SLSVPSNTL; LSVPSNTLT;
SVPSNTLTS; VPSNTLTSS; PSNTLTSST; SNTLTSSTW; NTLTSSTWD; TLTSSTWDS; LTSSTWDSI;
TSSTWDSIP; SSTWDSIPY; STWDSIPYI; TWDSIPYIG; WDSIPYIGC; DSIPYIGCP; SIPYIGCPS;
IPYIGCPST; PYIGCPSTL; YIGCPSTLW; IGCPSTLWV; GCPSTLWVL; CPSTLWVLL; PSTLWVLLF;
STLWVLLFI; TLWVLLFIR; LWVLLFIRS; WVLLFIRSL; VLLFIRSLS; LLFIRSLSK; LFIRSLSKK;
FIRSLSKKE; IRSLSKKEI; RSLSKKEIG; GFFTDLFLR; FFTDLFLRR; FTDLFLRRI; TDLFLRRIL;
DLFLRRILK; LFLRRILKY; FLRRILKYL; LRRILKYLA; RRILKYLAR; RILKYLARP; ILKYLARPL;
LKYLARPLH; KYLARPLHC; YLARPLHCC; LARPLHCCV; ARPLHCCVP; RPLHCCVPE; PLHCCVPEL;
LHCCVPELL; HCCVPELLV; CCVPELLVN; CVPELLVNR; VPELLVNRP; PELLVNRPQ; ELLVNRPQI;
LLVNRPQIS; LVNRPQISA; VNRPQISAA; NRPQISAAE; RPQISAAET; PQISAAETY; QISAAETYR;
ISAAETYRL; SAAETYRLS; AAETYRLSA; AETYRLSAL; ETYRLSALQ; TYRLSALQR; YRLSALQRG;
RLSALQRGP; LSALQRGPT; SALQRGPTP; ALQRGPTPC; LQRGPTPCS; QRGPTPCSS; RGPTPCSSS;
GPTPCSSSN; PTPCSSSNT; TPCSSSNTV; PCSSSNTVV; CSSSNTVVA; SSSNTVVAV; SSNTVVAVL;
SNTVVAVLV; NTVVAVLVT; STGGTFSPP; TGGTFSPPV; GGTFSPPVK; GTFSPPVKV; TFSPPVKVP;
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FLLGSGTQH; LLGSGTQHS; LGSGTQHST; GSGTQHSTG; ALWSVFITW; LWSVFITWD; WSVFITWDW;
SVFITWDWA; VFITWDWAV; FITWDWAVG; ITWDWAVGF; TWDWAVGFL; WDWAVGFLG; DWAVGFLGV;
WAVGFLGVI; AVGFLGVIV; VGFLGVIVP; GFLGVIVPS; FLGVIVPSG; LGVIVPSGY; GVIVPSGYF;
VIVPSGYFD; IVPSGYFDL; FISTPCISK; ISTPCISKG; STPCISKGS; TPCISKGSP; PCISKGSPP;
CISKGSPPT; ISKGSPPTA; SKGSPPTAK; KGSPPTAKK; GSPPTAKKW; SPPTAKKWK; PPTAKKWKL;
PTAKKWKLL; TAKKWKLLP; IGFPPPCSC; GFPPPCSCT; FPPPCSCTF; PPPCSCTFC; PPCSCTFCD;
PCSCTFCDP; CSCTFCDPA; RLSMLVIPI; LSMLVIPIT; SMLVIPITS; MLVIPITSV; LVIPITSVC;
VIPITSVCT; IPITSVCTV; PITSVCTVT; ITSVCTVTA; TSVCTVTAS; SVCTVTASH; VCTVTASHI;
CTVTASHIS; TVTASHISR; VTASHISRF; TASHISRFP; ASHISRFPQ; SHISRFPQV; HISRFPQVR;
ISRFPQVRS; SRFPQVRSS; RFPQVRSSF; FPQVRSSFK; PQVRSSFKL; QVRSSFKLG; VRSSFKLGR;
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GSPISGFRK; SPISGFRKH; PISGFRKHS; ISGFRKHST; SGFRKHSTS; GFRKHSTSV; FRKHSTSVI;
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PFISSFGTC; FISSFGTCT; ISSFGTCTG; SSFGTCTGS; SFGTCTGSF; FGTCTGSFG; GTCTGSFGF;
TCTGSFGFL; CTGSFGFLG; TGSFGFLGA; GSFGFLGAA; SFGFLGAAP; FGFLGAAPG; GFLGAAPGH;
FLGAAPGHS; LGAAPGHSP; GAAPGHSPF; AAPGHSPFL; APGHSPFLL; PGHSPFLLV; GHSPFLLVG;
HSPFLLVGA; SPFLLVGAI; PFLLVGAIF; FLLVGAIFI; LLVGAIFIC; LVGAIFICF; VGAIFICFK;
GAIFICFKS; AIFICFKSR; IFICFKSRC; FICFKSRCY; ICFKSRCYS; CFKSRCYSP; FKSRCYSPV;
KSRCYSPVQ; SRCYSPVQA; RQHPLRSSS; QHPLRSSSL; HPLRSSSLI; PLRSSSLIS; LRSSSLIST;
RSSSLISTS; SSSLISTSW; SSLISTSWG; SLISTSWGN; LISTSWGNS; ISTSWGNSF; STSWGNSFF;
TSWGNSFFY; SWGNSFFYK; WGNSFFYKL; GNSFFYKLS; VHSLCNFFY; HSLCNFFYT; SLCNFFYTV;
LCNFFYTVS; CNFFYTVSI; NFFYTVSII; FFYTVSIIY; FYTVSIIYT; YTVSIIYTI; TVSIIYTIS;
VSIIYTISM; SIIYTISMA; IIYTISMAK; IYTISMAKM; YTISMAKMY; TISMAKMYT; ISMAKMYTG;
SMAKMYTGT; MAKMYTGTF; AKMYTGTFP; KMYTGTFPF; MYTGTFPFS; YTGTFPFSY; TGTFPFSYL;
GTFPFSYLS; TFPFSYLSN; FPFSYLSNH; GPNRGKIRI; PNRGKIRII; NRGKIRIIL; RGKIRIILL;
GKIRIILLN; KIRIILLNI; IRIILLNII; RIILLNIII; IILLNIIIK; ILLNIIIKV; LLNIIIKVY;
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YRGIYNCPG; RGIYNCPGS; GIYNCPGSF; IYNCPGSFL; YNCPGSFLQ; NCPGSFLQK; CPGSFLQKS;
PGSFLQKSS; GSFLQKSSQ; SFLQKSSQG; FLQKSSQGV; LQKSSQGVS; QKSSQGVSK; KSSQGVSKK;
SSQGVSKKS; SQGVSKKSF; QGVSKKSFC; GVSKKSFCS; VSKKSFCSS; SKKSFCSSL; KKSFCSSLQ;
KSFCSSLQF; SFCSSLQFL; GYRRYIIPN; YRRYIIPNN; RRYIIPNNM; RYIIPNNMP; YIIPNNMPQ;
IIPNNMPQS; IPNNMPQSL; PNNMPQSLG; NNMPQSLGN; NMPQSLGNS; MPQSLGNSS; PQSLGNSSK;
QSLGNSSKQ; SLGNSSKQR; LGNSSKQRR; GNSSKQRRT; NSSKQRRTP; SSKQRRTPM; SKQRRTPMP;
KQRRTPMPR; QRRTPMPRI; RRTPMPRIK; RTPMPRIKV; TPMPRIKVL; PMPRIKVLN; MPRIKVLNI;
PRIKVLNII; RIKVLNIIN; IKVLNIINK; KVLNIINKS; VLNIINKSI; LNIINKSIY; NIINKSIYT;
IINKSIYTR; INKSIYTRK; NKSIYTRKQ; KSIYTRKQN; SIYTRKQNI; IYTRKQNII; YTRKQNIIV;
TRKQNIIVL; RKQNIIVLI; KQNIIVLIW; QNIIVLIWV; NIIVLIWVK; IIVLIWVKQ; IVLIWVKQF;
VLIWVKQFQ; LIWVKQFQS; IWVKQFQSH; WVKQFQSHA; LLIEAYSGN; LIEAYSGNF; IEAYSGNFV;
EAYSGNFVI; AYSGNFVIP; YSGNFVIPI; SGNFVIPII; GNFVIPIIK; NFVIPIIKE; FVIPIIKEL;
VIPIIKELI; IPIIKELIP; PIIKELIPY; IIKELIPYL; IKELIPYLS; GTNTTNSLN; SSKPSNSPR;
SKPSNSPRS; KPSNSPRST; PSNSPRSTS; SNSPRSTSN; NSPRSTSNY; SPRSTSNYS; PRSTSNYSI;

RSTSNYSIC; STSNYSICL; TSNYSICLR; SNYSICLRS; GTCYALYSS; TCYALYSSK; CYALYSSKG; YALYSSKGC; ALYSSKGCN; LYSSKGCNL; YSSKGCNLN; SSKGCNLNF; SKGCNLNFY; KGCNLNFYS; GCNLNFYSS; CNLNFYSSS; NLNFYSSSS; LNFYSSSSL; NFYSSSSLP; FYSSSSLPS; YSSSSLPSS; SSSSLPSSN; SSSLPSSNF; SSLPSSNFS; SLPSSNFSH; KSCGSSSLR; SCGSSSLRY; CGSSSLRYT; GSSSLRYTG; SSSLRYTGN; SSTHEPGNT; STHEPGNTK; THEPGNTKK; HEPGNTKKK; EPGNTKKKG; PGNTKKKGL; GNTKKKGLL; NTKKKGLLT; ESFTESFTA; SFTESFTAG; FTESFTAGK; TESFTAGKA; ESFTAGKAV; SFTAGKAVV; FTAGKAVVL; TAGKAVVLL; AGKAVVLLF; GKAVVLLFF; KAVVLLFFP; AVVLLFFPS; VVLLFFPST; VLLFFPSTL; LLFFPSTLS; LFFPSTLSS; FFPSTLSSP; FPSTLSSPL; PSTLSSPLQ; STLSSPLQN; TLSSPLQNS; LSSPLQNSS; SSPLQNSSK; SPLQNSSKS; PLQNSSKSS; LQNSSKSSK; QNSSKSSKI; NSSKSSKIK; SSKSSKIKI; SKSSKIKIK; KSSKIKIKI; SSKIKIKIL; ALFFVPVQV; LFFVPVQVL; FFVPVQVLP; FVPVQVLPT; VPVQVLPTF; PVQVLPTFT; VQVLPTFTE; QVLPTFTEA; VLPTFTEAC; LPTFTEACR; PTFTEACRD; TFTEACRDS; FTEACRDSW; TEACRDSWR; EACRDSWRR; ACRDSWRRT; CRDSWRRTM; RDSWRRTMA; DSWRRTMAF; SWRRTMAFV; WRRTMAFVQ; RRTMAFVQF; RTMAFVQFN; TMAFVQFNW; MAFVQFNWG; AFVQFNWGQ; FVQFNWGQG; VQFNWGQGQ; QFNWGQGQD; FNWGQGQDS; ARKTCLSCT; RKTCLSCTF; KTCLSCTFL; TCLSCTFLP; CLSCTFLPE; LSCTFLPEV; SCTFLPEVM; CTFLPEVMV; TFLPEVMVW; FLPEVMVWL; LPEVMVWLH; PEVMVWLHS; EVMVWLHSM; VMVWLHSMG; MVWLHSMGK; VWLHSMGKQ; WLHSMGKQL; LHSMGKQLL; HSMGKQLLP; SMGKQLLPV; MGKQLLPVS; GKQLLPVSH; KQLLPVSHA; QLLPVSHAL; LLPVSHALS; LPVSHALSF; PVSHALSFL; VSHALSFLR; SHALSFLRS; HALSFLRSW; ALSFLRSWF; LSFLRSWFG; SFLRSWFGC; FLRSWFGCI; LRSWFGCIP; RSWFGCIPL; GHGLAAFHG; AAPPCGLFF; APPCGLFFY; PPCGLFFYN; PCGLFFYNI; EAEAASAST; AEAASASTL; EAASASTLS; AASASTLSL; ASASTLSLK; GLAKLFGEI; LAKLFGEIP; AKLFGEIPI; KLFGEIPIL; LFGEIPILL; FGEIPILLQ; GEIPILLQF; EIPILLQFL; IPILLQFLQ

10 mers:

MDKVLNREES; DKVLNREESM; KVLNREESME; VLNREESMEL; LNREESMELM; NREESMELMD; REESMELMDL; EESMELMDLL; ESMELMDLLG; SMELMDLLGL; MELMDLLGLE; ELMDLLGLER; LMDLLGLERA; MDLLGLERAA; DLLGLERAAW; LLGLERAAWG; LGLERAAWGN; GLERAAWGNL; LERAAWGNLP; ERAAWGNLPL; RAAWGNLPLM; AAWGNLPLMR; AWGNLPLMRK; WGNLPLMRKA; GNLPLMRKAY; NLPLMRKAYL; LPLMRKAYLR; PLMRKAYLRK; LMRKAYLRKC; MRKAYLRKCK; RKAYLRKCKE; KAYLRKCKEF; AYLRKCKEFH; YLRKCKEFHP; LRKCKEFHPD; RKCKEFHPDK; KCKEFHPDKG; CKEFHPDKGG; KEFHPDKGGD; EFHPDKGGDE; FHPDKGGDED; HPDKGGDEDK; PDKGGDEDKM; DKGGDEDKMK; KGGDEDKMKR; GGDEDKMKRM; GDEDKMKRMN; DEDKMKRMNT; EDKMKRMNTL; DKMKRMNTLY; KMKRMNTLYK; MKRMNTLYKK; KRMNTLYKKM; RMNTLYKKME; MNTLYKKMEQ; NTLYKKMEQD; TLYKKMEQDV; LYKKMEQDVK; YKKMEQDVKV; KKMEQDVKVA; KMEQDVKVAH; MEQDVKVAHQ; EQDVKVAHQP; QDVKVAHQPD; DVKVAHQPDF; VKVAHQPDFG; KVAHQPDFGT; VAHQPDFGTW; AHQPDFGTWS; HQPDFGTWSS; QPDFGTWSSS; PDFGTWSSSE; DFGTWSSSEV; FGTWSSSEVC; GTWSSSEVCA; TWSSSEVCAD; WSSSEVCADF; SSSEVCADFP; SSEVCADFPL; SEVCADFPLC; EVCADFPLCP; VCADFPLCPD; CADFPLCPDT; ADFPLCPDTL; DFPLCPDTLY; FPLCPDTLYC; PLCPDTLYCK; LCPDTLYCKE; CPDTLYCKEW; PDTLYCKEWP; DTLYCKEWPI; TLYCKEWPIC; LYCKEWPICS; YCKEWPICSK; CKEWPICSKK; KEWPICSKKP; EWPICSKKPS; WPICSKKPSV; PICSKKPSVH; ICSKKPSVHC; CSKKPSVHCP; SKKPSVHCPC; KKPSVHCPCM; KPSVHCPCML; PSVHCPCMLC; SVHCPCMLCQ; VHCPCMLCQL; HCPCMLCQLR; CPCMLCQLRL; PCMLCQLRLR; CMLCQLRLRH; MLCQLRLRHL; LCQLRLRHLN; CQLRLRHLNR; QLRLRHLNRK; LRLRHLNRKF; RLRHLNRKFL; LRHLNRKFLR; RHLNRKFLRK; HLNRKFLRKE; LNRKFLRKEP; NRKFLRKEPL; RKFLRKEPLV; KFLRKEPLVW; FLRKEPLVWI; LRKEPLVWID; RKEPLVWIDC; KEPLVWIDCY; EPLVWIDCYC; PLVWIDCYCI; LVWIDCYCID; VWIDCYCIDC; WIDCYCIDCF; IDCYCIDCFT; DCYCIDCFTQ; CYCIDCFTQW; YCIDCFTQWF; CIDCFTQWFG; IDCFTQWFGL; DCFTQWFGLD; CFTQWFGLDL; FTQWFGLDLT; TQWFGLDLTE; QWFGLDLTEE; WFGLDLTEET; FGLDLTEETL; GLDLTEETLQ; LDLTEETLQW; DLTEETLQWW; LTEETLQWWV; TEETLQWWVQ; EETLQWWVQI; ETLQWWVQII; TLQWWVQIIG; LQWWVQIIGE; QWWVQIIGET; WWVQIIGETP; WVQIIGETPF; VQIIGETPFR; QIIGETPFRD; IIGETPFRDL; IGETPFRDLK; GETPFRDLKL; KALSNYFFYR; ALSNYFFYRC; LSNYFFYRCQ; SNYFFYRCQP; NYFFYRCQPM; YFFYRCQPME; FFYRCQPMEQ; FYRCQPMEQK; YRCQPMEQKS; RCQPMEQKSG; CQPMEQKSGS; QPMEQKSGSP; PMEQKSGSPG; MEQKSGSPGG; EQKSGSPGGV; QKSGSPGGVP; KSGSPGGVPL; SGSPGGVPLM; GSPGGVPLMK; SPGGVPLMKN; PGGVPLMKNG; GGVPLMKNGM; GVPLMKNGMK; VPLMKNGMKI; PLMKNGMKIY; LMKNGMKIYF; MKNGMKIYFA; KNGMKIYFAM; NGMKIYFAMK; GMKIYFAMKI; MKIYFAMKIC; KIYFAMKICL; IYFAMKICLP; YFAMKICLPV; FAMKICLPVM; AMKICLPVMK; MKICLPVMKK; KICLPVMKKQ; ICLPVMKKQQ; CLPVMKKQQQ; LPVMKKQQQI; PVMKKQQQIL; VMKKQQQILN; MKKQQQILNT; KKQQQILNTQ; KQQQILNTQH; QQQILNTQHH; QQILNTQHHP; QILNTQHHPK; ILNTQHHPKK; LNTQHHPKKK; NTQHHPKKKE; TQHHPKKKER; KTLKTFPLIY; TLKTFPLIYT; LKTFPLIYTS; KTFPLIYTSF; TFPLIYTSFL; FPLIYTSFLV; PLIYTSFLVK; LIYTSFLVKL; IYTSFLVKLY; YTSFLVKLYL; TSFLVKLYLV; SFLVKLYLVI; FLVKLYLVIE; LVKLYLVIEP; VKLYLVIEPL; KLYLVIEPLP; LYLVIEPLPA; YLVIEPLPAL; LVIEPLPALL; VIEPLPALLC; IEPLPALLCI; EPLPALLCIL; PLPALLCILL; LPALLCILLK; PALLCILLKK; ALLCILLKKK; LLCILLKKKL; LCILLKKKLK; CILLKKKLKF; ILLKKKLKFC;

LLKKKLKFCI; LKKKLKFCIK; KKKLKFCIKN; KKLKFCIKNL; KLKFCIKNLW; LKFCIKNLWK;
KFCIKNLWKN; FCIKNLWKNI; CIKNLWKNIL; LLLVDTCVLG; LLVDTCVLGI; LVDTCVLGII;
VDTCVLGIIL; DTCVLGIILY; TCVLGIILYS; CVLGIILYSF; LHIDIEFLQL; HIDIEFLQLI;
IDIEFLQLII; DIEFLQLIIS; IEFLQLIISV; EFLQLIISVK; FLQLIISVKS; LQLIISVKSC;
QLIISVKSCV; LIISVKSCVP; IISVKSCVPL; ISVKSCVPLV; SVKSCVPLVF; FVRVLIRNTY;
VRVLIRNTYY; RVLIRNTYYI; VLIRNTYYIV; LIRNTYYIVP; RSMILAQKSL; SMILAQKSLK;
MILAQKSLKK; ILAQKSLKKQ; LAQKSLKKQS; AQKSLKKQSR; QKSLKKQSRC; KSLKKQSRCL;
SLKKQSRCLG; LKKQSRCLGN; RQSVRMCFYY; RSVKSVRKKT; SVKSVRKKTS; VKSVRKKTSL;
KSVRKKTSLI; SVRKKTSLIT; VRKKTSLITL; RKKTSLITLS; KKTSLITLSI; KTSLITLSIM;
TSLITLSIMK; SLITLSIMKS; LITLSIMKST; ITLSIMKSTL; TLSIMKSTLQ; LSIMKSTLQM;
SIMKSTLQML; IMKSTLQMLL; MKSTLQMLLF; KSTLQMLLFL; STLQMLLFLQ; TLQMLLFLQK;
LQMLLFLQKV; QMLLFLQKVK; MLLFLQKVKI; LLFLQKVKIK; LFLQKVKIKK; FLQKVKIKKV;
LQKVKIKKVF; QKVKIKKVFV; KVKIKKVFVS; VKIKKVFVSK; KIKKVFVSKQ; NNIWQVLLGC;
NIWQVLLGCT; IWQVLLGCTV; WQVLLGCTVC; QVLLGCTVCY; VLLGCTVCYL; LLGCTVCYLK;
LGCTVCYLKW; GCTVCYLKWI; CTVCYLKWIL; YLIFCTVLFS; LIFCTVLFSM; IFCTVLFSMY;
FCTVLFSMYL; CTVLFSMYLK; TVLFSMYLKE; VLFSMYLKED; LFSMYLKEDT; FSMYLKEDTG;
SMYLKEDTGY; MYLKEDTGYL; YLKEDTGYLK; LKEDTGYLKV; KEDTGYLKVP; EDTGYLKVPL;
DTGYLKVPLI; TGYLKVPLIV; GYLKVPLIVE; YLKVPLIVEK; LKVPLIVEKQ; KVPLIVEKQH;
KGQELNQRIC; GQELNQRICL; QELNQRICLQ; ELNQRICLQD; LNQRICLQDM; NQRICLQDME;
TKEPKYFHQA; KEPKYFHQAW; EPKYFHQAWL; PKYFHQAWLQ; MSILSLKPCK; SILSLKPCKL;
ILSLKPCKLD; LSLKPCKLDL; ENPYKTQSSY; NPYKTQSSYL; PYKTQSSYLK; YKTQSSYLKK;
KTQSSYLKKE; TQSSYLKKEF; QSSYLKKEFY; SSYLKKEFYK; SYLKKEFYKV; YLKKEFYKVE;
LILQLIYNLE; ILQLIYNLEL; LQLIYNLELL; QLIYNLELLN; LIYNLELLNG; IYNLELLNGR;
YNLELLNGRK; NLELLNGRKG; LELLNGRKGW; ELLNGRKGWI; LLNGRKGWIL; LNGRKGWILR;
NIIYAWGNVF; IIYAWGNVFL; IYAWGNVFLI; YAWGNVFLIL; AWGNVFLILQ; WGNVFLILQE;
GNVFLILQEK; NVFLILQEKR; VFLILQEKRI; FLILQEKRIQ; LILQEKRIQK; ILQEKRIQKL;
LQEKRIQKLK; QEKRIQKLKT; EKRIQKLKTL; KRIQKLKTLD; RIQKLKTLDM; IQKLKTLDMD;
QKLKTLDMDQ; KLKTLDMDQA; LKTLDMDQAL; KTLDMDQALN; TLDMDQALNP; LDMDQALNPN;
DMDQALNPNH; MDQALNPNHN; DQALNPNHNA; QALNPNHNAL; ALNPNHNALP; LNPNHNALPK;
NPNHNALPKS; PNHNALPKSQ; NHNALPKSQI; HNALPKSQIL; NALPKSQILQ; ALPKSQILQP;
LPKSQILQPL; PKSQILQPLL; KSQILQPLLK; SQILQPLLKI; QILQPLLKIP; ILQPLLKIPK;
LQPLLKIPKG; QPLLKIPKGQ; PLLKIPKGQT; LLKIPKGQTP; LKIPKGQTPI; KIPKGQTPIV;
IPKGQTPIVK; PKGQTPIVKS; KGQTPIVKSC; GQTPIVKSCI; QTPIVKSCIC; TPIVKSCICV;
PIVKSCICVK; IVKSCICVKA; VKSCICVKAF; KSCICVKAFS; SCICVKAFSV; CICVKAFSVL;
ICVKAFSVLK; CVKAFSVLKG; VKAFSVLKGL; KAFSVLKGLK; AFSVLKGLKH; FSVLKGLKHH;
SVLKGLKHHP; VLKGLKHHPQ; LKGLKHHPQN; KGLKHHPQNN; GLKHHPQNNT; LKHHPQNNTS;
KHHPQNNTSL; HHPQNNTSLK; HPQNNTSLKV; PQNNTSLKVA; QNNTSLKVAY; NNTSLKVAYT;
NTSLKVAYTK; TSLKVAYTKA; SLKVAYTKAA; LKVAYTKAAF; KVAYTKAAFI; VAYTKAAFIK;
AYTKAAFIKC; YTKAAFIKCI; TKAAFIKCIC; KAAFIKCICT; AAFIKCICTI; AFIKCICTIK;
FIKCICTIKA; IKCICTIKAP; KCICTIKAPV; SILVCNCPCL; ILVCNCPCLS; LVCNCPCLSI;
VCNCPCLSIY; CNCPCLSIYL; NCPCLSIYLI; CPCLSIYLII; PCLSIYLIIS; CLSIYLIISG;
LSIYLIISGS; SIYLIISGSP; IYLIISGSPG; YLIISGSPGS; LIISGSPGSL; IISGSPGSLS;
ISGSPGSLSV; SGSPGSLSVP; GSPGSLSVPS; SPGSLSVPSN; PGSLSVPSNT; GSLSVPSNTL;
SLSVPSNTLT; LSVPSNTLTS; SVPSNTLTSS; VPSNTLTSST; PSNTLTSSTW; SNTLTSSTWD;
NTLTSSTWDS; TLTSSTWDSI; LTSSTWDSIP; TSSTWDSIPY; SSTWDSIPYI; STWDSIPYIG;
TWDSIPYIGC; WDSIPYIGCP; DSIPYIGCPS; SIPYIGCPST; IPYIGCPSTL; PYIGCPSTLW;
YIGCPSTLWV; IGCPSTLWVL; GCPSTLWVLL; CPSTLWVLLF; PSTLWVLLFI; STLWVLLFIR;
TLWVLLFIRS; LWVLLFIRSL; WVLLFIRSLS; VLLFIRSLSK; LLFIRSLSKK; LFIRSLSKKE;
FIRSLSKKEI; IRSLSKKEIG; GFFTDLFLRR; FFTDLFLRRI; FTDLFLRRIL; TDLFLRRILK;
DLFLRRILKY; LFLRRILKYL; FLRRILKYLA; LRRILKYLAR; RRILKYLARP; RILKYLARPL;
ILKYLARPLH; LKYLARPLHC; KYLARPLHCC; YLARPLHCCV; LARPLHCCVP; ARPLHCCVPE;
RPLHCCVPEL; PLHCCVPELL; LHCCVPELLV; HCCVPELLVN; CCVPELLVNR; CVPELLVNRP;
VPELLVNRPQ; PELLVNRPQI; ELLVNRPQIS; LLVNRPQISA; LVNRPQISAA; VNRPQISAAE;
NRPQISAAET; RPQISAAETY; PQISAAETYR; QISAAETYRL; ISAAETYRLS; SAAETYRLSA;
AAETYRLSAL; AETYRLSALQ; ETYRLSALQR; TYRLSALQRG; YRLSALQRGP; RLSALQRGPT;
LSALQRGPTP; SALQRGPTPC; ALQRGPTPCS; LQRGPTPCSS; QRGPTPCSSS; RGPTPCSSSN;
GPTPCSSSNT; PTPCSSSNTV; TPCSSSNTVV; PCSSSNTVVA; CSSSNTVVAV; SSSNTVVAVL;
SSNTVVAVLV; SNTVVAVLVT; STGGTFSPPV; TGGTFSPPVK; GGTFSPPVKV; GTFSPPVKVP;
TFSPPVKVPK; FSPPVKVPKY; SPPVKVPKYL; PPVKVPKYLA; PVKVPKYLAF; VKVPKYLAFS;
KVPKYLAFSF; VPKYLAFSFL; PKYLAFSFLL; KYLAFSFLLG; YLAFSFLLGS; LAFSFLLGSG;
AFSFLLGSGT; FSFLLGSGTQ; SFLLGSGTQH; FLLGSGTQHS; LLGSGTQHST; LGSGTQHSTG;
ALWSVFITWD; LWSVFITWDW; WSVFITWDWA; SVFITWDWAV; VFITWDWAVG; FITWDWAVGF;
ITWDWAVGFL; TWDWAVGFLG; WDWAVGFLGV; DWAVGFLGVI; WAVGFLGVIV; AVGFLGVIVP;
VGFLGVIVPS; GFLGVIVPSG; FLGVIVPSGY; LGVIVPSGYF; GVIVPSGYFD; VIVPSGYFDL;
FISTPCISKG; ISTPCISKGS; STPCISKGSP; TPCISKGSPP; PCISKGSPPT; CISKGSPPTA;

ISKGSPPTAK; SKGSPPTAKK; KGSPPTAKKW; GSPPTAKKWK; SPPTAKKWKL; PPTAKKWKLL;
PTAKKWKLLP; IGFPPPCSCT; GFPPPCSCTF; FPPPCSCTFC; PPPCSCTFCD; PPCSCTFCDP;
PCSCTFCDPA; RLSMLVIPIT; LSMLVIPITS; SMLVIPITSV; MLVIPITSVC; LVIPITSVCT;
VIPITSVCTV; IPITSVCTVT; PITSVCTVTA; ITSVCTVTAS; TSVCTVTASH; SVCTVTASHI;
VCTVTASHIS; CTVTASHISR; TVTASHISRF; VTASHISRFP; TASHISRFPQ; ASHISRFPQV;
SHISRFPQVR; HISRFPQVRS; ISRFPQVRSS; SRFPQVRSSF; RFPQVRSSFK; FPQVRSSFKL;
PQVRSSFKLG; QVRSSFKLGR; VRSSFKLGRG; RSSFKLGRGI; SSFKLGRGIL; SFKLGRGILA;
FKLGRGILAV; KLGRGILAVL; QGSIFLSGLS; GSIFLSGLSL; SIFLSGLSLL; IFLSGLSLLK;
FLSGLSLLKS; LSGLSLLKSF; SGLSLLKSFS; GLSLLKSFSA; LSLLKSFSAL; SLLKSFSALS;
LLKSFSALSF; LKSFSALSFR; KSFSALSFRL; SFSALSFRLK; FSALSFRLKP; SALSFRLKPL;
ALSFRLKPLR; LSFRLKPLRF; SFRLKPLRFS; FRLKPLRFSS; RLKPLRFSSG; LKPLRFSSGS;
KPLRFSSGSP; PLRFSSGSPI; LRFSSGSPIS; RFSSGSPISG; FSSGSPISGF; SSGSPISGFR;
SGSPISGFRK; GSPISGFRKH; SPISGFRKHS; PISGFRKHST; ISGFRKHSTS; SGFRKHSTSV;
GFRKHSTSVI; FRKHSTSVIA; RKHSTSVIAS; KHSTSVIAST; HSTSVIASTP; STSVIASTPV;
TSVIASTPVL; SVIASTPVLT; VIASTPVLTS; IASTPVLTSR; ASTPVLTSRT; STPVLTSRTS;
TPVLTSRTST; PVLTSRTSTP; VLTSRTSTPP; LTSRTSTPPF; TSRTSTPPFI; SRTSTPPFIS;
RTSTPPFISS; TSTPPFISSF; STPPFISSFG; TPPFISSFGT; PPFISSFGTC; PFISSFGTCT;
FISSFGTCTG; ISSFGTCTGS; SSFGTCTGSF; SFGTCTGSFG; FGTCTGSFGF; GTCTGSFGFL;
TCTGSFGFLG; CTGSFGFLGA; TGSFGFLGAA; GSFGFLGAAP; SFGFLGAAPG; FGFLGAAPGH;
GFLGAAPGHS; FLGAAPGHSP; LGAAPGHSPF; GAAPGHSPFL; AAPGHSPFLL; APGHSPFLLV;
PGHSPFLLVG; GHSPFLLVGA; HSPFLLVGAI; SPFLLVGAIF; PFLLVGAIFI; FLLVGAIFIC;
LLVGAIFICF; LVGAIFICFK; VGAIFICFKS; GAIFICFKSR; AIFICFKSRC; IFICFKSRCY;
FICFKSRCYS; ICFKSRCYSP; CFKSRCYSPV; FKSRCYSPVQ; KSRCYSPVQA; RQHPLRSSSL;
QHPLRSSSLI; HPLRSSSLIS; PLRSSSLIST; LRSSSLISTS; RSSSLISTSW; SSSLISTSWG;
SSLISTSWGN; SLISTSWGNS; LISTSWGNSF; ISTSWGNSFF; STSWGNSFFY; TSWGNSFFYK;
SWGNSFFYKL; WGNSFFYKLS; VHSLCNFFYT; HSLCNFFYTV; SLCNFFYTVS; LCNFFYTVSI;
CNFFYTVSII; NFFYTVSIIY; FFYTVSIIYT; FYTVSIIYTI; YTVSIIYTIS; TVSIIYTISM;
VSIIYTISMA; SIIYTISMAK; IIYTISMAKM; IYTISMAKMY; YTISMAKMYT; TISMAKMYTG;
ISMAKMYTGT; SMAKMYTGTF; MAKMYTGTFP; AKMYTGTFPF; KMYTGTFPFS; MYTGTFPFSY;
YTGTFPFSYL; TGTFPFSYLS; GTFPFSYLSN; TFPFSYLSNH; GPNRGKIRII; PNRGKIRIIL;
NRGKIRIILL; RGKIRIILLN; GKIRIILLNI; KIRIILLNII; IRIILLNIII; RIILLNIIIK;
IILLNIIIKV; ILLNIIIKVY; LLNIIIKVYR; LNIIIKVYRG; NIIIKVYRGI; IIIKVYRGIY;
IIKVYRGIYN; IKVYRGIYNC; KVYRGIYNCP; VYRGIYNCPG; YRGIYNCPGS; RGIYNCPGSF;
GIYNCPGSFL; IYNCPGSFLQ; YNCPGSFLQK; NCPGSFLQKS; CPGSFLQKSS; PGSFLQKSSQ;
GSFLQKSSQG; SFLQKSSQGV; FLQKSSQGVS; LQKSSQGVSK; QKSSQGVSKK; KSSQGVSKKS;
SSQGVSKKSF; SQGVSKKSFC; QGVSKKSFCS; GVSKKSFCSS; VSKKSFCSSL; SKKSFCSSLQ;
KKSFCSSLQF; KSFCSSLQFL; GYRRYIIPNN; YRRYIIPNNM; RRYIIPNNMP; RYIIPNNMPQ;
YIIPNNMPQS; IIPNNMPQSL; IPNNMPQSLG; PNNMPQSLGN; NNMPQSLGNS; NMPQSLGNSS;
MPQSLGNSSK; PQSLGNSSKQ; QSLGNSSKQR; SLGNSSKQRR; LGNSSKQRRT; GNSSKQRRTP;
NSSKQRRTPM; SSKQRRTPMP; SKQRRTPMPR; KQRRTPMPRI; QRRTPMPRIK; RRTPMPRIKV;
RTPMPRIKVL; TPMPRIKVLN; PMPRIKVLNI; MPRIKVLNII; PRIKVLNIIN; RIKVLNIINK;
IKVLNIINKS; KVLNIINKSI; VLNIINKSIY; LNIINKSIYT; NIINKSIYTR; IINKSIYTRK;
INKSIYTRKQ; NKSIYTRKQN; KSIYTRKQNI; SIYTRKQNII; IYTRKQNIIV; YTRKQNIIVL;
TRKQNIIVLI; RKQNIIVLIW; KQNIIVLIWV; QNIIVLIWVK; NIIVLIWVKQ; IIVLIWVKQF;
IVLIWVKQFQ; VLIWVKQFQS; LIWVKQFQSH; IWVKQFQSHA; LLIEAYSGNF; LIEAYSGNFV;
IEAYSGNFVI; EAYSGNFVIP; AYSGNFVIPI; YSGNFVIPII; SGNFVIPIIK; GNFVIPIIKE;
NFVIPIIKEL; FVIPIIKELI; VIPIIKELIP; IPIIKELIPY; PIIKELIPYL; IIKELIPYLS;
SSKPSNSPRS; SKPSNSPRST; KPSNSPRSTS; PSNSPRSTSN; SNSPRSTSNY; NSPRSTSNYS;
SPRSTSNYSI; PRSTSNYSIC; RSTSNYSICL; STSNYSICLR; TSNYSICLRS; GTCYALYSSK;
TCYALYSSKG; CYALYSSKGC; YALYSSKGCN; ALYSSKGCNL; LYSSKGCNLN; YSSKGCNLNF;
SSKGCNLNFY; SKGCNLNFYS; KGCNLNFYSS; GCNLNFYSSS; CNLNFYSSSS; NLNFYSSSSL;
LNFYSSSSLP; NFYSSSSLPS; FYSSSSLPSS; YSSSSLPSSN; SSSSLPSSNF; SSSLPSSNFS;
SSLPSSNFSH; KSCGSSSLRY; SCGSSSLRYT; CGSSSLRYTG; GSSSLRYTGN; SSTHEPGNTK;
STHEPGNTKK; THEPGNTKKK; HEPGNTKKKG; EPGNTKKKGL; PGNTKKKGLL; GNTKKKGLLT;
ESFTESFTAG; SFTESFTAGK; FTESFTAGKA; TESFTAGKAV; ESFTAGKAVV; SFTAGKAVVL;
FTAGKAVVLL; TAGKAVVLLF; AGKAVVLLFF; GKAVVLLFFP; KAVVLLFFPS; AVVLLFFPST;
VVLLFFPSTL; VLLFFPSTLS; LLFFPSTLSS; LFFPSTLSSP; FFPSTLSSPL; FPSTLSSPLQ;
PSTLSSPLQN; STLSSPLQNS; TLSSPLQNSS; LSSPLQNSSK; SSPLQNSSKS; SPLQNSSKSS;
PLQNSSKSSK; LQNSSKSSKI; QNSSKSSKIK; NSSKSSKIKI; SSKSSKIKIK; SKSSKIKIKI;
KSSKIKIKIL; ALFFVPVQVL; LFFVPVQVLP; FFVPVQVLPT; FVPVQVLPTF; VPVQVLPTFT;
PVQVLPTFTE; VQVLPTFTEA; QVLPTFTEAC; VLPTFTEACR; LPTFTEACRD; PTFTEACRDS;
TFTEACRDSW; FTEACRDSWR; TEACRDSWRR; EACRDSWRRT; ACRDSWRRTM; CRDSWRRTMA;
RDSWRRTMAF; DSWRRTMAFV; SWRRTMAFVQ; WRRTMAFVQF; RRTMAFVQFN; RTMAFVQFNW;
TMAFVQFNWG; MAFVQFNWGQ; AFVQFNWGQG; FVQFNWGQGQ; VQFNWGQGQD; QFNWGQGQDS;
ARKTCLSCTF; RKTCLSCTFL; KTCLSCTFLP; TCLSCTFLPE; CLSCTFLPEV; LSCTFLPEVM;

SCTFLPEVMV; CTFLPEVMVW; TFLPEVMVWL; FLPEVMVWLH; LPEVMVWLHS; PEVMVWLHSM; EVMVWLHSMG; VMVWLHSMGK; MVWLHSMGKQ; VWLHSMGKQL; WLHSMGKQLL; LHSMGKQLLP; HSMGKQLLPV; SMGKQLLPVS; MGKQLLPVSH; GKQLLPVSHA; KQLLPVSHAL; QLLPVSHALS; LLPVSHALSF; LPVSHALSFL; PVSHALSFLR; VSHALSFLRS; SHALSFLRSW; HALSFLRSWF; ALSFLRSWFG; LSFLRSWFGC; SFLRSWFGCI; FLRSWFGCIP; LRSWFGCIPL; AAPPCGLFFY; APPCGLFFYN; PPCGLFFYNI; EAEAASASTL; AEAASASTLS; EAASASTLSL; AASASTLSLK; GLAKLFGEIP; LAKLFGEIPI; AKLFGEIPIL; KLFGEIPILL; LFGEIPILLQ; FGEIPILLQF; GEIPILLQFL; EIPILLQFLQ

11 mers:

MDKVLNREESM; DKVLNREESME; KVLNREESMEL; VLNREESMELM; LNREESMELMD; NREESMELMDL; REESMELMDLL; EESMELMDLLG; ESMELMDLLGL; SMELMDLLGLE; MELMDLLGLER; ELMDLLGLERA; LMDLLGLERAA; MDLLGLERAAW; DLLGLERAAWG; LLGLERAAWGN; LGLERAAWGNL; GLERAAWGNLP; LERAAWGNLPL; ERAAWGNLPLM; RAAWGNLPLMR; AAWGNLPLMRK; AWGNLPLMRKA; WGNLPLMRKAY; GNLPLMRKAYL; NLPLMRKAYLR; LPLMRKAYLRK; PLMRKAYLRKC; LMRKAYLRKCK; MRKAYLRKCKE; RKAYLRKCKEF; KAYLRKCKEFH; AYLRKCKEFHP; YLRKCKEFHPD; LRKCKEFHPDK; RKCKEFHPDKG; KCKEFHPDKGG; CKEFHPDKGGD; KEFHPDKGGDE; EFHPDKGGDED; FHPDKGGDEDK; HPDKGGDEDKM; PDKGGDEDKMK; DKGGDEDKMKR; KGGDEDKMKRM; GGDEDKMKRMN; GDEDKMKRMNT; DEDKMKRMNTL; EDKMKRMNTLY; DKMKRMNTLYK; KMKRMNTLYKK; MKRMNTLYKKM; KRMNTLYKKME; RMNTLYKKMEQ; MNTLYKKMEQD; NTLYKKMEQDV; TLYKKMEQDVK; LYKKMEQDVKV; YKKMEQDVKVA; KKMEQDVKVAH; KMEQDVKVAHQ; MEQDVKVAHQP; EQDVKVAHQPD; QDVKVAHQPDF; DVKVAHQPDFG; VKVAHQPDFGT; KVAHQPDFGTW; VAHQPDFGTWS; AHQPDFGTWSS; HQPDFGTWSSS; QPDFGTWSSSE; PDFGTWSSSEV; DFGTWSSSEVC; FGTWSSSEVCA; GTWSSSEVCAD; TWSSSEVCADF; WSSSEVCADFP; SSSEVCADFPL; SSEVCADFPLC; SEVCADFPLCP; EVCADFPLCPD; VCADFPLCPDT; CADFPLCPDTL; ADFPLCPDTLY; DFPLCPDTLYC; FPLCPDTLYCK; PLCPDTLYCKE; LCPDTLYCKEW; CPDTLYCKEWP; PDTLYCKEWPI; DTLYCKEWPIC; TLYCKEWPICS; LYCKEWPICSK; YCKEWPICSKK; CKEWPICSKKP; KEWPICSKKPS; EWPICSKKPSV; WPICSKKPSVH; PICSKKPSVHC; ICSKKPSVHCP; CSKKPSVHCPC; SKKPSVHCPCM; KKPSVHCPCML; KPSVHCPCMLC; PSVHCPCMLCQ; SVHCPCMLCQL; VHCPCMLCQLR; HCPCMLCQLRL; CPCMLCQLRLR; PCMLCQLRLRH; CMLCQLRLRHL; MLCQLRLRHLN; LCQLRLRHLNR; CQLRLRHLNRK; QLRLRHLNRKF; LRLRHLNRKFL; RLRHLNRKFLR; LRHLNRKFLRK; RHLNRKFLRKE; HLNRKFLRKEP; LNRKFLRKEPL; NRKFLRKEPLV; RKFLRKEPLVW; KFLRKEPLVWI; FLRKEPLVWID; LRKEPLVWIDC; RKEPLVWIDCY; KEPLVWIDCYC; EPLVWIDCYCI; PLVWIDCYCID; LVWIDCYCIDC; VWIDCYCIDCF; WIDCYCIDCFT; IDCYCIDCFTQ; DCYCIDCFTQW; CYCIDCFTQWF; YCIDCFTQWFG; CIDCFTQWFGL; IDCFTQWFGLD; DCFTQWFGLDL; CFTQWFGLDLT; FTQWFGLDLTE; TQWFGLDLTEE; QWFGLDLTEET; WFGLDLTEETL; FGLDLTEETLQ; GLDLTEETLQW; LDLTEETLQWW; DLTEETLQWWV; LTEETLQWWVQ; TEETLQWWVQI; EETLQWWVQII; ETLQWWVQIIG; TLQWWVQIIGE; LQWWVQIIGET; QWWVQIIGETP; WWVQIIGETPF; WVQIIGETPFR; VQIIGETPFRD; QIIGETPFRDL; IIGETPFRDLK; IGETPFRDLKL; KALSNYFFYRC; ALSNYFFYRCQ; LSNYFFYRCQP; SNYFFYRCQPM; NYFFYRCQPME; YFFYRCQPMEQ; FFYRCQPMEQK; FYRCQPMEQKS; YRCQPMEQKSG; RCQPMEQKSGS; CQPMEQKSGSP; QPMEQKSGSPG; PMEQKSGSPGG; MEQKSGSPGGV; EQKSGSPGGVP; QKSGSPGGVPL; KSGSPGGVPLM; SGSPGGVPLMK; GSPGGVPLMKN; SPGGVPLMKNG; PGGVPLMKNGM; GGVPLMKNGMK; GVPLMKNGMKI; VPLMKNGMKIY; PLMKNGMKIYF; LMKNGMKIYFA; MKNGMKIYFAM; KNGMKIYFAMK; NGMKIYFAMKI; GMKIYFAMKIC; MKIYFAMKICL; KIYFAMKICLP; IYFAMKICLPV; YFAMKICLPVM; FAMKICLPVMK; AMKICLPVMKK; MKICLPVMKKQ; KICLPVMKKQQ; ICLPVMKKQQQ; CLPVMKKQQQI; LPVMKKQQQIL; PVMKKQQQILN; VMKKQQQILNT; MKKQQQILNTQ; KKQQQILNTQH; KQQQILNTQHH; QQQILNTQHHP; QQILNTQHHPK; QILNTQHHPKK; ILNTQHHPKKK; LNTQHHPKKKE; NTQHHPKKKER; KTLKTFPLIYT; TLKTFPLIYTS; LKTFPLIYTSF; KTFPLIYTSFL; TFPLIYTSFLV; FPLIYTSFLVK; PLIYTSFLVKL; LIYTSFLVKLY; IYTSFLVKLYL; YTSFLVKLYLV; TSFLVKLYLVI; SFLVKLYLVIE; FLVKLYLVIEP; LVKLYLVIEPL; VKLYLVIEPLP; KLYLVIEPLPA; LYLVIEPLPAL; YLVIEPLPALL; LVIEPLPALLC; VIEPLPALLCI; IEPLPALLCIL; EPLPALLCILL; PLPALLCILLK; LPALLCILLKK; PALLCILLKKK; ALLCILLKKKL; LLCILLKKKLK; LCILLKKKLKF; CILLKKKLKFC; ILLKKKLKFCI; LLKKKLKFCIK; LKKKLKFCIKN; KKKLKFCIKNL; KKLKFCIKNLW; KLKFCIKNLWK; LKFCIKNLWKN; KFCIKNLWKNI; FCIKNLWKNIL; LLLVDTCVLGI; LLVDTCVLGII; LVDTCVLGIIL; VDTCVLGIILY; DTCVLGIILYS; TCVLGIILYSF; LHIDIEFLQLI; HIDIEFLQLII; IDIEFLQLIIS; DIEFLQLIISV; IEFLQLIISVK; EFLQLIISVKS; FLQLIISVKSC; LQLIISVKSCV; QLIISVKSCVP; LIISVKSCVPL; IISVKSCVPLV; ISVKSCVPLVF; FVRVLIRNTYY; VRVLIRNTYYI; RVLIRNTYYIV; VLIRNTYYIVP; RSMILAQKSLK; SMILAQKSLKK; MILAQKSLKKQ; ILAQKSLKKQS; LAQKSLKKQSR; AQKSLKKQSRC; QKSLKKQSRCL; KSLKKQSRCLG; SLKKQSRCLGN; RSVKSVRKKTS; SVKSVRKKTSL; VKSVRKKTSLI; KSVRKKTSLIT; SVRKKTSLITL; VRKKTSLITLS; RKKTSLITLSI; KKTSLITLSIM; KTSLITLSIMK; TSLITLSIMKS; SLITLSIMKST; LITLSIMKSTL; ITLSIMKSTLQ; TLSIMKSTLQM; LSIMKSTLQML; SIMKSTLQMLL; IMKSTLQMLLF; MKSTLQMLLFL; KSTLQMLLFLQ; STLQMLLFLQK; TLQMLLFLQKV; LQMLLFLQKVK; QMLLFLQKVKI; MLLFLQKVKIK; LLFLQKVKIKK; LFLQKVKIKKV; FLQKVKIKKVF; LQKVKIKKVFV; QKVKIKKVFVS; KVKIKKVFVSK; VKIKKVFVSKQ; NNIWQVLLGCT; NIWQVLLGCTV; IWQVLLGCTVC; WQVLLGCTVCY; QVLLGCTVCYL; VLLGCTVCYLK; LLGCTVCYLKW; LGCTVCYLKWI; GCTVCYLKWIL; YLIFCTVLFSM; LIFCTVLFSMY; IFCTVLFSMYL; FCTVLFSMYLK; CTVLFSMYLKE; TVLFSMYLKED; VLFSMYLKEDT; LFSMYLKEDTG; FSMYLKEDTGY; SMYLKEDTGYL; MYLKEDTGYLK; YLKEDTGYLKV; LKEDTGYLKVP;

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FLGVIVPSGYF; LGVIVPSGYFD; GVIVPSGYFDL; FISTPCISKGS; ISTPCISKGSP; STPCISKGSPP;
TPCISKGSPPT; PCISKGSPPTA; CISKGSPPTAK; ISKGSPPTAKK; SKGSPPTAKKW; KGSPPTAKKWK;
GSPPTAKKWKL; SPPTAKKWKLL; PPTAKKWKLLP; IGFPPPCSCTF; GFPPPCSCTFC; FPPPCSCTFCD;
PPPCSCTFCDP; PPCSCTFCDPA; RLSMLVIPITS; LSMLVIPITSV; SMLVIPITSVC; MLVIPITSVCT;
LVIPITSVCTV; VIPITSVCTVT; IPITSVCTVTA; PITSVCTVTAS; ITSVCTVTASH; TSVCTVTASHI;
SVCTVTASHIS; VCTVTASHISR; CTVTASHISRF; TVTASHISRFP; VTASHISRFPQ; TASHISRFPQV;
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TSVIASTPVLT; SVIASTPVLTS; VIASTPVLTSR; IASTPVLTSRT; ASTPVLTSRTS; STPVLTSRTST;
TPVLTSRTSTP; PVLTSRTSTPP; VLTSRTSTPPF; LTSRTSTPPFI; TSRTSTPPFIS; SRTSTPPFISS;
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FISSFGTCTGS; ISSFGTCTGSF; SSFGTCTGSFG; SFGTCTGSFGF; FGTCTGSFGFL; GTCTGSFGFLG;
TCTGSFGFLGA; CTGSFGFLGAA; TGSFGFLGAAP; GSFGFLGAAPG; SFGFLGAAPGH; FGFLGAAPGHS;

GFLGAAPGHSP; FLGAAPGHSPF; LGAAPGHSPFL; GAAPGHSPFLL; AAPGHSPFLLV; APGHSPFLLVG; PGHSPFLLVGA; GHSPFLLVGAI; HSPFLLVGAIF; SPFLLVGAIFI; PFLLVGAIFIC; FLLVGAIFICF; LLVGAIFICFK; LVGAIFICFKS; VGAIFICFKSR; GAIFICFKSRC; AIFICFKSRCY; IFICFKSRCYS; FICFKSRCYSP; ICFKSRCYSPV; CFKSRCYSPVQ; FKSRCYSPVQA; RQHPLRSSSLI; QHPLRSSSLIS; HPLRSSSLIST; PLRSSSLISTS; LRSSSLISTSW; RSSSLISTSWG; SSSLISTSWGN; SSLISTSWGNS; SLISTSWGNSF; LISTSWGNSFF; ISTSWGNSFFY; STSWGNSFFYK; TSWGNSFFYKL; SWGNSFFYKLS; VHSLCNFFYTV; HSLCNFFYTVS; SLCNFFYTVSI; LCNFFYTVSII; CNFFYTVSIIY; NFFYTVSIIYT; FFYTVSIIYTI; FYTVSIIYTIS; YTVSIIYTISM; TVSIIYTISMA; VSIIYTISMAK; SIIYTISMAKM; IIYTISMAKMY; IYTISMAKMYT; YTISMAKMYTG; TISMAKMYTGT; ISMAKMYTGTF; SMAKMYTGTFP; MAKMYTGTFPF; AKMYTGTFPFS; KMYTGTFPFSY; MYTGTFPFSYL; YTGTFPFSYLS; TGTFPFSYLSN; GTFPFSYLSNH; GPNRGKIRIIL; PNRGKIRIILL; NRGKIRIILLN; RGKIRIILLNI; GKIRIILLNII; KIRIILLNIII; IRIILLNIIIK; RIILLNIIIKV; IILLNIIIKVY; ILLNIIIKVYR; LLNIIIKVYRG; LNIIIKVYRGI; NIIIKVYRGIY; IIIKVYRGIYN; IIKVYRGIYNC; IKVYRGIYNCP; KVYRGIYNCPG; VYRGIYNCPGS; YRGIYNCPGSF; RGIYNCPGSFL; GIYNCPGSFLQ; IYNCPGSFLQK; YNCPGSFLQKS; NCPGSFLQKSS; CPGSFLQKSSQ; PGSFLQKSSQG; GSFLQKSSQGV; SFLQKSSQGVS; FLQKSSQGVSK; LQKSSQGVSKK; QKSSQGVSKKS; KSSQGVSKKSF; SSQGVSKKSFC; SQGVSKKSFCS; QGVSKKSFCSS; GVSKKSFCSSL; VSKKSFCSSLQ; SKKSFCSSLQF; KKSFCSSLQFL; GYRRYIIPNNM; YRRYIIPNNMP; RRYIIPNNMPQ; RYIIPNNMPQS; YIIPNNMPQSL; IIPNNMPQSLG; IPNNMPQSLGN; PNNMPQSLGNS; NNMPQSLGNSS; NMPQSLGNSSK; MPQSLGNSSKQ; PQSLGNSSKQR; QSLGNSSKQRR; SLGNSSKQRRT; LGNSSKQRRTP; GNSSKQRRTPM; NSSKQRRTPMP; SSKQRRTPMPR; SKQRRTPMPRI; KQRRTPMPRIK; QRRTPMPRIKV; RRTPMPRIKVL; RTPMPRIKVLN; TPMPRIKVLNI; PMPRIKVLNII; MPRIKVLNIIN; PRIKVLNIINK; RIKVLNIINKS; IKVLNIINKSI; KVLNIINKSIY; VLNIINKSIYT; LNIINKSIYTR; NIINKSIYTRK; IINKSIYTRKQ; INKSIYTRKQN; NKSIYTRKQNI; KSIYTRKQNII; SIYTRKQNIIV; IYTRKQNIIVL; YTRKQNIIVLI; TRKQNIIVLIW; RKQNIIVLIWV; KQNIIVLIWVK; QNIIVLIWVKQ; NIIVLIWVKQF; IIVLIWVKQFQ; IVLIWVKQFQS; VLIWVKQFQSH; LIWVKQFQSHA; LLIEAYSGNFV; LIEAYSGNFVI; IEAYSGNFVIP; EAYSGNFVIPI; AYSGNFVIPII; YSGNFVIPIIK; SGNFVIPIIKE; GNFVIPIIKEL; NFVIPIIKELI; FVIPIIKELIP; VIPIIKELIPY; IPIIKELIPYL; PIIKELIPYLS; SSKPSNSPRST; SKPSNSPRSTS; KPSNSPRSTSN; PSNSPRSTSNY; SNSPRSTSNYS; NSPRSTSNYSI; SPRSTSNYSIC; PRSTSNYSICL; RSTSNYSICLR; STSNYSICLRS; GTCYALYSSKG; TCYALYSSKGC; CYALYSSKGCN; YALYSSKGCNL; ALYSSKGCNLN; LYSSKGCNLNF; YSSKGCNLNFY; SSKGCNLNFYS; SKGCNLNFYSS; KGCNLNFYSSS; GCNLNFYSSSS; CNLNFYSSSSL; NLNFYSSSSLP; LNFYSSSSLPS; NFYSSSSLPSS; FYSSSSLPSSN; YSSSSLPSSNF; SSSSLPSSNFS; SSSLPSSNFSH; KSCGSSSLRYT; SCGSSSLRYTG; CGSSSLRYTGN; SSTHEPGNTKK; STHEPGNTKKK; THEPGNTKKKG; HEPGNTKKKGL; EPGNTKKKGLL; PGNTKKKGLLT; ESFTESFTAGK; SFTESFTAGKA; FTESFTAGKAV; TESFTAGKAVV; ESFTAGKAVVL; SFTAGKAVVLL; FTAGKAVVLLF; TAGKAVVLLFF; AGKAVVLLFFP; GKAVVLLFFPS; KAVVLLFFPST; AVVLLFFPSTL; VVLLFFPSTLS; VLLFFPSTLSS; LLFFPSTLSSP; LFFPSTLSSPL; FFPSTLSSPLQ; FPSTLSSPLQN; PSTLSSPLQNS; STLSSPLQNSS; TLSSPLQNSSK; LSSPLQNSSKS; SSPLQNSSKSS; SPLQNSSKSSK; PLQNSSKSSKI; LQNSSKSSKIK; QNSSKSSKIKI; NSSKSSKIKIK; SSKSSKIKIKI; SKSSKIKIKIL; ALFFVPVQVLP; LFFVPVQVLPT; FFVPVQVLPTF; FVPVQVLPTFT; VPVQVLPTFTE; PVQVLPTFTEA; VQVLPTFTEAC; QVLPTFTEACR; VLPTFTEACRD; LPTFTEACRDS; PTFTEACRDSW; TFTEACRDSWR; FTEACRDSWRR; TEACRDSWRRT; EACRDSWRRTM; ACRDSWRRTMA; CRDSWRRTMAF; RDSWRRTMAFV; DSWRRTMAFVQ; SWRRTMAFVQF; WRRTMAFVQFN; RRTMAFVQFNW; RTMAFVQFNWG; TMAFVQFNWGQ; MAFVQFNWGQG; AFVQFNWGQGQ; FVQFNWGQGQD; VQFNWGQGQDS; ARKTCLSCTFL; RKTCLSCTFLP; KTCLSCTFLPE; TCLSCTFLPEV; CLSCTFLPEVM; LSCTFLPEVMV; SCTFLPEVMVW; CTFLPEVMVWL; TFLPEVMVWLH; FLPEVMVWLHS; LPEVMVWLHSM; PEVMVWLHSMG; EVMVWLHSMGK; VMVWLHSMGKQ; MVWLHSMGKQL; VWLHSMGKQLL; WLHSMGKQLLP; LHSMGKQLLPV; HSMGKQLLPVS; SMGKQLLPVSH; MGKQLLPVSHA; GKQLLPVSHAL; KQLLPVSHALS; QLLPVSHALSF; LLPVSHALSFL; LPVSHALSFLR; PVSHALSFLRS; VSHALSFLRSW; SHALSFLRSWF; HALSFLRSWFG; ALSFLRSWFGC; LSFLRSWFGCI; SFLRSWFGCIP; FLRSWFGCIPL; AAPPCGLFFYN; APPCGLFFYNI; EAEAASASTLS; AEAASASTLSL; EAASASTLSLK; GLAKLFGEIPI; LAKLFGEIPIL; AKLFGEIPILL; KLFGEIPILLQ; LFGEIPILLQF; FGEIPILLQFL; GEIPILLQFLQ

BK virus complementary reading frame 2

8 mers:

WIKFLTGK; IKFLTGKN; KFLTGKNP; FLTGKNPW; LTGKNPWS; TGKNPWSS; GKNPWSSW; KNPWSSWT; NPWSSWTF; ALKELPGE; LKELPGEI; KELPGEIF; ELPGEIFP; GSVRNFTL; SVRNFTLT; VRNFTLTK; RNFTLTKG; NFTLTKGA; FTLTKGAT; TLTKGATR; LTKGATRI; TKGATRIK; ILCIKKWS; LCIKKWSR; CIKKWSRM; LISLILEP; ISLILEPG; SLILEPGV; LILEPGVA; ILEPGVAQ; LEPGVAQR; EPGVAQRF; PGVAQRFV; GVAQRFVL; VAQRFVLI; AQRFVLIF; QRFVLIFL; RFVLIFLF; FVLIFLFA; VLIFLFAQ; LIFLFAQI; IFLFAQIP; FLFAQIPC; LFAQIPCT; FAQIPCTA; AQIPCTAR; QIPCTARN; IPCTARNG; PCTARNGL; CTARNGLF; TARNGLFV; ARNGLFVP; RNGLFVPK; NGLFVPKS; GLFVPKSL; LFVPKSLL; FVPKSLLC; VPKSLLCT; PKSLLCTA; KSLLCTAL; SLLCTALA; LLCTALAC; LCTALACY; CTALACYV; TALACYVS; ALACYVSL; LACYVSLD; IATALTAS; ATALTASH; TALTASHS; ALTASHSG; LTASHSGL; TASHSGLA; LKKLCNGG; KKLCNGGS; KLCNGGSK; LEKLPSEI;

SFKVTNLY; FKVTNLYL; KVTNLYLD; VTNLYLDK; VIIFFIGA; IIFFIGAN; IFFIGANL;
FFIGANLW; FIGANLWN; IGANLWNR; GANLWNRR; ANLWNRRV; NLWNRRVG; LWNRRVGV;
WNRRVGVL; NRRVGVLV; RRVGVLVE; RVGVLVEF; VGVLVEFL; RSNSRFST; SNSRFSTL;
NSRFSTLN; SRFSTLNT; RFSTLNTT; FSTLNTTQ; STLNTTQK; TLNTTQKK; LNTTQKKK;
NTTQKKKK; TTQKKKKG; TQKKKKGR; QKKKKGRR; KKKKGRRP; NPCLLCCV; PCLLCCVY;
CLLCCVYY; KTYGKIFC; TYGKIFCN; YGKIFCNF; GKIFCNFY; YYILFNST; FLSKAVYL;
RSIPYYRR; SIPYYRRK; IPYYRRKH; PYYRRKHS; YYRRKHSR; YRRKHSRG; RRKHSRGL;
RKHSRGLK; KHSRGLKG; HSRGLKGA; RNKAGVLE; NKAGVLEI; KAGVLEIN; AGVLEINY;
GCVFIIRY; CVFIIRYV; VFIIRYVF; FIIRYVFR; IIRYVFRI; IRYVFRIS; RYVFRISI;
YVFRISIQ; VFRISIQC; FRISIQCR; RISIQCRG; ISIQCRGV; KVSEKRPA; VSEKRPAL;
SEKRPALS; EKRPALSL; KALCKCYY; ALCKCYYF; LCKCYYFC; CKCYYFCR; KCYYFCRK;
KSKKYLSA; SKKYLSAS; KKYLSASS; KYLSASSR; YLSASSRY; LSASSRYS; SASSRYSF;
ASSRYSFS; KKSRYPSY; KSRYPSYD; SRYPSYDQ; RYPSYDQG; YPSYDQGR; PSYDQGRN;
SYDQGRNA; YDQGRNAN; DQGRNANR; QGRNANRK; GRNANRKI; RNANRKIQ; NANRKIQS;
ANRKIQSY; NRKIQSYI; RKIQSYIR; NGFNIWSS; GFNIWSSW; FNIWSSWK; NIWSSWKC;
IWSSWKCC; WSSWKCCT; SSWKCCTR; SWKCCTRT; WKCCTRTI; KCCTRTIY; CCTRTIYG;
CTRTIYGR; TRTIYGRC; RTIYGRCC; TIYGRCCL; IYGRCCLA; YGRCCLAA; GRCCLAAL;
RCCLAALF; CCLAALFA; CLAALFAT; FFALYCFQ; FALYCFQC; ALYCFQCT; WKNNTSCR;
KNNTSCRV; NNTSCRVI; NTSCRVIR; TSCRVIRF; SCRVIRFV; CRVIRFVW; RVIRFVWW;
SLKCKPTH; LKCKPTHG; KCKPTHGK; CKPTHGKA; KPTHGKAN; PTHGKANL; ARCSYRSV;
RCSYRSVH; CSYRSVHG; SYRSVHGC; YRSVHGCF; IKGFAFRT; KGFAFRTW; GFAFRTWN;
FAFRTWNK; AFRTWNKQ; FRTWNKQF; RTWNKQFR; TWNKQFRQ; WNKQFRQF; NKQFRQFE;
KQFRQFER; QFRQFERL; FRQFERLF; RQFERLFR; QFERLFRW; FERLFRWK; ERLFRWKC;
GKFRKETF; KFRKETFK; FRKETFKQ; RKETFKQK; KETFKQKN; ETFKQKNP; TFKQKNPN;
FKQKNPNI; KQKNPNIS; QKNPNIST; KNPNISTR; NPNISTRL; PNISTRLG; NISTRLGY;
ISTRLGYN; STRLGYNE; AQNIFKKI; QNIFKKIL; NIFKKILT; IFKKILTK; FKKILTKL;
KKILTKLR; KILTKLRV; ILTKLRVL; LTKLRVLT; KKNFTKWN; KNFTKWND; NFTKWNDL;
FTKWNDLV; TKWNDLVA; KWNDLVAT; WNDLVATA; NDLVATAN; DLVATANL; LVATANLV;
DKYVYFFK; KYVYFFKD; YVYFFKDE; VYFFKDEI; YMHGEMYS; YYKRRGFR; YKRRGFRN;
RLWTWIKH; IPITMLFP; PITMLFPS; ITMLFPSL; TMLFPSLR; MLFPSLRY; LFPSLRYF;
FPSLRYFS; PSLRYFSP; SLRYFSPC; RFPKVRPP; NTTPKITQ; TTPKITQA; KWLIQKQH;
WLIQKQHL; LIQKQHLL; IQKQHLLN; QKQHLLNV; KQHLLNVY; QHLLNVYV; HLLNVYVQ;
KHLFKAFW; HLFKAFWF; LFKAFWFA; FKAFWFAI; KAFWFAIV; AFWFAIVP; FWFAIVPV;
WFAIVPVC; FAIVPVCQ; AIVPVCQY; IVPVCQYI; VPVCQYIL; PVCQYILS; VCQYILSY;
CQYILSYL; QYILSYLG; YILSYLGP; ILSYLGPL; LSYLGPLE; SYLGPLEV; YLGPLEVF;
LGPLEVFL; GPLEVFLC; PLEVFLCH; LEVFLCHQ; EVFLCHQT; VFLCHQTP; PLLPGIPY;
LLPGIPYH; LPGIPYHT; AAHPLSGF; AHPLSGFS; HPLSGFSC; PLSGFSCL; GHLAKRKL;
HLAKRKLG; LAKRKLGK; AKRKLGKD; KRKLGKDS; RKLGKDSL; KLGKDSLQ; LGKDSLQI;
GKDSLQIF; KDSLQIFF; DSLQIFFS; SLQIFFSG; LQIFFSGG; QIFFSGGS; NILQGLST;
ILQGLSTV; LQGLSTVV; QGLSTVVF; GLSTVVFQ; LSTVVFQS; STVVFQSC; TGHKYQQL;
GHKYQQLK; HKYQQLKH; KYQQLKHT; YQQLKHTG; QQLKHTGY; QLKHTGYQ; LKHTGYQL;
KHTGYQLY; HTGYQLYK; TGYQLYKE; GYQLYKEA; YQLYKEAP; QLYKEAPH; LYKEAPHP;
YKEAPHPV; KEAPHPVH; EAPHPVHL; APHPVHLA; PHPVHLAT; HPVHLATL; PVHLATLW;
LCWSHEVL; CWSHEVLG; WSHEVLGE; SHEVLGEH; HEVLGEHF; EVLGEHFP; VLGEHFPL;
LGEHFPLL; HFHFYWDQ; FHFYWDQV; HFYWDQVP; FYWDQVPS; YWDQVPST; WDQVPSTQ;
DQVPSTQL; QVPSTQLD; VPSTQLDK; PSTQLDKH; STQLDKHC; TQLDKHCF; QLDKHCFC;
LDKHCFCP; DKHCFCPN; KHCFCPNR; HCFCPNRP; CFCPNRPY; FCPNRPYG; CPNRPYGQ;
PNRPYGQY; NRPYGQYS; RPYGQYSL; PYGQYSLP; YGQYSLPG; GQYSLPGT; QYSLPGTG;
YSLPGTGL; SLPGTGLL; LPGTGLLG; PGTGLLGF; YHQGTLTC; HQGTLTCN; QGTLTCNS;
GTLTCNSL; TLTCNSLA; LTCNSLAL; TCNSLALP; CNSLALPA; NSLALPAF; SLALPAFP;
LALPAFPR; ALPAFPRV; LPAFPRVL; PAFPRVLH; AFPRVLHL; FPRVLHLQ; PRVLHLQQ;
RVLHLQQR; VLHLQQRS; LHLQQRSG; HLQQRSGN; LQQRSGNY; QQRSGNYC; QRSGNYCL;
RSGNYCLE; VFLHHAHA; FLHHAHAL; LHHAHALF; HHAHALFV; HAHALFVT; AHALFVTL;
HALFVTLH; ALFVTLHE; LFVTLHEG; PLFVQLQP; LFVQLQPP; FVQLQPPT; VQLQPPTS;
QLQPPTSV; LQPPTSVD; QPPTSVDF; PPTSVDFH; PTSVDFHR; TSVDFHRL; SVDFHRLG;
VDFHRLGP; DFHRLGPH; FHRLGPHL; HRLGPHLN; RLGPHLNW; LGPHLNWG; GPHLNWGG;
PHLNWGGE; HLNWGGEF; LNWGGEFL; NWGGEFLL; WGGEFLLC; GGEFLLCC; GEFLLCCN;
EFLLCCNR; FLLCCNRE; LLCCNREA; LCCNREAF; CCNREAFF; CNREAFFS; NREAFFSL;
REAFFSLG; EAFFSLGY; AFFSLGYH; FFSLGYHC; SHFQHLAL; HFQHLALD; GFHLDPPF;
FHLDPPFL; HLDPPFLG; LDPPFLGL; DPPFLGLG; PPFLGLGS; PFLGLGSI; FLGLGSIL;
LGLGSILP; GLGSILPL; LLELLLLL; LELLLLLL; ELLLLLLL; LLLLLLLV; LLLLLLVV;
LLLLLVVL; LLLLVVLA; LLLVVLAL; LLVVLALA; LVVLALAR; VVLALARV; VLALARVP;
LALARVPL; ALARVPLA; LARVPLAF; ARVPLAFW; RVPLAFWE; VPLAFWEL; PLAFWELP;
LAFWELPL; AFWELPLD; FWELPLDT; WELPLDTL; ELPLDTLL; LPLDTLLF; PLDTLLFF;
LDTLLFFW; DTLLFFWL; TLLFFWLG; LLFFWLGP; LFFWLGPS; FFWLGPSS; FWLGPSSY;

WLGPSSYA; LGPSSYAS; GPSSYASR; PSSYASRA; SSYASRAG; SYASRAGV; YASRAGVT;
ASRAGVTV; SRAGVTVP; RAGVTVPY; AGVTVPYR; GVTVPYRP; VTVPYRPR; TVPYRPRS;
VPYRPRSK; PYRPRSKG; YRPRSKGN; RPRSKGNI; PRSKGNIH; LAPPGAIV; APPGAIVF;
PPGAIVFS; PGAIVFSI; GAIVFSIN; AIVFSINS; IVFSINSP; VFSINSPE; FSINSPEC;
SINSPECT; INSPECTL; NSPECTLC; FLKSILCV; LKSILCVT; KSILCVTS; SILCVTSS;
ILCVTSSI; LCVTSSIL; CVTSSILS; VTSSILSA; TSSILSAS; SSILSASS; SILSASSI;
ILSASSIL; VWPKCTRV; WPKCTRVP; PKCTRVPS; KCTRVPSL; CTRVPSLS; TRVPSLSA;
RVPSLSAT; VPSLSATC; PSLSATCL; SLSATCLT; LSATCLTI; SATCLTIE; ATCLTIEG;
TCLTIEGL; CLTIEGLI; LTIEGLIG; TIEGLIGE; IEGLIGER; EGLIGERS; GLIGERSE;
KFIGAFTI; FIGAFTIV; IGAFTIVQ; GAFTIVQV; AFTIVQVV; FTIVQVVS; TIVQVVSS;
IVQVVSSK; VQVVSSKN; QVVSSKNL; VVSSKNLA; VSSKNLAK; SSKNLAKE; SKNLAKES;
KNLAKESL; NLAKESLK; LAKESLKN; AKESLKNL; KESLKNLS; ESLKNLSV; SLKNLSVL;
LKNLSVLL; KNLSVLLC; NLSVLLCN; LSVLLCNS; SVLLCNSC; VLLCNSCE; LLCNSCEV;
LCNSCEVI; CNSCEVIE; NSCEVIEG; SCEVIEGI; CEVIEGIS; EVIEGISS; VIEGISSL;
IEGISSLI; EGISSLIT; GISSLITC; ISSLITCH; SSLITCHK; SLITCHKA; LITCHKAW;
ITCHKAWE; TCHKAWEI; CHKAWEIV; HKAWEIVA; KAWEIVAN; AWEIVANK; WEIVANKE;
EIVANKEG; IVANKEGP; VANKEGPQ; ANKEGPQC; NKEGPQCL; KEGPQCLG; EGPQCLGS;
GPQCLGSR; PQCLGSRY; ILLTKVFT; LLTKVFTP; LTKVFTPG; TKVFTPGN; KVFTPGNR;
VFTPGNRI; FTPGNRIS; YSSGLNNS; SSGLNNSK; SGLNNSKA; GLNNSKAM; LNNSKAMP;
NNSKAMPD; NSKAMPDC; SQSSKNLY; QSSKNLYP; SSKNLYPT; AKELIPLT; KELIPLTV;
IKAANPAI; KAANPAIA; AANPAIAP; ANPAIAPG; NPAIAPGA; PAIAPGAP; AIAPGAPA;
IAPGAPAI; APGAPAIT; PGAPAITA; GAPAITAY; APAITAYV; GVRPIAAI; VRPIAAIA;
RPIAAIAS; PIAAIASE; IAAIASEV; AAIASEVL; AIASEVLV; IASEVLVM; ASEVLVMP;
SEVLVMPS; EVLVMPST; VLVMPSTV; LVMPSTVA; VMPSTVAR; MPSTVARD; PSTVARDA;
STVARDAI; TSIAAAAS; SIAAAASP; IAAAASPA; AAAASPAA; AAASPAAI; AASPAAIS;
ASPAAISA; SPAAISAT; PAAISATE; AAISATEN; AISATENP; ISATENPV; SATENPVA;
ATENPVAA; TENPVAAA; ENPVAAAA; NPVAAAAS; PVAAAASD; VAAAASDT; AAAASDTL;
AAASDTLA; AASDTLAT; ASDTLATR; SDTLATRS; DTLATRSP; TLATRSPK; LATRSPKS;
ATRSPKSA; TRSPKSAR; RSPKSARA; SPKSARAA; PKSARAAP; KSARAAPM; SARAAPMN;
ARAAPMNL; RAAPMNLE; AAPMNLEI; APMNLEIQ; PMNLEIQK; MNLEIQKK; NLEIQKKR;
LEIQKKRD; EIQKKRDY; IQKKRDYL; QKKRDYLP; KKRDYLPR; KRDYLPRS; RDYLPRSL;
DYLPRSLL; YLPRSLLQ; LPRSLLQS; PRSLLQSL; RSLLQSLL; SLLQSLLQ; LLQSLLQQ;
LQSLLQQV; QSLLQQVK; SLLQQVKQ; LLQQVKQW; LQQVKQWY; QQVKQWYF; QVKQWYFC;
VKQWYFCF; KQWYFCFS; QWYFCFSR; WYFCFSRL; YFCFSRLH; FCFSRLHC; CFSRLHCL;
FSRLHCLH; SRLHCLHL; RLHCLHLY; LHCLHLYK; HCLHLYKI; CLHLYKIP; LHLYKIPA;
HLYKIPAK; LYKIPAKA; YKIPAKAL; KIPAKALK; KSSELFFL; SSELFFLF; SELFFLFQ;
ELFFLFQS; LFFLFQSR; FFLFQSRF; FLFQSRFY; LFQSRFYQ; FQSRFYQL; QSRFYQLS;
SRFYQLSL; RFYQLSLK; FYQLSLKL; YQLSLKLV; QLSLKLVV; LSLKLVVT; SLKLVVTA;
LKLVVTAG; KLVVTAGA; LVVTAGAE; VVTAGAEP; VTAGAEPW; TAGAEPWP; AGAEPWPL;
GAEPWPLS; AEPWPLSS; EPWPLSSL; PWPLSSLT; WPLSSLTG; PLSSLTGD; LSSLTGDK;
SSLTGDKA; SLTGDKAK; LTGDKAKI; TGDKAKIP; GDKAKIPR; DKAKIPRL; KAKIPRLA;
AKIPRLAK; KIPRLAKH; IPRLAKHV; PRLAKHVC; RLAKHVCH; LAKHVCHA; AKHVCHAL;
KHVCHALS; HVCHALSF; VCHALSFL; CHALSFLR; HALSFLRS; ALSFLRSW; LSFLRSWF;
SFLRSWFG; FLRSWFGC; LRSWFGCI; RSWFGCIP; SWFGCIPW; WFGCIPWV; FGCIPWVS;
GCIPWVSS; CIPWVSSS; IPWVSSSS; PWVSSSSL; GHGLAAFP; HGLAAFPC; GLAAFPCE;
LAAFPCES; AAFPCESC; AFPCESCT; FPCESCTF; PCESCTFL; CESCTFLP; ESCTFLPE;
SCTFLPEV; CTFLPEVM; TFLPEVMV; FLPEVMVW; LPEVMVWL; PEVMVWLH; EVMVWLHS;
VMVWLHSM; MVWLHSMG; VWLHSMGK; WLHSMGKQ; LHSMGKQL; HSMGKQLL; SMGKQLLP;
MGKQLLPV; GKQLLPVA; KQLLPVAF; QLLPVAFF; LLPVAFFF; LPVAFFFI; PVAFFFII;
VAFFFIIY; AFFFIIYK; FFFIIYKR; FFIIYKRP; FIIYKRPR; IIYKRPRP; IYKRPRPP;
YKRPRPPL; KRPRPPLP; RPRPPLPP; PRPPLPPP; RPPLPPPF; PPLPPPFL; PLPPPFLS;
LPPPFLSS; PPPFLSSS; PPFLSSSK; PFLSSSKG; FLSSSKGV; LSSSKGVE; SSSKGVEA;
SSKGVEAF; SKGVEAFS; KGVEAFSE; GVEAFSEA; QNYLGKSL; NYLGKSLF; YLGKSLFF;
LGKSLFFC; GKSLFFCN; KSLFFCNF; SLFFCNFC; LFFCNFCK

9 mers:
WIKFLTGKN; IKFLTGKNP; KFLTGKNPW; FLTGKNPWS; LTGKNPWSS; TGKNPWSSW; GKNPWSSWT;
KNPWSSWTF; ALKELPGEI; LKELPGEIF; KELPGEIFP; GSVRNFTLT; SVRNFTLTK; VRNFTLTKG;
RNFTLTKGA; NFTLTKGAT; FTLTKGATR; TLTKGATRI; LTKGATRIK; ILCIKKWSR; LCIKKWSRM;
LISLILEPG; ISLILEPGV; SLILEPGVA; LILEPGVAQ; ILEPGVAQR; LEPGVAQRF; EPGVAQRFV;
PGVAQRFVL; GVAQRFVLI; VAQRFVLIF; AQRFVLIFL; QRFVLIFLF; RFVLIFLFA; FVLIFLFAQ;
VLIFLFAQI; LIFLFAQIP; IFLFAQIPC; FLFAQIPCT; LFAQIPCTA; FAQIPCTAR; AQIPCTARN;
QIPCTARNG; IPCTARNGL; PCTARNGLF; CTARNGLFV; TARNGLFVP; ARNGLFVPK; RNGLFVPKS;
NGLFVPKSL; GLFVPKSLL; LFVPKSLLC; FVPKSLLCT; VPKSLLCTA; PKSLLCTAL; KSLLCTALA;
SLLCTALAC; LLCTALACY; LCTALACYV; CTALACYVS; TALACYVSL; ALACYVSLD; IATALTASH;
ATALTASHS; TALTASHSG; ALTASHSGL; LTASHSGLA; LKKLCNGGS; KKLCNGGSK; SFKVTNLYL;

FKVTNLYLD; KVTNLYLDK; VIIFFIGAN; IIFFIGANL; IFFIGANLW; FFIGANLWN; FIGANLWNR;
IGANLWNRR; GANLWNRRV; ANLWNRRVG; NLWNRRVGV; LWNRRVGVL; WNRRVGVLV; NRRVGVLVE;
RRVGVLVEF; RVGVLVEFL; RSNSRFSTL; SNSRFSTLN; NSRFSTLNT; SRFSTLNTT; RFSTLNTTQ;
FSTLNTTQK; STLNTTQKK; TLNTTQKKK; LNTTQKKKK; NTTQKKKKG; TTQKKKKGR; TQKKKKGRR;
QKKKKGRRP; NPCLLCCVY; PCLLCCVYY; KTYGKIFCN; TYGKIFCNF; YGKIFCNFY; RSIPYYRRK;
SIPYYRRKH; IPYYRRKHS; PYYRRKHSR; YYRRKHSRG; YRRKHSRGL; RRKHSRGLK; RKHSRGLKG;
KHSRGLKGA; RNKAGVLEI; NKAGVLEIN; KAGVLEINY; GCVFIIRYV; CVFIIRYVF; VFIIRYVFR;
FIIRYVFRI; IIRYVFRIS; IRYVFRISI; RYVFRISIQ; YVFRISIQC; VFRISIQCR; FRISIQCRG;
RISIQCRGV; KVSEKRPAL; VSEKRPALS; SEKRPALSL; KALCKCYYF; ALCKCYYFC; LCKCYYFCR;
CKCYYFCRK; KSKKYLSAS; SKKYLSASS; KKYLSASSR; KYLSASSRY; YLSASSRYS; LSASSRYSF;
SASSRYSFS; KKSRYPSYD; KSRYPSYDQ; SRYPSYDQG; RYPSYDQGR; YPSYDQGRN; PSYDQGRNA;
SYDQGRNAN; YDQGRNANR; DQGRNANRK; QGRNANRKI; GRNANRKIQ; RNANRKIQS; NANRKIQSY;
ANRKIQSYI; NRKIQSYIR; NGFNIWSSW; GFNIWSSWK; FNIWSSWKC; NIWSSWKCC; IWSSWKCCT;
WSSWKCCTR; SSWKCCTRT; SWKCCTRTI; WKCCTRTIY; KCCTRTIYG; CCTRTIYGR; CTRTIYGRC;
TRTIYGRCC; RTIYGRCCL; TIYGRCCLA; IYGRCCLAA; YGRCCLAAL; GRCCLAALF; RCCLAALFA;
CCLAALFAT; FFALYCFQC; FALYCFQCT; WKNNTSCRV; KNNTSCRVI; NNTSCRVIR; NTSCRVIRF;
TSCRVIRFV; SCRVIRFVW; CRVIRFVWW; SLKCKPTHG; LKCKPTHGK; KCKPTHGKA; CKPTHGKAN;
KPTHGKANL; ARCSYRSVH; RCSYRSVHG; CSYRSVHGC; SYRSVHGCF; IKGFAFRTW; KGFAFRTWN;
GFAFRTWNK; FAFRTWNKQ; AFRTWNKQF; FRTWNKQFR; RTWNKQFRQ; TWNKQFRQF; WNKQFRQFE;
NKQFRQFER; KQFRQFERL; QFRQFERLF; FRQFERLFR; RQFERLFRW; QFERLFRWK; FERLFRWKC;
GKFRKETFK; KFRKETFKQ; FRKETFKQK; RKETFKQKN; KETFKQKNP; ETFKQKNPN; TFKQKNPNI;
FKQKNPNIS; KQKNPNIST; QKNPNISTR; KNPNISTRL; NPNISTRLG; PNISTRLGY; NISTRLGYN;
ISTRLGYNE; AQNIFKKIL; QNIFKKILT; NIFKKILTK; IFKKILTKL; FKKILTKLR; KKILTKLRV;
KILTKLRVL; ILTKLRVLT; KKNFTKWND; KNFTKWNDL; NFTKWNDLV; FTKWNDLVA; TKWNDLVAT;
KWNDLVATA; WNDLVATAN; NDLVATANL; DLVATANLV; DKYVYFFKD; KYVYFFKDE; YVYFFKDEI;
YYKRRGFRN; IPITMLFPS; PITMLFPSL; ITMLFPSLR; TMLFPSLRY; MLFPSLRYF; LFPSLRYFS;
FPSLRYFSP; PSLRYFSPC; NTTPKITQA; KWLIQKQHL; WLIQKQHLL; LIQKQHLLN; IQKQHLLNV;
QKQHLLNVY; KQHLLNVYV; QHLLNVYVQ; KHLFKAFWF; HLFKAFWFA; LFKAFWFAI; FKAFWFAIV;
KAFWFAIVP; AFWFAIVPV; FWFAIVPVC; WFAIVPVCQ; FAIVPVCQY; AIVPVCQYI; IVPVCQYIL;
VPVCQYILS; PVCQYILSY; VCQYILSYL; CQYILSYLG; QYILSYLGP; YILSYLGPL; ILSYLGPLE;
LSYLGPLEV; SYLGPLEVF; YLGPLEVFL; LGPLEVFLC; GPLEVFLCH; PLEVFLCHQ; LEVFLCHQT;
EVFLCHQTP; PLLPGIPYH; LLPGIPYHT; AAHPLSGFS; AHPLSGFSC; HPLSGFSCL; GHLAKRKLG;
HLAKRKLGK; LAKRKLGKD; AKRKLGKDS; KRKLGKDSL; RKLGKDSLQ; KLGKDSLQI; LGKDSLQIF;
GKDSLQIFF; KDSLQIFFS; DSLQIFFSG; SLQIFFSGG; LQIFFSGGS; NILQGLSTV; ILQGLSTVV;
LQGLSTVVF; QGLSTVVFQ; GLSTVVFQS; LSTVVFQSC; TGHKYQQLK; GHKYQQLKH; HKYQQLKHT;
KYQQLKHTG; YQQLKHTGY; QQLKHTGYQ; QLKHTGYQL; LKHTGYQLY; KHTGYQLYK; HTGYQLYKE;
TGYQLYKEA; GYQLYKEAP; YQLYKEAPH; QLYKEAPHP; LYKEAPHPV; YKEAPHPVH; KEAPHPVHL;
EAPHPVHLA; APHPVHLAT; PHPVHLATL; HPVHLATLW; LCWSHEVLG; CWSHEVLGE; WSHEVLGEH;
SHEVLGEHF; HEVLGEHFP; EVLGEHFPL; VLGEHFPLL; HFHFYWDQV; FHFYWDQVP; HFYWDQVPS;
FYWDQVPST; YWDQVPSTQ; WDQVPSTQL; DQVPSTQLD; QVPSTQLDK; VPSTQLDKH; PSTQLDKHC;
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HQGTLTCNS; QGTLTCNSL; GTLTCNSLA; TLTCNSLAL; LTCNSLALP; TCNSLALPA; CNSLALPAF;
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FPRVLHLQQ; PRVLHLQQR; RVLHLQQRS; VLHLQQRSG; LHLQQRSGN; HLQQRSGNY; LQQRSGNYC;
QQRSGNYCL; QRSGNYCLE; VFLHHAHAL; FLHHAHALF; LHHAHALFV; HHAHALFVT; HAHALFVTL;
AHALFVTLH; HALFVTLHE; ALFVTLHEG; PLFVQLQPP; LFVQLQPPT; FVQLQPPTS; VQLQPPTSV;
QLQPPTSVD; LQPPTSVDF; QPPTSVDFH; PPTSVDFHR; PTSVDFHRL; TSVDFHRLG; SVDFHRLGP;
VDFHRLGPH; DFHRLGPHL; FHRLGPHLN; HRLGPHLNW; RLGPHLNWG; LGPHLNWGG; GPHLNWGGE;
PHLNWGGEF; HLNWGGEFL; LNWGGEFLL; NWGGEFLLC; WGGEFLLCC; GGEFLLCCN; GEFLLCCNR;
EFLLCCNRE; FLLCCNREA; LLCCNREAF; LCCNREAFF; CCNREAFFS; CNREAFFSL; NREAFFSLG;
REAFFSLGY; EAFFSLGYH; AFFSLGYHC; SHFQHLALD; GFHLDPPFL; FHLDPPFLG; HLDPPFLGL;
LDPPFLGLG; DPPFLGLGS; PPFLGLGSI; PFLGLGSIL; FLGLGSILP; LGLGSILPL; LLELLLLLL;
LELLLLLLL; ELLLLLLLV; LLLLLLLVV; LLLLLLVVL; LLLLLVVLA; LLLLVVLAL; LLLVVLALA;
LLVVLALAR; LVVLALARV; VVLALARVP; VLALARVPL; LALARVPLA; ALARVPLAF; LARVPLAFW;
ARVPLAFWE; RVPLAFWEL; VPLAFWELP; PLAFWELPL; LAFWELPLD; AFWELPLDT; FWELPLDTL;
WELPLDTLL; ELPLDTLLF; LPLDTLLFF; PLDTLLFFW; LDTLLFFWL; DTLLFFWLG; TLLFFWLGP;
LLFFWLGPS; LFFWLGPSS; FFWLGPSSY; FWLGPSSYA; WLGPSSYAS; LGPSSYASR; GPSSYASRA;
PSSYASRAG; SSYASRAGV; SYASRAGVT; YASRAGVTV; ASRAGVTVP; SRAGVTVPY; RAGVTVPYR;
AGVTVPYRP; GVTVPYRPR; VTVPYRPRS; TVPYRPRSK; VPYRPRSKG; PYRPRSKGN; YRPRSKGNI;
RPRSKGNIH; LAPPGAIVF; APPGAIVFS; PPGAIVFSI; PGAIVFSIN; GAIVFSINS; AIVFSINSP;
IVFSINSPE; VFSINSPEC; FSINSPECT; SINSPECTL; INSPECTLC; FLKSILCVT; LKSILCVTS;
KSILCVTSS; SILCVTSSI; ILCVTSSIL; LCVTSSILS; CVTSSILSA; VTSSILSAS; TSSILSASS;
SSILSASSI; SILSASSIL; VWPKCTRVP; WPKCTRVPS; PKCTRVPSL; KCTRVPSLS; CTRVPSLSA;

TRVPSLSAT; RVPSLSATC; VPSLSATCL; PSLSATCLT; SLSATCLTI; LSATCLTIE; SATCLTIEG;
ATCLTIEGL; TCLTIEGLI; CLTIEGLIG; LTIEGLIGE; TIEGLIGER; IEGLIGERS; EGLIGERSE;
KFIGAFTIV; FIGAFTIVQ; IGAFTIVQV; GAFTIVQVV; AFTIVQVVS; FTIVQVVSS; TIVQVVSSK;
IVQVVSSKN; VQVVSSKNL; QVVSSKNLA; VVSSKNLAK; VSSKNLAKE; SSKNLAKES; SKNLAKESL;
KNLAKESLK; NLAKESLKN; LAKESLKNL; AKESLKNLS; KESLKNLSV; ESLKNLSVL; SLKNLSVLL;
LKNLSVLLC; KNLSVLLCN; NLSVLLCNS; LSVLLCNSC; SVLLCNSCE; VLLCNSCEV; LLCNSCEVI;
LCNSCEVIE; CNSCEVIEG; NSCEVIEGI; SCEVIEGIS; CEVIEGISS; EVIEGISSL; VIEGISSLI;
IEGISSLIT; EGISSLITC; GISSLITCH; ISSLITCHK; SSLITCHKA; SLITCHKAW; LITCHKAWE;
ITCHKAWEI; TCHKAWEIV; CHKAWEIVA; HKAWEIVAN; KAWEIVANK; AWEIVANKE; WEIVANKEG;
EIVANKEGP; IVANKEGPQ; VANKEGPQC; ANKEGPQCL; NKEGPQCLG; KEGPQCLGS; EGPQCLGSR;
GPQCLGSRY; ILLTKVFTP; LLTKVFTPG; LTKVFTPGN; TKVFTPGNR; KVFTPGNRI; VFTPGNRIS;
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VRPIAAIAS; RPIAAIASE; PIAAIASEV; IAAIASEVL; AAIASEVLV; AIASEVLVM; IASEVLVMP;
ASEVLVMPS; SEVLVMPST; EVLVMPSTV; VLVMPSTVA; LVMPSTVAR; VMPSTVARD; MPSTVARDA;
PSTVARDAI; TSIAAAASP; SIAAAASPA; IAAAASPAA; AAAASPAAI; AAASPAAIS; AASPAAISA;
ASPAAISAT; SPAAISATE; PAAISATEN; AAISATENP; AISATENPV; ISATENPVA; SATENPVAA;
ATENPVAAA; TENPVAAAA; ENPVAAAAS; NPVAAAASD; PVAAAASDT; VAAAASDTL; AAAASDTLA;
AAASDTLAT; AASDTLATR; ASDTLATRS; SDTLATRSP; DTLATRSPK; TLATRSPKS; LATRSPKSA;
ATRSPKSAR; TRSPKSARA; RSPKSARAA; SPKSARAAP; PKSARAAPM; KSARAAPMN; SARAAPMNL;
ARAAPMNLE; RAAPMNLEI; AAPMNLEIQ; APMNLEIQK; PMNLEIQKK; MNLEIQKKR; NLEIQKKRD;
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VKQWYFCFS; KQWYFCFSR; QWYFCFSRL; WYFCFSRLH; YFCFSRLHC; FCFSRLHCL; CFSRLHCLH;
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HLYKIPAKA; LYKIPAKAL; YKIPAKALK; KSSELFFLF; SSELFFLFQ; SELFFLFQS; ELFFLFQSR;
LFFLFQSRF; FFLFQSRFY; FLFQSRFYQ; LFQSRFYQL; FQSRFYQLS; QSRFYQLSL; SRFYQLSLK;
RFYQLSLKL; FYQLSLKLV; YQLSLKLVV; QLSLKLVVT; LSLKLVVTA; SLKLVVTAG; LKLVVTAGA;
KLVVTAGAE; LVVTAGAEP; VVTAGAEPW; VTAGAEPWP; TAGAEPWPL; AGAEPWPLS; GAEPWPLSS;
AEPWPLSSL; EPWPLSSLT; PWPLSSLTG; WPLSSLTGD; PLSSLTGDK; LSSLTGDKA; SSLTGDKAK;
SLTGDKAKI; LTGDKAKIP; TGDKAKIPR; GDKAKIPRL; DKAKIPRLA; KAKIPRLAK; AKIPRLAKH;
KIPRLAKHV; IPRLAKHVC; PRLAKHVCH; RLAKHVCHA; LAKHVCHAL; AKHVCHALS; KHVCHALSF;
HVCHALSFL; VCHALSFLR; CHALSFLRS; HALSFLRSW; ALSFLRSWF; LSFLRSWFG; SFLRSWFGC;
FLRSWFGCI; LRSWFGCIP; RSWFGCIPW; SWFGCIPWV; WFGCIPWVS; FGCIPWVSS; GCIPWVSSS;
CIPWVSSSS; IPWVSSSSL; GHGLAAFPC; HGLAAFPCE; GLAAFPCES; LAAFPCESC; AAFPCESCT;
AFPCESCTF; FPCESCTFL; PCESCTFLP; CESCTFLPE; ESCTFLPEV; SCTFLPEVM; CTFLPEVMV;
TFLPEVMVW; FLPEVMVWL; LPEVMVWLH; PEVMVWLHS; EVMVWLHSM; VMVWLHSMG; MVWLHSMGK;
VWLHSMGKQ; WLHSMGKQL; LHSMGKQLL; HSMGKQLLP; SMGKQLLPV; MGKQLLPVA; GKQLLPVAF;
KQLLPVAFF; QLLPVAFFF; LLPVAFFFI; LPVAFFFII; PVAFFFIIY; VAFFFIIYK; AFFFIIYKR;
FFFIIYKRP; FFIIYKRPR; FIIYKRPRP; IIYKRPRPP; IYKRPRPPL; YKRPRPPLP; KRPRPPLPP;
RPRPPLPPP; PRPPLPPPF; RPPLPPPFL; PPLPPPFLS; PLPPPFLSS; LPPPFLSSS; PPPFLSSSK;
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KGVEAFSEA; QNYLGKSLF; NYLGKSLFF; YLGKSLFFC; LGKSLFFCN; GKSLFFCNF; KSLFFCNFC;
SLFFCNFCK

10 mers:
WIKFLTGKNP; IKFLTGKNPW; KFLTGKNPWS; FLTGKNPWSS; LTGKNPWSSW; TGKNPWSSWT;
GKNPWSSWTF; ALKELPGEIF; LKELPGEIFP; GSVRNFTLTK; SVRNFTLTKG; VRNFTLTKGA;
RNFTLTKGAT; NFTLTKGATR; FTLTKGATRI; TLTKGATRIK; ILCIKKWSRM; LISLILEPGV;
ISLILEPGVA; SLILEPGVAQ; LILEPGVAQR; ILEPGVAQRF; LEPGVAQRFV; EPGVAQRFVL;
PGVAQRFVLI; GVAQRFVLIF; VAQRFVLIFL; AQRFVLIFLF; QRFVLIFLFA; RFVLIFLFAQ;
FVLIFLFAQI; VLIFLFAQIP; LIFLFAQIPC; IFLFAQIPCT; FLFAQIPCTA; LFAQIPCTAR;
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TARNGLFVPK; ARNGLFVPKS; RNGLFVPKSL; NGLFVPKSLL; GLFVPKSLLC; LFVPKSLLCT;
FVPKSLLCTA; VPKSLLCTAL; PKSLLCTALA; KSLLCTALAC; SLLCTALACY; LLCTALACYV;
LCTALACYVS; CTALACYVSL; TALACYVSLD; IATALTASHS; ATALTASHSG; TALTASHSGL;
ALTASHSGLA; LKKLCNGGSK; SFKVTNLYLD; FKVTNLYLDK; VIIFFIGANL; IIFFIGANLW;
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RYVFRISIQC; YVFRISIQCR; VFRISIQCRG; FRISIQCRGV; KVSEKRPALS; VSEKRPALSL;
KALCKCYYFC; ALCKCYYFCR; LCKCYYFCRK; KSKKYLSASS; SKKYLSASSR; KKYLSASSRY;
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KQHLLNVYVQ; KHLFKAFWFA; HLFKAFWFAI; LFKAFWFAIV; FKAFWFAIVP; KAFWFAIVPV;
AFWFAIVPVC; FWFAIVPVCQ; WFAIVPVCQY; FAIVPVCQYI; AIVPVCQYIL; IVPVCQYILS;
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KHTGYQLYKE; HTGYQLYKEA; TGYQLYKEAP; GYQLYKEAPH; YQLYKEAPHP; QLYKEAPHPV;
LYKEAPHPVH; YKEAPHPVHL; KEAPHPVHLA; EAPHPVHLAT; APHPVHLATL; PHPVHLATLW;
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QLDKHCFCPN; LDKHCFCPNR; DKHCFCPNRP; KHCFCPNRPY; HCFCPNRPYG; CFCPNRPYGQ;
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LFVQLQPPTS; FVQLQPPTSV; VQLQPPTSVD; QLQPPTSVDF; LQPPTSVDFH; QPPTSVDFHR;
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EFLLCCNREA; FLLCCNREAF; LLCCNREAFF; LCCNREAFFS; CCNREAFFSL; CNREAFFSLG;
NREAFFSLGY; REAFFSLGYH; EAFFSLGYHC; GFHLDPPFLG; FHLDPPFLGL; HLDPPFLGLG;
LDPPFLGLGS; DPPFLGLGSI; PPFLGLGSIL; PFLGLGSILP; FLGLGSILPL; LLELLLLLLL;
LELLLLLLLV; ELLLLLLLVV; LLLLLLLVVL; LLLLLVVLA; LLLLLVVLAL; LLLLVVLALA;
LLLVVLALAR; LLVVLALARV; LVVLALARVP; VVLALARVPL; VLALARVPLA; LALARVPLAF;
ALARVPLAFW; LARVPLAFWE; ARVPLAFWEL; RVPLAFWELP; VPLAFWELPL; PLAFWELPLD;
LAFWELPLDT; AFWELPLDTL; FWELPLDTLL; WELPLDTLLF; ELPLDTLLFF; LPLDTLLFFW;
PLDTLLFFWL; LDTLLFFWLG; DTLLFFWLGP; TLLFFWLGPS; LLFFWLGPSS; LFFWLGPSSY;
FFWLGPSSYA; FWLGPSSYAS; WLGPSSYASR; LGPSSYASRA; GPSSYASRAG; PSSYASRAGV;
SSYASRAGVT; SYASRAGVTV; YASRAGVTVP; ASRAGVTVPY; SRAGVTVPYR; RAGVTVPYRP;
AGVTVPYRPR; GVTVPYRPRS; VTVPYRPRSK; TVPYRPRSKG; VPYRPRSKGN; PYRPRSKGNI;
YRPRSKGNIH; LAPPGAIVFS; APPGAIVFSI; PPGAIVFSIN; PGAIVFSINS; GAIVFSINSP;
AIVFSINSPE; IVFSINSPEC; VFSINSPECT; FSINSPECTL; SINSPECTLC; FLKSILCVTS;
LKSILCVTSS; KSILCVTSSI; SILCVTSSIL; ILCVTSSILS; LCVTSSILSA; CVTSSILSAS;
VTSSILSASS; TSSILSASSI; SSILSASSIL; VWPKCTRVPS; WPKCTRVPSL; PKCTRVPSLS;
KCTRVPSLSA; CTRVPSLSAT; TRVPSLSATC; RVPSLSATCL; VPSLSATCLT; PSLSATCLTI;
SLSATCLTIE; LSATCLTIEG; SATCLTIEGL; ATCLTIEGLI; TCLTIEGLIG; CLTIEGLIGE;
LTIEGLIGER; TIEGLIGERS; IEGLIGERSE; KFIGAFTIVQ; FIGAFTIVQV; IGAFTIVQVV;
GAFTIVQVVS; AFTIVQVVSS; FTIVQVVSSK; TIVQVVSSKN; IVQVVSSKNL; VQVVSSKNLA;

QVVSSKNLAK; VVSSKNLAKE; VSSKNLAKES; SSKNLAKESL; SKNLAKESLK; KNLAKESLKN;
NLAKESLKNL; LAKESLKNLS; AKESLKNLSV; KESLKNLSVL; ESLKNLSVLL; SLKNLSVLLC;
LKNLSVLLCN; KNLSVLLCNS; NLSVLLCNSC; LSVLLCNSCE; SVLLCNSCEV; VLLCNSCEVI;
LLCNSCEVIE; LCNSCEVIEG; CNSCEVIEGI; NSCEVIEGIS; SCEVIEGISS; CEVIEGISSL;
EVIEGISSLI; VIEGISSLIT; IEGISSLITC; EGISSLITCH; GISSLITCHK; ISSLITCHKA;
SSLITCHKAW; SLITCHKAWE; LITCHKAWEI; ITCHKAWEIV; TCHKAWEIVA; CHKAWEIVAN;
HKAWEIVANK; KAWEIVANKE; AWEIVANKEG; WEIVANKEGP; EIVANKEGPQ; IVANKEGPQC;
VANKEGPQCL; ANKEGPQCLG; NKEGPQCLGS; KEGPQCLGSR; EGPQCLGSRY; ILLTKVFTPG;
LLTKVFTPGN; LTKVFTPGNR; TKVFTPGNRI; KVFTPGNRIS; YSSGLNNSKA; SSGLNNSKAM;
SGLNNSKAMP; GLNNSKAMPD; LNNSKAMPDC; SQSSKNLYPT; IKAANPAIAP; KAANPAIAPG;
AANPAIAPGA; ANPAIAPGAP; NPAIAPGAPA; PAIAPGAPAI; AIAPGAPAIT; IAPGAPAITA;
APGAPAITAY; PGAPAITAYV; GVRPIAAIAS; VRPIAAIASE; RPIAAIASEV; PIAAIASEVL;
IAAIASEVLV; AAIASEVLVM; AIASEVLVMP; IASEVLVMPS; ASEVLVMPST; SEVLVMPSTV;
EVLVMPSTVA; VLVMPSTVAR; LVMPSTVARD; VMPSTVARDA; MPSTVARDAI; TSIAAAASPA;
SIAAAASPAA; IAAAASPAAI; AAAASPAAIS; AAASPAAISA; AASPAAISAT; ASPAAISATE;
SPAAISATEN; PAAISATENP; AAISATENPV; AISATENPVA; ISATENPVAA; SATENPVAAA;
ATENPVAAAA; TENPVAAAAS; ENPVAAAASD; NPVAAAASDT; PVAAAASDTL; VAAAASDTLA;
AAAASDTLAT; AAASDTLATR; AASDTLATRS; ASDTLATRSP; SDTLATRSPK; DTLATRSPKS;
TLATRSPKSA; LATRSPKSAR; ATRSPKSARA; TRSPKSARAA; RSPKSARAAP; SPKSARAAPM;
PKSARAAPMN; KSARAAPMNL; SARAAPMNLE; ARAAPMNLEI; RAAPMNLEIQ; AAPMNLEIQK;
APMNLEIQKK; PMNLEIQKKR; MNLEIQKKRD; NLEIQKKRDY; LEIQKKRDYL; EIQKKRDYLP;
IQKKRDYLPR; QKKRDYLPRS; KKRDYLPRSL; KRDYLPRSLL; RDYLPRSLLQ; DYLPRSLLQS;
YLPRSLLQSL; LPRSLLQSLL; PRSLLQSLLQ; RSLLQSLLQQ; SLLQSLLQQV; LLQSLLQQVK;
LQSLLQQVKQ; QSLLQQVKQW; SLLQQVKQWY; LLQQVKQWYF; LQQVKQWYFC; QQVKQWYFCF;
QVKQWYFCFS; VKQWYFCFSR; KQWYFCFSRL; QWYFCFSRLH; WYFCFSRLHC; YFCFSRLHCL;
FCFSRLHCLH; CFSRLHCLHL; FSRLHCLHLY; SRLHCLHLYK; RLHCLHLYKI; LHCLHLYKIP;
HCLHLYKIPA; CLHLYKIPAK; LHLYKIPAKA; HLYKIPAKAL; LYKIPAKALK; KSSELFFLFQ;
SSELFFLFQS; SELFFLFQSR; ELFFLFQSRF; LFFLFQSRFY; FFLFQSRFYQ; FLFQSRFYQL;
LFQSRFYQLS; FQSRFYQLSL; QSRFYQLSLK; SRFYQLSLKL; RFYQLSLKLV; FYQLSLKLVV;
YQLSLKLVVT; QLSLKLVVTA; LSLKLVVTAG; SLKLVVTAGA; LKLVVTAGAE; KLVVTAGAEP;
LVVTAGAEPW; VVTAGAEPWP; VTAGAEPWPL; TAGAEPWPLS; AGAEPWPLSS; GAEPWPLSSL;
AEPWPLSSLT; EPWPLSSLTG; PWPLSSLTGD; WPLSSLTGDK; PLSSLTGDKA; LSSLTGDKAK;
SSLTGDKAKI; SLTGDKAKIP; LTGDKAKIPR; TGDKAKIPRL; GDKAKIPRLA; DKAKIPRLAK;
KAKIPRLAKH; AKIPRLAKHV; KIPRLAKHVC; IPRLAKHVCH; PRLAKHVCHA; RLAKHVCHAL;
LAKHVCHALS; AKHVCHALSF; KHVCHALSFL; HVCHALSFLR; VCHALSFLRS; CHALSFLRSW;
HALSFLRSWF; ALSFLRSWFG; LSFLRSWFGC; SFLRSWFGCI; FLRSWFGCIP; LRSWFGCIPW;
RSWFGCIPWV; SWFGCIPWVS; WFGCIPWVSS; FGCIPWVSSS; GCIPWVSSSS; CIPWVSSSSL;
GHGLAAFPCE; HGLAAFPCES; GLAAFPCESC; LAAFPCESCT; AAFPCESCTF; AFPCESCTFL;
FPCESCTFLP; PCESCTFLPE; CESCTFLPEV; ESCTFLPEVM; SCTFLPEVMV; CTFLPEVMVW;
TFLPEVMVWL; FLPEVMVWLH; LPEVMVWLHS; PEVMVWLHSM; EVMVWLHSMG; VMVWLHSMGK;
MVWLHSMGKQ; VWLHSMGKQL; WLHSMGKQLL; LHSMGKQLLP; HSMGKQLLPV; SMGKQLLPVA;
MGKQLLPVAF; GKQLLPVAFF; KQLLPVAFFF; QLLPVAFFFI; LLPVAFFFII; LPVAFFFIIY;
PVAFFFIIYK; VAFFFIIYKR; AFFFIIYKRP; FFFIIYKRPR; FFIIYKRPRP; FIIYKRPRPP;
IIYKRPRPPL; IYKRPRPPLP; YKRPRPPLPP; KRPRPPLPPP; RPRPPLPPPF; PRPPLPPPFL;
RPPLPPPFLS; PPLPPPFLSS; PLPPPFLSSS; LPPPFLSSSK; PPPFLSSSKG; PPFLSSSKGV;
PFLSSSKGVE; FLSSSKGVEA; LSSSKGVEAF; SSSKGVEAFS; SSKGVEAFSE; SKGVEAFSEA;
QNYLGKSLFF; NYLGKSLFFC; YLGKSLFFCN; LGKSLFFCNF; GKSLFFCNFC; KSLFFCNFCK

11 mers:
WIKFLTGKNPW; IKFLTGKNPWS; KFLTGKNPWSS; FLTGKNPWSSW; LTGKNPWSSWT; TGKNPWSSWTF;
ALKELPGEIFP; GSVRNFTLTKG; SVRNFTLTKGA; VRNFTLTKGAT; RNFTLTKGATR; NFTLTKGATRI;
FTLTKGATRIK; LISLILEPGVA; ISLILEPGVAQ; SLILEPGVAQR; LILEPGVAQRF; ILEPGVAQRFV;
LEPGVAQRFVL; EPGVAQRFVLI; PGVAQRFVLIF; GVAQRFVLIFL; VAQRFVLIFLF; AQRFVLIFLFA;
QRFVLIFLFAQ; RFVLIFLFAQI; FVLIFLFAQIP; VLIFLFAQIPC; LIFLFAQIPCT; IFLFAQIPCTA;
FLFAQIPCTAR; LFAQIPCTARN; FAQIPCTARNG; AQIPCTARNGL; QIPCTARNGLF; IPCTARNGLFV;
PCTARNGLFVP; CTARNGLFVPK; TARNGLFVPKS; ARNGLFVPKSL; RNGLFVPKSLL; NGLFVPKSLLC;
GLFVPKSLLCT; LFVPKSLLCTA; FVPKSLLCTAL; VPKSLLCTALA; PKSLLCTALAC; KSLLCTALACY;
SLLCTALACYV; LLCTALACYVS; LCTALACYVSL; CTALACYVSLD; IATALTASHSG; ATALTASHSGL;
TALTASHSGLA; SFKVTNLYLDK; VIIFFIGANLW; IIFFIGANLWN; IFFIGANLWNR; FFIGANLWNRR;
FIGANLWNRRV; IGANLWNRRVG; GANLWNRRVGV; ANLWNRRVGVL; NLWNRRVGVLV; LWNRRVGVLVE;
WNRRVGVLVEF; NRRVGVLVEFL; RSNSRFSTLNT; SNSRFSTLNTT; NSRFSTLNTTQ; SRFSTLNTTQK;
RFSTLNTTQKK; FSTLNTTQKKK; STLNTTQKKKK; TLNTTQKKKKG; LNTTQKKKKGR; NTTQKKKKGRR;
TTQKKKKGRRP; KTYGKIFCNFY; RSIPYYRRKHS; SIPYYRRKHSR; IPYYRRKHSRG; PYYRRKHSRGL;
YYRRKHSRGLK; YRRKHSRGLKG; RRKHSRGLKGA; RNKAGVLEINY; GCVFIIRYVFR; CVFIIRYVFRI;
VFIIRYVFRIS; FIIRYVFRISI; IIRYVFRISIQ; IRYVFRISIQC; RYVFRISIQCR; YVFRISIQCRG;
VFRISIQCRGV; KVSEKRPALSL; KALCKCYYFCR; ALCKCYYFCRK; KSKKYLSASSR; SKKYLSASSRY;

KKYLSASSRYS; KYLSASSRYSF; YLSASSRYSFS; KKSRYPSYDQG; KSRYPSYDQGR; SRYPSYDQGRN;
RYPSYDQGRNA; YPSYDQGRNAN; PSYDQGRNANR; SYDQGRNANRK; YDQGRNANRKI; DQGRNANRKIQ;
QGRNANRKIQS; GRNANRKIQSY; RNANRKIQSYI; NANRKIQSYIR; NGFNIWSSWKC; GFNIWSSWKCC;
FNIWSSWKCCT; NIWSSWKCCTR; IWSSWKCCTRT; WSSWKCCTRTI; SSWKCCTRTIY; SWKCCTRTIYG;
WKCCTRTIYGR; KCCTRTIYGRC; CCTRTIYGRCC; CTRTIYGRCCL; TRTIYGRCCLA; RTIYGRCCLAA;
TIYGRCCLAAL; IYGRCCLAALF; YGRCCLAALFA; GRCCLAALFAT; WKNNTSCRVIR; KNNTSCRVIRF;
NNTSCRVIRFV; NTSCRVIRFVW; TSCRVIRFVWW; SLKCKPTHGKA; LKCKPTHGKAN; KCKPTHGKANL;
ARCSYRSVHGC; RCSYRSVHGCF; IKGFAFRTWNK; KGFAFRTWNKQ; GFAFRTWNKQF; FAFRTWNKQFR;
AFRTWNKQFRQ; FRTWNKQFRQF; RTWNKQFRQFE; TWNKQFRQFER; WNKQFRQFERL; NKQFRQFERLF;
KQFRQFERLFR; QFRQFERLFRW; FRQFERLFRWK; RQFERLFRWKC; GKFRKETFKQK; KFRKETFKQKN;
FRKETFKQKNP; RKETFKQKNPN; KETFKQKNPNI; ETFKQKNPNIS; TFKQKNPNIST; FKQKNPNISTR;
KQKNPNISTRL; QKNPNISTRLG; KNPNISTRLGY; NPNISTRLGYN; PNISTRLGYNE; AQNIFKKILTK;
QNIFKKILTKL; NIFKKILTKLR; IFKKILTKLRV; FKKILTKLRVL; KKILTKLRVLT; KKNFTKWNDLV;
KNFTKWNDLVA; NFTKWNDLVAT; FTKWNDLVATA; TKWNDLVATAN; KWNDLVATANL; WNDLVATANLV;
DKYVYFFKDEI; IPITMLFPSLR; PITMLFPSLRY; ITMLFPSLRYF; TMLFPSLRYFS; MLFPSLRYFSP;
LFPSLRYFSPC; KWLIQKQHLLN; WLIQKQHLLNV; LIQKQHLLNVY; IQKQHLLNVYV; QKQHLLNVYVQ;
KHLFKAFWFAI; HLFKAFWFAIV; LFKAFWFAIVP; FKAFWFAIVPV; KAFWFAIVPVC; AFWFAIVPVCQ;
FWFAIVPVCQY; WFAIVPVCQYI; FAIVPVCQYIL; AIVPVCQYILS; IVPVCQYILSY; VPVCQYILSYL;
PVCQYILSYLG; VCQYILSYLGP; CQYILSYLGPL; QYILSYLGPLE; YILSYLGPLEV; ILSYLGPLEVF;
LSYLGPLEVFL; SYLGPLEVFLC; YLGPLEVFLCH; LGPLEVFLCHQ; GPLEVFLCHQT; PLEVFLCHQTP;
AAHPLSGFSCL; GHLAKRKLGKD; HLAKRKLGKDS; LAKRKLGKDSL; AKRKLGKDSLQ; KRKLGKDSLQI;
RKLGKDSLQIF; KLGKDSLQIFF; LGKDSLQIFFS; GKDSLQIFFSG; KDSLQIFFSGG; DSLQIFFSGGS;
NILQGLSTVVF; ILQGLSTVVFQ; LQGLSTVVFQS; QGLSTVVFQSC; TGHKYQQLKHT; GHKYQQLKHTG;
HKYQQLKHTGY; KYQQLKHTGYQ; YQQLKHTGYQL; QQLKHTGYQLY; QLKHTGYQLYK; LKHTGYQLYKE;
KHTGYQLYKEA; HTGYQLYKEAP; TGYQLYKEAPH; GYQLYKEAPHP; YQLYKEAPHPV; QLYKEAPHPVH;
LYKEAPHPVHL; YKEAPHPVHLA; KEAPHPVHLAT; EAPHPVHLATL; APHPVHLATLW; LCWSHEVLGEH;
CWSHEVLGEHF; WSHEVLGEHFP; SHEVLGEHFPL; HEVLGEHFPLL; HFHFYWDQVPS; FHFYWDQVPST;
HFYWDQVPSTQ; FYWDQVPSTQL; YWDQVPSTQLD; WDQVPSTQLDK; DQVPSTQLDKH; QVPSTQLDKHC;
VPSTQLDKHCF; PSTQLDKHCFC; STQLDKHCFCP; TQLDKHCFCPN; QLDKHCFCPNR; LDKHCFCPNRP;
DKHCFCPNRPY; KHCFCPNRPYG; HCFCPNRPYGQ; CFCPNRPYGQY; FCPNRPYGQYS; CPNRPYGQYSL;
PNRPYGQYSLP; NRPYGQYSLPG; RPYGQYSLPGT; PYGQYSLPGTG; YGQYSLPGTGL; GQYSLPGTGLL;
QYSLPGTGLLG; YSLPGTGLLGF; YHQGTLTCNSL; HQGTLTCNSLA; QGTLTCNSLAL; GTLTCNSLALP;
TLTCNSLALPA; LTCNSLALPAF; TCNSLALPAFP; CNSLALPAFPR; NSLALPAFPRV; SLALPAFPRVL;
LALPAFPRVLH; ALPAFPRVLHL; LPAFPRVLHLQ; PAFPRVLHLQQ; AFPRVLHLQQR; FPRVLHLQQRS;
PRVLHLQQRSG; RVLHLQQRSGN; VLHLQQRSGNY; LHLQQRSGNYC; HLQQRSGNYCL; LQQRSGNYCLE;
VFLHHAHALFV; FLHHAHALFVT; LHHAHALFVTL; HHAHALFVTLH; HAHALFVTLHE; AHALFVTLHEG;
PLFVQLQPPTS; LFVQLQPPTSV; FVQLQPPTSVD; VQLQPPTSVDF; QLQPPTSVDFH; LQPPTSVDFHR;
QPPTSVDFHRL; PPTSVDFHRLG; PTSVDFHRLGP; TSVDFHRLGPH; SVDFHRLGPHL; VDFHRLGPHLN;
DFHRLGPHLNW; FHRLGPHLNWG; HRLGPHLNWGG; RLGPHLNWGGE; LGPHLNWGGEF; GPHLNWGGEFL;
PHLNWGGEFLL; HLNWGGEFLLC; LNWGGEFLLCC; NWGGEFLLCCN; WGGEFLLCCNR; GGEFLLCCNRE;
GEFLLCCNREA; EFLLCCNREAF; FLLCCNREAFF; LLCCNREAFFS; LCCNREAFFSL; CCNREAFFSLG;
CNREAFFSLGY; NREAFFSLGYH; REAFFSLGYHC; GFHLDPPFLGL; FHLDPPFLGLG; HLDPPFLGLGS;
LDPPFLGLGSI; DPPFLGLGSIL; PPFLGLGSILP; PFLGLGSILPL; LLELLLLLLLV; LELLLLLLLVV;
ELLLLLLLVVL; LLLLLLLVVLA; LLLLLLVVLAL; LLLLLVVLALA; LLLLVVLALAR; LLLVVLALARV;
LLVVLALARVP; LVVLALARVPL; VVLALARVPLA; VLALARVPLAF; LALARVPLAFW; ALARVPLAFWE;
LARVPLAFWEL; ARVPLAFWELP; RVPLAFWELPL; VPLAFWELPLD; PLAFWELPLDT; LAFWELPLDTL;
AFWELPLDTLL; FWELPLDTLLF; WELPLDTLLFF; ELPLDTLLFFW; LPLDTLLFFWL; PLDTLLFFWLG;
LDTLLFFWLGP; DTLLFFWLGPS; TLLFFWLGPSS; LLFFWLGPSSY; LFFWLGPSSYA; FFWLGPSSYAS;
FWLGPSSYASR; WLGPSSYASRA; LGPSSYASRAG; GPSSYASRAGV; PSSYASRAGVT; SSYASRAGVTV;
SYASRAGVTVP; YASRAGVTVPY; ASRAGVTVPYR; SRAGVTVPYRP; RAGVTVPYRPR; AGVTVPYRPRS;
GVTVPYRPRSK; VTVPYRPRSKG; TVPYRPRSKGN; VPYRPRSKGNI; PYRPRSKGNIH; LAPPGAIVFSI;
APPGAIVFSIN; PPGAIVFSINS; PGAIVFSINSP; GAIVFSINSPE; AIVFSINSPEC; IVFSINSPECT;
VFSINSPECTL; FSINSPECTLC; FLKSILCVTSS; LKSILCVTSSI; KSILCVTSSIL; SILCVTSSILS;
ILCVTSSILSA; LCVTSSILSAS; CVTSSILSASS; VTSSILSASSI; TSSILSASSIL; VWPKCTRVPSL;
WPKCTRVPSLS; PKCTRVPSLSA; KCTRVPSLSAT; CTRVPSLSATC; TRVPSLSATCL; RVPSLSATCLT;
VPSLSATCLTI; PSLSATCLTIE; SLSATCLTIEG; LSATCLTIEGL; SATCLTIEGLI; ATCLTIEGLIG;
TCLTIEGLIGE; CLTIEGLIGER; LTIEGLIGERS; TIEGLIGERSE; KFIGAFTIVQV; FIGAFTIVQVV;
IGAFTIVQVVS; GAFTIVQVVSS; AFTIVQVVSSK; FTIVQVVSSKN; TIVQVVSSKNL; IVQVVSSKNLA;
VQVVSSKNLAK; QVVSSKNLAKE; VVSSKNLAKES; VSSKNLAKESL; SSKNLAKESLK; SKNLAKESLKN;
KNLAKESLKNL; NLAKESLKNLS; LAKESLKNLSV; AKESLKNLSVL; KESLKNLSVLL; ESLKNLSVLLC;
SLKNLSVLLCN; LKNLSVLLCNS; KNLSVLLCNSC; NLSVLLCNSCE; LSVLLCNSCEV; SVLLCNSCEVI;
VLLCNSCEVIE; LLCNSCEVIEG; LCNSCEVIEGI; CNSCEVIEGIS; NSCEVIEGISS; SCEVIEGISSL;
CEVIEGISSLI; EVIEGISSLIT; VIEGISSLITC; IEGISSLITCH; EGISSLITCHK; GISSLITCHKA;
ISSLITCHKAW; SSLITCHKAWE; SLITCHKAWEI; LITCHKAWEIV; ITCHKAWEIVA; TCHKAWEIVAN;
CHKAWEIVANK; HKAWEIVANKE; KAWEIVANKEG; AWEIVANKEGP; WEIVANKEGPQ; EIVANKEGPQC;

IVANKEGPQCL; VANKEGPQCLG; ANKEGPQCLGS; NKEGPQCLGSR; KEGPQCLGSRY; ILLTKVFTPGN; LLTKVFTPGNR; LTKVFTPGNRI; TKVFTPGNRIS; YSSGLNNSKAM; SSGLNNSKAMP; SGLNNSKAMPD; GLNNSKAMPDC; IKAANPAIAPG; KAANPAIAPGA; AANPAIAPGAP; ANPAIAPGAPA; NPAIAPGAPAI; PAIAPGAPAIT; AIAPGAPAITA; IAPGAPAITAY; APGAPAITAYV; GVRPIAAIASE; VRPIAAIASEV; RPIAAIASEVL; PIAAIASEVLV; IAAIASEVLVM; AAIASEVLVMP; AIASEVLVMPS; IASEVLVMPST; ASEVLVMPSTV; SEVLVMPSTVA; EVLVMPSTVAR; VLVMPSTVARD; LVMPSTVARDA; VMPSTVARDAI; TSIAAAASPAA; SIAAAASPAAI; IAAAASPAAIS; AAAASPAAISA; AAASPAAISAT; AASPAAISATE; ASPAAISATEN; SPAAISATENP; PAAISATENPV; AAISATENPVA; AISATENPVAA; ISATENPVAAA; SATENPVAAAA; ATENPVAAAAS; TENPVAAAASD; ENPVAAAASDT; NPVAAAASDTL; PVAAAASDTLA; VAAAASDTLAT; AAAASDTLATR; AAASDTLATRS; AASDTLATRSP; ASDTLATRSPK; SDTLATRSPKS; DTLATRSPKSA; TLATRSPKSAR; LATRSPKSARA; ATRSPKSARAA; TRSPKSARAAP; RSPKSARAAPM; SPKSARAAPMN; PKSARAAPMNL; KSARAAPMNLE; SARAAPMNLEI; ARAAPMNLEIQ; RAAPMNLEIQK; AAPMNLEIQKK; APMNLEIQKKR; PMNLEIQKKRD; MNLEIQKKRDY; NLEIQKKRDYL; LEIQKKRDYLP; EIQKKRDYLPR; IQKKRDYLPRS; QKKRDYLPRSL; KKRDYLPRSLL; KRDYLPRSLLQ; RDYLPRSLLQS; DYLPRSLLQSL; YLPRSLLQSLL; LPRSLLQSLLQ; PRSLLQSLLQQ; RSLLQSLLQQV; SLLQSLLQQVK; LLQSLLQQVKQ; LQSLLQQVKQW; QSLLQQVKQWY; SLLQQVKQWYF; LLQQVKQWYFC; LQQVKQWYFCF; QQVKQWYFCFS; QVKQWYFCFSR; VKQWYFCFSRL; KQWYFCFSRLH; QWYFCFSRLHC; WYFCFSRLHCL; YFCFSRLHCLH; FCFSRLHCLHL; CFSRLHCLHLY; FSRLHCLHLYK; SRLHCLHLYKI; RLHCLHLYKIP; LHCLHLYKIPA; HCLHLYKIPAK; CLHLYKIPAKA; LHLYKIPAKAL; HLYKIPAKALK; KSSELFFLFQS; SSELFFLFQSR; SELFFLFQSRF; ELFFLFQSRFY; LFFLFQSRFYQ; FFLFQSRFYQL; FLFQSRFYQLS; LFQSRFYQLSL; FQSRFYQLSLK; QSRFYQLSLKL; SRFYQLSLKLV; RFYQLSLKLVV; FYQLSLKLVVT; YQLSLKLVVTA; QLSLKLVVTAG; LSLKLVVTAGA; SLKLVVTAGAE; LKLVVTAGAEP; KLVVTAGAEPW; LVVTAGAEPWP; VVTAGAEPWPL; VTAGAEPWPLS; TAGAEPWPLSS; AGAEPWPLSSL; GAEPWPLSSLT; AEPWPLSSLTG; EPWPLSSLTGD; PWPLSSLTGDK; WPLSSLTGDKA; PLSSLTGDKAK; LSSLTGDKAKI; SSLTGDKAKIP; SLTGDKAKIPR; LTGDKAKIPRL; TGDKAKIPRLA; GDKAKIPRLAK; DKAKIPRLAKH; KAKIPRLAKHV; AKIPRLAKHVC; KIPRLAKHVCH; IPRLAKHVCHA; PRLAKHVCHAL; RLAKHVCHALS; LAKHVCHALSF; AKHVCHALSFL; KHVCHALSFLR; HVCHALSFLRS; VCHALSFLRSW; CHALSFLRSWF; HALSFLRSWFG; ALSFLRSWFGC; LSFLRSWFGCI; SFLRSWFGCIP; FLRSWFGCIPW; LRSWFGCIPWV; RSWFGCIPWVS; SWFGCIPWVSS; WFGCIPWVSSS; FGCIPWVSSSS; GCIPWVSSSSL; GHGLAAFPCES; HGLAAFPCESC; GLAAFPCESCT; LAAFPCESCTF; AAFPCESCTFL; AFPCESCTFLP; FPCESCTFLPE; PCESCTFLPEV; CESCTFLPEVM; ESCTFLPEVMV; SCTFLPEVMVW; CTFLPEVMVWL; TFLPEVMVWLH; FLPEVMVWLHS; LPEVMVWLHSM; PEVMVWLHSMG; EVMVWLHSMGK; VMVWLHSMGKQ; MVWLHSMGKQL; VWLHSMGKQLL; WLHSMGKQLLP; LHSMGKQLLPV; HSMGKQLLPVA; SMGKQLLPVAF; MGKQLLPVAFF; GKQLLPVAFFF; KQLLPVAFFFI; QLLPVAFFFII; LLPVAFFFIIY; LPVAFFFIIYK; PVAFFFIIYKR; VAFFFIIYKRP; AFFFIIYKRPR; FFFIIYKRPRP; FFIIYKRPRPP; FIIYKRPRPPL; IIYKRPRPPLP; IYKRPRPPLPP; YKRPRPPLPPP; KRPRPPLPPPF; RPRPPLPPPFL; PRPPLPPPFLS; RPPLPPPFLSS; PPLPPPFLSSS; PLPPPFLSSSK; LPPPFLSSSKG; PPPFLSSSKGV; PPFLSSSKGVE; PFLSSSKGVEA; FLSSSKGVEAF; LSSSKGVEAFS; SSSKGVEAFSE; SSKGVEAFSEA; QNYLGKSLFFC; NYLGKSLFFCN; YLGKSLFFCNF; LGKSLFFCNFC; GKSLFFCNFCK

BK virus complementary reading frame 3

8 mers:

QGRIHGAH; GRIHGAHG; RIHGAHGP; IHGAHGPF; HGAHGPFR; GAHGPFRP; KSCLGKSS; SCLGKSSL; CLGKSSLN; LGKSSLNE; GKSSLNEK; KSSLNEKS; SSLNEKSL; SLNEKSLF; LNEKSLFK; NEKSLFKE; EKSLFKEV; NEENEYFV; KNGAGCKG; NGAGCKGS; GAGCKGSS; AGCKGSSS; GCKGSSSA; FSSLPRYP; SSLPRYPV; SLPRYPVL; LPRYPVLQ; PRYPVLQG; RYPVLQGM; YPVLQGMA; PVLQGMAY; VLQGMAYL; LQGMAYLF; QGMAYLFQ; GMAYLFQK; MAYLFQKA; AYLFQKAF; YLFQKAFC; LFQKAFCA; FQKAFCAL; QKAFCALP; KAFCALPL; AFCALPLH; FCALPLHA; CALPLHAM; ALPLHAMS; LPLHAMSA; KIFKKRAL; IFKKRALG; FKKRALGL; KKRALGLD; KRALGLDR; RALGLDRL; ALGLDRLL; LGLDRLLL; GLDRLLLH; LLHTVVWL; LHTVVWLR; HTVVWLRP; TVVWLRPN; RNSAMVGP; NSAMVGPN; SAMVGPNN; AMVGPNNW; MVGPNNWR; VGPNNWRN; GPNNWRNS; PNNWRNSL; NNWRNSLQ; NWRNSLQR; WRNSLQRS; RNSLQRSK; NSLQRSKA; SLQRSKAL; LQRSKALR; INNKILKG; NNKILKGP; NKILKGPK; VPTYGTEE; PTYGTEEW; TYGTEEWE; YGTEEWES; GTEEWESW; TEEWESWW; EEWESWWS; EWESWWSS; WESWWSSF; ESWWSSFN; SWWSSFNE; WWSSFNEK; WSSFNEKW; SSFNEKWD; SFNEKWDE; FNEKWDED; NEKWDEDL; EKWDEDLF; KWDEDLFC; WDEDLFCH; DEDLFCHE; EDLFCHED; DLFCHEDM; LFCHEDMF; FCHEDMFA; CHEDMFAS; HEDMFASD; EDMFASDE; DMFASDEE; MFASDEEA; FASDEEAT; ASDEEATA; SDEEATAD; DEEATADS; EEATADSQ; EATADSQH; ATADSQHS; TADSQHST; ADSQHSTP; DSQHSTPP; SQHSTPPK; QHSTPPKK; HSTPPKKK; STPPKKKR; TPPKKKRK; PPKKKRKV; PKKKRKVE; KKKRKVED; KKRKVEDP; KRKVEDPK; RKVEDPKD; KVEDPKDF; VEDPKDFP; EDPKDFPS; DPKDFPSD; PKDFPSDL; KDFPSDLH; DFPSDLHQ; FPSDLHQF; PSDLHQFL; SDLHQFLS; DLHQFLSQ; LHQFLSQA; HQFLSQAV; QFLSQAVF; FLSQAVFS; LSQAVFSN; SQAVFSNR; QAVFSNRT; AVFSNRTL; VFSNRTLA; FSNRTLAC; SNRTLACF; NRTLACFA; RTLACFAV; TLACFAVY; LACFAVYT; ACFAVYTT; CFAVYTTK; FAVYTTKE; AVYTTKEK; VYTTKEKA; YTTKEKAQ; TTKEKAQI; TKEKAQIL; KEKAQILY; EKAQILYK; KAQILYKK; AQILYKKL; QILYKKLM;

ILYKKLME; LYKKLMEK; YKKLMEKY; KKLMEKYS; KLMEKYSV; LMEKYSVT; MEKYSVTF;
EKYSVTFI; KYSVTFIS; YSVTFISR; SVTFISRH; VTFISRHM; TFISRHMC; FISRHMCA;
ISRHMCAG; SRHMCAGH; RHMCAGHN; HMCAGHNI; MCAGHNII; CAGHNIIF; AGHNIIFF;
GHNIIFFL; HNIIFFLT; NIIFFLTP; IIFFLTPH; IFFLTPHR; FFLTPHRH; FLTPHRHR;
LTPHRHRV; TPHRHRVS; PHRHRVSA; HRHRVSAI; RHRVSAIN; HRVSAINN; RVSAINNF;
VSAINNFC; SAINNFCQ; AINNFCQK; INNFCQKL; NNFCQKLC; NFCQKLCT; FCQKLCTF;
CQKLCTFS; QKLCTFSF; KLCTFSFL; LCTFSFLI; CTFSFLIC; TFSFLICK; FSFLICKG;
SFLICKGV; FLICKGVN; LICKGVNK; ICKGVNKE; CKGVNKEY; KGVNKEYL; GVNKEYLL;
VNKEYLLY; NKEYLLYS; KEYLLYSA; EYLLYSAL; YLLYSALT; LLYSALTR; LYSALTRD;
YSALTRDP; SALTRDPY; ALTRDPYH; LTRDPYHT; TRDPYHTI; RDPYHTIE; DPYHTIEE;
PYHTIEES; YHTIEESI; HTIEESIQ; TIEESIQG; IEESIQGG; EESIQGGL; ESIQGGLK;
SIQGGLKE; IQGGLKEH; QGGLKEHD; GGLKEHDF; GLKEHDFS; LKEHDFSP; KEHDFSPE;
EHDFSPEE; HDFSPEEP; DFSPEEPE; FSPEEPEE; SPEEPEET; PEEPEETK; EEPEETKQ;
EPEETKQV; PEETKQVS; EETKQVSW; ETKQVSWK; TKQVSWKL; KQVSWKLI; QVSWKLIT;
VSWKLITE; SWKLITEY; WKLITEYA; KLITEYAV; LITEYAVE; ITEYAVET; TEYAVETK;
EYAVETKC; YAVETKCE; AVETKCED; VETKCEDV; ETKCEDVF; TKCEDVFL; KCEDVFLL;
CEDVFLLL; EDVFLLLG; DVFLLLGM; VFLLLGMY; FLLLGMYL; LLLGMYLE; LLGMYLEF;
LGMYLEFQ; GMYLEFQY; MYLEFQYN; YLEFQYNV; LEFQYNVE; EFQYNVEE; FQYNVEEC;
QYNVEECK; YNVEECKK; NVEECKKC; VEECKKCQ; EECKKCQK; ECKKCQKK; CKKCQKKD;
KKCQKKDQ; KCQKKDQP; CQKKDQPY; QKKDQPYH; KKDQPYHF; KDQPYHFK; DQPYHFKY;
QPYHFKYH; PYHFKYHE; YHFKYHEK; HFKYHEKH; FKYHEKHF; KYHEKHFA; YHEKHFAN;
HEKHFANA; EKHFANAI; KHFANAII; HFANAIIF; FANAIIFA; ANAIIFAE; NAIIFAES;
AIIFAESK; IIFAESKN; IFAESKNQ; FAESKNQK; AESKNQKS; ESKNQKSI; SKNQKSIC;
KNQKSICQ; NQKSICQQ; QKSICQQA; KSICQQAV; SICQQAVD; ICQQAVDT; CQQAVDTV;
QQAVDTVL; QAVDTVLA; AVDTVLAK; VDTVLAKK; DTVLAKKR; TVLAKKRV; VLAKKRVD;
LAKKRVDT; AKKRVDTL; KKRVDTLH; KRVDTLHM; RVDTLHMT; VDTLHMTR; DTLHMTRE;
TLHMTREE; LHMTREEM; HMTREEML; MTREEMLT; TREEMLTE; REEMLTER; EEMLTERF;
EMLTERFN; MLTERFNH; LTERFNHI; TERFNHIL; ERFNHILD; RFNHILDK; FNHILDKM;
NHILDKMD; HILDKMDL; ILDKMDLI; LDKMDLIF; DKMDLIFG; KMDLIFGA; MDLIFGAH;
DLIFGAHG; LIFGAHGN; IFGAHGNA; FGAHGNAV; GAHGNAVL; AHGNAVLE; HGNAVLEQ;
GNAVLEQY; NAVLEQYM; AVLEQYMA; VLEQYMAG; LEQYMAGV; EQYMAGVA; QYMAGVAW;
YMAGVAWL; MAGVAWLH; AGVAWLHC; GVAWLHCL; VAWLHCLL; AWLHCLLP; WLHCLLPK;
LHCLLPKM; HCLLPKMD; CLLPKMDS; LLPKMDSV; LPKMDSVI; PKMDSVIF; KMDSVIFD;
MDSVIFDF; DSVIFDFL; SVIFDFLH; VIFDFLHC; IFDFLHCI; FDFLHCIV; DFLHCIVF;
FLHCIVFN; LHCIVFNV; HCIVFNVP; CIVFNVPK; IVFNVPKR; VFNVPKRR; FNVPKRRY;
NVPKRRYW; VPKRRYWL; PKRRYWLF; KRRYWLFK; RRYWLFKG; RYWLFKGP; YWLFKGPI;
WLFKGPID; LFKGPIDS; FKGPIDSG; KGPIDSGK; GPIDSGKT; PIDSGKTT; IDSGKTTL;
DSGKTTLA; SGKTTLAA; GKTTLAAG; KTTLAAGL; TTLAAGLL; TLAAGLLD; LAAGLLDL;
AAGLLDLC; AGLLDLCG; GLLDLCGG; LLDLCGGK; LDLCGGKA; DLCGGKAL; LCGGKALN;
CGGKALNV; GGKALNVN; GKALNVNL; KALNVNLP; ALNVNLPM; LNVNLPME; NVNLPMER;
VNLPMERL; NLPMERLT; LPMERLTF; PMERLTFE; MERLTFEL; ERLTFELG; RLTFELGV;
LTFELGVA; TFELGVAI; FELGVAID; ELGVAIDQ; LGVAIDQY; GVAIDQYM; VAIDQYMV;
AIDQYMVV; IDQYMVVF; DQYMVVFE; QYMVVFED; YMVVFEDV; MVVFEDVK; VVFEDVKG;
VFEDVKGT; FEDVKGTG; EDVKGTGA; DVKGTGAE; VKGTGAES; KGTGAESK; GTGAESKD;
TGAESKDL; GAESKDLP; AESKDLPS; ESKDLPSG; SKDLPSGH; KDLPSGHG; DLPSGHGI;
LPSGHGIN; PSGHGINN; SGHGINNL; GHGINNLD; HGINNLDS; GINNLDSL; INNLDSLR;
NNLDSLRD; NLDSLRDY; LDSLRDYL; DSLRDYLD; SLRDYLDG; LRDYLDGS; RDYLDGSV;
DYLDGSVK; YLDGSVKV; LDGSVKVN; DGSVKVNL; GSVKVNLE; SVKVNLEK; VKVNLEKK;
KVNLEKKH; VNLEKKHL; NLEKKHLN; LEKKHLNK; EKKHLNKR; KKHLNKRT; KHLNKRTQ;
HLNKRTQI; LNKRTQIF; NKRTQIFP; KRTQIFPP; RTQIFPPG; TQIFPPGL; QIFPPGLV;
IFPPGLVT; FPPGLVTM; PPGLVTMN; PGLVTMNE; GLVTMNEY; LVTMNEYP; VTMNEYPV;
TMNEYPVP; MNEYPVPK; NEYPVPKT; EYPVPKTL; YPVPKTLQ; PVPKTLQA; VPKTLQAR;
PKTLQARF; KTLQARFV; TLQARFVR; LQARFVRQ; QARFVRQI; ARFVRQID; RFVRQIDF;
FVRQIDFR; VRQIDFRP; RQIDFRPK; QIDFRPKI; IDFRPKIY; DFRPKIYL; FRPKIYLR;
RPKIYLRK; PKIYLRKS; KIYLRKSL; IYLRKSLQ; YLRKSLQN; LRKSLQNS; RKSLQNSE;
KSLQNSEF; SLQNSEFL; LQNSEFLL; QNSEFLLE; NSEFLLEK; SEFLLEKR; EFLLEKRI;
FLLEKRIL; LLEKRILQ; LEKRILQS; EKRILQSG; KRILQSGM; RILQSGMT; ILQSGMTL;
LQSGMTLL; QSGMTLLL; SGMTLLLL; GMTLLLLL; MTLLLLLI; TLLLLLIW; LLLLLIWF;
LLLLIWFR; LLLIWFRP; LLIWFRPV; LIWFRPVA; IWFRPVAD; WFRPVADF; FRPVADFA;
RPVADFAT; PVADFATD; VADFATDI; ADFATDIQ; DFATDIQS; FATDIQSR; ATDIQSRI;
TDIQSRIV; DIQSRIVE; IQSRIVEW; QSRIVEWK; SRIVEWKE; RIVEWKER; IVEWKERL;
VEWKERLD; EWKERLDS; WKERLDSE; KERLDSEI; ERLDSEIS; RLDSEISM; LDSEISMY;
DSEISMYT; SEISMYTF; EISMYTFS; ISMYTFSR; SMYTFSRM; MYTFSRMK; YTFSRMKY;
TFSRMKYN; FSRMKYNI; SRMKYNIC; RMKYNICM; MKYNICMG; KYNICMGK; YNICMGKC;
NICMGKCI; ICMGKCIL; CMGKCILD; MGKCILDI; GKCILDIT; KCILDITR; CILDITRE;

ILDITREE; LDITREED; DITREEDS; ITREEDSE; TREEDSET; REEDSETE; EEDSETED;
EDSETEDS; DSETEDSG; SETEDSGH; ETEDSGHG; TEDSGHGS; EDSGHGSS; DSGHGSST;
SGHGSSTE; GHGSSTES; HGSSTESQ; GSSTESQS; SSTESQSQ; STESQSQC; TESQSQCS;
ESQSQCSS; SQSQCSSQ; QSQCSSQV; SQCSSQVS; QCSSQVSD; CSSQVSDT; SSQVSDTS;
SQVSDTSA; QVSDTSAP; VSDTSAPA; SDTSAPAE; DTSAPAED; TSAPAEDS; SAPAEDSQ;
APAEDSQR; PAEDSQRS; AEDSQRSD; EDSQRSDP; DSQRSDPH; SQRSDPHS; QRSDPHSQ;
RSDPHSQE; SDPHSQEL; DPHSQELH; PHSQELHL; HSQELHLC; SQELHLCK; QELHLCKG;
ELHLCKGF; LHLCKGFQ; HLCKGFQC; LCKGFQCF; CKGFQCFK; KGFQCFKR; GFQCFKRP;
FQCFKRPK; QCFKRPKT; CFKRPKTP; FKRPKTPP; KRPKTPPP; RPKTPPPK; HKLKSGLY;
KLKSGLYK; LKSGLYKS; KSGLYKSS; SGLYKSSI; GLYKSSIY; MYMYNKST; YMYNKSTC;
MYNKSTCL; YNKSTCLK; NKSTCLKH; KSTCLKHF; STCLKHFG; TCLKHFGL; CLKHFGLQ;
LKHFGLQL; KHFGLQLS; HFGLQLSL; FGLQLSLF; GLQLSLFV; LQLSLFVN; QLSLFVNI;
LSLFVNIS; SLFVNISY; LFVNISYH; FVNISYHI; VNISYHIW; NISYHIWV; ISYHIWVP;
SYHIWVPW; YHIWVPWK; HIWVPWKS; IWVPWKSF; WVPWKSFC; VPWKSFCA; PWKSFCAI;
WKSFCAIK; KSFCAIKH; SFCAIKHP; FCAIKHPN; CAIKHPNL; AIKHPNLF; IKHPNLFY;
KHPNLFYL; HPNLFYLG; PNLFYLGF; NLFYLGFH; LFYLGFHT; FYLGFHTI; YLGFHTIH;
LGFHTIHR; GFHTIHRL; FHTIHRLP; HTIHRLPI; TIHRLPIH; IHRLPIHS; HRLPIHSL;
RLPIHSLG; LPIHSLGS; PIHSLGSP; IHSLGSPV; HSLGSPVY; SLGSPVYK; LGSPVYKV;
GSPVYKVT; QKGNWVRI; KGNWVRIL; GNWVRILY; NWVRILYR; WVRILYRS; VRILYRSF;
RILYRSFS; ILYRSFSQ; LYRSFSQA; YRSFSQAD; RSFSQADL; SFSQADLK; FSQADLKI;
SQADLKIS; QADLKISC; ADLKISCK; DLKISCKA; LKISCKAS; KISCKASP; ISCKASPL;
SCKASPLL; CKASPLLC; KASPLLCS; ASPLLCSR; SPLLCSRA; PLLCSRAV; LLCSRAVS;
LCSRAVSK; CSRAVSKQ; SRAVSKQA; RAVSKQAT; AVSKQATN; VSKQATNI; SKQATNIS;
KQATNISS; NIQAISFT; IQAISFTK; QAISFTKR; AISFTKRP; ISFTKRPH; SFTKRPHT;
FTKRPHTL; TKRPHTLF; KRPHTLFI; QHCGSCVG; HCGSCVGH; CGSCVGHM; GSCVGHMK;
SCVGHMKY; CVGHMKYW; VGHMKYWG; GHMKYWGN; HMKYWGNI; MKYWGNIF; KYWGNIFP;
YWGNIFPS; WGNIFPSC; GNIFPSCE; NIFPSCES; IFPSCESP; FPSCESPK; PSCESPKI;
SCESPKIP; CESPKIPS; ESPKIPSI; SPKIPSIF; PKIPSIFI; KIPSIFIS; IPSIFIST;
PSIFISTG; SIFISTGI; IFISTGIR; FISTGIRY; ISTGIRYP; STGIRYPA; TGIRYPAL;
GIRYPALN; IRYPALNW; RYPALNWI; YPALNWIS; PALNWISI; ALNWISIV; LNWISIVF;
NWISIVFV; WISIVFVQ; ISIVFVQI; SIVFVQIG; IVFVQIGL; VFVQIGLM; FVQIGLMV;
VQIGLMVS; QIGLMVSI; IGLMVSIH; GLMVSIHY; LMVSIHYL; MVSIHYLG; VSIHYLGL;
SIHYLGLG; IHYLGLGC; HYLGLGCW; YLGLGCWV; LGLGCWVF; GLGCWVFR; LGCWVFRG;
GCWVFRGY; CWVFRGYS; WVFRGYST; VFRGYSTI; FRGYSTIR; RGYSTIRV; GYSTIRVL;
HSLHFQGF; SLHFQGFS; LHFQGFST; HFQGFSTY; FQGFSTYS; QGFSTYSK; GFSTYSKE;
FSTYSKEV; STYSKEVE; TYSKEVEI; YSKEVEIT; SKEVEITA; KEVEITAL; EVEITALN;
VEITALNR; EITALNRF; ITALNRFS; TALNRFSS; ALNRFSST; LNRFSSTM; NRFSSTML;
RFSSTMLM; FSSTMLMH; SSTMLMHF; STMLMHFL; PCMKVKHA; CMKVKHAS; MKVKHASY;
KVKHASYS; VKHASYSN; KHASYSNN; HASYSNNL; ASYSNNLC; SYSNNLCL; YSNNLCLY;
SNNLCLYS; NNLCLYSY; NLCLYSYS; LCLYSYSL; CLYSYSLP; LYSYSLPH; YSYSLPHQ;
IGEGNSCC; GEGNSCCA; EGNSCCAV; GNSCCAVT; NSCCAVTG; SCCAVTGK; CCAVTGKH;
CAVTGKHF; AVTGKHFS; VTGKHFSL; TGKHFSLW; GKHFSLWA; KHFSLWAI; HFSLWAIT;
FSLWAITA; SLWAITAK; LWAITAKV; WAITAKVI; AITAKVIF; ITAKVIFS; TAKVIFST;
TKAPKVFI; KAPKVFIW; APKVFIWI; PKVFIWIP; KVFIWIPH; VFIWIPHF; FIWIPHFW;
IWIPHFWV; EAFYLCNS; AFYLCNSI; FYLCNSIY; YLCNSIYP; LCNSIYPS; CNSIYPSF;
NSIYPSFN; SIYPSFNF; FWHLHGFL; WHLHGFLW; HLHGFLWL; LHGFLWLF; HGFLWLFG;
GFLWLFGS; FLWLFGSC; LWLFGSCP; WLFGSCPW; LFGSCPWT; FGSCPWTL; GSCPWTLS;
SCPWTLSF; CPWTLSFS; PWTLSFSF; WTLSFSFG; TLSFSFGW; LSFSFGWG; SFSFGWGH;
FSFGWGHL; SFGWGHLH; FGWGHLHM; GWGHLHML; WGHLHMLQ; GHLHMLQE; HLHMLQEQ;
LHMLQEQV; HMLQEQVL; MLQEQVLQ; LQEQVLQS; QEQVLQSR; EQVLQSRT; QVLQSRTG;
VLQSRTGL; LQSRTGLE; QSRTGLEV; SRTGLEVK; RTGLEVKA; TGLEVKAT; GLEVKATS;
LEVKATSI; EVKATSIE; VKATSIEE; KATSIEEQ; ATSIEEQF; TSIEEQFF; SIEEQFFD;
TLLNVHFV; LLNVHFVD; LNVHFVDF; NVHFVDFL; VHFVDFLS; HFVDFLSP; FVDFLSPF;
VDFLSPFF; DFLSPFFV; LLLYCQHH; LLYCQHHL; LYCQHHLY; YCQHHLYY; CQHHLYYK;
QHHLYYKY; HHLYYKYG; HLYYKYGQ; LYYKYGQN; YYKYGQNV; YKYGQNVH; KYGQNVHG;
YGQNVHGY; GQNVHGYL; QNVHGYLP; NVHGYLPF; VHGYLPFQ; HGYLPFQL; GYLPFQLL;
YLPFQLLV; GKDQNNIV; KDQNNIVE; DQNNIVEY; QNNIVEYN; NNIVEYNY; NIVEYNYK;
IVEYNYKS; VEYNYKSL; KIFLFFSA; IFLFFSAI; FLFFSAIP; LFFSAIPV; FFSAIPVR;
FSAIPVRL; QTKKDPNA; QKYLHQET; KYLHQETE; YLHQETEY; LHQETEYH; HQETEYHS;
QETEYHST; ETEYHSTH; TEYHSTHL; EYHSTHLG; TIPKPCLI; IPKPCLIA; PKPCLIAD;
KPCLIADR; PCLIADRG; CLIADRGL; LIADRGLQ; IADRGLQW; ADRGLQWK; DRGLQWKL;
RGLQWKLC; GLQWKLCD; LQWKLCDP; QWKLCDPN; WKLCDPNH; KLCDPNHQ; LCDPNHQR;
CDPNHQRT; DPNHQRTY; PNHQRTYT; NHQRTYTL; HQRTYTLL; QRTYTLLE; RTYTLLEL;
TYTLLELR; YTLLELRN; QFELKQQT; FELKQQTQ; ELKQQTQQ; PQEHQQLQ; QEHQQLQH;
EHQQLQHM; HQQLQHMF; QQLQHMFE; QLQHMFEE; LQHMFEEL; QHMFEELG; HMFEELGL;

PLRYLLCP; LRYLLCPL; RYLLCPLQ; QGMQFELL; QQQPPQQQ; QQPPQQQF; QPPQQQFQ;
PPQQQFQP; PQQQFQPL; QQQFQPLK; QQFQPLKI; QFQPLKIL; FQPLKILW; QPLKILWQ;
PLKILWQQ; LKILWQQQ; KILWQQQP; ILWQQQPQ; LWQQQPQI; WQQQPQIH; QQQPQIHW;
QQPQIHWQ; QPQIHWQL; PQIHWQLG; QIHWQLGP; IHWQLGPP; HWQLGPPK; WQLGPPKV;
QLGPPKVL; LGPPKVLE; GPPKVLEQ; PPKVLEQH; PKVLEQHP; TWKYKKKG; WKYKKKGI;
KYKKKGIT; YKKKGITY; KKKGITYL; KKGITYLG; KGITYLGV; GITYLGVF; ITYLGVFY;
TYLGVFYR; YLGVFYRV; LGVFYRVF; GVFYRVFY; VFYRVFYS; FYRVFYSR; SSGTFVFP;
SGTFVFPV; GTFVFPVY; TFVFPVYT; FVFPVYTV; VFPVYTVF; FPVYTVFT; PVYTVFTS;
VYTVFTST; YTVFTSTK; TVFTSTKF; VFTSTKFQ; FTSTKFQQ; TSTKFQQK; STKFQQKL;
NKNKNPLS; KNKNPLSS; NKNPLSSF; KNPLSSFF; NPLSSFFC; PLSSFFCS; LSSFFCSS;
SSFFCSSP; SFFCSSPG; FFCSSPGF; FCSSPGFT; CSSPGFTN; SSPGFTNF; SPGFTNFH;
QLAQNHGL; LAQNHGLC; AQNHGLCP; QNHGLCPV; LGTRPRFL; GTRPRFLG; TRPRFLGS;
RPRFLGSQ; PRFLGSQN; RFLGSQNM; FLGSQNMS; LGSQNMSV; GSQNMSVM; SQNMSVMH;
QNMSVMHF; NMSVMHFP; MSVMHFPS; GHGLAAFH; HGLAAFHG; AAPPCESC; APPCESCT;
PPCESCTF; PCESCTFL; CESCTFLP; ESCTFLPE; SCTFLPEV; CTFLPEVM; TFLPEVMV;
FLPEVMVW; LPEVMVWL; PEVMVWLH; EVMVWLHS; VMVWLHSP; MVWLHSPV; VWLHSPVS;
WLHSPVSH; LHSPVSHA; HSPVSHAL; SPVSHALS; PVSHALSF; VSHALSFL; SHALSFLR;
HALSFLRS; ALSFLRSW; LSFLRSWF; SFLRSWFG; FLRSWFGC; LRSWFGCI; RSWFGCIP;
SWFGCIPW; WFGCIPWV; FGCIPWVS; GCIPWVSS; CIPWVSSS; IPWVSSSS; PWVSSSSL;
WVSSSSLW; VSSSSLWP; SSSSLWPF; SSSLWPFF; SSLWPFFL; YIRGRGRL; IRGRGRLC;
RGRGRLCL; GRGRLCLH; RGRLCLHP; GRLCLHPF; RLCLHPFS; LCLHPFSQ; CLHPFSQV;
LHPFSQVV; HPFSQVVR; PFSQVVRV; FSQVVRVW; SQVVRVWR; QVVRVWRL; VVRVWRLF;
VRVWRLFL; RVWRLFLR; VWRLFLRP; WRLFLRPS; RLFLRPSK; LFLRPSKT; FLRPSKTI;
LRPSKTIW; RPSKTIWG; PSKTIWGN; SKTIWGNP; KTIWGNPY; TIWGNPYS; IWGNPYSF;
WGNPYSFA; GNPYSFAI; NPYSFAIF; PYSFAIFA; YSFAIFAK

9 mers:
QGRIHGAHG; GRIHGAHGP; RIHGAHGPF; IHGAHGPFR; HGAHGPFRP; KSCLGKSSL; SCLGKSSLN;
CLGKSSLNE; LGKSSLNEK; GKSSLNEKS; KSSLNEKSL; SSLNEKSLF; SLNEKSLFK; LNEKSLFKE;
NEKSLFKEV; KNGAGCKGS; NGAGCKGSS; GAGCKGSSS; AGCKGSSSA; FSSLPRYPV; SSLPRYPVL;
SLPRYPVLQ; LPRYPVLQG; PRYPVLQGM; RYPVLQGMA; YPVLQGMAY; PVLQGMAYL; VLQGMAYLF;
LQGMAYLFQ; QGMAYLFQK; GMAYLFQKA; MAYLFQKAF; AYLFQKAFC; YLFQKAFCA; LFQKAFCAL;
FQKAFCALP; QKAFCALPL; KAFCALPLH; AFCALPLHA; FCALPLHAM; CALPLHAMS; ALPLHAMSA;
KIFKKRALG; IFKKRALGL; FKKRALGLD; KKRALGLDR; KRALGLDRL; RALGLDRLL; ALGLDRLLL;
LGLDRLLLH; LLHTVVWLR; LHTVVWLRP; HTVVWLRPN; RNSAMVGPN; NSAMVGPNN; SAMVGPNNW;
AMVGPNNWR; MVGPNNWRN; VGPNNWRNS; GPNNWRNSL; PNNWRNSLQ; NNWRNSLQR; NWRNSLQRS;
WRNSLQRSK; RNSLQRSKA; NSLQRSKAL; SLQRSKALR; INNKILKGP; NNKILKGPK; VPTYGTEEW;
PTYGTEEWE; TYGTEEWES; YGTEEWESW; GTEEWESWW; TEEWESWWS; EEWESWWSS; EWESWWSSF;
WESWWSSFN; ESWWSSFNE; SWWSSFNEK; WWSSFNEKW; WSSFNEKWD; SSFNEKWDE; SFNEKWDED;
FNEKWDEDL; NEKWDEDLF; EKWDEDLFC; KWDEDLFCH; WDEDLFCHE; DEDLFCHED; EDLFCHEDM;
DLFCHEDMF; LFCHEDMFA; FCHEDMFAS; CHEDMFASD; HEDMFASDE; EDMFASDEE; DMFASDEEA;
MFASDEEAT; FASDEEATA; ASDEEATAD; SDEEATADS; DEEATADSQ; EEATADSQH; EATADSQHS;
ATADSQHST; TADSQHSTP; ADSQHSTPP; DSQHSTPPK; SQHSTPPKK; QHSTPPKKK; HSTPPKKKR;
STPPKKKRK; TPPKKKRKV; PPKKKRKVE; PKKKRKVED; KKKRKVEDP; KKRKVEDPK; KRKVEDPKD;
RKVEDPKDF; KVEDPKDFP; VEDPKDFPS; EDPKDFPSD; DPKDFPSDL; PKDFPSDLH; KDFPSDLHQ;
DFPSDLHQF; FPSDLHQFL; PSDLHQFLS; SDLHQFLSQ; DLHQFLSQA; LHQFLSQAV; HQFLSQAVF;
QFLSQAVFS; FLSQAVFSN; LSQAVFSNR; SQAVFSNRT; QAVFSNRTL; AVFSNRTLA; VFSNRTLAC;
FSNRTLACF; SNRTLACFA; NRTLACFAV; RTLACFAVY; TLACFAVYT; LACFAVYTT; ACFAVYTTK;
CFAVYTTKE; FAVYTTKEK; AVYTTKEKA; VYTTKEKAQ; YTTKEKAQI; TTKEKAQIL; TKEKAQILY;
KEKAQILYK; EKAQILYKK; KAQILYKKL; AQILYKKLM; QILYKKLME; ILYKKLMEK; LYKKLMEKY;
YKKLMEKYS; KKLMEKYSV; KLMEKYSVT; LMEKYSVTF; MEKYSVTFI; EKYSVTFIS; KYSVTFISR;
YSVTFISRH; SVTFISRHM; VTFISRHMC; TFISRHMCA; FISRHMCAG; ISRHMCAGH; SRHMCAGHN;
RHMCAGHNI; HMCAGHNII; MCAGHNIIF; CAGHNIIFF; AGHNIIFFL; GHNIIFFLT; HNIIFFLTP;
NIIFFLTPH; IIFFLTPHR; IFFLTPHRH; FFLTPHRHR; FLTPHRHRV; LTPHRHRVS; TPHRHRVSA;
PHRHRVSAI; HRHRVSAIN; RHRVSAINN; HRVSAINNF; RVSAINNFC; VSAINNFCQ; SAINNFCQK;
AINNFCQKL; INNFCQKLC; NNFCQKLCT; NFCQKLCTF; FCQKLCTFS; CQKLCTFSF; QKLCTFSFL;
KLCTFSFLI; LCTFSFLIC; CTFSFLICK; TFSFLICKG; FSFLICKGV; SFLICKGVN; FLICKGVNK;
LICKGVNKE; ICKGVNKEY; CKGVNKEYL; KGVNKEYLL; GVNKEYLLY; VNKEYLLYS; NKEYLLYSA;
KEYLLYSAL; EYLLYSALT; YLLYSALTR; LLYSALTRD; LYSALTRDP; YSALTRDPY; SALTRDPYH;
ALTRDPYHT; LTRDPYHTI; TRDPYHTIE; RDPYHTIEE; DPYHTIEES; PYHTIEESI; YHTIEESIQ;
HTIEESIQG; TIEESIQGG; IEESIQGGL; EESIQGGLK; ESIQGGLKE; SIQGGLKEH; IQGGLKEHD;
QGGLKEHDF; GGLKEHDFS; GLKEHDFSP; LKEHDFSPE; KEHDFSPEE; EHDFSPEEP; HDFSPEEPE;
DFSPEEPEE; FSPEEPEET; SPEEPEETK; PEEPEETKQ; EEPEETKQV; EPEETKQVS; PEETKQVSW;
EETKQVSWK; ETKQVSWKL; TKQVSWKLI; KQVSWKLIT; QVSWKLITE; VSWKLITEY; SWKLITEYA;
WKLITEYAV; KLITEYAVE; LITEYAVET; ITEYAVETK; TEYAVETKC; EYAVETKCE; YAVETKCED;

AVETKCEDV; VETKCEDVF; ETKCEDVFL; TKCEDVFLL; KCEDVFLLL; CEDVFLLLG; EDVFLLLGM;
DVFLLLGMY; VFLLLGMYL; FLLLGMYLE; LLLGMYLEF; LLGMYLEFQ; LGMYLEFQY; GMYLEFQYN;
MYLEFQYNV; YLEFQYNVE; LEFQYNVEE; EFQYNVEEC; FQYNVEECK; QYNVEECKK; YNVEECKKC;
NVEECKKCQ; VEECKKCQK; EECKKCQKK; ECKKCQKKD; CKKCQKKDQ; KKCQKKDQP; KCQKKDQPY;
CQKKDQPYH; QKKDQPYHF; KKDQPYHFK; KDQPYHFKY; DQPYHFKYH; QPYHFKYHE; PYHFKYHEK;
YHFKYHEKH; HFKYHEKHF; FKYHEKHFA; KYHEKHFAN; YHEKHFANA; HEKHFANAI; EKHFANAII;
KHFANAIIF; HFANAIIFA; FANAIIFAE; ANAIIFAES; NAIIFAESK; AIIFAESKN; IIFAESKNQ;
IFAESKNQK; FAESKNQKS; AESKNQKSI; ESKNQKSIC; SKNQKSICQ; KNQKSICQQ; NQKSICQQA;
QKSICQQAV; KSICQQAVD; SICQQAVDT; ICQQAVDTV; CQQAVDTVL; QQAVDTVLA; QAVDTVLAK;
AVDTVLAKK; VDTVLAKKR; DTVLAKKRV; TVLAKKRVD; VLAKKRVDT; LAKKRVDTL; AKKRVDTLH;
KKRVDTLHM; KRVDTLHMT; RVDTLHMTR; VDTLHMTRE; DTLHMTREE; TLHMTREEM; LHMTREEML;
HMTREEMLT; MTREEMLTE; TREEMLTER; REEMLTERF; EEMLTERFN; EMLTERFNH; MLTERFNHI;
LTERFNHIL; TERFNHILD; ERFNHILDK; RFNHILDKM; FNHILDKMD; NHILDKMDL; HILDKMDLI;
ILDKMDLIF; LDKMDLIFG; DKMDLIFGA; KMDLIFGAH; MDLIFGAHG; DLIFGAHGN; LIFGAHGNA;
IFGAHGNAV; FGAHGNAVL; GAHGNAVLE; AHGNAVLEQ; HGNAVLEQY; GNAVLEQYM; NAVLEQYMA;
AVLEQYMAG; VLEQYMAGV; LEQYMAGVA; EQYMAGVAW; QYMAGVAWL; YMAGVAWLH; MAGVAWLHC;
AGVAWLHCL; GVAWLHCLL; VAWLHCLLP; AWLHCLLPK; WLHCLLPKM; LHCLLPKMD; HCLLPKMDS;
CLLPKMDSV; LLPKMDSVI; LPKMDSVIF; PKMDSVIFD; KMDSVIFDF; MDSVIFDFL; DSVIFDFLH;
SVIFDFLHC; VIFDFLHCI; IFDFLHCIV; FDFLHCIVF; DFLHCIVFN; FLHCIVFNV; LHCIVFNVP;
HCIVFNVPK; CIVFNVPKR; IVFNVPKRR; VFNVPKRRY; FNVPKRRYW; NVPKRRYWL; VPKRRYWLF;
PKRRYWLFK; KRRYWLFKG; RRYWLFKGP; RYWLFKGPI; YWLFKGPID; WLFKGPIDS; LFKGPIDSG;
FKGPIDSGK; KGPIDSGKT; GPIDSGKTT; PIDSGKTTL; IDSGKTTLA; DSGKTTLAA; SGKTTLAAG;
GKTTLAAGL; KTTLAAGLL; TTLAAGLLD; TLAAGLLDL; LAAGLLDLC; AAGLLDLCG; AGLLDLCGG;
GLLDLCGGK; LLDLCGGKA; LDLCGGKAL; DLCGGKALN; LCGGKALNV; CGGKALNVN; GGKALNVNL;
GKALNVNLP; KALNVNLPM; ALNVNLPME; LNVNLPMER; NVNLPMERL; VNLPMERLT; NLPMERLTF;
LPMERLTFE; PMERLTFEL; MERLTFELG; ERLTFELGV; RLTFELGVA; LTFELGVAI; TFELGVAID;
FELGVAIDQ; ELGVAIDQY; LGVAIDQYM; GVAIDQYMV; VAIDQYMVV; AIDQYMVVF; IDQYMVVFE;
DQYMVVFED; QYMVVFEDV; YMVVFEDVK; MVVFEDVKG; VVFEDVKGT; VFEDVKGTG; FEDVKGTGA;
EDVKGTGAE; DVKGTGAES; VKGTGAESK; KGTGAESKD; GTGAESKDL; TGAESKDLP; GAESKDLPS;
AESKDLPSG; ESKDLPSGH; SKDLPSGHG; KDLPSGHGI; DLPSGHGIN; LPSGHGINN; PSGHGINNL;
SGHGINNLD; GHGINNLDS; HGINNLDSL; GINNLDSLR; INNLDSLRD; NNLDSLRDY; NLDSLRDYL;
LDSLRDYLD; DSLRDYLDG; SLRDYLDGS; LRDYLDGSV; RDYLDGSVK; DYLDGSVKV; YLDGSVKVN;
LDGSVKVNL; DGSVKVNLE; GSVKVNLEK; SVKVNLEKK; VKVNLEKKH; KVNLEKKHL; VNLEKKHLN;
NLEKKHLNK; LEKKHLNKR; EKKHLNKRT; KKHLNKRTQ; KHLNKRTQI; HLNKRTQIF; LNKRTQIFP;
NKRTQIFPP; KRTQIFPPG; RTQIFPPGL; TQIFPPGLV; QIFPPGLVT; IFPPGLVTM; FPPGLVTMN;
PPGLVTMNE; PGLVTMNEY; GLVTMNEYP; LVTMNEYPV; VTMNEYPVP; TMNEYPVPK; MNEYPVPKT;
NEYPVPKTL; EYPVPKTLQ; YPVPKTLQA; PVPKTLQAR; VPKTLQARF; PKTLQARFV; KTLQARFVR;
TLQARFVRQ; LQARFVRQI; QARFVRQID; ARFVRQIDF; RFVRQIDFR; FVRQIDFRP; VRQIDFRPK;
RQIDFRPKI; QIDFRPKIY; IDFRPKIYL; DFRPKIYLR; FRPKIYLRK; RPKIYLRKS; PKIYLRKSL;
KIYLRKSLQ; IYLRKSLQN; YLRKSLQNS; LRKSLQNSE; RKSLQNSEF; KSLQNSEFL; SLQNSEFLL;
LQNSEFLLE; QNSEFLLEK; NSEFLLEKR; SEFLLEKRI; EFLLEKRIL; FLLEKRILQ; LLEKRILQS;
LEKRILQSG; EKRILQSGM; KRILQSGMT; RILQSGMTL; ILQSGMTLL; LQSGMTLLL; QSGMTLLLL;
SGMTLLLLL; GMTLLLLLI; MTLLLLLIW; TLLLLLIWF; LLLLLIWFR; LLLLIWFRP; LLLIWFRPV;
LLIWFRPVA; LIWFRPVAD; IWFRPVADF; WFRPVADFA; FRPVADFAT; RPVADFATD; PVADFATDI;
VADFATDIQ; ADFATDIQS; DFATDIQSR; FATDIQSRI; ATDIQSRIV; TDIQSRIVE; DIQSRIVEW;
IQSRIVEWK; QSRIVEWKE; SRIVEWKER; RIVEWKERL; IVEWKERLD; VEWKERLDS; EWKERLDSE;
WKERLDSEI; KERLDSEIS; ERLDSEISM; RLDSEISMY; LDSEISMYT; DSEISMYTF; SEISMYTFS;
EISMYTFSR; ISMYTFSRM; SMYTFSRMK; MYTFSRMKY; YTFSRMKYN; TFSRMKYNI; FSRMKYNIC;
SRMKYNICM; RMKYNICMG; MKYNICMGK; KYNICMGKC; YNICMGKCI; NICMGKCIL; ICMGKCILD;
CMGKCILDI; MGKCILDIT; GKCILDITR; KCILDITRE; CILDITREE; ILDITREED; LDITREEDS;
DITREEDSE; ITREEDSET; TREEDSETE; REEDSETED; EEDSETEDS; EDSETEDSG; DSETEDSGH;
SETEDSGHG; ETEDSGHGS; TEDSGHGSS; EDSGHGSST; DSGHGSSTE; SGHGSSTES; GHGSSTESQ;
HGSSTESQS; GSSTESQSQ; SSTESQSQC; STESQSQCS; TESQSQCSS; ESQSQCSSQ; SQSQCSSQV;
QSQCSSQVS; SQCSSQVSD; QCSSQVSDT; CSSQVSDTS; SSQVSDTSA; SQVSDTSAP; QVSDTSAPA;
VSDTSAPAE; SDTSAPAED; DTSAPAEDS; TSAPAEDSQ; SAPAEDSQR; APAEDSQRS; PAEDSQRSD;
AEDSQRSDP; EDSQRSDPH; DSQRSDPHS; SQRSDPHSQ; QRSDPHSQE; RSDPHSQEL; SDPHSQELH;
DPHSQELHL; PHSQELHLC; HSQELHLCK; SQELHLCKG; QELHLCKGF; ELHLCKGFQ; LHLCKGFQC;
HLCKGFQCF; LCKGFQCFK; CKGFQCFKR; KGFQCFKRP; GFQCFKRPK; FQCFKRPKT; QCFKRPKTP;
CFKRPKTPP; FKRPKTPPP; KRPKTPPPK; HKLKSGLYK; KLKSGLYKS; LKSGLYKSS; KSGLYKSSI;
SGLYKSSIY; MYMYNKSTC; YMYNKSTCL; MYNKSTCLK; YNKSTCLKH; NKSTCLKHF; KSTCLKHFG;
STCLKHFGL; TCLKHFGLQ; CLKHFGLQL; LKHFGLQLS; KHFGLQLSL; HFGLQLSLF; FGLQLSLFV;
GLQLSLFVN; LQLSLFVNI; QLSLFVNIS; LSLFVNISY; SLFVNISYH; LFVNISYHI; FVNISYHIW;
VNISYHIWV; NISYHIWVP; ISYHIWVPW; SYHIWVPWK; YHIWVPWKS; HIWVPWKSF; IWVPWKSFC;
WVPWKSFCA; VPWKSFCAI; PWKSFCAIK; WKSFCAIKH; KSFCAIKHP; SFCAIKHPN; FCAIKHPNL;
CAIKHPNLF; AIKHPNLFY; IKHPNLFYL; KHPNLFYLG; HPNLFYLGF; PNLFYLGFH; NLFYLGFHT;

LFYLGFHTI; FYLGFHTIH; YLGFHTIHR; LGFHTIHRL; GFHTIHRLP; FHTIHRLPI; HTIHRLPIH; TIHRLPIHS; IHRLPIHSL; HRLPIHSLG; RLPIHSLGS; LPIHSLGSP; PIHSLGSPV; IHSLGSPVY; HSLGSPVYK; SLGSPVYKV; LGSPVYKVT; QKGNWVRIL; KGNWVRILY; GNWVRILYR; NWVRILYRS; WVRILYRSF; VRILYRSFS; RILYRSFSQ; ILYRSFSQA; LYRSFSQAD; YRSFSQADL; RSFSQADLK; SFSQADLKI; FSQADLKIS; SQADLKISC; QADLKISCK; ADLKISCKA; DLKISCKAS; LKISCKASP; KISCKASPL; ISCKASPLL; SCKASPLLC; CKASPLLCS; KASPLLCSR; ASPLLCSRA; SPLLCSRAV; PLLCSRAVS; LLCSRAVSK; LCSRAVSKQ; CSRAVSKQA; SRAVSKQAT; RAVSKQATN; AVSKQATNI; VSKQATNIS; SKQATNISS; NIQAISFTK; IQAISFTKR; QAISFTKRP; AISFTKRPH; ISFTKRPHT; SFTKRPHTL; FTKRPHTLF; TKRPHTLFI; QHCGSCVGH; HCGSCVGHM; CGSCVGHMK; GSCVGHMKY; SCVGHMKYW; CVGHMKYWG; VGHMKYWGN; GHMKYWGNI; HMKYWGNIF; MKYWGNIFP; KYWGNIFPS; YWGNIFPSC; WGNIFPSCE; GNIFPSCES; NIFPSCESP; IFPSCESPK; FPSCESPKI; PSCESPKIP; SCESPKIPS; CESPKIPSI; ESPKIPSIF; SPKIPSIFI; PKIPSIFIS; KIPSIFIST; IPSIFISTG; PSIFISTGI; SIFISTGIR; IFISTGIRY; FISTGIRYP; ISTGIRYPA; STGIRYPAL; TGIRYPALN; GIRYPALNW; IRYPALNWI; RYPALNWIS; YPALNWISI; PALNWISIV; ALNWISIVF; LNWISIVFV; NWISIVFVQ; WISIVFVQI; ISIVFVQIG; SIVFVQIGL; IVFVQIGLM; VFVQIGLMV; FVQIGLMVS; VQIGLMVSI; QIGLMVSIH; IGLMVSIHY; GLMVSIHYL; LMVSIHYLG; MVSIHYLGL; VSIHYLGLG; SIHYLGLGC; IHYLGLGCW; HYLGLGCWV; YLGLGCWVF; LGLGCWVFR; GLGCWVFRG; LGCWVFRGY; GCWVFRGYS; CWVFRGYST; WVFRGYSTI; VFRGYSTIR; FRGYSTIRV; RGYSTIRVL; HSLHFQGFS; SLHFQGFST; LHFQGFSTY; HFQGFSTYS; FQGFSTYSK; QGFSTYSKE; GFSTYSKEV; FSTYSKEVE; STYSKEVEI; TYSKEVEIT; YSKEVEITA; SKEVEITAL; KEVEITALN; EVEITALNR; VEITALNRF; EITALNRFS; ITALNRFSS; TALNRFSST; ALNRFSSTM; LNRFSSTML; NRFSSTMLM; RFSSTMLMH; FSSTMLMHF; SSTMLMHFL; PCMKVKHAS; CMKVKHASY; MKVKHASYS; KVKHASYSN; VKHASYSNN; KHASYSNNL; HASYSNNLC; ASYSNNLCL; SYSNNLCLY; YSNNLCLYS; SNNLCLYSY; NNLCLYSYS; NLCLYSYSL; LCLYSYSLP; CLYSYSLPH; LYSYSLPHQ; IGEGNSCCA; GEGNSCCAV; EGNSCCAVT; GNSCCAVTG; NSCCAVTGK; SCCAVTGKH; CCAVTGKHF; CAVTGKHFS; AVTGKHFSL; VTGKHFSLW; TGKHFSLWA; GKHFSLWAI; KHFSLWAIT; HFSLWAITA; FSLWAITAK; SLWAITAKV; LWAITAKVI; WAITAKVIF; AITAKVIFS; ITAKVIFST; TKAPKVFIW; KAPKVFIWI; APKVFIWIP; PKVFIWIPH; KVFIWIPHF; VFIWIPHFW; FIWIPHFWV; EAFYLCNSI; AFYLCNSIY; FYLCNSIYP; YLCNSIYPS; LCNSIYPSF; CNSIYPSFN; NSIYPSFNF; FWHLHGFLW; WHLHGFLWL; HLHGFLWLF; LHGFLWLFG; HGFLWLFGS; GFLWLFGSC; FLWLFGSCP; LWLFGSCPW; WLFGSCPWT; LFGSCPWTL; FGSCPWTLS; GSCPWTLSF; SCPWTLSFS; CPWTLSFSF; PWTLSFSFG; WTLSFSFGW; TLSFSFGWG; LSFSFGWGH; SFSFGWGHL; FSFGWGHLH; SFGWGHLHM; FGWGHLHML; GWGHLHMLQ; WGHLHMLQE; GHLHMLQEQ; HLHMLQEQV; LHMLQEQVL; HMLQEQVLQ; MLQEQVLQS; LQEQVLQSR; QEQVLQSRT; EQVLQSRTG; QVLQSRTGL; VLQSRTGLE; LQSRTGLEV; QSRTGLEVK; SRTGLEVKA; RTGLEVKAT; TGLEVKATS; GLEVKATSI; LEVKATSIE; EVKATSIEE; VKATSIEEQ; KATSIEEQF; ATSIEEQFF; TSIEEQFFD; TLLNVHFVD; LLNVHFVDF; LNVHFVDFL; NVHFVDFLS; VHFVDFLSP; HFVDFLSPF; FVDFLSPFF; VDFLSPFFV; LLLYCQHHL; LLYCQHHLY; LYCQHHLYY; YCQHHLYYK; CQHHLYYKY; QHHLYYKYG; HHLYYKYGQ; HLYYKYGQN; LYYKYGQNV; YYKYGQNVH; YKYGQNVHG; KYGQNVHGY; YGQNVHGYL; GQNVHGYLP; QNVHGYLPF; NVHGYLPFQ; VHGYLPFQL; HGYLPFQLL; GYLPFQLLV; GKDQNNIVE; KDQNNIVEY; DQNNIVEYN; QNNIVEYNY; NNIVEYNYK; NIVEYNYKS; IVEYNYKSL; KIFLFFSAI; IFLFFSAIP; FLFFSAIPV; LFFSAIPVR; FFSAIPVRL; QKYLHQETE; KYLHQETEY; YLHQETEYH; LHQETEYHS; HQETEYHST; QETEYHSTH; ETEYHSTHL; TEYHSTHLG; TIPKPCLIA; IPKPCLIAD; PKPCLIADR; KPCLIADRG; PCLIADRGL; CLIADRGLQ; LIADRGLQW; IADRGLQWK; ADRGLQWKL; DRGLQWKLC; RGLQWKLCD; GLQWKLCDP; LQWKLCDPN; QWKLCDPNH; WKLCDPNHQ; KLCDPNHQR; LCDPNHQRT; CDPNHQRTY; DPNHQRTYT; PNHQRTYTL; NHQRTYTLL; HQRTYTLLE; QRTYTLLEL; RTYTLLELR; TYTLLELRN; QFELKQQTQ; FELKQQTQQ; PQEHQQLQH; QEHQQLQHM; EHQQLQHMF; HQQLQHMFE; QQLQHMFEE; QLQHMFEEL; LQHMFEELG; QHMFEELGL; PLRYLLCPL; LRYLLCPLQ; QQQPPQQQF; QQPPQQQFQ; QPPQQQFQP; PPQQQFQPL; PQQQFQPLK; QQQFQPLKI; QQFQPLKIL; QFQPLKILW; FQPLKILWQ; QPLKILWQQ; PLKILWQQQ; LKILWQQQP; KILWQQQPQ; ILWQQQPQI; LWQQQPQIH; WQQQPQIHW; QQQPQIHWQ; QQPQIHWQL; QPQIHWQLG; PQIHWQLGP; QIHWQLGPP; IHWQLGPPK; HWQLGPPKV; WQLGPPKVL; QLGPPKVLE; LGPPKVLEQ; GPPKVLEQH; PPKVLEQHP; TWKYKKKGI; WKYKKKGIT; KYKKKGITY; YKKKGITYL; KKKGITYLG; KKGITYLGV; KGITYLGVF; GITYLGVFY; ITYLGVFYR; TYLGVFYRV; YLGVFYRVF; LGVFYRVFY; GVFYRVFYS; VFYRVFYSR; SSGTFVFPV; SGTFVFPVY; GTFVFPVYT; TFVFPVYTV; FVFPVYTVF; VFPVYTVFT; FPVYTVFTS; PVYTVFTST; VYTVFTSTK; YTVFTSTKF; TVFTSTKFQ; VFTSTKFQQ; FTSTKFQQK; TSTKFQQKL; NKNKNPLSS; KNKNPLSSF; NKNPLSSFF; KNPLSSFFC; NPLSSFFCS; PLSSFFCSS; LSSFFCSSP; SSFFCSSPG; SFFCSSPGF; FFCSSPGFT; FCSSPGFTN; CSSPGFTNF; SSPGFTNFH; QLAQNHGLC; LAQNHGLCP; AQNHGLCPV; LGTRPRFLG; GTRPRFLGS; TRPRFLGSQ; RPRFLGSQN; PRFLGSQNM; RFLGSQNMS; FLGSQNMSV; LGSQNMSVM; GSQNMSVMH; SQNMSVMHF; QNMSVMHFP; NMSVMHFPS; GHGLAAFHG; AAPPCESCT; APPCESCTF; PPCESCTFL; PCESCTFLP; CESCTFLPE; ESCTFLPEV; SCTFLPEVM; CTFLPEVMV; TFLPEVMVW; FLPEVMVWL; LPEVMVWLH; PEVMVWLHS; EVMVWLHSP; VMVWLHSPV; MVWLHSPVS; VWLHSPVSH; WLHSPVSHA; LHSPVSHAL; HSPVSHALS; SPVSHALSF; PVSHALSFL; VSHALSFLR; SHALSFLRS; HALSFLRSW; ALSFLRSWF; LSFLRSWFG; SFLRSWFGC; FLRSWFGCI; LRSWFGCIP; RSWFGCIPW; SWFGCIPWV; WFGCIPWVS; FGCIPWVSS; GCIPWVSSS; CIPWVSSSS; IPWVSSSSL; PWVSSSSLW; WVSSSSLWP; VSSSSLWPF; SSSSLWPFF; SSSLWPFFL;

YIRGRGRLC; IRGRGRLCL; RGRGRLCLH; GRGRLCLHP; RGRLCLHPF; GRLCLHPFS; RLCLHPFSQ;
LCLHPFSQV; CLHPFSQVV; LHPFSQVVR; HPFSQVVRV; PFSQVVRVW; FSQVVRVWR; SQVVRVWRL;
QVVRVWRLF; VVRVWRLFL; VRVWRLFLR; RVWRLFLRP; VWRLFLRPS; WRLFLRPSK; RLFLRPSKT;
LFLRPSKTI; FLRPSKTIW; LRPSKTIWG; RPSKTIWGN; PSKTIWGNP; SKTIWGNPY; KTIWGNPYS;
TIWGNPYSF; IWGNPYSFA; WGNPYSFAI; GNPYSFAIF; NPYSFAIFA; PYSFAIFAK

10 mers:
QGRIHGAHGP; GRIHGAHGPF; RIHGAHGPFR; IHGAHGPFRP; KSCLGKSSLN; SCLGKSSLNE;
CLGKSSLNEK; LGKSSLNEKS; GKSSLNEKSL; KSSLNEKSLF; SSLNEKSLFK; SLNEKSLFKE;
LNEKSLFKEV; KNGAGCKGSS; NGAGCKGSSS; GAGCKGSSSA; FSSLPRYPVL; SSLPRYPVLQ;
SLPRYPVLQG; LPRYPVLQGM; PRYPVLQGMA; RYPVLQGMAY; YPVLQGMAYL; PVLQGMAYLF;
VLQGMAYLFQ; LQGMAYLFQK; QGMAYLFQKA; GMAYLFQKAF; MAYLFQKAFC; AYLFQKAFCA;
YLFQKAFCAL; LFQKAFCALP; FQKAFCALPL; QKAFCALPLH; KAFCALPLHA; AFCALPLHAM;
FCALPLHAMS; CALPLHAMSA; KIFKKRALGL; IFKKRALGLD; FKKRALGLDR; KKRALGLDRL;
KRALGLDRLL; RALGLDRLLL; ALGLDRLLLH; LLHTVVWLRP; LHTVVWLRPN; RNSAMVGPNN;
NSAMVGPNNW; SAMVGPNNWR; AMVGPNNWRN; MVGPNNWRNS; VGPNNWRNSL; GPNNWRNSLQ;
PNNWRNSLQR; NNWRNSLQRS; NWRNSLQRSK; WRNSLQRSKA; RNSLQRSKAL; NSLQRSKALR;
INNKILKGPK; VPTYGTEEWE; PTYGTEEWES; TYGTEEWESW; YGTEEWESWW; GTEEWESWWS;
TEEWESWWSS; EEWESWWSSF; EWESWWSSFN; WESWWSSFNE; ESWWSSFNEK; SWWSSFNEKW;
WWSSFNEKWD; WSSFNEKWDE; SSFNEKWDED; SFNEKWDEDL; FNEKWDEDLF; NEKWDEDLFC;
EKWDEDLFCH; KWDEDLFCHE; WDEDLFCHED; DEDLFCHEDM; EDLFCHEDMF; DLFCHEDMFA;
LFCHEDMFAS; FCHEDMFASD; CHEDMFASDE; HEDMFASDEE; EDMFASDEEA; DMFASDEEAT;
MFASDEEATA; FASDEEATAD; ASDEEATADS; SDEEATADSQ; DEEATADSQH; EEATADSQHS;
EATADSQHST; ATADSQHSTP; TADSQHSTPP; ADSQHSTPPK; DSQHSTPPKK; SQHSTPPKKK;
QHSTPPKKKR; HSTPPKKKRK; STPPKKKRKV; TPPKKKRKVE; PPKKKRKVED; PKKKRKVEDP;
KKKRKVEDPK; KKRKVEDPKD; KRKVEDPKDF; RKVEDPKDFP; KVEDPKDFPS; VEDPKDFPSD;
EDPKDFPSDL; DPKDFPSDLH; PKDFPSDLHQ; KDFPSDLHQF; DFPSDLHQFL; FPSDLHQFLS;
PSDLHQFLSQ; SDLHQFLSQA; DLHQFLSQAV; LHQFLSQAVF; HQFLSQAVFS; QFLSQAVFSN;
FLSQAVFSNR; LSQAVFSNRT; SQAVFSNRTL; QAVFSNRTLA; AVFSNRTLAC; VFSNRTLACF;
FSNRTLACFA; SNRTLACFAV; NRTLACFAVY; RTLACFAVYT; TLACFAVYTT; LACFAVYTTK;
ACFAVYTTKE; CFAVYTTKEK; FAVYTTKEKA; AVYTTKEKAQ; VYTTKEKAQI; YTTKEKAQIL;
TTKEKAQILY; TKEKAQILYK; KEKAQILYKK; EKAQILYKKL; KAQILYKKLM; AQILYKKLME;
QILYKKLMEK; ILYKKLMEKY; LYKKLMEKYS; YKKLMEKYSV; KKLMEKYSVT; KLMEKYSVTF;
LMEKYSVTFI; MEKYSVTFIS; EKYSVTFISR; KYSVTFISRH; YSVTFISRHM; SVTFISRHMC;
VTFISRHMCA; TFISRHMCAG; FISRHMCAGH; ISRHMCAGHN; SRHMCAGHNI; RHMCAGHNII;
HMCAGHNIIF; MCAGHNIIFF; CAGHNIIFFL; AGHNIIFFLT; GHNIIFFLTP; HNIIFFLTPH;
NIIFFLTPHR; IIFFLTPHRH; IFFLTPHRHR; FFLTPHRHRV; FLTPHRHRVS; LTPHRHRVSA;
TPHRHRVSAI; PHRHRVSAIN; HRHRVSAINN; RHRVSAINNF; HRVSAINNFC; RVSAINNFCQ;
VSAINNFCQK; SAINNFCQKL; AINNFCQKLC; INNFCQKLCT; NNFCQKLCTF; NFCQKLCTFS;
FCQKLCTFSF; CQKLCTFSFL; QKLCTFSFLI; KLCTFSFLIC; LCTFSFLICK; CTFSFLICKG;
TFSFLICKGV; FSFLICKGVN; SFLICKGVNK; FLICKGVNKE; LICKGVNKEY; ICKGVNKEYL;
CKGVNKEYLL; KGVNKEYLLY; GVNKEYLLYS; VNKEYLLYSA; NKEYLLYSAL; KEYLLYSALT;
EYLLYSALTR; YLLYSALTRD; LLYSALTRDP; LYSALTRDPY; YSALTRDPYH; SALTRDPYHT;
ALTRDPYHTI; LTRDPYHTIE; TRDPYHTIEE; RDPYHTIEES; DPYHTIEESI; PYHTIEESIQ;
YHTIEESIQG; HTIEESIQGG; TIEESIQGGL; IEESIQGGLK; EESIQGGLKE; ESIQGGLKEH;
SIQGGLKEHD; IQGGLKEHDF; QGGLKEHDFS; GGLKEHDFSP; GLKEHDFSPE; LKEHDFSPEE;
KEHDFSPEEP; EHDFSPEEPE; HDFSPEEPEE; DFSPEEPEET; FSPEEPEETK; SPEEPEETKQ;
PEEPEETKQV; EEPEETKQVS; EPEETKQVSW; PEETKQVSWK; EETKQVSWKL; ETKQVSWKLI;
TKQVSWKLIT; KQVSWKLITE; QVSWKLITEY; VSWKLITEYA; SWKLITEYAV; WKLITEYAVE;
KLITEYAVET; LITEYAVETK; ITEYAVETKC; TEYAVETKCE; EYAVETKCED; YAVETKCEDV;
AVETKCEDVF; VETKCEDVFL; ETKCEDVFLL; TKCEDVFLLL; KCEDVFLLLG; CEDVFLLLGM;
EDVFLLLGMY; DVFLLLGMYL; VFLLLGMYLE; FLLLGMYLEF; LLLGMYLEFQ; LLGMYLEFQY;
LGMYLEFQYN; GMYLEFQYNV; MYLEFQYNVE; YLEFQYNVEE; LEFQYNVEEC; EFQYNVEECK;
FQYNVEECKK; QYNVEECKKC; YNVEECKKCQ; NVEECKKCQK; VEECKKCQKK; EECKKCQKKD;
ECKKCQKKDQ; CKKCQKKDQP; KKCQKKDQPY; KCQKKDQPYH; CQKKDQPYHF; QKKDQPYHFK;
KKDQPYHFKY; KDQPYHFKYH; DQPYHFKYHE; QPYHFKYHEK; PYHFKYHEKH; YHFKYHEKHF;
HFKYHEKHFA; FKYHEKHFAN; KYHEKHFANA; YHEKHFANAI; HEKHFANAII; EKHFANAIIF;
KHFANAIIFA; HFANAIIFAE; FANAIIFAES; ANAIIFAESK; NAIIFAESKN; AIIFAESKNQ;
IIFAESKNQK; IFAESKNQKS; FAESKNQKSI; AESKNQKSIC; ESKNQKSICQ; SKNQKSICQQ;
KNQKSICQQA; NQKSICQQAV; QKSICQQAVD; KSICQQAVDT; SICQQAVDTV; ICQQAVDTVL;
CQQAVDTVLA; QQAVDTVLAK; QAVDTVLAKK; AVDTVLAKKR; VDTVLAKKRV; DTVLAKKRVD;
TVLAKKRVDT; VLAKKRVDTL; LAKKRVDTLH; AKKRVDTLHM; KKRVDTLHMT; KRVDTLHMTR;
RVDTLHMTRE; VDTLHMTREE; DTLHMTREEM; TLHMTREEML; LHMTREEMLT; HMTREEMLTE;
MTREEMLTER; TREEMLTERF; REEMLTERFN; EEMLTERFNH; EMLTERFNHI; MLTERFNHIL;
LTERFNHILD; TERFNHILDK; ERFNHILDKM; RFNHILDKMD; FNHILDKMDL; NHILDKMDLI;

HILDKMDLIF; ILDKMDLIFG; LDKMDLIFGA; DKMDLIFGAH; KMDLIFGAHG; MDLIFGAHGN;
DLIFGAHGNA; LIFGAHGNAV; IFGAHGNAVL; FGAHGNAVLE; GAHGNAVLEQ; AHGNAVLEQY;
HGNAVLEQYM; GNAVLEQYMA; NAVLEQYMAG; AVLEQYMAGV; VLEQYMAGVA; LEQYMAGVAW;
EQYMAGVAWL; QYMAGVAWLH; YMAGVAWLHC; MAGVAWLHCL; AGVAWLHCLL; GVAWLHCLLP;
VAWLHCLLPK; AWLHCLLPKM; WLHCLLPKMD; LHCLLPKMDS; HCLLPKMDSV; CLLPKMDSVI;
LLPKMDSVIF; LPKMDSVIFD; PKMDSVIFDF; KMDSVIFDFL; MDSVIFDFLH; DSVIFDFLHC;
SVIFDFLHCI; VIFDFLHCIV; IFDFLHCIVF; FDFLHCIVFN; DFLHCIVFNV; FLHCIVFNVP;
LHCIVFNVPK; HCIVFNVPKR; CIVFNVPKRR; IVFNVPKRRY; VFNVPKRRYW; FNVPKRRYWL;
NVPKRRYWLF; VPKRRYWLFK; PKRRYWLFKG; KRRYWLFKGP; RRYWLFKGPI; RYWLFKGPID;
YWLFKGPIDS; WLFKGPIDSG; LFKGPIDSGK; FKGPIDSGKT; KGPIDSGKTT; GPIDSGKTTL;
PIDSGKTTLA; IDSGKTTLAA; DSGKTTLAAG; SGKTTLAAGL; GKTTLAAGLL; KTTLAAGLLD;
TTLAAGLLDL; TLAAGLLDLC; LAAGLLDLCG; AAGLLDLCGG; AGLLDLCGGK; GLLDLCGGKA;
LLDLCGGKAL; LDLCGGKALN; DLCGGKALNV; LCGGKALNVN; CGGKALNVNL; GGKALNVNLP;
GKALNVNLPM; KALNVNLPME; ALNVNLPMER; LNVNLPMERL; NVNLPMERLT; VNLPMERLTF;
NLPMERLTFE; LPMERLTFEL; PMERLTFELG; MERLTFELGV; ERLTFELGVA; RLTFELGVAI;
LTFELGVAID; TFELGVAIDQ; FELGVAIDQY; ELGVAIDQYM; LGVAIDQYMV; GVAIDQYMVV;
VAIDQYMVVF; AIDQYMVVFE; IDQYMVVFED; DQYMVVFEDV; QYMVVFEDVK; YMVVFEDVKG;
MVVFEDVKGT; VVFEDVKGTG; VFEDVKGTGA; FEDVKGTGAE; EDVKGTGAES; DVKGTGAESK;
VKGTGAESKD; KGTGAESKDL; GTGAESKDLP; TGAESKDLPS; GAESKDLPSG; AESKDLPSGH;
ESKDLPSGHG; SKDLPSGHGI; KDLPSGHGIN; DLPSGHGINN; LPSGHGINNL; PSGHGINNLD;
SGHGINNLDS; GHGINNLDSL; HGINNLDSLR; GINNLDSLRD; INNLDSLRDY; NNLDSLRDYL;
NLDSLRDYLD; LDSLRDYLDG; DSLRDYLDGS; SLRDYLDGSV; LRDYLDGSVK; RDYLDGSVKV;
DYLDGSVKVN; YLDGSVKVNL; LDGSVKVNLE; DGSVKVNLEK; GSVKVNLEKK; SVKVNLEKKH;
VKVNLEKKHL; KVNLEKKHLN; VNLEKKHLNK; NLEKKHLNKR; LEKKHLNKRT; EKKHLNKRTQ;
KKHLNKRTQI; KHLNKRTQIF; HLNKRTQIFP; LNKRTQIFPP; NKRTQIFPPG; KRTQIFPPGL;
RTQIFPPGLV; TQIFPPGLVT; QIFPPGLVTM; IFPPGLVTMN; FPPGLVTMNE; PPGLVTMNEY;
PGLVTMNEYP; GLVTMNEYPV; LVTMNEYPVP; VTMNEYPVPK; TMNEYPVPKT; MNEYPVPKTL;
NEYPVPKTLQ; EYPVPKTLQA; YPVPKTLQAR; PVPKTLQARF; VPKTLQARFV; PKTLQARFVR;
KTLQARFVRQ; TLQARFVRQI; LQARFVRQID; QARFVRQIDF; ARFVRQIDFR; RFVRQIDFRP;
FVRQIDFRPK; VRQIDFRPKI; RQIDFRPKIY; QIDFRPKIYL; IDFRPKIYLR; DFRPKIYLRK;
FRPKIYLRKS; RPKIYLRKSL; PKIYLRKSLQ; KIYLRKSLQN; IYLRKSLQNS; YLRKSLQNSE;
LRKSLQNSEF; RKSLQNSEFL; KSLQNSEFLL; SLQNSEFLLE; LQNSEFLLEK; QNSEFLLEKR;
NSEFLLEKRI; SEFLLEKRIL; EFLLEKRILQ; FLLEKRILQS; LLEKRILQSG; LEKRILQSGM;
EKRILQSGMT; KRILQSGMTL; RILQSGMTLL; ILQSGMTLLL; LQSGMTLLLL; QSGMTLLLLL;
SGMTLLLLLI; GMTLLLLLIW; MTLLLLLIWF; TLLLLLIWFR; LLLLLIWFRP; LLLLIWFRPV;
LLLIWFRPVA; LLIWFRPVAD; LIWFRPVADF; IWFRPVADFA; WFRPVADFAT; FRPVADFATD;
RPVADFATDI; PVADFATDIQ; VADFATDIQS; ADFATDIQSR; DFATDIQSRI; FATDIQSRIV;
ATDIQSRIVE; TDIQSRIVEW; DIQSRIVEWK; IQSRIVEWKE; QSRIVEWKER; SRIVEWKERL;
RIVEWKERLD; IVEWKERLDS; VEWKERLDSE; EWKERLDSEI; WKERLDSEIS; KERLDSEISM;
ERLDSEISMY; RLDSEISMYT; LDSEISMYTF; DSEISMYTFS; SEISMYTFSR; EISMYTFSRM;
ISMYTFSRMK; SMYTFSRMKY; MYTFSRMKYN; YTFSRMKYNI; TFSRMKYNIC; FSRMKYNICM;
SRMKYNICMG; RMKYNICMGK; MKYNICMGKC; KYNICMGKCI; YNICMGKCIL; NICMGKCILD;
ICMGKCILDI; CMGKCILDIT; MGKCILDITR; GKCILDITRE; KCILDITREE; CILDITREED;
ILDITREEDS; LDITREEDSE; DITREEDSET; ITREEDSETE; TREEDSETED; REEDSETEDS;
EEDSETEDSG; EDSETEDSGH; DSETEDSGHG; SETEDSGHGS; ETEDSGHGSS; TEDSGHGSST;
EDSGHGSSTE; DSGHGSSTES; SGHGSSTESQ; GHGSSTESQS; HGSSTESQSQ; GSSTESQSQC;
SSTESQSQCS; STESQSQCSS; TESQSQCSSQ; ESQSQCSSQV; SQSQCSSQVS; QSQCSSQVSD;
SQCSSQVSDT; QCSSQVSDTS; CSSQVSDTSA; SSQVSDTSAP; SQVSDTSAPA; QVSDTSAPAE;
VSDTSAPAED; SDTSAPAEDS; DTSAPAEDSQ; TSAPAEDSQR; SAPAEDSQRS; APAEDSQRSD;
PAEDSQRSDP; AEDSQRSDPH; EDSQRSDPHS; DSQRSDPHSQ; SQRSDPHSQE; QRSDPHSQEL;
RSDPHSQELH; SDPHSQELHL; DPHSQELHLC; PHSQELHLCK; HSQELHLCKG; SQELHLCKGF;
QELHLCKGFQ; ELHLCKGFQC; LHLCKGFQCF; HLCKGFQCFK; LCKGFQCFKR; CKGFQCFKRP;
KGFQCFKRPK; GFQCFKRPKT; FQCFKRPKTP; QCFKRPKTPP; CFKRPKTPPP; FKRPKTPPPK;
HKLKSGLYKS; KLKSGLYKSS; LKSGLYKSSI; KSGLYKSSIY; MYMYNKSTCL; YMYNKSTCLK;
MYNKSTCLKH; YNKSTCLKHF; NKSTCLKHFG; KSTCLKHFGL; STCLKHFGLQ; TCLKHFGLQL;
CLKHFGLQLS; LKHFGLQLSL; KHFGLQLSLF; HFGLQLSLFV; FGLQLSLFVN; GLQLSLFVNI;
LQLSLFVNIS; QLSLFVNISY; LSLFVNISYH; SLFVNISYHI; LFVNISYHIW; FVNISYHIWV;
VNISYHIWVP; NISYHIWVPW; ISYHIWVPWK; SYHIWVPWKS; YHIWVPWKSF; HIWVPWKSFC;
IWVPWKSFCA; WVPWKSFCAI; VPWKSFCAIK; PWKSFCAIKH; WKSFCAIKHP; KSFCAIKHPN;
SFCAIKHPNL; FCAIKHPNLF; CAIKHPNLFY; AIKHPNLFYL; IKHPNLFYLG; KHPNLFYLGF;
HPNLFYLGFH; PNLFYLGFHT; NLFYLGFHTI; LFYLGFHTIH; FYLGFHTIHR; YLGFHTIHRL;
LGFHTIHRLP; GFHTIHRLPI; FHTIHRLPIH; HTIHRLPIHS; TIHRLPIHSL; IHRLPIHSLG;
HRLPIHSLGS; RLPIHSLGSP; LPIHSLGSPV; PIHSLGSPVY; IHSLGSPVYK; HSLGSPVYKV;
SLGSPVYKVT; QKGNWVRILY; KGNWVRILYR; GNWVRILYRS; NWVRILYRSF; WVRILYRSFS;
VRILYRSFSQ; RILYRSFSQA; ILYRSFSQAD; LYRSFSQADL; YRSFSQADLK; RSFSQADLKI;

SFSQADLKIS; FSQADLKISC; SQADLKISCK; QADLKISCKA; ADLKISCKAS; DLKISCKASP;
LKISCKASPL; KISCKASPLL; ISCKASPLLC; SCKASPLLCS; CKASPLLCSR; KASPLLCSRA;
ASPLLCSRAV; SPLLCSRAVS; PLLCSRAVSK; LLCSRAVSKQ; LCSRAVSKQA; CSRAVSKQAT;
SRAVSKQATN; RAVSKQATNI; AVSKQATNIS; VSKQATNISS; NIQAISFTKR; IQAISFTKRP;
QAISFTKRPH; AISFTKRPHT; ISFTKRPHTL; SFTKRPHTLF; FTKRPHTLFI; QHCGSCVGHM;
HCGSCVGHMK; CGSCVGHMKY; GSCVGHMKYW; SCVGHMKYWG; CVGHMKYWGN; VGHMKYWGNI;
GHMKYWGNIF; HMKYWGNIFP; MKYWGNIFPS; KYWGNIFPSC; YWGNIFPSCE; WGNIFPSCES;
GNIFPSCESP; NIFPSCESPK; IFPSCESPKI; FPSCESPKIP; PSCESPKIPS; SCESPKIPSI;
CESPKIPSIF; ESPKIPSIFI; SPKIPSIFIS; PKIPSIFIST; KIPSIFISTG; IPSIFISTGI;
PSIFISTGIR; SIFISTGIRY; IFISTGIRYP; FISTGIRYPA; ISTGIRYPAL; STGIRYPALN;
TGIRYPALNW; GIRYPALNWI; IRYPALNWIS; RYPALNWISI; YPALNWISIV; PALNWISIVF;
ALNWISIVFV; LNWISIVFVQ; NWISIVFVQI; WISIVFVQIG; ISIVFVQIGL; SIVFVQIGLM;
IVFVQIGLMV; VFVQIGLMVS; FVQIGLMVSI; VQIGLMVSIH; QIGLMVSIHY; IGLMVSIHYL;
GLMVSIHYLG; LMVSIHYLGL; MVSIHYLGLG; VSIHYLGLGC; SIHYLGLGCW; IHYLGLGCWV;
HYLGLGCWVF; YLGLGCWVFR; LGLGCWVFRG; GLGCWVFRGY; LGCWVFRGYS; GCWVFRGYST;
CWVFRGYSTI; WVFRGYSTIR; VFRGYSTIRV; FRGYSTIRVL; HSLHFQGFST; SLHFQGFSTY;
LHFQGFSTYS; HFQGFSTYSK; FQGFSTYSKE; QGFSTYSKEV; GFSTYSKEVE; FSTYSKEVEI;
STYSKEVEIT; TYSKEVEITA; YSKEVEITAL; SKEVEITALN; KEVEITALNR; EVEITALNRF;
VEITALNRFS; EITALNRFSS; ITALNRFSST; TALNRFSSTM; ALNRFSSTML; LNRFSSTMLM;
NRFSSTMLMH; RFSSTMLMHF; FSSTMLMHFL; PCMKVKHASY; CMKVKHASYS; MKVKHASYSN;
KVKHASYSNN; VKHASYSNNL; KHASYSNNLC; HASYSNNLCL; ASYSNNLCLY; SYSNNLCLYS;
YSNNLCLYSY; SNNLCLYSYS; NNLCLYSYSL; NLCLYSYSLP; LCLYSYSLPH; CLYSYSLPHQ;
IGEGNSCCAV; GEGNSCCAVT; EGNSCCAVTG; GNSCCAVTGK; NSCCAVTGKH; SCCAVTGKHF;
CCAVTGKHFS; CAVTGKHFSL; AVTGKHFSLW; VTGKHFSLWA; TGKHFSLWAI; GKHFSLWAIT;
KHFSLWAITA; HFSLWAITAK; FSLWAITAKV; SLWAITAKVI; LWAITAKVIF; WAITAKVIFS;
AITAKVIFST; TKAPKVFIWI; KAPKVFIWIP; APKVFIWIPH; PKVFIWIPHF; KVFIWIPHFW;
VFIWIPHFWV; EAFYLCNSIY; AFYLCNSIYP; FYLCNSIYPS; YLCNSIYPSF; LCNSIYPSFN;
CNSIYPSFNF; FWHLHGFLWL; WHLHGFLWLF; HLHGFLWLFG; LHGFLWLFGS; HGFLWLFGSC;
GFLWLFGSCP; FLWLFGSCPW; LWLFGSCPWT; WLFGSCPWTL; LFGSCPWTLS; FGSCPWTLSF;
GSCPWTLSFS; SCPWTLSFSF; CPWTLSFSFG; PWTLSFSFGW; WTLSFSFGWG; TLSFSFGWGH;
LSFSFGWGHL; SFSFGWGHLH; FSFGWGHLHM; SFGWGHLHML; FGWGHLHMLQ; GWGHLHMLQE;
WGHLHMLQEQ; GHLHMLQEQV; HLHMLQEQVL; LHMLQEQVLQ; HMLQEQVLQS; MLQEQVLQSR;
LQEQVLQSRT; QEQVLQSRTG; EQVLQSRTGL; QVLQSRTGLE; VLQSRTGLEV; LQSRTGLEVK;
QSRTGLEVKA; SRTGLEVKAT; RTGLEVKATS; TGLEVKATSI; GLEVKATSIE; LEVKATSIEE;
EVKATSIEEQ; VKATSIEEQF; KATSIEEQFF; ATSIEEQFFD; TLLNVHFVDF; LLNVHFVDFL;
LNVHFVDFLS; NVHFVDFLSP; VHFVDFLSPF; HFVDFLSPFF; FVDFLSPFFV; LLLYCQHHLY;
LLYCQHHLYY; LYCQHHLYYK; YCQHHLYYKY; CQHHLYYKYG; QHHLYYKYGQ; HHLYYKYGQN;
HLYYKYGQNV; LYYKYGQNVH; YYKYGQNVHG; YKYGQNVHGY; KYGQNVHGYL; YGQNVHGYLP;
GQNVHGYLPF; QNVHGYLPFQ; NVHGYLPFQL; VHGYLPFQLL; HGYLPFQLLV; GKDQNNIVEY;
KDQNNIVEYN; DQNNIVEYNY; QNNIVEYNYK; NNIVEYNYKS; NIVEYNYKSL; KIFLFFSAIP;
IFLFFSAIPV; FLFFSAIPVR; LFFSAIPVRL; QKYLHQETEY; KYLHQETEYH; YLHQETEYHS;
LHQETEYHST; HQETEYHSTH; QETEYHSTHL; ETEYHSTHLG; TIPKPCLIAD; IPKPCLIADR;
PKPCLIADRG; KPCLIADRGL; PCLIADRGLQ; CLIADRGLQW; LIADRGLQWK; IADRGLQWKL;
ADRGLQWKLC; DRGLQWKLCD; RGLQWKLCDP; GLQWKLCDPN; LQWKLCDPNH; QWKLCDPNHQ;
WKLCDPNHQR; KLCDPNHQRT; LCDPNHQRTY; CDPNHQRTYT; DPNHQRTYTL; PNHQRTYTLL;
NHQRTYTLLE; HQRTYTLLEL; QRTYTLLELR; RTYTLLELRN; QFELKQQTQQ; PQEHQQLQHM;
QEHQQLQHMF; EHQQLQHMFE; HQQLQHMFEE; QQLQHMFEEL; QLQHMFEELG; LQHMFEELGL;
PLRYLLCPLQ; QQQPPQQQFQ; QQPPQQQFQP; QPPQQQFQPL; PPQQQFQPLK; PQQQFQPLKI;
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LKILWQQQPQ; KILWQQQPQI; ILWQQQPQIH; LWQQQPQIHW; WQQQPQIHWQ; QQQPQIHWQL;
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WQLGPPKVLE; QLGPPKVLEQ; LGPPKVLEQH; GPPKVLEQHP; TWKYKKKGIT; WKYKKKGITY;
KYKKKGITYL; YKKKGITYLG; KKKGITYLGV; KKGITYLGVF; KGITYLGVFY; GITYLGVFYR;
ITYLGVFYRV; TYLGVFYRVF; YLGVFYRVFY; LGVFYRVFYS; GVFYRVFYSR; SSGTFVFPVY;
SGTFVFPVYT; GTFVFPVYTV; TFVFPVYTVF; FVFPVYTVFT; VFPVYTVFTS; FPVYTVFTST;
PVYTVFTSTK; VYTVFTSTKF; YTVFTSTKFQ; TVFTSTKFQQ; VFTSTKFQQK; FTSTKFQQKL;
NKNKNPLSSF; KNKNPLSSFF; NKNPLSSFFC; KNPLSSFFCS; NPLSSFFCSS; PLSSFFCSSP;
LSSFFCSSPG; SSFFCSSPGF; SFFCSSPGFT; FFCSSPGFTN; FCSSPGFTNF; CSSPGFTNFH;
QLAQNHGLCP; LAQNHGLCPV; LGTRPRFLGS; GTRPRFLGSQ; TRPRFLGSQN; RPRFLGSQNM;
PRFLGSQNMS; RFLGSQNMSV; FLGSQNMSVM; LGSQNMSVMH; GSQNMSVMHF; SQNMSVMHFP;
QNMSVMHFPS; AAPPCESCTF; APPCESCTFL; PPCESCTFLP; PCESCTFLPE; CESCTFLPEV;
ESCTFLPEVM; SCTFLPEVMV; CTFLPEVMVW; TFLPEVMVWL; FLPEVMVWLH; LPEVMVWLHS;
PEVMVWLHSP; EVMVWLHSPV; VMVWLHSPVS; MVWLHSPVSH; VWLHSPVSHA; WLHSPVSHAL;
LHSPVSHALS; HSPVSHALSF; SPVSHALSFL; PVSHALSFLR; VSHALSFLRS; SHALSFLRSW;
HALSFLRSWF; ALSFLRSWFG; LSFLRSWFGC; SFLRSWFGCI; FLRSWFGCIP; LRSWFGCIPW;

RSWFGCIPWV; SWFGCIPWVS; WFGCIPWVSS; FGCIPWVSSS; GCIPWVSSSS; CIPWVSSSSL;
IPWVSSSSLW; PWVSSSSLWP; WVSSSSLWPF; VSSSSLWPFF; SSSSLWPFFL; YIRGRGRLCL;
IRGRGRLCLH; RGRGRLCLHP; GRGRLCLHPF; RGRLCLHPFS; GRLCLHPFSQ; RLCLHPFSQV;
LCLHPFSQVV; CLHPFSQVVR; LHPFSQVVRV; HPFSQVVRVW; PFSQVVRVWR; FSQVVRVWRL;
SQVVRVWRLF; QVVRVWRLFL; VVRVWRLFLR; VRVWRLFLRP; RVWRLFLRPS; VWRLFLRPSK;
WRLFLRPSKT; RLFLRPSKTI; LFLRPSKTIW; FLRPSKTIWG; LRPSKTIWGN; RPSKTIWGNP;
PSKTIWGNPY; SKTIWGNPYS; KTIWGNPYSF; TIWGNPYSFA; IWGNPYSFAI; WGNPYSFAIF;
GNPYSFAIFA; NPYSFAIFAK

11 mers:
QGRIHGAHGPF; GRIHGAHGPFR; RIHGAHGPFRP; KSCLGKSSLNE; SCLGKSSLNEK; CLGKSSLNEKS;
LGKSSLNEKSL; GKSSLNEKSLF; KSSLNEKSLFK; SSLNEKSLFKE; SLNEKSLFKEV; KNGAGCKGSSS;
NGAGCKGSSSA; FSSLPRYPVLQ; SSLPRYPVLQG; SLPRYPVLQGM; LPRYPVLQGMA; PRYPVLQGMAY;
RYPVLQGMAYL; YPVLQGMAYLF; PVLQGMAYLFQ; VLQGMAYLFQK; LQGMAYLFQKA; QGMAYLFQKAF;
GMAYLFQKAFC; MAYLFQKAFCA; AYLFQKAFCAL; YLFQKAFCALP; LFQKAFCALPL; FQKAFCALPLH;
QKAFCALPLHA; KAFCALPLHAM; AFCALPLHAMS; FCALPLHAMSA; KIFKKRALGLD; IFKKRALGLDR;
FKKRALGLDRL; KKRALGLDRLL; KRALGLDRLLL; RALGLDRLLLH; LLHTVVWLRPN; RNSAMVGPNNW;
NSAMVGPNNWR; SAMVGPNNWRN; AMVGPNNWRNS; MVGPNNWRNSL; VGPNNWRNSLQ; GPNNWRNSLQR;
PNNWRNSLQRS; NNWRNSLQRSK; NWRNSLQRSKA; WRNSLQRSKAL; RNSLQRSKALR; VPTYGTEEWES;
PTYGTEEWESW; TYGTEEWESWW; YGTEEWESWWS; GTEEWESWWSS; TEEWESWWSSF; EEWESWWSSFN;
EWESWWSSFNE; WESWWSSFNEK; ESWWSSFNEKW; SWWSSFNEKWD; WWSSFNEKWDE; WSSFNEKWDED;
SSFNEKWDEDL; SFNEKWDEDLF; FNEKWDEDLFC; NEKWDEDLFCH; EKWDEDLFCHE; KWDEDLFCHED;
WDEDLFCHEDM; DEDLFCHEDMF; EDLFCHEDMFA; DLFCHEDMFAS; LFCHEDMFASD; FCHEDMFASDE;
CHEDMFASDEE; HEDMFASDEEA; EDMFASDEEAT; DMFASDEEATA; MFASDEEATAD; FASDEEATADS;
ASDEEATADSQ; SDEEATADSQH; DEEATADSQHS; EEATADSQHST; EATADSQHSTP; ATADSQHSTPP;
TADSQHSTPPK; ADSQHSTPPKK; DSQHSTPPKKK; SQHSTPPKKKR; QHSTPPKKKRK; HSTPPKKKRKV;
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KRKVEDPKDFP; RKVEDPKDFPS; KVEDPKDFPSD; VEDPKDFPSDL; EDPKDFPSDLH; DPKDFPSDLHQ;
PKDFPSDLHQF; KDFPSDLHQFL; DFPSDLHQFLS; FPSDLHQFLSQ; PSDLHQFLSQA; SDLHQFLSQAV;
DLHQFLSQAVF; LHQFLSQAVFS; HQFLSQAVFSN; QFLSQAVFSNR; FLSQAVFSNRT; LSQAVFSNRTL;
SQAVFSNRTLA; QAVFSNRTLAC; AVFSNRTLACF; VFSNRTLACFA; FSNRTLACFAV; SNRTLACFAVY;
NRTLACFAVYT; RTLACFAVYTT; TLACFAVYTTK; LACFAVYTTKE; ACFAVYTTKEK; CFAVYTTKEKA;
FAVYTTKEKAQ; AVYTTKEKAQI; VYTTKEKAQIL; YTTKEKAQILY; TTKEKAQILYK; TKEKAQILYKK;
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LYKKLMEKYSV; YKKLMEKYSVT; KKLMEKYSVTF; KLMEKYSVTFI; LMEKYSVTFIS; MEKYSVTFISR;
EKYSVTFISRH; KYSVTFISRHM; YSVTFISRHMC; SVTFISRHMCA; VTFISRHMCAG; TFISRHMCAGH;
FISRHMCAGHN; ISRHMCAGHNI; SRHMCAGHNII; RHMCAGHNIIF; HMCAGHNIIFF; MCAGHNIIFFL;
CAGHNIIFFLT; AGHNIIFFLTP; GHNIIFFLTPH; HNIIFFLTPHR; NIIFFLTPHRH; IIFFLTPHRHR;
IFFLTPHRHRV; FFLTPHRHRVS; FLTPHRHRVSA; LTPHRHRVSAI; TPHRHRVSAIN; PHRHRVSAINN;
HRHRVSAINNF; RHRVSAINNFC; HRVSAINNFCQ; RVSAINNFCQK; VSAINNFCQKL; SAINNFCQKLC;
AINNFCQKLCT; INNFCQKLCTF; NNFCQKLCTFS; NFCQKLCTFSF; FCQKLCTFSFL; CQKLCTFSFLI;
QKLCTFSFLIC; KLCTFSFLICK; LCTFSFLICKG; CTFSFLICKGV; TFSFLICKGVN; FSFLICKGVNK;
SFLICKGVNKE; FLICKGVNKEY; LICKGVNKEYL; ICKGVNKEYLL; CKGVNKEYLLY; KGVNKEYLLYS;
GVNKEYLLYSA; VNKEYLLYSAL; NKEYLLYSALT; KEYLLYSALTR; EYLLYSALTRD; YLLYSALTRDP;
LLYSALTRDPY; LYSALTRDPYH; YSALTRDPYHT; SALTRDPYHTI; ALTRDPYHTIE; LTRDPYHTIEE;
TRDPYHTIEES; RDPYHTIEESI; DPYHTIEESIQ; PYHTIEESIQG; YHTIEESIQGG; HTIEESIQGGL;
TIEESIQGGLK; IEESIQGGLKE; EESIQGGLKEH; ESIQGGLKEHD; SIQGGLKEHDF; IQGGLKEHDFS;
QGGLKEHDFSP; GGLKEHDFSPE; GLKEHDFSPEE; LKEHDFSPEEP; KEHDFSPEEPE; EHDFSPEEPEE;
HDFSPEEPEET; DFSPEEPEETK; FSPEEPEETKQ; SPEEPEETKQV; PEEPEETKQVS; EEPEETKQVSW;
EPEETKQVSWK; PEETKQVSWKL; EETKQVSWKLI; ETKQVSWKLIT; TKQVSWKLITE; KQVSWKLITEY;
QVSWKLITEYA; VSWKLITEYAV; SWKLITEYAVE; WKLITEYAVET; KLITEYAVETK; LITEYAVETKC;
ITEYAVETKCE; TEYAVETKCED; EYAVETKCEDV; YAVETKCEDVF; AVETKCEDVFL; VETKCEDVFLL;
ETKCEDVFLLL; TKCEDVFLLLG; KCEDVFLLLGM; CEDVFLLLGMY; EDVFLLLGMYL; DVFLLLGMYLE;
VFLLLGMYLEF; FLLLGMYLEFQ; LLLGMYLEFQY; LLGMYLEFQYN; LGMYLEFQYNV; GMYLEFQYNVE;
MYLEFQYNVEE; YLEFQYNVEEC; LEFQYNVEECK; EFQYNVEECKK; FQYNVEECKKC; QYNVEECKKCQ;
YNVEECKKCQK; NVEECKKCQKK; VEECKKCQKKD; EECKKCQKKDQ; ECKKCQKKDQP; CKKCQKKDQPY;
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DQPYHFKYHEK; QPYHFKYHEKH; PYHFKYHEKHF; YHFKYHEKHFA; HFKYHEKHFAN; FKYHEKHFANA;
KYHEKHFANAI; YHEKHFANAII; HEKHFANAIIF; EKHFANAIIFA; KHFANAIIFAE; HFANAIIFAES;
FANAIIFAESK; ANAIIFAESKN; NAIIFAESKNQ; AIIFAESKNQK; IIFAESKNQKS; IFAESKNQKSI;
FAESKNQKSIC; AESKNQKSICQ; ESKNQKSICQQ; SKNQKSICQQA; KNQKSICQQAV; NQKSICQQAVD;
QKSICQQAVDT; KSICQQAVDTV; SICQQAVDTVL; ICQQAVDTVLA; CQQAVDTVLAK; QQAVDTVLAKK;
QAVDTVLAKKR; AVDTVLAKKRV; VDTVLAKKRVD; DTVLAKKRVDT; TVLAKKRVDTL; VLAKKRVDTLH;
LAKKRVDTLHM; AKKRVDTLHMT; KKRVDTLHMTR; KRVDTLHMTRE; RVDTLHMTREE; VDTLHMTREEM;
DTLHMTREEML; TLHMTREEMLT; LHMTREEMLTE; HMTREEMLTER; MTREEMLTERF; TREEMLTERFN;
REEMLTERFNH; EEMLTERFNHI; EMLTERFNHIL; MLTERFNHILD; LTERFNHILDK; TERFNHILDKM;

ERFNHILDKMD; RFNHILDKMDL; FNHILDKMDLI; NHILDKMDLIF; HILDKMDLIFG; ILDKMDLIFGA;
LDKMDLIFGAH; DKMDLIFGAHG; KMDLIFGAHGN; MDLIFGAHGNA; DLIFGAHGNAV; LIFGAHGNAVL;
IFGAHGNAVLE; FGAHGNAVLEQ; GAHGNAVLEQY; AHGNAVLEQYM; HGNAVLEQYMA; GNAVLEQYMAG;
NAVLEQYMAGV; AVLEQYMAGVA; VLEQYMAGVAW; LEQYMAGVAWL; EQYMAGVAWLH; QYMAGVAWLHC;
YMAGVAWLHCL; MAGVAWLHCLL; AGVAWLHCLLP; GVAWLHCLLPK; VAWLHCLLPKM; AWLHCLLPKMD;
WLHCLLPKMDS; LHCLLPKMDSV; HCLLPKMDSVI; CLLPKMDSVIF; LLPKMDSVIFD; LPKMDSVIFDF;
PKMDSVIFDFL; KMDSVIFDFLH; MDSVIFDFLHC; DSVIFDFLHCI; SVIFDFLHCIV; VIFDFLHCIVF;
IFDFLHCIVFN; FDFLHCIVFNV; DFLHCIVFNVP; FLHCIVFNVPK; LHCIVFNVPKR; HCIVFNVPKRR;
CIVFNVPKRRY; IVFNVPKRRYW; VFNVPKRRYWL; FNVPKRRYWLF; NVPKRRYWLFK; VPKRRYWLFKG;
PKRRYWLFKGP; KRRYWLFKGPI; RRYWLFKGPID; RYWLFKGPIDS; YWLFKGPIDSG; WLFKGPIDSGK;
LFKGPIDSGKT; FKGPIDSGKTT; KGPIDSGKTTL; GPIDSGKTTLA; PIDSGKTTLAA; IDSGKTTLAAG;
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LAAGLLDLCGG; AAGLLDLCGGK; AGLLDLCGGKA; GLLDLCGGKAL; LLDLCGGKALN; LDLCGGKALNV;
DLCGGKALNVN; LCGGKALNVNL; CGGKALNVNLP; GGKALNVNLPM; GKALNVNLPME; KALNVNLPMER;
ALNVNLPMERL; LNVNLPMERLT; NVNLPMERLTF; VNLPMERLTFE; NLPMERLTFEL; LPMERLTFELG;
PMERLTFELGV; MERLTFELGVA; ERLTFELGVAI; RLTFELGVAID; LTFELGVAIDQ; TFELGVAIDQY;
FELGVAIDQYM; ELGVAIDQYMV; LGVAIDQYMVV; GVAIDQYMVVF; VAIDQYMVVFE; AIDQYMVVFED;
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KDLPSGHGINN; DLPSGHGINNL; LPSGHGINNLD; PSGHGINNLDS; SGHGINNLDSL; GHGINNLDSLR;
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VNLEKKHLNKR; NLEKKHLNKRT; LEKKHLNKRTQ; EKKHLNKRTQI; KKHLNKRTQIF; KHLNKRTQIFP;
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QIFPPGLVTMN; IFPPGLVTMNE; FPPGLVTMNEY; PPGLVTMNEYP; PGLVTMNEYPV; GLVTMNEYPVP;
LVTMNEYPVPK; VTMNEYPVPKT; TMNEYPVPKTL; MNEYPVPKTLQ; NEYPVPKTLQA; EYPVPKTLQAR;
YPVPKTLQARF; PVPKTLQARFV; VPKTLQARFVR; PKTLQARFVRQ; KTLQARFVRQI; TLQARFVRQID;
LQARFVRQIDF; QARFVRQIDFR; ARFVRQIDFRP; RFVRQIDFRPK; FVRQIDFRPKI; VRQIDFRPKIY;
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PKIYLRKSLQN; KIYLRKSLQNS; IYLRKSLQNSE; YLRKSLQNSEF; LRKSLQNSEFL; RKSLQNSEFLL;
KSLQNSEFLLE; SLQNSEFLLEK; LQNSEFLLEKR; QNSEFLLEKRI; NSEFLLEKRIL; SEFLLEKRILQ;
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LIWFRPVADFA; IWFRPVADFAT; WFRPVADFATD; FRPVADFATDI; RPVADFATDIQ; PVADFATDIQS;
VADFATDIQSR; ADFATDIQSRI; DFATDIQSRIV; FATDIQSRIVE; ATDIQSRIVEW; TDIQSRIVEWK;
DIQSRIVEWKE; IQSRIVEWKER; QSRIVEWKERL; SRIVEWKERLD; RIVEWKERLDS; IVEWKERLDSE;
VEWKERLDSEI; EWKERLDSEIS; WKERLDSEISM; KERLDSEISMY; ERLDSEISMYT; RLDSEISMYTF;
LDSEISMYTFS; DSEISMYTFSR; SEISMYTFSRM; EISMYTFSRMK; ISMYTFSRMKY; SMYTFSRMKYN;
MYTFSRMKYNI; YTFSRMKYNIC; TFSRMKYNICM; FSRMKYNICMG; SRMKYNICMGK; RMKYNICMGKC;
MKYNICMGKCI; KYNICMGKCIL; YNICMGKCILD; NICMGKCILDI; ICMGKCILDIT; CMGKCILDITR;
MGKCILDITRE; GKCILDITREE; KCILDITREED; CILDITREEDS; ILDITREEDSE; LDITREEDSET;
DITREEDSETE; ITREEDSETED; TREEDSETEDS; REEDSETEDSG; EEDSETEDSGH; EDSETEDSGHG;
DSETEDSGHGS; SETEDSGHGSS; ETEDSGHGSST; TEDSGHGSSTE; EDSGHGSSTES; DSGHGSSTESQ;
SGHGSSTESQS; GHGSSTESQSQ; HGSSTESQSQC; GSSTESQSQCS; SSTESQSQCSS; STESQSQCSSQ;
TESQSQCSSQV; ESQSQCSSQVS; SQSQCSSQVSD; QSQCSSQVSDT; SQCSSQVSDTS; QCSSQVSDTSA;
CSSQVSDTSAP; SSQVSDTSAPA; SQVSDTSAPAE; QVSDTSAPAED; VSDTSAPAEDS; SDTSAPAEDSQ;
DTSAPAEDSQR; TSAPAEDSQRS; SAPAEDSQRSD; APAEDSQRSDP; PAEDSQRSDPH; AEDSQRSDPHS;
EDSQRSDPHSQ; DSQRSDPHSQE; SQRSDPHSQEL; QRSDPHSQELH; RSDPHSQELHL; SDPHSQELHLC;
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FQCFKRPKTPP; QCFKRPKTPPP; CFKRPKTPPPK; HKLKSGLYKSS; KLKSGLYKSSI; LKSGLYKSSIY;
MYMYNKSTCLK; YMYNKSTCLKH; MYNKSTCLKHF; YNKSTCLKHFG; NKSTCLKHFGL; KSTCLKHFGLQ;
STCLKHFGLQL; TCLKHFGLQLS; CLKHFGLQLSL; LKHFGLQLSLF; KHFGLQLSLFV; HFGLQLSLFVN;
FGLQLSLFVNI; GLQLSLFVNIS; LQLSLFVNISY; QLSLFVNISYH; LSLFVNISYHI; SLFVNISYHIW;
LFVNISYHIWV; FVNISYHIWVP; VNISYHIWVPW; NISYHIWVPWK; ISYHIWVPWKS; SYHIWVPWKSF;
YHIWVPWKSFC; HIWVPWKSFCA; IWVPWKSFCAI; WVPWKSFCAIK; VPWKSFCAIKH; PWKSFCAIKHP;
WKSFCAIKHPN; KSFCAIKHPNL; SFCAIKHPNLF; FCAIKHPNLFY; CAIKHPNLFYL; AIKHPNLFYLG;
IKHPNLFYLGF; KHPNLFYLGFH; HPNLFYLGFHT; PNLFYLGFHTI; NLFYLGFHTIH; LFYLGFHTIHR;
FYLGFHTIHRL; YLGFHTIHRLP; LGFHTIHRLPI; GFHTIHRLPIH; FHTIHRLPIHS; HTIHRLPIHSL;
TIHRLPIHSLG; IHRLPIHSLGS; HRLPIHSLGSP; RLPIHSLGSPV; LPIHSLGSPVY; PIHSLGSPVYK;
IHSLGSPVYKV; HSLGSPVYKVT; QKGNWVRILYR; KGNWVRILYRS; GNWVRILYRSF; NWVRILYRSFS;
WVRILYRSFSQ; VRILYRSFSQA; RILYRSFSQAD; ILYRSFSQADL; LYRSFSQADLK; YRSFSQADLKI;

RSFSQADLKIS; SFSQADLKISC; FSQADLKISCK; SQADLKISCKA; QADLKISCKAS; ADLKISCKASP;
DLKISCKASPL; LKISCKASPLL; KISCKASPLLC; ISCKASPLLCS; SCKASPLLCSR; CKASPLLCSRA;
KASPLLCSRAV; ASPLLCSRAVS; SPLLCSRAVSK; PLLCSRAVSKQ; LLCSRAVSKQA; LCSRAVSKQAT;
CSRAVSKQATN; SRAVSKQATNI; RAVSKQATNIS; AVSKQATNISS; NIQAISFTKRP; IQAISFTKRPH;
QAISFTKRPHT; AISFTKRPHTL; ISFTKRPHTLF; SFTKRPHTLFI; QHCGSCVGHMK; HCGSCVGHMKY;
CGSCVGHMKYW; GSCVGHMKYWG; SCVGHMKYWGN; CVGHMKYWGNI; VGHMKYWGNIF; GHMKYWGNIFP;
HMKYWGNIFPS; MKYWGNIFPSC; KYWGNIFPSCE; YWGNIFPSCES; WGNIFPSCESP; GNIFPSCESPK;
NIFPSCESPKI; IFPSCESPKIP; FPSCESPKIPS; PSCESPKIPSI; SCESPKIPSIF; CESPKIPSIFI;
ESPKIPSIFIS; SPKIPSIFIST; PKIPSIFISTG; KIPSIFISTGI; IPSIFISTGIR; PSIFISTGIRY;
SIFISTGIRYP; IFISTGIRYPA; FISTGIRYPAL; ISTGIRYPALN; STGIRYPALNW; TGIRYPALNWI;
GIRYPALNWIS; IRYPALNWISI; RYPALNWISIV; YPALNWISIVF; PALNWISIVFV; ALNWISIVFVQ;
LNWISIVFVQI; NWISIVFVQIG; WISIVFVQIGL; ISIVFVQIGLM; SIVFVQIGLMV; IVFVQIGLMVS;
VFVQIGLMVSI; FVQIGLMVSIH; VQIGLMVSIHY; QIGLMVSIHYL; IGLMVSIHYLG; GLMVSIHYLGL;
LMVSIHYLGLG; MVSIHYLGLGC; VSIHYLGLGCW; SIHYLGLGCWV; IHYLGLGCWVF; HYLGLGCWVFR;
YLGLGCWVFRG; LGLGCWVFRGY; GLGCWVFRGYS; LGCWVFRGYST; GCWVFRGYSTI; CWVFRGYSTIR;
WVFRGYSTIRV; VFRGYSTIRVL; HSLHFQGFSTY; SLHFQGFSTYS; LHFQGFSTYSK; HFQGFSTYSKE;
FQGFSTYSKEV; QGFSTYSKEVE; GFSTYSKEVEI; FSTYSKEVEIT; STYSKEVEITA; TYSKEVEITAL;
YSKEVEITALN; SKEVEITALNR; KEVEITALNRF; EVEITALNRFS; VEITALNRFSS; EITALNRFSST;
ITALNRFSSTM; TALNRFSSTML; ALNRFSSTMLM; LNRFSSTMLMH; NRFSSTMLMHF; RFSSTMLMHFL;
PCMKVKHASYS; CMKVKHASYSN; MKVKHASYSNN; KVKHASYSNNL; VKHASYSNNLC; KHASYSNNLCL;
HASYSNNLCLY; ASYSNNLCLYS; SYSNNLCLYSY; YSNNLCLYSYS; SNNLCLYSYSL; NNLCLYSYSLP;
NLCLYSYSLPH; LCLYSYSLPHQ; IGEGNSCCAVT; GEGNSCCAVTG; EGNSCCAVTGK; GNSCCAVTGKH;
NSCCAVTGKHF; SCCAVTGKHFS; CCAVTGKHFSL; CAVTGKHFSLW; AVTGKHFSLWA; VTGKHFSLWAI;
TGKHFSLWAIT; GKHFSLWAITA; KHFSLWAITAK; HFSLWAITAKV; FSLWAITAKVI; SLWAITAKVIF;
LWAITAKVIFS; WAITAKVIFST; TKAPKVFIWIP; KAPKVFIWIPH; APKVFIWIPHF; PKVFIWIPHFW;
KVFIWIPHFWV; EAFYLCNSIYP; AFYLCNSIYPS; FYLCNSIYPSF; YLCNSIYPSFN; LCNSIYPSFNF;
FWHLHGFLWLF; WHLHGFLWLFG; HLHGFLWLFGS; LHGFLWLFGSC; HGFLWLFGSCP; GFLWLFGSCPW;
FLWLFGSCPWT; LWLFGSCPWTL; WLFGSCPWTLS; LFGSCPWTLSF; FGSCPWTLSFS; GSCPWTLSFSF;
SCPWTLSFSFG; CPWTLSFSFGW; PWTLSFSFGWG; WTLSFSFGWGH; TLSFSFGWGHL; LSFSFGWGHLH;
SFSFGWGHLHM; FSFGWGHLHML; SFGWGHLHMLQ; FGWGHLHMLQE; GWGHLHMLQEQ; WGHLHMLQEQV;
GHLHMLQEQVL; HLHMLQEQVLQ; LHMLQEQVLQS; HMLQEQVLQSR; MLQEQVLQSRT; LQEQVLQSRTG;
QEQVLQSRTGL; EQVLQSRTGLE; QVLQSRTGLEV; VLQSRTGLEVK; LQSRTGLEVKA; QSRTGLEVKAT;
SRTGLEVKATS; RTGLEVKATSI; TGLEVKATSIE; GLEVKATSIEE; LEVKATSIEEQ; EVKATSIEEQF;
VKATSIEEQFF; KATSIEEQFFD; TLLNVHFVDFL; LLNVHFVDFLS; LNVHFVDFLSP; NVHFVDFLSPF;
VHFVDFLSPFF; HFVDFLSPFFV; LLLYCQHHLYY; LLYCQHHLYYK; LYCQHHLYYKY; YCQHHLYYKYG;
CQHHLYYKYGQ; QHHLYYKYGQN; HHLYYKYGQNV; HLYYKYGQNVH; LYYKYGQNVHG; YYKYGQNVHGY;
YKYGQNVHGYL; KYGQNVHGYLP; YGQNVHGYLPF; GQNVHGYLPFQ; QNVHGYLPFQL; NVHGYLPFQLL;
VHGYLPFQLLV; GKDQNNIVEYN; KDQNNIVEYNY; DQNNIVEYNYK; QNNIVEYNYKS; NNIVEYNYKSL;
KIFLFFSAIPV; IFLFFSAIPVR; FLFFSAIPVRL; QKYLHQETEYH; KYLHQETEYHS; YLHQETEYHST;
LHQETEYHSTH; HQETEYHSTHL; QETEYHSTHLG; TIPKPCLIADR; IPKPCLIADRG; PKPCLIADRGL;
KPCLIADRGLQ; PCLIADRGLQW; CLIADRGLQWK; LIADRGLQWKL; IADRGLQWKLC; ADRGLQWKLCD;
DRGLQWKLCDP; RGLQWKLCDPN; GLQWKLCDPNH; LQWKLCDPNHQ; QWKLCDPNHQR; WKLCDPNHQRT;
KLCDPNHQRTY; LCDPNHQRTYT; CDPNHQRTYTL; DPNHQRTYTLL; PNHQRTYTLLE; NHQRTYTLLEL;
HQRTYTLLELR; QRTYTLLELRN; PQEHQQLQHMF; QEHQQLQHMFE; EHQQLQHMFEE; HQQLQHMFEEL;
QQLQHMFEELG; QLQHMFEELGL; QQQPPQQQFQP; QQPPQQQFQPL; QPPQQQFQPLK; PPQQQFQPLKI;
PQQQFQPLKIL; QQQFQPLKILW; QQFQPLKILWQ; QFQPLKILWQQ; FQPLKILWQQQ; QPLKILWQQQP;
PLKILWQQQPQ; LKILWQQQPQI; KILWQQQPQIH; ILWQQQPQIHW; LWQQQPQIHWQ; WQQQPQIHWQL;
QQQPQIHWQLG; QQPQIHWQLGP; QPQIHWQLGPP; PQIHWQLGPPK; QIHWQLGPPKV; IHWQLGPPKVL;
HWQLGPPKVLE; WQLGPPKVLEQ; QLGPPKVLEQH; LGPPKVLEQHP; TWKYKKKGITY; WKYKKKGITYL;
KYKKKGITYLG; YKKKGITYLGV; KKKGITYLGVF; KKGITYLGVFY; KGITYLGVFYR; GITYLGVFYRV;
ITYLGVFYRVF; TYLGVFYRVFY; YLGVFYRVFYS; LGVFYRVFYSR; SSGTFVFPVYT; SGTFVFPVYTV;
GTFVFPVYTVF; TFVFPVYTVFT; FVFPVYTVFTS; VFPVYTVFTST; FPVYTVFTSTK; PVYTVFTSTKF;
VYTVFTSTKFQ; YTVFTSTKFQQ; TVFTSTKFQQK; VFTSTKFQQKL; NKNKNPLSSFF; KNKNPLSSFFC;
NKNPLSSFFCS; KNPLSSFFCSS; NPLSSFFCSSP; PLSSFFCSSPG; LSSFFCSSPGF; SSFFCSSPGFT;
SFFCSSPGFTN; FFCSSPGFTNF; FCSSPGFTNFH; QLAQNHGLCPV; LGTRPRFLGSQ; GTRPRFLGSQN;
TRPRFLGSQNM; RPRFLGSQNMS; PRFLGSQNMSV; RFLGSQNMSVM; FLGSQNMSVMH; LGSQNMSVMHF;
GSQNMSVMHFP; SQNMSVMHFPS; AAPPCESCTFL; APPCESCTFLP; PPCESCTFLPE; PCESCTFLPEV;
CESCTFLPEVM; ESCTFLPEVMV; SCTFLPEVMVW; CTFLPEVMVWL; TFLPEVMVWLH; FLPEVMVWLHS;
LPEVMVWLHSP; PEVMVWLHSPV; EVMVWLHSPVS; VMVWLHSPVSH; MVWLHSPVSHA; VWLHSPVSHAL;
WLHSPVSHALS; LHSPVSHALSF; HSPVSHALSFL; SPVSHALSFLR; PVSHALSFLRS; VSHALSFLRSW;
SHALSFLRSWF; HALSFLRSWFG; ALSFLRSWFGC; LSFLRSWFGCI; SFLRSWFGCIP; FLRSWFGCIPW;
LRSWFGCIPWV; RSWFGCIPWVS; SWFGCIPWVSS; WFGCIPWVSSS; FGCIPWVSSSS; GCIPWVSSSSL;
CIPWVSSSSLW; IPWVSSSSLWP; PWVSSSSLWPF; WVSSSSLWPFF; VSSSSLWPFFL; YIRGRGRLCLH;
IRGRGRLCLHP; RGRGRLCLHPF; GRGRLCLHPFS; RGRLCLHPFSQ; GRLCLHPFSQV; RLCLHPFSQVV
LCLHPFSQVVR; CLHPFSQVVRV; LHPFSQVVRVW; HPFSQVVRVWR; PFSQVVRVWRL; FSQVVRVWRLF;

SQVVRVWRLFL; QVVRVWRLFLR; VVRVWRLFLRP; VRVWRLFLRPS; RVWRLFLRPSK; VWRLFLRPSKT; WRLFLRPSKTI; RLFLRPSKTIW; LFLRPSKTIWG; FLRPSKTIWGN; LRPSKTIWGNP; RPSKTIWGNPY; PSKTIWGNPYS; SKTIWGNPYSF; KTIWGNPYSFA; TIWGNPYSFAI; IWGNPYSFAIF; WGNPYSFAIFA; GNPYSFAIFAK

Preferred BK virus fragments of VP2-3 capable of interacting with one or more MHC class 1 molecules are listed in Table J.

Table J: Prediction of BK virus VP2-3 protein specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
107	KVSTVGLY	0.435	454	WB	VP2-3	A0101
140	FVNNIQYL	0.674	33	SB	VP2-3	A0201
80	FAALIQTV	0.581	93	WB	VP2-3	A0201
195	FLEETTWT	0.576	98	WB	VP2-3	A0201
5	ALLGDLVA	0.564	111	WB	VP2-3	A0201
43	SLATVEGI	0.559	118	WB	VP2-3	A0201
293	MLPLLLGL	0.552	127	WB	VP2-3	A0201
40	QIASLATV	0.533	155	WB	VP2-3	A0201
61	GLTPQTYA	0.533	155	WB	VP2-3	A0201
296	LLLGLYGT	0.529	163	WB	VP2-3	A0201
76	AIAGFAAL	0.469	311	WB	VP2-3	A0201
89	GISSLAQV	0.456	358	WB	VP2-3	A0201
297	LLGLYGTV	0.439	433	WB	VP2-3	A0201
132	ILFPGVNT	0.434	457	WB	VP2-3	A0201
140	FVNNIQYL	0.869	4	SB	VP2-3	A0202
293	MLPLLLGL	0.799	8	SB	VP2-3	A0202
80	FAALIQTV	0.745	15	SB	VP2-3	A0202
43	SLATVEGI	0.730	18	SB	VP2-3	A0202
61	GLTPQTYA	0.709	23	SB	VP2-3	A0202
195	FLEETTWT	0.686	29	SB	VP2-3	A0202
76	AIAGFAAL	0.667	36	SB	VP2-3	A0202
89	GISSLAQV	0.640	49	SB	VP2-3	A0202
3	ALALLGDL	0.630	54	WB	VP2-3	A0202
297	LLGLYGTV	0.607	69	WB	VP2-3	A0202
40	QIASLATV	0.606	71	WB	VP2-3	A0202
0	MGAALALL	0.581	92	WB	VP2-3	A0202
112	GLYQQSGM	0.575	99	WB	VP2-3	A0202
287	RTAPQWML	0.543	139	WB	VP2-3	A0202
6	LLGDLVAS	0.539	146	WB	VP2-3	A0202
157	FATISQAL	0.530	162	WB	VP2-3	A0202
10	LVASVSEA	0.524	173	WB	VP2-3	A0202
296	LLLGLYGT	0.477	287	WB	VP2-3	A0202
155	SLFATISQ	0.473	298	WB	VP2-3	A0202
86	TVTGISSL	0.461	341	WB	VP2-3	A0202
62	LTPQTYAV	0.458	352	WB	VP2-3	A0202
114	YQQSGMAL	0.445	405	WB	VP2-3	A0202
13	SVSEAAAA	0.433	461	WB	VP2-3	A0202
18	AAATGFSV	0.427	490	WB	VP2-3	A0202
132	ILFPGVNT	0.427	491	WB	VP2-3	A0202
43	SLATVEGI	0.798	8	SB	VP2-3	A0203
140	FVNNIQYL	0.775	11	SB	VP2-3	A0203
297	LLGLYGTV	0.773	11	SB	VP2-3	A0203
40	QIASLATV	0.748	15	SB	VP2-3	A0203
80	FAALIQTV	0.730	18	SB	VP2-3	A0203
61	GLTPQTYA	0.706	24	SB	VP2-3	A0203
89	GISSLAQV	0.701	25	SB	VP2-3	A0203

76	AIAGFAAL	0.701	25	SB	VP2-3	A0203
83	LIQTVTGI	0.666	37	SB	VP2-3	A0203
18	AAATGFSV	0.649	44	SB	VP2-3	A0203
3	ALALLGDL	0.643	47	SB	VP2-3	A0203
112	GLYQQSGM	0.624	58	WB	VP2-3	A0203
10	LVASVSEA	0.604	72	WB	VP2-3	A0203
114	YQQSGMAL	0.558	119	WB	VP2-3	A0203
296	LLLGLYGT	0.552	127	WB	VP2-3	A0203
195	FLEETTWT	0.540	144	WB	VP2-3	A0203
132	ILFPGVNT	0.534	154	WB	VP2-3	A0203
62	LTPQTYAV	0.523	175	WB	VP2-3	A0203
69	VIAGAPGA	0.516	187	WB	VP2-3	A0203
161	SQALWHVI	0.493	241	WB	VP2-3	A0203
86	TVTGISSL	0.464	330	WB	VP2-3	A0203
5	ALLGDLVA	0.455	364	WB	VP2-3	A0203
13	SVSEAAAA	0.454	368	WB	VP2-3	A0203
268	SVHSGEFI	0.440	426	WB	VP2-3	A0203
167	VIRDDIPA	0.435	450	WB	VP2-3	A0203
297	LLGLYGTV	0.613	66	WB	VP2-3	A0204
43	SLATVEGI	0.584	90	WB	VP2-3	A0204
140	FVNNIQYL	0.522	175	WB	VP2-3	A0204
80	FAALIQTV	0.522	176	WB	VP2-3	A0204
287	RTAPQWML	0.509	203	WB	VP2-3	A0204
114	YQQSGMAL	0.793	9	SB	VP2-3	A0206
80	FAALIQTV	0.748	15	SB	VP2-3	A0206
18	AAATGFSV	0.743	16	SB	VP2-3	A0206
140	FVNNIQYL	0.719	20	SB	VP2-3	A0206
39	VQIASLAT	0.713	22	SB	VP2-3	A0206
161	SQALWHVI	0.700	25	SB	VP2-3	A0206
40	QIASLATV	0.665	37	SB	VP2-3	A0206
75	GAIAGFAA	0.665	37	SB	VP2-3	A0206
76	AIAGFAAL	0.657	40	SB	VP2-3	A0206
293	MLPLLLGL	0.644	47	SB	VP2-3	A0206
94	AQVGYRFF	0.637	50	WB	VP2-3	A0206
62	LTPQTYAV	0.598	77	WB	VP2-3	A0206
214	IQDYYSNL	0.578	96	WB	VP2-3	A0206
201	WTIVNAPI	0.563	112	WB	VP2-3	A0206
195	FLEETTWT	0.551	129	WB	VP2-3	A0206
296	LLLGLYGT	0.550	129	WB	VP2-3	A0206
89	GISSLAQV	0.537	149	WB	VP2-3	A0206
5	ALLGDLVA	0.535	153	WB	VP2-3	A0206
157	FATISQAL	0.507	207	WB	VP2-3	A0206
13	SVSEAAAA	0.502	217	WB	VP2-3	A0206
287	RTAPQWML	0.501	221	WB	VP2-3	A0206
61	GLTPQTYA	0.499	226	WB	VP2-3	A0206
23	FSVAEIAA	0.479	279	WB	VP2-3	A0206
297	LLGLYGTV	0.477	286	WB	VP2-3	A0206
45	ATVEGITT	0.475	292	WB	VP2-3	A0206
4	LALLGDLV	0.460	346	WB	VP2-3	A0206
101	FSDWDHKV	0.454	366	WB	VP2-3	A0206
10	LVASVSEA	0.443	412	WB	VP2-3	A0206
132	ILFPGVNT	0.441	425	WB	VP2-3	A0206
247	SIDNADSI	0.437	440	WB	VP2-3	A0206
303	TVTPALEA	0.437	443	WB	VP2-3	A0206
43	SLATVEGI	0.433	463	WB	VP2-3	A0206
35	AAIEVQIA	0.427	493	WB	VP2-3	A0206
5	ALLGDLVA	0.884	3	SB	VP2-3	A0211
293	MLPLLLGL	0.861	4	SB	VP2-3	A0211
61	GLTPQTYA	0.856	4	SB	VP2-3	A0211

297	LLGLYGTV	0.852	4	SB	VP2-3	A0211
146	YLDPRHWG	0.842	5	SB	VP2-3	A0211
89	GISSLAQV	0.841	5	SB	VP2-3	A0211
155	SLFATISQ	0.823	6	SB	VP2-3	A0211
76	AIAGFAAL	0.819	7	SB	VP2-3	A0211
43	SLATVEGI	0.812	7	SB	VP2-3	A0211
40	QIASLATV	0.801	8	SB	VP2-3	A0211
296	LLLGLYGT	0.762	13	SB	VP2-3	A0211
140	FVNNIQYL	0.727	19	SB	VP2-3	A0211
132	ILFPGVNT	0.718	21	SB	VP2-3	A0211
80	FAALIQTV	0.692	27	SB	VP2-3	A0211
195	FLEETTWT	0.687	29	SB	VP2-3	A0211
86	TVTGISSL	0.686	29	SB	VP2-3	A0211
101	FSDWDHKV	0.685	30	SB	VP2-3	A0211
62	LTPQTYAV	0.680	32	SB	VP2-3	A0211
18	AAATGFSV	0.673	34	SB	VP2-3	A0211
112	GLYQQSGM	0.663	38	SB	VP2-3	A0211
287	RTAPQWML	0.657	40	SB	VP2-3	A0211
247	SIDNADSI	0.657	40	SB	VP2-3	A0211
250	NADSIEEV	0.652	43	SB	VP2-3	A0211
262	DLRNKESV	0.628	56	WB	VP2-3	A0211
299	GLYGTVTP	0.595	79	WB	VP2-3	A0211
6	LLGDLVAS	0.595	79	WB	VP2-3	A0211
292	WMLPLLLG	0.555	123	WB	VP2-3	A0211
268	SVHSGEFI	0.540	145	WB	VP2-3	A0211
303	TVTPALEA	0.519	182	WB	VP2-3	A0211
3	ALALLGDL	0.514	191	WB	VP2-3	A0211
32	EAAAAIEV	0.514	192	WB	VP2-3	A0211
191	SLARFLEE	0.502	217	WB	VP2-3	A0211
13	SVSEAAAA	0.493	240	WB	VP2-3	A0211
69	VIAGAPGA	0.467	317	WB	VP2-3	A0211
4	LALLGDLV	0.450	382	WB	VP2-3	A0211
167	VIRDDIPA	0.450	384	WB	VP2-3	A0211
293	MLPLLLGL	0.799	8	SB	VP2-3	A0212
297	LLGLYGTV	0.778	11	SB	VP2-3	A0212
5	ALLGDLVA	0.772	11	SB	VP2-3	A0212
76	AIAGFAAL	0.741	16	SB	VP2-3	A0212
146	YLDPRHWG	0.731	18	SB	VP2-3	A0212
43	SLATVEGI	0.730	18	SB	VP2-3	A0212
296	LLLGLYGT	0.725	19	SB	VP2-3	A0212
140	FVNNIQYL	0.685	30	SB	VP2-3	A0212
40	QIASLATV	0.664	37	SB	VP2-3	A0212
112	GLYQQSGM	0.661	39	SB	VP2-3	A0212
132	ILFPGVNT	0.661	39	SB	VP2-3	A0212
80	FAALIQTV	0.654	42	SB	VP2-3	A0212
155	SLFATISQ	0.649	44	SB	VP2-3	A0212
62	LTPQTYAV	0.635	51	WB	VP2-3	A0212
61	GLTPQTYA	0.635	51	WB	VP2-3	A0212
195	FLEETTWT	0.616	63	WB	VP2-3	A0212
89	GISSLAQV	0.615	64	WB	VP2-3	A0212
262	DLRNKESV	0.607	70	WB	VP2-3	A0212
6	LLGDLVAS	0.562	114	WB	VP2-3	A0212
114	YQQSGMAL	0.562	114	WB	VP2-3	A0212
69	VIAGAPGA	0.521	178	WB	VP2-3	A0212
101	FSDWDHKV	0.505	211	WB	VP2-3	A0212
18	AAATGFSV	0.490	249	WB	VP2-3	A0212
287	RTAPQWML	0.482	270	WB	VP2-3	A0212
299	GLYGTVTP	0.463	335	WB	VP2-3	A0212
3	ALALLGDL	0.450	383	WB	VP2-3	A0212
213	YIQDYYSN	0.440	430	WB	VP2-3	A0212

297	LLGLYGTV	0.869	4	SB	VP2-3	A0216
61	GLTPQTYA	0.801	8	SB	VP2-3	A0216
89	GISSLAQV	0.801	8	SB	VP2-3	A0216
40	QIASLATV	0.770	11	SB	VP2-3	A0216
262	DLRNKESV	0.743	16	SB	VP2-3	A0216
76	AIAGFAAL	0.723	20	SB	VP2-3	A0216
155	SLFATISQ	0.689	28	SB	VP2-3	A0216
140	FVNNIQYL	0.684	30	SB	VP2-3	A0216
293	MLPLLLGL	0.670	35	SB	VP2-3	A0216
5	ALLGDLVA	0.656	41	SB	VP2-3	A0216
80	FAALIQTV	0.647	45	SB	VP2-3	A0216
195	FLEETTWT	0.641	48	SB	VP2-3	A0216
43	SLATVEGI	0.614	64	WB	VP2-3	A0216
18	AAATGFSV	0.614	65	WB	VP2-3	A0216
86	TVTGISSL	0.612	66	WB	VP2-3	A0216
112	GLYQQSGM	0.597	78	WB	VP2-3	A0216
132	ILFPGVNT	0.596	79	WB	VP2-3	A0216
62	LTPQTYAV	0.580	93	WB	VP2-3	A0216
250	NADSIEEV	0.545	136	WB	VP2-3	A0216
296	LLLGLYGT	0.536	152	WB	VP2-3	A0216
146	YLDPRHWG	0.527	167	WB	VP2-3	A0216
32	EAAAAIEV	0.507	206	WB	VP2-3	A0216
247	SIDNADSI	0.502	219	WB	VP2-3	A0216
268	SVHSGEFI	0.451	380	WB	VP2-3	A0216
250	NADSIEEV	0.620	61	WB	VP2-3	A0219
40	QIASLATV	0.614	65	WB	VP2-3	A0219
18	AAATGFSV	0.612	66	WB	VP2-3	A0219
293	MLPLLLGL	0.609	68	WB	VP2-3	A0219
43	SLATVEGI	0.596	78	WB	VP2-3	A0219
146	YLDPRHWG	0.579	95	WB	VP2-3	A0219
80	FAALIQTV	0.579	95	WB	VP2-3	A0219
296	LLLGLYGT	0.567	108	WB	VP2-3	A0219
140	FVNNIQYL	0.565	110	WB	VP2-3	A0219
89	GISSLAQV	0.562	114	WB	VP2-3	A0219
297	LLGLYGTV	0.543	139	WB	VP2-3	A0219
61	GLTPQTYA	0.537	150	WB	VP2-3	A0219
76	AIAGFAAL	0.526	168	WB	VP2-3	A0219
5	ALLGDLVA	0.523	174	WB	VP2-3	A0219
62	LTPQTYAV	0.508	205	WB	VP2-3	A0219
86	TVTGISSL	0.502	220	WB	VP2-3	A0219
195	FLEETTWT	0.500	223	WB	VP2-3	A0219
32	EAAAAIEV	0.455	364	WB	VP2-3	A0219
132	ILFPGVNT	0.452	374	WB	VP2-3	A0219
114	YQQSGMAL	0.451	378	WB	VP2-3	A0219
262	DLRNKESV	0.442	418	WB	VP2-3	A0219
107	KVSTVGLY	0.604	72	WB	VP2-3	A0301
322	VSRGSSQK	0.592	83	WB	VP2-3	A0301
335	ASAKTTNK	0.580	93	WB	VP2-3	A0301
239	HVNFGHTY	0.472	302	WB	VP2-3	A0301
335	ASAKTTNK	0.732	18	SB	VP2-3	A1101
270	HSGEFIEK	0.611	67	WB	VP2-3	A1101
257	VTQRMDLR	0.584	90	WB	VP2-3	A1101
107	KVSTVGLY	0.575	98	WB	VP2-3	A1101
339	TTNKRRSR	0.528	165	WB	VP2-3	A1101
92	SLAQVGYR	0.509	202	WB	VP2-3	A1101
175	ITSQELQR	0.479	280	WB	VP2-3	A1101
91	SSLAQVGY	0.475	293	WB	VP2-3	A1101
322	VSRGSSQK	0.474	297	WB	VP2-3	A1101
176	TSQELQRR	0.469	312	WB	VP2-3	A1101

97	GYRFFSDW	0.582	91	WB	VP2-3	A2301
145	QYLDPRHW	0.515	190	WB	VP2-3	A2301
133	LFPGVNTF	0.508	205	WB	VP2-3	A2301
100	FFSDWDHK	0.478	283	WB	VP2-3	A2301
217	YYSNLSPI	0.443	412	WB	VP2-3	A2301
194	RFLEETTW	0.435	453	WB	VP2-3	A2301
217	YYSNLSPI	0.742	16	SB	VP2-3	A2402
133	LFPGVNTF	0.635	51	WB	VP2-3	A2402
291	QWMLPLLL	0.529	163	WB	VP2-3	A2402
97	GYRFFSDW	0.659	40	SB	VP2-3	A2403
194	RFLEETTW	0.644	47	SB	VP2-3	A2403
217	YYSNLSPI	0.636	51	WB	VP2-3	A2403
133	LFPGVNTF	0.624	58	WB	VP2-3	A2403
145	QYLDPRHW	0.611	67	WB	VP2-3	A2403
304	VTPALEAY	0.815	7	SB	VP2-3	A2602
256	EVTQRMDL	0.685	30	SB	VP2-3	A2602
122	ELFNPDEY	0.657	40	SB	VP2-3	A2602
287	RTAPQWML	0.612	66	WB	VP2-3	A2602
239	HVNFGHTY	0.607	69	WB	VP2-3	A2602
107	KVSTVGLY	0.569	105	WB	VP2-3	A2602
76	AIAGFAAL	0.544	138	WB	VP2-3	A2602
267	ESVHSGEF	0.496	232	WB	VP2-3	A2602
158	ATISQALW	0.474	296	WB	VP2-3	A2602
140	FVNNIQYL	0.465	324	WB	VP2-3	A2602
210	FYNYIQDY	0.674	34	SB	VP2-3	A2902
239	HVNFGHTY	0.663	38	SB	VP2-3	A2902
123	LFNPDEYY	0.588	86	WB	VP2-3	A2902
139	TFVNNIQY	0.582	91	WB	VP2-3	A2902
122	ELFNPDEY	0.546	136	WB	VP2-3	A2902
211	YNYIQDYY	0.522	177	WB	VP2-3	A2902
107	KVSTVGLY	0.502	219	WB	VP2-3	A2902
204	VNAPINFY	0.450	383	WB	VP2-3	A2902
322	VSRGSSQK	0.699	26	SB	VP2-3	A3001
331	KGTRASAK	0.573	101	WB	VP2-3	A3001
228	MVRQVAER	0.521	178	WB	VP2-3	A3001
342	KRRSRSSR	0.469	312	WB	VP2-3	A3001
335	ASAKTTNK	0.448	393	WB	VP2-3	A3001
324	RGSSQKAK	0.442	420	WB	VP2-3	A3001
107	KVSTVGLY	0.586	88	WB	VP2-3	A3002
210	FYNYIQDY	0.499	226	WB	VP2-3	A3002
339	TTNKRRSR	0.798	8	SB	VP2-3	A3101
228	MVRQVAER	0.756	13	SB	VP2-3	A3101
327	SQKAKGTR	0.755	14	SB	VP2-3	A3101
257	VTQRMDLR	0.637	50	WB	VP2-3	A3101
336	SAKTTNKR	0.631	53	WB	VP2-3	A3101
187	FFRDSLAR	0.594	80	WB	VP2-3	A3101
92	SLAQVGYR	0.593	81	WB	VP2-3	A3101
218	YSNLSPIR	0.579	95	WB	VP2-3	A3101
162	QALWHVIR	0.557	120	WB	VP2-3	A3101
176	TSQELQRR	0.511	198	WB	VP2-3	A3101
179	ELQRRTER	0.476	288	WB	VP2-3	A3101
182	RRTERFFR	0.473	299	WB	VP2-3	A3101
143	NIQYLDPR	0.430	474	WB	VP2-3	A3101

179	ELQRRTER	0.741	16	SB	VP2-3	A3301
228	MVRQVAER	0.701	25	SB	VP2-3	A3301
187	FFRDSLAR	0.688	29	SB	VP2-3	A3301
339	TTNKRRSR	0.662	38	SB	VP2-3	A3301
143	NIQYLDPR	0.508	205	WB	VP2-3	A3301
228	MVRQVAER	0.823	6	SB	VP2-3	A6801
339	TTNKRRSR	0.774	11	SB	VP2-3	A6801
175	ITSQELQR	0.722	20	SB	VP2-3	A6801
92	SLAQVGYR	0.704	24	SB	VP2-3	A6801
218	YSNLSPIR	0.701	25	SB	VP2-3	A6801
253	SIEEVTQR	0.642	48	SB	VP2-3	A6801
143	NIQYLDPR	0.634	52	WB	VP2-3	A6801
162	QALWHVIR	0.599	76	WB	VP2-3	A6801
179	ELQRRTER	0.592	82	WB	VP2-3	A6801
257	VTQRMDLR	0.581	92	WB	VP2-3	A6801
336	SAKTTNKR	0.571	103	WB	VP2-3	A6801
176	TSQELQRR	0.567	107	WB	VP2-3	A6801
270	HSGEFIEK	0.558	119	WB	VP2-3	A6801
239	HVNFGHTY	0.520	180	WB	VP2-3	A6801
138	NTFVNNIQ	0.471	305	WB	VP2-3	A6801
122	ELFNPDEY	0.441	425	WB	VP2-3	A6801
100	FFSDWDHK	0.434	458	WB	VP2-3	A6801
32	EAAAAIEV	0.852	4	SB	VP2-3	A6802
80	FAALIQTV	0.773	11	SB	VP2-3	A6802
86	TVTGISSL	0.765	12	SB	VP2-3	A6802
201	WTIVNAPI	0.749	15	SB	VP2-3	A6802
55	EAIAAIGL	0.732	18	SB	VP2-3	A6802
140	FVNNIQYL	0.714	22	SB	VP2-3	A6802
199	TTWTIVNA	0.686	29	SB	VP2-3	A6802
62	LTPQTYAV	0.667	36	SB	VP2-3	A6802
244	HTYSIDNA	0.652	43	SB	VP2-3	A6802
287	RTAPQWML	0.650	44	SB	VP2-3	A6802
40	QIASLATV	0.640	49	SB	VP2-3	A6802
0	MGAALALL	0.635	51	WB	VP2-3	A6802
52	TTSEAIAA	0.624	58	WB	VP2-3	A6802
27	EIAAGEAA	0.616	63	WB	VP2-3	A6802
21	TGFSVAEI	0.588	86	WB	VP2-3	A6802
10	LVASVSEA	0.583	90	WB	VP2-3	A6802
18	AAATGFSV	0.561	115	WB	VP2-3	A6802
76	AIAGFAAL	0.537	149	WB	VP2-3	A6802
53	TSEAIAAI	0.500	223	WB	VP2-3	A6802
303	TVTPALEA	0.475	293	WB	VP2-3	A6802
185	ERFFRDSL	0.472	301	WB	VP2-3	A6802
256	EVTQRMDL	0.455	363	WB	VP2-3	A6802
157	FATISQAL	0.452	375	WB	VP2-3	A6802
23	FSVAEIAA	0.451	380	WB	VP2-3	A6802
13	SVSEAAAA	0.446	400	WB	VP2-3	A6802
38	EVQIASLA	0.440	427	WB	VP2-3	A6802
43	SLATVEGI	0.440	430	WB	VP2-3	A6802
250	NADSIEEV	0.433	460	WB	VP2-3	A6802
32	EAAAAIEV	0.788	9	SB	VP2-3	A6901
199	TTWTIVNA	0.689	28	SB	VP2-3	A6901
201	WTIVNAPI	0.671	35	SB	VP2-3	A6901
40	QIASLATV	0.635	52	WB	VP2-3	A6901
55	EAIAAIGL	0.619	61	WB	VP2-3	A6901
134	FPGVNTFV	0.612	66	WB	VP2-3	A6901
80	FAALIQTV	0.611	67	WB	VP2-3	A6901
101	FSDWDHKV	0.563	112	WB	VP2-3	A6901
27	EIAAGEAA	0.546	135	WB	VP2-3	A6901

62	LTPQTYAV	0.541	143	WB	VP2-3	A6901
140	FVNNIQYL	0.534	154	WB	VP2-3	A6901
244	HTYSIDNA	0.533	156	WB	VP2-3	A6901
250	NADSIEEV	0.521	178	WB	VP2-3	A6901
52	TTSEAIAA	0.511	198	WB	VP2-3	A6901
18	AAATGFSV	0.493	241	WB	VP2-3	A6901
287	RTAPQWML	0.476	289	WB	VP2-3	A6901
222	SPIRPSMV	0.469	313	WB	VP2-3	A6901
289	APQWMLPL	0.773	11	SB	VP2-3	B0702
225	RPSMVRQV	0.705	24	SB	VP2-3	B0702
222	SPIRPSMV	0.604	72	WB	VP2-3	B0702
153	GPSLFATI	0.482	272	WB	VP2-3	B0702
134	FPGVNTFV	0.477	287	WB	VP2-3	B0702
63	TPQTYAVI	0.476	289	WB	VP2-3	B0702
73	APGAIAGF	0.460	343	WB	VP2-3	B0702
114	YQQSGMAL	0.579	94	WB	VP2-3	B1501
180	LQRRTERF	0.557	120	WB	VP2-3	B1501
94	AQVGYRFF	0.550	129	WB	VP2-3	B1501
239	HVNFGHTY	0.550	130	WB	VP2-3	B1501
203	IVNAPINF	0.498	228	WB	VP2-3	B1501
39	VQIASLAT	0.466	321	WB	VP2-3	B1501
107	KVSTVGLY	0.464	331	WB	VP2-3	B1501
161	SQALWHVI	0.446	400	WB	VP2-3	B1501
127	DEYYDILF	0.753	14	SB	VP2-3	B1801
37	IEVQIASL	0.745	15	SB	VP2-3	B1801
233	AEREGTHV	0.477	286	WB	VP2-3	B1801
182	RRTERFFR	0.519	182	WB	VP2-3	B2705
342	KRRSRSSR	0.514	192	WB	VP2-3	B2705
259	QRMDLRNK	0.511	197	WB	VP2-3	B2705
320	RRVSRGSS	0.459	349	WB	VP2-3	B2705
294	LPLLLGLY	0.729	18	SB	VP2-3	B3501
16	EAAAATGF	0.672	34	SB	VP2-3	B3501
239	HVNFGHTY	0.639	49	SB	VP2-3	B3501
206	APINFYNY	0.606	71	WB	VP2-3	B3501
157	FATISQAL	0.598	77	WB	VP2-3	B3501
289	APQWMLPL	0.579	95	WB	VP2-3	B3501
139	TFVNNIQY	0.501	221	WB	VP2-3	B3501
93	LAQVGYRF	0.486	261	WB	VP2-3	B3501
123	LFNPDEYY	0.476	289	WB	VP2-3	B3501
73	APGAIAGF	0.469	313	WB	VP2-3	B3501
114	YQQSGMAL	0.547	134	WB	VP2-3	B3901
37	IEVQIASL	0.623	59	WB	VP2-3	B4001
272	GEFIEKTI	0.558	118	WB	VP2-3	B4001
127	DEYYDILF	0.459	346	WB	VP2-3	B4001
235	REGTHVNF	0.445	404	WB	VP2-3	B4001
233	AEREGTHV	0.430	476	WB	VP2-3	B4001
235	REGTHVNF	0.564	111	WB	VP2-3	B4002
197	EETTWTIV	0.485	263	WB	VP2-3	B4002
272	GEFIEKTI	0.467	318	WB	VP2-3	B4002
26	AEIAAGEA	0.493	240	WB	VP2-3	B4403
235	REGTHVNF	0.426	497	WB	VP2-3	B4403
26	AEIAAGEA	0.624	58	WB	VP2-3	B4501

233	AEREGTHV	0.483	269	WB	VP2-3	B4501
197	EETTWTIV	0.443	413	WB	VP2-3	B4501
153	GPSLFATI	0.494	238	WB	VP2-3	B5101
63	TPQTYAVI	0.493	241	WB	VP2-3	B5101
294	LPLLLGLY	0.483	269	WB	VP2-3	B5101
134	FPGVNTFV	0.466	321	WB	VP2-3	B5101
222	SPIRPSMV	0.440	427	WB	VP2-3	B5101
206	APINFYNY	0.677	32	SB	VP2-3	B5301
134	FPGVNTFV	0.594	81	WB	VP2-3	B5301
63	TPQTYAVI	0.488	254	WB	VP2-3	B5301
153	GPSLFATI	0.467	320	WB	VP2-3	B5301
134	FPGVNTFV	0.703	24	SB	VP2-3	B5401
294	LPLLLGLY	0.526	168	WB	VP2-3	B5401
80	FAALIQTV	0.437	443	WB	VP2-3	B5401
158	ATISQALW	0.681	31	SB	VP2-3	B5801
194	RFLEETTW	0.580	93	WB	VP2-3	B5801
287	RTAPQWML	0.551	129	WB	VP2-3	B5801
203	IVNAPINF	0.463	332	WB	VP2-3	B5801
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138	NTFVNNIQY	0.453	373	WB	VP2-3	A0101
195	FLEETTWTI	0.822	6	SB	VP2-3	A0201
6	LLGDLVASV	0.810	7	SB	VP2-3	A0201
292	WMLPLLLGL	0.786	10	SB	VP2-3	A0201
213	YIQDYYSNL	0.758	13	SB	VP2-3	A0201
61	GLTPQTYAV	0.678	32	SB	VP2-3	A0201
82	ALIQTVTGI	0.643	47	SB	VP2-3	A0201
299	GLYGTVTPA	0.622	59	WB	VP2-3	A0201
159	TISQALWHV	0.608	69	WB	VP2-3	A0201
39	VQIASLATV	0.593	81	WB	VP2-3	A0201
296	LLLGLYGTV	0.532	157	WB	VP2-3	A0201
155	SLFATISQA	0.509	203	WB	VP2-3	A0201
3	ALALLGDLV	0.509	203	WB	VP2-3	A0201
76	AIAGFAALI	0.477	288	WB	VP2-3	A0201
17	AAAATGFSV	0.471	307	WB	VP2-3	A0201
100	FFSDWDHKV	0.465	327	WB	VP2-3	A0201
191	SLARFLEET	0.427	492	WB	VP2-3	A0201
61	GLTPQTYAV	0.877	3	SB	VP2-3	A0202
6	LLGDLVASV	0.801	8	SB	VP2-3	A0202
195	FLEETTWTI	0.800	8	SB	VP2-3	A0202
3	ALALLGDLV	0.789	9	SB	VP2-3	A0202
213	YIQDYYSNL	0.759	13	SB	VP2-3	A0202
159	TISQALWHV	0.692	27	SB	VP2-3	A0202
155	SLFATISQA	0.675	33	SB	VP2-3	A0202
292	WMLPLLLGL	0.671	35	SB	VP2-3	A0202
299	GLYGTVTPA	0.656	41	SB	VP2-3	A0202
82	ALIQTVTGI	0.656	41	SB	VP2-3	A0202
191	SLARFLEET	0.649	44	SB	VP2-3	A0202
10	LVASVSEAA	0.578	96	WB	VP2-3	A0202
52	TTSEAIAAI	0.559	118	WB	VP2-3	A0202
76	AIAGFAALI	0.550	130	WB	VP2-3	A0202
296	LLLGLYGTV	0.537	149	WB	VP2-3	A0202
39	VQIASLATV	0.505	211	WB	VP2-3	A0202
33	AAAAIEVQI	0.497	231	WB	VP2-3	A0202
220	NLSPIRPSM	0.483	269	WB	VP2-3	A0202

80	FAALIQTVT	0.482	272	WB	VP2-3	A0202
112	GLYQQSGMA	0.457	356	WB	VP2-3	A0202
75	GAIAGFAAL	0.449	388	WB	VP2-3	A0202
17	AAAATGFSV	0.447	396	WB	VP2-3	A0202
65	QTYAVIAGA	0.445	405	WB	VP2-3	A0202
36	AIEVQIASL	0.443	413	WB	VP2-3	A0202
136	GVNTFVNNI	0.436	444	WB	VP2-3	A0202
132	ILFPGVNTF	0.435	454	WB	VP2-3	A0202
100	FFSDWDHKV	0.428	488	WB	VP2-3	A0202
6	LLGDLVASV	0.941	1	SB	VP2-3	A0203
299	GLYGTVTPA	0.900	2	SB	VP2-3	A0203
61	GLTPQTYAV	0.878	3	SB	VP2-3	A0203
82	ALIQTVTGI	0.870	4	SB	VP2-3	A0203
39	VQIASLATV	0.845	5	SB	VP2-3	A0203
213	YIQDYYSNL	0.840	5	SB	VP2-3	A0203
292	WMLPLLLGL	0.787	10	SB	VP2-3	A0203
296	LLLGLYGTV	0.779	10	SB	VP2-3	A0203
195	FLEETTWTI	0.757	13	SB	VP2-3	A0203
112	GLYQQSGMA	0.739	16	SB	VP2-3	A0203
155	SLFATISQA	0.730	18	SB	VP2-3	A0203
65	QTYAVIAGA	0.690	28	SB	VP2-3	A0203
3	ALALLGDLV	0.687	29	SB	VP2-3	A0203
69	VIAGAPGAI	0.670	35	SB	VP2-3	A0203
136	GVNTFVNNI	0.666	37	SB	VP2-3	A0203
76	AIAGFAALI	0.664	37	SB	VP2-3	A0203
191	SLARFLEET	0.663	38	SB	VP2-3	A0203
159	TISQALWHV	0.608	69	WB	VP2-3	A0203
85	QTVTGISSL	0.606	70	WB	VP2-3	A0203
52	TTSEAIAAI	0.586	88	WB	VP2-3	A0203
167	VIRDDIPAI	0.553	125	WB	VP2-3	A0203
17	AAAATGFSV	0.540	145	WB	VP2-3	A0203
75	GAIAGFAAL	0.515	190	WB	VP2-3	A0203
10	LVASVSEAA	0.487	258	WB	VP2-3	A0203
18	AAATGFSVA	0.483	269	WB	VP2-3	A0203
20	ATGFSVAEI	0.460	344	WB	VP2-3	A0203
79	GFAALIQTV	0.447	396	WB	VP2-3	A0203
220	NLSPIRPSM	0.428	485	WB	VP2-3	A0203
6	LLGDLVASV	0.693	27	SB	VP2-3	A0204
195	FLEETTWTI	0.675	33	SB	VP2-3	A0204
61	GLTPQTYAV	0.670	35	SB	VP2-3	A0204
82	ALIQTVTGI	0.615	64	WB	VP2-3	A0204
155	SLFATISQA	0.590	84	WB	VP2-3	A0204
296	LLLGLYGTV	0.582	91	WB	VP2-3	A0204
100	FFSDWDHKV	0.570	104	WB	VP2-3	A0204
17	AAAATGFSV	0.494	238	WB	VP2-3	A0204
292	WMLPLLLGL	0.493	241	WB	VP2-3	A0204
213	YIQDYYSNL	0.491	246	WB	VP2-3	A0204
299	GLYGTVTPA	0.468	317	WB	VP2-3	A0204
159	TISQALWHV	0.463	333	WB	VP2-3	A0204
191	SLARFLEET	0.455	365	WB	VP2-3	A0204
39	VQIASLATV	0.928	2	SB	VP2-3	A0206
292	WMLPLLLGL	0.907	2	SB	VP2-3	A0206
195	FLEETTWTI	0.894	3	SB	VP2-3	A0206
61	GLTPQTYAV	0.849	5	SB	VP2-3	A0206
159	TISQALWHV	0.830	6	SB	VP2-3	A0206
6	LLGDLVASV	0.811	7	SB	VP2-3	A0206
75	GAIAGFAAL	0.805	8	SB	VP2-3	A0206
68	AVIAGAPGA	0.768	12	SB	VP2-3	A0206
17	AAAATGFSV	0.719	20	SB	VP2-3	A0206
82	ALIQTVTGI	0.701	25	SB	VP2-3	A0206

296	LLLGLYGTV	0.688	29	SB	VP2-3	A0206
45	ATVEGITTT	0.678	32	SB	VP2-3	A0206
94	AQVGYRFFS	0.625	57	WB	VP2-3	A0206
146	YLDPRHWGP	0.622	59	WB	VP2-3	A0206
213	YIQDYYSNL	0.593	81	WB	VP2-3	A0206
52	TTSEAIAAI	0.579	94	WB	VP2-3	A0206
10	LVASVSEAA	0.547	133	WB	VP2-3	A0206
129	YYDILFPGV	0.545	137	WB	VP2-3	A0206
288	TAPQWMLPL	0.544	139	WB	VP2-3	A0206
114	YQQSGMALE	0.542	141	WB	VP2-3	A0206
246	YSIDNADSI	0.520	180	WB	VP2-3	A0206
18	AAATGFSVA	0.517	186	WB	VP2-3	A0206
299	GLYGTVTPA	0.516	189	WB	VP2-3	A0206
85	QTVTGISSL	0.511	198	WB	VP2-3	A0206
76	AIAGFAALI	0.511	198	WB	VP2-3	A0206
29	AAGEAAAAI	0.508	205	WB	VP2-3	A0206
132	ILFPGVNTF	0.505	210	WB	VP2-3	A0206
230	RQVAEREGT	0.497	230	WB	VP2-3	A0206
3	ALALLGDLV	0.496	234	WB	VP2-3	A0206
65	QTYAVIAGA	0.478	282	WB	VP2-3	A0206
5	ALLGDLVAS	0.462	337	WB	VP2-3	A0206
167	VIRDDIPAI	0.444	409	WB	VP2-3	A0206
115	QQSGMALEL	0.438	437	WB	VP2-3	A0206
61	GLTPQTYAV	0.969	1	SB	VP2-3	A0211
6	LLGDLVASV	0.968	1	SB	VP2-3	A0211
296	LLLGLYGTV	0.950	1	SB	VP2-3	A0211
292	WMLPLLLGL	0.944	1	SB	VP2-3	A0211
195	FLEETTWTI	0.936	2	SB	VP2-3	A0211
159	TISQALWHV	0.904	2	SB	VP2-3	A0211
155	SLFATISQA	0.891	3	SB	VP2-3	A0211
299	GLYGTVTPA	0.884	3	SB	VP2-3	A0211
100	FFSDWDHKV	0.872	4	SB	VP2-3	A0211
146	YLDPRHWGP	0.871	4	SB	VP2-3	A0211
3	ALALLGDLV	0.860	4	SB	VP2-3	A0211
213	YIQDYYSNL	0.850	5	SB	VP2-3	A0211
220	NLSPIRPSM	0.829	6	SB	VP2-3	A0211
132	ILFPGVNTF	0.826	6	SB	VP2-3	A0211
76	AIAGFAALI	0.816	7	SB	VP2-3	A0211
191	SLARFLEET	0.802	8	SB	VP2-3	A0211
82	ALIQTVTGI	0.775	11	SB	VP2-3	A0211
129	YYDILFPGV	0.734	17	SB	VP2-3	A0211
92	SLAQVGYRF	0.679	32	SB	VP2-3	A0211
79	GFAALIQTV	0.662	38	SB	VP2-3	A0211
5	ALLGDLVAS	0.660	39	SB	VP2-3	A0211
112	GLYQQSGMA	0.658	40	SB	VP2-3	A0211
17	AAAATGFSV	0.657	41	SB	VP2-3	A0211
295	PLLLGLYGT	0.632	53	WB	VP2-3	A0211
133	LFPGVNTFV	0.594	80	WB	VP2-3	A0211
167	VIRDDIPAI	0.594	81	WB	VP2-3	A0211
253	SIEEVTQRM	0.567	108	WB	VP2-3	A0211
86	TVTGISSLA	0.472	303	WB	VP2-3	A0211
288	TAPQWMLPL	0.472	304	WB	VP2-3	A0211
27	EIAAGEAAA	0.450	383	WB	VP2-3	A0211
6	LLGDLVASV	0.931	2	SB	VP2-3	A0212
61	GLTPQTYAV	0.924	2	SB	VP2-3	A0212
296	LLLGLYGTV	0.910	2	SB	VP2-3	A0212
292	WMLPLLLGL	0.910	2	SB	VP2-3	A0212
213	YIQDYYSNL	0.894	3	SB	VP2-3	A0212
195	FLEETTWTI	0.892	3	SB	VP2-3	A0212
146	YLDPRHWGP	0.842	5	SB	VP2-3	A0212

100	FFSDWDHKV	0.833	6	SB	VP2-3	A0212
299	GLYGTVTPA	0.769	12	SB	VP2-3	A0212
159	TISQALWHV	0.717	21	SB	VP2-3	A0212
132	ILFPGVNTF	0.716	21	SB	VP2-3	A0212
167	VIRDDIPAI	0.698	26	SB	VP2-3	A0212
155	SLFATISQA	0.679	32	SB	VP2-3	A0212
82	ALIQTVTGI	0.678	32	SB	VP2-3	A0212
191	SLARFLEET	0.662	38	SB	VP2-3	A0212
3	ALALLGDLV	0.654	42	SB	VP2-3	A0212
129	YYDILFPGV	0.650	43	SB	VP2-3	A0212
220	NLSPIRPSM	0.622	59	WB	VP2-3	A0212
5	ALLGDLVAS	0.593	82	WB	VP2-3	A0212
79	GFAALIQTV	0.532	157	WB	VP2-3	A0212
133	LFPGVNTFV	0.528	164	WB	VP2-3	A0212
295	PLLLGLYGT	0.485	261	WB	VP2-3	A0212
27	EIAAGEAAA	0.471	306	WB	VP2-3	A0212
17	AAAATGFSV	0.450	383	WB	VP2-3	A0212
76	AIAGFAALI	0.448	393	WB	VP2-3	A0212
253	SIEEVTQRM	0.430	475	WB	VP2-3	A0212
6	LLGDLVASV	0.934	2	SB	VP2-3	A0216
61	GLTPQTYAV	0.916	2	SB	VP2-3	A0216
296	LLLGLYGTV	0.886	3	SB	VP2-3	A0216
159	TISQALWHV	0.864	4	SB	VP2-3	A0216
195	FLEETTWTI	0.847	5	SB	VP2-3	A0216
155	SLFATISQA	0.847	5	SB	VP2-3	A0216
299	GLYGTVTPA	0.835	5	SB	VP2-3	A0216
213	YIQDYYSNL	0.801	8	SB	VP2-3	A0216
100	FFSDWDHKV	0.789	9	SB	VP2-3	A0216
133	LFPGVNTFV	0.782	10	SB	VP2-3	A0216
292	WMLPLLLGL	0.764	12	SB	VP2-3	A0216
3	ALALLGDLV	0.763	12	SB	VP2-3	A0216
191	SLARFLEET	0.721	20	SB	VP2-3	A0216
82	ALIQTVTGI	0.677	33	SB	VP2-3	A0216
220	NLSPIRPSM	0.650	44	SB	VP2-3	A0216
76	AIAGFAALI	0.635	51	WB	VP2-3	A0216
17	AAAATGFSV	0.610	67	WB	VP2-3	A0216
132	ILFPGVNTF	0.584	90	WB	VP2-3	A0216
112	GLYQQSGMA	0.570	104	WB	VP2-3	A0216
92	SLAQVGYRF	0.552	127	WB	VP2-3	A0216
79	GFAALIQTV	0.522	176	WB	VP2-3	A0216
6	LLGDLVASV	0.930	2	SB	VP2-3	A0219
292	WMLPLLLGL	0.899	2	SB	VP2-3	A0219
61	GLTPQTYAV	0.888	3	SB	VP2-3	A0219
195	FLEETTWTI	0.848	5	SB	VP2-3	A0219
159	TISQALWHV	0.840	5	SB	VP2-3	A0219
100	FFSDWDHKV	0.782	10	SB	VP2-3	A0219
213	YIQDYYSNL	0.736	17	SB	VP2-3	A0219
296	LLLGLYGTV	0.726	19	SB	VP2-3	A0219
146	YLDPRHWGP	0.682	31	SB	VP2-3	A0219
82	ALIQTVTGI	0.643	47	SB	VP2-3	A0219
17	AAAATGFSV	0.629	55	WB	VP2-3	A0219
155	SLFATISQA	0.603	73	WB	VP2-3	A0219
299	GLYGTVTPA	0.564	111	WB	VP2-3	A0219
295	PLLLGLYGT	0.553	125	WB	VP2-3	A0219
129	YYDILFPGV	0.529	163	WB	VP2-3	A0219
220	NLSPIRPSM	0.528	164	WB	VP2-3	A0219
167	VIRDDIPAI	0.507	208	WB	VP2-3	A0219
132	ILFPGVNTF	0.504	214	WB	VP2-3	A0219
3	ALALLGDLV	0.475	291	WB	VP2-3	A0219

321	RVSRGSSQK	0.719	20	SB	VP2-3	A0301
334	RASAKTTNK	0.651	43	SB	VP2-3	A0301
203	IVNAPINFY	0.555	123	WB	VP2-3	A0301
293	MLPLLLGLY	0.473	299	WB	VP2-3	A0301
334	RASAKTTNK	0.729	18	SB	VP2-3	A1101
321	RVSRGSSQK	0.724	19	SB	VP2-3	A1101
91	SSLAQVGYR	0.688	29	SB	VP2-3	A1101
203	IVNAPINFY	0.666	37	SB	VP2-3	A1101
99	RFFSDWDHK	0.496	234	WB	VP2-3	A1101
158	ATISQALWH	0.460	345	WB	VP2-3	A1101
161	SQALWHVIR	0.457	356	WB	VP2-3	A1101
174	AITSQELQR	0.448	392	WB	VP2-3	A1101
139	TFVNNIQYL	0.584	90	WB	VP2-3	A2301
187	FFRDSLARF	0.577	97	WB	VP2-3	A2301
113	LYQQSGMAL	0.564	111	WB	VP2-3	A2301
132	ILFPGVNTF	0.521	178	WB	VP2-3	A2301
300	LYGTVTPAL	0.518	183	WB	VP2-3	A2301
216	DYYSNLSPI	0.482	271	WB	VP2-3	A2301
310	AYEDGPNQK	0.478	283	WB	VP2-3	A2301
202	TIVNAPINF	0.466	322	WB	VP2-3	A2301
99	RFFSDWDHK	0.466	323	WB	VP2-3	A2301
92	SLAQVGYRF	0.459	348	WB	VP2-3	A2301
300	LYGTVTPAL	0.661	39	SB	VP2-3	A2402
216	DYYSNLSPI	0.637	50	WB	VP2-3	A2402
156	LFATISQAL	0.560	116	WB	VP2-3	A2402
113	LYQQSGMAL	0.530	160	WB	VP2-3	A2402
200	TWTIVNAPI	0.452	374	WB	VP2-3	A2402
113	LYQQSGMAL	0.743	16	SB	VP2-3	A2403
139	TFVNNIQYL	0.591	83	WB	VP2-3	A2403
187	FFRDSLARF	0.572	102	WB	VP2-3	A2403
300	LYGTVTPAL	0.502	218	WB	VP2-3	A2403
292	WMLPLLLGL	0.426	498	WB	VP2-3	A2403
122	ELFNPDEYY	0.557	120	WB	VP2-3	A2601
303	TVTPALEAY	0.843	5	SB	VP2-3	A2602
203	IVNAPINFY	0.823	6	SB	VP2-3	A2602
122	ELFNPDEYY	0.792	9	SB	VP2-3	A2602
85	QTVTGISSL	0.778	11	SB	VP2-3	A2602
213	YIQDYYSNL	0.629	55	WB	VP2-3	A2602
293	MLPLLLGLY	0.578	96	WB	VP2-3	A2602
179	ELQRRTERF	0.551	128	WB	VP2-3	A2602
36	AIEVQIASL	0.518	183	WB	VP2-3	A2602
138	NTFVNNIQY	0.503	215	WB	VP2-3	A2602
187	FFRDSLARF	0.468	316	WB	VP2-3	A2602
202	TIVNAPINF	0.447	398	WB	VP2-3	A2602
62	LTPQTYAVI	0.442	416	WB	VP2-3	A2602
210	FYNYIQDYY	0.765	12	SB	VP2-3	A2902
122	ELFNPDEYY	0.716	21	SB	VP2-3	A2902
138	NTFVNNIQY	0.580	94	WB	VP2-3	A2902
203	IVNAPINFY	0.465	327	WB	VP2-3	A2902
209	NFYNYIQDY	0.457	357	WB	VP2-3	A2902
293	MLPLLLGLY	0.446	402	WB	VP2-3	A2902
99	RFFSDWDHK	0.765	12	SB	VP2-3	A3001
321	RVSRGSSQK	0.639	49	SB	VP2-3	A3001
334	RASAKTTNK	0.593	81	WB	VP2-3	A3001
186	RFFRDSLAR	0.501	222	WB	VP2-3	A3001

329	KAKGTRASA	0.446	401	WB	VP2-3	A3001
210	FYNYIQDYY	0.594	80	WB	VP2-3	A3002
203	IVNAPINFY	0.508	205	WB	VP2-3	A3002
293	MLPLLLGLY	0.466	321	WB	VP2-3	A3002
338	KTTNKRRSR	0.829	6	SB	VP2-3	A3101
316	NQKKRRVSR	0.804	8	SB	VP2-3	A3101
227	SMVRQVAER	0.772	11	SB	VP2-3	A3101
186	RFFRDSLAR	0.765	12	SB	VP2-3	A3101
91	SSLAQVGYR	0.756	13	SB	VP2-3	A3101
161	SQALWHVIR	0.641	48	SB	VP2-3	A3101
326	SSQKAKGTR	0.632	53	WB	VP2-3	A3101
334	RASAKTTNK	0.583	91	WB	VP2-3	A3101
217	YYSNLSPIR	0.570	105	WB	VP2-3	A3101
336	SAKTTNKRR	0.537	149	WB	VP2-3	A3101
99	RFFSDWDHK	0.504	214	WB	VP2-3	A3101
335	ASAKTTNKR	0.479	280	WB	VP2-3	A3101
321	RVSRGSSQK	0.435	453	WB	VP2-3	A3101
256	EVTQRMDLR	0.709	23	SB	VP2-3	A3301
316	NQKKRRVSR	0.703	24	SB	VP2-3	A3301
252	DSIEEVTQR	0.585	89	WB	VP2-3	A3301
341	NKRRSRSSR	0.463	333	WB	VP2-3	A3301
256	EVTQRMDLR	0.844	5	SB	VP2-3	A6801
252	DSIEEVTQR	0.787	10	SB	VP2-3	A6801
138	NTFVNNIQY	0.711	22	SB	VP2-3	A6801
175	ITSQELQRR	0.650	44	SB	VP2-3	A6801
279	IAPGGANQR	0.616	63	WB	VP2-3	A6801
217	YYSNLSPIR	0.607	70	WB	VP2-3	A6801
91	SSLAQVGYR	0.605	71	WB	VP2-3	A6801
227	SMVRQVAER	0.599	76	WB	VP2-3	A6801
335	ASAKTTNKR	0.531	160	WB	VP2-3	A6801
122	ELFNPDEYY	0.510	201	WB	VP2-3	A6801
210	FYNYIQDYY	0.503	217	WB	VP2-3	A6801
174	AITSQELQR	0.462	338	WB	VP2-3	A6801
142	NNIQYLDPR	0.461	341	WB	VP2-3	A6801
326	SSQKAKGTR	0.457	357	WB	VP2-3	A6801
321	RVSRGSSQK	0.456	360	WB	VP2-3	A6801
303	TVTPALEAY	0.454	367	WB	VP2-3	A6801
161	SQALWHVIR	0.451	379	WB	VP2-3	A6801
203	IVNAPINFY	0.449	388	WB	VP2-3	A6801
338	KTTNKRRSR	0.428	487	WB	VP2-3	A6801
336	SAKTTNKRR	0.427	493	WB	VP2-3	A6801
65	QTYAVIAGA	0.846	5	SB	VP2-3	A6802
52	TTSEAIAAI	0.827	6	SB	VP2-3	A6802
86	TVTGISSLA	0.764	12	SB	VP2-3	A6802
10	LVASVSEAA	0.709	23	SB	VP2-3	A6802
198	ETTWTIVNA	0.691	28	SB	VP2-3	A6802
85	QTVTGISSL	0.677	32	SB	VP2-3	A6802
16	EAAAATGFS	0.649	44	SB	VP2-3	A6802
267	ESVHSGEFI	0.602	73	WB	VP2-3	A6802
27	EIAAGEAAA	0.596	79	WB	VP2-3	A6802
17	AAAATGFSV	0.574	100	WB	VP2-3	A6802
249	DNADSIEEV	0.562	114	WB	VP2-3	A6802
166	HVIRDDIPA	0.561	115	WB	VP2-3	A6802
159	TISQALWHV	0.550	130	WB	VP2-3	A6802
88	TGISSLAQV	0.536	151	WB	VP2-3	A6802
48	EGITTTSEA	0.535	152	WB	VP2-3	A6802
246	YSIDNADSI	0.523	174	WB	VP2-3	A6802

76	AIAGFAALI	0.521	177	WB	VP2-3	A6802
55	EAIAAIGLT	0.484	267	WB	VP2-3	A6802
80	FAALIQTVT	0.481	273	WB	VP2-3	A6802
152	WGPSLFATI	0.478	284	WB	VP2-3	A6802
33	AAAAIEVQI	0.458	353	WB	VP2-3	A6802
288	TAPQWMLPL	0.443	416	WB	VP2-3	A6802
51	TTTSEAIAA	0.433	463	WB	VP2-3	A6802
65	QTYAVIAGA	0.710	23	SB	VP2-3	A6901
198	ETTWTIVNA	0.703	24	SB	VP2-3	A6901
52	TTSEAIAAI	0.684	30	SB	VP2-3	A6901
159	TISQALWHV	0.622	59	WB	VP2-3	A6901
292	WMLPLLLGL	0.604	72	WB	VP2-3	A6901
17	AAAATGFSV	0.601	74	WB	VP2-3	A6901
27	EIAAGEAAA	0.579	94	WB	VP2-3	A6901
195	FLEETTWTI	0.570	104	WB	VP2-3	A6901
288	TAPQWMLPL	0.545	137	WB	VP2-3	A6901
6	LLGDLVASV	0.506	209	WB	VP2-3	A6901
296	LLLGLYGTV	0.472	301	WB	VP2-3	A6901
100	FFSDWDHKV	0.429	484	WB	VP2-3	A6901
225	RPSMVRQVA	0.705	24	SB	VP2-3	B0702
172	IPAITSQEL	0.628	55	WB	VP2-3	B0702
148	DPRHWGPSL	0.610	67	WB	VP2-3	B0702
289	APQWMLPLL	0.598	77	WB	VP2-3	B0702
314	GPNQKKRRV	0.530	162	WB	VP2-3	B0702
206	APINFYNYI	0.475	294	WB	VP2-3	B0702
132	ILFPGVNTF	0.606	70	WB	VP2-3	B1501
203	IVNAPINFY	0.578	96	WB	VP2-3	B1501
180	LQRRTERFF	0.558	118	WB	VP2-3	B1501
115	QQSGMALEL	0.503	216	WB	VP2-3	B1501
39	VQIASLATV	0.477	287	WB	VP2-3	B1501
122	ELFNPDEYY	0.439	432	WB	VP2-3	B1501
92	SLAQVGYRF	0.428	489	WB	VP2-3	B1501
184	TERFFRDSL	0.622	59	WB	VP2-3	B1801
292	WMLPLLLGL	0.590	84	WB	VP2-3	B1801
148	DPRHWGPSL	0.584	90	WB	VP2-3	B1801
54	SEAIAAIGL	0.546	135	WB	VP2-3	B1801
255	EEVTQRMDL	0.451	380	WB	VP2-3	B1801
15	SEAAAATGF	0.435	449	WB	VP2-3	B1801
320	RRVSRGSSQ	0.507	206	WB	VP2-3	B2705
303	TVTPALEAY	0.686	29	SB	VP2-3	B3501
172	IPAITSQEL	0.611	67	WB	VP2-3	B3501
125	NPDEYYDIL	0.606	71	WB	VP2-3	B3501
238	THVNFGHTY	0.550	130	WB	VP2-3	B3501
156	LFATISQAL	0.521	178	WB	VP2-3	B3501
67	YAVIAGAPG	0.510	199	WB	VP2-3	B3501
288	TAPQWMLPL	0.508	204	WB	VP2-3	B3501
289	APQWMLPLL	0.499	225	WB	VP2-3	B3501
132	ILFPGVNTF	0.484	265	WB	VP2-3	B3501
80	FAALIQTVT	0.470	310	WB	VP2-3	B3501
63	TPQTYAVIA	0.453	372	WB	VP2-3	B3501
28	IAAGEAAAA	0.446	400	WB	VP2-3	B3501
134	FPGVNTFVN	0.445	405	WB	VP2-3	B3501
205	NAPINFYNY	0.437	442	WB	VP2-3	B3501
13	SVSEAAAAT	0.433	461	WB	VP2-3	B3501
75	GAIAGFAAL	0.429	483	WB	VP2-3	B3501

54	SEAIAAIGL	0.703	24	SB	VP2-3	B4001
31	GEAAAAIEV	0.632	53	WB	VP2-3	B4001
255	EEVTQRMDL	0.542	141	WB	VP2-3	B4001
15	SEAAAATGF	0.509	202	WB	VP2-3	B4001
184	TERFFRDSL	0.467	319	WB	VP2-3	B4001
266	KESVHSGEF	0.574	99	WB	VP2-3	B4002
255	EEVTQRMDL	0.532	158	WB	VP2-3	B4002
272	GEFIEKTIA	0.496	232	WB	VP2-3	B4002
15	SEAAAATGF	0.495	235	WB	VP2-3	B4002
54	SEAIAAIGL	0.445	405	WB	VP2-3	B4002
54	SEAIAAIGL	0.492	243	WB	VP2-3	B4403
15	SEAAAATGF	0.476	288	WB	VP2-3	B4403
26	AEIAAGEAA	0.466	322	WB	VP2-3	B4403
26	AEIAAGEAA	0.639	49	SB	VP2-3	B4501
255	EEVTQRMDL	0.521	178	WB	VP2-3	B4501
31	GEAAAAIEV	0.456	361	WB	VP2-3	B4501
197	EETTWTIVN	0.432	464	WB	VP2-3	B4501
206	APINFYNYI	0.497	230	WB	VP2-3	B5101
294	LPLLLGLYG	0.451	381	WB	VP2-3	B5101
206	APINFYNYI	0.608	69	WB	VP2-3	B5301
289	APQWMLPLL	0.545	136	WB	VP2-3	B5301
157	FATISQALW	0.522	176	WB	VP2-3	B5301
206	APINFYNYI	0.614	64	WB	VP2-3	B5401
73	APGAIAGFA	0.573	100	WB	VP2-3	B5401
119	MALELFNPD	0.511	199	WB	VP2-3	B5401
134	FPGVNTFVN	0.502	218	WB	VP2-3	B5401
294	LPLLLGLYG	0.488	254	WB	VP2-3	B5401
63	TPQTYAVIA	0.478	282	WB	VP2-3	B5401
80	FAALIQTVT	0.464	329	WB	VP2-3	B5401
157	FATISQALW	0.723	19	SB	VP2-3	B5801
90	ISSLAQVGY	0.546	136	WB	VP2-3	B5801
96	VGYRFFSDW	0.481	274	WB	VP2-3	B5801
	10-mers					
237	GTHVNFGHTY	0.517	185	WB	VP2-3	A0101
5	ALLGDLVASV	0.820	6	SB	VP2-3	A0201
132	ILFPGVNTFV	0.785	10	SB	VP2-3	A0201
299	GLYGTVTPAL	0.721	20	SB	VP2-3	A0201
195	FLEETTWTIV	0.703	24	SB	VP2-3	A0201
155	SLFATISQAL	0.632	53	WB	VP2-3	A0201
114	YQQSGMALEL	0.529	162	WB	VP2-3	A0201
158	ATISQALWHV	0.476	288	WB	VP2-3	A0201
199	TTWTIVNAPI	0.473	298	WB	VP2-3	A0201
61	GLTPQTYAVI	0.471	305	WB	VP2-3	A0201
112	GLYQQSGMAL	0.455	364	WB	VP2-3	A0201
260	RMDLRNKESV	0.442	418	WB	VP2-3	A0201
220	NLSPIRPSMV	0.436	445	WB	VP2-3	A0201
163	ALWHVIRDDI	0.430	476	WB	VP2-3	A0201
132	ILFPGVNTFV	0.798	8	SB	VP2-3	A0202
5	ALLGDLVASV	0.785	10	SB	VP2-3	A0202
155	SLFATISQAL	0.742	16	SB	VP2-3	A0202
299	GLYGTVTPAL	0.680	32	SB	VP2-3	A0202

112	GLYQQSGMAL	0.654	42	SB	VP2-3	A0202
195	FLEETTWTIV	0.589	85	WB	VP2-3	A0202
3	ALALLGDLVA	0.583	91	WB	VP2-3	A0202
191	SLARFLEETT	0.557	120	WB	VP2-3	A0202
114	YQQSGMALEL	0.554	124	WB	VP2-3	A0202
296	LLLGLYGTVT	0.537	149	WB	VP2-3	A0202
138	NTFVNNIQYL	0.525	170	WB	VP2-3	A0202
220	NLSPIRPSMV	0.519	182	WB	VP2-3	A0202
158	ATISQALWHV	0.501	222	WB	VP2-3	A0202
10	LVASVSEAAA	0.479	280	WB	VP2-3	A0202
61	GLTPQTYAVI	0.466	322	WB	VP2-3	A0202
124	FNPDEYYDIL	0.461	342	WB	VP2-3	A0202
295	PLLLGLYGTV	0.450	382	WB	VP2-3	A0202
260	RMDLRNKESV	0.447	397	WB	VP2-3	A0202
293	MLPLLLGLYG	0.427	492	WB	VP2-3	A0202
2	AALALLGDLV	0.426	498	WB	VP2-3	A0202
132	ILFPGVNTFV	0.888	3	SB	VP2-3	A0203
5	ALLGDLVASV	0.868	4	SB	VP2-3	A0203
195	FLEETTWTIV	0.820	7	SB	VP2-3	A0203
299	GLYGTVTPAL	0.803	8	SB	VP2-3	A0203
220	NLSPIRPSMV	0.788	9	SB	VP2-3	A0203
112	GLYQQSGMAL	0.756	14	SB	VP2-3	A0203
61	GLTPQTYAVI	0.703	24	SB	VP2-3	A0203
155	SLFATISQAL	0.700	25	SB	VP2-3	A0203
239	HVNFGHTYSI	0.663	38	SB	VP2-3	A0203
287	RTAPQWMLPL	0.629	55	WB	VP2-3	A0203
260	RMDLRNKESV	0.533	156	WB	VP2-3	A0203
191	SLARFLEETT	0.530	161	WB	VP2-3	A0203
68	AVIAGAPGAI	0.529	163	WB	VP2-3	A0203
158	ATISQALWHV	0.516	187	WB	VP2-3	A0203
24	SVAEIAAGEA	0.513	193	WB	VP2-3	A0203
114	YQQSGMALEL	0.513	194	WB	VP2-3	A0203
35	AAIEVQIASL	0.509	203	WB	VP2-3	A0203
295	PLLLGLYGTV	0.503	217	WB	VP2-3	A0203
69	VIAGAPGAIA	0.490	248	WB	VP2-3	A0203
3	ALALLGDLVA	0.472	303	WB	VP2-3	A0203
10	LVASVSEAAA	0.471	304	WB	VP2-3	A0203
75	GAIAGFAALI	0.453	373	WB	VP2-3	A0203
85	QTVTGISSLA	0.440	425	WB	VP2-3	A0203
43	SLATVEGITT	0.431	473	WB	VP2-3	A0203
132	ILFPGVNTFV	0.738	17	SB	VP2-3	A0204
195	FLEETTWTIV	0.686	30	SB	VP2-3	A0204
5	ALLGDLVASV	0.678	32	SB	VP2-3	A0204
155	SLFATISQAL	0.630	54	WB	VP2-3	A0204
158	ATISQALWHV	0.567	108	WB	VP2-3	A0204
299	GLYGTVTPAL	0.485	263	WB	VP2-3	A0204
112	GLYQQSGMAL	0.468	317	WB	VP2-3	A0204
287	RTAPQWMLPL	0.457	356	WB	VP2-3	A0204
5	ALLGDLVASV	0.873	3	SB	VP2-3	A0206
195	FLEETTWTIV	0.869	4	SB	VP2-3	A0206
132	ILFPGVNTFV	0.865	4	SB	VP2-3	A0206
114	YQQSGMALEL	0.803	8	SB	VP2-3	A0206
158	ATISQALWHV	0.779	10	SB	VP2-3	A0206
35	AAIEVQIASL	0.711	22	SB	VP2-3	A0206
75	GAIAGFAALI	0.649	44	SB	VP2-3	A0206
287	RTAPQWMLPL	0.626	57	WB	VP2-3	A0206
299	GLYGTVTPAL	0.599	76	WB	VP2-3	A0206
68	AVIAGAPGAI	0.591	83	WB	VP2-3	A0206
67	YAVIAGAPGA	0.588	86	WB	VP2-3	A0206

84	IQTVTGISSL	0.569	105	WB	VP2-3	A0206
2	AALALLGDLV	0.550	129	WB	VP2-3	A0206
94	AQVGYRFFSD	0.537	150	WB	VP2-3	A0206
146	YLDPRHWGPS	0.525	169	WB	VP2-3	A0206
260	RMDLRNKESV	0.525	170	WB	VP2-3	A0206
166	HVIRDDIPAI	0.513	193	WB	VP2-3	A0206
288	TAPQWMLPLL	0.507	208	WB	VP2-3	A0206
155	SLFATISQAL	0.500	223	WB	VP2-3	A0206
39	VQIASLATVE	0.488	254	WB	VP2-3	A0206
24	SVAEIAAGEA	0.488	255	WB	VP2-3	A0206
194	RFLEETTWTI	0.480	276	WB	VP2-3	A0206
10	LVASVSEAAA	0.470	309	WB	VP2-3	A0206
112	GLYQQSGMAL	0.466	322	WB	VP2-3	A0206
220	NLSPIRPSMV	0.460	344	WB	VP2-3	A0206
159	TISQALWHVI	0.458	353	WB	VP2-3	A0206
17	AAAATGFSVA	0.457	354	WB	VP2-3	A0206
45	ATVEGITTTS	0.454	365	WB	VP2-3	A0206
231	QVAEREGTHV	0.453	371	WB	VP2-3	A0206
78	AGFAALIQTV	0.448	394	WB	VP2-3	A0206
115	QQSGMALELF	0.438	437	WB	VP2-3	A0206
81	AALIQTVTGI	0.433	460	WB	VP2-3	A0206
61	GLTPQTYAVI	0.432	466	WB	VP2-3	A0206
132	ILFPGVNTFV	0.975	1	SB	VP2-3	A0211
5	ALLGDLVASV	0.972	1	SB	VP2-3	A0211
155	SLFATISQAL	0.940	1	SB	VP2-3	A0211
299	GLYGTVTPAL	0.939	1	SB	VP2-3	A0211
195	FLEETTWTIV	0.931	2	SB	VP2-3	A0211
260	RMDLRNKESV	0.912	2	SB	VP2-3	A0211
220	NLSPIRPSMV	0.891	3	SB	VP2-3	A0211
295	PLLLGLYGTV	0.885	3	SB	VP2-3	A0211
112	GLYQQSGMAL	0.864	4	SB	VP2-3	A0211
61	GLTPQTYAVI	0.850	5	SB	VP2-3	A0211
146	YLDPRHWGPS	0.740	16	SB	VP2-3	A0211
191	SLARFLEETT	0.737	17	SB	VP2-3	A0211
128	EYYDILFPGV	0.731	18	SB	VP2-3	A0211
159	TISQALWHVI	0.674	34	SB	VP2-3	A0211
102	SDWDHKVSTV	0.641	48	SB	VP2-3	A0211
292	WMLPLLLGLY	0.638	50	WB	VP2-3	A0211
163	ALWHVIRDDI	0.620	60	WB	VP2-3	A0211
3	ALALLGDLVA	0.616	63	WB	VP2-3	A0211
92	SLAQVGYRFF	0.615	64	WB	VP2-3	A0211
158	ATISQALWHV	0.598	77	WB	VP2-3	A0211
99	RFFSDWDHKV	0.596	79	WB	VP2-3	A0211
287	RTAPQWMLPL	0.585	89	WB	VP2-3	A0211
78	AGFAALIQTV	0.570	105	WB	VP2-3	A0211
43	SLATVEGITT	0.568	107	WB	VP2-3	A0211
223	PIRPSMVRQV	0.566	109	WB	VP2-3	A0211
296	LLLGLYGTVT	0.548	133	WB	VP2-3	A0211
38	EVQIASLATV	0.532	158	WB	VP2-3	A0211
114	YQQSGMALEL	0.530	162	WB	VP2-3	A0211
194	RFLEETTWTI	0.518	184	WB	VP2-3	A0211
239	HVNFGHTYSI	0.510	199	WB	VP2-3	A0211
24	SVAEIAAGEA	0.497	230	WB	VP2-3	A0211
171	DIPAITSQEL	0.484	265	WB	VP2-3	A0211
231	QVAEREGTHV	0.484	265	WB	VP2-3	A0211
288	TAPQWMLPLL	0.470	310	WB	VP2-3	A0211
16	EAAAATGFSV	0.464	330	WB	VP2-3	A0211
87	VTGISSLAQV	0.454	366	WB	VP2-3	A0211
6	LLGDLVASVS	0.453	372	WB	VP2-3	A0211
35	AAIEVQIASL	0.437	439	WB	VP2-3	A0211

132 ILFPGVNTFV	0.943	1	SB	VP2-3	A0212
5 ALLGDLVASV	0.935	2	SB	VP2-3	A0212
195 FLEETTWTIV	0.906	2	SB	VP2-3	A0212
299 GLYGTVTPAL	0.904	2	SB	VP2-3	A0212
155 SLFATISQAL	0.880	3	SB	VP2-3	A0212
260 RMDLRNKESV	0.826	6	SB	VP2-3	A0212
220 NLSPIRPSMV	0.779	10	SB	VP2-3	A0212
112 GLYQQSGMAL	0.778	11	SB	VP2-3	A0212
295 PLLLGLYGTV	0.757	13	SB	VP2-3	A0212
191 SLARFLEETT	0.661	39	SB	VP2-3	A0212
61 GLTPQTYAVI	0.654	42	SB	VP2-3	A0212
163 ALWHVIRDDI	0.638	50	WB	VP2-3	A0212
128 EYYDILFPGV	0.616	63	WB	VP2-3	A0212
146 YLDPRHWGPS	0.615	64	WB	VP2-3	A0212
114 YQQSGMALEL	0.540	145	WB	VP2-3	A0212
296 LLLGLYGTVT	0.537	149	WB	VP2-3	A0212
102 SDWDHKVSTV	0.537	150	WB	VP2-3	A0212
231 QVAEREGTHV	0.480	278	WB	VP2-3	A0212
292 WMLPLLLGLY	0.456	358	WB	VP2-3	A0212
158 ATISQALWHV	0.442	419	WB	VP2-3	A0212
99 RFFSDWDHKV	0.441	423	WB	VP2-3	A0212
213 YIQDYYSNLS	0.431	472	WB	VP2-3	A0212
132 ILFPGVNTFV	0.955	1	SB	VP2-3	A0216
5 ALLGDLVASV	0.929	2	SB	VP2-3	A0216
299 GLYGTVTPAL	0.896	3	SB	VP2-3	A0216
195 FLEETTWTIV	0.888	3	SB	VP2-3	A0216
220 NLSPIRPSMV	0.866	4	SB	VP2-3	A0216
155 SLFATISQAL	0.857	4	SB	VP2-3	A0216
295 PLLLGLYGTV	0.819	7	SB	VP2-3	A0216
260 RMDLRNKESV	0.787	9	SB	VP2-3	A0216
112 GLYQQSGMAL	0.782	10	SB	VP2-3	A0216
61 GLTPQTYAVI	0.651	43	SB	VP2-3	A0216
191 SLARFLEETT	0.648	45	SB	VP2-3	A0216
158 ATISQALWHV	0.620	60	WB	VP2-3	A0216
102 SDWDHKVSTV	0.575	99	WB	VP2-3	A0216
163 ALWHVIRDDI	0.562	114	WB	VP2-3	A0216
231 QVAEREGTHV	0.553	125	WB	VP2-3	A0216
128 EYYDILFPGV	0.552	126	WB	VP2-3	A0216
38 EVQIASLATV	0.550	130	WB	VP2-3	A0216
223 PIRPSMVRQV	0.520	179	WB	VP2-3	A0216
43 SLATVEGITT	0.498	229	WB	VP2-3	A0216
99 RFFSDWDHKV	0.498	229	WB	VP2-3	A0216
171 DIPAITSQEL	0.485	262	WB	VP2-3	A0216
87 VTGISSLAQV	0.455	363	WB	VP2-3	A0216
16 EAAAATGFSV	0.451	379	WB	VP2-3	A0216
114 YQQSGMALEL	0.446	401	WB	VP2-3	A0216
78 AGFAALIQTV	0.438	434	WB	VP2-3	A0216
3 ALALLGDLVA	0.434	456	WB	VP2-3	A0216
59 AIGLTPQTYA	0.433	460	WB	VP2-3	A0216
296 LLLGLYGTVT	0.427	492	WB	VP2-3	A0216
5 ALLGDLVASV	0.918	2	SB	VP2-3	A0219
195 FLEETTWTIV	0.849	5	SB	VP2-3	A0219
299 GLYGTVTPAL	0.826	6	SB	VP2-3	A0219
220 NLSPIRPSMV	0.768	12	SB	VP2-3	A0219
155 SLFATISQAL	0.750	14	SB	VP2-3	A0219
260 RMDLRNKESV	0.698	26	SB	VP2-3	A0219
295 PLLLGLYGTV	0.664	37	SB	VP2-3	A0219
61 GLTPQTYAVI	0.545	137	WB	VP2-3	A0219
114 YQQSGMALEL	0.523	175	WB	VP2-3	A0219
128 EYYDILFPGV	0.521	177	WB	VP2-3	A0219

159 TISQALWHVI	0.498	228	WB	VP2-3	A0219
16 EAAAATGFSV	0.480	277	WB	VP2-3	A0219
112 GLYQQSGMAL	0.441	424	WB	VP2-3	A0219
158 ATISQALWHV	0.439	430	WB	VP2-3	A0219
268 SVHSGEFIEK	0.544	139	WB	VP2-3	A0301
329 KAKGTRASAK	0.506	208	WB	VP2-3	A0301
320 RRVSRGSSQK	0.471	306	WB	VP2-3	A0301
202 TIVNAPINFY	0.464	331	WB	VP2-3	A0301
292 WMLPLLLGLY	0.456	358	WB	VP2-3	A0301
268 SVHSGEFIEK	0.783	10	SB	VP2-3	A1101
257 VTQRMDLRNK	0.698	26	SB	VP2-3	A1101
160 ISQALWHVIR	0.561	115	WB	VP2-3	A1101
329 KAKGTRASAK	0.536	152	WB	VP2-3	A1101
202 TIVNAPINFY	0.497	230	WB	VP2-3	A1101
90 ISSLAQVGYR	0.464	329	WB	VP2-3	A1101
212 NYIQDYYSNL	0.652	43	SB	VP2-3	A2301
186 RFFRDSLARF	0.651	43	SB	VP2-3	A2301
194 RFLEETTWTI	0.548	132	WB	VP2-3	A2301
201 WTIVNAPINF	0.547	135	WB	VP2-3	A2301
310 AYEDGPNQKK	0.490	250	WB	VP2-3	A2301
245 TYSIDNADSI	0.489	252	WB	VP2-3	A2301
91 SSLAQVGYRF	0.461	340	WB	VP2-3	A2301
179 ELQRRTERFF	0.429	482	WB	VP2-3	A2301
212 NYIQDYYSNL	0.650	44	SB	VP2-3	A2402
194 RFLEETTWTI	0.609	69	WB	VP2-3	A2402
151 HWGPSLFATI	0.540	145	WB	VP2-3	A2402
245 TYSIDNADSI	0.529	162	WB	VP2-3	A2402
186 RFFRDSLARF	0.484	266	WB	VP2-3	A2402
156 LFATISQALW	0.476	290	WB	VP2-3	A2402
194 RFLEETTWTI	0.667	36	SB	VP2-3	A2403
186 RFFRDSLARF	0.659	39	SB	VP2-3	A2403
212 NYIQDYYSNL	0.619	62	WB	VP2-3	A2403
245 TYSIDNADSI	0.461	341	WB	VP2-3	A2403
291 QWMLPLLLGL	0.429	481	WB	VP2-3	A2403
202 TIVNAPINFY	0.620	60	WB	VP2-3	A2601
252 DSIEEVTQRM	0.617	63	WB	VP2-3	A2601
202 TIVNAPINFY	0.801	8	SB	VP2-3	A2602
302 GTVTPALEAY	0.771	11	SB	VP2-3	A2602
287 RTAPQWMLPL	0.760	13	SB	VP2-3	A2602
201 WTIVNAPINF	0.744	15	SB	VP2-3	A2602
179 ELQRRTERFF	0.735	17	SB	VP2-3	A2602
171 DIPAITSQEL	0.532	158	WB	VP2-3	A2602
166 HVIRDDIPAI	0.531	159	WB	VP2-3	A2602
131 DILFPGVNTF	0.488	253	WB	VP2-3	A2602
38 EVQIASLATV	0.471	304	WB	VP2-3	A2602
209 NFYNYIQDYY	0.572	102	WB	VP2-3	A2902
204 VNAPINFYNY	0.549	131	WB	VP2-3	A2902
292 WMLPLLLGLY	0.547	134	WB	VP2-3	A2902
329 KAKGTRASAK	0.783	10	SB	VP2-3	A3001
322 VSRGSSQKAK	0.757	13	SB	VP2-3	A3001
268 SVHSGEFIEK	0.678	32	SB	VP2-3	A3001
180 LQRRTERFFR	0.485	263	WB	VP2-3	A3001
237 GTHVNFGHTY	0.479	281	WB	VP2-3	A3001

89 GISSLAQVGY	0.518	184	WB	VP2-3	A3002
292 WMLPLLLGLY	0.511	198	WB	VP2-3	A3002
209 NFYNYIQDYY	0.475	292	WB	VP2-3	A3002
202 TIVNAPINFY	0.437	443	WB	VP2-3	A3002
180 LQRRTERFFR	0.756	14	SB	VP2-3	A3101
334 RASAKTTNKR	0.645	46	SB	VP2-3	A3101
337 AKTTNKRRSR	0.606	71	WB	VP2-3	A3101
160 ISQALWHVIR	0.591	83	WB	VP2-3	A3101
174 AITSQELQRR	0.577	97	WB	VP2-3	A3101
177 SQELQRRTER	0.543	140	WB	VP2-3	A3101
329 KAKGTRASAK	0.520	180	WB	VP2-3	A3101
90 ISSLAQVGYR	0.491	246	WB	VP2-3	A3101
340 TNKRRSRSSR	0.489	252	WB	VP2-3	A3101
226 PSMVRQVAER	0.471	305	WB	VP2-3	A3101
335 ASAKTTNKRR	0.455	363	WB	VP2-3	A3101
315 PNQKKRRVSR	0.448	393	WB	VP2-3	A3101
216 DYYSNLSPIR	0.588	86	WB	VP2-3	A3301
180 LQRRTERFFR	0.560	116	WB	VP2-3	A3301
160 ISQALWHVIR	0.507	206	WB	VP2-3	A3301
278 TIAPGGANQR	0.743	16	SB	VP2-3	A6801
309 EAYEDGPNQK	0.741	16	SB	VP2-3	A6801
90 ISSLAQVGYR	0.713	22	SB	VP2-3	A6801
216 DYYSNLSPIR	0.707	23	SB	VP2-3	A6801
268 SVHSGEFIEK	0.645	46	SB	VP2-3	A6801
185 ERFFRDSLAR	0.541	142	WB	VP2-3	A6801
334 RASAKTTNKR	0.535	152	WB	VP2-3	A6801
202 TIVNAPINFY	0.532	158	WB	VP2-3	A6801
160 ISQALWHVIR	0.498	228	WB	VP2-3	A6801
255 EEVTQRMDLR	0.495	237	WB	VP2-3	A6801
209 NFYNYIQDYY	0.464	329	WB	VP2-3	A6801
221 LSPIRPSMVR	0.439	434	WB	VP2-3	A6801
16 EAAAATGFSV	0.886	3	SB	VP2-3	A6802
199 TTWTIVNAPI	0.877	3	SB	VP2-3	A6802
32 EAAAAIEVQI	0.797	8	SB	VP2-3	A6802
138 NTFVNNIQYL	0.763	12	SB	VP2-3	A6802
239 HVNFGHTYSI	0.707	23	SB	VP2-3	A6802
287 RTAPQWMLPL	0.692	28	SB	VP2-3	A6802
24 SVAEIAAGEA	0.669	36	SB	VP2-3	A6802
51 TTTSEAIAAI	0.664	38	SB	VP2-3	A6802
205 NAPINFYNYI	0.663	38	SB	VP2-3	A6802
27 EIAAGEAAAA	0.642	47	SB	VP2-3	A6802
48 EGITTTSEAI	0.641	48	SB	VP2-3	A6802
85 QTVTGISSLA	0.637	50	WB	VP2-3	A6802
38 EVQIASLATV	0.608	69	WB	VP2-3	A6802
171 DIPAITSQEL	0.587	86	WB	VP2-3	A6802
10 LVASVSEAAA	0.570	105	WB	VP2-3	A6802
128 EYYDILFPGV	0.563	113	WB	VP2-3	A6802
220 NLSPIRPSMV	0.549	130	WB	VP2-3	A6802
132 ILFPGVNTFV	0.545	138	WB	VP2-3	A6802
166 HVIRDDIPAI	0.535	152	WB	VP2-3	A6802
155 SLFATISQAL	0.516	188	WB	VP2-3	A6802
159 TISQALWHVI	0.500	223	WB	VP2-3	A6802
28 IAAGEAAAAI	0.487	257	WB	VP2-3	A6802
231 QVAEREGTHV	0.474	296	WB	VP2-3	A6802
158 ATISQALWHV	0.457	357	WB	VP2-3	A6802
41 IASLATVEGI	0.435	450	WB	VP2-3	A6802

16	EAAAATGFSV	0.809	7	SB	VP2-3	A6901
199	TTWTIVNAPI	0.775	11	SB	VP2-3	A6901
128	EYYDILFPGV	0.674	34	SB	VP2-3	A6901
38	EVQIASLATV	0.655	41	SB	VP2-3	A6901
138	NTFVNNIQYL	0.647	45	SB	VP2-3	A6901
158	ATISQALWHV	0.607	69	WB	VP2-3	A6901
32	EAAAAIEVQI	0.603	73	WB	VP2-3	A6901
27	EIAAGEAAAA	0.569	105	WB	VP2-3	A6901
239	HVNFGHTYSI	0.516	187	WB	VP2-3	A6901
287	RTAPQWMLPL	0.511	198	WB	VP2-3	A6901
166	HVIRDDIPAI	0.505	210	WB	VP2-3	A6901
132	ILFPGVNTFV	0.497	229	WB	VP2-3	A6901
231	QVAEREGTHV	0.482	271	WB	VP2-3	A6901
5	ALLGDLVASV	0.460	346	WB	VP2-3	A6901
51	TTTSEAIAAI	0.451	381	WB	VP2-3	A6901
87	VTGISSLAQV	0.440	426	WB	VP2-3	A6901
288	TAPQWMLPLL	0.437	441	WB	VP2-3	A6901
24	SVAEIAAGEA	0.434	456	WB	VP2-3	A6901
289	APQWMLPLLL	0.641	48	SB	VP2-3	B0702
225	RPSMVRQVAE	0.621	60	WB	VP2-3	B0702
148	DPRHWGPSLF	0.517	185	WB	VP2-3	B0702
73	APGAIAGFAA	0.513	194	WB	VP2-3	B0702
292	WMLPLLLGLY	0.543	140	WB	VP2-3	B1501
115	QQSGMALELF	0.542	141	WB	VP2-3	B1501
114	YQQSGMALEL	0.537	150	WB	VP2-3	B1501
84	IQTVTGISSL	0.522	176	WB	VP2-3	B1501
155	SLFATISQAL	0.494	238	WB	VP2-3	B1501
230	RQVAEREGTH	0.480	276	WB	VP2-3	B1501
92	SLAQVGYRFF	0.475	291	WB	VP2-3	B1501
58	AAIGLTPQTY	0.469	311	WB	VP2-3	B1501
237	GTHVNFGHTY	0.447	398	WB	VP2-3	B1501
299	GLYGTVTPAL	0.434	457	WB	VP2-3	B1501
201	WTIVNAPINF	0.426	497	WB	VP2-3	B1501
233	AEREGTHVNF	0.711	22	SB	VP2-3	B1801
121	LELFNPDEYY	0.515	189	WB	VP2-3	B1801
178	QELQRRTERF	0.507	207	WB	VP2-3	B1801
37	IEVQIASLAT	0.487	257	WB	VP2-3	B1801
148	DPRHWGPSLF	0.482	273	WB	VP2-3	B1801
292	WMLPLLLGLY	0.445	407	WB	VP2-3	B1801
320	RRVSRGSSQK	0.631	54	WB	VP2-3	B2705
98	YRFFSDWDHK	0.450	383	WB	VP2-3	B2705
125	NPDEYYDILF	0.757	13	SB	VP2-3	B3501
58	AAIGLTPQTY	0.566	109	WB	VP2-3	B3501
148	DPRHWGPSLF	0.544	138	WB	VP2-3	B3501
28	IAAGEAAAAI	0.514	192	WB	VP2-3	B3501
202	TIVNAPINFY	0.476	289	WB	VP2-3	B3501
67	YAVIAGAPGA	0.456	358	WB	VP2-3	B3501
292	WMLPLLLGLY	0.447	397	WB	VP2-3	B3501
209	NFYNYIQDYY	0.429	480	WB	VP2-3	B3501
114	YQQSGMALEL	0.466	323	WB	VP2-3	B3901
233	AEREGTHVNF	0.508	204	WB	VP2-3	B4001
254	IEEVTQRMDL	0.497	230	WB	VP2-3	B4001
266	KESVHSGEFI	0.457	355	WB	VP2-3	B4002
233	AEREGTHVNF	0.450	382	WB	VP2-3	B4002

26	AEIAAGEAAA	0.461	340	WB	VP2-3 B4403
26	AEIAAGEAAA	0.637	50	WB	VP2-3 B4501
197	EETTWTIVNA	0.481	273	WB	VP2-3 B4501
233	AEREGTHVNF	0.474	297	WB	VP2-3 B4501
294	LPLLLGLYGT	0.583	91	WB	VP2-3 B5101
289	APQWMLPLLL	0.580	94	WB	VP2-3 B5301
125	NPDEYYDILF	0.476	289	WB	VP2-3 B5301
294	LPLLLGLYGT	0.816	7	SB	VP2-3 B5401
73	APGAIAGFAA	0.666	36	SB	VP2-3 B5401
134	FPGVNTFVNN	0.529	163	WB	VP2-3 B5401
192	LARFLEETTW	0.441	422	WB	VP2-3 B5701
283	GANQRTAPQW	0.661	39	SB	VP2-3 B5801
192	LARFLEETTW	0.570	105	WB	VP2-3 B5801
201	WTIVNAPINF	0.543	139	WB	VP2-3 B5801
156	LFATISQALW	0.490	247	WB	VP2-3 B5801
287	RTAPQWMLPL	0.462	337	WB	VP2-3 B5801
91	SSLAQVGYRF	0.439	432	WB	VP2-3 B5801
	11-mers				
201	WTIVNAPINFY	0.505	212	WB	VP2-3 A0101
146	YLDPRHWGPSL	0.844	5	SB	VP2-3 A0201
247	SIDNADSIEEV	0.608	69	WB	VP2-3 A0201
157	FATISQALWHV	0.499	226	WB	VP2-3 A0201
297	LLGLYGTVTPA	0.443	413	WB	VP2-3 A0201
61	GLTPQTYAVIA	0.440	428	WB	VP2-3 A0201
80	FAALIQTVTGI	0.740	16	SB	VP2-3 A0202
146	YLDPRHWGPSL	0.686	29	SB	VP2-3 A0202
297	LLGLYGTVTPA	0.612	66	WB	VP2-3 A0202
293	MLPLLLGLYGT	0.607	69	WB	VP2-3 A0202
61	GLTPQTYAVIA	0.598	77	WB	VP2-3 A0202
24	SVAEIAAGEAA	0.577	96	WB	VP2-3 A0202
157	FATISQALWHV	0.572	102	WB	VP2-3 A0202
52	TTSEAIAAIGL	0.559	117	WB	VP2-3 A0202
40	QIASLATVEGI	0.554	124	WB	VP2-3 A0202
287	RTAPQWMLPLL	0.542	142	WB	VP2-3 A0202
247	SIDNADSIEEV	0.539	146	WB	VP2-3 A0202
92	SLAQVGYRFFS	0.525	170	WB	VP2-3 A0202
10	LVASVSEAAAA	0.525	170	WB	VP2-3 A0202
59	AIGLTPQTYAV	0.518	183	WB	VP2-3 A0202
86	TVTGISSLAQV	0.493	241	WB	VP2-3 A0202
43	SLATVEGITTT	0.487	258	WB	VP2-3 A0202
3	ALALLGDLVAS	0.480	278	WB	VP2-3 A0202
34	AAAIEVQIASL	0.471	305	WB	VP2-3 A0202
83	LIQTVTGISSL	0.467	318	WB	VP2-3 A0202
1	GAALALLGDLV	0.467	320	WB	VP2-3 A0202
244	HTYSIDNADSI	0.466	324	WB	VP2-3 A0202
155	SLFATISQALW	0.458	350	WB	VP2-3 A0202
274	FIEKTIAPGGA	0.427	490	WB	VP2-3 A0202
140	FVNNIQYLDPR	0.427	492	WB	VP2-3 A0202
146	YLDPRHWGPSL	0.801	8	SB	VP2-3 A0203
297	LLGLYGTVTPA	0.759	13	SB	VP2-3 A0203

83 LIQTVTGISSL	0.719	20	SB	VP2-3	A0203
293 MLPLLLGLYGT	0.711	22	SB	VP2-3	A0203
80 FAALIQTVTGI	0.669	36	SB	VP2-3	A0203
43 SLATVEGITTT	0.657	40	SB	VP2-3	A0203
59 AIGLTPQTYAV	0.639	49	SB	VP2-3	A0203
61 GLTPQTYAVIA	0.610	67	WB	VP2-3	A0203
18 AAATGFSVAEI	0.562	114	WB	VP2-3	A0203
40 QIASLATVEGI	0.559	118	WB	VP2-3	A0203
86 TVTGISSLAQV	0.542	141	WB	VP2-3	A0203
287 RTAPQWMLPLL	0.526	168	WB	VP2-3	A0203
274 FIEKTIAPGGA	0.518	183	WB	VP2-3	A0203
10 LVASVSEAAAA	0.513	193	WB	VP2-3	A0203
4 LALLGDLVASV	0.490	248	WB	VP2-3	A0203
24 SVAEIAAGEAA	0.488	253	WB	VP2-3	A0203
34 AAAIEVQIASL	0.478	283	WB	VP2-3	A0203
327 SQKAKGTRASA	0.474	294	WB	VP2-3	A0203
247 SIDNADSIEEV	0.455	365	WB	VP2-3	A0203
157 FATISQALWHV	0.447	396	WB	VP2-3	A0203
101 FSDWDHKVSTV	0.447	398	WB	VP2-3	A0203
67 YAVIAGAPGAI	0.430	477	WB	VP2-3	A0203
146 YLDPRHWGPSL	0.615	64	WB	VP2-3	A0204
29 AAGEAAAAIEV	0.520	180	WB	VP2-3	A0204
59 AIGLTPQTYAV	0.517	185	WB	VP2-3	A0204
297 LLGLYGTVTPA	0.495	236	WB	VP2-3	A0204
247 SIDNADSIEEV	0.488	255	WB	VP2-3	A0204
43 SLATVEGITTT	0.466	322	WB	VP2-3	A0204
146 YLDPRHWGPSL	0.882	3	SB	VP2-3	A0206
214 IQDYYSNLSPI	0.767	12	SB	VP2-3	A0206
230 RQVAEREGTHV	0.764	12	SB	VP2-3	A0206
157 FATISQALWHV	0.747	15	SB	VP2-3	A0206
114 YQQSGMALELF	0.741	16	SB	VP2-3	A0206
247 SIDNADSIEEV	0.659	40	SB	VP2-3	A0206
29 AAGEAAAAIEV	0.632	53	WB	VP2-3	A0206
287 RTAPQWMLPLL	0.614	64	WB	VP2-3	A0206
80 FAALIQTVTGI	0.614	65	WB	VP2-3	A0206
35 AAIEVQIASLA	0.587	86	WB	VP2-3	A0206
37 IEVQIASLATV	0.586	88	WB	VP2-3	A0206
24 SVAEIAAGEAA	0.580	93	WB	VP2-3	A0206
4 LALLGDLVASV	0.580	94	WB	VP2-3	A0206
101 FSDWDHKVSTV	0.577	97	WB	VP2-3	A0206
15 SEAAAATGFSV	0.572	102	WB	VP2-3	A0206
86 TVTGISSLAQV	0.557	120	WB	VP2-3	A0206
59 AIGLTPQTYAV	0.537	150	WB	VP2-3	A0206
293 MLPLLLGLYGT	0.536	151	WB	VP2-3	A0206
58 AAIGLTPQTYA	0.531	159	WB	VP2-3	A0206
10 LVASVSEAAAA	0.524	173	WB	VP2-3	A0206
18 AAATGFSVAEI	0.509	203	WB	VP2-3	A0206
68 AVIAGAPGAIA	0.503	215	WB	VP2-3	A0206
84 IQTVTGISSLA	0.500	223	WB	VP2-3	A0206
52 TTSEAIAAIGL	0.457	357	WB	VP2-3	A0206
1 GAALALLGDLV	0.454	366	WB	VP2-3	A0206
297 LLGLYGTVTPA	0.442	420	WB	VP2-3	A0206
13 SVSEAAAATGF	0.441	423	WB	VP2-3	A0206
45 ATVEGITTTSE	0.429	481	WB	VP2-3	A0206
146 YLDPRHWGPSL	0.969	1	SB	VP2-3	A0211
247 SIDNADSIEEV	0.903	2	SB	VP2-3	A0211
86 TVTGISSLAQV	0.868	4	SB	VP2-3	A0211
61 GLTPQTYAVIA	0.808	7	SB	VP2-3	A0211
92 SLAQVGYRFFS	0.759	13	SB	VP2-3	A0211

59	AIGLTPQTYAV	0.737	17	SB	VP2-3 A0211
122	ELFNPDEYYDI	0.669	35	SB	VP2-3 A0211
43	SLATVEGITTT	0.657	40	SB	VP2-3 A0211
29	AAGEAAAAIEV	0.644	46	SB	VP2-3 A0211
4	LALLGDLVASV	0.626	56	WB	VP2-3 A0211
287	RTAPQWMLPLL	0.626	57	WB	VP2-3 A0211
131	DILFPGVNTFV	0.620	60	WB	VP2-3 A0211
101	FSDWDHKVSTV	0.615	64	WB	VP2-3 A0211
157	FATISQALWHV	0.608	69	WB	VP2-3 A0211
293	MLPLLLGLYGT	0.597	78	WB	VP2-3 A0211
132	ILFPGVNTFVN	0.565	110	WB	VP2-3 A0211
297	LLGLYGTVTPA	0.547	134	WB	VP2-3 A0211
76	AIAGFAALIQT	0.537	150	WB	VP2-3 A0211
292	WMLPLLLGLYG	0.526	167	WB	VP2-3 A0211
24	SVAEIAAGEAA	0.526	168	WB	VP2-3 A0211
253	SIEEVTQRMDL	0.525	170	WB	VP2-3 A0211
296	LLLGLYGTVTP	0.523	174	WB	VP2-3 A0211
98	YRFFSDWDHKV	0.515	190	WB	VP2-3 A0211
6	LLGDLVASVSE	0.504	213	WB	VP2-3 A0211
27	EIAAGEAAAAI	0.496	234	WB	VP2-3 A0211
194	RFLEETTWTIV	0.476	288	WB	VP2-3 A0211
155	SLFATISQALW	0.468	315	WB	VP2-3 A0211
5	ALLGDLVASVS	0.465	325	WB	VP2-3 A0211
83	LIQTVTGISSL	0.454	369	WB	VP2-3 A0211
77	IAGFAALIQTV	0.449	386	WB	VP2-3 A0211
278	TIAPGGANQRT	0.438	437	WB	VP2-3 A0211
191	SLARFLEETTW	0.437	444	WB	VP2-3 A0211
299	GLYGTVTPALE	0.429	482	WB	VP2-3 A0211
146	YLDPRHWGPSL	0.942	1	SB	VP2-3 A0212
247	SIDNADSIEEV	0.724	19	SB	VP2-3 A0212
59	AIGLTPQTYAV	0.677	32	SB	VP2-3 A0212
61	GLTPQTYAVIA	0.591	83	WB	VP2-3 A0212
43	SLATVEGITTT	0.566	109	WB	VP2-3 A0212
122	ELFNPDEYYDI	0.556	121	WB	VP2-3 A0212
4	LALLGDLVASV	0.541	143	WB	VP2-3 A0212
293	MLPLLLGLYGT	0.513	194	WB	VP2-3 A0212
6	LLGDLVASVSE	0.507	207	WB	VP2-3 A0212
83	LIQTVTGISSL	0.499	226	WB	VP2-3 A0212
253	SIEEVTQRMDL	0.493	242	WB	VP2-3 A0212
292	WMLPLLLGLYG	0.489	251	WB	VP2-3 A0212
92	SLAQVGYRFFS	0.479	281	WB	VP2-3 A0212
86	TVTGISSLAQV	0.475	292	WB	VP2-3 A0212
157	FATISQALWHV	0.435	454	WB	VP2-3 A0212
132	ILFPGVNTFVN	0.434	457	WB	VP2-3 A0212
213	YIQDYYSNLSP	0.433	464	WB	VP2-3 A0212
98	YRFFSDWDHKV	0.432	468	WB	VP2-3 A0212
296	LLLGLYGTVTP	0.431	473	WB	VP2-3 A0212
146	YLDPRHWGPSL	0.908	2	SB	VP2-3 A0216
247	SIDNADSIEEV	0.852	4	SB	VP2-3 A0216
86	TVTGISSLAQV	0.811	7	SB	VP2-3 A0216
59	AIGLTPQTYAV	0.755	14	SB	VP2-3 A0216
29	AAGEAAAAIEV	0.714	22	SB	VP2-3 A0216
92	SLAQVGYRFFS	0.674	34	SB	VP2-3 A0216
131	DILFPGVNTFV	0.671	35	SB	VP2-3 A0216
43	SLATVEGITTT	0.635	52	WB	VP2-3 A0216
61	GLTPQTYAVIA	0.633	53	WB	VP2-3 A0216
297	LLGLYGTVTPA	0.621	60	WB	VP2-3 A0216
83	LIQTVTGISSL	0.526	169	WB	VP2-3 A0216
157	FATISQALWHV	0.524	172	WB	VP2-3 A0216
122	ELFNPDEYYDI	0.508	205	WB	VP2-3 A0216

4 LALLGDLVASV	0.499	225	WB	VP2-3	A0216
77 IAGFAALIQTV	0.459	350	WB	VP2-3	A0216
76 AIAGFAALIQT	0.458	351	WB	VP2-3	A0216
146 YLDPRHWGPSL	0.941	1	SB	VP2-3	A0219
247 SIDNADSIEEV	0.699	26	SB	VP2-3	A0219
86 TVTGISSLAQV	0.670	35	SB	VP2-3	A0219
59 AIGLTPQTYAV	0.566	109	WB	VP2-3	A0219
4 LALLGDLVASV	0.537	149	WB	VP2-3	A0219
157 FATISQALWHV	0.530	161	WB	VP2-3	A0219
83 LIQTVTGISSL	0.499	225	WB	VP2-3	A0219
332 GTRASAKTTNK	0.622	59	WB	VP2-3	A0301
321 RVSRGSSQKAK	0.580	93	WB	VP2-3	A0301
203 IVNAPINFYNY	0.501	220	WB	VP2-3	A0301
339 TTNKRRSRSSR	0.487	258	WB	VP2-3	A0301
203 IVNAPINFYNY	0.678	32	SB	VP2-3	A1101
339 TTNKRRSRSSR	0.651	43	SB	VP2-3	A1101
277 KTIAPGGANQR	0.634	52	WB	VP2-3	A1101
321 RVSRGSSQKAK	0.626	57	WB	VP2-3	A1101
332 GTRASAKTTNK	0.606	70	WB	VP2-3	A1101
89 GISSLAQVGYR	0.521	177	WB	VP2-3	A1101
136 GVNTFVNNIQY	0.517	185	WB	VP2-3	A1101
159 TISQALWHVIR	0.481	274	WB	VP2-3	A1101
176 TSQELQRRTER	0.476	289	WB	VP2-3	A1101
140 FVNNIQYLDPR	0.469	313	WB	VP2-3	A1101
267 ESVHSGEFIEK	0.437	442	WB	VP2-3	A1101
200 TWTIVNAPINF	0.630	54	WB	VP2-3	A2301
97 GYRFFSDWDHK	0.623	59	WB	VP2-3	A2301
113 LYQQSGMALEL	0.597	77	WB	VP2-3	A2301
186 RFFRDSLARFL	0.449	389	WB	VP2-3	A2301
200 TWTIVNAPINF	0.612	66	WB	VP2-3	A2402
113 LYQQSGMALEL	0.533	156	WB	VP2-3	A2402
113 LYQQSGMALEL	0.750	14	SB	VP2-3	A2403
186 RFFRDSLARFL	0.485	263	WB	VP2-3	A2403
91 SSLAQVGYRFF	0.459	347	WB	VP2-3	A2403
201 WTIVNAPINFY	0.672	34	SB	VP2-3	A2601
109 STVGLYQQSGM	0.619	61	WB	VP2-3	A2601
201 WTIVNAPINFY	0.930	2	SB	VP2-3	A2602
109 STVGLYQQSGM	0.769	12	SB	VP2-3	A2602
27 EIAAGEAAAAI	0.765	12	SB	VP2-3	A2602
287 RTAPQWMLPLL	0.678	32	SB	VP2-3	A2602
203 IVNAPINFYNY	0.672	34	SB	VP2-3	A2602
13 SVSEAAAATGF	0.566	109	WB	VP2-3	A2602
88 TGISSLAQVGY	0.498	228	WB	VP2-3	A2602
291 QWMLPLLLGLY	0.553	126	WB	VP2-3	A2902
203 IVNAPINFYNY	0.517	185	WB	VP2-3	A2902
236 EGTHVNFGHTY	0.485	262	WB	VP2-3	A2902
208 INFYNYIQDYY	0.471	304	WB	VP2-3	A2902
136 GVNTFVNNIQY	0.468	317	WB	VP2-3	A2902
319 KRRVSRGSSQK	0.802	8	SB	VP2-3	A3001
332 GTRASAKTTNK	0.790	9	SB	VP2-3	A3001
97 GYRFFSDWDHK	0.743	16	SB	VP2-3	A3001
321 RVSRGSSQKAK	0.684	30	SB	VP2-3	A3001

203 IVNAPINFYNY	0.460	345	WB	VP2-3	A3002
339 TTNKRRSRSSR	0.837	5	SB	VP2-3	A3101
277 KTIAPGGANQR	0.682	31	SB	VP2-3	A3101
334 RASAKTTNKRR	0.664	37	SB	VP2-3	A3101
336 SAKTTNKRRSR	0.656	41	SB	VP2-3	A3101
140 FVNNIQYLDPR	0.655	41	SB	VP2-3	A3101
176 TSQELQRRTER	0.645	46	SB	VP2-3	A3101
179 ELQRRTERFFR	0.636	51	WB	VP2-3	A3101
225 RPSMVRQVAER	0.580	94	WB	VP2-3	A3101
324 RGSSQKAKGTR	0.569	105	WB	VP2-3	A3101
89 GISSLAQVGYR	0.567	108	WB	VP2-3	A3101
159 TISQALWHVIR	0.483	268	WB	VP2-3	A3101
332 GTRASAKTTNK	0.446	401	WB	VP2-3	A3101
220 NLSPIRPSMVR	0.432	465	WB	VP2-3	A3101
179 ELQRRTERFFR	0.812	7	SB	VP2-3	A3301
339 TTNKRRSRSSR	0.738	17	SB	VP2-3	A3301
140 FVNNIQYLDPR	0.519	181	WB	VP2-3	A3301
176 TSQELQRRTER	0.516	188	WB	VP2-3	A3301
220 NLSPIRPSMVR	0.506	210	WB	VP2-3	A3301
159 TISQALWHVIR	0.465	326	WB	VP2-3	A3301
339 TTNKRRSRSSR	0.848	5	SB	VP2-3	A6801
140 FVNNIQYLDPR	0.795	9	SB	VP2-3	A6801
159 TISQALWHVIR	0.758	13	SB	VP2-3	A6801
256 EVTQRMDLRNK	0.719	20	SB	VP2-3	A6801
179 ELQRRTERFFR	0.714	22	SB	VP2-3	A6801
309 EAYEDGPNQKK	0.713	22	SB	VP2-3	A6801
267 ESVHSGEFIEK	0.706	24	SB	VP2-3	A6801
220 NLSPIRPSMVR	0.687	29	SB	VP2-3	A6801
250 NADSIEEVTQR	0.655	41	SB	VP2-3	A6801
176 TSQELQRRTER	0.647	45	SB	VP2-3	A6801
201 WTIVNAPINFY	0.600	75	WB	VP2-3	A6801
89 GISSLAQVGYR	0.591	83	WB	VP2-3	A6801
277 KTIAPGGANQR	0.588	86	WB	VP2-3	A6801
172 IPAITSQELQR	0.515	190	WB	VP2-3	A6801
225 RPSMVRQVAER	0.438	438	WB	VP2-3	A6801
215 QDYYSNLSPIR	0.437	444	WB	VP2-3	A6801
198 ETTWTIVNAPI	0.863	4	SB	VP2-3	A6802
86 TVTGISSLAQV	0.804	8	SB	VP2-3	A6802
16 EAAAATGFSVA	0.777	11	SB	VP2-3	A6802
80 FAALIQTVTGI	0.761	13	SB	VP2-3	A6802
27 EIAAGEAAAAI	0.759	13	SB	VP2-3	A6802
244 HTYSIDNADSI	0.756	13	SB	VP2-3	A6802
52 TTSEAIAAIGL	0.729	18	SB	VP2-3	A6802
24 SVAEIAAGEAA	0.724	19	SB	VP2-3	A6802
40 QIASLATVEGI	0.649	44	SB	VP2-3	A6802
32 EAAAAIEVQIA	0.633	52	WB	VP2-3	A6802
10 LVASVSEAAAA	0.605	71	WB	VP2-3	A6802
131 DILFPGVNTFV	0.561	115	WB	VP2-3	A6802
287 RTAPQWMLPLL	0.551	129	WB	VP2-3	A6802
259 QRMDLRNKESV	0.550	129	WB	VP2-3	A6802
122 ELFNPDEYYDI	0.549	131	WB	VP2-3	A6802
46 TVEGITTTSEA	0.537	150	WB	VP2-3	A6802
157 FATISQALWHV	0.500	223	WB	VP2-3	A6802
109 STVGLYQQSGM	0.495	235	WB	VP2-3	A6802
204 VNAPINFYNYI	0.467	319	WB	VP2-3	A6802
18 AAATGFSVAEI	0.465	326	WB	VP2-3	A6802
23 FSVAEIAAGEA	0.463	333	WB	VP2-3	A6802
15 SEAAAATGFSV	0.457	356	WB	VP2-3	A6802

98	YRFFSDWDHKV	0.453	371	WB	VP2-3	A6802
50	ITTTSEAIAAI	0.442	419	WB	VP2-3	A6802
67	YAVIAGAPGAI	0.439	430	WB	VP2-3	A6802
0	MGAALALLGDL	0.426	497	WB	VP2-3	A6802
198	ETTWTIVNAPI	0.765	12	SB	VP2-3	A6901
27	EIAAGEAAAAI	0.722	20	SB	VP2-3	A6901
131	DILFPGVNTFV	0.706	23	SB	VP2-3	A6901
157	FATISQALWHV	0.625	58	WB	VP2-3	A6901
52	TTSEAIAAIGL	0.581	93	WB	VP2-3	A6901
244	HTYSIDNADSI	0.559	117	WB	VP2-3	A6901
86	TVTGISSLAQV	0.494	237	WB	VP2-3	A6901
24	SVAEIAAGEAA	0.491	245	WB	VP2-3	A6901
67	YAVIAGAPGAI	0.465	326	WB	VP2-3	A6901
146	YLDPRHWGPSL	0.462	338	WB	VP2-3	A6901
29	AAGEAAAAIEV	0.456	360	WB	VP2-3	A6901
101	FSDWDHKVSTV	0.443	416	WB	VP2-3	A6901
294	LPLLLGLYGTV	0.439	433	WB	VP2-3	A6901
40	QIASLATVEGI	0.436	448	WB	VP2-3	A6901
287	RTAPQWMLPLL	0.433	459	WB	VP2-3	A6901
73	APGAIAGFAAL	0.671	35	SB	VP2-3	B0702
222	SPIRPSMVRQV	0.530	162	WB	VP2-3	B0702
67	YAVIAGAPGAI	0.489	251	WB	VP2-3	B0702
114	YQQSGMALELF	0.567	108	WB	VP2-3	B1501
201	WTIVNAPINFY	0.536	151	WB	VP2-3	B1501
203	IVNAPINFYNY	0.501	221	WB	VP2-3	B1501
13	SVSEAAAATGF	0.500	223	WB	VP2-3	B1501
264	RNKESVHSGEF	0.488	254	WB	VP2-3	B1501
57	IAAIGLTPQTY	0.455	361	WB	VP2-3	B1501
37	IEVQIASLATV	0.605	71	WB	VP2-3	B1801
127	DEYYDILFPGV	0.591	83	WB	VP2-3	B1801
178	QELQRRTERFF	0.466	323	WB	VP2-3	B1801
130	YDILFPGVNTF	0.426	495	WB	VP2-3	B1801
182	RRTERFFRDSL	0.564	111	WB	VP2-3	B2705
319	KRRVSRGSSQK	0.498	227	WB	VP2-3	B2705
320	RRVSRGSSQKA	0.461	342	WB	VP2-3	B2705
286	QRTAPQWMLPL	0.430	477	WB	VP2-3	B2705
119	MALELFNPDEY	0.799	8	SB	VP2-3	B3501
57	IAAIGLTPQTY	0.701	25	SB	VP2-3	B3501
67	YAVIAGAPGAI	0.605	71	WB	VP2-3	B3501
13	SVSEAAAATGF	0.558	119	WB	VP2-3	B3501
201	WTIVNAPINFY	0.508	204	WB	VP2-3	B3501
73	APGAIAGFAAL	0.500	224	WB	VP2-3	B3501
301	YGTVTPALEAY	0.466	322	WB	VP2-3	B3501
11	VASVSEAAAAT	0.445	404	WB	VP2-3	B3501
146	YLDPRHWGPSL	0.500	223	WB	VP2-3	B3901
211	YNYIQDYYSNL	0.445	405	WB	VP2-3	B3901
31	GEAAAAIEVQI	0.587	87	WB	VP2-3	B4001
15	SEAAAATGFSV	0.513	194	WB	VP2-3	B4001
37	IEVQIASLATV	0.477	287	WB	VP2-3	B4001
127	DEYYDILFPGV	0.451	380	WB	VP2-3	B4001
178	QELQRRTERFF	0.497	231	WB	VP2-3	B4002
26	AEIAAGEAAAA	0.428	489	WB	VP2-3	B4002

26 AEIAAGEAAAA	0.484	264	WB	VP2-3	B4403
26 AEIAAGEAAAA	0.620	61	WB	VP2-3	B4501
294 LPLLLGLYGTV	0.749	15	SB	VP2-3	B5101
134 FPGVNTFVNNI	0.632	53	WB	VP2-3	B5101
134 FPGVNTFVNNI	0.791	9	SB	VP2-3	B5301
294 LPLLLGLYGTV	0.479	281	WB	VP2-3	B5301
119 MALELFNPDEY	0.477	287	WB	VP2-3	B5301
294 LPLLLGLYGTV	0.839	5	SB	VP2-3	B5401
134 FPGVNTFVNNI	0.750	14	SB	VP2-3	B5401
63 TPQTYAVIAGA	0.491	245	WB	VP2-3	B5401
80 FAALIQTVTGI	0.454	369	WB	VP2-3	B5401
222 SPIRPSMVRQV	0.451	378	WB	VP2-3	B5401
90 ISSLAQVGYRF	0.685	30	SB	VP2-3	B5801
191 SLARFLEETTW	0.631	54	WB	VP2-3	B5801
155 SLFATISQALW	0.572	102	WB	VP2-3	B5801
57 IAAIGLTPQTY	0.539	145	WB	VP2-3	B5801
282 GGANQRTAPQW	0.529	162	WB	VP2-3	B5801
287 RTAPQWMLPLL	0.488	253	WB	VP2-3	B5801

Preferred BK virus fragments of VP1 capable of interacting with one or more MHC class 1 molecules are listed in Table K.

Table K: Prediction of BK virus VP1 protein specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
196	YLDKNNAY	0.756	14	SB	VP1	A0101
108	LMWEAVTV	0.819	7	SB	VP1	A0201
243	VLLDEQGV	0.703	24	SB	VP1	A0201
83	KMLPCYST	0.657	41	SB	VP1	A0201
40	GVDAITEV	0.595	79	WB	VP1	A0201
281	GLARYFKI	0.591	83	WB	VP1	A0201
106	NLLMWEAV	0.580	94	WB	VP1	A0201
84	MLPCYSTA	0.562	114	WB	VP1	A0201
107	LLMWEAVT	0.498	229	WB	VP1	A0201
281	GLARYFKI	0.717	21	SB	VP1	A0202
108	LMWEAVTV	0.668	36	SB	VP1	A0202
84	MLPCYSTA	0.666	37	SB	VP1	A0202
243	VLLDEQGV	0.663	38	SB	VP1	A0202
262	SAADICGL	0.662	38	SB	VP1	A0202
40	GVDAITEV	0.633	52	WB	VP1	A0202
34	VLEVKTGV	0.510	200	WB	VP1	A0202
152	FAVGGDPL	0.508	205	WB	VP1	A0202
121	GITSMLNL	0.475	291	WB	VP1	A0202
125	MLNLHAGS	0.470	310	WB	VP1	A0202
25	KLLIKGGV	0.457	354	WB	VP1	A0202
107	LLMWEAVT	0.451	379	WB	VP1	A0202
238	NTATTVLL	0.447	394	WB	VP1	A0202
84	MLPCYSTA	0.841	5	SB	VP1	A0203
108	LMWEAVTV	0.784	10	SB	VP1	A0203
27	LIKGGVEV	0.779	10	SB	VP1	A0203
281	GLARYFKI	0.762	13	SB	VP1	A0203
243	VLLDEQGV	0.746	15	SB	VP1	A0203
236	VTNTATTV	0.674	33	SB	VP1	A0203
25	KLLIKGGV	0.657	41	SB	VP1	A0203
106	NLLMWEAV	0.643	47	SB	VP1	A0203
34	VLEVKTGV	0.635	51	WB	VP1	A0203
233	VLHVTNTA	0.633	52	WB	VP1	A0203
107	LLMWEAVT	0.563	113	WB	VP1	A0203
262	SAADICGL	0.538	148	WB	VP1	A0203
188	VMNTDHKA	0.531	159	WB	VP1	A0203
83	KMLPCYST	0.509	203	WB	VP1	A0203
125	MLNLHAGS	0.509	203	WB	VP1	A0203
326	SQVEEVRV	0.501	221	WB	VP1	A0203
229	NVPPVLHV	0.492	244	WB	VP1	A0203
121	GITSMLNL	0.490	248	WB	VP1	A0203
40	GVDAITEV	0.488	255	WB	VP1	A0203
294	SVKNPYPI	0.470	308	WB	VP1	A0203
112	AVTVKTEV	0.456	358	WB	VP1	A0203
119	VIGITSML	0.439	433	WB	VP1	A0203
108	LMWEAVTV	0.780	10	SB	VP1	A0204

243	VLLDEQGV	0.740	16	SB	VP1	A0204
25	KLLIKGGV	0.582	91	WB	VP1	A0204
281	GLARYFKI	0.510	201	WB	VP1	A0204
34	VLEVKTGV	0.498	228	WB	VP1	A0204
236	VTNTATTV	0.489	253	WB	VP1	A0204
326	SQVEEVRV	0.453	371	WB	VP1	A0204
106	NLLMWEAV	0.441	423	WB	VP1	A0204
27	LIKGGVEV	0.432	465	WB	VP1	A0204
40	GVDAITEV	0.431	472	WB	VP1	A0204
108	LMWEAVTV	0.852	4	SB	VP1	A0206
326	SQVEEVRV	0.789	9	SB	VP1	A0206
106	NLLMWEAV	0.731	18	SB	VP1	A0206
152	FAVGGDPL	0.729	18	SB	VP1	A0206
243	VLLDEQGV	0.720	20	SB	VP1	A0206
40	GVDAITEV	0.691	28	SB	VP1	A0206
21	VQVPKLLI	0.685	30	SB	VP1	A0206
84	MLPCYSTA	0.624	58	WB	VP1	A0206
83	KMLPCYST	0.623	59	WB	VP1	A0206
354	GQLQTKMV	0.584	89	WB	VP1	A0206
229	NVPPVLHV	0.574	99	WB	VP1	A0206
25	KLLIKGGV	0.543	139	WB	VP1	A0206
262	SAADICGL	0.513	193	WB	VP1	A0206
236	VTNTATTV	0.506	208	WB	VP1	A0206
281	GLARYFKI	0.505	211	WB	VP1	A0206
144	VQGSNFHF	0.481	275	WB	VP1	A0206
112	AVTVKTEV	0.454	368	WB	VP1	A0206
276	TQQWRGLA	0.439	434	WB	VP1	A0206
184	AQSQVMNT	0.432	465	WB	VP1	A0206
147	SNFHFFAV	0.432	467	WB	VP1	A0206
108	LMWEAVTV	0.966	1	SB	VP1	A0211
243	VLLDEQGV	0.965	1	SB	VP1	A0211
106	NLLMWEAV	0.910	2	SB	VP1	A0211
40	GVDAITEV	0.856	4	SB	VP1	A0211
27	LIKGGVEV	0.838	5	SB	VP1	A0211
229	NVPPVLHV	0.830	6	SB	VP1	A0211
25	KLLIKGGV	0.823	6	SB	VP1	A0211
349	YIDRQGQL	0.819	7	SB	VP1	A0211
281	GLARYFKI	0.788	9	SB	VP1	A0211
84	MLPCYSTA	0.786	10	SB	VP1	A0211
196	YLDKNNAY	0.751	14	SB	VP1	A0211
83	KMLPCYST	0.746	15	SB	VP1	A0211
34	VLEVKTGV	0.731	18	SB	VP1	A0211
101	DLTCGNLL	0.639	49	SB	VP1	A0211
262	SAADICGL	0.614	65	WB	VP1	A0211
97	NLNEDLTC	0.603	73	WB	VP1	A0211
188	VMNTDHKA	0.602	74	WB	VP1	A0211
233	VLHVTNTA	0.594	80	WB	VP1	A0211
112	AVTVKTEV	0.578	96	WB	VP1	A0211
320	PMYGMESQ	0.573	102	WB	VP1	A0211
326	SQVEEVRV	0.548	133	WB	VP1	A0211
332	RVFDGTEQ	0.542	141	WB	VP1	A0211
333	VFDGTEQL	0.505	211	WB	VP1	A0211
254	CKADSLYV	0.500	224	WB	VP1	A0211
236	VTNTATTV	0.498	229	WB	VP1	A0211
124	SMLNLHAG	0.491	246	WB	VP1	A0211
121	GITSMLNL	0.481	276	WB	VP1	A0211
147	SNFHFFAV	0.471	305	WB	VP1	A0211
107	LLMWEAVT	0.456	358	WB	VP1	A0211
252	PLCKADSL	0.453	370	WB	VP1	A0211
223	TYTGGENV	0.451	378	WB	VP1	A0211

339	QLPGDPDM	0.440	428	WB	VP1	A0211
119	VIGITSML	0.437	439	WB	VP1	A0211
243	VLLDEQGV	0.938	1	SB	VP1	A0212
108	LMWEAVTV	0.932	2	SB	VP1	A0212
106	NLLMWEAV	0.866	4	SB	VP1	A0212
27	LIKGGVEV	0.758	13	SB	VP1	A0212
281	GLARYFKI	0.738	17	SB	VP1	A0212
34	VLEVKTGV	0.730	18	SB	VP1	A0212
196	YLDKNNAY	0.708	23	SB	VP1	A0212
25	KLLIKGGV	0.691	28	SB	VP1	A0212
349	YIDRQGQL	0.659	40	SB	VP1	A0212
84	MLPCYSTA	0.645	46	SB	VP1	A0212
40	GVDAITEV	0.626	57	WB	VP1	A0212
229	NVPPVLHV	0.625	57	WB	VP1	A0212
320	PMYGMESQ	0.570	104	WB	VP1	A0212
188	VMNTDHKA	0.557	120	WB	VP1	A0212
233	VLHVTNTA	0.537	149	WB	VP1	A0212
83	KMLPCYST	0.496	234	WB	VP1	A0212
339	QLPGDPDM	0.474	295	WB	VP1	A0212
107	LLMWEAVT	0.462	337	WB	VP1	A0212
124	SMLNLHAG	0.437	443	WB	VP1	A0212
50	FLNPEMGD	0.437	444	WB	VP1	A0212
236	VTNTATTV	0.435	450	WB	VP1	A0212
97	NLNEDLTC	0.431	469	WB	VP1	A0212
326	SQVEEVRV	0.429	483	WB	VP1	A0212
108	LMWEAVTV	0.930	2	SB	VP1	A0216
243	VLLDEQGV	0.867	4	SB	VP1	A0216
106	NLLMWEAV	0.829	6	SB	VP1	A0216
27	LIKGGVEV	0.816	7	SB	VP1	A0216
229	NVPPVLHV	0.794	9	SB	VP1	A0216
40	GVDAITEV	0.784	10	SB	VP1	A0216
281	GLARYFKI	0.745	15	SB	VP1	A0216
34	VLEVKTGV	0.709	23	SB	VP1	A0216
84	MLPCYSTA	0.699	26	SB	VP1	A0216
349	YIDRQGQL	0.698	26	SB	VP1	A0216
25	KLLIKGGV	0.668	36	SB	VP1	A0216
112	AVTVKTEV	0.647	45	SB	VP1	A0216
252	PLCKADSL	0.627	56	WB	VP1	A0216
101	DLTCGNLL	0.529	163	WB	VP1	A0216
233	VLHVTNTA	0.520	179	WB	VP1	A0216
119	VIGITSML	0.493	241	WB	VP1	A0216
83	KMLPCYST	0.490	250	WB	VP1	A0216
320	PMYGMESQ	0.474	296	WB	VP1	A0216
236	VTNTATTV	0.470	309	WB	VP1	A0216
196	YLDKNNAY	0.461	339	WB	VP1	A0216
321	MYGMESQV	0.456	360	WB	VP1	A0216
152	FAVGGDPL	0.438	439	WB	VP1	A0216
223	TYTGGENV	0.434	457	WB	VP1	A0216
108	LMWEAVTV	0.930	2	SB	VP1	A0219
243	VLLDEQGV	0.896	3	SB	VP1	A0219
106	NLLMWEAV	0.798	8	SB	VP1	A0219
40	GVDAITEV	0.662	38	SB	VP1	A0219
229	NVPPVLHV	0.606	70	WB	VP1	A0219
27	LIKGGVEV	0.540	144	WB	VP1	A0219
349	YIDRQGQL	0.526	168	WB	VP1	A0219
34	VLEVKTGV	0.485	262	WB	VP1	A0219
254	CKADSLYV	0.484	265	WB	VP1	A0219
196	YLDKNNAY	0.451	381	WB	VP1	A0219
236	VTNTATTV	0.446	399	WB	VP1	A0219

333	VFDGTEQL	0.439	432	WB	VP1	A0219
281	GLARYFKI	0.434	456	WB	VP1	A0219
101	DLTCGNLL	0.430	474	WB	VP1	A0219
289	RLRKRSVK	0.776	11	SB	VP1	A0301
308	LINRRTQK	0.697	26	SB	VP1	A0301
164	VLMNYRTK	0.693	27	SB	VP1	A0301
127	NLHAGSQK	0.656	41	SB	VP1	A0301
165	LMNYRTKY	0.467	318	WB	VP1	A0301
280	RGLARYFK	0.446	399	WB	VP1	A0301
352	RQGQLQTK	0.432	468	WB	VP1	A0301
187	QVMNTDHK	0.705	24	SB	VP1	A1101
164	VLMNYRTK	0.620	60	WB	VP1	A1101
308	LINRRTQK	0.613	65	WB	VP1	A1101
280	RGLARYFK	0.596	79	WB	VP1	A1101
22	QVPKLLIK	0.510	200	WB	VP1	A1101
31	GVEVLEVK	0.506	210	WB	VP1	A1101
11	GAAPKKPK	0.444	408	WB	VP1	A1101
352	RQGQLQTK	0.436	447	WB	VP1	A1101
298	PYPISFLL	0.570	104	WB	VP1	A2301
259	LYVSAADI	0.509	203	WB	VP1	A2301
144	VQGSNFHF	0.499	225	WB	VP1	A2301
109	MWEAVTVK	0.470	310	WB	VP1	A2301
284	RYFKIRLR	0.448	393	WB	VP1	A2301
298	PYPISFLL	0.771	11	SB	VP1	A2402
202	AYPVECWI	0.672	34	SB	VP1	A2402
259	LYVSAADI	0.538	148	WB	VP1	A2402
302	SFLLSDLI	0.533	156	WB	VP1	A2402
144	VQGSNFHF	0.441	422	WB	VP1	A2402
202	AYPVECWI	0.721	20	SB	VP1	A2403
298	PYPISFLL	0.614	65	WB	VP1	A2403
259	LYVSAADI	0.464	329	WB	VP1	A2403
118	EVIGITSM	0.834	6	SB	VP1	A2601
118	EVIGITSM	0.909	2	SB	VP1	A2602
315	KVDGQPMY	0.730	18	SB	VP1	A2602
196	YLDKNNAY	0.675	33	SB	VP1	A2602
182	PTAQSQVM	0.599	76	WB	VP1	A2602
217	NTRYFGTY	0.573	101	WB	VP1	A2602
349	YIDRQGQL	0.555	123	WB	VP1	A2602
327	QVEEVRVF	0.491	245	WB	VP1	A2602
190	NTDHKAYL	0.463	332	WB	VP1	A2602
238	NTATTVLL	0.462	338	WB	VP1	A2602
196	YLDKNNAY	0.550	130	WB	VP1	A2902
165	LMNYRTKY	0.498	228	WB	VP1	A2902
289	RLRKRSVK	0.873	3	SB	VP1	A3001
280	RGLARYFK	0.802	8	SB	VP1	A3001
187	QVMNTDHK	0.563	113	WB	VP1	A3001
308	LINRRTQK	0.535	153	WB	VP1	A3001
164	VLMNYRTK	0.534	153	WB	VP1	A3001
285	YFKIRLRK	0.497	231	WB	VP1	A3001
284	RYFKIRLR	0.452	377	WB	VP1	A3001
127	NLHAGSQK	0.426	497	WB	VP1	A3001
315	KVDGQPMY	0.436	447	WB	VP1	A3002
165	LMNYRTKY	0.431	473	WB	VP1	A3002

284	RYFKIRLR	0.898	3	SB	VP1	A3101
280	RGLARYFK	0.716	21	SB	VP1	A3101
289	RLRKRSVK	0.670	35	SB	VP1	A3101
282	LARYFKIR	0.663	38	SB	VP1	A3101
277	QQWRGLAR	0.643	47	SB	VP1	A3101
285	YFKIRLRK	0.581	93	WB	VP1	A3101
304	LLSDLINR	0.569	106	WB	VP1	A3101
308	LINRRTQK	0.542	141	WB	VP1	A3101
273	SSGTQQWR	0.503	215	WB	VP1	A3101
164	VLMNYRTK	0.434	458	WB	VP1	A3101
345	DMIRYIDR	0.767	12	SB	VP1	A3301
284	RYFKIRLR	0.631	54	WB	VP1	A3301
282	LARYFKIR	0.515	190	WB	VP1	A3301
285	YFKIRLRK	0.504	213	WB	VP1	A3301
277	QQWRGLAR	0.444	410	WB	VP1	A3301
187	QVMNTDHK	0.708	23	SB	VP1	A6801
345	DMIRYIDR	0.627	56	WB	VP1	A6801
325	ESQVEEVR	0.606	70	WB	VP1	A6801
85	LPCYSTAR	0.568	107	WB	VP1	A6801
127	NLHAGSQK	0.503	217	WB	VP1	A6801
304	LLSDLINR	0.497	230	WB	VP1	A6801
308	LINRRTQK	0.497	231	WB	VP1	A6801
284	RYFKIRLR	0.488	254	WB	VP1	A6801
162	QGVLMNYR	0.487	257	WB	VP1	A6801
305	LSDLINRR	0.439	431	WB	VP1	A6801
282	LARYFKIR	0.438	439	WB	VP1	A6801
238	NTATTVLL	0.723	19	SB	VP1	A6802
262	SAADICGL	0.718	21	SB	VP1	A6802
118	EVIGITSM	0.718	21	SB	VP1	A6802
147	SNFHFFAV	0.659	39	SB	VP1	A6802
229	NVPPVLHV	0.647	45	SB	VP1	A6802
297	NPYPISFL	0.515	191	WB	VP1	A6802
152	FAVGGDPL	0.506	210	WB	VP1	A6802
88	YSTARIPL	0.473	300	WB	VP1	A6802
294	SVKNPYPI	0.458	351	WB	VP1	A6802
254	CKADSLYV	0.441	421	WB	VP1	A6802
108	LMWEAVTV	0.730	18	SB	VP1	A6901
238	NTATTVLL	0.636	51	WB	VP1	A6901
157	DPLEMQGV	0.635	51	WB	VP1	A6901
297	NPYPISFL	0.557	120	WB	VP1	A6901
118	EVIGITSM	0.548	132	WB	VP1	A6901
229	NVPPVLHV	0.545	137	WB	VP1	A6901
106	NLLMWEAV	0.539	147	WB	VP1	A6901
262	SAADICGL	0.441	421	WB	VP1	A6901
19	EPVQVPKL	0.431	471	WB	VP1	A6901
142	KPVQGSNF	0.685	30	SB	VP1	B0702
297	NPYPISFL	0.489	251	WB	VP1	B0702
16	KPKEPVQV	0.433	462	WB	VP1	B0702
95	LPNLNEDL	0.428	488	WB	VP1	B0702
68	HLSAENAF	0.555	123	WB	VP1	B1501
165	LMNYRTKY	0.542	142	WB	VP1	B1501
161	MQGVLMNY	0.509	202	WB	VP1	B1501
144	VQGSNFHF	0.453	369	WB	VP1	B1501
196	YLDKNNAY	0.448	393	WB	VP1	B1501
246	DEQGVGPL	0.554	124	WB	VP1	B1801

324	MESQVEEV	0.449	389	WB	VP1	B1801
159	LEMQGVLM	0.439	432	WB	VP1	B1801
283	ARYFKIRL	0.453	371	WB	VP1	B2705
292	KRSVKNPY	0.436	446	WB	VP1	B2705
279	WRGLARYF	0.426	496	WB	VP1	B2705
152	FAVGGDPL	0.737	17	SB	VP1	B3501
142	KPVQGSNF	0.631	54	WB	VP1	B3501
19	EPVQVPKL	0.547	134	WB	VP1	B3501
196	YLDKNNAY	0.544	138	WB	VP1	B3501
118	EVIGITSM	0.533	157	WB	VP1	B3501
95	LPNLNEDL	0.482	270	WB	VP1	B3501
299	YPISFLLS	0.480	278	WB	VP1	B3501
68	HLSAENAF	0.472	304	WB	VP1	B3501
297	NPYPISFL	0.470	309	WB	VP1	B3501
227	GENVPPVL	0.576	98	WB	VP1	B4001
159	LEMQGVLM	0.513	194	WB	VP1	B4001
324	MESQVEEV	0.433	462	WB	VP1	B4001
246	DEQGVGPL	0.430	476	WB	VP1	B4001
227	GENVPPVL	0.457	357	WB	VP1	B4002
71	AENAFESD	0.469	312	WB	VP1	B4501
340	LPGDPDMI	0.621	60	WB	VP1	B5101
230	VPPVLHVT	0.446	401	WB	VP1	B5101
203	YPVECWIP	0.426	498	WB	VP1	B5101
297	NPYPISFL	0.568	107	WB	VP1	B5301
142	KPVQGSNF	0.533	156	WB	VP1	B5301
19	EPVQVPKL	0.525	171	WB	VP1	B5301
340	LPGDPDMI	0.522	176	WB	VP1	B5301
95	LPNLNEDL	0.434	456	WB	VP1	B5301
299	YPISFLLS	0.612	66	WB	VP1	B5401
203	YPVECWIP	0.524	172	WB	VP1	B5401
230	VPPVLHVT	0.521	178	WB	VP1	B5401
85	LPCYSTAR	0.450	382	WB	VP1	B5401
340	LPGDPDMI	0.436	448	WB	VP1	B5401
272	NSSGTQQW	0.527	166	WB	VP1	B5701
201	NAYPVECW	0.479	280	WB	VP1	B5701
201	NAYPVECW	0.691	28	SB	VP1	B5801
272	NSSGTQQW	0.675	33	SB	VP1	B5801
	9-mers					
107	LLMWEAVTV	0.761	13	SB	VP1	A0201
83	KMLPCYSTA	0.724	19	SB	VP1	A0201
26	LLIKGGVEV	0.573	101	WB	VP1	A0201
323	GMESQVEEV	0.550	129	WB	VP1	A0201
332	RVFDGTEQL	0.550	130	WB	VP1	A0201
107	LLMWEAVTV	0.769	12	SB	VP1	A0202
332	RVFDGTEQL	0.681	31	SB	VP1	A0202
323	GMESQVEEV	0.678	32	SB	VP1	A0202
26	LLIKGGVEV	0.632	53	WB	VP1	A0202
83	KMLPCYSTA	0.540	145	WB	VP1	A0202
308	LINRRTQKV	0.539	146	WB	VP1	A0202

61	NLRGYSQHL	0.534	154	WB	VP1	A0202
127	NLHAGSQKV	0.529	163	WB	VP1	A0202
43	AITEVECFL	0.504	213	WB	VP1	A0202
118	EVIGITSML	0.480	277	WB	VP1	A0202
304	LLSDLINRR	0.474	295	WB	VP1	A0202
268	GLFTNSSGT	0.463	333	WB	VP1	A0202
339	QLPGDPDMI	0.455	363	WB	VP1	A0202
146	GSNFHFFAV	0.439	430	WB	VP1	A0202
236	VTNTATTVL	0.439	434	WB	VP1	A0202
107	LLMWEAVTV	0.839	5	SB	VP1	A0203
308	LINRRTQKV	0.820	6	SB	VP1	A0203
26	LLIKGGVEV	0.818	7	SB	VP1	A0203
127	NLHAGSQKV	0.786	10	SB	VP1	A0203
83	KMLPCYSTA	0.761	13	SB	VP1	A0203
27	LIKGGVEVL	0.623	59	WB	VP1	A0203
61	NLRGYSQHL	0.616	64	WB	VP1	A0203
332	RVFDGTEQL	0.609	68	WB	VP1	A0203
323	GMESQVEEV	0.604	72	WB	VP1	A0203
222	GTYTGGENV	0.586	88	WB	VP1	A0203
258	SLYVSAADI	0.570	104	WB	VP1	A0203
268	GLFTNSSGT	0.535	153	WB	VP1	A0203
235	HVTNTATTV	0.512	195	WB	VP1	A0203
320	PMYGMESQV	0.509	203	WB	VP1	A0203
125	MLNLHAGSQ	0.480	277	WB	VP1	A0203
114	TVKTEVIGI	0.476	288	WB	VP1	A0203
287	KIRLRKRSV	0.452	374	WB	VP1	A0203
236	VTNTATTVL	0.450	384	WB	VP1	A0203
107	LLMWEAVTV	0.751	14	SB	VP1	A0204
26	LLIKGGVEV	0.688	29	SB	VP1	A0204
323	GMESQVEEV	0.648	45	SB	VP1	A0204
127	NLHAGSQKV	0.613	65	WB	VP1	A0204
308	LINRRTQKV	0.547	133	WB	VP1	A0204
83	KMLPCYSTA	0.504	214	WB	VP1	A0204
33	EVLEVKTGV	0.476	289	WB	VP1	A0204
43	AITEVECFL	0.428	488	WB	VP1	A0204
107	LLMWEAVTV	0.865	4	SB	VP1	A0206
26	LLIKGGVEV	0.808	7	SB	VP1	A0206
332	RVFDGTEQL	0.797	8	SB	VP1	A0206
83	KMLPCYSTA	0.723	20	SB	VP1	A0206
235	HVTNTATTV	0.591	83	WB	VP1	A0206
144	VQGSNFHFF	0.586	88	WB	VP1	A0206
146	GSNFHFFAV	0.555	123	WB	VP1	A0206
43	AITEVECFL	0.542	142	WB	VP1	A0206
326	SQVEEVRVF	0.472	303	WB	VP1	A0206
39	TGVDAITEV	0.460	344	WB	VP1	A0206
127	NLHAGSQKV	0.451	378	WB	VP1	A0206
107	LLMWEAVTV	0.952	1	SB	VP1	A0211
26	LLIKGGVEV	0.946	1	SB	VP1	A0211
127	NLHAGSQKV	0.943	1	SB	VP1	A0211
320	PMYGMESQV	0.941	1	SB	VP1	A0211
332	RVFDGTEQL	0.923	2	SB	VP1	A0211
83	KMLPCYSTA	0.869	4	SB	VP1	A0211
43	AITEVECFL	0.830	6	SB	VP1	A0211
33	EVLEVKTGV	0.818	7	SB	VP1	A0211
61	NLRGYSQHL	0.804	8	SB	VP1	A0211
323	GMESQVEEV	0.800	8	SB	VP1	A0211
308	LINRRTQKV	0.688	29	SB	VP1	A0211
235	HVTNTATTV	0.687	29	SB	VP1	A0211
242	TVLLDEQGV	0.669	35	SB	VP1	A0211

196	YLDKNNAYP	0.642	48	SB	VP1	A0211
339	QLPGDPDMI	0.623	59	WB	VP1	A0211
101	DLTCGNLLM	0.603	73	WB	VP1	A0211
54	EMGDPDDNL	0.589	85	WB	VP1	A0211
27	LIKGGVEVL	0.568	107	WB	VP1	A0211
258	SLYVSAADI	0.564	111	WB	VP1	A0211
176	TITPKNPTA	0.543	140	WB	VP1	A0211
349	YIDRQGQLQ	0.525	169	WB	VP1	A0211
222	GTYTGGENV	0.521	178	WB	VP1	A0211
124	SMLNLHAGS	0.494	238	WB	VP1	A0211
108	LMWEAVTVK	0.489	251	WB	VP1	A0211
39	TGVDAITEV	0.488	253	WB	VP1	A0211
94	PLPNLNEDL	0.487	256	WB	VP1	A0211
255	KADSLYVSA	0.475	292	WB	VP1	A0211
118	EVIGITSML	0.472	304	WB	VP1	A0211
201	NAYPVECWI	0.470	310	WB	VP1	A0211
106	NLLMWEAVT	0.467	320	WB	VP1	A0211
268	GLFTNSSGT	0.463	332	WB	VP1	A0211
244	LLDEQGVGP	0.443	415	WB	VP1	A0211
26	LLIKGGVEV	0.905	2	SB	VP1	A0212
107	LLMWEAVTV	0.903	2	SB	VP1	A0212
127	NLHAGSQKV	0.895	3	SB	VP1	A0212
320	PMYGMESQV	0.883	3	SB	VP1	A0212
61	NLRGYSQHL	0.837	5	SB	VP1	A0212
33	EVLEVKTGV	0.810	7	SB	VP1	A0212
332	RVFDGTEQL	0.768	12	SB	VP1	A0212
308	LINRRTQKV	0.710	23	SB	VP1	A0212
43	AITEVECFL	0.696	26	SB	VP1	A0212
323	GMESQVEEV	0.680	31	SB	VP1	A0212
242	TVLLDEQGV	0.643	47	SB	VP1	A0212
196	YLDKNNAYP	0.604	72	WB	VP1	A0212
54	EMGDPDDNL	0.597	78	WB	VP1	A0212
83	KMLPCYSTA	0.575	99	WB	VP1	A0212
339	QLPGDPDMI	0.548	132	WB	VP1	A0212
108	LMWEAVTVK	0.537	149	WB	VP1	A0212
268	GLFTNSSGT	0.534	155	WB	VP1	A0212
222	GTYTGGENV	0.527	166	WB	VP1	A0212
27	LIKGGVEVL	0.505	212	WB	VP1	A0212
124	SMLNLHAGS	0.492	243	WB	VP1	A0212
244	LLDEQGVGP	0.484	266	WB	VP1	A0212
164	VLMNYRTKY	0.481	274	WB	VP1	A0212
94	PLPNLNEDL	0.480	276	WB	VP1	A0212
235	HVTNTATTV	0.457	356	WB	VP1	A0212
304	LLSDLINRR	0.443	414	WB	VP1	A0212
258	SLYVSAADI	0.436	449	WB	VP1	A0212
349	YIDRQGQLQ	0.435	452	WB	VP1	A0212
201	NAYPVECWI	0.435	453	WB	VP1	A0212
26	LLIKGGVEV	0.935	2	SB	VP1	A0216
320	PMYGMESQV	0.926	2	SB	VP1	A0216
127	NLHAGSQKV	0.887	3	SB	VP1	A0216
107	LLMWEAVTV	0.872	3	SB	VP1	A0216
332	RVFDGTEQL	0.838	5	SB	VP1	A0216
61	NLRGYSQHL	0.835	5	SB	VP1	A0216
43	AITEVECFL	0.834	6	SB	VP1	A0216
323	GMESQVEEV	0.826	6	SB	VP1	A0216
235	HVTNTATTV	0.762	13	SB	VP1	A0216
33	EVLEVKTGV	0.742	16	SB	VP1	A0216
308	LINRRTQKV	0.701	25	SB	VP1	A0216
83	KMLPCYSTA	0.653	42	SB	VP1	A0216
54	EMGDPDDNL	0.649	44	SB	VP1	A0216

201	NAYPVECWI	0.593	81	WB	VP1	A0216
111	EAVTVKTEV	0.540	145	WB	VP1	A0216
39	TGVDAITEV	0.524	171	WB	VP1	A0216
118	EVIGITSML	0.513	194	WB	VP1	A0216
196	YLDKNNAYP	0.512	196	WB	VP1	A0216
339	QLPGDPDMI	0.491	245	WB	VP1	A0216
222	GTYTGGENV	0.485	262	WB	VP1	A0216
27	LIKGGVEVL	0.467	318	WB	VP1	A0216
176	TITPKNPTA	0.462	336	WB	VP1	A0216
94	PLPNLNEDL	0.426	496	WB	VP1	A0216
127	NLHAGSQKV	0.862	4	SB	VP1	A0219
107	LLMWEAVTV	0.811	7	SB	VP1	A0219
320	PMYGMESQV	0.786	10	SB	VP1	A0219
26	LLIKGGVEV	0.776	11	SB	VP1	A0219
332	RVFDGTEQL	0.762	13	SB	VP1	A0219
323	GMESQVEEV	0.643	47	SB	VP1	A0219
61	NLRGYSQHL	0.621	60	WB	VP1	A0219
54	EMGDPDDNL	0.581	93	WB	VP1	A0219
235	HVTNTATTV	0.537	150	WB	VP1	A0219
33	EVLEVKTGV	0.529	162	WB	VP1	A0219
308	LINRRTQKV	0.528	165	WB	VP1	A0219
39	TGVDAITEV	0.492	242	WB	VP1	A0219
108	LMWEAVTVK	0.442	417	WB	VP1	A0219
27	LIKGGVEVL	0.438	437	WB	VP1	A0219
284	RYFKIRLRK	0.643	47	SB	VP1	A0301
108	LMWEAVTVK	0.570	104	WB	VP1	A0301
134	KVHENGGGK	0.525	170	WB	VP1	A0301
164	VLMNYRTKY	0.453	370	WB	VP1	A0301
163	GVLMNYRTK	0.440	426	WB	VP1	A0301
163	GVLMNYRTK	0.621	60	WB	VP1	A1101
186	SQVMNTDHK	0.599	76	WB	VP1	A1101
284	RYFKIRLRK	0.586	88	WB	VP1	A1101
276	TQQWRGLAR	0.561	115	WB	VP1	A1101
134	KVHENGGGK	0.556	121	WB	VP1	A1101
284	RYFKIRLRK	0.724	19	SB	VP1	A2301
87	CYSTARIPL	0.572	102	WB	VP1	A2301
143	PVQGSNFHF	0.555	123	WB	VP1	A2301
348	RYIDRQGQL	0.538	147	WB	VP1	A2301
144	VQGSNFHFF	0.480	277	WB	VP1	A2301
144	VQGSNFHFF	0.521	178	WB	VP1	A2402
348	RYIDRQGQL	0.506	210	WB	VP1	A2402
348	RYIDRQGQL	0.602	73	WB	VP1	A2403
195	AYLDKNNAY	0.502	218	WB	VP1	A2403
278	QWRGLARYF	0.434	457	WB	VP1	A2403
118	EVIGITSML	0.663	38	SB	VP1	A2601
160	EMQGVLMNY	0.553	126	WB	VP1	A2601
118	EVIGITSML	0.898	3	SB	VP1	A2602
160	EMQGVLMNY	0.659	39	SB	VP1	A2602
36	EVKTGVDAI	0.584	90	WB	VP1	A2602
164	VLMNYRTKY	0.620	61	WB	VP1	A2902
188	VMNTDHKAY	0.535	153	WB	VP1	A2902
195	AYLDKNNAY	0.524	172	WB	VP1	A2902

284	RYFKIRLRK	0.812	7	SB	VP1	A3001
134	KVHENGGGK	0.791	9	SB	VP1	A3001
163	GVLMNYRTK	0.563	113	WB	VP1	A3001
291	RKRSVKNPY	0.543	141	WB	VP1	A3001
169	RTKYPQGTI	0.492	243	WB	VP1	A3001
191	TDHKAYLDK	0.436	444	WB	VP1	A3001
287	KIRLRKRSV	0.436	446	WB	VP1	A3001
289	RLRKRSVKN	0.436	447	WB	VP1	A3001
186	SQVMNTDHK	0.434	455	WB	VP1	A3001
161	MQGVLMNYR	0.811	7	SB	VP1	A3101
285	YFKIRLRKR	0.800	8	SB	VP1	A3101
284	RYFKIRLRK	0.762	13	SB	VP1	A3101
276	TQQWRGLAR	0.627	56	WB	VP1	A3101
84	MLPCYSTAR	0.578	95	WB	VP1	A3101
304	LLSDLINRR	0.573	101	WB	VP1	A3101
281	GLARYFKIR	0.520	180	WB	VP1	A3101
108	LMWEAVTVK	0.502	219	WB	VP1	A3101
303	FLLSDLINR	0.441	422	WB	VP1	A3101
285	YFKIRLRKR	0.782	10	SB	VP1	A3301
307	DLINRRTQK	0.659	39	SB	VP1	A3301
272	NSSGTQQWR	0.732	18	SB	VP1	A6801
84	MLPCYSTAR	0.720	20	SB	VP1	A6801
307	DLINRRTQK	0.593	81	WB	VP1	A6801
324	MESQVEEVR	0.548	132	WB	VP1	A6801
304	LLSDLINRR	0.543	140	WB	VP1	A6801
118	EVIGITSML	0.509	202	WB	VP1	A6801
161	MQGVLMNYR	0.437	442	WB	VP1	A6801
284	RYFKIRLRK	0.437	444	WB	VP1	A6801
118	EVIGITSML	0.903	2	SB	VP1	A6802
111	EAVTVKTEV	0.739	16	SB	VP1	A6802
33	EVLEVKTGV	0.728	18	SB	VP1	A6802
39	TGVDAITEV	0.683	30	SB	VP1	A6802
297	NPYPISFLL	0.632	53	WB	VP1	A6802
332	RVFDGTEQL	0.578	95	WB	VP1	A6802
145	QGSNFHFFA	0.563	113	WB	VP1	A6802
201	NAYPVECWI	0.556	121	WB	VP1	A6802
187	QVMNTDHKA	0.527	167	WB	VP1	A6802
146	GSNFHFFAV	0.497	231	WB	VP1	A6802
293	RSVKNPYPI	0.457	357	WB	VP1	A6802
261	VSAADICGL	0.455	364	WB	VP1	A6802
235	HVTNTATTV	0.444	410	WB	VP1	A6802
229	NVPPVLHVT	0.441	422	WB	VP1	A6802
297	NPYPISFLL	0.673	34	SB	VP1	A6901
118	EVIGITSML	0.636	51	WB	VP1	A6901
235	HVTNTATTV	0.546	136	WB	VP1	A6901
107	LLMWEAVTV	0.499	225	WB	VP1	A6901
201	NAYPVECWI	0.485	262	WB	VP1	A6901
111	EAVTVKTEV	0.483	268	WB	VP1	A6901
225	TGGENVPPV	0.469	311	WB	VP1	A6901
222	GTYTGGENV	0.437	440	WB	VP1	A6901
127	NLHAGSQKV	0.433	463	WB	VP1	A6901
332	RVFDGTEQL	0.430	474	WB	VP1	A6901
85	LPCYSTARI	0.692	28	SB	VP1	B0702
13	APKKPKEPV	0.688	29	SB	VP1	B0702
1	APTKRKGEC	0.619	61	WB	VP1	B0702
282	LARYFKIRL	0.535	153	WB	VP1	B0702
287	KIRLRKRSV	0.520	179	WB	VP1	B0702

181	NPTAQSQVM	0.498	227	WB	VP1	B0702
79	SPDRKMLPC	0.482	272	WB	VP1	B0702
19	EPVQVPKLL	0.474	295	WB	VP1	B0702
251	GPLCKADSL	0.455	364	WB	VP1	B0702
287	KIRLRKRSV	0.431	472	WB	VP1	B0801
326	SQVEEVRVF	0.598	77	WB	VP1	B1501
188	VMNTDHKAY	0.589	85	WB	VP1	B1501
313	TQKVDGQPM	0.566	108	WB	VP1	B1501
277	QQWRGLARY	0.543	140	WB	VP1	B1501
160	EMQGVLMNY	0.456	360	WB	VP1	B1501
295	VKNPYPISF	0.595	79	WB	VP1	B1801
117	TEVIGITSM	0.472	303	WB	VP1	B1801
288	IRLRKRSVK	0.523	174	WB	VP1	B2705
279	WRGLARYFK	0.486	259	WB	VP1	B2705
181	NPTAQSQVM	0.758	13	SB	VP1	B3501
57	DPDDNLRGY	0.613	65	WB	VP1	B3501
157	DPLEMQGVL	0.577	97	WB	VP1	B3501
142	KPVQGSNFH	0.574	99	WB	VP1	B3501
297	NPYPISFLL	0.568	107	WB	VP1	B3501
151	FFAVGGDPL	0.565	110	WB	VP1	B3501
67	QHLSAENAF	0.495	235	WB	VP1	B3501
203	YPVECWIPD	0.491	247	WB	VP1	B3501
19	EPVQVPKLL	0.475	292	WB	VP1	B3501
42	DAITEVECF	0.468	317	WB	VP1	B3501
95	LPNLNEDLT	0.441	424	WB	VP1	B3501
136	HENGGGKPV	0.448	391	WB	VP1	B4001
47	VECFLNPEM	0.431	469	WB	VP1	B4001
71	AENAFESDS	0.600	75	WB	VP1	B4501
85	LPCYSTARI	0.659	39	SB	VP1	B5101
19	EPVQVPKLL	0.475	292	WB	VP1	B5101
297	NPYPISFLL	0.459	350	WB	VP1	B5101
85	LPCYSTARI	0.655	41	SB	VP1	B5301
297	NPYPISFLL	0.623	59	WB	VP1	B5301
19	EPVQVPKLL	0.535	152	WB	VP1	B5301
95	LPNLNEDLT	0.636	51	WB	VP1	B5401
85	LPCYSTARI	0.591	83	WB	VP1	B5401
203	YPVECWIPD	0.481	273	WB	VP1	B5401
299	YPISFLLSD	0.435	452	WB	VP1	B5401
102	LTCGNLLMW	0.453	371	WB	VP1	B5701
102	LTCGNLLMW	0.624	58	WB	VP1	B5801
	10-mers					
196	YLDKNNAYPV	0.866	4	SB	VP1	A0201
108	LMWEAVTVKT	0.691	28	SB	VP1	A0201
84	MLPCYSTARI	0.675	33	SB	VP1	A0201
106	NLLMWEAVTV	0.634	52	WB	VP1	A0201
224	YTGGENVPPV	0.608	69	WB	VP1	A0201
260	YVSAADICGL	0.589	85	WB	VP1	A0201
244	LLDEQGVGPL	0.537	150	WB	VP1	A0201
25	KLLIKGGVEV	0.517	185	WB	VP1	A0201
188	VMNTDHKAYL	0.504	214	WB	VP1	A0201

281 GLARYFKIRL	0.482	271	WB	VP1	A0201
322 YGMESQVEEV	0.465	325	WB	VP1	A0201
26 LLIKGGVEVL	0.465	328	WB	VP1	A0201
196 YLDKNNAYPV	0.722	20	SB	VP1	A0202
260 YVSAADICGL	0.676	33	SB	VP1	A0202
244 LLDEQGVGPL	0.652	43	SB	VP1	A0202
26 LLIKGGVEVL	0.621	60	WB	VP1	A0202
188 VMNTDHKAYL	0.613	66	WB	VP1	A0202
84 MLPCYSTARI	0.604	72	WB	VP1	A0202
106 NLLMWEAVTV	0.571	104	WB	VP1	A0202
224 YTGGENVPPV	0.554	124	WB	VP1	A0202
281 GLARYFKIRL	0.520	179	WB	VP1	A0202
303 FLLSDLINRR	0.495	236	WB	VP1	A0202
304 LLSDLINRRT	0.487	257	WB	VP1	A0202
322 YGMESQVEEV	0.470	308	WB	VP1	A0202
25 KLLIKGGVEV	0.462	338	WB	VP1	A0202
38 KTGVDAITEV	0.453	372	WB	VP1	A0202
255 KADSLYVSAA	0.442	419	WB	VP1	A0202
84 MLPCYSTARI	0.854	4	SB	VP1	A0203
196 YLDKNNAYPV	0.801	8	SB	VP1	A0203
244 LLDEQGVGPL	0.704	24	SB	VP1	A0203
188 VMNTDHKAYL	0.702	25	SB	VP1	A0203
26 LLIKGGVEVL	0.663	38	SB	VP1	A0203
106 NLLMWEAVTV	0.660	39	SB	VP1	A0203
224 YTGGENVPPV	0.611	67	WB	VP1	A0203
260 YVSAADICGL	0.606	70	WB	VP1	A0203
25 KLLIKGGVEV	0.596	79	WB	VP1	A0203
281 GLARYFKIRL	0.590	84	WB	VP1	A0203
304 LLSDLINRRT	0.530	162	WB	VP1	A0203
108 LMWEAVTVKT	0.467	319	WB	VP1	A0203
233 VLHVTNTATT	0.462	338	WB	VP1	A0203
352 RQGQLQTKMV	0.448	391	WB	VP1	A0203
236 VTNTATTVLL	0.446	399	WB	VP1	A0203
38 KTGVDAITEV	0.441	424	WB	VP1	A0203
307 DLINRRTQKV	0.438	437	WB	VP1	A0203
196 YLDKNNAYPV	0.658	40	SB	VP1	A0204
25 KLLIKGGVEV	0.650	44	SB	VP1	A0204
244 LLDEQGVGPL	0.598	77	WB	VP1	A0204
224 YTGGENVPPV	0.596	78	WB	VP1	A0204
108 LMWEAVTVKT	0.548	133	WB	VP1	A0204
106 NLLMWEAVTV	0.541	142	WB	VP1	A0204
38 KTGVDAITEV	0.517	185	WB	VP1	A0204
322 YGMESQVEEV	0.499	226	WB	VP1	A0204
188 VMNTDHKAYL	0.473	299	WB	VP1	A0204
26 LLIKGGVEVL	0.468	315	WB	VP1	A0204
89 STARIPLPNL	0.433	459	WB	VP1	A0204
196 YLDKNNAYPV	0.873	3	SB	VP1	A0206
144 VQGSNFHFFA	0.733	17	SB	VP1	A0206
106 NLLMWEAVTV	0.694	27	SB	VP1	A0206
260 YVSAADICGL	0.677	32	SB	VP1	A0206
84 MLPCYSTARI	0.671	35	SB	VP1	A0206
244 LLDEQGVGPL	0.637	50	WB	VP1	A0206
224 YTGGENVPPV	0.606	71	WB	VP1	A0206
38 KTGVDAITEV	0.590	84	WB	VP1	A0206
25 KLLIKGGVEV	0.588	86	WB	VP1	A0206
186 SQVMNTDHKA	0.588	86	WB	VP1	A0206
352 RQGQLQTKMV	0.559	118	WB	VP1	A0206
152 FAVGGDPLEM	0.550	129	WB	VP1	A0206

26 LLIKGGVEVL	0.549	131	WB	VP1	A0206
322 YGMESQVEEV	0.514	191	WB	VP1	A0206
277 QQWRGLARYF	0.509	202	WB	VP1	A0206
108 LMWEAVTVKT	0.503	216	WB	VP1	A0206
161 MQGVLMNYRT	0.428	486	WB	VP1	A0206
196 YLDKNNAYPV	0.976	1	SB	VP1	A0211
106 NLLMWEAVTV	0.926	2	SB	VP1	A0211
244 LLDEQGVGPL	0.906	2	SB	VP1	A0211
25 KLLIKGGVEV	0.849	5	SB	VP1	A0211
26 LLIKGGVEVL	0.843	5	SB	VP1	A0211
224 YTGGENVPPV	0.820	7	SB	VP1	A0211
281 GLARYFKIRL	0.817	7	SB	VP1	A0211
252 PLCKADSLYV	0.801	8	SB	VP1	A0211
188 VMNTDHKAYL	0.798	8	SB	VP1	A0211
84 MLPCYSTARI	0.773	11	SB	VP1	A0211
307 DLINRRTQKV	0.751	14	SB	VP1	A0211
108 LMWEAVTVKT	0.740	16	SB	VP1	A0211
260 YVSAADICGL	0.693	27	SB	VP1	A0211
349 YIDRQGQLQT	0.652	43	SB	VP1	A0211
304 LLSDLINRRT	0.628	55	WB	VP1	A0211
322 YGMESQVEEV	0.608	69	WB	VP1	A0211
155 GGDPLEMQGV	0.597	78	WB	VP1	A0211
315 KVDGQPMYGM	0.593	82	WB	VP1	A0211
124 SMLNLHAGSQ	0.578	96	WB	VP1	A0211
38 KTGVDAITEV	0.533	156	WB	VP1	A0211
268 GLFTNSSGTQ	0.499	226	WB	VP1	A0211
243 VLLDEQGVGP	0.427	494	WB	VP1	A0211
196 YLDKNNAYPV	0.940	1	SB	VP1	A0212
106 NLLMWEAVTV	0.863	4	SB	VP1	A0212
26 LLIKGGVEVL	0.799	8	SB	VP1	A0212
244 LLDEQGVGPL	0.763	12	SB	VP1	A0212
281 GLARYFKIRL	0.762	13	SB	VP1	A0212
224 YTGGENVPPV	0.734	17	SB	VP1	A0212
188 VMNTDHKAYL	0.728	19	SB	VP1	A0212
108 LMWEAVTVKT	0.718	21	SB	VP1	A0212
25 KLLIKGGVEV	0.705	24	SB	VP1	A0212
84 MLPCYSTARI	0.659	40	SB	VP1	A0212
260 YVSAADICGL	0.646	46	SB	VP1	A0212
307 DLINRRTQKV	0.625	57	WB	VP1	A0212
252 PLCKADSLYV	0.620	60	WB	VP1	A0212
304 LLSDLINRRT	0.541	143	WB	VP1	A0212
349 YIDRQGQLQT	0.533	157	WB	VP1	A0212
155 GGDPLEMQGV	0.513	195	WB	VP1	A0212
243 VLLDEQGVGP	0.504	213	WB	VP1	A0212
303 FLLSDLINRR	0.481	274	WB	VP1	A0212
322 YGMESQVEEV	0.474	297	WB	VP1	A0212
124 SMLNLHAGSQ	0.430	477	WB	VP1	A0212
196 YLDKNNAYPV	0.945	1	SB	VP1	A0216
106 NLLMWEAVTV	0.882	3	SB	VP1	A0216
252 PLCKADSLYV	0.866	4	SB	VP1	A0216
281 GLARYFKIRL	0.844	5	SB	VP1	A0216
307 DLINRRTQKV	0.820	7	SB	VP1	A0216
26 LLIKGGVEVL	0.800	8	SB	VP1	A0216
25 KLLIKGGVEV	0.779	10	SB	VP1	A0216
244 LLDEQGVGPL	0.740	16	SB	VP1	A0216
224 YTGGENVPPV	0.726	19	SB	VP1	A0216
84 MLPCYSTARI	0.723	19	SB	VP1	A0216
188 VMNTDHKAYL	0.662	38	SB	VP1	A0216
108 LMWEAVTVKT	0.606	70	WB	VP1	A0216

260	YVSAADICGL	0.545	136	WB	VP1 A0216
38	KTGVDAITEV	0.510	199	WB	VP1 A0216
304	LLSDLINRRT	0.477	285	WB	VP1 A0216
349	YIDRQGQLQT	0.470	309	WB	VP1 A0216
28	IKGGVEVLEV	0.430	478	WB	VP1 A0216
196	YLDKNNAYPV	0.940	1	SB	VP1 A0219
106	NLLMWEAVTV	0.763	12	SB	VP1 A0219
224	YTGGENVPPV	0.678	32	SB	VP1 A0219
26	LLIKGGVEVL	0.671	35	SB	VP1 A0219
260	YVSAADICGL	0.656	41	SB	VP1 A0219
244	LLDEQGVGPL	0.644	46	SB	VP1 A0219
108	LMWEAVTVKT	0.615	64	WB	VP1 A0219
188	VMNTDHKAYL	0.555	122	WB	VP1 A0219
84	MLPCYSTARI	0.508	204	WB	VP1 A0219
322	YGMESQVEEV	0.492	243	WB	VP1 A0219
252	PLCKADSLYV	0.482	270	WB	VP1 A0219
307	DLINRRTQKV	0.457	354	WB	VP1 A0219
25	KLLIKGGVEV	0.429	484	WB	VP1 A0219
107	LLMWEAVTVK	0.689	28	SB	VP1 A0301
283	ARYFKIRLRK	0.645	46	SB	VP1 A0301
287	KIRLRKRSVK	0.641	48	SB	VP1 A0301
83	KMLPCYSTAR	0.532	157	WB	VP1 A0301
171	KYPQGTITPK	0.503	216	WB	VP1 A0301
278	QWRGLARYFK	0.449	387	WB	VP1 A0301
190	NTDHKAYLDK	0.449	388	WB	VP1 A0301
125	MLNLHAGSQK	0.679	32	SB	VP1 A1101
275	GTQQWRGLAR	0.611	67	WB	VP1 A1101
107	LLMWEAVTVK	0.606	70	WB	VP1 A1101
185	QSQVMNTDHK	0.571	103	WB	VP1 A1101
20	PVQVPKLLIK	0.498	228	WB	VP1 A1101
190	NTDHKAYLDK	0.491	247	WB	VP1 A1101
83	KMLPCYSTAR	0.430	478	WB	VP1 A1101
143	PVQGSNFHFF	0.511	199	WB	VP1 A2301
171	KYPQGTITPK	0.457	356	WB	VP1 A2301
284	RYFKIRLRKR	0.441	423	WB	VP1 A2301
187	QVMNTDHKAY	0.752	14	SB	VP1 A2602
46	EVECFLNPEM	0.733	17	SB	VP1 A2602
315	KVDGQPMYGM	0.715	21	SB	VP1 A2602
294	SVKNPYPISF	0.643	47	SB	VP1 A2602
89	STARIPLPNL	0.602	74	WB	VP1 A2602
143	PVQGSNFHFF	0.581	92	WB	VP1 A2602
260	YVSAADICGL	0.510	201	WB	VP1 A2602
116	KTEVIGITSM	0.460	343	WB	VP1 A2602
187	QVMNTDHKAY	0.558	119	WB	VP1 A2902
163	GVLMNYRTKY	0.462	337	WB	VP1 A2902
287	KIRLRKRSVK	0.842	5	SB	VP1 A3001
278	QWRGLARYFK	0.767	12	SB	VP1 A3001
6	KGECPGAAPK	0.695	27	SB	VP1 A3001
16	KPKEPVQVPK	0.691	28	SB	VP1 A3001
171	KYPQGTITPK	0.665	37	SB	VP1 A3001
125	MLNLHAGSQK	0.599	76	WB	VP1 A3001
185	QSQVMNTDHK	0.499	225	WB	VP1 A3001
83	KMLPCYSTAR	0.463	333	WB	VP1 A3001
282	LARYFKIRLR	0.426	496	WB	VP1 A3001

284	RYFKIRLRKR	0.859	4	SB	VP1 A3101
83	KMLPCYSTAR	0.777	11	SB	VP1 A3101
282	LARYFKIRLR	0.689	28	SB	VP1 A3101
287	KIRLRKRSVK	0.682	31	SB	VP1 A3101
160	EMQGVLMNYR	0.668	36	SB	VP1 A3101
278	QWRGLARYFK	0.657	40	SB	VP1 A3101
275	GTQQWRGLAR	0.580	93	WB	VP1 A3101
283	ARYFKIRLRK	0.575	99	WB	VP1 A3101
302	SFLLSDLINR	0.565	110	WB	VP1 A3101
160	EMQGVLMNYR	0.552	127	WB	VP1 A3301
302	SFLLSDLINR	0.464	328	WB	VP1 A3301
282	LARYFKIRLR	0.443	412	WB	VP1 A3301
284	RYFKIRLRKR	0.438	439	WB	VP1 A3301
73	NAFESDSPDR	0.798	8	SB	VP1 A6801
160	EMQGVLMNYR	0.747	15	SB	VP1 A6801
125	MLNLHAGSQK	0.647	45	SB	VP1 A6801
282	LARYFKIRLR	0.540	145	WB	VP1 A6801
271	TNSSGTQQWR	0.508	205	WB	VP1 A6801
107	LLMWEAVTVK	0.504	213	WB	VP1 A6801
118	EVIGITSMLN	0.492	243	WB	VP1 A6801
54	EMGDPDDNLR	0.481	275	WB	VP1 A6801
185	QSQVMNTDHK	0.480	278	WB	VP1 A6801
303	FLLSDLINRR	0.453	372	WB	VP1 A6801
275	GTQQWRGLAR	0.443	413	WB	VP1 A6801
145	QGSNFHFFAV	0.746	15	SB	VP1 A6802
241	TTVLLDEQGV	0.705	24	SB	VP1 A6802
260	YVSAADICGL	0.681	31	SB	VP1 A6802
84	MLPCYSTARI	0.661	39	SB	VP1 A6802
89	STARIPLPNL	0.658	40	SB	VP1 A6802
111	EAVTVKTEVI	0.641	48	SB	VP1 A6802
322	YGMESQVEEV	0.619	61	WB	VP1 A6802
224	YTGGENVPPV	0.529	163	WB	VP1 A6802
104	CGNLLMWEAV	0.498	228	WB	VP1 A6802
200	NNAYPVECWI	0.458	354	WB	VP1 A6802
42	DAITEVECFL	0.447	397	WB	VP1 A6802
319	QPMYGMESQV	0.444	411	WB	VP1 A6802
224	YTGGENVPPV	0.750	14	SB	VP1 A6901
196	YLDKNNAYPV	0.662	38	SB	VP1 A6901
89	STARIPLPNL	0.596	79	WB	VP1 A6901
106	NLLMWEAVTV	0.558	119	WB	VP1 A6901
322	YGMESQVEEV	0.518	184	WB	VP1 A6901
46	EVECFLNPEM	0.482	271	WB	VP1 A6901
19	EPVQVPKLLI	0.478	283	WB	VP1 A6901
319	QPMYGMESQV	0.476	289	WB	VP1 A6901
157	DPLEMQGVLM	0.439	432	WB	VP1 A6901
142	KPVQGSNFHF	0.666	37	SB	VP1 B0702
299	YPISFLLSDL	0.604	72	WB	VP1 B0702
235	HVTNTATTVL	0.525	170	WB	VP1 B0702
319	QPMYGMESQV	0.457	357	WB	VP1 B0702
93	IPLPNLNEDL	0.429	484	WB	VP1 B0702
66	SQHLSAENAF	0.595	79	WB	VP1 B1501
313	TQKVDGQPMY	0.589	85	WB	VP1 B1501
187	QVMNTDHKAY	0.570	104	WB	VP1 B1501
277	QQWRGLARYF	0.566	109	WB	VP1 B1501
276	TQQWRGLARY	0.565	110	WB	VP1 B1501
294	SVKNPYPISF	0.507	207	WB	VP1 B1501

194	KAYLDKNNAY	0.474	297	WB	VP1	B1501
261	VSAADICGLF	0.433	461	WB	VP1	B1501
26	LLIKGGVEVL	0.430	478	WB	VP1	B1501
159	LEMQGVLMNY	0.712	22	SB	VP1	B1801
117	TEVIGITSML	0.548	133	WB	VP1	B1801
215	NENTRYFGTY	0.514	192	WB	VP1	B1801
110	WEAVTVKTEV	0.509	202	WB	VP1	B1801
32	VEVLEVKTGV	0.462	335	WB	VP1	B1801
283	ARYFKIRLRK	0.558	119	WB	VP1	B2705
152	FAVGGDPLEM	0.756	13	SB	VP1	B3501
157	DPLEMQGVLM	0.715	21	SB	VP1	B3501
211	DPSRNENTRY	0.683	30	SB	VP1	B3501
340	LPGDPDMIRY	0.676	33	SB	VP1	B3501
142	KPVQGSNFHF	0.645	46	SB	VP1	B3501
187	QVMNTDHKAY	0.604	72	WB	VP1	B3501
194	KAYLDKNNAY	0.600	75	WB	VP1	B3501
299	YPISFLLSDL	0.560	117	WB	VP1	B3501
46	EVECFLNPEM	0.533	156	WB	VP1	B3501
79	SPDRKMLPCY	0.513	194	WB	VP1	B3501
95	LPNLNEDLTC	0.454	367	WB	VP1	B3501
251	GPLCKADSLY	0.435	453	WB	VP1	B3501
117	TEVIGITSML	0.570	104	WB	VP1	B4001
324	MESQVEEVRV	0.475	293	WB	VP1	B4001
53	PEMGDPDDNL	0.473	298	WB	VP1	B4001
99	NEDLTCGNLL	0.471	304	WB	VP1	B4001
110	WEAVTVKTEV	0.428	488	WB	VP1	B4001
215	NENTRYFGTY	0.430	476	WB	VP1	B4402
71	AENAFESDSP	0.495	235	WB	VP1	B4501
19	EPVQVPKLLI	0.654	42	SB	VP1	B5101
299	YPISFLLSDL	0.557	120	WB	VP1	B5101
19	EPVQVPKLLI	0.658	40	SB	VP1	B5301
299	YPISFLLSDL	0.604	72	WB	VP1	B5301
142	KPVQGSNFHF	0.531	159	WB	VP1	B5301
340	LPGDPDMIRY	0.523	174	WB	VP1	B5301
79	SPDRKMLPCY	0.468	315	WB	VP1	B5301
211	DPSRNENTRY	0.468	316	WB	VP1	B5301
23	VPKLLIKGGV	0.607	70	WB	VP1	B5401
231	PPVLHVTNTA	0.590	84	WB	VP1	B5401
85	LPCYSTARIP	0.533	157	WB	VP1	B5401
19	EPVQVPKLLI	0.463	332	WB	VP1	B5401
203	YPVECWIPDP	0.456	358	WB	VP1	B5401
270	FTNSSGTQQW	0.478	285	WB	VP1	B5701
270	FTNSSGTQQW	0.738	16	SB	VP1	B5801
199	KNNAYPVECW	0.634	52	WB	VP1	B5801
261	VSAADICGLF	0.458	351	WB	VP1	B5801
	11-mers					
83	KMLPCYSTARI	0.778	11	SB	VP1	A0201
107	LLMWEAVTVKT	0.594	80	WB	VP1	A0201
243	VLLDEQGVGPL	0.577	97	WB	VP1	A0201

303 FLLSDLINRRT	0.551	129	WB	VP1	A0201
233 VLHVTNTATTV	0.497	230	WB	VP1	A0201
144 VQGSNFHFFAV	0.461	342	WB	VP1	A0201
125 MLNLHAGSQKV	0.459	348	WB	VP1	A0201
187 QVMNTDHKAYL	0.444	407	WB	VP1	A0201
323 GMESQVEEVRV	0.434	458	WB	VP1	A0201
125 MLNLHAGSQKV	0.757	13	SB	VP1	A0202
97 NLNEDLTCGNL	0.678	32	SB	VP1	A0202
243 VLLDEQGVGPL	0.618	62	WB	VP1	A0202
83 KMLPCYSTARI	0.597	78	WB	VP1	A0202
107 LLMWEAVTVKT	0.592	82	WB	VP1	A0202
323 GMESQVEEVRV	0.558	119	WB	VP1	A0202
144 VQGSNFHFFAV	0.548	133	WB	VP1	A0202
233 VLHVTNTATTV	0.506	209	WB	VP1	A0202
187 QVMNTDHKAYL	0.482	270	WB	VP1	A0202
303 FLLSDLINRRT	0.438	436	WB	VP1	A0202
125 MLNLHAGSQKV	0.897	3	SB	VP1	A0203
27 LIKGGVEVLEV	0.784	10	SB	VP1	A0203
83 KMLPCYSTARI	0.744	15	SB	VP1	A0203
233 VLHVTNTATTV	0.743	16	SB	VP1	A0203
97 NLNEDLTCGNL	0.709	23	SB	VP1	A0203
243 VLLDEQGVGPL	0.708	23	SB	VP1	A0203
61 NLRGYSQHLSA	0.693	27	SB	VP1	A0203
107 LLMWEAVTVKT	0.605	71	WB	VP1	A0203
134 KVHENGGGKPV	0.574	99	WB	VP1	A0203
144 VQGSNFHFFAV	0.520	180	WB	VP1	A0203
294 SVKNPYPISFL	0.475	292	WB	VP1	A0203
346 MIRYIDRQGQL	0.471	306	WB	VP1	A0203
323 GMESQVEEVRV	0.459	348	WB	VP1	A0203
303 FLLSDLINRRT	0.454	367	WB	VP1	A0203
125 MLNLHAGSQKV	0.687	29	SB	VP1	A0204
233 VLHVTNTATTV	0.655	41	SB	VP1	A0204
243 VLLDEQGVGPL	0.629	55	WB	VP1	A0204
134 KVHENGGGKPV	0.544	138	WB	VP1	A0204
323 GMESQVEEVRV	0.544	138	WB	VP1	A0204
83 KMLPCYSTARI	0.497	230	WB	VP1	A0204
144 VQGSNFHFFAV	0.476	290	WB	VP1	A0204
107 LLMWEAVTVKT	0.464	328	WB	VP1	A0204
195 AYLDKNNAYPV	0.460	345	WB	VP1	A0204
25 KLLIKGGVEVL	0.443	415	WB	VP1	A0204
224 YTGGENVPPVL	0.428	487	WB	VP1	A0204
144 VQGSNFHFFAV	0.865	4	SB	VP1	A0206
83 KMLPCYSTARI	0.720	20	SB	VP1	A0206
125 MLNLHAGSQKV	0.576	97	WB	VP1	A0206
243 VLLDEQGVGPL	0.571	103	WB	VP1	A0206
318 GQPMYGMESQV	0.519	181	WB	VP1	A0206
107 LLMWEAVTVKT	0.498	229	WB	VP1	A0206
187 QVMNTDHKAYL	0.485	261	WB	VP1	A0206
233 VLHVTNTATTV	0.435	450	WB	VP1	A0206
303 FLLSDLINRRT	0.433	462	WB	VP1	A0206
243 VLLDEQGVGPL	0.906	2	SB	VP1	A0211
233 VLHVTNTATTV	0.899	2	SB	VP1	A0211
125 MLNLHAGSQKV	0.897	3	SB	VP1	A0211
83 KMLPCYSTARI	0.831	6	SB	VP1	A0211
27 LIKGGVEVLEV	0.813	7	SB	VP1	A0211
323 GMESQVEEVRV	0.770	12	SB	VP1	A0211
244 LLDEQGVGPLC	0.735	17	SB	VP1	A0211

61	NLRGYSQHLSA	0.703	24	SB	VP1	A0211
304	LLSDLINRRTQ	0.696	26	SB	VP1	A0211
25	KLLIKGGVEVL	0.681	31	SB	VP1	A0211
134	KVHENGGGKPV	0.674	34	SB	VP1	A0211
97	NLNEDLTCGNL	0.669	35	SB	VP1	A0211
195	AYLDKNNAYPV	0.636	51	WB	VP1	A0211
303	FLLSDLINRRT	0.612	66	WB	VP1	A0211
164	VLMNYRTKYPQ	0.607	70	WB	VP1	A0211
223	TYTGGENVPPV	0.585	89	WB	VP1	A0211
196	YLDKNNAYPVE	0.560	116	WB	VP1	A0211
107	LLMWEAVTVKT	0.551	128	WB	VP1	A0211
235	HVTNTATTVLL	0.525	171	WB	VP1	A0211
22	QVPKLLIKGGV	0.523	174	WB	VP1	A0211
268	GLFTNSSGTQQ	0.506	209	WB	VP1	A0211
339	QLPGDPDMIRY	0.501	222	WB	VP1	A0211
144	VQGSNFHFFAV	0.500	224	WB	VP1	A0211
187	QVMNTDHKAYL	0.499	225	WB	VP1	A0211
11	GAAPKKPKEPV	0.474	297	WB	VP1	A0211
224	YTGGENVPPVL	0.472	302	WB	VP1	A0211
160	EMQGVLMNYRT	0.468	317	WB	VP1	A0211
349	YIDRQGQLQTK	0.450	385	WB	VP1	A0211
240	ATTVLLDEQGV	0.437	443	WB	VP1	A0211
233	VLHVTNTATTV	0.838	5	SB	VP1	A0212
243	VLLDEQGVGPL	0.823	6	SB	VP1	A0212
125	MLNLHAGSQKV	0.813	7	SB	VP1	A0212
323	GMESQVEEVRV	0.713	22	SB	VP1	A0212
27	LIKGGVEVLEV	0.697	26	SB	VP1	A0212
61	NLRGYSQHLSA	0.690	28	SB	VP1	A0212
144	VQGSNFHFFAV	0.652	42	SB	VP1	A0212
244	LLDEQGVGPLC	0.645	46	SB	VP1	A0212
304	LLSDLINRRTQ	0.599	76	WB	VP1	A0212
83	KMLPCYSTARI	0.596	79	WB	VP1	A0212
164	VLMNYRTKYPQ	0.576	98	WB	VP1	A0212
196	YLDKNNAYPVE	0.569	106	WB	VP1	A0212
303	FLLSDLINRRT	0.561	115	WB	VP1	A0212
224	YTGGENVPPVL	0.543	140	WB	VP1	A0212
25	KLLIKGGVEVL	0.530	161	WB	VP1	A0212
107	LLMWEAVTVKT	0.511	199	WB	VP1	A0212
97	NLNEDLTCGNL	0.491	247	WB	VP1	A0212
195	AYLDKNNAYPV	0.490	249	WB	VP1	A0212
349	YIDRQGQLQTK	0.465	325	WB	VP1	A0212
154	VGGDPLEMQGV	0.464	329	WB	VP1	A0212
160	EMQGVLMNYRT	0.460	345	WB	VP1	A0212
108	LMWEAVTVKTE	0.438	434	WB	VP1	A0212
233	VLHVTNTATTV	0.865	4	SB	VP1	A0216
125	MLNLHAGSQKV	0.827	6	SB	VP1	A0216
323	GMESQVEEVRV	0.804	8	SB	VP1	A0216
27	LIKGGVEVLEV	0.752	14	SB	VP1	A0216
243	VLLDEQGVGPL	0.724	19	SB	VP1	A0216
83	KMLPCYSTARI	0.660	39	SB	VP1	A0216
61	NLRGYSQHLSA	0.647	45	SB	VP1	A0216
187	QVMNTDHKAYL	0.643	47	SB	VP1	A0216
164	VLMNYRTKYPQ	0.619	61	WB	VP1	A0216
195	AYLDKNNAYPV	0.616	64	WB	VP1	A0216
11	GAAPKKPKEPV	0.542	142	WB	VP1	A0216
294	SVKNPYPISFL	0.530	162	WB	VP1	A0216
318	GQPMYGMESQV	0.525	170	WB	VP1	A0216
25	KLLIKGGVEVL	0.517	186	WB	VP1	A0216
223	TYTGGENVPPV	0.512	196	WB	VP1	A0216
268	GLFTNSSGTQQ	0.495	236	WB	VP1	A0216

97 NLNEDLTCGNL	0.481	274	WB	VP1	A0216
22 QVPKLLIKGGV	0.478	284	WB	VP1	A0216
304 LLSDLINRRTQ	0.474	295	WB	VP1	A0216
160 EMQGVLMNYRT	0.464	329	WB	VP1	A0216
31 GVEVLEVKTGV	0.459	348	WB	VP1	A0216
144 VQGSNFHFFAV	0.456	361	WB	VP1	A0216
235 HVTNTATTVLL	0.454	368	WB	VP1	A0216
303 FLLSDLINRRT	0.453	372	WB	VP1	A0216
249 GVGPLCKADSL	0.450	383	WB	VP1	A0216
220 YFGTYTGGENV	0.447	394	WB	VP1	A0216
37 VKTGVDAITEV	0.439	433	WB	VP1	A0216
134 KVHENGGGKPV	0.434	454	WB	VP1	A0216
233 VLHVTNTATTV	0.703	24	SB	VP1	A0219
125 MLNLHAGSQKV	0.697	26	SB	VP1	A0219
243 VLLDEQGVGPL	0.673	34	SB	VP1	A0219
27 LIKGGVEVLEV	0.581	93	WB	VP1	A0219
144 VQGSNFHFFAV	0.546	135	WB	VP1	A0219
323 GMESQVEEVRV	0.511	198	WB	VP1	A0219
83 KMLPCYSTARI	0.501	221	WB	VP1	A0219
223 TYTGGENVPPV	0.457	357	WB	VP1	A0219
154 VGGDPLEMQGV	0.443	413	WB	VP1	A0219
224 YTGGENVPPVL	0.428	485	WB	VP1	A0219
124 SMLNLHAGSQK	0.698	26	SB	VP1	A0301
289 RLRKRSVKNPY	0.560	117	WB	VP1	A0301
281 GLARYFKIRLR	0.520	180	WB	VP1	A0301
106 NLLMWEAVTVK	0.478	285	WB	VP1	A0301
270 FTNSSGTQQWR	0.447	395	WB	VP1	A0301
124 SMLNLHAGSQK	0.754	14	SB	VP1	A1101
184 AQSQVMNTDHK	0.640	49	SB	VP1	A1101
301 ISFLLSDLINR	0.631	54	WB	VP1	A1101
277 QQWRGLARYFK	0.573	101	WB	VP1	A1101
73 NAFESDSPDRK	0.538	148	WB	VP1	A1101
275 GTQQWRGLARY	0.477	288	WB	VP1	A1101
106 NLLMWEAVTVK	0.462	336	WB	VP1	A1101
161 MQGVLMNYRTK	0.448	390	WB	VP1	A1101
312 RTQKVDGQPMY	0.441	421	WB	VP1	A1101
282 LARYFKIRLRK	0.432	467	WB	VP1	A1101
305 LSDLINRRTQK	0.431	473	WB	VP1	A1101
259 LYVSAADICGL	0.573	102	WB	VP1	A2301
298 PYPISFLLSDL	0.474	295	WB	VP1	A2301
298 PYPISFLLSDL	0.564	111	WB	VP1	A2402
167 NYRTKYPQGTI	0.552	128	WB	VP1	A2402
278 QWRGLARYFKI	0.438	439	WB	VP1	A2402
65 YSQHLSAENAF	0.655	41	SB	VP1	A2403
298 PYPISFLLSDL	0.628	56	WB	VP1	A2403
259 LYVSAADICGL	0.536	151	WB	VP1	A2403
269 LFTNSSGTQQW	0.434	458	WB	VP1	A2403
118 EVIGITSMLNL	0.705	24	SB	VP1	A2601
78 DSPDRKMLPCY	0.602	74	WB	VP1	A2601
118 EVIGITSMLNL	0.894	3	SB	VP1	A2602
294 SVKNPYPISFL	0.778	11	SB	VP1	A2602
78 DSPDRKMLPCY	0.715	21	SB	VP1	A2602
260 YVSAADICGLF	0.691	28	SB	VP1	A2602
339 QLPGDPDMIRY	0.669	35	SB	VP1	A2602

187	QVMNTDHKAYL	0.618	62	WB	VP1	A2602
275	GTQQWRGLARY	0.593	81	WB	VP1	A2602
312	RTQKVDGQPMY	0.482	273	WB	VP1	A2602
289	RLRKRSVKNPY	0.805	8	SB	VP1	A3001
282	LARYFKIRLRK	0.787	10	SB	VP1	A3001
6	KGECPGAAPKK	0.656	41	SB	VP1	A3001
134	KVHENGGGKPV	0.525	169	WB	VP1	A3001
132	SQKVHENGGGK	0.508	205	WB	VP1	A3001
312	RTQKVDGQPMY	0.498	227	WB	VP1	A3001
277	QQWRGLARYFK	0.477	286	WB	VP1	A3001
161	MQGVLMNYRTK	0.455	362	WB	VP1	A3001
291	RKRSVKNPYPI	0.432	468	WB	VP1	A3001
312	RTQKVDGQPMY	0.474	295	WB	VP1	A3002
277	QQWRGLARYFK	0.695	27	SB	VP1	A3101
301	ISFLLSDLINR	0.646	46	SB	VP1	A3101
302	SFLLSDLINRR	0.634	52	WB	VP1	A3101
270	FTNSSGTQQWR	0.615	64	WB	VP1	A3101
124	SMLNLHAGSQK	0.602	74	WB	VP1	A3101
281	GLARYFKIRLR	0.598	77	WB	VP1	A3101
282	LARYFKIRLRK	0.457	355	WB	VP1	A3101
161	MQGVLMNYRTK	0.453	371	WB	VP1	A3101
82	RKMLPCYSTAR	0.428	486	WB	VP1	A3101
301	ISFLLSDLINR	0.516	187	WB	VP1	A3301
302	SFLLSDLINRR	0.486	259	WB	VP1	A3301
270	FTNSSGTQQWR	0.792	9	SB	VP1	A6801
301	ISFLLSDLINR	0.717	21	SB	VP1	A6801
73	NAFESDSPDRK	0.709	23	SB	VP1	A6801
72	ENAFESDSPDR	0.595	80	WB	VP1	A6801
322	YGMESQVEEVR	0.478	284	WB	VP1	A6801
282	LARYFKIRLRK	0.478	284	WB	VP1	A6801
118	EVIGITSMLNL	0.811	7	SB	VP1	A6802
187	QVMNTDHKAYL	0.666	36	SB	VP1	A6802
22	QVPKLLIKGGV	0.649	44	SB	VP1	A6802
235	HVTNTATTVLL	0.487	257	WB	VP1	A6802
330	EVRVFDGTEQL	0.471	306	WB	VP1	A6802
103	TCGNLLMWEAV	0.457	354	WB	VP1	A6802
118	EVIGITSMLNL	0.681	31	SB	VP1	A6901
33	EVLEVKTGVDA	0.574	99	WB	VP1	A6901
187	QVMNTDHKAYL	0.533	155	WB	VP1	A6901
299	YPISFLLSDLI	0.456	361	WB	VP1	A6901
224	YTGGENVPPVL	0.454	366	WB	VP1	A6901
235	HVTNTATTVLL	0.449	389	WB	VP1	A6901
85	LPCYSTARIPL	0.805	8	SB	VP1	B0702
142	KPVQGSNFHFF	0.686	29	SB	VP1	B0702
13	APKKPKEPVQV	0.564	112	WB	VP1	B0702
1	APTKRKGECPG	0.493	242	WB	VP1	B0702
16	KPKEPVQVPKL	0.491	245	WB	VP1	B0702
178	TPKNPTAQSQV	0.486	259	WB	VP1	B0702
299	YPISFLLSDLI	0.435	452	WB	VP1	B0702
285	YFKIRLRKRSV	0.492	244	WB	VP1	B0801
276	TQQWRGLARYF	0.585	89	WB	VP1	B1501
289	RLRKRSVKNPY	0.578	96	WB	VP1	B1501

186 SQVMNTDHKAY	0.565	110	WB	VP1	B1501
65 YSQHLSAENAF	0.559	118	WB	VP1	B1501
260 YVSAADICGLF	0.550	130	WB	VP1	B1501
312 RTQKVDGQPMY	0.427	492	WB	VP1	B1501
324 MESQVEEVRVF	0.678	32	SB	VP1	B1801
45 TEVECFLNPEM	0.554	124	WB	VP1	B1801
75 FESDSPDRKML	0.525	171	WB	VP1	B1801
110 WEAVTVKTEVI	0.483	267	WB	VP1	B1801
311 RRTQKVDGQPM	0.521	177	WB	VP1	B2705
277 QQWRGLARYFK	0.429	480	WB	VP1	B2705
142 KPVQGSNFHFF	0.739	16	SB	VP1	B3501
203 YPVECWIPDPS	0.712	22	SB	VP1	B3501
85 LPCYSTARIPL	0.676	33	SB	VP1	B3501
211 DPSRNENTRYF	0.625	57	WB	VP1	B3501
65 YSQHLSAENAF	0.609	68	WB	VP1	B3501
151 FFAVGGDPLEM	0.579	95	WB	VP1	B3501
260 YVSAADICGLF	0.578	96	WB	VP1	B3501
299 YPISFLLSDLI	0.498	227	WB	VP1	B3501
52 NPEMGDPDDNL	0.470	310	WB	VP1	B3501
193 HKAYLDKNNAY	0.461	342	WB	VP1	B3501
149 FHFFAVGGDPL	0.586	88	WB	VP1	B3901
234 LHVTNTATTVL	0.579	94	WB	VP1	B3901
224 YTGGENVPPVL	0.498	227	WB	VP1	B3901
75 FESDSPDRKML	0.556	121	WB	VP1	B4001
45 TEVECFLNPEM	0.446	402	WB	VP1	B4001
45 TEVECFLNPEM	0.451	379	WB	VP1	B4002
45 TEVECFLNPEM	0.477	287	WB	VP1	B4403
71 AENAFESDSPD	0.487	257	WB	VP1	B4501
299 YPISFLLSDLI	0.706	24	SB	VP1	B5101
340 LPGDPDMIRYI	0.600	75	WB	VP1	B5101
230 VPPVLHVTNTA	0.508	206	WB	VP1	B5101
85 LPCYSTARIPL	0.492	243	WB	VP1	B5101
299 YPISFLLSDLI	0.735	17	SB	VP1	B5301
340 LPGDPDMIRYI	0.564	112	WB	VP1	B5301
142 KPVQGSNFHFF	0.534	154	WB	VP1	B5301
85 LPCYSTARIPL	0.434	455	WB	VP1	B5301
299 YPISFLLSDLI	0.778	11	SB	VP1	B5401
230 VPPVLHVTNTA	0.720	20	SB	VP1	B5401
203 YPVECWIPDPS	0.657	40	SB	VP1	B5401
93 IPLPNLNEDLT	0.542	142	WB	VP1	B5401
85 LPCYSTARIPL	0.510	200	WB	VP1	B5401
340 LPGDPDMIRYI	0.458	350	WB	VP1	B5401
293 RSVKNPYPISF	0.691	28	SB	VP1	B5801

Preferred BK virus fragments of small T antigen capable of interacting with one or more MHC class 1 molecules are listed in Table L.

Table L: Prediction of BK virus small t protein specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
124	FLRKEPLV	0.663	38	SB	Small t	A0201
11	ELMDLLGL	0.599	76	WB	Small t	A0201
153	TLQWWVQI	0.543	141	WB	Small t	A0201
74	GTWNSSEV	0.542	141	WB	Small t	A0201
154	LQWWVQII	0.520	179	WB	Small t	A0201
110	CMLCQLRL	0.509	202	WB	Small t	A0201
21	AAWGNLPL	0.473	297	WB	Small t	A0201
60	KMEQDVKV	0.452	375	WB	Small t	A0201
11	ELMDLLGL	0.762	13	SB	Small t	A0202
124	FLRKEPLV	0.715	21	SB	Small t	A0202
9	SMELMDLL	0.628	56	WB	Small t	A0202
50	KMKRMNTL	0.586	88	WB	Small t	A0202
60	KMEQDVKV	0.505	211	WB	Small t	A0202
27	PLMRKAYL	0.488	254	WB	Small t	A0202
110	CMLCQLRL	0.475	292	WB	Small t	A0202
124	FLRKEPLV	0.863	4	SB	Small t	A0203
50	KMKRMNTL	0.758	13	SB	Small t	A0203
11	ELMDLLGL	0.712	22	SB	Small t	A0203
153	TLQWWVQI	0.690	28	SB	Small t	A0203
110	CMLCQLRL	0.515	189	WB	Small t	A0203
105	SVHCPCML	0.430	474	WB	Small t	A0203
60	KMEQDVKV	0.429	484	WB	Small t	A0203
60	KMEQDVKV	0.615	64	WB	Small t	A0204
124	FLRKEPLV	0.573	100	WB	Small t	A0204
153	TLQWWVQI	0.524	172	WB	Small t	A0204
11	ELMDLLGL	0.521	178	WB	Small t	A0204
50	KMKRMNTL	0.443	412	WB	Small t	A0204
154	LQWWVQII	0.679	32	SB	Small t	A0206
74	GTWNSSEV	0.645	46	SB	Small t	A0206
11	ELMDLLGL	0.594	80	WB	Small t	A0206
124	FLRKEPLV	0.581	92	WB	Small t	A0206
21	AAWGNLPL	0.571	104	WB	Small t	A0206
110	CMLCQLRL	0.496	233	WB	Small t	A0206
142	TQWFGLDL	0.494	239	WB	Small t	A0206
153	TLQWWVQI	0.468	315	WB	Small t	A0206
60	KMEQDVKV	0.427	490	WB	Small t	A0206
11	ELMDLLGL	0.904	2	SB	Small t	A0211
124	FLRKEPLV	0.865	4	SB	Small t	A0211
153	TLQWWVQI	0.861	4	SB	Small t	A0211
60	KMEQDVKV	0.845	5	SB	Small t	A0211
14	DLLGLERA	0.725	19	SB	Small t	A0211
74	GTWNSSEV	0.720	20	SB	Small t	A0211
110	CMLCQLRL	0.666	37	SB	Small t	A0211
27	PLMRKAYL	0.666	37	SB	Small t	A0211

21	AAWGNLPL	0.638	50	WB	Small t	A0211
9	SMELMDLL	0.635	51	WB	Small t	A0211
56	TLYKKMEQ	0.625	57	WB	Small t	A0211
50	KMKRMNTL	0.582	92	WB	Small t	A0211
146	GLDLTEET	0.563	113	WB	Small t	A0211
3	VLNREESM	0.494	239	WB	Small t	A0211
105	SVHCPCML	0.430	474	WB	Small t	A0211
148	DLTEETLQ	0.428	487	WB	Small t	A0211
124	FLRKEPLV	0.884	3	SB	Small t	A0212
11	ELMDLLGL	0.842	5	SB	Small t	A0212
153	TLQWWVQI	0.692	28	SB	Small t	A0212
60	KMEQDVKV	0.666	37	SB	Small t	A0212
3	VLNREESM	0.639	49	SB	Small t	A0212
27	PLMRKAYL	0.597	78	WB	Small t	A0212
110	CMLCQLRL	0.580	94	WB	Small t	A0212
50	KMKRMNTL	0.579	94	WB	Small t	A0212
14	DLLGLERA	0.523	174	WB	Small t	A0212
74	GTWNSSEV	0.521	178	WB	Small t	A0212
56	TLYKKMEQ	0.520	180	WB	Small t	A0212
21	AAWGNLPL	0.511	197	WB	Small t	A0212
9	SMELMDLL	0.426	495	WB	Small t	A0212
124	FLRKEPLV	0.876	3	SB	Small t	A0216
27	PLMRKAYL	0.829	6	SB	Small t	A0216
11	ELMDLLGL	0.740	16	SB	Small t	A0216
74	GTWNSSEV	0.734	17	SB	Small t	A0216
60	KMEQDVKV	0.732	18	SB	Small t	A0216
153	TLQWWVQI	0.684	30	SB	Small t	A0216
56	TLYKKMEQ	0.662	38	SB	Small t	A0216
50	KMKRMNTL	0.651	43	SB	Small t	A0216
21	AAWGNLPL	0.600	75	WB	Small t	A0216
110	CMLCQLRL	0.577	97	WB	Small t	A0216
14	DLLGLERA	0.566	109	WB	Small t	A0216
9	SMELMDLL	0.532	158	WB	Small t	A0216
146	GLDLTEET	0.453	370	WB	Small t	A0216
3	VLNREESM	0.429	482	WB	Small t	A0216
11	ELMDLLGL	0.807	8	SB	Small t	A0219
124	FLRKEPLV	0.736	17	SB	Small t	A0219
21	AAWGNLPL	0.637	51	WB	Small t	A0219
153	TLQWWVQI	0.608	69	WB	Small t	A0219
27	PLMRKAYL	0.589	85	WB	Small t	A0219
110	CMLCQLRL	0.548	133	WB	Small t	A0219
74	GTWNSSEV	0.540	145	WB	Small t	A0219
116	RLRHLNRK	0.728	19	SB	Small t	A0301
53	RMNTLYKK	0.719	20	SB	Small t	A0301
119	HLNRKFLR	0.676	33	SB	Small t	A0301
28	LMRKAYLK	0.671	35	SB	Small t	A0301
31	KAYLKKCK	0.506	210	WB	Small t	A0301
53	RMNTLYKK	0.727	19	SB	Small t	A1101
31	KAYLKKCK	0.639	49	SB	Small t	A1101
52	KRMNTLYK	0.454	367	WB	Small t	A1101
119	HLNRKFLR	0.443	415	WB	Small t	A1101
160	IIGETPFR	0.438	436	WB	Small t	A1101
28	LMRKAYLK	0.435	452	WB	Small t	A1101
131	VWIDCYCI	0.479	280	WB	Small t	A2301
92	LYCKEWPI	0.458	351	WB	Small t	A2301

131	VWIDCYCI	0.675	33	SB	Small t	A2402
92	LYCKEWPI	0.622	60	WB	Small t	A2402
11	ELMDLLGL	0.486	259	WB	Small t	A2601
159	QIIGETPF	0.823	6	SB	Small t	A2602
80	EVCADFPL	0.594	80	WB	Small t	A2602
66	KVAHQPDF	0.563	112	WB	Small t	A2602
11	ELMDLLGL	0.500	224	WB	Small t	A2602
86	PLCPDTLY	0.515	189	WB	Small t	A2902
116	RLRHLNRK	0.810	7	SB	Small t	A3001
28	LMRKAYLK	0.805	8	SB	Small t	A3001
53	RMNTLYKK	0.672	34	SB	Small t	A3001
31	KAYLKKCK	0.628	55	WB	Small t	A3001
52	KRMNTLYK	0.620	60	WB	Small t	A3001
29	MRKAYLKK	0.612	66	WB	Small t	A3001
120	LNRKFLRK	0.571	104	WB	Small t	A3001
119	HLNRKFLR	0.850	5	SB	Small t	A3101
53	RMNTLYKK	0.816	7	SB	Small t	A3101
111	MLCQLRLR	0.684	30	SB	Small t	A3101
28	LMRKAYLK	0.646	46	SB	Small t	A3101
116	RLRHLNRK	0.541	142	WB	Small t	A3101
160	IIGETPFR	0.540	145	WB	Small t	A3101
31	KAYLKKCK	0.504	214	WB	Small t	A3101
119	HLNRKFLR	0.745	15	SB	Small t	A3301
111	MLCQLRLR	0.521	177	WB	Small t	A3301
160	IIGETPFR	0.469	313	WB	Small t	A3301
163	ETPFRDLK	0.799	8	SB	Small t	A6801
111	MLCQLRLR	0.725	19	SB	Small t	A6801
119	HLNRKFLR	0.654	42	SB	Small t	A6801
160	IIGETPFR	0.568	107	WB	Small t	A6801
80	EVCADFPL	0.773	11	SB	Small t	A6802
11	ELMDLLGL	0.583	90	WB	Small t	A6802
8	ESMELMDL	0.563	113	WB	Small t	A6802
105	SVHCPCML	0.510	200	WB	Small t	A6802
19	ERAAWGNL	0.434	456	WB	Small t	A6802
11	ELMDLLGL	0.667	36	SB	Small t	A6901
80	EVCADFPL	0.549	131	WB	Small t	A6901
74	GTWNSSEV	0.545	137	WB	Small t	A6901
85	FPLCPDTL	0.537	150	WB	Small t	A6901
21	AAWGNLPL	0.513	193	WB	Small t	A6901
8	ESMELMDL	0.453	372	WB	Small t	A6901
103	KPSVHCPC	0.540	145	WB	Small t	B0702
21	AAWGNLPL	0.482	270	WB	Small t	B0702
26	LPLMRKAY	0.431	472	WB	Small t	B0702
50	KMKRMNTL	0.479	282	WB	Small t	B0801
33	YLKKCKEF	0.446	401	WB	Small t	B0801
159	QIIGETPF	0.529	163	WB	Small t	B1501
33	YLKKCKEF	0.496	232	WB	Small t	B1501
50	KMKRMNTL	0.474	294	WB	Small t	B1501
52	KRMNTLYK	0.623	58	WB	Small t	B2705

29	MRKAYLKK	0.430	477	WB	Small t	B2705
26	LPLMRKAY	0.749	15	SB	Small t	B3501
85	FPLCPDTL	0.706	24	SB	Small t	B3501
21	AAWGNLPL	0.509	203	WB	Small t	B3501
159	QIIGETPF	0.457	355	WB	Small t	B3501
5	NREESMEL	0.555	123	WB	Small t	B3901
162	GETPFRDL	0.607	69	WB	Small t	B4001
6	REESMELM	0.511	197	WB	Small t	B4001
6	REESMELM	0.433	463	WB	Small t	B4002
151	EETLQWWV	0.428	488	WB	Small t	B4002
150	TEETLQWW	0.443	414	WB	Small t	B4402
151	EETLQWWV	0.426	497	WB	Small t	B4403
151	EETLQWWV	0.447	397	WB	Small t	B4501
-						
85	FPLCPDTL	0.509	202	WB	Small t	B5101
108	CPCMLCQL	0.480	276	WB	Small t	B5101
26	LPLMRKAY	0.636	51	WB	Small t	B5301
85	FPLCPDTL	0.559	117	WB	Small t	B5301
26	LPLMRKAY	0.482	271	WB	Small t	B5401
149	LTEETLQW	0.602	74	WB	Small t,	B5701
149	LTEETLQW	0.555	123	WB	Small t	B5801
66	KVAHQPDF	0.491	246	WB	Small t	B5801
16	LGLERAAW	0.439	430	WB	Small t	B5801
	9-mers					
91	TLYCKEWPI	0.629	55	WB	Small t	A0201
153	TLQWWVQII	0.605	71	WB	Small t	A0201
130	LVWIDCYCI	0.509	201	WB	Small t	A0201
91	TLYCKEWPI	0.697	26	SB	Small t	A0202
146	GLDLTEETL	0.429	483	WB	Small t	A0202
153	TLQWWVQII	0.838	5	SB	Small t	A0203
91	TLYCKEWPI	0.728	18	SB	Small t	A0203
20	RAAWGNLPL	0.491	246	WB	Small t	A0203
53	RMNTLYKKM	0.490	249	WB	Small t	A0203
153	TLQWWVQII	0.535	152	WB	Small t	A0204
91	TLYCKEWPI	0.525	170	WB	Small t	A0204
59	KKMEQDVKV	0.514	191	WB	Small t	A0204
158	VQIIGETPF	0.700	25	SB	Small t	A0206
142	TQWFGLDLT	0.667	36	SB	Small t	A0206
91	TLYCKEWPI	0.660	39	SB	Small t	A0206
20	RAAWGNLPL	0.634	52	WB	Small t	A0206
79	SEVCADFPL	0.515	189	WB	Small t	A0206
10	MELMDLLGL	0.496	233	WB	Small t	A0206
21	AAWGNLPLM	0.457	357	WB	Small t	A0206
146	GLDLTEETL	0.857	4	SB	Small t	A0211
91	TLYCKEWPI	0.856	4	SB	Small t	A0211

153	TLQWWVQII	0.797	8	SB	Small t	A0211
20	RAAWGNLPL	0.620	61	WB	Small t	A0211
14	DLLGLERAA	0.614	65	WB	Small t	A0211
86	PLCPDTLYC	0.564	111	WB	Small t	A0211
130	LVWIDCYCI	0.505	210	WB	Small t	A0211
73	FGTWNSSEV	0.481	274	WB	Small t	A0211
21	AAWGNLPLM	0.448	394	WB	Small t	A0211
152	ETLQWWVQI	0.445	404	WB	Small t	A0211
98	PICSKKPSV	0.436	448	WB	Small t	A0211
129	PLVWIDCYC	0.432	465	WB	Small t	A0211
146	GLDLTEETL	0.773	11	SB	Small t	A0212
91	TLYCKEWPI	0.751	14	SB	Small t	A0212
153	TLQWWVQII	0.666	37	SB	Small t	A0212
14	DLLGLERAA	0.548	133	WB	Small t	A0212
141	FTQWFGLDL	0.521	178	WB	Small t	A0212
98	PICSKKPSV	0.430	474	WB	Small t	A0212
146	GLDLTEETL	0.773	11	SB	Small t	A0216
91	TLYCKEWPI	0.720	20	SB	Small t	A0216
98	PICSKKPSV	0.617	62	WB	Small t	A0216
153	TLQWWVQII	0.518	184	WB	Small t	A0216
129	PLVWIDCYC	0.472	302	WB	Small t	A0216
146	GLDLTEETL	0.704	24	SB	Small t	A0219
153	TLQWWVQII	0.531	160	WB	Small t	A0219
21	AAWGNLPLM	0.506	209	WB	Small t	A0219
91	TLYCKEWPI	0.505	211	WB	Small t	A0219
119	HLNRKFLRK	0.834	6	SB	Small t	A0301
28	LMRKAYLKK	0.703	24	SB	Small t	A0301
50	KMKRMNTLY	0.654	42	SB	Small t	A0301
27	PLMRKAYLK	0.578	96	WB	Small t	A0301
114	QLRLRHLNR	0.447	397	WB	Small t	A0301
119	HLNRKFLRK	0.694	27	SB	Small t	A1101
27	PLMRKAYLK	0.576	98	WB	Small t	A1101
159	QIIGETPFR	0.516	187	WB	Small t	A1101
32	AYLKKCKEF	0.708	23	SB	Small t	A2301
32	AYLKKCKEF	0.523	174	WB	Small t	A2402
32	AYLKKCKEF	0.859	4	SB	Small t	A2403
68	AHQPDFGTW	0.542	142	WB	Small t	A2403
8	ESMELMDLL	0.463	335	WB	Small t	A2601
163	ETPFRDLKL	0.795	9	SB	Small t	A2602
152	ETLQWWVQI	0.499	225	WB	Small t	A2602
8	ESMELMDLL	0.476	290	WB	Small t	A2602
50	KMKRMNTLY	0.576	98	WB	Small t	A2902
85	FPLCPDTLY	0.475	291	WB	Small t	A2902
28	LMRKAYLKK	0.830	6	SB	Small t	A3001
51	MKRMNTLYK	0.827	6	SB	Small t	A3001
36	KCKEFHPDK	0.817	7	SB	Small t	A3001
114	QLRLRHLNR	0.516	187	WB	Small t	A3001
50	KMKRMNTLY	0.501	220	WB	Small t	A3001
119	HLNRKFLRK	0.445	405	WB	Small t	A3001
27	PLMRKAYLK	0.439	431	WB	Small t	A3001

52	KRMNTLYKK	0.435	453	WB	Small t	A3001
50	KMKRMNTLY	0.561	115	WB	Small t	A3002
118	RHLNRKFLR	0.820	7	SB	Small t	A3101
110	CMLCQLRLR	0.649	44	SB	Small t	A3101
114	QLRLRHLNR	0.628	56	WB	Small t	A3101
50	KMKRMNTLY	0.540	144	WB	Small t	A3101
119	HLNRKFLRK	0.514	191	WB	Small t	A3101
28	LMRKAYLKK	0.436	447	WB	Small t	A3101
114	QLRLRHLNR	0.699	25	SB	Small t	A3301
159	QIIGETPFR	0.822	6	SB	Small t	A6801
108	CPCMLCQLR	0.553	125	WB	Small t	A6801
8	ESMELMDLL	0.767	12	SB	Small t	A6802
139	DCFTQWFGL	0.659	40	SB	Small t	A6802
73	FGTWNSSEV	0.580	94	WB	Small t	A6802
152	ETLQWWVQI	0.522	175	WB	Small t	A6802
134	DCYCIDCFT	0.491	247	WB	Small t	A6802
163	ETPFRDLKL	0.490	247	WB	Small t	A6802
152	ETLQWWVQI	0.832	6	SB	Small t	A6901
8	ESMELMDLL	0.609	68	WB	Small t	A6901
91	TLYCKEWPI	0.506	210	WB	Small t	A6901
130	LVWIDCYCI	0.492	244	WB	Small t	A6901
21	AAWGNLPLM	0.483	267	WB	Small t	A6901
20	RAAWGNLPL	0.721	20	SB	Small t	B0702
26	LPLMRKAYL	0.719	20	SB	Small t	B0702
103	KPSVHCPCM	0.431	472	WB	Small t	B0702
158	VQIIGETPF	0.615	64	WB	Small t	B1501
50	KMKRMNTLY	0.561	115	WB	Small t	B1501
116	RLRHLNRKF	0.503	216	WB	Small t	B1501
20	RAAWGNLPL	0.444	411	WB	Small t	B1501
10	MELMDLLGL	0.722	20	SB	Small t	B1801
150	TEETLQWWV	0.497	230	WB	Small t	B1801
79	SEVCADFPL	0.470	308	WB	Small t	B1801
52	KRMNTLYKK	0.656	41	SB	Small t	B2705
85	FPLCPDTLY	0.805	8	SB	Small t	B3501
128	EPLVWIDCY	0.750	14	SB	Small t	B3501
20	RAAWGNLPL	0.618	62	WB	Small t	B3501
21	AAWGNLPLM	0.545	137	WB	Small t	B3501
103	KPSVHCPCM	0.451	377	WB	Small t	B3501
10	MELMDLLGL	0.751	14	SB	Small t	B4001
79	SEVCADFPL	0.738	16	SB	Small t	B4001
7	EESMELMDL	0.561	115	WB	Small t	B4001
18	LERAAWGNL	0.497	231	WB	Small t	B4001
79	SEVCADFPL	0.455	365	WB	Small t	B4002
79	SEVCADFPL	0.591	83	WB	Small t	B4403
151	EETLQWWVQ	0.463	334	WB	Small t	B4403
85	FPLCPDTLY	0.710	23	SB	Small t	B5301
128	EPLVWIDCY	0.651	43	SB	Small t	B5301

26	LPLMRKAYL	0.625	57	WB	Small t	B5301
97	WPICSKKPS	0.548	132	WB	Small t	B5401
149	LTEETLQWW	0.564	112	WB	Small t	B5701
124	FLRKEPLVW	0.534	154	WB	Small t	B5801
20	RAAWGNLPL	0.460	344	WB	Small t	B5801
	10-mers					
124	FLRKEPLVWI	0.574	100	WB	Small t	A0201
56	TLYKKMEQDV	0.485	263	WB	Small t	A0201
12	LMDLLGLERA	0.456	361	WB	Small t	A0201
3	VLNREESMEL	0.434	454	WB	Small t	A0201
111	MLCQLRLRHL	0.647	45	SB	Small t	A0202
124	FLRKEPLVWI	0.608	69	WB	Small t	A0202
12	LMDLLGLERA	0.607	70	WB	Small t	A0202
3	VLNREESMEL	0.562	114	WB	Small t	A0202
56	TLYKKMEQDV	0.516	187	WB	Small t	A0202
145	FGLDLTEETL	0.516	188	WB	Small t	A0202
9	SMELMDLLGL	0.507	206	WB	Small t	A0202
25	NLPLMRKAYL	0.483	269	WB	Small t	A0202
124	FLRKEPLVWI	0.870	4	SB	Small t	A0203
56	TLYKKMEQDV	0.707	23	SB	Small t	A0203
3	VLNREESMEL	0.666	37	SB	Small t	A0203
111	MLCQLRLRHL	0.549	131	WB	Small t	A0203
12	LMDLLGLERA	0.468	314	WB	Small t	A0203
9	SMELMDLLGL	0.462	338	WB	Small t	A0203
116	RLRHLNRKFL	0.429	484	WB	Small t	A0203
149	LTEETLQWWV	0.571	104	WB	Small t	A0204
3	VLNREESMEL	0.557	120	WB	Small t	A0204
124	FLRKEPLVWI	0.500	223	WB	Small t	A0204
149	LTEETLQWWV	0.581	93	WB	Small t	A0206
154	LQWWVQIIGE	0.521	177	WB	Small t	A0206
20	RAAWGNLPLM	0.518	184	WB	Small t	A0206
142	TQWFGLDLTE	0.463	334	WB	Small t	A0206
124	FLRKEPLVWI	0.430	474	WB	Small t	A0206
56	TLYKKMEQDV	0.875	3	SB	Small t	A0211
3	VLNREESMEL	0.824	6	SB	Small t	A0211
149	LTEETLQWWV	0.779	10	SB	Small t	A0211
12	LMDLLGLERA	0.757	13	SB	Small t	A0211
124	FLRKEPLVWI	0.715	21	SB	Small t	A0211
9	SMELMDLLGL	0.706	24	SB	Small t	A0211
111	MLCQLRLRHL	0.689	28	SB	Small t	A0211
25	NLPLMRKAYL	0.682	31	SB	Small t	A0211
129	PLVWIDCYCI	0.681	31	SB	Small t	A0211
116	RLRHLNRKFL	0.554	124	WB	Small t	A0211
146	GLDLTEETLQ	0.516	188	WB	Small t	A0211
17	GLERAAWGNL	0.502	219	WB	Small t	A0211
145	FGLDLTEETL	0.451	381	WB	Small t	A0211
56	TLYKKMEQDV	0.893	3	SB	Small t	A0212
3	VLNREESMEL	0.788	9	SB	Small t	A0212
124	FLRKEPLVWI	0.756	13	SB	Small t	A0212
149	LTEETLQWWV	0.727	19	SB	Small t	A0212
12	LMDLLGLERA	0.604	72	WB	Small t	A0212

111	MLCQLRLRHL	0.584	90	WB	Small t A0212
9	SMELMDLLGL	0.579	95	WB	Small t A0212
145	FGLDLTEETL	0.484	264	WB	Small t A0212
25	NLPLMRKAYL	0.477	287	WB	Small t A0212
116	RLRHLNRKFL	0.449	386	WB	Small t A0212
17	GLERAAWGNL	0.430	474	WB	Small t A0212
56	TLYKKMEQDV	0.842	5	SB	Small t A0216
3	VLNREESMEL	0.768	12	SB	Small t A0216
25	NLPLMRKAYL	0.703	24	SB	Small t A0216
124	FLRKEPLVWI	0.687	29	SB	Small t A0216
149	LTEETLQWWV	0.632	53	WB	Small t A0216
111	MLCQLRLRHL	0.627	56	WB	Small t A0216
116	RLRHLNRKFL	0.566	110	WB	Small t A0216
17	GLERAAWGNL	0.545	137	WB	Small t A0216
129	PLVWIDCYCI	0.522	175	WB	Small t A0216
12	LMDLLGLERA	0.484	265	WB	Small t A0216
9	SMELMDLLGL	0.468	316	WB	Small t A0216
149	LTEETLQWWV	0.627	56	WB	Small t A0219
3	VLNREESMEL	0.573	101	WB	Small t A0219
56	TLYKKMEQDV	0.570	104	WB	Small t A0219
124	FLRKEPLVWI	0.551	128	WB	Small t A0219
12	LMDLLGLERA	0.486	260	WB	Small t A0219
50	KMKRMNTLYK	0.754	14	SB	Small t A0301
118	RHLNRKFLRK	0.678	32	SB	Small t A0301
27	PLMRKAYLKK	0.663	38	SB	Small t A0301
114	QLRLRHLNRK	0.562	114	WB	Small t A0301
22	AWGNLPLMRK	0.533	156	WB	Small t A0301
26	LPLMRKAYLK	0.500	222	WB	Small t A0301
50	KMKRMNTLYK	0.700	25	SB	Small t A1101
27	PLMRKAYLKK	0.478	284	WB	Small t A1101
21	AAWGNLPLMR	0.475	293	WB	Small t A1101
22	AWGNLPLMRK	0.449	387	WB	Small t A1101
86	PLCPDTLYCK	0.444	410	WB	Small t A1101
135	CYCIDCFTQW	0.623	58	WB	Small t A2301
57	LYKKMEQDVK	0.531	160	WB	Small t A2301
136	YCIDCFTQWF	0.433	463	WB	Small t A2301
135	CYCIDCFTQW	0.616	63	WB	Small t A2403
123	KFLRKEPLVW	0.549	132	WB	Small t A2403
64	DVKVAHQPDF	0.665	37	SB	Small t A2602
152	ETLQWWVQII	0.483	269	WB	Small t A2602
84	DFPLCPDTLY	0.458	353	WB	Small t A2902
50	KMKRMNTLYK	0.848	5	SB	Small t A3001
114	QLRLRHLNRK	0.729	18	SB	Small t A3001
51	MKRMNTLYKK	0.685	30	SB	Small t A3001
27	PLMRKAYLKK	0.500	224	WB	Small t A3001
116	RLRHLNRKFL	0.497	231	WB	Small t A3001
29	MRKAYLKKCK	0.488	255	WB	Small t A3001
117	LRHLNRKFLR	0.676	33	SB	Small t A3101
113	CQLRLRHLNR	0.674	34	SB	Small t A3101
50	KMKRMNTLYK	0.640	49	SB	Small t A3101
51	MKRMNTLYKK	0.468	316	WB	Small t A3101

118	RHLNRKFLRK	0.446	400	WB	Small t	A3101
11	ELMDLLGLER	0.512	196	WB	Small t	A3301
117	LRHLNRKFLR	0.430	476	WB	Small t	A3301
11	ELMDLLGLER	0.720	20	SB	Small t	A6801
90	DTLYCKEWPI	0.574	99	WB	Small t	A6802
152	ETLQWWVQII	0.456	358	WB	Small t	A6802
19	ERAAWGNLPL	0.452	375	WB	Small t	A6802
152	ETLQWWVQII	0.795	9	SB	Small t	A6901
90	DTLYCKEWPI	0.586	88	WB	Small t	A6901
149	LTEETLQWWV	0.575	98	WB	Small t	A6901
97	WPICSKKPSV	0.518	184	WB	Small t	A6901
103	KPSVHCPCML	0.703	24	SB	Small t	B0702
97	WPICSKKPSV	0.563	113	WB	Small t	B0702
116	RLRHLNRKFL	0.471	304	WB	Small t	B0702
157	WVQIIGETPF	0.540	145	WB	Small t	B1501
52	KRMNTLYKKM	0.591	83	WB	Small t	B2705
157	WVQIIGETPF	0.638	50	WB	Small t	B3501
20	RAAWGNLPLM	0.595	80	WB	Small t	B3501
136	YCIDCFTQWF	0.429	483	WB	Small t	B3501
19	ERAAWGNLPL	0.539	147	WB	Small t	B3901
6	REESMELMDL	0.707	23	SB	Small t	B4001
162	GETPFRDLKL	0.618	62	WB	Small t	B4001
7	EESMELMDLL	0.488	253	WB	Small t	B4001
7	EESMELMDLL	0.482	271	WB	Small t	B4002
127	KEPLVWIDCY	0.429	481	WB	Small t	B4402
151	EETLQWWVQI	0.495	235	WB	Small t	B4403
127	KEPLVWIDCY	0.434	456	WB	Small t	B4403
97	WPICSKKPSV	0.434	454	WB	Small t	B5101
97	WPICSKKPSV	0.735	17	SB	Small t	B5401
26	LPLMRKAYLK	0.511	197	WB	Small t	B5401
67	VAHQPDFGTW	0.448	393	WB	Small t	B5701
123	KFLRKEPLVW	0.620	60	WB	Small t	B5801
67	VAHQPDFGTW	0.537	149	WB	Small t	B5801
20	RAAWGNLPLM	0.485	263	WB	Small t	B5801
31	KAYLKKCKEF	0.431	473	WB	Small t	B5801
	11-mers					
11	ELMDLLGLERA	0.458	351	WB	Small t	A0201
2	KVLNREESMEL	0.432	467	WB	Small t	A0201
11	ELMDLLGLERA	0.582	92	WB	Small t	A0202
137	CIDCFTQWFGL	0.516	187	WB	Small t	A0202
3	VLNREESMELM	0.491	245	WB	Small t	A0202
148	DLTEETLQWWV	0.445	404	WB	Small t	A0202

11	ELMDLLGLERA	0.652	42	SB	Small t A0203
110	CMLCQLRLRHL	0.520	180	WB	Small t A0203
3	VLNREESMELM	0.473	298	WB	Small t A0203
105	SVHCPCMLCQL	0.449	389	WB	Small t A0203
2	KVLNREESMEL	0.525	170	WB	Small t A0204
148	DLTEETLQWWV	0.453	372	WB	Small t A0204
105	SVHCPCMLCQL	0.450	384	WB	Small t A0204
2	KVLNREESMEL	0.620	61	WB	Small t A0206
154	LQWWVQIIGET	0.600	75	WB	Small t A0206
137	CIDCFTQWFGL	0.565	110	WB	Small t A0206
142	TQWFGLDLTEE	0.519	182	WB	Small t A0206
132	WIDCYCIDCFT	0.435	452	WB	Small t A0206
148	DLTEETLQWWV	0.957	1	SB	Small t A0211
11	ELMDLLGLERA	0.815	7	SB	Small t A0211
137	CIDCFTQWFGL	0.698	26	SB	Small t A0211
12	LMDLLGLERAA	0.669	35	SB	Small t A0211
2	KVLNREESMEL	0.597	77	WB	Small t A0211
105	SVHCPCMLCQL	0.539	146	WB	Small t A0211
3	VLNREESMELM	0.535	153	WB	Small t A0211
148	DLTEETLQWWV	0.806	8	SB	Small t A0212
11	ELMDLLGLERA	0.654	42	SB	Small t A0212
12	LMDLLGLERAA	0.577	96	WB	Small t A0212
137	CIDCFTQWFGL	0.551	128	WB	Small t A0212
3	VLNREESMELM	0.514	192	WB	Small t A0212
2	KVLNREESMEL	0.481	273	WB	Small t A0212
148	DLTEETLQWWV	0.886	3	SB	Small t A0216
11	ELMDLLGLERA	0.650	43	SB	Small t A0216
2	KVLNREESMEL	0.514	191	WB	Small t A0216
105	SVHCPCMLCQL	0.496	233	WB	Small t A0216
137	CIDCFTQWFGL	0.440	427	WB	Small t A0216
148	DLTEETLQWWV	0.849	5	SB	Small t A0219
11	ELMDLLGLERA	0.602	73	WB	Small t A0219
137	CIDCFTQWFGL	0.566	109	WB	Small t A0219
50	KMKRMNTLYKK	0.667	36	SB	Small t A0301
116	RLRHLNRKFLR	0.645	46	SB	Small t A0301
56	TLYKKMEQDVK	0.645	46	SB	Small t A0301
21	AAWGNLPLMRK	0.508	205	WB	Small t A0301
28	LMRKAYLKKCK	0.454	369	WB	Small t A0301
160	IIGETPFRDLK	0.432	464	WB	Small t A0301
21	AAWGNLPLMRK	0.742	16	SB	Small t A1101
56	TLYKKMEQDVK	0.640	49	SB	Small t A1101
50	KMKRMNTLYKK	0.634	52	WB	Small t A1101
160	IIGETPFRDLK	0.632	53	WB	Small t A1101
113	CQLRLRHLNRK	0.537	149	WB	Small t A1101
20	RAAWGNLPLMR	0.531	160	WB	Small t A1101
135	CYCIDCFTQWF	0.785	10	SB	Small t A2301
131	VWIDCYCIDCF	0.697	26	SB	Small t A2301
92	LYCKEWPICSK	0.544	139	WB	Small t A2301
156	WWVQIIGETPF	0.530	161	WB	Small t A2301
75	TWNSSEVCADF	0.493	240	WB	Small t A2301
131	VWIDCYCIDCF	0.708	23	SB	Small t A2402

135	CYCIDCFTQWF	0.672	34	SB	Small t A2402
156	WWVQIIGETPF	0.515	190	WB	Small t A2402
123	KFLRKEPLVWI	0.489	251	WB	Small t A2402
75	TWNSSEVCADF	0.462	339	WB	Small t A2402
135	CYCIDCFTQWF	0.775	11	SB	Small t A2403
123	KFLRKEPLVWI	0.525	170	WB	Small t A2403
75	TWNSSEVCADF	0.428	485	WB	Small t A2403
8	ESMELMDLLGL	0.474	297	WB	Small t A2601
159	QIIGETPFRDL	0.618	62	WB	Small t A2602
8	ESMELMDLLGL	0.433	462	WB	Small t A2602
50	KMKRMNTLYKK	0.760	13	SB	Small t A3001
28	LMRKAYLKKCK	0.745	15	SB	Small t A3001
116	RLRHLNRKFLR	0.667	36	SB	Small t A3001
117	LRHLNRKFLRK	0.531	160	WB	Small t A3001
34	LKKCKEFHPDK	0.429	482	WB	Small t A3001
116	RLRHLNRKFLR	0.853	4	SB	Small t A3101
50	KMKRMNTLYKK	0.838	5	SB	Small t A3101
20	RAAWGNLPLMR	0.617	63	WB	Small t A3101
157	WVQIIGETPFR	0.496	232	WB	Small t A3101
112	LCQLRLRHLNR	0.451	380	WB	Small t A3101
31	KAYLKKCKEFH	0.448	392	WB	Small t A3101
113	CQLRLRHLNRK	0.434	458	WB	Small t A3101
28	LMRKAYLKKCK	0.433	461	WB	Small t A3101
116	RLRHLNRKFLR	0.594	80	WB	Small t A3301
157	WVQIIGETPFR	0.716	21	SB	Small t A6801
20	RAAWGNLPLMR	0.562	114	WB	Small t A6801
56	TLYKKMEQDVK	0.549	131	WB	Small t A6801
25	NLPLMRKAYLK	0.482	272	WB	Small t A6801
108	CPCMLCQLRLR	0.467	319	WB	Small t A6801
8	ESMELMDLLGL	0.653	42	SB	Small t A6802
77	NSSEVCADFPL	0.649	44	SB	Small t A6802
11	ELMDLLGLERA	0.570	105	WB	Small t A6802
105	SVHCPCMLCQL	0.506	209	WB	Small t A6802
137	CIDCFTQWFGL	0.468	315	WB	Small t A6802
128	EPLVWIDCYCI	0.606	71	WB	Small t A6901
8	ESMELMDLLGL	0.560	116	WB	Small t A6901
11	ELMDLLGLERA	0.539	145	WB	Small t A6901
148	DLTEETLQWWV	0.482	273	WB	Small t A6901
55	NTLYKKMEQDV	0.432	464	WB	Small t A6901
114	QLRLRHLNRKF	0.463	333	WB	Small t B0801
114	QLRLRHLNRKF	0.473	298	WB	Small t B1501
18	LERAAWGNLPL	0.572	102	WB	Small t B1801
41	HPDKGGDEDKM	0.545	136	WB	Small t B3501
97	WPICSKKPSVH	0.529	164	WB	Small t B3501
156	WWVQIIGETPF	0.482	270	WB	Small t B3501
6	REESMELMDLL	0.673	34	SB	Small t B4001
18	LERAAWGNLPL	0.630	54	WB	Small t B4001
47	DEDKMKRMNTL	0.434	458	WB	Small t B4001
6	REESMELMDLL	0.511	198	WB	Small t B4002

151 EETLQWWVQII	0.500	224	WB	Small t	B4002
128 EPLVWIDCYCI	0.605	72	WB	Small t	B5101
128 EPLVWIDCYCI	0.529	163	WB	Small t	B5301
85 FPLCPDTLYCK	0.471	304	WB	Small t	B5401
66 KVAHQPDFGTW	0.658	40	SB	Small t	B5801
122 RKFLRKEPLVW	0.499	225	WB	Small t	B5801

Preferred BK virus fragments of large T antigen capable of interacting with one or more MHC class 1 molecules are listed in Table M.

Table M: Prediction of BK virus Large T protein specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
77	NSSEVPTY	0.514	193	WB	Large T	A0101
611	YTFSRMKY	0.480	276	WB	Large T	A0101
175	KLMEKYSV	0.847	5	SB	Large T	A0201
388	YMAGVAWL	0.833	6	SB	Large T	A0201
287	FLLLGMYL	0.807	8	SB	Large T	A0201
501	YLDGSVKV	0.800	8	SB	Large T	A0201
272	KLITEYAV	0.733	18	SB	Large T	A0201
469	YMVVFEDV	0.711	22	SB	Large T	A0201
579	LLIWFRPV	0.705	24	SB	Large T	A0201
372	KMDLIFGA	0.695	27	SB	Large T	A0201
155	RTLACFAV	0.663	38	SB	Large T	A0201
293	YLEFQYNV	0.656	41	SB	Large T	A0201
527	VTMNEYPV	0.629	55	WB	Large T	A0201
563	FLLEKRIL	0.620	61	WB	Large T	A0201
322	FANAIIFA	0.612	66	WB	Large T	A0201
231	YLLYSALT	0.611	67	WB	Large T	A0201
557	SLQNSEFL	0.608	69	WB	Large T	A0201
11	ELMDLLGL	0.599	76	WB	Large T	A0201
215	KLCTFSFL	0.590	84	WB	Large T	A0201
457	RLTFELGV	0.587	86	WB	Large T	A0201
398	LLPKMDSV	0.582	91	WB	Large T	A0201
465	AIDQYMVV	0.565	111	WB	Large T	A0201
369	ILDKMDLI	0.551	128	WB	Large T	A0201
74	GTWNSSEV	0.542	141	WB	Large T	A0201
603	RLDSEISM	0.535	153	WB	Large T	A0201
569	ILQSGMTL	0.529	164	WB	Large T	A0201
573	GMTLLLLL	0.519	181	WB	Large T	A0201
146	FLSQAVFS	0.495	234	WB	Large T	A0201
21	AAWGNLPL	0.473	297	WB	Large T	A0201
448	ALNVNLPM	0.468	316	WB	Large T	A0201
609	SMYTFSRM	0.459	347	WB	Large T	A0201
574	MTLLLLLI	0.458	350	WB	Large T	A0201
60	KMEQDVKV	0.452	375	WB	Large T	A0201
388	YMAGVAWL	0.861	4	SB	Large T	A0202
175	KLMEKYSV	0.858	4	SB	Large T	A0202
293	YLEFQYNV	0.811	7	SB	Large T	A0202
287	FLLLGMYL	0.800	8	SB	Large T	A0202
272	KLITEYAV	0.772	11	SB	Large T	A0202
11	ELMDLLGL	0.762	13	SB	Large T	A0202
146	FLSQAVFS	0.740	16	SB	Large T	A0202
322	FANAIIFA	0.740	16	SB	Large T	A0202
215	KLCTFSFL	0.732	18	SB	Large T	A0202
398	LLPKMDSV	0.721	20	SB	Large T	A0202
501	YLDGSVKV	0.716	21	SB	Large T	A0202
557	SLQNSEFL	0.712	22	SB	Large T	A0202
570	LQSGMTLL	0.696	26	SB	Large T	A0202
372	KMDLIFGA	0.672	34	SB	Large T	A0202

457	RLTFELGV	0.666	37	SB	Large T	A0202
573	GMTLLLLL	0.655	41	SB	Large T	A0202
579	LLIWFRPV	0.643	47	SB	Large T	A0202
9	SMELMDLL	0.628	56	WB	Large T	A0202
469	YMVVFEDV	0.606	70	WB	Large T	A0202
558	LQNSEFLL	0.596	78	WB	Large T	A0202
563	FLLEKRIL	0.593	81	WB	Large T	A0202
50	KMKRMNTL	0.586	88	WB	Large T	A0202
369	ILDKMDLI	0.585	89	WB	Large T	A0202
391	GVAWLHCL	0.577	96	WB	Large T	A0202
491	GINNLDSL	0.576	98	WB	Large T	A0202
184	FISRHMCA	0.571	103	WB	Large T	A0202
514	HLNKRTQI	0.561	115	WB	Large T	A0202
377	FGAHGNAV	0.549	131	WB	Large T	A0202
569	ILQSGMTL	0.546	135	WB	Large T	A0202
527	VTMNEYPV	0.533	156	WB	Large T	A0202
226	GVNKEYLL	0.525	171	WB	Large T	A0202
448	ALNVNLPM	0.512	196	WB	Large T	A0202
355	HMTREEML	0.510	200	WB	Large T	A0202
60	KMEQDVKV	0.505	211	WB	Large T	A0202
27	PLMRKAYL	0.488	254	WB	Large T	A0202
603	RLDSEISM	0.481	276	WB	Large T	A0202
144	HQFLSQAV	0.472	301	WB	Large T	A0202
465	AIDQYMVV	0.458	353	WB	Large T	A0202
155	RTLACFAV	0.443	412	WB	Large T	A0202
609	SMYTFSRM	0.442	419	WB	Large T	A0202
464	VAIDQYMV	0.429	483	WB	Large T	A0202
388	YMAGVAWL	0.893	3	SB	Large T	A0203
579	LLIWFRPV	0.884	3	SB	Large T	A0203
175	KLMEKYSV	0.870	4	SB	Large T	A0203
501	YLDGSVKV	0.811	7	SB	Large T	A0203
457	RLTFELGV	0.781	10	SB	Large T	A0203
287	FLLLGMYL	0.780	10	SB	Large T	A0203
272	KLITEYAV	0.779	10	SB	Large T	A0203
398	LLPKMDSV	0.777	11	SB	Large T	A0203
293	YLEFQYNV	0.769	12	SB	Large T	A0203
50	KMKRMNTL	0.758	13	SB	Large T	A0203
469	YMVVFEDV	0.736	17	SB	Large T	A0203
11	ELMDLLGL	0.712	22	SB	Large T	A0203
569	ILQSGMTL	0.711	22	SB	Large T	A0203
322	FANAIIFA	0.697	26	SB	Large T	A0203
184	FISRHMCA	0.689	28	SB	Large T	A0203
514	HLNKRTQI	0.680	31	SB	Large T	A0203
609	SMYTFSRM	0.642	48	SB	Large T	A0203
563	FLLEKRIL	0.628	55	WB	Large T	A0203
372	KMDLIFGA	0.622	59	WB	Large T	A0203
570	LQSGMTLL	0.608	69	WB	Large T	A0203
215	KLCTFSFL	0.607	70	WB	Large T	A0203
391	GVAWLHCL	0.570	104	WB	Large T	A0203
448	ALNVNLPM	0.556	122	WB	Large T	A0203
188	HMCAGHNI	0.551	128	WB	Large T	A0203
527	VTMNEYPV	0.548	132	WB	Large T	A0203
573	GMTLLLLL	0.535	153	WB	Large T	A0203
520	QIFPPGLV	0.531	159	WB	Large T	A0203
146	FLSQAVFS	0.528	165	WB	Large T	A0203
144	HQFLSQAV	0.527	166	WB	Large T	A0203
491	GINNLDSL	0.526	168	WB	Large T	A0203
557	SLQNSEFL	0.517	186	WB	Large T	A0203
465	AIDQYMVV	0.513	193	WB	Large T	A0203
155	RTLACFAV	0.509	202	WB	Large T	A0203
464	VAIDQYMV	0.497	232	WB	Large T	A0203

551	KIYLRKSL	0.489	252	WB	Large T	A0203
369	ILDKMDLI	0.466	321	WB	Large T	A0203
654	SQVSDTSA	0.462	338	WB	Large T	A0203
231	YLLYSALT	0.453	372	WB	Large T	A0203
199	LTPHRHRV	0.447	394	WB	Large T	A0203
60	KMEQDVKV	0.429	484	WB	Large T	A0203
615	RMKYNICM	0.427	490	WB	Large T	A0203
175	KLMEKYSV	0.762	13	SB	Large T	A0204
388	YMAGVAWL	0.708	23	SB	Large T	A0204
272	KLITEYAV	0.652	43	SB	Large T	A0204
527	VTMNEYPV	0.635	52	WB	Large T	A0204
579	LLIWFRPV	0.627	56	WB	Large T	A0204
60	KMEQDVKV	0.615	64	WB	Large T	A0204
287	FLLLGMYL	0.601	75	WB	Large T	A0204
569	ILQSGMTL	0.572	102	WB	Large T	A0204
501	YLDGSVKV	0.571	104	WB	Large T	A0204
557	SLQNSEFL	0.565	110	WB	Large T	A0204
563	FLLEKRIL	0.554	124	WB	Large T	A0204
293	YLEFQYNV	0.537	149	WB	Large T	A0204
215	KLCTFSFL	0.534	154	WB	Large T	A0204
11	ELMDLLGL	0.521	178	WB	Large T	A0204
469	YMVVFEDV	0.512	195	WB	Large T	A0204
464	VAIDQYMV	0.512	196	WB	Large T	A0204
536	KTLQARFV	0.494	239	WB	Large T	A0204
155	RTLACFAV	0.475	293	WB	Large T	A0204
398	LLPKMDSV	0.460	345	WB	Large T	A0204
465	AIDQYMVV	0.459	349	WB	Large T	A0204
457	RLTFELGV	0.448	393	WB	Large T	A0204
50	KMKRMNTL	0.443	412	WB	Large T	A0204
175	KLMEKYSV	0.879	3	SB	Large T	A0206
155	RTLACFAV	0.822	6	SB	Large T	A0206
272	KLITEYAV	0.820	6	SB	Large T	A0206
579	LLIWFRPV	0.813	7	SB	Large T	A0206
287	FLLLGMYL	0.784	10	SB	Large T	A0206
654	SQVSDTSA	0.782	10	SB	Large T	A0206
501	YLDGSVKV	0.771	11	SB	Large T	A0206
388	YMAGVAWL	0.737	17	SB	Large T	A0206
469	YMVVFEDV	0.730	18	SB	Large T	A0206
267	KQVSWKLI	0.720	20	SB	Large T	A0206
144	HQFLSQAV	0.705	24	SB	Large T	A0206
372	KMDLIFGA	0.695	27	SB	Large T	A0206
570	LQSGMTLL	0.694	27	SB	Large T	A0206
296	FQYNVEEC	0.688	29	SB	Large T	A0206
457	RLTFELGV	0.678	32	SB	Large T	A0206
398	LLPKMDSV	0.673	34	SB	Large T	A0206
558	LQNSEFLL	0.665	37	SB	Large T	A0206
338	CQQAVDTV	0.654	42	SB	Large T	A0206
322	FANAIIFA	0.648	45	SB	Large T	A0206
465	AIDQYMVV	0.646	45	SB	Large T	A0206
74	GTWNSSEV	0.645	46	SB	Large T	A0206
527	VTMNEYPV	0.615	64	WB	Large T	A0206
293	YLEFQYNV	0.613	65	WB	Large T	A0206
11	ELMDLLGL	0.594	80	WB	Large T	A0206
536	KTLQARFV	0.593	81	WB	Large T	A0206
464	VAIDQYMV	0.572	102	WB	Large T	A0206
21	AAWGNLPL	0.571	104	WB	Large T	A0206
383	AVLEQYMA	0.539	146	WB	Large T	A0206
563	FLLEKRIL	0.534	155	WB	Large T	A0206
574	MTLLLLLI	0.517	185	WB	Large T	A0206
215	KLCTFSFL	0.512	195	WB	Large T	A0206

184	FISRHMCA	0.511	197	WB	Large T	A0206
519	TQIFPPGL	0.505	210	WB	Large T	A0206
377	FGAHGNAV	0.470	308	WB	Large T	A0206
335	KSICQQAV	0.469	311	WB	Large T	A0206
369	ILDKMDLI	0.464	328	WB	Large T	A0206
520	QIFPPGLV	0.458	352	WB	Large T	A0206
391	GVAWLHCL	0.457	355	WB	Large T	A0206
231	YLLYSALT	0.451	380	WB	Large T	A0206
569	ILQSGMTL	0.445	406	WB	Large T	A0206
339	QQAVDTVL	0.443	414	WB	Large T	A0206
146	FLSQAVFS	0.438	436	WB	Large T	A0206
169	AQILYKKL	0.435	453	WB	Large T	A0206
60	KMEQDVKV	0.427	490	WB	Large T	A0206
501	YLDGSVKV	0.977	1	SB	Large T	A0211
388	YMAGVAWL	0.963	1	SB	Large T	A0211
175	KLMEKYSV	0.945	1	SB	Large T	A0211
287	FLLLGMYL	0.937	1	SB	Large T	A0211
579	LLIWFRPV	0.922	2	SB	Large T	A0211
465	AIDQYMVV	0.919	2	SB	Large T	A0211
272	KLITEYAV	0.906	2	SB	Large T	A0211
11	ELMDLLGL	0.904	2	SB	Large T	A0211
398	LLPKMDSV	0.900	2	SB	Large T	A0211
457	RLTFELGV	0.899	2	SB	Large T	A0211
293	YLEFQYNV	0.897	3	SB	Large T	A0211
557	SLQNSEFL	0.882	3	SB	Large T	A0211
569	ILQSGMTL	0.870	4	SB	Large T	A0211
469	YMVVFEDV	0.866	4	SB	Large T	A0211
563	FLLEKRIL	0.862	4	SB	Large T	A0211
603	RLDSEISM	0.848	5	SB	Large T	A0211
60	KMEQDVKV	0.845	5	SB	Large T	A0211
369	ILDKMDLI	0.828	6	SB	Large T	A0211
573	GMTLLLLL	0.824	6	SB	Large T	A0211
215	KLCTFSFL	0.821	6	SB	Large T	A0211
520	QIFPPGLV	0.811	7	SB	Large T	A0211
609	SMYTFSRM	0.780	10	SB	Large T	A0211
372	KMDLIFGA	0.777	11	SB	Large T	A0211
464	VAIDQYMV	0.743	16	SB	Large T	A0211
14	DLLGLERA	0.725	19	SB	Large T	A0211
74	GTWNSSEV	0.720	20	SB	Large T	A0211
391	GVAWLHCL	0.719	20	SB	Large T	A0211
485	DLPSGHGI	0.719	21	SB	Large T	A0211
155	RTLACFAV	0.693	27	SB	Large T	A0211
442	DLCGGKAL	0.686	29	SB	Large T	A0211
231	YLLYSALT	0.682	31	SB	Large T	A0211
536	KTLQARFV	0.668	36	SB	Large T	A0211
355	HMTREEML	0.667	36	SB	Large T	A0211
27	PLMRKAYL	0.666	37	SB	Large T	A0211
406	IFDFLHCV	0.646	46	SB	Large T	A0211
514	HLNKRTQI	0.642	48	SB	Large T	A0211
21	AAWGNLPL	0.638	50	WB	Large T	A0211
9	SMELMDLL	0.635	51	WB	Large T	A0211
56	TLYKKMEQ	0.625	57	WB	Large T	A0211
188	HMCAGHNI	0.618	62	WB	Large T	A0211
576	LLLLLIWF	0.614	64	WB	Large T	A0211
146	FLSQAVFS	0.597	78	WB	Large T	A0211
383	AVLEQYMA	0.594	81	WB	Large T	A0211
405	VIFDFLHC	0.587	87	WB	Large T	A0211
344	TVLAKKRV	0.583	91	WB	Large T	A0211
50	KMKRMNTL	0.582	92	WB	Large T	A0211
288	LLLGMYLE	0.577	96	WB	Large T	A0211
448	ALNVNLPM	0.573	100	WB	Large T	A0211

368	HILDKMDL	0.570	104	WB	Large T	A0211
527	VTMNEYPV	0.561	115	WB	Large T	A0211
150	AVFSNRTL	0.555	122	WB	Large T	A0211
184	FISRHMCA	0.545	137	WB	Large T	A0211
199	LTPHRHRV	0.543	140	WB	Large T	A0211
551	KIYLRKSL	0.523	173	WB	Large T	A0211
3	VLNREESM	0.494	239	WB	Large T	A0211
491	GINNLDSL	0.485	262	WB	Large T	A0211
291	GMYLEFQY	0.468	315	WB	Large T	A0211
350	RVDTLHMT	0.466	322	WB	Large T	A0211
142	DLHQFLSQ	0.459	348	WB	Large T	A0211
401	KMDSVIFD	0.458	350	WB	Large T	A0211
673	HLCKGFQC	0.458	350	WB	Large T	A0211
289	LLGMYLEF	0.450	383	WB	Large T	A0211
577	LLLLIWFR	0.450	384	WB	Large T	A0211
439	GLLDLCGG	0.448	390	WB	Large T	A0211
501	YLDGSVKV	0.940	1	SB	Large T	A0212
388	YMAGVAWL	0.924	2	SB	Large T	A0212
175	KLMEKYSV	0.912	2	SB	Large T	A0212
287	FLLLGMYL	0.903	2	SB	Large T	A0212
398	LLPKMDSV	0.879	3	SB	Large T	A0212
469	YMVVFEDV	0.878	3	SB	Large T	A0212
293	YLEFQYNV	0.872	4	SB	Large T	A0212
579	LLIWFRPV	0.853	4	SB	Large T	A0212
563	FLLEKRIL	0.852	4	SB	Large T	A0212
272	KLITEYAV	0.852	4	SB	Large T	A0212
465	AIDQYMVV	0.843	5	SB	Large T	A0212
11	ELMDLLGL	0.842	5	SB	Large T	A0212
569	ILQSGMTL	0.821	6	SB	Large T	A0212
457	RLTFELGV	0.787	10	SB	Large T	A0212
557	SLQNSEFL	0.757	13	SB	Large T	A0212
609	SMYTFSRM	0.711	22	SB	Large T	A0212
464	VAIDQYMV	0.698	26	SB	Large T	A0212
60	KMEQDVKV	0.666	37	SB	Large T	A0212
355	HMTREEML	0.663	38	SB	Large T	A0212
603	RLDSEISM	0.662	38	SB	Large T	A0212
368	HILDKMDL	0.659	39	SB	Large T	A0212
3	VLNREESM	0.639	49	SB	Large T	A0212
184	FISRHMCA	0.635	52	WB	Large T	A0212
405	VIFDFLHC	0.629	55	WB	Large T	A0212
215	KLCTFSFL	0.615	64	WB	Large T	A0212
369	ILDKMDLI	0.609	68	WB	Large T	A0212
27	PLMRKAYL	0.597	78	WB	Large T	A0212
372	KMDLIFGA	0.588	86	WB	Large T	A0212
50	KMKRMNTL	0.579	94	WB	Large T	A0212
520	QIFPPGLV	0.577	96	WB	Large T	A0212
573	GMTLLLLL	0.577	96	WB	Large T	A0212
527	VTMNEYPV	0.571	104	WB	Large T	A0212
188	HMCAGHNI	0.546	135	WB	Large T	A0212
14	DLLGLERA	0.523	174	WB	Large T	A0212
442	DLCGGKAL	0.521	178	WB	Large T	A0212
74	GTWNSSEV	0.521	178	WB	Large T	A0212
56	TLYKKMEQ	0.520	180	WB	Large T	A0212
485	DLPSGHGI	0.518	183	WB	Large T	A0212
21	AAWGNLPL	0.511	197	WB	Large T	A0212
391	GVAWLHCL	0.511	199	WB	Large T	A0212
231	YLLYSALT	0.504	213	WB	Large T	A0212
288	LLLGMYLE	0.486	259	WB	Large T	A0212
514	HLNKRTQI	0.480	276	WB	Large T	A0212
199	LTPHRHRV	0.477	285	WB	Large T	A0212
155	RTLACFAV	0.476	290	WB	Large T	A0212

377	FGAHGNAV	0.461	340	WB	Large T	A0212
146	FLSQAVFS	0.442	418	WB	Large T	A0212
9	SMELMDLL	0.426	495	WB	Large T	A0212
501	YLDGSVKV	0.928	2	SB	Large T	A0216
388	YMAGVAWL	0.917	2	SB	Large T	A0216
175	KLMEKYSV	0.905	2	SB	Large T	A0216
398	LLPKMDSV	0.895	3	SB	Large T	A0216
287	FLLLGMYL	0.891	3	SB	Large T	A0216
293	YLEFQYNV	0.849	5	SB	Large T	A0216
557	SLQNSEFL	0.846	5	SB	Large T	A0216
569	ILQSGMTL	0.836	5	SB	Large T	A0216
272	KLITEYAV	0.832	6	SB	Large T	A0216
465	AIDQYMVV	0.829	6	SB	Large T	A0216
27	PLMRKAYL	0.829	6	SB	Large T	A0216
579	LLIWFRPV	0.804	8	SB	Large T	A0216
215	KLCTFSFL	0.784	10	SB	Large T	A0216
11	ELMDLLGL	0.740	16	SB	Large T	A0216
74	GTWNSSEV	0.734	17	SB	Large T	A0216
60	KMEQDVKV	0.732	18	SB	Large T	A0216
457	RLTFELGV	0.727	19	SB	Large T	A0216
469	YMVVFEDV	0.718	21	SB	Large T	A0216
563	FLLEKRIL	0.709	23	SB	Large T	A0216
520	QIFPPGLV	0.701	25	SB	Large T	A0216
514	HLNKRTQI	0.689	29	SB	Large T	A0216
369	ILDKMDLI	0.673	34	SB	Large T	A0216
56	TLYKKMEQ	0.662	38	SB	Large T	A0216
50	KMKRMNTL	0.651	43	SB	Large T	A0216
609	SMYTFSRM	0.647	45	SB	Large T	A0216
603	RLDSEISM	0.626	56	WB	Large T	A0216
355	HMTREEML	0.623	58	WB	Large T	A0216
21	AAWGNLPL	0.600	75	WB	Large T	A0216
442	DLCGGKAL	0.597	78	WB	Large T	A0216
573	GMTLLLLL	0.595	79	WB	Large T	A0216
464	VAIDQYMV	0.593	82	WB	Large T	A0216
344	TVLAKKRV	0.583	91	WB	Large T	A0216
199	LTPHRHRV	0.568	106	WB	Large T	A0216
14	DLLGLERA	0.566	109	WB	Large T	A0216
485	DLPSGHGI	0.550	130	WB	Large T	A0216
536	KTLQARFV	0.548	132	WB	Large T	A0216
9	SMELMDLL	0.532	158	WB	Large T	A0216
391	GVAWLHCL	0.522	176	WB	Large T	A0216
150	AVFSNRTL	0.516	187	WB	Large T	A0216
188	HMCAGHNI	0.512	195	WB	Large T	A0216
527	VTMNEYPV	0.506	210	WB	Large T	A0216
146	FLSQAVFS	0.504	213	WB	Large T	A0216
231	YLLYSALT	0.501	220	WB	Large T	A0216
491	GINNLDSL	0.476	290	WB	Large T	A0216
184	FISRHMCA	0.474	296	WB	Large T	A0216
551	KIYLRKSL	0.468	315	WB	Large T	A0216
155	RTLACFAV	0.465	327	WB	Large T	A0216
673	HLCKGFQC	0.463	334	WB	Large T	A0216
448	ALNVNLPM	0.442	418	WB	Large T	A0216
372	KMDLIFGA	0.442	419	WB	Large T	A0216
406	IFDFLHCV	0.433	460	WB	Large T	A0216
3	VLNREESM	0.429	482	WB	Large T	A0216
501	YLDGSVKV	0.939	1	SB	Large T	A0219
388	YMAGVAWL	0.930	2	SB	Large T	A0219
287	FLLLGMYL	0.835	5	SB	Large T	A0219
11	ELMDLLGL	0.807	8	SB	Large T	A0219
175	KLMEKYSV	0.800	8	SB	Large T	A0219

569	ILQSGMTL	0.780	10	SB	Large T	A0219
398	LLPKMDSV	0.713	22	SB	Large T	A0219
293	YLEFQYNV	0.711	22	SB	Large T	A0219
557	SLQNSEFL	0.660	39	SB	Large T	A0219
465	AIDQYMVV	0.659	39	SB	Large T	A0219
272	KLITEYAV	0.651	43	SB	Large T	A0219
21	AAWGNLPL	0.637	51	WB	Large T	A0219
457	RLTFELGV	0.599	76	WB	Large T	A0219
27	PLMRKAYL	0.589	85	WB	Large T	A0219
603	RLDSEISM	0.574	100	WB	Large T	A0219
369	ILDKMDLI	0.567	108	WB	Large T	A0219
469	YMVVFEDV	0.565	111	WB	Large T	A0219
579	LLIWFRPV	0.564	112	WB	Large T	A0219
563	FLLEKRIL	0.555	123	WB	Large T	A0219
485	DLPSGHGI	0.542	142	WB	Large T	A0219
74	GTWNSSEV	0.540	145	WB	Large T	A0219
464	VAIDQYMV	0.507	208	WB	Large T	A0219
355	HMTREEML	0.497	230	WB	Large T	A0219
372	KMDLIFGA	0.431	469	WB	Large T	A0219
406	IFDFLHCV	0.429	482	WB	Large T	A0219
573	GMTLLLLL	0.426	497	WB	Large T	A0219
53	RMNTLYKK	0.719	20	SB	Large T	A0301
232	LLYSALTR	0.673	34	SB	Large T	A0301
28	LMRKAYLK	0.671	35	SB	Large T	A0301
394	WLHCLLPK	0.536	150	WB	Large T	A0301
208	AINNFCQK	0.529	162	WB	Large T	A0301
161	AVYTTKEK	0.526	169	WB	Large T	A0301
577	LLLLIWFR	0.513	193	WB	Large T	A0301
365	RFNHILDK	0.512	196	WB	Large T	A0301
291	GMYLEFQY	0.507	207	WB	Large T	A0301
31	KAYLKKCK	0.506	210	WB	Large T	A0301
608	ISMYTFSR	0.489	252	WB	Large T	A0301
413	VVFNVPKR	0.483	270	WB	Large T	A0301
121	SQHSTPPK	0.481	274	WB	Large T	A0301
156	TLACFAVY	0.475	294	WB	Large T	A0301
222	LICKGVNK	0.438	435	WB	Large T	A0301
195	IIFFLTPH	0.434	456	WB	Large T	A0301
412	CVVFNVPK	0.428	486	WB	Large T	A0301
208	AINNFCQK	0.764	12	SB	Large T	A1101
161	AVYTTKEK	0.761	13	SB	Large T	A1101
121	SQHSTPPK	0.746	15	SB	Large T	A1101
325	AIIFAESK	0.737	17	SB	Large T	A1101
341	AVDTVLAK	0.732	18	SB	Large T	A1101
53	RMNTLYKK	0.727	19	SB	Large T	A1101
608	ISMYTFSR	0.721	20	SB	Large T	A1101
544	RQIDFRPK	0.709	23	SB	Large T	A1101
505	SVKVNLEK	0.695	27	SB	Large T	A1101
168	KAQILYKK	0.672	34	SB	Large T	A1101
412	CVVFNVPK	0.665	37	SB	Large T	A1101
669	SQELHLCK	0.657	40	SB	Large T	A1101
31	KAYLKKCK	0.639	49	SB	Large T	A1101
218	TFSFLICK	0.626	57	WB	Large T	A1101
413	VVFNVPKR	0.613	65	WB	Large T	A1101
537	TLQARFVR	0.609	68	WB	Large T	A1101
470	MVVFEDVK	0.604	72	WB	Large T	A1101
404	SVIFDFLH	0.596	79	WB	Large T	A1101
222	LICKGVNK	0.581	93	WB	Large T	A1101
560	NSEFLLEK	0.574	100	WB	Large T	A1101
611	YTFSRMKY	0.568	107	WB	Large T	A1101
148	SQAVFSNR	0.553	125	WB	Large T	A1101

450	NVNLPMER	0.526	168	WB	Large T	A1101
394	WLHCLLPK	0.499	226	WB	Large T	A1101
291	GMYLEFQY	0.497	231	WB	Large T	A1101
617	KYNICMGK	0.464	328	WB	Large T	A1101
247	ESIQGGLK	0.464	331	WB	Large T	A1101
577	LLLLIWFR	0.462	338	WB	Large T	A1101
52	KRMNTLYK	0.454	367	WB	Large T	A1101
678	FQCFKRPK	0.440	426	WB	Large T	A1101
28	LMRKAYLK	0.435	452	WB	Large T	A1101
365	RFNHILDK	0.427	494	WB	Large T	A1101
408	DFLHCVVF	0.671	35	SB	Large T	A2301
541	RFVRQIDF	0.664	37	SB	Large T	A2301
610	MYTFSRMK	0.660	39	SB	Large T	A2301
321	HFANAIIF	0.633	53	WB	Large T	A2301
172	LYKKLMEK	0.626	57	WB	Large T	A2301
104	LFCHEDMF	0.617	63	WB	Large T	A2301
500	DYLDGSVK	0.609	68	WB	Large T	A2301
582	WFRPVADF	0.608	69	WB	Large T	A2301
230	EYLLYSAL	0.601	75	WB	Large T	A2301
617	KYNICMGK	0.599	76	WB	Large T	A2301
205	RVSAINNF	0.504	214	WB	Large T	A2301
387	QYMAGVAW	0.502	219	WB	Large T	A2301
576	LLLLLIWF	0.493	241	WB	Large T	A2301
92	WWSSFNEK	0.492	243	WB	Large T	A2301
145	QFLSQAVF	0.489	252	WB	Large T	A2301
365	RFNHILDK	0.475	292	WB	Large T	A2301
556	KSLQNSEF	0.460	343	WB	Large T	A2301
159	CFAVYTTK	0.441	423	WB	Large T	A2301
230	EYLLYSAL	0.680	32	SB	Large T	A2402
145	QFLSQAVF	0.522	176	WB	Large T	A2402
408	DFLHCVVF	0.519	182	WB	Large T	A2402
531	EYPVPKTL	0.510	199	WB	Large T	A2402
321	HFANAIIF	0.507	206	WB	Large T	A2402
422	YWLFKGPI	0.506	210	WB	Large T	A2402
541	RFVRQIDF	0.460	344	WB	Large T	A2402
387	QYMAGVAW	0.445	405	WB	Large T	A2402
387	QYMAGVAW	0.768	12	SB	Large T	A2403
582	WFRPVADF	0.765	12	SB	Large T	A2403
145	QFLSQAVF	0.713	22	SB	Large T	A2403
541	RFVRQIDF	0.706	24	SB	Large T	A2403
321	HFANAIIF	0.691	28	SB	Large T	A2403
230	EYLLYSAL	0.591	83	WB	Large T	A2403
408	DFLHCVVF	0.567	108	WB	Large T	A2403
556	KSLQNSEF	0.546	135	WB	Large T	A2403
104	LFCHEDMF	0.497	230	WB	Large T	A2403
531	EYPVPKTL	0.496	233	WB	Large T	A2403
611	YTFSRMKY	0.680	31	SB	Large T	A2601
285	DVFLLLGM	0.588	86	WB	Large T	A2601
11	ELMDLLGL	0.486	259	WB	Large T	A2601
611	YTFSRMKY	0.903	2	SB	Large T	A2602
285	DVFLLLGM	0.810	7	SB	Large T	A2602
280	ETKCEDVF	0.737	17	SB	Large T	A2602
66	KVAHQPDF	0.563	112	WB	Large T	A2602
11	ELMDLLGL	0.500	224	WB	Large T	A2602
463	GVAIDQYM	0.486	261	WB	Large T	A2602
80	EVPTYGTE	0.485	262	WB	Large T	A2602

291	GMYLEFQY	0.680	31	SB	Large T	A2902
286	VFLLLGMY	0.624	58	WB	Large T	A2902
611	YTFSRMKY	0.617	63	WB	Large T	A2902
156	TLACFAVY	0.552	127	WB	Large T	A2902
270	SWKLITEY	0.500	223	WB	Large T	A2902
121	SQHSTPPK	0.836	5	SB	Large T	A3001
419	KRRYWLFK	0.811	7	SB	Large T	A3001
28	LMRKAYLK	0.805	8	SB	Large T	A3001
544	RQIDFRPK	0.771	11	SB	Large T	A3001
683	RPKTPPPK	0.740	16	SB	Large T	A3001
505	SVKVNLEK	0.732	18	SB	Large T	A3001
53	RMNTLYKK	0.672	34	SB	Large T	A3001
394	WLHCLLPK	0.669	36	SB	Large T	A3001
309	KDQPYHFK	0.647	45	SB	Large T	A3001
31	KAYLKKCK	0.628	55	WB	Large T	A3001
52	KRMNTLYK	0.620	60	WB	Large T	A3001
161	AVYTTKEK	0.613	65	WB	Large T	A3001
29	MRKAYLKK	0.612	66	WB	Large T	A3001
594	QSRIVEWK	0.594	80	WB	Large T	A3001
168	KAQILYKK	0.583	91	WB	Large T	A3001
549	RPKIYLRK	0.571	103	WB	Large T	A3001
172	LYKKLMEK	0.566	109	WB	Large T	A3001
130	KRKVEDPK	0.560	116	WB	Large T	A3001
617	KYNICMGK	0.549	131	WB	Large T	A3001
610	MYTFSRMK	0.541	142	WB	Large T	A3001
365	RFNHILDK	0.516	188	WB	Large T	A3001
196	IFFLTPHR	0.458	350	WB	Large T	A3001
208	AINNFCQK	0.450	382	WB	Large T	A3001
237	LTRDPYHI	0.443	416	WB	Large T	A3001
205	RVSAINNF	0.506	210	WB	Large T	A3002
611	YTFSRMKY	0.440	428	WB	Large T	A3002
577	LLLLIWFR	0.818	7	SB	Large T	A3101
53	RMNTLYKK	0.816	7	SB	Large T	A3101
608	ISMYTFSR	0.791	9	SB	Large T	A3101
537	TLQARFVR	0.773	11	SB	Large T	A3101
196	IFFLTPHR	0.772	11	SB	Large T	A3101
414	VFNVPKRR	0.682	31	SB	Large T	A3101
148	SQAVFSNR	0.678	32	SB	Large T	A3101
180	YSVTFISR	0.672	34	SB	Large T	A3101
676	KGFQCFKR	0.671	35	SB	Large T	A3101
413	VVFNVPKR	0.665	37	SB	Large T	A3101
617	KYNICMGK	0.648	45	SB	Large T	A3101
28	LMRKAYLK	0.646	46	SB	Large T	A3101
544	RQIDFRPK	0.646	46	SB	Large T	A3101
232	LLYSALTR	0.630	55	WB	Large T	A3101
168	KAQILYKK	0.618	62	WB	Large T	A3101
542	FVRQIDFR	0.590	84	WB	Large T	A3101
589	FSKDIQSR	0.590	84	WB	Large T	A3101
596	RIVEWKER	0.580	93	WB	Large T	A3101
198	FLTPHRHR	0.569	106	WB	Large T	A3101
172	LYKKLMEK	0.550	129	WB	Large T	A3101
365	RFNHILDK	0.540	145	WB	Large T	A3101
610	MYTFSRMK	0.532	157	WB	Large T	A3101
450	NVNLPMER	0.515	189	WB	Large T	A3101
31	KAYLKKCK	0.504	214	WB	Large T	A3101
208	AINNFCQK	0.461	339	WB	Large T	A3101
155	RTLACFAV	0.460	345	WB	Large T	A3101
121	SQHSTPPK	0.452	376	WB	Large T	A3101

577	LLLLIWFR	0.795	9	SB	Large T	A3301
196	IFFLTPHR	0.758	13	SB	Large T	A3301
608	ISMYTFSR	0.631	54	WB	Large T	A3301
450	NVNLPMER	0.631	54	WB	Large T	A3301
542	FVRQIDFR	0.628	55	WB	Large T	A3301
537	TLQARFVR	0.608	69	WB	Large T	A3301
343	DTVLAKKR	0.575	99	WB	Large T	A3301
180	YSVTFISR	0.574	100	WB	Large T	A3301
589	FSKDIQSR	0.535	152	WB	Large T	A3301
547	DFRPKIYL	0.526	169	WB	Large T	A3301
500	DYLDGSVK	0.521	178	WB	Large T	A3301
198	FLTPHRHR	0.504	215	WB	Large T	A3301
265	ETKQVSWK	0.447	397	WB	Large T	A3301
265	ETKQVSWK	0.836	5	SB	Large T	A6801
608	ISMYTFSR	0.827	6	SB	Large T	A6801
470	MVVFEDVK	0.812	7	SB	Large T	A6801
180	YSVTFISR	0.805	8	SB	Large T	A6801
343	DTVLAKKR	0.798	8	SB	Large T	A6801
412	CVVFNVPK	0.772	11	SB	Large T	A6801
450	NVNLPMER	0.771	11	SB	Large T	A6801
542	FVRQIDFR	0.764	12	SB	Large T	A6801
611	YTFSRMKY	0.753	14	SB	Large T	A6801
610	MYTFSRMK	0.746	15	SB	Large T	A6801
413	VVFNVPKR	0.728	19	SB	Large T	A6801
247	ESIQGGLK	0.662	38	SB	Large T	A6801
232	LLYSALTR	0.652	43	SB	Large T	A6801
589	FSKDIQSR	0.648	44	SB	Large T	A6801
537	TLQARFVR	0.632	53	WB	Large T	A6801
196	IFFLTPHR	0.626	57	WB	Large T	A6801
577	LLLLIWFR	0.606	71	WB	Large T	A6801
218	TFSFLICK	0.597	78	WB	Large T	A6801
560	NSEFLLEK	0.575	99	WB	Large T	A6801
325	AIIFAESK	0.570	105	WB	Large T	A6801
198	FLTPHRHR	0.567	108	WB	Large T	A6801
505	SVKVNLEK	0.553	126	WB	Large T	A6801
167	EKAQILYK	0.548	132	WB	Large T	A6801
148	SQAVFSNR	0.536	151	WB	Large T	A6801
159	CFAVYTTK	0.531	159	WB	Large T	A6801
161	AVYTTKEK	0.529	163	WB	Large T	A6801
208	AINNFCQK	0.516	188	WB	Large T	A6801
328	FAESKNQK	0.505	212	WB	Large T	A6801
596	RIVEWKER	0.471	306	WB	Large T	A6801
492	INNLDSLR	0.464	329	WB	Large T	A6801
156	TLACFAVY	0.458	351	WB	Large T	A6801
124	STPPKKKR	0.453	371	WB	Large T	A6801
275	TEYAVETK	0.432	465	WB	Large T	A6801
123	HSTPPKKK	0.429	482	WB	Large T	A6801
404	SVIFDFLH	0.427	492	WB	Large T	A6801
313	YHFKYHEK	0.426	496	WB	Large T	A6801
322	FANAIIFA	0.703	24	SB	Large T	A6802
520	QIFPPGLV	0.669	35	SB	Large T	A6802
155	RTLACFAV	0.653	42	SB	Large T	A6802
377	FGAHGNAV	0.634	52	WB	Large T	A6802
527	VTMNEYPV	0.617	63	WB	Large T	A6802
403	DSVIFDFL	0.603	73	WB	Large T	A6802
11	ELMDLLGL	0.583	90	WB	Large T	A6802
189	MCAGHNII	0.575	99	WB	Large T	A6802
8	ESMELMDL	0.563	113	WB	Large T	A6802
199	LTPHRHRV	0.555	123	WB	Large T	A6802
178	EKYSVTFI	0.531	160	WB	Large T	A6802

388	YMAGVAWL	0.523	174	WB	Large T	A6802
574	MTLLLLLI	0.480	278	WB	Large T	A6802
464	VAIDQYMV	0.479	281	WB	Large T	A6802
579	LLIWFRPV	0.477	286	WB	Large T	A6802
649	QSQCSSQV	0.455	365	WB	Large T	A6802
19	ERAAWGNL	0.434	456	WB	Large T	A6802
434	TTLAAGLL	0.431	470	WB	Large T	A6802
216	LCTFSFLI	0.428	489	WB	Large T	A6802
520	QIFPPGLV	0.711	22	SB	Large T	A6901
11	ELMDLLGL	0.667	36	SB	Large T	A6901
155	RTLACFAV	0.636	51	WB	Large T	A6901
574	MTLLLLLI	0.613	66	WB	Large T	A6901
527	VTMNEYPV	0.575	99	WB	Large T	A6901
434	TTLAAGLL	0.571	103	WB	Large T	A6901
501	YLDGSVKV	0.546	135	WB	Large T	A6901
74	GTWNSSEV	0.545	137	WB	Large T	A6901
464	VAIDQYMV	0.523	175	WB	Large T	A6901
322	FANAIIFA	0.514	192	WB	Large T	A6901
21	AAWGNLPL	0.513	193	WB	Large T	A6901
579	LLIWFRPV	0.508	205	WB	Large T	A6901
287	FLLLGMYL	0.504	214	WB	Large T	A6901
388	YMAGVAWL	0.494	238	WB	Large T	A6901
340	QAVDTVLA	0.464	328	WB	Large T	A6901
8	ESMELMDL	0.453	372	WB	Large T	A6901
458	LTFELGVA	0.433	462	WB	Large T	A6901
377	FGAHGNAV	0.431	472	WB	Large T	A6901
383	AVLEQYMA	0.426	499	WB	Large T	A6901
453	LPMERLTF	0.735	17	SB	Large T	B0702
417	VPKRRYWL	0.608	69	WB	Large T	B0702
399	LPKMDSVI	0.500	223	WB	Large T	B0702
21	AAWGNLPL	0.482	270	WB	Large T	B0702
139	FPSDLHQF	0.479	281	WB	Large T	B0702
26	LPLMRKAY	0.431	472	WB	Large T	B0702
417	VPKRRYWL	0.555	123	WB	Large T	B0801
50	KMKRMNTL	0.479	282	WB	Large T	B0801
33	YLKKCKEF	0.446	401	WB	Large T	B0801
205	RVSAINNF	0.544	139	WB	Large T	B1501
306	CQKKDQPY	0.511	199	WB	Large T	B1501
339	QQAVDTVL	0.504	214	WB	Large T	B1501
615	RMKYNICM	0.498	228	WB	Large T	B1501
33	YLKKCKEF	0.496	232	WB	Large T	B1501
388	YMAGVAWL	0.493	240	WB	Large T	B1501
611	YTFSRMKY	0.492	244	WB	Large T	B1501
291	GMYLEFQY	0.486	261	WB	Large T	B1501
144	HQFLSQAV	0.476	288	WB	Large T	B1501
50	KMKRMNTL	0.474	294	WB	Large T	B1501
156	TLACFAVY	0.469	311	WB	Large T	B1501
570	LQSGMTLL	0.441	424	WB	Large T	B1501
89	WESWWSSF	0.814	7	SB	Large T	B1801
455	MERLTFEL	0.686	29	SB	Large T	B1801
606	SEISMYTF	0.646	45	SB	Large T	B1801
177	MEKYSVTF	0.627	56	WB	Large T	B1801
363	TERFNHIL	0.449	388	WB	Large T	B1801
86	TEEWESWW	0.434	458	WB	Large T	B1801
52	KRMNTLYK	0.623	58	WB	Large T	B2705
567	KRILQSGM	0.555	122	WB	Large T	B2705

544	RQIDFRPK	0.533	155	WB	Large T	B2705
419	KRRYWLFK	0.506	209	WB	Large T	B2705
349	KRVDTLHM	0.461	341	WB	Large T	B2705
29	MRKAYLKK	0.430	477	WB	Large T	B2705
139	FPSDLHQF	0.796	9	SB	Large T	B3501
522	FPPGLVTM	0.773	11	SB	Large T	B3501
453	LPMERLTF	0.752	14	SB	Large T	B3501
26	LPLMRKAY	0.749	15	SB	Large T	B3501
235	SALTRDPY	0.599	76	WB	Large T	B3501
382	NAVLEQYM	0.558	119	WB	Large T	B3501
111	FASDEEAT	0.538	148	WB	Large T	B3501
156	TLACFAVY	0.533	156	WB	Large T	B3501
321	HFANAIIF	0.513	193	WB	Large T	B3501
21	AAWGNLPL	0.509	203	WB	Large T	B3501
77	NSSEVPTY	0.502	218	WB	Large T	B3501
98	EKWDEDLF	0.451	381	WB	Large T	B3501
145	QFLSQAVF	0.450	384	WB	Large T	B3501
89	WESWWSSF	0.445	407	WB	Large T	B3501
5	NREESMEL	0.555	123	WB	Large T	B3901
339	QQAVDTVL	0.464	330	WB	Large T	B3901
388	YMAGVAWL	0.429	483	WB	Large T	B3901
455	MERLTFEL	0.676	33	SB	Large T	B4001
363	TERFNHIL	0.626	57	WB	Large T	B4001
283	CEDVFLLL	0.595	80	WB	Large T	B4001
606	SEISMYTF	0.593	81	WB	Large T	B4001
6	REESMELM	0.511	197	WB	Large T	B4001
177	MEKYSVTF	0.487	257	WB	Large T	B4001
246	EESIQGGL	0.432	465	WB	Large T	B4001
606	SEISMYTF	0.568	107	WB	Large T	B4002
89	WESWWSSF	0.495	237	WB	Large T	B4002
166	KEKAQILY	0.489	250	WB	Large T	B4002
359	EEMLTERF	0.489	251	WB	Large T	B4002
246	EESIQGGL	0.464	328	WB	Large T	B4002
177	MEKYSVTF	0.454	367	WB	Large T	B4002
264	EETKQVSW	0.446	403	WB	Large T	B4002
6	REESMELM	0.433	463	WB	Large T	B4002
264	EETKQVSW	0.514	193	WB	Large T	B4402
606	SEISMYTF	0.472	303	WB	Large T	B4402
86	TEEWESWW	0.464	329	WB	Large T	B4402
166	KEKAQILY	0.461	342	WB	Large T	B4402
359	EEMLTERF	0.449	388	WB	Large T	B4402
606	SEISMYTF	0.549	131	WB	Large T	B4403
359	EEMLTERF	0.526	167	WB	Large T	B4403
359	EEMLTERF	0.512	196	WB	Large T	B4501
329	AESKNQKS	0.443	415	WB	Large T	B4501
246	EESIQGGL	0.433	460	WB	Large T	B4501
481	AESKDLPS	0.431	470	WB	Large T	B4501
522	FPPGLVTM	0.629	55	WB	Large T	B5101
453	LPMERLTF	0.621	60	WB	Large T	B5101
399	LPKMDSVI	0.598	77	WB	Large T	B5101
453	LPMERLTF	0.755	14	SB	Large T	B5301
139	FPSDLHQF	0.729	18	SB	Large T	B5301
26	LPLMRKAY	0.636	51	WB	Large T	B5301

399	LPKMDSVI	0.632	53	WB	Large T	B5301
522	FPPGLVTM	0.582	91	WB	Large T	B5301
522	FPPGLVTM	0.577	97	WB	Large T	B5401
322	FANAIIFA	0.511	198	WB	Large T	B5401
26	LPLMRKAY	0.482	271	WB	Large T	B5401
82	PTYGTEEW	0.517	186	WB	Large T	B5701
93	WSSFNEKW	0.678	32	SB	Large T	B5801
556	KSLQNSEF	0.602	74	WB	Large T	B5801
593	IQSRIVEW	0.573	101	WB	Large T	B5801
205	RVSAINNF	0.525	169	WB	Large T	B5801
82	PTYGTEEW	0.504	215	WB	Large T	B5801
66	KVAHQPDF	0.491	246	WB	Large T	B5801
16	LGLERAAW	0.439	430	WB	Large T	B5801
77	NSSEVPTY	0.431	469	WB	Large T	B5801
	9-mers					
603	RLDSEISMY	0.648	44	SB	Large T	A0101
226	GVNKEYLLY	0.477	286	WB	Large T	A0101
234	YSALTRDPY	0.471	304	WB	Large T	A0101
409	FLHCVVFNV	0.891	3	SB	Large T	A0201
405	VIFDFLHCV	0.842	5	SB	Large T	A0201
215	KLCTFSFLI	0.747	15	SB	Large T	A0201
198	FLTPHRHRV	0.693	27	SB	Large T	A0201
578	LLLIWFRPV	0.690	28	SB	Large T	A0201
384	VLEQYMAGV	0.680	31	SB	Large T	A0201
557	SLQNSEFLL	0.658	40	SB	Large T	A0201
397	CLLPKMDSV	0.639	49	SB	Large T	A0201
569	ILQSGMTLL	0.614	64	WB	Large T	A0201
175	KLMEKYSVT	0.580	94	WB	Large T	A0201
435	TLAAGLLDL	0.578	95	WB	Large T	A0201
361	MLTERFNHI	0.562	114	WB	Large T	A0201
579	LLIWFRPVA	0.505	212	WB	Large T	A0201
573	GMTLLLLLI	0.494	237	WB	Large T	A0201
368	HILDKMDLI	0.488	254	WB	Large T	A0201
621	CMGKCILDI	0.465	327	WB	Large T	A0201
394	WLHCLLPKM	0.443	412	WB	Large T	A0201
156	TLACFAVYT	0.437	440	WB	Large T	A0201
409	FLHCVVFNV	0.885	3	SB	Large T	A0202
198	FLTPHRHRV	0.824	6	SB	Large T	A0202
361	MLTERFNHI	0.774	11	SB	Large T	A0202
569	ILQSGMTLL	0.765	12	SB	Large T	A0202
405	VIFDFLHCV	0.742	16	SB	Large T	A0202
384	VLEQYMAGV	0.728	19	SB	Large T	A0202
494	NLDSLRDYL	0.687	29	SB	Large T	A0202
557	SLQNSEFLL	0.676	33	SB	Large T	A0202
570	LQSGMTLLL	0.676	33	SB	Large T	A0202
397	CLLPKMDSV	0.658	40	SB	Large T	A0202
402	MDSVIFDFL	0.642	48	SB	Large T	A0202
215	KLCTFSFLI	0.640	49	SB	Large T	A0202
497	SLRDYLDGS	0.630	54	WB	Large T	A0202
463	GVAIDQYMV	0.614	65	WB	Large T	A0202
435	TLAAGLLDL	0.605	71	WB	Large T	A0202
175	KLMEKYSVT	0.560	116	WB	Large T	A0202
573	GMTLLLLLI	0.558	119	WB	Large T	A0202
156	TLACFAVYT	0.554	124	WB	Large T	A0202
289	LLGMYLEFQ	0.542	142	WB	Large T	A0202

648	SQSQCSSQV	0.542	142	WB	Large T	A0202
391	GVAWLHCLL	0.529	163	WB	Large T	A0202
219	FSFLICKGV	0.528	165	WB	Large T	A0202
208	AINNFCQKL	0.524	173	WB	Large T	A0202
191	AGHNIIFFL	0.514	191	WB	Large T	A0202
111	FASDEEATA	0.506	208	WB	Large T	A0202
139	FPSDLHQFL	0.505	211	WB	Large T	A0202
236	ALTRDPYHI	0.501	220	WB	Large T	A0202
589	FSKDIQSRI	0.499	226	WB	Large T	A0202
526	LVTMNEYPV	0.493	240	WB	Large T	A0202
146	FLSQAVFSN	0.480	278	WB	Large T	A0202
578	LLLIWFRPV	0.466	321	WB	Large T	A0202
377	FGAHGNAVL	0.465	327	WB	Large T	A0202
458	LTFELGVAI	0.452	376	WB	Large T	A0202
572	SGMTLLLLL	0.450	385	WB	Large T	A0202
398	LLPKMDSVI	0.448	392	WB	Large T	A0202
368	HILDKMDLI	0.438	438	WB	Large T	A0202
409	FLHCVVFNV	0.911	2	SB	Large T	A0203
198	FLTPHRHRV	0.891	3	SB	Large T	A0203
361	MLTERFNHI	0.884	3	SB	Large T	A0203
384	VLEQYMAGV	0.838	5	SB	Large T	A0203
578	LLLIWFRPV	0.819	7	SB	Large T	A0203
397	CLLPKMDSV	0.815	7	SB	Large T	A0203
569	ILQSGMTLL	0.803	8	SB	Large T	A0203
405	VIFDFLHCV	0.796	9	SB	Large T	A0203
435	TLAAGLLDL	0.744	16	SB	Large T	A0203
175	KLMEKYSVT	0.694	27	SB	Large T	A0203
457	RLTFELGVA	0.683	30	SB	Large T	A0203
497	SLRDYLDGS	0.596	79	WB	Large T	A0203
579	LLIWFRPVA	0.575	99	WB	Large T	A0203
553	YLRKSLQNS	0.569	105	WB	Large T	A0203
215	KLCTFSFLI	0.566	108	WB	Large T	A0203
236	ALTRDPYHI	0.540	144	WB	Large T	A0203
375	LIFGAHGNA	0.540	145	WB	Large T	A0203
573	GMTLLLLLI	0.537	150	WB	Large T	A0203
570	LQSGMTLLL	0.528	165	WB	Large T	A0203
156	TLACFAVYT	0.527	166	WB	Large T	A0203
648	SQSQCSSQV	0.520	179	WB	Large T	A0203
391	GVAWLHCLL	0.517	185	WB	Large T	A0203
398	LLPKMDSVI	0.516	188	WB	Large T	A0203
394	WLHCLLPKM	0.513	194	WB	Large T	A0203
464	VAIDQYMVV	0.512	195	WB	Large T	A0203
188	HMCAGHNII	0.510	199	WB	Large T	A0203
519	TQIFPPGLV	0.506	210	WB	Large T	A0203
208	AINNFCQKL	0.501	220	WB	Large T	A0203
368	HILDKMDLI	0.496	232	WB	Large T	A0203
20	RAAWGNLPL	0.491	246	WB	Large T	A0203
53	RMNTLYKKM	0.490	249	WB	Large T	A0203
568	RILQSGMTL	0.485	263	WB	Large T	A0203
538	LQARFVRQI	0.458	352	WB	Large T	A0203
289	LLGMYLEFQ	0.456	360	WB	Large T	A0203
557	SLQNSEFLL	0.447	396	WB	Large T	A0203
596	RIVEWKERL	0.441	423	WB	Large T	A0203
463	GVAIDQYMV	0.432	464	WB	Large T	A0203
198	FLTPHRHRV	0.766	12	SB	Large T	A0204
409	FLHCVVFNV	0.744	15	SB	Large T	A0204
405	VIFDFLHCV	0.645	46	SB	Large T	A0204
578	LLLIWFRPV	0.640	48	SB	Large T	A0204
384	VLEQYMAGV	0.607	70	WB	Large T	A0204
464	VAIDQYMVV	0.564	111	WB	Large T	A0204

557	SLQNSEFLL	0.552	127	WB	Large T	A0204
59	KKMEQDVKV	0.514	191	WB	Large T	A0204
526	LVTMNEYPV	0.512	196	WB	Large T	A0204
435	TLAAGLLDL	0.489	251	WB	Large T	A0204
292	MYLEFQYNV	0.488	255	WB	Large T	A0204
569	ILQSGMTLL	0.485	264	WB	Large T	A0204
208	AINNFCQKL	0.474	296	WB	Large T	A0204
397	CLLPKMDSV	0.468	315	WB	Large T	A0204
175	KLMEKYSVT	0.464	329	WB	Large T	A0204
361	MLTERFNHI	0.447	395	WB	Large T	A0204
236	ALTRDPYHI	0.447	398	WB	Large T	A0204
215	KLCTFSFLI	0.445	404	WB	Large T	A0204
361	MLTERFNHI	0.848	5	SB	Large T	A0206
397	CLLPKMDSV	0.834	6	SB	Large T	A0206
409	FLHCVVFNV	0.819	7	SB	Large T	A0206
578	LLLIWFRPV	0.801	8	SB	Large T	A0206
198	FLTPHRHRV	0.793	9	SB	Large T	A0206
405	VIFDFLHCV	0.746	15	SB	Large T	A0206
544	RQIDFRPKI	0.739	16	SB	Large T	A0206
648	SQSQCSSQV	0.729	18	SB	Large T	A0206
384	VLEQYMAGV	0.692	27	SB	Large T	A0206
570	LQSGMTLLL	0.683	30	SB	Large T	A0206
596	RIVEWKERL	0.674	34	SB	Large T	A0206
568	RILQSGMTL	0.638	50	WB	Large T	A0206
20	RAAWGNLPL	0.634	52	WB	Large T	A0206
435	TLAAGLLDL	0.583	91	WB	Large T	A0206
215	KLCTFSFLI	0.560	116	WB	Large T	A0206
464	VAIDQYMVV	0.560	117	WB	Large T	A0206
368	HILDKMDLI	0.550	130	WB	Large T	A0206
339	QQAVDTVLA	0.549	131	WB	Large T	A0206
569	ILQSGMTLL	0.520	180	WB	Large T	A0206
111	FASDEEATA	0.520	180	WB	Large T	A0206
267	KQVSWKLIT	0.516	188	WB	Large T	A0206
579	LLIWFRPVA	0.507	206	WB	Large T	A0206
458	LTFELGVAI	0.503	216	WB	Large T	A0206
10	MELMDLLGL	0.496	233	WB	Large T	A0206
391	GVAWLHCLL	0.476	291	WB	Large T	A0206
287	FLLLGMYLE	0.473	298	WB	Large T	A0206
519	TQIFPPGLV	0.470	308	WB	Large T	A0206
288	LLLGMYLEF	0.469	312	WB	Large T	A0206
447	KALNVNLPM	0.457	357	WB	Large T	A0206
21	AAWGNLPLM	0.457	357	WB	Large T	A0206
394	WLHCLLPKM	0.451	379	WB	Large T	A0206
526	LVTMNEYPV	0.441	421	WB	Large T	A0206
175	KLMEKYSVT	0.439	432	WB	Large T	A0206
148	SQAVFSNRT	0.438	437	WB	Large T	A0206
198	FLTPHRHRV	0.978	1	SB	Large T	A0211
405	VIFDFLHCV	0.968	1	SB	Large T	A0211
409	FLHCVVFNV	0.933	2	SB	Large T	A0211
397	CLLPKMDSV	0.929	2	SB	Large T	A0211
384	VLEQYMAGV	0.926	2	SB	Large T	A0211
557	SLQNSEFLL	0.912	2	SB	Large T	A0211
494	NLDSLRDYL	0.903	2	SB	Large T	A0211
569	ILQSGMTLL	0.890	3	SB	Large T	A0211
435	TLAAGLLDL	0.890	3	SB	Large T	A0211
215	KLCTFSFLI	0.876	3	SB	Large T	A0211
578	LLLIWFRPV	0.862	4	SB	Large T	A0211
563	FLLEKRILQ	0.862	4	SB	Large T	A0211
579	LLIWFRPVA	0.849	5	SB	Large T	A0211
292	MYLEFQYNV	0.832	6	SB	Large T	A0211

388	YMAGVAWLH	0.799	8	SB	Large T	A0211
463	GVAIDQYMV	0.796	9	SB	Large T	A0211
428	PIDSGKTTL	0.778	11	SB	Large T	A0211
573	GMTLLLLLI	0.771	11	SB	Large T	A0211
500	DYLDGSVKV	0.751	14	SB	Large T	A0211
454	PMERLTFEL	0.736	17	SB	Large T	A0211
288	LLLGMYLEF	0.733	17	SB	Large T	A0211
526	LVTMNEYPV	0.733	18	SB	Large T	A0211
391	GVAWLHCLL	0.725	19	SB	Large T	A0211
464	VAIDQYMVV	0.721	20	SB	Large T	A0211
568	RILQSGMTL	0.720	20	SB	Large T	A0211
142	DLHQFLSQA	0.703	24	SB	Large T	A0211
361	MLTERFNHI	0.692	28	SB	Large T	A0211
236	ALTRDPYHI	0.685	30	SB	Large T	A0211
596	RIVEWKERL	0.685	30	SB	Large T	A0211
156	TLACFAVYT	0.663	38	SB	Large T	A0211
287	FLLLGMYLE	0.659	40	SB	Large T	A0211
208	AINNFCQKL	0.637	50	WB	Large T	A0211
575	TLLLLLIWF	0.632	53	WB	Large T	A0211
20	RAAWGNLPL	0.620	61	WB	Large T	A0211
14	DLLGLERAA	0.614	65	WB	Large T	A0211
289	LLGMYLEFQ	0.602	74	WB	Large T	A0211
603	RLDSEISMY	0.592	82	WB	Large T	A0211
368	HILDKMDLI	0.590	84	WB	Large T	A0211
576	LLLLLIWFR	0.575	99	WB	Large T	A0211
394	WLHCLLPKM	0.569	106	WB	Large T	A0211
353	TLHMTREEM	0.558	119	WB	Large T	A0211
273	LITEYAVET	0.545	137	WB	Large T	A0211
398	LLPKMDSVI	0.535	152	WB	Large T	A0211
401	KMDSVIFDF	0.531	160	WB	Large T	A0211
146	FLSQAVFSN	0.527	166	WB	Large T	A0211
188	HMCAGHNII	0.524	172	WB	Large T	A0211
406	IFDFLHCVV	0.519	181	WB	Large T	A0211
648	SQSQCSSQV	0.514	191	WB	Large T	A0211
458	LTFELGVAI	0.508	204	WB	Large T	A0211
497	SLRDYLDGS	0.503	216	WB	Large T	A0211
501	YLDGSVKVN	0.501	220	WB	Large T	A0211
171	ILYKKLMEK	0.485	264	WB	Large T	A0211
73	FGTWNSSEV	0.481	274	WB	Large T	A0211
609	SMYTFSRMK	0.474	295	WB	Large T	A0211
416	NVPKRRYWL	0.464	330	WB	Large T	A0211
109	DMFASDEEA	0.459	346	WB	Large T	A0211
139	FPSDLHQFL	0.459	349	WB	Large T	A0211
439	GLLDLCGGK	0.452	377	WB	Large T	A0211
465	AIDQYMVVF	0.449	389	WB	Large T	A0211
21	AAWGNLPLM	0.448	394	WB	Large T	A0211
521	IFPPGLVTM	0.438	438	WB	Large T	A0211
175	KLMEKYSVT	0.437	440	WB	Large T	A0211
457	RLTFELGVA	0.430	478	WB	Large T	A0211
150	AVFSNRTLA	0.428	486	WB	Large T	A0211
198	FLTPHRHRV	0.950	1	SB	Large T	A0212
405	VIFDFLHCV	0.944	1	SB	Large T	A0212
384	VLEQYMAGV	0.915	2	SB	Large T	A0212
397	CLLPKMDSV	0.909	2	SB	Large T	A0212
409	FLHCVVFNV	0.905	2	SB	Large T	A0212
435	TLAAGLLDL	0.836	5	SB	Large T	A0212
569	ILQSGMTLL	0.822	6	SB	Large T	A0212
292	MYLEFQYNV	0.776	11	SB	Large T	A0212
578	LLLIWFRPV	0.774	11	SB	Large T	A0212
557	SLQNSEFLL	0.763	12	SB	Large T	A0212
563	FLLEKRILQ	0.736	17	SB	Large T	A0212

464	VAIDQYMVV	0.723	20	SB	Large T	A0212
494	NLDSLRDYL	0.711	22	SB	Large T	A0212
361	MLTERFNHI	0.692	27	SB	Large T	A0212
579	LLIWFRPVA	0.684	30	SB	Large T	A0212
288	LLLGMYLEF	0.636	51	WB	Large T	A0212
497	SLRDYLDGS	0.636	51	WB	Large T	A0212
215	KLCTFSFLI	0.619	61	WB	Large T	A0212
596	RIVEWKERL	0.610	68	WB	Large T	A0212
388	YMAGVAWLH	0.607	69	WB	Large T	A0212
287	FLLLGMYLE	0.598	77	WB	Large T	A0212
428	PIDSGKTTL	0.561	115	WB	Large T	A0212
14	DLLGLERAA	0.548	133	WB	Large T	A0212
454	PMERLTFEL	0.545	137	WB	Large T	A0212
526	LVTMNEYPV	0.533	155	WB	Large T	A0212
458	LTFELGVAI	0.531	160	WB	Large T	A0212
236	ALTRDPYHI	0.525	171	WB	Large T	A0212
208	AINNFCQKL	0.521	177	WB	Large T	A0212
500	DYLDGSVKV	0.517	185	WB	Large T	A0212
111	FASDEEATA	0.507	206	WB	Large T	A0212
289	LLGMYLEFQ	0.505	212	WB	Large T	A0212
188	HMCAGHNII	0.504	214	WB	Large T	A0212
368	HILDKMDLI	0.496	232	WB	Large T	A0212
398	LLPKMDSVI	0.494	239	WB	Large T	A0212
463	GVAIDQYMV	0.481	275	WB	Large T	A0212
401	KMDSVIFDF	0.477	286	WB	Large T	A0212
171	ILYKKLMEK	0.476	289	WB	Large T	A0212
568	RILQSGMTL	0.453	370	WB	Large T	A0212
139	FPSDLHQFL	0.450	385	WB	Large T	A0212
394	WLHCLLPKM	0.439	434	WB	Large T	A0212
198	FLTPHRHRV	0.957	1	SB	Large T	A0216
405	VIFDFLHCV	0.924	2	SB	Large T	A0216
384	VLEQYMAGV	0.898	2	SB	Large T	A0216
397	CLLPKMDSV	0.898	3	SB	Large T	A0216
409	FLHCVVFNV	0.881	3	SB	Large T	A0216
569	ILQSGMTLL	0.861	4	SB	Large T	A0216
494	NLDSLRDYL	0.860	4	SB	Large T	A0216
557	SLQNSEFLL	0.844	5	SB	Large T	A0216
454	PMERLTFEL	0.756	13	SB	Large T	A0216
428	PIDSGKTTL	0.749	15	SB	Large T	A0216
578	LLLIWFRPV	0.694	27	SB	Large T	A0216
435	TLAAGLLDL	0.679	32	SB	Large T	A0216
526	LVTMNEYPV	0.669	36	SB	Large T	A0216
289	LLGMYLEFQ	0.657	40	SB	Large T	A0216
215	KLCTFSFLI	0.657	41	SB	Large T	A0216
142	DLHQFLSQA	0.655	41	SB	Large T	A0216
292	MYLEFQYNV	0.655	41	SB	Large T	A0216
563	FLLEKRILQ	0.646	45	SB	Large T	A0216
596	RIVEWKERL	0.646	46	SB	Large T	A0216
236	ALTRDPYHI	0.645	46	SB	Large T	A0216
416	NVPKRRYWL	0.628	55	WB	Large T	A0216
463	GVAIDQYMV	0.626	57	WB	Large T	A0216
361	MLTERFNHI	0.601	74	WB	Large T	A0216
156	TLACFAVYT	0.590	84	WB	Large T	A0216
208	AINNFCQKL	0.578	96	WB	Large T	A0216
568	RILQSGMTL	0.574	99	WB	Large T	A0216
500	DYLDGSVKV	0.539	146	WB	Large T	A0216
398	LLPKMDSVI	0.537	149	WB	Large T	A0216
579	LLIWFRPVA	0.529	163	WB	Large T	A0216
391	GVAWLHCLL	0.519	181	WB	Large T	A0216
353	TLHMTREEM	0.510	200	WB	Large T	A0216
619	NICMGKCIL	0.500	224	WB	Large T	A0216

648	SQSQCSSQV	0.495	236	WB	Large T	A0216
171	ILYKKLMEK	0.463	333	WB	Large T	A0216
464	VAIDQYMVV	0.456	359	WB	Large T	A0216
188	HMCAGHNII	0.440	428	WB	Large T	A0216
368	HILDKMDLI	0.426	497	WB	Large T	A0216
198	FLTPHRHRV	0.947	1	SB	Large T	A0219
405	VIFDFLHCV	0.932	2	SB	Large T	A0219
409	FLHCVVFNV	0.879	3	SB	Large T	A0219
397	CLLPKMDSV	0.868	4	SB	Large T	A0219
569	ILQSGMTLL	0.849	5	SB	Large T	A0219
435	TLAAGLLDL	0.795	9	SB	Large T	A0219
384	VLEQYMAGV	0.766	12	SB	Large T	A0219
494	NLDSLRDYL	0.716	21	SB	Large T	A0219
428	PIDSGKTTL	0.697	26	SB	Large T	A0219
557	SLQNSEFLL	0.621	60	WB	Large T	A0219
578	LLLIWFRPV	0.588	86	WB	Large T	A0219
292	MYLEFQYNV	0.530	162	WB	Large T	A0219
526	LVTMNEYPV	0.519	182	WB	Large T	A0219
361	MLTERFNHI	0.518	183	WB	Large T	A0219
500	DYLDGSVKV	0.508	205	WB	Large T	A0219
21	AAWGNLPLM	0.506	209	WB	Large T	A0219
454	PMERLTFEL	0.461	340	WB	Large T	A0219
236	ALTRDPYHI	0.459	349	WB	Large T	A0219
146	FLSQAVFSN	0.428	486	WB	Large T	A0219
171	ILYKKLMEK	0.858	4	SB	Large T	A0301
609	SMYTFSRMK	0.762	13	SB	Large T	A0301
28	LMRKAYLKK	0.703	24	SB	Large T	A0301
195	IIFFLTPHR	0.658	40	SB	Large T	A0301
50	KMKRMNTLY	0.654	42	SB	Large T	A0301
217	CTFSFLICK	0.640	49	SB	Large T	A0301
221	FLICKGVNK	0.633	52	WB	Large T	A0301
528	TMNEYPVPK	0.599	76	WB	Large T	A0301
155	RTLACFAVY	0.595	79	WB	Large T	A0301
27	PLMRKAYLK	0.578	96	WB	Large T	A0301
226	GVNKEYLLY	0.545	137	WB	Large T	A0301
121	SQHSTPPKK	0.490	248	WB	Large T	A0301
231	YLLYSALTR	0.475	294	WB	Large T	A0301
341	AVDTVLAKK	0.472	302	WB	Large T	A0301
576	LLLLLIWFR	0.467	318	WB	Large T	A0301
668	HSQELHLCK	0.464	331	WB	Large T	A0301
504	GSVKVNLEK	0.452	376	WB	Large T	A0301
509	NLEKKHLNK	0.452	377	WB	Large T	A0301
350	RVDTLHMTR	0.444	409	WB	Large T	A0301
603	RLDSEISMY	0.433	461	WB	Large T	A0301
217	CTFSFLICK	0.826	6	SB	Large T	A1101
528	TMNEYPVPK	0.817	7	SB	Large T	A1101
609	SMYTFSRMK	0.802	8	SB	Large T	A1101
207	SAINNFCQK	0.774	11	SB	Large T	A1101
171	ILYKKLMEK	0.747	15	SB	Large T	A1101
668	HSQELHLCK	0.730	18	SB	Large T	A1101
341	AVDTVLAKK	0.703	24	SB	Large T	A1101
195	IIFFLTPHR	0.686	30	SB	Large T	A1101
504	GSVKVNLEK	0.679	32	SB	Large T	A1101
121	SQHSTPPKK	0.674	33	SB	Large T	A1101
147	LSQAVFSNR	0.654	42	SB	Large T	A1101
536	KTLQARFVR	0.650	44	SB	Large T	A1101
155	RTLACFAVY	0.646	46	SB	Large T	A1101
340	QAVDTVLAK	0.602	74	WB	Large T	A1101
505	SVKVNLEKK	0.583	91	WB	Large T	A1101

27	PLMRKAYLK	0.576	98	WB	Large T	A1101
120	DSQHSTPPK	0.567	108	WB	Large T	A1101
393	AWLHCLLPK	0.566	109	WB	Large T	A1101
413	VVFNVPKRR	0.559	118	WB	Large T	A1101
439	GLLDLCGGK	0.551	129	WB	Large T	A1101
324	NAIIFAESK	0.539	146	WB	Large T	A1101
350	RVDTLHMTR	0.529	163	WB	Large T	A1101
226	GVNKEYLLY	0.518	184	WB	Large T	A1101
607	EISMYTFSR	0.496	233	WB	Large T	A1101
274	ITEYAVETK	0.491	247	WB	Large T	A1101
593	IQSRIVEWK	0.489	252	WB	Large T	A1101
491	GINNLDSLR	0.488	254	WB	Large T	A1101
296	FQYNVEECK	0.478	285	WB	Large T	A1101
576	LLLLLIWFR	0.466	321	WB	Large T	A1101
91	SWWSSFNEK	0.461	340	WB	Large T	A1101
158	ACFAVYTTK	0.456	360	WB	Large T	A1101
221	FLICKGVNK	0.446	399	WB	Large T	A1101
32	AYLKKCKEF	0.708	23	SB	Large T	A2301
581	IWFRPVADF	0.678	32	SB	Large T	A2301
312	PYHFKYHEK	0.647	45	SB	Large T	A2301
91	SWWSSFNEK	0.552	126	WB	Large T	A2301
387	QYMAGVAWL	0.546	135	WB	Large T	A2301
190	CAGHNIIFF	0.527	166	WB	Large T	A2301
401	KMDSVIFDF	0.522	176	WB	Large T	A2301
286	VFLLLGMYL	0.518	183	WB	Large T	A2301
292	MYLEFQYNV	0.512	196	WB	Large T	A2301
138	DFPSDLHQF	0.501	220	WB	Large T	A2301
314	HFKYHEKHF	0.501	222	WB	Large T	A2301
575	TLLLLLIWF	0.496	233	WB	Large T	A2301
213	CQKLCTFSF	0.485	263	WB	Large T	A2301
393	AWLHCLLPK	0.471	305	WB	Large T	A2301
288	LLLGMYLEF	0.464	331	WB	Large T	A2301
320	KHFANAIIF	0.463	334	WB	Large T	A2301
327	IFAESKNQK	0.458	352	WB	Large T	A2301
610	MYTFSRMKY	0.455	365	WB	Large T	A2301
211	NFCQKLCTF	0.454	368	WB	Large T	A2301
612	TFSRMKYNI	0.440	427	WB	Large T	A2301
88	EWESWWSSF	0.597	78	WB	Large T	A2402
387	QYMAGVAWL	0.587	87	WB	Large T	A2402
138	DFPSDLHQF	0.544	138	WB	Large T	A2402
241	PYHIIEESI	0.536	150	WB	Large T	A2402
32	AYLKKCKEF	0.523	174	WB	Large T	A2402
581	IWFRPVADF	0.503	216	WB	Large T	A2402
468	QYMVVFEDV	0.502	219	WB	Large T	A2402
612	TFSRMKYNI	0.451	381	WB	Large T	A2402
286	VFLLLGMYL	0.434	456	WB	Large T	A2402
417	VPKRRYWLF	0.432	466	WB	Large T	A2402
32	AYLKKCKEF	0.859	4	SB	Large T	A2403
387	QYMAGVAWL	0.773	11	SB	Large T	A2403
138	DFPSDLHQF	0.618	62	WB	Large T	A2403
320	KHFANAIIF	0.569	105	WB	Large T	A2403
521	IFPPGLVTM	0.551	129	WB	Large T	A2403
68	AHQPDFGTW	0.542	142	WB	Large T	A2403
286	VFLLLGMYL	0.532	158	WB	Large T	A2403
581	IWFRPVADF	0.506	209	WB	Large T	A2403
401	KMDSVIFDF	0.462	338	WB	Large T	A2403
190	CAGHNIIFF	0.458	351	WB	Large T	A2403
468	QYMVVFEDV	0.446	400	WB	Large T	A2403
211	NFCQKLCTF	0.433	461	WB	Large T	A2403

285	DVFLLLGMY	0.689	29	SB	Large T	A2601
265	ETKQVSWKL	0.506	209	WB	Large T	A2601
8	ESMELMDLL	0.463	335	WB	Large T	A2601
285	DVFLLLGMY	0.923	2	SB	Large T	A2602
465	AIDQYMVVF	0.801	8	SB	Large T	A2602
280	ETKCEDVFL	0.742	16	SB	Large T	A2602
545	QIDFRPKIY	0.724	19	SB	Large T	A2602
138	DFPSDLHQF	0.617	63	WB	Large T	A2602
226	GVNKEYLLY	0.612	66	WB	Large T	A2602
155	RTLACFAVY	0.609	68	WB	Large T	A2602
152	FSNRTLACF	0.590	84	WB	Large T	A2602
265	ETKQVSWKL	0.518	183	WB	Large T	A2602
8	ESMELMDLL	0.476	290	WB	Large T	A2602
103	DLFCHEDMF	0.457	358	WB	Large T	A2602
450	NVNLPMERL	0.447	396	WB	Large T	A2602
164	TTKEKAQIL	0.437	441	WB	Large T	A2602
290	LGMYLEFQY	0.593	81	WB	Large T	A2902
50	KMKRMNTLY	0.576	98	WB	Large T	A2902
269	VSWKLITEY	0.552	127	WB	Large T	A2902
285	DVFLLLGMY	0.538	148	WB	Large T	A2902
226	GVNKEYLLY	0.508	204	WB	Large T	A2902
610	MYTFSRMKY	0.474	295	WB	Large T	A2902
414	VFNVPKRRY	0.429	480	WB	Large T	A2902
28	LMRKAYLKK	0.830	6	SB	Large T	A3001
51	MKRMNTLYK	0.827	6	SB	Large T	A3001
36	KCKEFHPDK	0.817	7	SB	Large T	A3001
418	PKRRYWLFK	0.813	7	SB	Large T	A3001
121	SQHSTPPKK	0.755	14	SB	Large T	A3001
682	KRPKTPPPK	0.723	19	SB	Large T	A3001
528	TMNEYPVPK	0.716	21	SB	Large T	A3001
677	GFQCFKRPK	0.683	30	SB	Large T	A3001
120	DSQHSTPPK	0.675	33	SB	Large T	A3001
674	LCKGFQCFK	0.669	36	SB	Large T	A3001
129	KKRKVEDPK	0.666	37	SB	Large T	A3001
158	ACFAVYTTK	0.657	40	SB	Large T	A3001
536	KTLQARFVR	0.637	51	WB	Large T	A3001
505	SVKVNLEKK	0.634	52	WB	Large T	A3001
609	SMYTFSRMK	0.598	77	WB	Large T	A3001
166	KEKAQILYK	0.579	95	WB	Large T	A3001
312	PYHFKYHEK	0.574	100	WB	Large T	A3001
195	IIFFLTPHR	0.569	105	WB	Large T	A3001
393	AWLHCLLPK	0.519	181	WB	Large T	A3001
50	KMKRMNTLY	0.501	220	WB	Large T	A3001
340	QAVDTVLAK	0.481	273	WB	Large T	A3001
274	ITEYAVETK	0.481	274	WB	Large T	A3001
124	STPPKKKRK	0.478	282	WB	Large T	A3001
171	ILYKKLMEK	0.467	318	WB	Large T	A3001
411	HCVVFNVPK	0.465	325	WB	Large T	A3001
27	PLMRKAYLK	0.439	431	WB	Large T	A3001
544	RQIDFRPKI	0.437	440	WB	Large T	A3001
668	HSQELHLCK	0.436	445	WB	Large T	A3001
52	KRMNTLYKK	0.435	453	WB	Large T	A3001
50	KMKRMNTLY	0.561	115	WB	Large T	A3002
401	KMDSVIFDF	0.525	169	WB	Large T	A3002
172	LYKKLMEKY	0.524	172	WB	Large T	A3002
285	DVFLLLGMY	0.509	201	WB	Large T	A3002
610	MYTFSRMKY	0.502	218	WB	Large T	A3002

226	GVNKEYLLY	0.497	231	WB	Large T	A3002
603	RLDSEISMY	0.483	269	WB	Large T	A3002
536	KTLQARFVR	0.856	4	SB	Large T	A3101
576	LLLLLIWFR	0.848	5	SB	Large T	A3101
179	KYSVTFISR	0.844	5	SB	Large T	A3101
541	RFVRQIDFR	0.836	5	SB	Large T	A3101
147	LSQAVFSNR	0.821	6	SB	Large T	A3101
547	DFRPKIYLR	0.799	8	SB	Large T	A3101
195	IIFFLTPHR	0.720	20	SB	Large T	A3101
528	TMNEYPVPK	0.713	22	SB	Large T	A3101
350	RVDTLHMTR	0.712	22	SB	Large T	A3101
197	FFLTPHRHR	0.682	31	SB	Large T	A3101
491	GINNLDSLR	0.668	36	SB	Large T	A3101
413	VVFNVPKRR	0.651	43	SB	Large T	A3101
607	EISMYTFSR	0.604	72	WB	Large T	A3101
155	RTLACFAVY	0.573	101	WB	Large T	A3101
609	SMYTFSRMK	0.567	108	WB	Large T	A3101
217	CTFSFLICK	0.563	113	WB	Large T	A3101
50	KMKRMNTLY	0.540	144	WB	Large T	A3101
91	SWWSSFNEK	0.515	190	WB	Large T	A3101
123	HSTPPKKKR	0.487	257	WB	Large T	A3101
292	MYLEFQYNV	0.476	289	WB	Large T	A3101
677	GFQCFKRPK	0.472	301	WB	Large T	A3101
231	YLLYSALTR	0.438	439	WB	Large T	A3101
28	LMRKAYLKK	0.436	447	WB	Large T	A3101
547	DFRPKIYLR	0.938	1	SB	Large T	A3301
576	LLLLLIWFR	0.827	6	SB	Large T	A3301
607	EISMYTFSR	0.826	6	SB	Large T	A3301
195	IIFFLTPHR	0.692	27	SB	Large T	A3301
588	DFSKDIQSR	0.669	35	SB	Large T	A3301
197	FFLTPHRHR	0.615	64	WB	Large T	A3301
147	LSQAVFSNR	0.592	82	WB	Large T	A3301
231	YLLYSALTR	0.473	299	WB	Large T	A3301
607	EISMYTFSR	0.908	2	SB	Large T	A6801
412	CVVFNVPKR	0.851	5	SB	Large T	A6801
195	IIFFLTPHR	0.838	5	SB	Large T	A6801
217	CTFSFLICK	0.813	7	SB	Large T	A6801
324	NAIIFAESK	0.796	9	SB	Large T	A6801
207	SAINNFCQK	0.749	15	SB	Large T	A6801
160	FAVYTTKEK	0.721	20	SB	Large T	A6801
274	ITEYAVETK	0.648	44	SB	Large T	A6801
147	LSQAVFSNR	0.643	47	SB	Large T	A6801
536	KTLQARFVR	0.643	47	SB	Large T	A6801
231	YLLYSALTR	0.628	56	WB	Large T	A6801
616	MKYNICMGK	0.625	58	WB	Large T	A6801
491	GINNLDSLR	0.625	58	WB	Large T	A6801
413	VVFNVPKRR	0.622	60	WB	Large T	A6801
560	NSEFLLEKR	0.620	61	WB	Large T	A6801
609	SMYTFSRMK	0.595	80	WB	Large T	A6801
167	EKAQILYKK	0.595	80	WB	Large T	A6801
610	MYTFSRMKY	0.588	86	WB	Large T	A6801
576	LLLLLIWFR	0.573	101	WB	Large T	A6801
469	YMVVFEDVK	0.567	108	WB	Large T	A6801
296	FQYNVEECK	0.534	153	WB	Large T	A6801
123	HSTPPKKKR	0.530	162	WB	Large T	A6801
340	QAVDTVLAK	0.527	167	WB	Large T	A6801
668	HSQELHLCK	0.512	196	WB	Large T	A6801
505	SVKVNLEKK	0.501	220	WB	Large T	A6801
120	DSQHSTPPK	0.485	263	WB	Large T	A6801

528	TMNEYPVPK	0.481	275	WB	Large T	A6801
171	ILYKKLMEK	0.479	281	WB	Large T	A6801
504	GSVKVNLEK	0.451	380	WB	Large T	A6801
285	DVFLLLGMY	0.450	385	WB	Large T	A6801
449	LNVNLPMER	0.448	390	WB	Large T	A6801
350	RVDTLHMTR	0.441	422	WB	Large T	A6801
403	DSVIFDFLH	0.439	432	WB	Large T	A6801
388	YMAGVAWLH	0.437	440	WB	Large T	A6801
588	DFSKDIQSR	0.437	444	WB	Large T	A6801
547	DFRPKIYLR	0.427	492	WB	Large T	A6801
8	ESMELMDLL	0.767	12	SB	Large T	A6802
409	FLHCVVFNV	0.700	25	SB	Large T	A6802
402	MDSVIFDFL	0.694	27	SB	Large T	A6802
450	NVNLPMERL	0.691	28	SB	Large T	A6802
219	FSFLICKGV	0.689	28	SB	Large T	A6802
265	ETKQVSWKL	0.607	70	WB	Large T	A6802
280	ETKCEDVFL	0.589	85	WB	Large T	A6802
416	NVPKRRYWL	0.585	89	WB	Large T	A6802
526	LVTMNEYPV	0.585	89	WB	Large T	A6802
405	VIFDFLHCV	0.583	91	WB	Large T	A6802
73	FGTWNSSEV	0.580	94	WB	Large T	A6802
458	LTFELGVAI	0.577	96	WB	Large T	A6802
371	DKMDLIFGA	0.565	110	WB	Large T	A6802
589	FSKDIQSRI	0.558	119	WB	Large T	A6802
198	FLTPHRHRV	0.543	140	WB	Large T	A6802
519	TQIFPPGLV	0.515	189	WB	Large T	A6802
377	FGAHGNAVL	0.502	218	WB	Large T	A6802
156	TLACFAVYT	0.493	239	WB	Large T	A6802
464	VAIDQYMVV	0.486	261	WB	Large T	A6802
468	QYMVVFEDV	0.482	271	WB	Large T	A6802
608	ISMYTFSRM	0.465	326	WB	Large T	A6802
343	DTVLAKKRV	0.459	348	WB	Large T	A6802
361	MLTERFNHI	0.450	382	WB	Large T	A6802
191	AGHNIIFFL	0.447	396	WB	Large T	A6802
154	NRTLACFAV	0.432	468	WB	Large T	A6802
458	LTFELGVAI	0.702	25	SB	Large T	A6901
405	VIFDFLHCV	0.691	28	SB	Large T	A6901
409	FLHCVVFNV	0.683	30	SB	Large T	A6901
578	LLLIWFRPV	0.630	54	WB	Large T	A6901
8	ESMELMDLL	0.609	68	WB	Large T	A6901
368	HILDKMDLI	0.587	87	WB	Large T	A6901
139	FPSDLHQFL	0.553	125	WB	Large T	A6901
292	MYLEFQYNV	0.522	176	WB	Large T	A6901
21	AAWGNLPLM	0.483	267	WB	Large T	A6901
198	FLTPHRHRV	0.481	274	WB	Large T	A6901
265	ETKQVSWKL	0.457	355	WB	Large T	A6901
500	DYLDGSVKV	0.449	389	WB	Large T	A6901
464	VAIDQYMVV	0.431	472	WB	Large T	A6901
20	RAAWGNLPL	0.721	20	SB	Large T	B0702
26	LPLMRKAYL	0.719	20	SB	Large T	B0702
200	TPHRHRVSA	0.662	38	SB	Large T	B0702
532	YPVPKTLQA	0.651	43	SB	Large T	B0702
399	LPKMDSVIF	0.516	187	WB	Large T	B0702
568	RILQSGMTL	0.499	226	WB	Large T	B0702
81	VPTYGTEEW	0.497	232	WB	Large T	B0702
139	FPSDLHQFL	0.467	320	WB	Large T	B0702
417	VPKRRYWLF	0.461	339	WB	Large T	B0702
417	VPKRRYWLF	0.587	87	WB	Large T	B0801

144	HQFLSQAVF	0.618	62	WB	Large T	B1501
234	YSALTRDPY	0.569	105	WB	Large T	B1501
50	KMKRMNTLY	0.561	115	WB	Large T	B1501
213	CQKLCTFSF	0.528	165	WB	Large T	B1501
155	RTLACFAVY	0.522	176	WB	Large T	B1501
514	HLNKRTQIF	0.501	221	WB	Large T	B1501
288	LLLGMYLEF	0.495	236	WB	Large T	B1501
570	LQSGMTLLL	0.479	280	WB	Large T	B1501
152	FSNRTLACF	0.468	315	WB	Large T	B1501
176	LMEKYSVTF	0.466	324	WB	Large T	B1501
20	RAAWGNLPL	0.444	411	WB	Large T	B1501
388	YMAGVAWLH	0.439	434	WB	Large T	B1501
10	MELMDLLGL	0.722	20	SB	Large T	B1801
530	NEYPVPKTL	0.706	24	SB	Large T	B1801
670	QELHLCKGF	0.692	27	SB	Large T	B1801
229	KEYLLYSAL	0.571	104	WB	Large T	B1801
664	SENPHSQEL	0.520	179	WB	Large T	B1801
52	KRMNTLYKK	0.656	41	SB	Large T	B2705
548	FRPKIYLRK	0.526	169	WB	Large T	B2705
420	RRYWLFKGP	0.518	184	WB	Large T	B2705
364	ERFNHILDK	0.460	343	WB	Large T	B2705
614	SRMKYNICM	0.452	375	WB	Large T	B2705
540	ARFVRQIDF	0.436	448	WB	Large T	B2705
682	KRPKTPPPK	0.430	477	WB	Large T	B2705
399	LPKMDSVIF	0.752	14	SB	Large T	B3501
139	FPSDLHQFL	0.633	52	WB	Large T	B3501
20	RAAWGNLPL	0.618	62	WB	Large T	B3501
234	YSALTRDPY	0.565	111	WB	Large T	B3501
447	KALNVNLPM	0.561	115	WB	Large T	B3501
21	AAWGNLPLM	0.545	137	WB	Large T	B3501
189	MCAGHNIIF	0.537	149	WB	Large T	B3501
111	FASDEEATA	0.509	202	WB	Large T	B3501
534	VPKTLQARF	0.498	229	WB	Large T	B3501
81	VPTYGTEEW	0.486	260	WB	Large T	B3501
269	VSWKLITEY	0.463	334	WB	Large T	B3501
285	DVFLLLGMY	0.447	394	WB	Large T	B3501
532	YPVPKTLQA	0.445	403	WB	Large T	B3501
176	LMEKYSVTF	0.441	423	WB	Large T	B3501
155	RTLACFAVY	0.434	455	WB	Large T	B3501
666	NPHSQELHL	0.426	495	WB	Large T	B3501
377	FGAHGNAVL	0.547	133	WB	Large T	B3901
10	MELMDLLGL	0.751	14	SB	Large T	B4001
229	KEYLLYSAL	0.690	28	SB	Large T	B4001
664	SENPHSQEL	0.681	31	SB	Large T	B4001
530	NEYPVPKTL	0.592	82	WB	Large T	B4001
7	EESMELMDL	0.561	115	WB	Large T	B4001
245	IEESIQGGL	0.552	127	WB	Large T	B4001
561	SEFLLEKRI	0.498	227	WB	Large T	B4001
18	LERAAWGNL	0.497	231	WB	Large T	B4001
358	REEMLTERF	0.441	422	WB	Large T	B4001
664	SENPHSQEL	0.630	54	WB	Large T	B4002
229	KEYLLYSAL	0.583	91	WB	Large T	B4002
606	SEISMYTFS	0.489	252	WB	Large T	B4002
279	VETKCEDVF	0.469	314	WB	Large T	B4002
177	MEKYSVTFI	0.462	335	WB	Large T	B4002

606	SEISMYTFS	0.521	177	WB	Large T	B4403
561	SEFLLEKRI	0.458	353	WB	Large T	B4403
664	SENPHSQEL	0.446	403	WB	Large T	B4403
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329	AESKNQKSI	0.497	229	WB	Large T	B4501
453	LPMERLTFE	0.451	378	WB	Large T	B5101
139	FPSDLHQFL	0.438	437	WB	Large T	B5101
81	VPTYGTEEW	0.673	34	SB	Large T	B5301
399	LPKMDSVIF	0.628	55	WB	Large T	B5301
26	LPLMRKAYL	0.625	57	WB	Large T	B5301
666	NPHSQELHL	0.553	126	WB	Large T	B5301
139	FPSDLHQFL	0.509	202	WB	Large T	B5301
574	MTLLLLLIW	0.454	366	WB	Large T	B5301
522	FPPGLVTMN	0.672	34	SB	Large T	B5401
200	TPHRHRVSA	0.530	162	WB	Large T	B5401
219	FSFLICKGV	0.453	373	WB	Large T	B5401
453	LPMERLTFE	0.432	466	WB	Large T	B5401
574	MTLLLLLIW	0.446	399	WB	Large T	B5701
401	KMDSVIFDF	0.615	64	WB	Large T	B5801
574	MTLLLLLIW	0.594	80	WB	Large T	B5801
152	FSNRTLACF	0.562	114	WB	Large T	B5801
84	YGTEEWESW	0.553	125	WB	Large T	B5801
20	RAAWGNLPL	0.460	344	WB	Large T	B5801
447	KALNVNLPM	0.442	419	WB	Large T	B5801
269	VSWKLITEY	0.429	482	WB	Large T	B5801
	10-mers					
164	TTKEKAQILY	0.528	165	WB	Large T	A0101
401	KMDSVIFDFL	0.830	6	SB	Large T	A0201
291	GMYLEFQYNV	0.761	13	SB	Large T	A0201
405	VIFDFLHCVV	0.679	32	SB	Large T	A0201
525	GLVTMNEYPV	0.676	33	SB	Large T	A0201
501	YLDGSVKVNL	0.671	35	SB	Large T	A0201
569	ILQSGMTLLL	0.658	40	SB	Large T	A0201
577	LLLLIWFRPV	0.657	40	SB	Large T	A0201
383	AVLEQYMAGV	0.637	50	WB	Large T	A0201
361	MLTERFNHIL	0.616	63	WB	Large T	A0201
176	LMEKYSVTFI	0.609	68	WB	Large T	A0201
404	SVIFDFLHCV	0.585	89	WB	Large T	A0201
603	RLDSEISMYT	0.583	90	WB	Large T	A0201
497	SLRDYLDGSV	0.570	104	WB	Large T	A0201
272	KLITEYAVET	0.543	140	WB	Large T	A0201
578	LLLIWFRPVA	0.503	216	WB	Large T	A0201
563	FLLEKRILQS	0.500	222	WB	Large T	A0201
56	TLYKKMEQDV	0.485	263	WB	Large T	A0201
528	TMNEYPVPKT	0.457	354	WB	Large T	A0201
12	LMDLLGLERA	0.456	361	WB	Large T	A0201
568	RILQSGMTLL	0.454	367	WB	Large T	A0201
288	LLLGMYLEFQ	0.448	391	WB	Large T	A0201
3	VLNREESMEL	0.434	454	WB	Large T	A0201
401	KMDSVIFDFL	0.773	11	SB	Large T	A0202
603	RLDSEISMYT	0.720	20	SB	Large T	A0202
569	ILQSGMTLLL	0.716	21	SB	Large T	A0202

291	GMYLEFQYNV	0.681	31	SB	Large T A0202
525	GLVTMNEYPV	0.674	33	SB	Large T A0202
497	SLRDYLDGSV	0.665	37	SB	Large T A0202
405	VIFDFLHCVV	0.649	44	SB	Large T A0202
501	YLDGSVKVNL	0.648	44	SB	Large T A0202
288	LLLGMYLEFQ	0.645	46	SB	Large T A0202
577	LLLLIWFRPV	0.628	55	WB	Large T A0202
287	FLLLGMYLEF	0.618	62	WB	Large T A0202
570	LQSGMTLLLL	0.609	69	WB	Large T A0202
12	LMDLLGLERA	0.607	70	WB	Large T A0202
388	YMAGVAWLHC	0.582	91	WB	Large T A0202
156	TLACFAVYTT	0.566	109	WB	Large T A0202
175	KLMEKYSVTF	0.566	109	WB	Large T A0202
3	VLNREESMEL	0.562	114	WB	Large T A0202
397	CLLPKMDSVI	0.561	115	WB	Large T A0202
285	DVFLLLGMYL	0.560	117	WB	Large T A0202
435	TLAAGLLDLC	0.550	130	WB	Large T A0202
361	MLTERFNHIL	0.543	140	WB	Large T A0202
383	AVLEQYMAGV	0.535	153	WB	Large T A0202
353	TLHMTREEML	0.532	157	WB	Large T A0202
461	ELGVAIDQYM	0.520	180	WB	Large T A0202
56	TLYKKMEQDV	0.516	187	WB	Large T A0202
103	DLFCHEDMFA	0.516	187	WB	Large T A0202
463	GVAIDQYMVV	0.509	202	WB	Large T A0202
9	SMELMDLLGL	0.507	206	WB	Large T A0202
142	DLHQFLSQAV	0.497	230	WB	Large T A0202
611	YTFSRMKYNI	0.493	240	WB	Large T A0202
272	KLITEYAVET	0.492	243	WB	Large T A0202
375	LIFGAHGNAV	0.491	247	WB	Large T A0202
563	FLLEKRILQS	0.488	253	WB	Large T A0202
440	LLDLCGGKAL	0.488	255	WB	Large T A0202
25	NLPLMRKAYL	0.483	269	WB	Large T A0202
568	RILQSGMTLL	0.478	285	WB	Large T A0202
176	LMEKYSVTFI	0.471	305	WB	Large T A0202
236	ALTRDPYHII	0.461	341	WB	Large T A0202
493	NNLDSLRDYL	0.454	366	WB	Large T A0202
572	SGMTLLLLLI	0.453	371	WB	Large T A0202
148	SQAVFSNRTL	0.450	383	WB	Large T A0202
439	GLLDLCGGKA	0.445	406	WB	Large T A0202
609	SMYTFSRMKY	0.445	406	WB	Large T A0202
345	VLAKKRVDTL	0.445	407	WB	Large T A0202
360	EMLTERFNHI	0.440	427	WB	Large T A0202
578	LLLIWFRPVA	0.438	435	WB	Large T A0202
556	KSLQNSEFLL	0.437	441	WB	Large T A0202
213	CQKLCTFSFL	0.433	461	WB	Large T A0202
497	SLRDYLDGSV	0.883	3	SB	Large T A0203
361	MLTERFNHIL	0.815	7	SB	Large T A0203
291	GMYLEFQYNV	0.792	9	SB	Large T A0203
525	GLVTMNEYPV	0.769	12	SB	Large T A0203
383	AVLEQYMAGV	0.755	14	SB	Large T A0203
569	ILQSGMTLLL	0.731	18	SB	Large T A0203
375	LIFGAHGNAV	0.731	18	SB	Large T A0203
577	LLLLIWFRPV	0.708	23	SB	Large T A0203
56	TLYKKMEQDV	0.707	23	SB	Large T A0203
405	VIFDFLHCVV	0.674	34	SB	Large T A0203
3	VLNREESMEL	0.666	37	SB	Large T A0203
457	RLTFELGVAI	0.665	37	SB	Large T A0203
404	SVIFDFLHCV	0.654	42	SB	Large T A0203
501	YLDGSVKVNL	0.627	56	WB	Large T A0203
345	VLAKKRVDTL	0.625	57	WB	Large T A0203
176	LMEKYSVTFI	0.611	67	WB	Large T A0203

156	TLACFAVYTT	0.600	75	WB	Large T	A0203
236	ALTRDPYHII	0.576	98	WB	Large T	A0203
401	KMDSVIFDFL	0.549	132	WB	Large T	A0203
537	TLQARFVRQI	0.548	132	WB	Large T	A0203
439	GLLDLCGGKA	0.546	136	WB	Large T	A0203
570	LQSGMTLLLL	0.542	142	WB	Large T	A0203
568	RILQSGMTLL	0.541	143	WB	Large T	A0203
397	CLLPKMDSVI	0.534	154	WB	Large T	A0203
611	YTFSRMKYNI	0.521	177	WB	Large T	A0203
142	DLHQFLSQAV	0.503	217	WB	Large T	A0203
603	RLDSEISMYT	0.488	254	WB	Large T	A0203
578	LLLIWFRPVA	0.485	261	WB	Large T	A0203
272	KLITEYAVET	0.485	263	WB	Large T	A0203
213	CQKLCTFSFL	0.480	277	WB	Large T	A0203
463	GVAIDQYMVV	0.473	298	WB	Large T	A0203
12	LMDLLGLERA	0.468	314	WB	Large T	A0203
528	TMNEYPVPKT	0.465	326	WB	Large T	A0203
9	SMELMDLLGL	0.462	338	WB	Large T	A0203
333	NQKSICQQAV	0.456	361	WB	Large T	A0203
336	SICQQAVDTV	0.435	451	WB	Large T	A0203
383	AVLEQYMAGV	0.666	37	SB	Large T	A0204
525	GLVTMNEYPV	0.603	73	WB	Large T	A0204
577	LLLLIWFRPV	0.591	83	WB	Large T	A0204
361	MLTERFNHIL	0.573	101	WB	Large T	A0204
497	SLRDYLDGSV	0.565	110	WB	Large T	A0204
336	SICQQAVDTV	0.557	120	WB	Large T	A0204
3	VLNREESMEL	0.557	120	WB	Large T	A0204
291	GMYLEFQYNV	0.549	132	WB	Large T	A0204
405	VIFDFLHCVV	0.533	155	WB	Large T	A0204
375	LIFGAHGNAV	0.515	190	WB	Large T	A0204
537	TLQARFVRQI	0.496	234	WB	Large T	A0204
236	ALTRDPYHII	0.494	238	WB	Large T	A0204
401	KMDSVIFDFL	0.484	266	WB	Large T	A0204
528	TMNEYPVPKT	0.473	300	WB	Large T	A0204
345	VLAKKRVDTL	0.461	339	WB	Large T	A0204
175	KLMEKYSVTF	0.451	380	WB	Large T	A0204
569	ILQSGMTLLL	0.446	401	WB	Large T	A0204
176	LMEKYSVTFI	0.437	440	WB	Large T	A0204
463	GVAIDQYMVV	0.434	454	WB	Large T	A0204
518	RTQIFPPGLV	0.431	473	WB	Large T	A0204
383	AVLEQYMAGV	0.832	6	SB	Large T	A0206
404	SVIFDFLHCV	0.773	11	SB	Large T	A0206
401	KMDSVIFDFL	0.762	13	SB	Large T	A0206
577	LLLLIWFRPV	0.744	15	SB	Large T	A0206
570	LQSGMTLLLL	0.714	22	SB	Large T	A0206
525	GLVTMNEYPV	0.698	26	SB	Large T	A0206
291	GMYLEFQYNV	0.682	31	SB	Large T	A0206
405	VIFDFLHCVV	0.674	33	SB	Large T	A0206
568	RILQSGMTLL	0.670	35	SB	Large T	A0206
361	MLTERFNHIL	0.650	43	SB	Large T	A0206
375	LIFGAHGNAV	0.644	47	SB	Large T	A0206
287	FLLLGMYLEF	0.607	70	WB	Large T	A0206
497	SLRDYLDGSV	0.596	79	WB	Large T	A0206
267	KQVSWKLITE	0.564	112	WB	Large T	A0206
175	KLMEKYSVTF	0.553	125	WB	Large T	A0206
148	SQAVFSNRTL	0.535	153	WB	Large T	A0206
20	RAAWGNLPLM	0.518	184	WB	Large T	A0206
388	YMAGVAWLHC	0.510	201	WB	Large T	A0206
213	CQKLCTFSFL	0.505	212	WB	Large T	A0206
272	KLITEYAVET	0.494	237	WB	Large T	A0206

578	LLLIWFRPVA	0.494	238	WB	Large T	A0206
336	SICQQAVDTV	0.493	242	WB	Large T	A0206
501	YLDGSVKVNL	0.487	257	WB	Large T	A0206
569	ILQSGMTLLL	0.483	269	WB	Large T	A0206
520	QIFPPGLVTM	0.482	272	WB	Large T	A0206
338	CQQAVDTVLA	0.481	275	WB	Large T	A0206
277	YAVETKCEDV	0.480	278	WB	Large T	A0206
155	RTLACFAVYT	0.469	312	WB	Large T	A0206
563	FLLEKRILQS	0.454	368	WB	Large T	A0206
603	RLDSEISMYT	0.445	405	WB	Large T	A0206
397	CLLPKMDSVI	0.441	422	WB	Large T	A0206
457	RLTFELGVAI	0.437	440	WB	Large T	A0206
207	SAINNFCQKL	0.433	463	WB	Large T	A0206
463	GVAIDQYMVV	0.429	481	WB	Large T	A0206
501	YLDGSVKVNL	0.958	1	SB	Large T	A0211
405	VIFDFLHCVV	0.936	2	SB	Large T	A0211
525	GLVTMNEYPV	0.915	2	SB	Large T	A0211
291	GMYLEFQYNV	0.909	2	SB	Large T	A0211
569	ILQSGMTLLL	0.902	2	SB	Large T	A0211
142	DLHQFLSQAV	0.898	3	SB	Large T	A0211
497	SLRDYLDGSV	0.895	3	SB	Large T	A0211
401	KMDSVIFDFL	0.890	3	SB	Large T	A0211
577	LLLLIWFRPV	0.888	3	SB	Large T	A0211
56	TLYKKMEQDV	0.875	3	SB	Large T	A0211
361	MLTERFNHIL	0.874	3	SB	Large T	A0211
383	AVLEQYMAGV	0.866	4	SB	Large T	A0211
442	DLCGGKALNV	0.854	4	SB	Large T	A0211
375	LIFGAHGNAV	0.829	6	SB	Large T	A0211
3	VLNREESMEL	0.824	6	SB	Large T	A0211
288	LLLGMYLEFQ	0.816	7	SB	Large T	A0211
603	RLDSEISMYT	0.797	9	SB	Large T	A0211
404	SVIFDFLHCV	0.791	9	SB	Large T	A0211
236	ALTRDPYHII	0.782	10	SB	Large T	A0211
388	YMAGVAWLHC	0.782	10	SB	Large T	A0211
12	LMDLLGLERA	0.757	13	SB	Large T	A0211
287	FLLLGMYLEF	0.747	15	SB	Large T	A0211
463	GVAIDQYMVV	0.742	16	SB	Large T	A0211
336	SICQQAVDTV	0.736	17	SB	Large T	A0211
345	VLAKKRVDTL	0.725	19	SB	Large T	A0211
353	TLHMTREEML	0.722	20	SB	Large T	A0211
568	RILQSGMTLL	0.720	20	SB	Large T	A0211
440	LLDLCGGKAL	0.713	22	SB	Large T	A0211
578	LLLIWFRPVA	0.712	22	SB	Large T	A0211
563	FLLEKRILQS	0.708	23	SB	Large T	A0211
9	SMELMDLLGL	0.706	24	SB	Large T	A0211
439	GLLDLCGGKA	0.690	28	SB	Large T	A0211
520	QIFPPGLVTM	0.684	30	SB	Large T	A0211
25	NLPLMRKAYL	0.682	31	SB	Large T	A0211
457	RLTFELGVAI	0.675	33	SB	Large T	A0211
156	TLACFAVYTT	0.669	35	SB	Large T	A0211
435	TLAAGLLDLC	0.649	44	SB	Large T	A0211
397	CLLPKMDSVI	0.648	44	SB	Large T	A0211
197	FFLTPHRHRV	0.635	51	WB	Large T	A0211
537	TLQARFVRQI	0.630	55	WB	Large T	A0211
609	SMYTFSRMKY	0.624	58	WB	Large T	A0211
176	LMEKYSVTFI	0.612	66	WB	Large T	A0211
175	KLMEKYSVTF	0.575	98	WB	Large T	A0211
103	DLFCHEDMFA	0.573	101	WB	Large T	A0211
289	LLGMYLEFQY	0.539	146	WB	Large T	A0211
428	PIDSGKTTLA	0.534	155	WB	Large T	A0211
272	KLITEYAVET	0.531	160	WB	Large T	A0211

545	QIDFRPKIYL	0.527	166	WB	Large T A0211
575	TLLLLLIWFR	0.518	183	WB	Large T A0211
198	FLTPHRHRVS	0.517	185	WB	Large T A0211
528	TMNEYPVPKT	0.509	203	WB	Large T A0211
17	GLERAAWGNL	0.502	219	WB	Large T A0211
384	VLEQYMAGVA	0.492	244	WB	Large T A0211
277	YAVETKCEDV	0.480	278	WB	Large T A0211
124	STPPKKKRKV	0.477	287	WB	Large T A0211
360	EMLTERFNHI	0.458	351	WB	Large T A0211
171	ILYKKLMEKY	0.456	358	WB	Large T A0211
369	ILDKMDLIFG	0.442	418	WB	Large T A0211
215	KLCTFSFLIC	0.432	464	WB	Large T A0211
461	ELGVAIDQYM	0.429	479	WB	Large T A0211
501	YLDGSVKVNL	0.900	2	SB	Large T A0212
405	VIFDFLHCVV	0.897	3	SB	Large T A0212
56	TLYKKMEQDV	0.893	3	SB	Large T A0212
291	GMYLEFQYNV	0.886	3	SB	Large T A0212
497	SLRDYLDGSV	0.867	4	SB	Large T A0212
383	AVLEQYMAGV	0.855	4	SB	Large T A0212
525	GLVTMNEYPV	0.825	6	SB	Large T A0212
361	MLTERFNHIL	0.824	6	SB	Large T A0212
375	LIFGAHGNAV	0.806	8	SB	Large T A0212
142	DLHQFLSQAV	0.795	9	SB	Large T A0212
3	VLNREESMEL	0.788	9	SB	Large T A0212
401	KMDSVIFDFL	0.784	10	SB	Large T A0212
569	ILQSGMTLLL	0.783	10	SB	Large T A0212
577	LLLLIWFRPV	0.783	10	SB	Large T A0212
388	YMAGVAWLHC	0.765	12	SB	Large T A0212
345	VLAKKRVDTL	0.754	14	SB	Large T A0212
288	LLLGMYLEFQ	0.715	21	SB	Large T A0212
287	FLLLGMYLEF	0.683	30	SB	Large T A0212
563	FLLEKRILQS	0.666	37	SB	Large T A0212
442	DLCGGKALNV	0.657	40	SB	Large T A0212
397	CLLPKMDSVI	0.632	53	WB	Large T A0212
12	LMDLLGLERA	0.604	72	WB	Large T A0212
404	SVIFDFLHCV	0.604	72	WB	Large T A0212
9	SMELMDLLGL	0.579	95	WB	Large T A0212
603	RLDSEISMYT	0.573	101	WB	Large T A0212
236	ALTRDPYHII	0.570	104	WB	Large T A0212
277	YAVETKCEDV	0.569	106	WB	Large T A0212
578	LLLIWFRPVA	0.558	119	WB	Large T A0212
353	TLHMTREEML	0.552	126	WB	Large T A0212
197	FFLTPHRHRV	0.549	131	WB	Large T A0212
520	QIFPPGLVTM	0.543	139	WB	Large T A0212
176	LMEKYSVTFI	0.536	150	WB	Large T A0212
175	KLMEKYSVTF	0.528	165	WB	Large T A0212
463	GVAIDQYMVV	0.500	222	WB	Large T A0212
336	SICQQAVDTV	0.495	235	WB	Large T A0212
457	RLTFELGVAI	0.489	252	WB	Large T A0212
198	FLTPHRHRVS	0.484	266	WB	Large T A0212
609	SMYTFSRMKY	0.480	276	WB	Large T A0212
171	ILYKKLMEKY	0.477	285	WB	Large T A0212
25	NLPLMRKAYL	0.477	287	WB	Large T A0212
439	GLLDLCGGKA	0.476	288	WB	Large T A0212
611	YTFSRMKYNI	0.472	304	WB	Large T A0212
435	TLAAGLLDLC	0.461	342	WB	Large T A0212
440	LLDLCGGKAL	0.459	349	WB	Large T A0212
568	RILQSGMTLL	0.458	352	WB	Large T A0212
360	EMLTERFNHI	0.457	354	WB	Large T A0212
537	TLQARFVRQI	0.452	375	WB	Large T A0212
17	GLERAAWGNL	0.430	474	WB	Large T A0212

528	TMNEYPVPKT	0.428	488	WB	Large T A0212
525	GLVTMNEYPV	0.882	3	SB	Large T A0216
405	VIFDFLHCVV	0.863	4	SB	Large T A0216
497	SLRDYLDGSV	0.861	4	SB	Large T A0216
56	TLYKKMEQDV	0.842	5	SB	Large T A0216
291	GMYLEFQYNV	0.841	5	SB	Large T A0216
569	ILQSGMTLLL	0.838	5	SB	Large T A0216
501	YLDGSVKVNL	0.833	6	SB	Large T A0216
361	MLTERFNHIL	0.812	7	SB	Large T A0216
142	DLHQFLSQAV	0.809	7	SB	Large T A0216
401	KMDSVIFDFL	0.806	8	SB	Large T A0216
442	DLCGGKALNV	0.802	8	SB	Large T A0216
375	LIFGAHGNAV	0.773	11	SB	Large T A0216
3	VLNREESMEL	0.768	12	SB	Large T A0216
345	VLAKKRVDTL	0.765	12	SB	Large T A0216
577	LLLLIWFRPV	0.743	16	SB	Large T A0216
383	AVLEQYMAGV	0.739	16	SB	Large T A0216
336	SICQQAVDTV	0.721	20	SB	Large T A0216
25	NLPLMRKAYL	0.703	24	SB	Large T A0216
288	LLLGMYLEFQ	0.679	32	SB	Large T A0216
176	LMEKYSVTFI	0.675	33	SB	Large T A0216
236	ALTRDPYHII	0.671	35	SB	Large T A0216
353	TLHMTREEML	0.668	36	SB	Large T A0216
404	SVIFDFLHCV	0.647	45	SB	Large T A0216
603	RLDSEISMYT	0.630	54	WB	Large T A0216
197	FFLTPHRHRV	0.615	64	WB	Large T A0216
388	YMAGVAWLHC	0.602	73	WB	Large T A0216
568	RILQSGMTLL	0.598	77	WB	Large T A0216
156	TLACFAVYTT	0.567	108	WB	Large T A0216
397	CLLPKMDSVI	0.562	114	WB	Large T A0216
461	ELGVAIDQYM	0.550	130	WB	Large T A0216
17	GLERAAWGNL	0.545	137	WB	Large T A0216
103	DLFCHEDMFA	0.537	149	WB	Large T A0216
463	GVAIDQYMVV	0.534	155	WB	Large T A0216
537	TLQARFVRQI	0.528	165	WB	Large T A0216
563	FLLEKRILQS	0.511	198	WB	Large T A0216
545	QIDFRPKIYL	0.493	240	WB	Large T A0216
12	LMDLLGLERA	0.484	265	WB	Large T A0216
287	FLLLGMYLEF	0.483	270	WB	Large T A0216
289	LLGMYLEFQY	0.482	270	WB	Large T A0216
439	GLLDLCGGKA	0.477	287	WB	Large T A0216
9	SMELMDLLGL	0.468	316	WB	Large T A0216
673	HLCKGFQCFK	0.468	317	WB	Large T A0216
520	QIFPPGLVTM	0.463	334	WB	Large T A0216
190	CAGHNIIFFL	0.447	397	WB	Large T A0216
440	LLDLCGGKAL	0.445	406	WB	Large T A0216
124	STPPKKKRKV	0.438	439	WB	Large T A0216
578	LLLIWFRPVA	0.428	485	WB	Large T A0216
501	YLDGSVKVNL	0.885	3	SB	Large T A0219
569	ILQSGMTLLL	0.833	6	SB	Large T A0219
401	KMDSVIFDFL	0.761	13	SB	Large T A0219
361	MLTERFNHIL	0.747	15	SB	Large T A0219
405	VIFDFLHCVV	0.704	24	SB	Large T A0219
291	GMYLEFQYNV	0.679	32	SB	Large T A0219
142	DLHQFLSQAV	0.676	33	SB	Large T A0219
577	LLLLIWFRPV	0.646	45	SB	Large T A0219
525	GLVTMNEYPV	0.631	54	WB	Large T A0219
497	SLRDYLDGSV	0.622	59	WB	Large T A0219
388	YMAGVAWLHC	0.582	91	WB	Large T A0219
3	VLNREESMEL	0.573	101	WB	Large T A0219

288	LLLGMYLEFQ	0.572	102	WB	Large T	A0219
56	TLYKKMEQDV	0.570	104	WB	Large T	A0219
375	LIFGAHGNAV	0.565	110	WB	Large T	A0219
442	DLCGGKALNV	0.557	120	WB	Large T	A0219
383	AVLEQYMAGV	0.556	122	WB	Large T	A0219
236	ALTRDPYHII	0.545	137	WB	Large T	A0219
345	VLAKKRVDTL	0.515	189	WB	Large T	A0219
603	RLDSEISMYT	0.498	227	WB	Large T	A0219
12	LMDLLGLERA	0.486	260	WB	Large T	A0219
397	CLLPKMDSVI	0.475	293	WB	Large T	A0219
404	SVIFDFLHCV	0.474	294	WB	Large T	A0219
435	TLAAGLLDLC	0.459	347	WB	Large T	A0219
197	FFLTPHRHRV	0.449	389	WB	Large T	A0219
353	TLHMTREEML	0.433	463	WB	Large T	A0219
537	TLQARFVRQI	0.427	492	WB	Large T	A0219
170	QILYKKLMEK	0.764	12	SB	Large T	A0301
50	KMKRMNTLYK	0.754	14	SB	Large T	A0301
615	RMKYNICMGK	0.751	14	SB	Large T	A0301
608	ISMYTFSRMK	0.734	17	SB	Large T	A0301
609	SMYTFSRMKY	0.707	23	SB	Large T	A0301
527	VTMNEYPVPK	0.691	28	SB	Large T	A0301
673	HLCKGFQCFK	0.668	36	SB	Large T	A0301
27	PLMRKAYLKK	0.663	38	SB	Large T	A0301
157	LACFAVYTTK	0.654	42	SB	Large T	A0301
392	VAWLHCLLPK	0.582	92	WB	Large T	A0301
575	TLLLLLIWFR	0.574	100	WB	Large T	A0301
220	SFLICKGVNK	0.554	124	WB	Large T	A0301
22	AWGNLPLMRK	0.533	156	WB	Large T	A0301
326	IIFAESKNQK	0.519	181	WB	Large T	A0301
26	LPLMRKAYLK	0.500	222	WB	Large T	A0301
558	LQNSEFLLEK	0.484	265	WB	Large T	A0301
311	QPYHFKYHEK	0.465	326	WB	Large T	A0301
417	VPKRRYWLFK	0.462	338	WB	Large T	A0301
206	VSAINNFCQK	0.448	391	WB	Large T	A0301
448	ALNVNLPMER	0.447	396	WB	Large T	A0301
273	LITEYAVETK	0.446	399	WB	Large T	A0301
171	ILYKKLMEKY	0.433	462	WB	Large T	A0301
527	VTMNEYPVPK	0.811	7	SB	Large T	A1101
608	ISMYTFSRMK	0.760	13	SB	Large T	A1101
392	VAWLHCLLPK	0.708	23	SB	Large T	A1101
558	LQNSEFLLEK	0.705	24	SB	Large T	A1101
50	KMKRMNTLYK	0.700	25	SB	Large T	A1101
326	IIFAESKNQK	0.695	27	SB	Large T	A1101
206	VSAINNFCQK	0.692	28	SB	Large T	A1101
609	SMYTFSRMKY	0.665	37	SB	Large T	A1101
575	TLLLLLIWFR	0.648	45	SB	Large T	A1101
170	QILYKKLMEK	0.643	47	SB	Large T	A1101
157	LACFAVYTTK	0.635	51	WB	Large T	A1101
673	HLCKGFQCFK	0.622	59	WB	Large T	A1101
90	ESWWSSFNEK	0.565	110	WB	Large T	A1101
615	RMKYNICMGK	0.556	121	WB	Large T	A1101
121	SQHSTPPKKK	0.552	127	WB	Large T	A1101
504	GSVKVNLEKK	0.541	143	WB	Large T	A1101
339	QQAVDTVLAK	0.540	145	WB	Large T	A1101
340	QAVDTVLAKK	0.534	154	WB	Large T	A1101
448	ALNVNLPMER	0.528	165	WB	Large T	A1101
194	NIIFFLTPHR	0.516	188	WB	Large T	A1101
27	PLMRKAYLKK	0.478	284	WB	Large T	A1101
21	AAWGNLPLMR	0.475	293	WB	Large T	A1101
273	LITEYAVETK	0.470	310	WB	Large T	A1101

120	DSQHSTPPKK	0.450	383	WB	Large T A1101
22	AWGNLPLMRK	0.449	387	WB	Large T A1101
220	SFLICKGVNK	0.445	404	WB	Large T A1101
468	QYMVVFEDVK	0.626	57	WB	Large T A2301
151	VFSNRTLACF	0.608	69	WB	Large T A2301
287	FLLLGMYLEF	0.575	99	WB	Large T A2301
582	WFRPVADFSK	0.548	133	WB	Large T A2301
57	LYKKMEQDVK	0.531	160	WB	Large T A2301
574	MTLLLLLIWF	0.524	171	WB	Large T A2301
83	TYGTEEWESW	0.500	224	WB	Large T A2301
406	IFDFLHCVVF	0.486	260	WB	Large T A2301
416	NVPKRRYWLF	0.477	288	WB	Large T A2301
220	SFLICKGVNK	0.469	311	WB	Large T A2301
159	CFAVYTTKEK	0.465	326	WB	Large T A2301
203	RHRVSAINNF	0.458	351	WB	Large T A2301
295	EFQYNVEECK	0.447	396	WB	Large T A2301
175	KLMEKYSVTF	0.446	401	WB	Large T A2301
91	SWWSSFNEKW	0.436	447	WB	Large T A2301
464	VAIDQYMVVF	0.430	478	WB	Large T A2301
212	FCQKLCTFSF	0.426	499	WB	Large T A2301
151	VFSNRTLACF	0.606	71	WB	Large T A2402
162	VYTTKEKAQI	0.518	183	WB	Large T A2402
617	KYNICMGKCI	0.510	200	WB	Large T A2402
416	NVPKRRYWLF	0.506	209	WB	Large T A2402
406	IFDFLHCVVF	0.483	269	WB	Large T A2402
83	TYGTEEWESW	0.472	301	WB	Large T A2402
138	DFPSDLHQFL	0.430	477	WB	Large T A2402
83	TYGTEEWESW	0.622	59	WB	Large T A2403
513	KHLNKRTQIF	0.548	132	WB	Large T A2403
287	FLLLGMYLEF	0.533	155	WB	Large T A2403
212	FCQKLCTFSF	0.510	201	WB	Large T A2403
162	VYTTKEKAQI	0.492	243	WB	Large T A2403
175	KLMEKYSVTF	0.491	245	WB	Large T A2403
151	VFSNRTLACF	0.479	280	WB	Large T A2403
313	YHFKYHEKHF	0.456	358	WB	Large T A2403
406	IFDFLHCVVF	0.453	370	WB	Large T A2403
416	NVPKRRYWLF	0.449	389	WB	Large T A2403
203	RHRVSAINNF	0.444	408	WB	Large T A2403
574	MTLLLLLIWF	0.429	480	WB	Large T A2403
164	TTKEKAQILY	0.552	127	WB	Large T A2601
607	EISMYTFSRM	0.466	322	WB	Large T A2601
607	EISMYTFSRM	0.857	4	SB	Large T A2602
520	QIFPPGLVTM	0.811	7	SB	Large T A2602
268	QVSWKLITEY	0.726	19	SB	Large T A2602
164	TTKEKAQILY	0.721	20	SB	Large T A2602
416	NVPKRRYWLF	0.714	22	SB	Large T A2602
533	PVPKTLQARF	0.685	30	SB	Large T A2602
64	DVKVAHQPDF	0.665	37	SB	Large T A2602
280	ETKCEDVFLL	0.646	46	SB	Large T A2602
285	DVFLLLGMYL	0.612	66	WB	Large T A2602
368	HILDKMDLIF	0.589	85	WB	Large T A2602
80	EVPTYGTEEW	0.587	86	WB	Large T A2602
184	FISRHMCAGH	0.532	158	WB	Large T A2602
163	YTTKEKAQIL	0.514	192	WB	Large T A2602
284	EDVFLLLGMY	0.470	308	WB	Large T A2602
138	DFPSDLHQFL	0.465	326	WB	Large T A2602
611	YTFSRMKYNI	0.465	327	WB	Large T A2602

574	MTLLLLLIWF	0.463	333	WB	Large T A2602
464	VAIDQYMVVF	0.457	354	WB	Large T A2602
404	SVIFDFLHCV	0.451	380	WB	Large T A2602
609	SMYTFSRMKY	0.700	25	SB	Large T A2902
413	VVFNVPKRRY	0.524	172	WB	Large T A2902
171	ILYKKLMEKY	0.501	221	WB	Large T A2902
289	LLGMYLEFQY	0.496	232	WB	Large T A2902
75	TWNSSEVPTY	0.466	321	WB	Large T A2902
268	QVSWKLITEY	0.455	364	WB	Large T A2902
50	KMKRMNTLYK	0.848	5	SB	Large T A3001
676	KGFQCFKRPK	0.733	17	SB	Large T A3001
681	FKRPKTPPPK	0.723	20	SB	Large T A3001
51	MKRMNTLYKK	0.685	30	SB	Large T A3001
615	RMKYNICMGK	0.677	33	SB	Large T A3001
527	VTMNEYPVPK	0.661	39	SB	Large T A3001
417	VPKRRYWLFK	0.637	50	WB	Large T A3001
121	SQHSTPPKKK	0.623	59	WB	Large T A3001
582	WFRPVADFSK	0.622	59	WB	Large T A3001
542	FVRQIDFRPK	0.556	121	WB	Large T A3001
608	ISMYTFSRMK	0.552	126	WB	Large T A3001
128	KKKRKVEDPK	0.548	132	WB	Large T A3001
547	DFRPKIYLRK	0.507	207	WB	Large T A3001
307	QKKDQPYHFK	0.501	220	WB	Large T A3001
27	PLMRKAYLKK	0.500	224	WB	Large T A3001
356	MTREEMLTER	0.494	238	WB	Large T A3001
29	MRKAYLKKCK	0.488	255	WB	Large T A3001
119	ADSQHSTPPK	0.460	344	WB	Large T A3001
363	TERFNHILDK	0.445	405	WB	Large T A3001
166	KEKAQILYKK	0.442	418	WB	Large T A3001
164	TTKEKAQILY	0.439	432	WB	Large T A3001
120	DSQHSTPPKK	0.428	485	WB	Large T A3001
233	LYSALTRDPY	0.534	155	WB	Large T A3002
609	SMYTFSRMKY	0.528	165	WB	Large T A3002
268	QVSWKLITEY	0.485	262	WB	Large T A3002
75	TWNSSEVPTY	0.446	400	WB	Large T A3002
575	TLLLLLIWFR	0.750	14	SB	Large T A3101
230	EYLLYSALTR	0.642	48	SB	Large T A3101
50	KMKRMNTLYK	0.640	49	SB	Large T A3101
674	LCKGFQCFKR	0.638	50	WB	Large T A3101
609	SMYTFSRMKY	0.623	58	WB	Large T A3101
615	RMKYNICMGK	0.604	72	WB	Large T A3101
194	NIIFFLTPHR	0.586	88	WB	Large T A3101
448	ALNVNLPMER	0.583	90	WB	Large T A3101
673	HLCKGFQCFK	0.573	101	WB	Large T A3101
146	FLSQAVFSNR	0.570	104	WB	Large T A3101
412	CVVFNVPKRR	0.565	110	WB	Large T A3101
196	IFFLTPHRHR	0.550	130	WB	Large T A3101
356	MTREEMLTER	0.548	132	WB	Large T A3101
349	KRVDTLHMTR	0.530	161	WB	Large T A3101
220	SFLICKGVNK	0.524	172	WB	Large T A3101
51	MKRMNTLYKK	0.468	316	WB	Large T A3101
157	LACFAVYTTK	0.456	358	WB	Large T A3101
535	PKTLQARFVR	0.445	403	WB	Large T A3101
606	SEISMYTFSR	0.445	404	WB	Large T A3101
594	QSRIVEWKER	0.442	417	WB	Large T A3101
205	RVSAINNFCQ	0.434	458	WB	Large T A3101
230	EYLLYSALTR	0.653	42	SB	Large T A3301

575 TLLLLLIWFR	0.600	76	WB	Large T	A3301
674 LCKGFQCFKR	0.537	150	WB	Large T	A3301
196 IFFLTPHRHR	0.529	162	WB	Large T	A3301
194 NIIFFLTPHR	0.529	163	WB	Large T	A3301
11 ELMDLLGLER	0.512	196	WB	Large T	A3301
146 FLSQAVFSNR	0.482	271	WB	Large T	A3301
178 EKYSVTFISR	0.464	330	WB	Large T	A3301
547 DFRPKIYLRK	0.429	482	WB	Large T	A3301
Large T A3301					
194 NIIFFLTPHR	0.866	4	SB	Large T	A6801
412 CVVFNVPKRR	0.785	10	SB	Large T	A6801
356 MTREEMLTER	0.784	10	SB	Large T	A6801
90 ESWWSSFNEK	0.756	13	SB	Large T	A6801
146 FLSQAVFSNR	0.739	16	SB	Large T	A6801
11 ELMDLLGLER	0.720	20	SB	Large T	A6801
178 EKYSVTFISR	0.713	22	SB	Large T	A6801
157 LACFAVYTTK	0.693	27	SB	Large T	A6801
608 ISMYTFSRMK	0.660	39	SB	Large T	A6801
673 HLCKGFQCFK	0.645	46	SB	Large T	A6801
230 EYLLYSALTR	0.644	47	SB	Large T	A6801
575 TLLLLLIWFR	0.643	47	SB	Large T	A6801
326 IIFAESKNQK	0.639	49	SB	Large T	A6801
273 LITEYAVETK	0.632	53	WB	Large T	A6801
206 VSAINNFCQK	0.629	55	WB	Large T	A6801
340 QAVDTVLAKK	0.623	59	WB	Large T	A6801
490 HGINNLDSLR	0.593	81	WB	Large T	A6801
475 DVKGTGAESK	0.581	93	WB	Large T	A6801
606 SEISMYTFSR	0.572	102	WB	Large T	A6801
592 DIQSRIVEWK	0.563	113	WB	Large T	A6801
311 QPYHFKYHEK	0.556	122	WB	Large T	A6801
527 VTMNEYPVPK	0.541	143	WB	Large T	A6801
295 EFQYNVEECK	0.539	146	WB	Large T	A6801
299 NVEECKKCQK	0.534	155	WB	Large T	A6801
159 CFAVYTTKEK	0.524	171	WB	Large T	A6801
296 FQYNVEECKK	0.510	200	WB	Large T	A6801
196 IFFLTPHRHR	0.505	212	WB	Large T	A6801
622 MGKCILDITR	0.480	277	WB	Large T	A6801
542 FVRQIDFRPK	0.478	282	WB	Large T	A6801
411 HCVVFNVPKR	0.476	290	WB	Large T	A6801
120 DSQHSTPPKK	0.461	341	WB	Large T	A6801
546 IDFRPKIYLR	0.437	443	WB	Large T	A6801
164 TTKEKAQILY	0.433	460	WB	Large T	A6801
404 SVIFDFLHCV	0.762	13	SB	Large T	A6802
611 YTFSRMKYNI	0.677	32	SB	Large T	A6802
285 DVFLLLGMYL	0.632	53	WB	Large T	A6802
322 FANAIIFAES	0.613	66	WB	Large T	A6802
280 ETKCEDVFLL	0.609	69	WB	Large T	A6802
462 LGVAIDQYMV	0.574	100	WB	Large T	A6802
607 EISMYTFSRM	0.562	114	WB	Large T	A6802
375 LIFGAHGNAV	0.557	120	WB	Large T	A6802
405 VIFDFLHCVV	0.536	151	WB	Large T	A6802
647 ESQSQCSSQV	0.517	185	WB	Large T	A6802
190 CAGHNIIFFL	0.488	253	WB	Large T	A6802
383 AVLEQYMAGV	0.479	281	WB	Large T	A6802
77 NSSEVPTYGT	0.467	320	WB	Large T	A6802
19 ERAAWGNLPL	0.452	375	WB	Large T	A6802
108 EDMFASDEEA	0.451	379	WB	Large T	A6802
265 ETKQVSWKLI	0.451	380	WB	Large T	A6802
207 SAINNFCQKL	0.440	428	WB	Large T	A6802
463 GVAIDQYMVV	0.433	459	WB	Large T	A6802

156	TLACFAVYTT	0.432	465	WB	Large T A6802
383	AVLEQYMAGV	0.745	15	SB	Large T A6901
404	SVIFDFLHCV	0.639	49	SB	Large T A6901
611	YTFSRMKYNI	0.596	79	WB	Large T A6901
375	LIFGAHGNAV	0.575	99	WB	Large T A6901
405	VIFDFLHCVV	0.552	127	WB	Large T A6901
360	EMLTERFNHI	0.545	137	WB	Large T A6901
520	QIFPPGLVTM	0.541	143	WB	Large T A6901
453	LPMERLTFEL	0.477	287	WB	Large T A6901
434	TTLAAGLLDL	0.466	324	WB	Large T A6901
277	YAVETKCEDV	0.458	352	WB	Large T A6901
197	FFLTPHRHRV	0.452	374	WB	Large T A6901
577	LLLLIWFRPV	0.435	451	WB	Large T A6901
285	DVFLLLGMYL	0.431	470	WB	Large T A6901
549	RPKIYLRKSL	0.785	10	SB	Large T B0702
200	TPHRHRVSAI	0.752	14	SB	Large T B0702
453	LPMERLTFEL	0.722	20	SB	Large T B0702
427	GPIDSGKTTL	0.704	24	SB	Large T B0702
486	LPSGHGINNL	0.573	101	WB	Large T B0702
584	RPVADFSKDI	0.560	117	WB	Large T B0702
549	RPKIYLRKSL	0.479	280	WB	Large T B0801
200	TPHRHRVSAI	0.453	373	WB	Large T B0801
544	RQIDFRPKIY	0.584	89	WB	Large T B1501
188	HMCAGHNIIF	0.577	97	WB	Large T B1501
175	KLMEKYSVTF	0.568	107	WB	Large T B1501
609	SMYTFSRMKY	0.536	150	WB	Large T B1501
148	SQAVFSNRTL	0.502	218	WB	Large T B1501
268	QVSWKLITEY	0.478	284	WB	Large T B1501
287	FLLLGMYLEF	0.475	292	WB	Large T B1501
249	IQGGLKEHDF	0.467	318	WB	Large T B1501
464	VAIDQYMVVF	0.445	406	WB	Large T B1501
570	LQSGMTLLLL	0.439	434	WB	Large T B1501
460	FELGVAIDQY	0.795	9	SB	Large T B1801
87	EEWESWWSSF	0.653	42	SB	Large T B1801
455	MERLTFELGV	0.576	98	WB	Large T B1801
574	MTLLLLLIWF	0.498	227	WB	Large T B1801
420	RRYWLFKGPI	0.605	71	WB	Large T B2705
52	KRMNTLYKKM	0.591	83	WB	Large T B2705
567	KRILQSGMTL	0.564	111	WB	Large T B2705
349	KRVDTLHMTR	0.487	258	WB	Large T B2705
517	KRTQIFPPGL	0.471	305	WB	Large T B2705
464	VAIDQYMVVF	0.679	32	SB	Large T B3501
453	LPMERLTFEL	0.600	75	WB	Large T B3501
20	RAAWGNLPLM	0.595	80	WB	Large T B3501
268	QVSWKLITEY	0.558	119	WB	Large T B3501
486	LPSGHGINNL	0.549	131	WB	Large T B3501
287	FLLLGMYLEF	0.479	279	WB	Large T B3501
523	PPGLVTMNEY	0.479	281	WB	Large T B3501
532	YPVPKTLQAR	0.470	310	WB	Large T B3501
139	FPSDLHQFLS	0.459	347	WB	Large T B3501
189	MCAGHNIIFF	0.451	379	WB	Large T B3501
389	MAGVAWLHCL	0.449	390	WB	Large T B3501
262	EPEETKQVSW	0.433	460	WB	Large T B3501
317	YHEKHFANAI	0.608	69	WB	Large T B3901

148	SQAVFSNRTL	0.545	137	WB	Large T B3901
19	ERAAWGNLPL	0.539	147	WB	Large T B3901
501	YLDGSVKVNL	0.498	228	WB	Large T B3901
6	REESMELMDL	0.707	23	SB	Large T B4001
561	SEFLLEKRIL	0.683	30	SB	Large T B4001
279	VETKCEDVFL	0.502	218	WB	Large T B4001
264	EETKQVSWKL	0.500	224	WB	Large T B4001
7	EESMELMDLL	0.488	253	WB	Large T B4001
455	MERLTFELGV	0.485	263	WB	Large T B4001
561	SEFLLEKRIL	0.595	80	WB	Large T B4002
7	EESMELMDLL	0.482	271	WB	Large T B4002
229	KEYLLYSALT	0.482	272	WB	Large T B4002
279	VETKCEDVFL	0.472	303	WB	Large T B4002
87	EEWESWWSSF	0.458	353	WB	Large T B4002
561	SEFLLEKRIL	0.496	233	WB	Large T B4403
606	SEISMYTFSR	0.427	493	WB	Large T B4403
453	LPMERLTFEL	0.695	27	SB	Large T B5101
240	DPYHIIEESI	0.492	244	WB	Large T B5101
486	LPSGHGINNL	0.447	397	WB	Large T B5101
453	LPMERLTFEL	0.721	20	SB	Large T B5301
262	EPEETKQVSW	0.716	21	SB	Large T B5301
486	LPSGHGINNL	0.585	89	WB	Large T B5301
427	GPIDSGKTTL	0.470	308	WB	Large T B5301
200	TPHRHRVSAI	0.457	356	WB	Large T B5301
139	FPSDLHQFLS	0.584	89	WB	Large T B5401
26	LPLMRKAYLK	0.511	197	WB	Large T B5401
160	FAVYTTKEKA	0.489	252	WB	Large T B5401
453	LPMERLTFEL	0.483	267	WB	Large T B5401
67	VAHQPDFGTW	0.448	393	WB	Large T B5701
67	VAHQPDFGTW	0.537	149	WB	Large T B5801
464	VAIDQYMVVF	0.503	216	WB	Large T B5801
20	RAAWGNLPLM	0.485	263	WB	Large T B5801
556	KSLQNSEFLL	0.475	293	WB	Large T B5801
175	KLMEKYSVTF	0.437	440	WB	Large T B5801
31	KAYLKKCKEF	0.431	473	WB	Large T B5801
591	KDIQSRIVEW	0.430	474	WB	Large T B5801
	11-mers				
163	YTTKEKAQILY	0.682	31	SB	Large T A0101
388	YMAGVAWLHCL	0.862	4	SB	Large T A0201
175	KLMEKYSVTFI	0.854	4	SB	Large T A0201
576	LLLLLIWFRPV	0.708	23	SB	Large T A0201
369	ILDKMDLIFGA	0.641	48	SB	Large T A0201
569	ILQSGMTLLLL	0.609	68	WB	Large T A0201
146	FLSQAVFSNRT	0.563	113	WB	Large T A0201
198	FLTPHRHRVSA	0.558	119	WB	Large T A0201
287	FLLLGMYLEFQ	0.530	162	WB	Large T A0201
568	RILQSGMTLLL	0.506	209	WB	Large T A0201
528	TMNEYPVPKTL	0.501	222	WB	Large T A0201
439	GLLDLCGGKAL	0.469	312	WB	Large T A0201
448	ALNVNLPMERL	0.469	313	WB	Large T A0201
577	LLLLIWFRPVA	0.462	336	WB	Large T A0201

11	ELMDLLGLERA	0.458	351	WB	Large T A0201
217	CTFSFLICKGV	0.447	398	WB	Large T A0201
152	FSNRTLACFAV	0.439	431	WB	Large T A0201
269	VSWKLITEYAV	0.439	432	WB	Large T A0201
570	LQSGMTLLLLL	0.434	457	WB	Large T A0201
2	KVLNREESMEL	0.432	467	WB	Large T A0201
388	YMAGVAWLHCL	0.869	4	SB	Large T A0202
175	KLMEKYSVTFI	0.858	4	SB	Large T A0202
189	MCAGHNIIFFL	0.726	19	SB	Large T A0202
198	FLTPHRHRVSA	0.718	21	SB	Large T A0202
146	FLSQAVFSNRT	0.718	21	SB	Large T A0202
570	LQSGMTLLLLL	0.667	36	SB	Large T A0202
569	ILQSGMTLLLL	0.666	36	SB	Large T A0202
448	ALNVNLPMERL	0.624	58	WB	Large T A0202
576	LLLLLIWFRPV	0.621	60	WB	Large T A0202
152	FSNRTLACFAV	0.601	74	WB	Large T A0202
287	FLLLGMYLEFQ	0.593	82	WB	Large T A0202
528	TMNEYPVPKTL	0.587	87	WB	Large T A0202
11	ELMDLLGLERA	0.582	92	WB	Large T A0202
243	HIIEESIQGGL	0.571	103	WB	Large T A0202
369	ILDKMDLIFGA	0.561	115	WB	Large T A0202
212	FCQKLCTFSFL	0.560	116	WB	Large T A0202
375	LIFGAHGNAVL	0.541	142	WB	Large T A0202
461	ELGVAIDQYMV	0.541	143	WB	Large T A0202
409	FLHCVVFNVPK	0.524	171	WB	Large T A0202
439	GLLDLCGGKAL	0.519	181	WB	Large T A0202
452	NLPMERLTFEL	0.515	189	WB	Large T A0202
407	FDFLHCVVFNV	0.493	239	WB	Large T A0202
3	VLNREESMELM	0.491	245	WB	Large T A0202
268	QVSWKLITEYA	0.488	255	WB	Large T A0202
290	LGMYLEFQYNV	0.481	273	WB	Large T A0202
217	CTFSFLICKGV	0.464	330	WB	Large T A0202
564	LLEKRILQSGM	0.447	398	WB	Large T A0202
222	LICKGVNKEYL	0.436	448	WB	Large T A0202
226	GVNKEYLLYSA	0.428	485	WB	Large T A0202
388	YMAGVAWLHCL	0.868	4	SB	Large T A0203
175	KLMEKYSVTFI	0.862	4	SB	Large T A0203
198	FLTPHRHRVSA	0.779	10	SB	Large T A0203
528	TMNEYPVPKTL	0.766	12	SB	Large T A0203
576	LLLLLIWFRPV	0.728	19	SB	Large T A0203
569	ILQSGMTLLLL	0.703	24	SB	Large T A0203
146	FLSQAVFSNRT	0.702	25	SB	Large T A0203
448	ALNVNLPMERL	0.668	36	SB	Large T A0203
11	ELMDLLGLERA	0.652	42	SB	Large T A0203
439	GLLDLCGGKAL	0.593	81	WB	Large T A0203
268	QVSWKLITEYA	0.577	97	WB	Large T A0203
570	LQSGMTLLLLL	0.548	132	WB	Large T A0203
226	GVNKEYLLYSA	0.540	144	WB	Large T A0203
243	HIIEESIQGGL	0.523	174	WB	Large T A0203
375	LIFGAHGNAVL	0.522	176	WB	Large T A0203
382	NAVLEQYMAGV	0.516	188	WB	Large T A0203
217	CTFSFLICKGV	0.515	190	WB	Large T A0203
374	DLIFGAHGNAV	0.511	197	WB	Large T A0203
404	SVIFDFLHCVV	0.498	229	WB	Large T A0203
152	FSNRTLACFAV	0.491	245	WB	Large T A0203
3	VLNREESMELM	0.473	298	WB	Large T A0203
287	FLLLGMYLEFQ	0.469	312	WB	Large T A0203
452	NLPMERLTFEL	0.465	327	WB	Large T A0203
369	ILDKMDLIFGA	0.464	328	WB	Large T A0203
568	RILQSGMTLLL	0.457	356	WB	Large T A0203

199	LTPHRHRVSAI	0.453	373	WB	Large T	A0203
471	VVFEDVKGTGA	0.450	383	WB	Large T	A0203
469	YMVVFEDVKGT	0.450	385	WB	Large T	A0203
388	YMAGVAWLHCL	0.691	28	SB	Large T	A0204
528	TMNEYPVPKTL	0.687	29	SB	Large T	A0204
175	KLMEKYSVTFI	0.670	35	SB	Large T	A0204
576	LLLLLIWFRPV	0.616	63	WB	Large T	A0204
198	FLTPHRHRVSA	0.583	91	WB	Large T	A0204
2	KVLNREESMEL	0.525	170	WB	Large T	A0204
569	ILQSGMTLLLL	0.449	386	WB	Large T	A0204
336	SICQQAVDTVL	0.431	472	WB	Large T	A0204
544	RQIDFRPKIYL	0.801	8	SB	Large T	A0206
388	YMAGVAWLHCL	0.796	9	SB	Large T	A0206
175	KLMEKYSVTFI	0.743	16	SB	Large T	A0206
576	LLLLLIWFRPV	0.738	16	SB	Large T	A0206
570	LQSGMTLLLLL	0.711	22	SB	Large T	A0206
198	FLTPHRHRVSA	0.706	24	SB	Large T	A0206
404	SVIFDFLHCVV	0.688	29	SB	Large T	A0206
152	FSNRTLACFAV	0.646	46	SB	Large T	A0206
568	RILQSGMTLLL	0.644	47	SB	Large T	A0206
369	ILDKMDLIFGA	0.622	59	WB	Large T	A0206
2	KVLNREESMEL	0.620	61	WB	Large T	A0206
148	SQAVFSNRTLA	0.618	62	WB	Large T	A0206
335	KSICQQAVDTV	0.568	106	WB	Large T	A0206
382	NAVLEQYMAGV	0.548	133	WB	Large T	A0206
519	TQIFPPGLVTM	0.539	146	WB	Large T	A0206
243	HIIEESIQGGL	0.519	182	WB	Large T	A0206
287	FLLLGMYLEFQ	0.515	191	WB	Large T	A0206
146	FLSQAVFSNRT	0.506	210	WB	Large T	A0206
569	ILQSGMTLLLL	0.487	256	WB	Large T	A0206
439	GLLDLCGGKAL	0.478	284	WB	Large T	A0206
213	CQKLCTFSFLI	0.469	312	WB	Large T	A0206
542	FVRQIDFRPKI	0.464	330	WB	Large T	A0206
267	KQVSWKLITEY	0.462	336	WB	Large T	A0206
471	VVFEDVKGTGA	0.460	343	WB	Large T	A0206
383	AVLEQYMAGVA	0.445	407	WB	Large T	A0206
577	LLLLIWFRPVA	0.444	408	WB	Large T	A0206
155	RTLACFAVYTT	0.442	419	WB	Large T	A0206
268	QVSWKLITEYA	0.438	437	WB	Large T	A0206
375	LIFGAHGNAVL	0.437	441	WB	Large T	A0206
452	NLPMERLTFEL	0.429	479	WB	Large T	A0206
296	FQYNVEECKKC	0.427	490	WB	Large T	A0206
388	YMAGVAWLHCL	0.966	1	SB	Large T	A0211
198	FLTPHRHRVSA	0.943	1	SB	Large T	A0211
576	LLLLLIWFRPV	0.898	3	SB	Large T	A0211
569	ILQSGMTLLLL	0.893	3	SB	Large T	A0211
439	GLLDLCGGKAL	0.887	3	SB	Large T	A0211
452	NLPMERLTFEL	0.875	3	SB	Large T	A0211
369	ILDKMDLIFGA	0.868	4	SB	Large T	A0211
528	TMNEYPVPKTL	0.858	4	SB	Large T	A0211
461	ELGVAIDQYMV	0.854	4	SB	Large T	A0211
287	FLLLGMYLEFQ	0.832	6	SB	Large T	A0211
454	PMERLTFELGV	0.823	6	SB	Large T	A0211
11	ELMDLLGLERA	0.815	7	SB	Large T	A0211
360	EMLTERFNHIL	0.779	10	SB	Large T	A0211
374	DLIFGAHGNAV	0.775	11	SB	Large T	A0211
175	KLMEKYSVTFI	0.773	11	SB	Large T	A0211
577	LLLLIWFRPVA	0.765	12	SB	Large T	A0211
568	RILQSGMTLLL	0.755	14	SB	Large T	A0211

288	LLLGMYLEFQY	0.753	14	SB	Large T A0211
341	AVDTVLAKKRV	0.752	14	SB	Large T A0211
448	ALNVNLPMERL	0.747	15	SB	Large T A0211
375	LIFGAHGNAVL	0.691	28	SB	Large T A0211
603	RLDSEISMYTF	0.681	31	SB	Large T A0211
404	SVIFDFLHCVV	0.671	35	SB	Large T A0211
12	LMDLLGLERAA	0.669	35	SB	Large T A0211
146	FLSQAVFSNRT	0.648	45	SB	Large T A0211
485	DLPSGHGINNL	0.644	47	SB	Large T A0211
563	FLLEKRILQSG	0.601	74	WB	Large T A0211
2	KVLNREESMEL	0.597	77	WB	Large T A0211
501	YLDGSVKVNLE	0.596	78	WB	Large T A0211
189	MCAGHNIIFFL	0.591	83	WB	Large T A0211
428	PIDSGKTTLAA	0.577	97	WB	Large T A0211
405	VIFDFLHCVVF	0.563	112	WB	Large T A0211
196	IFFLTPHRHRV	0.551	128	WB	Large T A0211
217	CTFSFLICKGV	0.550	130	WB	Large T A0211
269	VSWKLITEYAV	0.549	132	WB	Large T A0211
109	DMFASDEEATA	0.544	138	WB	Large T A0211
544	RQIDFRPKIYL	0.542	141	WB	Large T A0211
3	VLNREESMELM	0.535	153	WB	Large T A0211
557	SLQNSEFLLEK	0.517	186	WB	Large T A0211
533	PVPKTLQARFV	0.511	198	WB	Large T A0211
243	HIIEESIQGGL	0.500	224	WB	Large T A0211
401	KMDSVIFDFLH	0.486	260	WB	Large T A0211
222	LICKGVNKEYL	0.462	338	WB	Large T A0211
353	TLHMTREEMLT	0.459	349	WB	Large T A0211
232	LLYSALTRDPY	0.435	449	WB	Large T A0211
215	KLCTFSFLICK	0.435	452	WB	Large T A0211
573	GMTLLLLLIWF	0.433	459	WB	Large T A0211
423	WLFKGPIDSGK	0.428	487	WB	Large T A0211
388	YMAGVAWLHCL	0.936	1	SB	Large T A0212
198	FLTPHRHRVSA	0.906	2	SB	Large T A0212
439	GLLDLCGGKAL	0.823	6	SB	Large T A0212
528	TMNEYPVPKTL	0.817	7	SB	Large T A0212
576	LLLLLIWFRPV	0.817	7	SB	Large T A0212
454	PMERLTFELGV	0.806	8	SB	Large T A0212
569	ILQSGMTLLLL	0.801	8	SB	Large T A0212
287	FLLLGMYLEFQ	0.777	11	SB	Large T A0212
369	ILDKMDLIFGA	0.756	13	SB	Large T A0212
374	DLIFGAHGNAV	0.706	24	SB	Large T A0212
360	EMLTERFNHIL	0.682	31	SB	Large T A0212
461	ELGVAIDQYMV	0.658	40	SB	Large T A0212
288	LLLGMYLEFQY	0.655	41	SB	Large T A0212
11	ELMDLLGLERA	0.654	42	SB	Large T A0212
452	NLPMERLTFEL	0.645	46	SB	Large T A0212
563	FLLEKRILQSG	0.643	47	SB	Large T A0212
375	LIFGAHGNAVL	0.631	54	WB	Large T A0212
175	KLMEKYSVTFI	0.620	60	WB	Large T A0212
577	LLLLIWFRPVA	0.601	74	WB	Large T A0212
269	VSWKLITEYAV	0.598	77	WB	Large T A0212
12	LMDLLGLERAA	0.577	96	WB	Large T A0212
146	FLSQAVFSNRT	0.577	97	WB	Large T A0212
448	ALNVNLPMERL	0.574	100	WB	Large T A0212
341	AVDTVLAKKRV	0.549	132	WB	Large T A0212
485	DLPSGHGINNL	0.537	149	WB	Large T A0212
405	VIFDFLHCVVF	0.536	151	WB	Large T A0212
3	VLNREESMELM	0.514	192	WB	Large T A0212
423	WLFKGPIDSGK	0.499	225	WB	Large T A0212
2	KVLNREESMEL	0.481	273	WB	Large T A0212
404	SVIFDFLHCVV	0.458	350	WB	Large T A0212

564	LLEKRILQSGM	0.452	374	WB	Large T A0212
469	YMVVFEDVKGT	0.452	377	WB	Large T A0212
243	HIIEESIQGGL	0.441	421	WB	Large T A0212
222	LICKGVNKEYL	0.440	428	WB	Large T A0212
217	CTFSFLICKGV	0.437	444	WB	Large T A0212
196	IFFLTPHRHRV	0.436	445	WB	Large T A0212
189	MCAGHNIIFFL	0.432	469	WB	Large T A0212
471	VVFEDVKGTGA	0.426	495	WB	Large T A0212
388	YMAGVAWLHCL	0.907	2	SB	Large T A0216
198	FLTPHRHRVSA	0.867	4	SB	Large T A0216
461	ELGVAIDQYMV	0.859	4	SB	Large T A0216
569	ILQSGMTLLLL	0.824	6	SB	Large T A0216
452	NLPMERLTFEL	0.778	11	SB	Large T A0216
454	PMERLTFELGV	0.771	11	SB	Large T A0216
576	LLLLLIWFRPV	0.754	14	SB	Large T A0216
528	TMNEYPVPKTL	0.752	14	SB	Large T A0216
374	DLIFGAHGNAV	0.737	17	SB	Large T A0216
287	FLLLGMYLEFQ	0.712	22	SB	Large T A0216
341	AVDTVLAKKRV	0.711	22	SB	Large T A0216
369	ILDKMDLIFGA	0.696	26	SB	Large T A0216
448	ALNVNLPMERL	0.693	27	SB	Large T A0216
175	KLMEKYSVTFI	0.691	28	SB	Large T A0216
439	GLLDLCGGKAL	0.678	32	SB	Large T A0216
146	FLSQAVFSNRT	0.661	39	SB	Large T A0216
11	ELMDLLGLERA	0.650	43	SB	Large T A0216
485	DLPSGHGINNL	0.642	48	SB	Large T A0216
375	LIFGAHGNAVL	0.639	49	SB	Large T A0216
360	EMLTERFNHIL	0.631	54	WB	Large T A0216
222	LICKGVNKEYL	0.620	60	WB	Large T A0216
568	RILQSGMTLLL	0.559	118	WB	Large T A0216
196	IFFLTPHRHRV	0.554	124	WB	Large T A0216
533	PVPKTLQARFV	0.551	128	WB	Large T A0216
404	SVIFDFLHCVV	0.528	165	WB	Large T A0216
189	MCAGHNIIFFL	0.523	173	WB	Large T A0216
288	LLLGMYLEFQY	0.517	186	WB	Large T A0216
2	KVLNREESMEL	0.514	191	WB	Large T A0216
577	LLLLIWFRPVA	0.493	240	WB	Large T A0216
544	RQIDFRPKIYL	0.485	264	WB	Large T A0216
269	VSWKLITEYAV	0.483	267	WB	Large T A0216
161	AVYTTKEKAQI	0.475	293	WB	Large T A0216
109	DMFASDEEATA	0.457	355	WB	Large T A0216
388	YMAGVAWLHCL	0.952	1	SB	Large T A0219
569	ILQSGMTLLLL	0.841	5	SB	Large T A0219
198	FLTPHRHRVSA	0.685	30	SB	Large T A0219
576	LLLLLIWFRPV	0.681	31	SB	Large T A0219
287	FLLLGMYLEFQ	0.664	37	SB	Large T A0219
461	ELGVAIDQYMV	0.655	41	SB	Large T A0219
369	ILDKMDLIFGA	0.647	45	SB	Large T A0219
11	ELMDLLGLERA	0.602	73	WB	Large T A0219
454	PMERLTFELGV	0.584	90	WB	Large T A0219
448	ALNVNLPMERL	0.562	114	WB	Large T A0219
146	FLSQAVFSNRT	0.559	118	WB	Large T A0219
374	DLIFGAHGNAV	0.556	121	WB	Large T A0219
360	EMLTERFNHIL	0.537	149	WB	Large T A0219
528	TMNEYPVPKTL	0.532	157	WB	Large T A0219
485	DLPSGHGINNL	0.524	172	WB	Large T A0219
452	NLPMERLTFEL	0.507	206	WB	Large T A0219
341	AVDTVLAKKRV	0.499	226	WB	Large T A0219
439	GLLDLCGGKAL	0.485	262	WB	Large T A0219
189	MCAGHNIIFFL	0.462	337	WB	Large T A0219

175	KLMEKYSVTFI	0.454	367	WB	Large T	A0219
269	VSWKLITEYAV	0.448	394	WB	Large T	A0219
156	TLACFAVYTTK	0.728	18	SB	Large T	A0301
409	FLHCVVFNVPK	0.709	23	SB	Large T	A0301
215	KLCTFSFLICK	0.671	35	SB	Large T	A0301
50	KMKRMNTLYKK	0.667	36	SB	Large T	A0301
391	GVAWLHCLLPK	0.656	41	SB	Large T	A0301
205	RVSAINNFCQK	0.650	44	SB	Large T	A0301
56	TLYKKMEQDVK	0.645	46	SB	Large T	A0301
507	KVNLEKKHLNK	0.586	88	WB	Large T	A0301
219	FSFLICKGVNK	0.581	92	WB	Large T	A0301
195	IIFFLTPHRHR	0.575	99	WB	Large T	A0301
164	TTKEKAQILYK	0.549	131	WB	Large T	A0301
557	SLQNSEFLLEK	0.539	146	WB	Large T	A0301
272	KLITEYAVETK	0.533	156	WB	Large T	A0301
21	AAWGNLPLMRK	0.508	205	WB	Large T	A0301
416	NVPKRRYWLFK	0.507	206	WB	Large T	A0301
608	ISMYTFSRMKY	0.491	247	WB	Large T	A0301
574	MTLLLLLIWFR	0.485	261	WB	Large T	A0301
673	HLCKGFQCFKR	0.459	348	WB	Large T	A0301
28	LMRKAYLKKCK	0.454	369	WB	Large T	A0301
244	IIEESIQGGLK	0.448	393	WB	Large T	A0301
497	SLRDYLDGSVK	0.443	416	WB	Large T	A0301
423	WLFKGPIDSGK	0.432	464	WB	Large T	A0301
401	KMDSVIFDFLH	0.427	490	WB	Large T	A0301
391	GVAWLHCLLPK	0.825	6	SB	Large T	A1101
215	KLCTFSFLICK	0.800	8	SB	Large T	A1101
557	SLQNSEFLLEK	0.791	9	SB	Large T	A1101
205	RVSAINNFCQK	0.784	10	SB	Large T	A1101
574	MTLLLLLIWFR	0.768	12	SB	Large T	A1101
21	AAWGNLPLMRK	0.742	16	SB	Large T	A1101
164	TTKEKAQILYK	0.721	20	SB	Large T	A1101
156	TLACFAVYTTK	0.719	20	SB	Large T	A1101
526	LVTMNEYPVPK	0.716	21	SB	Large T	A1101
507	KVNLEKKHLNK	0.706	24	SB	Large T	A1101
325	AIIFAESKNQK	0.702	25	SB	Large T	A1101
169	AQILYKKLMEK	0.699	25	SB	Large T	A1101
118	TADSQHSTPPK	0.677	32	SB	Large T	A1101
416	NVPKRRYWLFK	0.651	43	SB	Large T	A1101
56	TLYKKMEQDVK	0.640	49	SB	Large T	A1101
50	KMKRMNTLYKK	0.634	52	WB	Large T	A1101
447	KALNVNLPMER	0.627	56	WB	Large T	A1101
322	FANAIIFAESK	0.620	61	WB	Large T	A1101
608	ISMYTFSRMKY	0.609	68	WB	Large T	A1101
219	FSFLICKGVNK	0.594	80	WB	Large T	A1101
338	CQQAVDTVLAK	0.593	81	WB	Large T	A1101
362	LTERFNHILDK	0.588	86	WB	Large T	A1101
409	FLHCVVFNVPK	0.555	122	WB	Large T	A1101
195	IIFFLTPHRHR	0.547	134	WB	Large T	A1101
437	AAGLLDLCGGK	0.547	134	WB	Large T	A1101
20	RAAWGNLPLMR	0.531	160	WB	Large T	A1101
272	KLITEYAVETK	0.526	169	WB	Large T	A1101
607	EISMYTFSRMK	0.523	174	WB	Large T	A1101
244	IIEESIQGGLK	0.506	209	WB	Large T	A1101
339	QQAVDTVLAKK	0.471	307	WB	Large T	A1101
467	DQYMVVFEDVK	0.445	404	WB	Large T	A1101
497	SLRDYLDGSVK	0.436	448	WB	Large T	A1101
581	IWFRPVADFSK	0.434	454	WB	Large T	A1101
312	PYHFKYHEKHF	0.709	23	SB	Large T	A2301

286	VFLLLGMYLEF	0.704	24	SB	Large T A2301
610	MYTFSRMKYNI	0.668	36	SB	Large T A2301
581	IWFRPVADFSK	0.626	57	WB	Large T A2301
500	DYLDGSVKVNL	0.598	77	WB	Large T A2301
211	NFCQKLCTFSF	0.575	99	WB	Large T A2301
83	TYGTEEWESWW	0.560	116	WB	Large T A2301
187	RHMCAGHNIIF	0.491	245	WB	Large T A2301
179	KYSVTFISRHM	0.485	263	WB	Large T A2301
316	KYHEKHFANAI	0.478	282	WB	Large T A2301
295	EFQYNVEECKK	0.478	283	WB	Large T A2301
617	KYNICMGKCIL	0.477	288	WB	Large T A2301
95	SFNEKWDEDLF	0.476	289	WB	Large T A2301
553	YLRKSLQNSEF	0.468	316	WB	Large T A2301
162	VYTTKEKAQIL	0.451	380	WB	Large T A2301
405	VIFDFLHCVVF	0.442	417	WB	Large T A2301
316	KYHEKHFANAI	0.677	33	SB	Large T A2402
286	VFLLLGMYLEF	0.676	33	SB	Large T A2402
312	PYHFKYHEKHF	0.617	62	WB	Large T A2402
610	MYTFSRMKYNI	0.570	105	WB	Large T A2402
83	TYGTEEWESWW	0.514	192	WB	Large T A2402
179	KYSVTFISRHM	0.513	193	WB	Large T A2402
162	VYTTKEKAQIL	0.482	272	WB	Large T A2402
211	NFCQKLCTFSF	0.461	341	WB	Large T A2402
286	VFLLLGMYLEF	0.742	16	SB	Large T A2403
316	KYHEKHFANAI	0.713	22	SB	Large T A2403
83	TYGTEEWESWW	0.653	42	SB	Large T A2403
312	PYHFKYHEKHF	0.613	66	WB	Large T A2403
397	CLLPKMDSVIF	0.571	103	WB	Large T A2403
162	VYTTKEKAQIL	0.563	112	WB	Large T A2403
365	RFNHILDKMDL	0.554	124	WB	Large T A2403
553	YLRKSLQNSEF	0.528	165	WB	Large T A2403
617	KYNICMGKCIL	0.509	202	WB	Large T A2403
211	NFCQKLCTFSF	0.504	213	WB	Large T A2403
95	SFNEKWDEDLF	0.478	285	WB	Large T A2403
187	RHMCAGHNIIF	0.466	321	WB	Large T A2403
163	YTTKEKAQILY	0.631	54	WB	Large T A2601
8	ESMELMDLLGL	0.474	297	WB	Large T A2601
163	YTTKEKAQILY	0.728	19	SB	Large T A2602
150	AVFSNRTLACF	0.703	24	SB	Large T A2602
170	QILYKKLMEKY	0.637	51	WB	Large T A2602
405	VIFDFLHCVVF	0.629	55	WB	Large T A2602
280	ETKCEDVFLLL	0.628	56	WB	Large T A2602
463	GVAIDQYMVVF	0.624	58	WB	Large T A2602
243	HIIEESIQGGL	0.535	153	WB	Large T A2602
356	MTREEMLTERF	0.491	247	WB	Large T A2602
142	DLHQFLSQAVF	0.472	304	WB	Large T A2602
450	NVNLPMERLTF	0.453	372	WB	Large T A2602
553	YLRKSLQNSEF	0.450	382	WB	Large T A2602
74	GTWNSSEVPTY	0.435	453	WB	Large T A2602
8	ESMELMDLLGL	0.433	462	WB	Large T A2602
221	FLICKGVNKEY	0.621	60	WB	Large T A2902
288	LLLGMYLEFQY	0.600	75	WB	Large T A2902
163	YTTKEKAQILY	0.475	293	WB	Large T A2902
286	VFLLLGMYLEF	0.470	307	WB	Large T A2902
170	QILYKKLMEKY	0.430	478	WB	Large T A2902
405	VIFDFLHCVVF	0.427	492	WB	Large T A2902

50	KMKRMNTLYKK	0.760	13	SB	Large T	A3001
28	LMRKAYLKKCK	0.745	15	SB	Large T	A3001
164	TTKEKAQILYK	0.727	19	SB	Large T	A3001
507	KVNLEKKHLNK	0.707	23	SB	Large T	A3001
680	CFKRPKTPPPK	0.688	29	SB	Large T	A3001
409	FLHCVVFNVPK	0.668	36	SB	Large T	A3001
497	SLRDYLDGSVK	0.662	38	SB	Large T	A3001
158	ACFAVYTTKEK	0.661	39	SB	Large T	A3001
416	NVPKRRYWLFK	0.594	80	WB	Large T	A3001
541	RFVRQIDFRPK	0.587	87	WB	Large T	A3001
215	KLCTFSFLICK	0.567	107	WB	Large T	A3001
348	KKRVDTLHMTR	0.563	112	WB	Large T	A3001
205	RVSAINNFCQK	0.546	136	WB	Large T	A3001
526	LVTMNEYPVPK	0.536	151	WB	Large T	A3001
306	CQKKDQPYHFK	0.508	204	WB	Large T	A3001
118	TADSQHSTPPK	0.505	211	WB	Large T	A3001
272	KLITEYAVETK	0.489	252	WB	Large T	A3001
156	TLACFAVYTTK	0.486	259	WB	Large T	A3001
557	SLQNSEFLLEK	0.482	271	WB	Large T	A3001
169	AQILYKKLMEK	0.470	309	WB	Large T	A3001
539	QARFVRQIDFR	0.458	353	WB	Large T	A3001
581	IWFRPVADFSK	0.451	378	WB	Large T	A3001
574	MTLLLLLIWFR	0.433	462	WB	Large T	A3001
34	LKKCKEFHPDK	0.429	482	WB	Large T	A3001
267	KQVSWKLITEY	0.523	175	WB	Large T	A3002
170	QILYKKLMEKY	0.442	420	WB	Large T	A3002
574	MTLLLLLIWFR	0.869	4	SB	Large T	A3101
50	KMKRMNTLYKK	0.838	5	SB	Large T	A3101
447	KALNVNLPMER	0.794	9	SB	Large T	A3101
145	QFLSQAVFSNR	0.744	15	SB	Large T	A3101
195	IIFFLTPHRHR	0.736	17	SB	Large T	A3101
673	HLCKGFQCFKR	0.670	35	SB	Large T	A3101
539	QARFVRQIDFR	0.653	42	SB	Large T	A3101
355	HMTREEMLTER	0.647	45	SB	Large T	A3101
205	RVSAINNFCQK	0.637	50	WB	Large T	A3101
558	LQNSEFLLEKR	0.626	57	WB	Large T	A3101
541	RFVRQIDFRPK	0.624	58	WB	Large T	A3101
20	RAAWGNLPLMR	0.617	63	WB	Large T	A3101
121	SQHSTPPKKKR	0.607	70	WB	Large T	A3101
621	CMGKCILDITR	0.587	87	WB	Large T	A3101
177	MEKYSVTFISR	0.582	91	WB	Large T	A3101
215	KLCTFSFLICK	0.554	124	WB	Large T	A3101
164	TTKEKAQILYK	0.536	151	WB	Large T	A3101
680	CFKRPKTPPPK	0.526	169	WB	Large T	A3101
534	VPKTLQARFVR	0.518	183	WB	Large T	A3101
193	HNIIFFLTPHR	0.500	223	WB	Large T	A3101
507	KVNLEKKHLNK	0.492	244	WB	Large T	A3101
306	CQKKDQPYHFK	0.486	259	WB	Large T	A3101
526	LVTMNEYPVPK	0.467	319	WB	Large T	A3101
229	KEYLLYSALTR	0.466	321	WB	Large T	A3101
593	IQSRIVEWKER	0.449	389	WB	Large T	A3101
31	KAYLKKCKEFH	0.448	392	WB	Large T	A3101
545	QIDFRPKIYLR	0.448	393	WB	Large T	A3101
401	KMDSVIFDFLH	0.443	415	WB	Large T	A3101
605	DSEISMYTFSR	0.438	435	WB	Large T	A3101
28	LMRKAYLKKCK	0.433	461	WB	Large T	A3101
574	MTLLLLLIWFR	0.838	5	SB	Large T	A3301
195	IIFFLTPHRHR	0.685	30	SB	Large T	A3301
605	DSEISMYTFSR	0.684	30	SB	Large T	A3301

539	QARFVRQIDFR	0.650	44	SB	Large T	A3301
145	QFLSQAVFSNR	0.639	49	SB	Large T	A3301
355	HMTREEMLTER	0.625	57	WB	Large T	A3301
673	HLCKGFQCFKR	0.606	70	WB	Large T	A3301
531	EYPVPKTLQAR	0.582	92	WB	Large T	A3301
545	QIDFRPKIYLR	0.484	264	WB	Large T	A3301
285	DVFLLLGMYLE	0.462	337	WB	Large T	A3301
416	NVPKRRYWLFK	0.441	424	WB	Large T	A3301
177	MEKYSVTFISR	0.440	428	WB	Large T	A3301
574	MTLLLLLIWFR	0.820	7	SB	Large T	A6801
607	EISMYTFSRMK	0.808	7	SB	Large T	A6801
322	FANAIIFAESK	0.780	10	SB	Large T	A6801
605	DSEISMYTFSR	0.765	12	SB	Large T	A6801
195	IIFFLTPHRHR	0.762	13	SB	Large T	A6801
156	TLACFAVYTTK	0.756	14	SB	Large T	A6801
205	RVSAINNFCQK	0.712	22	SB	Large T	A6801
539	QARFVRQIDFR	0.695	27	SB	Large T	A6801
219	FSFLICKGVNK	0.676	33	SB	Large T	A6801
193	HNIIFFLTPHR	0.673	34	SB	Large T	A6801
673	HLCKGFQCFKR	0.665	37	SB	Large T	A6801
164	TTKEKAQILYK	0.656	41	SB	Large T	A6801
355	HMTREEMLTER	0.654	42	SB	Large T	A6801
526	LVTMNEYPVPK	0.641	48	SB	Large T	A6801
416	NVPKRRYWLFK	0.635	51	WB	Large T	A6801
340	QAVDTVLAKKR	0.620	61	WB	Large T	A6801
409	FLHCVVFNVPK	0.589	85	WB	Large T	A6801
20	RAAWGNLPLMR	0.562	114	WB	Large T	A6801
325	AIIFAESKNQK	0.554	124	WB	Large T	A6801
56	TLYKKMEQDVK	0.549	131	WB	Large T	A6801
163	YTTKEKAQILY	0.548	132	WB	Large T	A6801
467	DQYMVVFEDVK	0.534	155	WB	Large T	A6801
391	GVAWLHCLLPK	0.521	178	WB	Large T	A6801
608	ISMYTFSRMKY	0.493	240	WB	Large T	A6801
295	EFQYNVEECKK	0.489	251	WB	Large T	A6801
25	NLPLMRKAYLK	0.482	272	WB	Large T	A6801
447	KALNVNLPMER	0.477	288	WB	Large T	A6801
545	QIDFRPKIYLR	0.471	305	WB	Large T	A6801
362	LTERFNHILDK	0.463	332	WB	Large T	A6801
177	MEKYSVTFISR	0.463	335	WB	Large T	A6801
145	QFLSQAVFSNR	0.460	343	WB	Large T	A6801
423	WLFKGPIDSGK	0.456	361	WB	Large T	A6801
118	TADSQHSTPPK	0.435	450	WB	Large T	A6801
557	SLQNSEFLLEK	0.430	477	WB	Large T	A6801
189	MCAGHNIIFFL	0.792	9	SB	Large T	A6802
217	CTFSFLICKGV	0.752	14	SB	Large T	A6802
404	SVIFDFLHCVV	0.734	17	SB	Large T	A6802
382	NAVLEQYMAGV	0.680	31	SB	Large T	A6802
403	DSVIFDFLHCV	0.654	42	SB	Large T	A6802
8	ESMELMDLLGL	0.653	42	SB	Large T	A6802
152	FSNRTLACFAV	0.617	62	WB	Large T	A6802
290	LGMYLEFQYNV	0.606	70	WB	Large T	A6802
462	LGVAIDQYMVV	0.591	83	WB	Large T	A6802
268	QVSWKLITEYA	0.576	98	WB	Large T	A6802
280	ETKCEDVFLLL	0.573	101	WB	Large T	A6802
11	ELMDLLGLERA	0.570	105	WB	Large T	A6802
234	YSALTRDPYHI	0.549	132	WB	Large T	A6802
388	YMAGVAWLHCL	0.531	159	WB	Large T	A6802
243	HIIEESIQGGL	0.507	206	WB	Large T	A6802
181	SVTFISRHMCA	0.503	216	WB	Large T	A6802
407	FDFLHCVVFNV	0.489	251	WB	Large T	A6802

374	DLIFGAHGNAV	0.480	277	WB	Large T	A6802
542	FVRQIDFRPKI	0.446	400	WB	Large T	A6802
212	FCQKLCTFSFL	0.433	460	WB	Large T	A6802
461	ELGVAIDQYMV	0.429	484	WB	Large T	A6802
388	YMAGVAWLHCL	0.652	42	SB	Large T	A6901
461	ELGVAIDQYMV	0.575	99	WB	Large T	A6901
374	DLIFGAHGNAV	0.573	102	WB	Large T	A6901
8	ESMELMDLLGL	0.560	116	WB	Large T	A6901
152	FSNRTLACFAV	0.541	143	WB	Large T	A6901
11	ELMDLLGLERA	0.539	145	WB	Large T	A6901
576	LLLLLIWFRPV	0.519	182	WB	Large T	A6901
404	SVIFDFLHCVV	0.512	196	WB	Large T	A6901
360	EMLTERFNHIL	0.498	228	WB	Large T	A6901
189	MCAGHNIIFFL	0.474	297	WB	Large T	A6901
243	HIIEESIQGGL	0.472	303	WB	Large T	A6901
382	NAVLEQYMAGV	0.470	309	WB	Large T	A6901
217	CTFSFLICKGV	0.457	355	WB	Large T	A6901
269	VSWKLITEYAV	0.443	414	WB	Large T	A6901
55	NTLYKKMEQDV	0.432	464	WB	Large T	A6901
532	YPVPKTLQARF	0.646	46	SB	Large T	B0702
553	YLRKSLQNSEF	0.492	244	WB	Large T	B0801
267	KQVSWKLITEY	0.566	109	WB	Large T	B1501
538	LQARFVRQIDF	0.565	110	WB	Large T	B1501
553	YLRKSLQNSEF	0.561	116	WB	Large T	B1501
188	HMCAGHNIIFF	0.554	124	WB	Large T	B1501
388	YMAGVAWLHCL	0.542	141	WB	Large T	B1501
221	FLICKGVNKEY	0.541	142	WB	Large T	B1501
544	RQIDFRPKIYL	0.521	178	WB	Large T	B1501
579	LLIWFRPVADF	0.518	183	WB	Large T	B1501
519	TQIFPPGLVTM	0.480	276	WB	Large T	B1501
232	LLYSALTRDPY	0.478	283	WB	Large T	B1501
405	VIFDFLHCVVF	0.474	295	WB	Large T	B1501
608	ISMYTFSRMKY	0.450	384	WB	Large T	B1501
150	AVFSNRTLACF	0.434	457	WB	Large T	B1501
570	LQSGMTLLLLL	0.429	483	WB	Large T	B1501
668	HSQELHLCKGF	0.426	495	WB	Large T	B1501
86	TEEWESWWSSF	0.650	44	SB	Large T	B1801
460	FELGVAIDQYM	0.643	47	SB	Large T	B1801
318	HEKHFANAIIF	0.625	57	WB	Large T	B1801
18	LERAAWGNLPL	0.572	102	WB	Large T	B1801
79	SEVPTYGTEEW	0.556	122	WB	Large T	B1801
601	KERLDSEISMY	0.505	210	WB	Large T	B1801
664	SENPHSQELHL	0.497	230	WB	Large T	B1801
532	YPVPKTLQARF	0.461	341	WB	Large T	B1801
614	SRMKYNICMGK	0.547	134	WB	Large T	B2705
567	KRILQSGMTLL	0.507	207	WB	Large T	B2705
544	RQIDFRPKIYL	0.450	382	WB	Large T	B2705
548	FRPKIYLRKSL	0.450	385	WB	Large T	B2705
522	FPPGLVTMNEY	0.812	7	SB	Large T	B3501
532	YPVPKTLQARF	0.780	10	SB	Large T	B3501
277	YAVETKCEDVF	0.742	16	SB	Large T	B3501
399	LPKMDSVIFDF	0.560	116	WB	Large T	B3501
41	HPDKGGDEDKM	0.545	136	WB	Large T	B3501
392	VAWLHCLLPKM	0.532	158	WB	Large T	B3501
139	FPSDLHQFLSQ	0.494	238	WB	Large T	B3501

232	LLYSALTRDPY	0.453	371	WB	Large T	B3501
459	TFELGVAIDQY	0.442	417	WB	Large T	B3501
317	YHEKHFANAII	0.586	88	WB	Large T	B3901
388	YMAGVAWLHCL	0.549	130	WB	Large T	B3901
6	REESMELMDLL	0.673	34	SB	Large T	B4001
664	SENPHSQELHL	0.668	36	SB	Large T	B4001
18	LERAAWGNLPL	0.630	54	WB	Large T	B4001
385	LEQYMAGVAWL	0.562	114	WB	Large T	B4001
460	FELGVAIDQYM	0.552	126	WB	Large T	B4001
279	VETKCEDVFLL	0.540	145	WB	Large T	B4001
606	SEISMYTFSRM	0.498	228	WB	Large T	B4001
133	VEDPKDFPSDL	0.446	399	WB	Large T	B4001
166	KEKAQILYKKL	0.440	428	WB	Large T	B4001
47	DEDKMKRMNTL	0.434	458	WB	Large T	B4001
664	SENPHSQELHL	0.540	144	WB	Large T	B4002
6	REESMELMDLL	0.511	198	WB	Large T	B4002
264	EETKQVSWKLI	0.502	219	WB	Large T	B4002
318	HEKHFANAIIF	0.459	347	WB	Large T	B4002
359	EEMLTERFNHI	0.445	403	WB	Large T	B4002
279	VETKCEDVFLL	0.432	464	WB	Large T	B4002
79	SEVPTYGTEEW	0.512	196	WB	Large T	B4402
261	EEPEETKQVSW	0.484	267	WB	Large T	B4402
561	SEFLLEKRILQ	0.477	287	WB	Large T	B4403
664	SENPHSQELHL	0.464	331	WB	Large T	B4403
606	SEISMYTFSRM	0.457	356	WB	Large T	B4403
79	SEVPTYGTEEW	0.452	375	WB	Large T	B4403
261	EEPEETKQVSW	0.438	438	WB	Large T	B4403
359	EEMLTERFNHI	0.482	271	WB	Large T	B4501
115	EEATADSQHST	0.450	383	WB	Large T	B4501
453	LPMERLTFELG	0.470	309	WB	Large T	B5101
532	YPVPKTLQARF	0.433	463	WB	Large T	B5101
522	FPPGLVTMNEY	0.689	28	SB	Large T	B5301
532	YPVPKTLQARF	0.645	46	SB	Large T	B5301
399	LPKMDSVIFDF	0.555	122	WB	Large T	B5301
277	YAVETKCEDVF	0.474	296	WB	Large T	B5301
453	LPMERLTFELG	0.580	93	WB	Large T	B5401
522	FPPGLVTMNEY	0.544	138	WB	Large T	B5401
427	GPIDSGKTTLA	0.508	204	WB	Large T	B5401
82	PTYGTEEWESW	0.576	98	WB	Large T	B5701
90	ESWWSSFNEKW	0.678	32	SB	Large T	B5801
66	KVAHQPDFGTW	0.658	40	SB	Large T	B5801
572	SGMTLLLLLIW	0.539	146	WB	Large T	B5801
413	VVFNVPKRRYW	0.527	167	WB	Large T	B5801
277	YAVETKCEDVF	0.495	235	WB	Large T	B5801
608	ISMYTFSRMKY	0.487	258	WB	Large T	B5801
82	PTYGTEEWESW	0.458	353	WB	Large T	B5801

Preferred BK virus fragments of agnoprotein capable of interacting with one or more MHC class 1 molecules are listed in Table N.

Table N: Prediction of BK virus Agnoprotein specific MHC class1, 8- , 9- ,10- ,11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHC/ database. The MHC class 1 molecules for which no binders were found are not listed.

pos	peptide	logscore	affinity(nM)	Bind Level	Protein Name	Allele
	8-mers					
36	FIFILELL	0.641	48	SB	Agno	A0201
59	STTALPAV	0.453	373	WB	Agno	A0201
36	FIFILELL	0.785	10	SB	Agno	A0202
12	QLSRQASV	0.702	25	SB	Agno	A0202
12	QLSRQASV	0.712	22	SB	Agno	A0203
59	STTALPAV	0.537	149	WB	Agno	A0203
36	FIFILELL	0.524	171	WB	Agno	A0203
32	AQRIFIFI	0.503	216	WB	Agno	A0203
6	NLVVLRQL	0.431	473	WB	Agno	A0203
12	QLSRQASV	0.508	206	WB	Agno	A0204
59	STTALPAV	0.489	252	WB	Agno	A0204
32	AQRIFIFI	0.646	46	SB	Agno	A0206
36	FIFILELL	0.585	89	WB	Agno	A0206
59	STTALPAV	0.582	92	WB	Agno	A0206
12	QLSRQASV	0.479	281	WB	Agno	A0206
38	FILELLLE	0.474	297	WB	Agno	A0206
-						
12	QLSRQASV	0.883	3	SB	Agno	A0211
36	FIFILELL	0.782	10	SB	Agno	A0211
59	STTALPAV	0.695	27	SB	Agno	A0211
6	NLVVLRQL	0.688	29	SB	Agno	A0211
12	QLSRQASV	0.825	6	SB	Agno	A0212
36	FIFILELL	0.705	24	SB	Agno	A0212
59	STTALPAV	0.504	214	WB	Agno	A0212
46	FCRGEDSV	0.502	219	WB	Agno	A0212
12	QLSRQASV	0.877	3	SB	Agno	A0216
36	FIFILELL	0.643	47	SB	Agno	A0216
6	NLVVLRQL	0.580	93	WB	Agno	A0216
59	STTALPAV	0.474	294	WB	Agno	A0216
1	FCEPKNLV	0.427	494	WB	Agno	A0216
12	QLSRQASV	0.746	15	SB	Agno	A0219
59	STTALPAV	0.455	364	WB	Agno	A0219
23	KTWTGTKK	0.662	38	SB	Agno	A0301
60	TTALPAVK	0.568	107	WB	Agno	A0301
8	VVLRQLSR	0.444	408	WB	Agno	A0301
13	LSRQASVK	0.436	444	WB	Agno	A0301
60	TTALPAVK	0.785	10	SB	Agno	A1101
23	KTWTGTKK	0.637	50	WB	Agno	A1101
8	VVLRQLSR	0.554	124	WB	Agno	A1101

16	QASVKVGK	0.458	351	WB	Agno	A1101
35	IFIFILEL	0.573	101	WB	Agno	A2301
31	RAQRIFIF	0.514	191	WB	Agno	A2301
37	IFILELLL	0.454	367	WB	Agno	A2301
37	IFILELLL	0.536	150	WB	Agno	A2402
35	IFIFILEL	0.478	284	WB	Agno	A2402
31	RAQRIFIF	0.431	472	WB	Agno	A2402
31	RAQRIFIF	0.449	386	WB	Agno	A2403
13	LSRQASVK	0.690	28	SB	Agno	A3001
23	KTWTGTKK	0.659	40	SB	Agno	A3001
27	GTKKRAQR	0.803	8	SB	Agno	A3101
23	KTWTGTKK	0.648	45	SB	Agno	A3101
8	VVLRQLSR	0.587	87	WB	Agno	A3101
41	ELLLEFCR	0.701	25	SB	Agno	A3301
27	GTKKRAQR	0.564	111	WB	Agno	A3301
8	VVLRQLSR	0.466	323	WB	Agno	A3301
60	TTALPAVK	0.774	11	SB	Agno	A6801
41	ELLLEFCR	0.627	56	WB	Agno	A6801
27	GTKKRAQR	0.537	150	WB	Agno	A6801
16	QASVKVGK	0.459	349	WB	Agno	A6801
51	DSVDGKNK	0.431	473	WB	Agno	A6801
59	STTALPAV	0.655	42	SB	Agno	A6802
33	QRIFIFIL	0.552	127	WB	Agno	A6802
36	FIFILELL	0.512	195	WB	Agno	A6802
59	STTALPAV	0.674	34	SB	Agno	A6901
36	FIFILELL	0.441	424	WB	Agno	A6901
63	LPAVKDSV	0.582	91	WB	Agno	B0702
3	EPKNLVVL	0.427	490	WB	Agno	B0702
33	QRIFIFIL	0.431	472	WB	Agno	B2705
3	EPKNLVVL	0.518	184	WB	Agno	B3501
63	LPAVKDSV	0.585	88	WB	Agno	B5101
3	EPKNLVVL	0.456	358	WB	Agno	B5301
63	LPAVKDSV	0.745	15	SB	Agno	B5401
31	RAQRIFIF	0.503	215	WB	Agno	B5801
	9-mers					
34	RIFIFILEL	0.674	34	SB	Agno	A0201
36	FIFILELLL	0.613	66	WB	Agno	A0201
11	RQLSRQASV	0.561	115	WB	Agno	A0201
62	ALPAVKDSV	0.503	215	WB	Agno	A0201
38	FILELLLEF	0.448	392	WB	Agno	A0201
36	FIFILELLL	0.698	26	SB	Agno	A0202
62	ALPAVKDSV	0.609	68	WB	Agno	A0202
34	RIFIFILEL	0.540	144	WB	Agno	A0202

11	RQLSRQASV	0.688	29	SB	Agno	A0203
62	ALPAVKDSV	0.667	36	SB	Agno	A0203
9	VLRQLSRQA	0.455	362	WB	Agno	A0203
34	RIFIFILEL	0.439	433	WB	Agno	A0203
62	ALPAVKDSV	0.515	190	WB	Agno	A0204
11	RQLSRQASV	0.855	4	SB	Agno	A0206
38	FILELLLEF	0.731	18	SB	Agno	A0206
62	ALPAVKDSV	0.588	86	WB	Agno	A0206
32	AQRIFIFIL	0.561	116	WB	Agno	A0206
58	KSTTALPAV	0.559	118	WB	Agno	A0206
34	RIFIFILEL	0.506	208	WB	Agno	A0206
31	RAQRIFIFI	0.487	256	WB	Agno	A0206
36	FIFILELLL	0.455	365	WB	Agno	A0206
62	ALPAVKDSV	0.927	2	SB	Agno	A0211
34	RIFIFILEL	0.836	5	SB	Agno	A0211
36	FIFILELLL	0.796	9	SB	Agno	A0211
38	FILELLLEF	0.621	60	WB	Agno	A0211
9	VLRQLSRQA	0.546	135	WB	Agno	A0211
11	RQLSRQASV	0.445	405	WB	Agno	A0211
62	ALPAVKDSV	0.904	2	SB	Agno	A0212
36	FIFILELLL	0.746	15	SB	Agno	A0212
34	RIFIFILEL	0.679	32	SB	Agno	A0212
38	FILELLLEF	0.614	65	WB	Agno	A0212
11	RQLSRQASV	0.545	138	WB	Agno	A0212
1	FCEPKNLVV	0.473	300	WB	Agno	A0212
42	LLLEFCRGE	0.465	327	WB	Agno	A0212
9	VLRQLSRQA	0.442	416	WB	Agno	A0212
62	ALPAVKDSV	0.922	2	SB	Agno	A0216
34	RIFIFILEL	0.732	18	SB	Agno	A0216
36	FIFILELLL	0.654	42	SB	Agno	A0216
11	RQLSRQASV	0.490	247	WB	Agno	A0216
62	ALPAVKDSV	0.778	11	SB	Agno	A0219
12	QLSRQASVK	0.643	47	SB	Agno	A0301
15	RQASVKVGK	0.538	148	WB	Agno	A0301
59	STTALPAVK	0.461	341	WB	Agno	A0301
59	STTALPAVK	0.825	6	SB	Agno	A1101
15	RQASVKVGK	0.624	58	WB	Agno	A1101
7	LVVLRQLSR	0.460	345	WB	Agno	A1101
35	IFIFILELL	0.514	192	WB	Agno	A2301
38	FILELLLEF	0.473	300	WB	Agno	A2301
35	IFIFILELL	0.610	67	WB	Agno	A2402
38	FILELLLEF	0.532	157	WB	Agno	A2403
38	FILELLLEF	0.598	77	WB	Agno	A2602
38	FILELLLEF	0.463	334	WB	Agno	A2902
21	VGKTWTGTK	0.528	165	WB	Agno	A3001
59	STTALPAVK	0.477	285	WB	Agno	A3001
29	KKRAQRIFI	0.452	377	WB	Agno	A3001

23	KTWTGTKKR	0.727	19	SB	Agno	A3101
15	RQASVKVGK	0.617	62	WB	Agno	A3101
26	TGTKKRAQR	0.524	172	WB	Agno	A3101
7	LVVLRQLSR	0.506	210	WB	Agno	A3101
59	STTALPAVK	0.486	260	WB	Agno	A3101
7	LVVLRQLSR	0.666	37	SB	Agno	A3301
3	EPKNLVVLR	0.510	201	WB	Agno	A3301
59	STTALPAVK	0.728	19	SB	Agno	A6801
3	EPKNLVVLR	0.667	36	SB	Agno	A6801
7	LVVLRQLSR	0.664	37	SB	Agno	A6801
31	RAQRIFIFI	0.609	68	WB	Agno	A6802
38	FILELLLEF	0.453	371	WB	Agno	B1801
15	RQASVKVGK	0.566	109	WB	Agno	B2705
30	KRAQRIFIF	0.523	174	WB	Agno	B2705
11	RQLSRQASV	0.449	390	WB	Agno	B2705
3						
38	FILELLLEF	0.505	211	WB	Agno	B3501
2	CEPKNLVVL	0.521	179	WB	Agno	B4001
17	ASVKVGKTW	0.443	414	WB	Agno	B5701
17	ASVKVGKTW	0.572	103	WB	Agno	B5801
	10-mers					
34	RIFIFILELL	0.605	71	WB	Agno	A0201
38	FILELLLEFC	0.449	388	WB	Agno	A0201
34	RIFIFILELL	0.719	20	SB	Agno	A0202
38	FILELLLEFC	0.622	59	WB	Agno	A0202
12	QLSRQASVKV	0.449	386	WB	Agno	A0202
12	QLSRQASVKV	0.588	86	WB	Agno	A0203
34	RIFIFILELL	0.456	359	WB	Agno	A0203
12	QLSRQASVKV	0.503	215	WB	Agno	A0204
38	FILELLLEFC	0.656	41	SB	Agno	A0206
34	RIFIFILELL	0.549	131	WB	Agno	A0206
61	TALPAVKDSV	0.450	382	WB	Agno	A0206
12	QLSRQASVKV	0.859	4	SB	Agno	A0211
34	RIFIFILELL	0.772	11	SB	Agno	A0211
38	FILELLLEFC	0.626	57	WB	Agno	A0211
61	TALPAVKDSV	0.569	106	WB	Agno	A0211
12	QLSRQASVKV	0.754	14	SB	Agno	A0212
38	FILELLLEFC	0.627	56	WB	Agno	A0212
34	RIFIFILELL	0.497	231	WB	Agno	A0212
61	TALPAVKDSV	0.433	461	WB	Agno	A0212
12	QLSRQASVKV	0.843	5	SB	Agno	A0216
34	RIFIFILELL	0.581	92	WB	Agno	A0216
61	TALPAVKDSV	0.550	130	WB	Agno	A0216
12	QLSRQASVKV	0.632	53	WB	Agno	A0219

61 TALPAVKDSV	0.549	131	WB	Agno	A0219
11 RQLSRQASVK	0.636	51	WB	Agno	A0301
58 KSTTALPAVK	0.532	158	WB	Agno	A0301
20 KVGKTWTGTK	0.496	234	WB	Agno	A0301
62 ALPAVKDSVK	0.452	375	WB	Agno	A0301
58 KSTTALPAVK	0.688	29	SB	Agno	A1101
20 KVGKTWTGTK	0.671	35	SB	Agno	A1101
11 RQLSRQASVK	0.620	60	WB	Agno	A1101
62 ALPAVKDSVK	0.445	404	WB	Agno	A1101
37 IFILELLLEF	0.695	27	SB	Agno	A2301
35 IFIFILELLL	0.487	256	WB	Agno	A2301
37 IFILELLLEF	0.663	38	SB	Agno	A2402
35 IFIFILELLL	0.622	59	WB	Agno	A2402
37 IFILELLLEF	0.663	38	SB	Agno	A2403
37 IFILELLLEF	0.470	309	WB	Agno	A2902
20 KVGKTWTGTK	0.787	10	SB	Agno	A3001
58 KSTTALPAVK	0.557	120	WB	Agno	A3001
11 RQLSRQASVK	0.509	202	WB	Agno	A3001
6 NLVVLRQLSR	0.567	108	WB	Agno	A3101
39 ILELLLEFCR	0.521	177	WB	Agno	A3101
25 WTGTKKRAQR	0.504	214	WB	Agno	A3101
39 ILELLLEFCR	0.523	173	WB	Agno	A3301
6 NLVVLRQLSR	0.485	262	WB	Agno	A3301
6 NLVVLRQLSR	0.604	72	WB	Agno	A6801
39 ILELLLEFCR	0.479	279	WB	Agno	A6801
25 WTGTKKRAQR	0.465	326	WB	Agno	A6801
33 QRIFIFILEL	0.528	164	WB	Agno	A6802
61 TALPAVKDSV	0.473	301	WB	Agno	A6802
34 RIFIFILELL	0.467	321	WB	Agno	A6802
61 TALPAVKDSV	0.448	394	WB	Agno	A6901
11 RQLSRQASVK	0.534	154	WB	Agno	B2705
14 SRQASVKVGK	0.516	188	WB	Agno	B2705
33 QRIFIFILEL	0.469	312	WB	Agno	B2705
16 QASVKVGKTW	0.632	53	WB	Agno	B5801
11-mers					
34 RIFIFILELLL	0.552	127	WB	Agno	A0201
11 RQLSRQASVKV	0.460	344	WB	Agno	A0201
43 LLEFCRGEDSV	0.586	87	WB	Agno	A0202
34 RIFIFILELLL	0.503	216	WB	Agno	A0202
9 VLRQLSRQASV	0.497	229	WB	Agno	A0202
9 VLRQLSRQASV	0.814	7	SB	Agno	A0203
11 RQLSRQASVKV	0.508	205	WB	Agno	A0203
43 LLEFCRGEDSV	0.483	267	WB	Agno	A0203
32 AQRIFIFILEL	0.446	400	WB	Agno	A0203
9 VLRQLSRQASV	0.447	398	WB	Agno	A0204

11 RQLSRQASVKV	0.776	11	SB	Agno	A0206
32 AQRIFIFILEL	0.584	90	WB	Agno	A0206
9 VLRQLSRQASV	0.887	3	SB	Agno	A0211
34 RIFIFILELLL	0.793	9	SB	Agno	A0211
43 LLEFCRGEDSV	0.747	15	SB	Agno	A0211
52 SVDGKNKSTTA	0.612	66	WB	Agno	A0211
11 RQLSRQASVKV	0.433	463	WB	Agno	A0211
36 FIFILELLLEF	0.429	481	WB	Agno	A0211
9 VLRQLSRQASV	0.876	3	SB	Agno	A0212
34 RIFIFILELLL	0.586	88	WB	Agno	A0212
43 LLEFCRGEDSV	0.585	89	WB	Agno	A0212
38 FILELLLEFCR	0.454	369	WB	Agno	A0212
11 RQLSRQASVKV	0.442	417	WB	Agno	A0212
9 VLRQLSRQASV	0.838	5	SB	Agno	A0216
43 LLEFCRGEDSV	0.725	19	SB	Agno	A0216
34 RIFIFILELLL	0.606	71	WB	Agno	A0216
60 TTALPAVKDSV	0.460	346	WB	Agno	A0216
52 SVDGKNKSTTA	0.455	365	WB	Agno	A0216
9 VLRQLSRQASV	0.674	33	SB	Agno	A0219
43 LLEFCRGEDSV	0.477	285	WB	Agno	A0219
20 KVGKTWTGTKK	0.660	39	SB	Agno	A0301
20 KVGKTWTGTKK	0.617	63	WB	Agno	A1101
61 TALPAVKDSVK	0.508	204	WB	Agno	A1101
36 FIFILELLLEF	0.535	152	WB	Agno	A2602
36 FIFILELLLEF	0.571	103	WB	Agno	A2902
13 LSRQASVKVGK	0.753	14	SB	Agno	A3001
20 KVGKTWTGTKK	0.713	22	SB	Agno	A3001
5 KNLVVLRQLSR	0.558	119	WB	Agno	A3101
24 TWTGTKKRAQR	0.496	232	WB	Agno	A3101
38 FILELLLEFCR	0.469	313	WB	Agno	A3101
38 FILELLLEFCR	0.616	63	WB	Agno	A3301
38 FILELLLEFCR	0.611	67	WB	Agno	A6801
24 TWTGTKKRAQR	0.442	419	WB	Agno	A6801
61 TALPAVKDSVK	0.439	434	WB	Agno	A6801
60 TTALPAVKDSV	0.850	5	SB	Agno	A6802
33 QRIFIFILELL	0.650	43	SB	Agno	A6802
60 TTALPAVKDSV	0.545	136	WB	Agno	A6901
32 AQRIFIFILEL	0.471	305	WB	Agno	B1501
36 FIFILELLLEF	0.436	448	WB	Agno	B1501
15 RQASVKVGKTW	0.427	491	WB	Agno	B1501
30 KRAQRIFIFIL	0.478	284	WB	Agno	B2705
36 FIFILELLLEF	0.451	378	WB	Agno	B3501
30 KRAQRIFIFIL	0.455	362	WB	Agno	B3901
15 RQASVKVGKTW	0.573	100	WB	Agno	B5801

Preferred BK virus fragments capable of interacting with one or more MHC class 2 molecules are listed in Table O.

Table O: Predicted MHC class 2 BK virus peptide sequences. Prediction of 13-, 14-, 15-, 16-mers from all 6 reading frames of the genome (access no #V01108) obtained using the program displayed in figure 2.

BK virus, reading frame 1			
13 mers:			
FCKNCKRIGISPN;	CKNCKRIGISPNS;	KNCKRIGISPNSF;	NCKRIGISPNSFA;
CKRIGISPNSFAR;	KRIGISPNSFARP;	RIGISPNSFARPQ;	IGISPNSFARPQK;
GISPNSFARPQKK;	ISPNSFARPQKKP;	SPNSFARPQKKPP;	PNSFARPQKKPPH;
NSFARPQKKPPHP;	SFARPQKKPPHPY;	FARPQKKPPHPYY;	ARPQKKPPHPYYL;
RPQKKPPHPYYLR;	PQKKPPHPYYLRE;	QKKPPHPYYLRER;	KKPPHPYYLRERV;
KPPHPYYLRERVE;	PPHPYYLRERVEA;	PHPYYLRERVEAE;	HPYYLRERVEAEA;
PYYLRERVEAEAA;	YYLRERVEAEAAS;	YLRERVEAEAASA;	LRERVEAEAASAS;
RERVEAEAASASY;	ERVEAEAASASYI;	RVEAEAASASYIL;	KKRPQGGAAYPWN;
KRPQGGAAYPWNA;	RPQGGAAYPWNAA;	PQGGAAYPWNAAK;	QGGAAYPWNAAKP;
PQEGKCMTHRGMQ;	QEGKCMTHRGMQP;	EGKCMTHRGMQPN;	GKCMTHRGMQPNH;
KCMTHRGMQPNHD;	CMTHRGMQPNHDL;	MTHRGMQPNHDLR;	THRGMQPNHDLRK;
HRGMQPNHDLRKE;	RGMQPNHDLRKES;	GMQPNHDLRKESA;	LTGRSCLPMECSQ;
TGRSCLPMECSQT;	GRSCLPMECSQTM;	RSCLPMECSQTMT;	SCLPMECSQTMTS;
CLPMECSQTMTSG;	LPMECSQTMTSGR;	PMECSQTMTSGRK;	MECSQTMTSGRKV;
ECSQTMTSGRKVH;	CSQTMTSGRKVHD;	SQTMTSGRKVHDR;	QTMTSGRKVHDRH;
TMTSGRKVHDRHV;	MTSGRKVHDRHVL;	TSGRKVHDRHVLR;	SGRKVHDRHVLRA;
ESWPCPQLNWTKA;	SWPCPQLNWTKAM;	WPCPQLNWTKAMV;	PCPQLNWTKAMVL;
CPQLNWTKAMVLR;	PQLNWTKAMVLRQ;	QLNWTKAMVLRQL;	LNWTKAMVLRQLS;
NWTKAMVLRQLSR;	WTKAMVLRQLSRQ;	TKAMVLRQLSRQA;	KAMVLRQLSRQAS;
AMVLRQLSRQASV;	MVLRQLSRQASVK;	VLRQLSRQASVKV;	LRQLSRQASVKVG;
RQLSRQASVKVGK;	QLSRQASVKVGKT;	LSRQASVKVGKTW;	SRQASVKVGKTWT;
RQASVKVGKTWTG;	QASVKVGKTWTGT;	ASVKVGKTWTGTK;	SVKVGKTWTGTKK;
VKVGKTWTGTKKR;	KVGKTWTGTKKRA;	VGKTWTGTKKRAQ;	GKTWTGTKKRAQR;
KTWTGTKKRAQRI;	TWTGTKKRAQRIF;	WTGTKKRAQRIFI;	TGTKKRAQRIFIF;
GTKKRAQRIFIFI;	TKKRAQRIFIFIL;	KKRAQRIFIFILE;	KRAQRIFIFILEL;
RAQRIFIFILELL;	AQRIFIFILELLL;	QRIFIFILELLLE;	RIFIFILELLLEF;
IFIFILELLLEFC;	FIFILELLLEFCR;	IFILELLLEFCRG;	FILELLLEFCRGE;
ILELLLEFCRGED;	LELLLEFCRGEDS;	ELLLEFCRGEDSV;	LLLEFCRGEDSVD;
LLEFCRGEDSVDG;	LEFCRGEDSVDGK;	EFCRGEDSVDGKN;	FCRGEDSVDGKNK;
CRGEDSVDGKNKS;	RGEDSVDGKNKST;	GEDSVDGKNKSTT;	EDSVDGKNKSTTA;
DSVDGKNKSTTAL;	SVDGKNKSTTALP;	VDGKNKSTTALPA;	DGKNKSTTALPAV;
GKNKSTTALPAVK;	KNKSTTALPAVKD;	NKSTTALPAVKDS;	KSTTALPAVKDSV;
STTALPAVKDSVK;	TTALPAVKDSVKD;	TALPAVKDSVKDS;	VSNPFFFVFPGSW;
SNPFFFVFPGSWV;	NPFFFVFPGSWVL;	PFFFVFPGSWVLL;	LPVYLRLLLPQDF;
PVYLRLLLPQDFQ;	VYLRLLLPQDFQW;	YLRLLLPQDFQWL;	LRLLLPQDFQWLK;
RLLLPQDFQWLKL;	LLLPQDFQWLKLL;	LLPQDFQWLKLLL;	LPQDFQWLKLLLG;
PQDFQWLKLLLGR;	QDFQWLKLLLGRL;	DFQWLKLLLGRLL;	FQWLKLLLGRLLL;
QWLKLLLGRLLLL;	LLVLLGLLLGLLL;	GISSLMIGITKFP;	ISSLMIGITKFPL;
ASISNQAWLWNCL;	SISNQAWLWNCLT;	ISNQAWLWNCLTQ;	SNQAWLWNCLTQM;
NQAWLWNCLTQMS;	QAWLWNCLTQMST;	AWLWNCLTQMSTM;	WLWNCLTQMSTMI;
LWNCLTQMSTMIF;	WNCLTQMSTMIFC;	NCLTQMSTMIFCF;	CLTQMSTMIFCFL;
LTQMSTMIFCFLV;	ILLLIIFNTLILG;	LLLIIFNTLILGI;	LLIIFNTLILGIG;
LIIFNTLILGIGV;	IIFNTLILGIGVL;	IFNTLILGIGVLL;	FNTLILGIGVLLC;
NTLILGIGVLLCL;	TLILGIGVLLCLL;	LILGIGVLLCLLL;	ILGIGVLLCLLLF;
LGIGVLLCLLLFP;	GIGVLLCLLLFPR;	IGVLLCLLLFPRL;	GVLLCLLLFPRLC;
VLLCLLLFPRLCG;	LLCLLLFPRLCGM;	LCLLLFPRLCGML;	CLLLFPRLCGMLL;
LLLFPRLCGMLLG;	LLFPRLCGMLLGM;	LFPRLCGMLLGMI;	FPRLCGMLLGMIY;

PRLCGMLLGMIYL; RLCGMLLGMIYLL; PHRNCREEQKDFL; HRNCREEQKDFLE;
RNCREEQKDFLET; NCREEQKDFLETP; CREEQKDFLETPW; REEQKDFLETPWL;
EEQKDFLETPWLD; EQKDFLETPWLDF; QKDFLETPWLDFW; KDFLETPWLDFWR;
DFLETPWLDFWRK; FLETPWLDFWRKL; LETPWLDFWRKLP; ETPWLDFWRKLPG;
TPWLDFWRKLPGQ; PWLDFWRKLPGQL; TFIIIFNNIILIF; FIIIFNNIILIFP;
IIIFNNIILIFPL; IIFNNIILIFPLL; IFNNIILIFPLLG; FNNIILIFPLLGP;
NNIILIFPLLGPQ; NIILIFPLLGPQW; IILIFPLLGPQWL; ILIFPLLGPQWLD;
LIFPLLGPQWLDK; LKGKVPVYILAIL; KGKVPVYILAILI; GKVPVYILAILIV;
KKLLPQEVLIKEL; KLLPQEVLIKELL; LLPQEVLIKELLL; LPQEVLIKELLLN;
PQEVLIKELLLNG; QEVLIKELLLNGC; EVLIKELLLNGCC; VLIKELLLNGCCL;
LIKELLLNGCCLY; IKELLLNGCCLYF; HLLLKHMKMAPTK; LLLKHMKMAPTKR;
LLKHMKMAPTKRK; LKHMKMAPTKRKG; KHMKMAPTKRKGE; HMKMAPTKRKGEC;
MKMAPTKRKGECP; KMAPTKRKGECPG; MAPTKRKGECPGA; APTKRKGECPGAA;
PTKRKGECPGAAP; TKRKGECPGAAPK; KRKGECPGAAPKK; RKGECPGAAPKKP;
KGECPGAAPKKPK; GECPGAAPKKPKE; ECPGAAPKKPKEP; CPGAAPKKPKEPV;
PGAAPKKPKEPVQ; GAAPKKPKEPVQV; AAPKKPKEPVQVP; APKKPKEPVQVPK;
PKKPKEPVQVPKL; KKPKEPVQVPKLL; KPKEPVQVPKLLI; PKEPVQVPKLLIK;
KEPVQVPKLLIKG; EPVQVPKLLIKGG; PVQVPKLLIKGGV; VQVPKLLIKGGVE;
QVPKLLIKGGVEV; VPKLLIKGGVEVL; PKLLIKGGVEVLE; KLLIKGGVEVLEV;
LLIKGGVEVLEVK; LIKGGVEVLEVKT; IKGGVEVLEVKTG; KGGVEVLEVKTGV;
GGVEVLEVKTGVD; GVEVLEVKTGVDA; VEVLEVKTGVDAI; EVLEVKTGVDAIT;
VLEVKTGVDAITE; LEVKTGVDAITEV; EVKTGVDAITEVE; VKTGVDAITEVEC;
KTGVDAITEVECF; TGVDAITEVECFL; GVDAITEVECFLN; VDAITEVECFLNP;
DAITEVECFLNPE; AITEVECFLNPEM; ITEVECFLNPEMG; TEVECFLNPEMGD;
EVECFLNPEMGDP; VECFLNPEMGDPD; ECFLNPEMGDPDE; CFLNPEMGDPDEN;
FLNPEMGDPDENL; LNPEMGDPDENLR; NPEMGDPDENLRG; PEMGDPDENLRGF;
EMGDPDENLRGFS; MGDPDENLRGFSL; GDPDENLRGFSLK; DPDENLRGFSLKL;
PDENLRGFSLKLS; DENLRGFSLKLSA; ENLRGFSLKLSAE; NLRGFSLKLSAEN;
LRGFSLKLSAEND; RGFSLKLSAENDF; GFSLKLSAENDFS; FSLKLSAENDFSS;
SLKLSAENDFSSD; LKLSAENDFSSDS; KLSAENDFSSDSP; LSAENDFSSDSPE;
SAENDFSSDSPER; AENDFSSDSPERK; ENDFSSDSPERKM; NDFSSDSPERKML;
DFSSDSPERKMLP; FSSDSPERKMLPC; SSDSPERKMLPCY; SDSPERKMLPCYS;
DSPERKMLPCYST; SPERKMLPCYSTA; PERKMLPCYSTAR; ERKMLPCYSTARI;
RKMLPCYSTARIP; KMLPCYSTARIPL; MLPCYSTARIPLP; LPCYSTARIPLPN;
PCYSTARIPLPNL; CYSTARIPLPNLN; YSTARIPLPNLNE; STARIPLPNLNED;
TARIPLPNLNEDL; ARIPLPNLNEDLT; RIPLPNLNEDLTC; IPLPNLNEDLTCG;
PLPNLNEDLTCGN; LPNLNEDLTCGNL; PNLNEDLTCGNLL; NLNEDLTCGNLLM;
LNEDLTCGNLLMW; NEDLTCGNLLMWE; EDLTCGNLLMWEA; DLTCGNLLMWEAV;
LTCGNLLMWEAVT; TCGNLLMWEAVTV; CGNLLMWEAVTVQ; GNLLMWEAVTVQT;
NLLMWEAVTVQTE; LLMWEAVTVQTEV; LMWEAVTVQTEVI; MWEAVTVQTEVIG;
WEAVTVQTEVIGI; EAVTVQTEVIGIT; AVTVQTEVIGITS; VTVQTEVIGITSM;
TVQTEVIGITSML; VQTEVIGITSMLN; QTEVIGITSMLNL; TEVIGITSMLNLH;
EVIGITSMLNLHA; VIGITSMLNLHAG; IGITSMLNLHAGS; GITSMLNLHAGSQ;
ITSMLNLHAGSQK; TSMLNLHAGSQKV; SMLNLHAGSQKVH; MLNLHAGSQKVHE;
LNLHAGSQKVHEH; NLHAGSQKVHEHG; LHAGSQKVHEHGG; HAGSQKVHEHGGG;
AGSQKVHEHGGGK; GSQKVHEHGGGKP; SQKVHEHGGGKPI; QKVHEHGGGKPIQ;
KVHEHGGGKPIQG; VHEHGGGKPIQGS; HEHGGGKPIQGSN; EHGGGKPIQGSNF;
HGGGKPIQGSNFH; GGGKPIQGSNFHF; GGKPIQGSNFHFF; GKPIQGSNFHFFA;
KPIQGSNFHFFAV; PIQGSNFHFFAVG; IQGSNFHFFAVGG; QGSNFHFFAVGGE;
GSNFHFFAVGGEP; SNFHFFAVGGEPL; NFHFFAVGGEPLE; FHFFAVGGEPLEM;
HFFAVGGEPLEMQ; FFAVGGEPLEMQG; FAVGGEPLEMQGV; AVGGEPLEMQGVL;
VGGEPLEMQGVLM; GGEPLEMQGVLMN; GEPLEMQGVLMNY; EPLEMQGVLMNYR;
PLEMQGVLMNYRS; LEMQGVLMNYRSK; EMQGVLMNYRSKY; MQGVLMNYRSKYP;
QGVLMNYRSKYPD; GVLMNYRSKYPDG; VLMNYRSKYPDGT; LMNYRSKYPDGTI;
MNYRSKYPDGTIT; NYRSKYPDGTITP; YRSKYPDGTITPK; RSKYPDGTITPKN;
SKYPDGTITPKNP; KYPDGTITPKNPT; YPDGTITPKNPTA; PDGTITPKNPTAQ;
DGTITPKNPTAQS; GTITPKNPTAQSQ; TITPKNPTAQSQV; ITPKNPTAQSQVM;
TPKNPTAQSQVMN; PKNPTAQSQVMNT; KNPTAQSQVMNTD; NPTAQSQVMNTDH;
PTAQSQVMNTDHK; TAQSQVMNTDHKA; AQSQVMNTDHKAY; QSQVMNTDHKAYL;

SQVMNTDHKAYLD; QVMNTDHKAYLDK; VMNTDHKAYLDKN; MNTDHKAYLDKNN;
NTDHKAYLDKNNA; TDHKAYLDKNNAY; DHKAYLDKNNAYP; HKAYLDKNNAYPV;
KAYLDKNNAYPVE; AYLDKNNAYPVEC; YLDKNNAYPVECW; LDKNNAYPVECWV;
DKNNAYPVECWVP; KNNAYPVECWVPD; NNAYPVECWVPDP; NAYPVECWVPDPS;
AYPVECWVPDPSR; YPVECWVPDPSRN; PVECWVPDPSRNE; VECWVPDPSRNEN;
ECWVPDPSRNENA; CWVPDPSRNENAR; WVPDPSRNENARY; VPDPSRNENARYF;
PDPSRNENARYFG; DPSRNENARYFGT; PSRNENARYFGTF; SRNENARYFGTFT;
RNENARYFGTFTG; NENARYFGTFTGG; ENARYFGTFTGGE; NARYFGTFTGGEN;
ARYFGTFTGGENV; RYFGTFTGGENVP; YFGTFTGGENVPP; FGTFTGGENVPPV;
GTFTGGENVPPVL; TFTGGENVPPVLH; FTGGENVPPVLHV; TGGENVPPVLHVT;
GGENVPPVLHVTN; GENVPPVLHVTNT; ENVPPVLHVTNTA; NVPPVLHVTNTAT;
VPPVLHVTNTATT; PPVLHVTNTATTV; PVLHVTNTATTVL; VLHVTNTATTVLL;
LHVTNTATTVLLD; HVTNTATTVLLDE; VTNTATTVLLDEQ; TNTATTVLLDEQG;
NTATTVLLDEQGV; TATTVLLDEQGVG; ATTVLLDEQGVGP; TTVLLDEQGVGPL;
TVLLDEQGVGPLC; VLLDEQGVGPLCK; LLDEQGVGPLCKA; LDEQGVGPLCKAD;
DEQGVGPLCKADS; EQGVGPLCKADSL; QGVGPLCKADSLY; GVGPLCKADSLYV;
VGPLCKADSLYVS; GPLCKADSLYVSA; PLCKADSLYVSAA; LCKADSLYVSAAD;
CKADSLYVSAADI; KADSLYVSAADIC; ADSLYVSAADICG; DSLYVSAADICGL;
SLYVSAADICGLF; LYVSAADICGLFT; YVSAADICGLFTN; VSAADICGLFTNS;
SAADICGLFTNSS; AADICGLFTNSSG; ADICGLFTNSSGT; DICGLFTNSSGTQ;
ICGLFTNSSGTQQ; CGLFTNSSGTQQW; GLFTNSSGTQQWR; LFTNSSGTQQWRG;
FTNSSGTQQWRGL; TNSSGTQQWRGLA; NSSGTQQWRGLAR; SSGTQQWRGLARY;
SGTQQWRGLARYF; GTQQWRGLARYFK; TQQWRGLARYFKI; QQWRGLARYFKIR;
QWRGLARYFKIRL; WRGLARYFKIRLR; RGLARYFKIRLRK; GLARYFKIRLRKR;
LARYFKIRLRKRS; ARYFKIRLRKRSV; RYFKIRLRKRSVK; YFKIRLRKRSVKN;
FKIRLRKRSVKNP; KIRLRKRSVKNPY; IRLRKRSVKNPYP; RLRKRSVKNPYPI;
LRKRSVKNPYPIS; RKRSVKNPYPISF; KRSVKNPYPISFL; RSVKNPYPISFLL;
SVKNPYPISFLLS; VKNPYPISFLLSD; KNPYPISFLLSDL; NPYPISFLLSDLI;
PYPISFLLSDLIN; YPISFLLSDLINR; PISFLLSDLINRR; ISFLLSDLINRRT;
SFLLSDLINRRTQ; FLLSDLINRRTQR; LLSDLINRRTQRV; LSDLINRRTQRVD;
SDLINRRTQRVDG; DLINRRTQRVDGQ; LINRRTQRVDGQP; INRRTQRVDGQPM;
NRRTQRVDGQPMY; RRTQRVDGQPMYG; RTQRVDGQPMYGM; TQRVDGQPMYGME;
QRVDGQPMYGMES; RVDGQPMYGMESQ; VDGQPMYGMESQV; DGQPMYGMESQVE;
GQPMYGMESQVEE; QPMYGMESQVEEV; PMYGMESQVEEVR; MYGMESQVEEVRV;
YGMESQVEEVRVF; GMESQVEEVRVFD; MESQVEEVRVFDG; ESQVEEVRVFDGT;
SQVEEVRVFDGTE; QVEEVRVFDGTER; VEEVRVFDGTERL; EEVRVFDGTERLP;
EVRVFDGTERLPG; VRVFDGTERLPGD; RVFDGTERLPGDP; VFDGTERLPGDPD;
FDGTERLPGDPDM; DGTERLPGDPDMI; GTERLPGDPDMIR; TERLPGDPDMIRY;
ERLPGDPDMIRYI; RLPGDPDMIRYID; LPGDPDMIRYIDK; PGDPDMIRYIDKQ;
GDPDMIRYIDKQG; DPDMIRYIDKQGQ; PDMIRYIDKQGQL; DMIRYIDKQGQLQ;
MIRYIDKQGQLQT; IRYIDKQGQLQTK; RYIDKQGQLQTKM; YIDKQGQLQTKML;
TGAFIVHIHLINA; GAFIVHIHLINAA; AFIVHIHLINAAF; FIVHIHLINAAFV;
ATFKLVLFWGWCF; TFKLVLFWGWCFR; FKLVLFWGWCFRP; KLVLFWGWCFRPF;
LVLFWGWCFRPFK; VLFWGWCFRPFKT; LFWGWCFRPFKTL; FWGWCFRPFKTLK;
WGWCFRPFKTLKA; GWCFRPFKTLKAF; WCFRPFKTLKAFT; CFRPFKTLKAFTQ;
FRPFKTLKAFTQM; RPFKTLKAFTQMQ; PFKTLKAFTQMQL; FKTLKAFTQMQLL;
KTLKAFTQMQLLT; TLKAFTQMQLLTM; LKAFTQMQLLTMG; KAFTQMQLLTMGV;
ILFSCNIKNTFPH; LFSCNIKNTFPHA; FSCNIKNTFPHAY; SCNIKNTFPHAYI;
CNIKNTFPHAYII; NIKNTFPHAYIIF; IKNTFPHAYIIFH; KNTFPHAYIIFHP;
KSIHTYLRIQPFL; SIHTYLRIQPFLP; IHTYLRIQPFLPF; HTYLRIQPFLPFN;
TYLRIQPFLPFNN; YLRIQPFLPFNNS; LRIQPFLPFNNSR; RIQPFLPFNNSRL;
IQPFLPFNNSRLY; QPFLPFNNSRLYI; PFLPFNNSRLYIS; FLPFNNSRLYISC;
LPFNNSRLYISCK; PFNNSRLYISCKI; FNNSRLYISCKIS; NNSRLYISCKISY;
NSRLYISCKISYR; SRLYISCKISYRP; RLYISCKISYRPK; LYISCKISYRPKP;
YISCKISYRPKPN; IYFGPKIYLSYKS; YFGPKIYLSYKSS; FGPKIYLSYKSSL;
GPKIYLSYKSSLQ; PKIYLSYKSSLQG; KIYLSYKSSLQGF; IYLSYKSSLQGFR;
YLSYKSSLQGFRD; LSYKSSLQGFRDR; SYKSSLQGFRDRI; YKSSLQGFRDRIL;
KSSLQGFRDRILI; SSLQGFRDRILIH; SLQGFRDRILIHC; LQGFRDRILIHCN;
QGFRDRILIHCNQ; GFRDRILIHCNQA; FRDRILIHCNQAW; RDRILIHCNQAWW;

DRILIHCNQAWWK; RILIHCNQAWWKY; ILIHCNQAWWKYL; LIHCNQAWWKYLG;
IHCNQAWWKYLGS; HCNQAWWKYLGSF; CNQAWWKYLGSFV; FSSCPFYIFKNNH;
SSCPFYIFKNNHV; SCPFYIFKNNHVL; CPFYIFKNNHVLI; PFYIFKNNHVLIY;
FYIFKNNHVLIYS; YIFKNNHVLIYSY; IFKNNHVLIYSYT; PVSSFRYIENNTV;
VSSFRYIENNTVQ; SSFRYIENNTVQK; SFRYIENNTVQKI; FRYIENNTVQKIK;
RYIENNTVQKIKY; YIENNTVQKIKYY; IENNTVQKIKYYR; ENNTVQKIKYYRI;
NNTVQKIKYYRIH; NTVQKIKYYRIHF; TVQKIKYYRIHFR; QTVQPSNTCHILF;
HFFPGHMKGIYSF; FFPGHMKGIYSFF; FPGHMKGIYSFFS; NCIYCLLTNTFLI;
CIYCLLTNTFLIF; IYCLLTNTFLIFT; YCLLTNTFLIFTF; CLLTNTFLIFTFC;
LLTNTFLIFTFCK; LTNTFLIFTFCKN; TNTFLIFTFCKNN; NTFLIFTFCKNNS;
TFLIFTFCKNNSI; FLIFTFCKNNSIC; LIFTFCKNNSICK; IFTFCKNNSICKV;
FTFCKNNSICKVL; TFCKNNSICKVLF; FCKNNSICKVLFM; CKNNSICKVLFMI;
KNNSICKVLFMIL; NNSICKVLFMILK; NSICKVLFMILKV; SICKVLFMILKVI;
ICKVLFMILKVIR; CKVLFMILKVIRL; KVLFMILKVIRLV; VLFMILKVIRLVF;
LFMILKVIRLVFF; FMILKVIRLVFFL; MILKVIRLVFFLT; ILKVIRLVFFLTL;
LKVIRLVFFLTLF; KVIRLVFFLTLFT; VIRLVFFLTLFTL; IRLVFFLTLFTLL;
RLVFFLTLFTLLY; LVFFLTLFTLLYI; VFFLTLFTLLYIV; FFLTLFTLLYIVL;
FLTLFTLLYIVLK; LTLFTLLYIVLKF; KHILTLCLYCILS; HILTLCLYCILSN;
FPRHLLCFFRLFW; PRHLLCFFRLFWA; RHLLCFFRLFWAK; HLLCFFRLFWAKI;
LLCFFRLFWAKIM; LCFFRLFWAKIML; CFFRLFWAKIMLL; APLNAFFYSMVWI;
PLNAFFYSMVWIS; LNAFFYSMVWISS; KTKGTQLLTEIIN; TKGTQLLTEIINC;
KGTQLLTEIINCR; GTQLLTEIINCRN; TQLLTEIINCRNS; QLLTEIINCRNSM;
LLTEIINCRNSMS; LTEIINCRNSMSM; TEIINCRNSMSMW; EIINCRNSMSMWS;
KEYNIMPSTHVST; EYNIMPSTHVSTN; YNIMPSTHVSTNK; NIMPSTHVSTNKS;
IMPSTHVSTNKSY; MPSTHVSTNKSYR; PSTHVSTNKSYRI; STHVSTNKSYRIF;
THVSTNKSYRIFF; HVSTNKSYRIFFH; VSTNKSYRIFFHK; STNKSYRIFFHKF;
TNKSYRIFFHKFF; NKSYRIFFHKFFI; KSYRIFFHKFFIQ; SYRIFFHKFFIQN;
YRIFFHKFFIQNL; RIFFHKFFIQNLS; IFFHKFFIQNLSF; FFHKFFIQNLSFF;
FHKFFIQNLSFFF; HKFFIQNLSFFFS; KFFIQNLSFFFSS; FFIQNLSFFFSSI;
FIQNLSFFFSSIH; IQNLSFFFSSIHS; QNLSFFFSSIHSK; NLSFFFSSIHSKA;
LSFFFSSIHSKAG; SFFFSSIHSKAGK; FFFSSIHSKAGKG; FFSSIHSKAGKGS;
FSSIHSKAGKGSI; SSIHSKAGKGSIT; SIHSKAGKGSITK; IHSKAGKGSITKY;
HSKAGKGSITKYS; SKAGKGSITKYSL; KAGKGSITKYSLT; AGKGSITKYSLTK;
GKGSITKYSLTKK; KGSITKYSLTKKL; GSITKYSLTKKLV; IRGKVFRVFYLSF;
RGKVFRVFYLSFF; GKVFRVFYLSFFF; KVFRVFYLSFFFG; VFRVFYLSFFFGW;
FRVFYLSFFFGWC; VLRICCCFFITGK; LRICCCFFITGKH; RICCCFFITGKHI;
ICCCFFITGKHIF; CCCFFITGKHIFM; CCFFITGKHIFMA; CFFITGKHIFMAK;
IFIPFFIKGTPPG; FIPFFIKGTPPGL; IPFFIKGTPPGLP; PFFIKGTPPGLPL;
FFIKGTPPGLPLF; FIKGTPPGLPLFC; IKGTPPGLPLFCS; KGTPPGLPLFCSI;
GTPPGLPLFCSIG; TPPGLPLFCSIGW; PPGLPLFCSIGWH; PGLPLFCSIGWHL;
SFRSLKGVSPIIW; FRSLKGVSPIIWT; RSLKGVSPIIWTH; SLKGVSPIIWTHH;
LKGVSPIIWTHHC; KGVSPIIWTHHCR; GVSPIIWTHHCRV; VSPIIWTHHCRVS;
SPIIWTHHCRVSS; PIIWTHHCRVSSV; IIWTHHCRVSSVR; IWTHHCRVSSVRS;
WTHHCRVSSVRSK; THHCRVSSVRSKP; HHCRVSSVRSKPN; HCRVSSVRSKPNH;
CRVSSVRSKPNHC; RVSSVRSKPNHCV; VSSVRSKPNHCVK; SSVRSKPNHCVKQ;
SVRSKPNHCVKQS; VRSKPNHCVKQSM; RSKPNHCVKQSMQ; QSIQTKGSFLKNF;
SIQTKGSFLKNFL; IQTKGSFLKNFLF; QTKGSFLKNFLFK; TKGSFLKNFLFKC;
KGSFLKNFLFKCL; GSFLKNFLFKCLN; SFLKNFLFKCLNL; FLKNFLFKCLNLS;
HSMQGQCTEGFLE; SMQGQCTEGFLEQ; MQGQCTEGFLEQI; QGQCTEGFLEQIG;
GQCTEGFLEQIGH; QCTEGFLEQIGHS; CTEGFLEQIGHSL; TEGFLEQIGHSLQ;
EGFLEQIGHSLQY; GFLEQIGHSLQYR; FLEQIGHSLQYRV; LEQIGHSLQYRVS;
EQIGHSLQYRVSG; QIGHSLQYRVSGQ; IGHSLQYRVSGQR; GHSLQYRVSGQRG;
HSLQYRVSGQRGK; SLQYRVSGQRGKS; LQYRVSGQRGKSA; QYRVSGQRGKSAQ;
YRVSGQRGKSAQT; RVSGQRGKSAQTS; VSGQRGKSAQTSE; SGQRGKSAQTSEL;
GQRGKSAQTSELL; QRGKSAQTSELLQ; RGKSAQTSELLQV; GKSAQTSELLQVP;
KSAQTSELLQVPK; SAQTSELLQVPKS; AQTSELLQVPKSG; ATFTSCSIFLYKV;
TFTSCSIFLYKVF; FTSCSIFLYKVFI; TSCSIFLYKVFIL; SCSIFLYKVFILF;
CSIFLYKVFILFI; SIFLYKVFILFIL; IFLYKVFILFILS; FLYKVFILFILSS;
LYKVFILFILSSS; YKVFILFILSSSP; KVFILFILSSSPP; VFILFILSSSPPL;

FILFILSSSPPLS; ILFILSSSPPLSG; AFLIKGRFPQAAL; FLIKGRFPQAALS;
LIKGRFPQAALSR; IKGRFPQAALSRP; KGRFPQAALSRPK; GRFPQAALSRPKR;
RFPQAALSRPKRS; FPQAALSRPKRSM; PQAALSRPKRSMS; QAALSRPKRSMSS;
AALSRPKRSMSSM; ALSRPKRSMSSMD; LSRPKRSMSSMDS; SRPKRSMSSMDSS;
RPKRSMSSMDSSL; PKRSMSSMDSSLL; KRSMSSMDSSLLR; RSMSSMDSSLLRT;
SMSSMDSSLLRTL; MSSMDSSLLRTLS

14 mers:
FCKNCKRIGISPNS; CKNCKRIGISPNSF; KNCKRIGISPNSFA;
NCKRIGISPNSFAR; CKRIGISPNSFARP; KRIGISPNSFARPQ;
RIGISPNSFARPQK; IGISPNSFARPQKK; GISPNSFARPQKKP;
ISPNSFARPQKKPP; SPNSFARPQKKPPH; PNSFARPQKKPPHP;
NSFARPQKKPPHPY; SFARPQKKPPHPYY; FARPQKKPPHPYYL;
ARPQKKPPHPYYLR; RPQKKPPHPYYLRE; PQKKPPHPYYLRER;
QKKPPHPYYLRERV; KKPPHPYYLRERVE; KPPHPYYLRERVEA;
PPHPYYLRERVEAE; PHPYYLRERVEAEA; HPYYLRERVEAEAA;
PYYLRERVEAEAAS; YYLRERVEAEAASA; YLRERVEAEAASAS;
LRERVEAEAASASY; RERVEAEAASASYI; ERVEAEAASASYIL;
KKRPQGGAAYPWNA; KRPQGGAAYPWNAA; RPQGGAAYPWNAAK;
PQGGAAYPWNAAKP; PQEGKCMTHRGMQP; QEGKCMTHRGMQPN;
EGKCMTHRGMQPNH; GKCMTHRGMQPNHD; KCMTHRGMQPNHDL;
CMTHRGMQPNHDLR; MTHRGMQPNHDLRK; THRGMQPNHDLRKE;
HRGMQPNHDLRKES; RGMQPNHDLRKESA; LTGRSCLPMECSQT;
TGRSCLPMECSQTM; GRSCLPMECSQTMT; RSCLPMECSQTMTS;
SCLPMECSQTMTSG; CLPMECSQTMTSGR; LPMECSQTMTSGRK;
PMECSQTMTSGRKV; MECSQTMTSGRKVH; ECSQTMTSGRKVHD;
CSQTMTSGRKVHDR; SQTMTSGRKVHDRH; QTMTSGRKVHDRHV;
TMTSGRKVHDRHVL; MTSGRKVHDRHVLR; TSGRKVHDRHVLRA;
ESWPCPQLNWTKAM; SWPCPQLNWTKAMV; WPCPQLNWTKAMVL;
PCPQLNWTKAMVLR; CPQLNWTKAMVLRQ; PQLNWTKAMVLRQL;
QLNWTKAMVLRQLS; LNWTKAMVLRQLSR; NWTKAMVLRQLSRQ;
WTKAMVLRQLSRQA; TKAMVLRQLSRQAS; KAMVLRQLSRQASV;
AMVLRQLSRQASVK; MVLRQLSRQASVKV; VLRQLSRQASVKVG;
LRQLSRQASVKVGK; RQLSRQASVKVGKT; QLSRQASVKVGKTW;
LSRQASVKVGKTWT; SRQASVKVGKTWTG; RQASVKVGKTWTGT;
QASVKVGKTWTGTK; ASVKVGKTWTGTKK; SVKVGKTWTGTKKR;
VKVGKTWTGTKKRA; KVGKTWTGTKKRAQ; VGKTWTGTKKRAQR;
GKTWTGTKKRAQRI; KTWTGTKKRAQRIF; TWTGTKKRAQRIFI;
WTGTKKRAQRIFIF; TGTKKRAQRIFIFI; GTKKRAQRIFIFIL;
TKKRAQRIFIFILE; KKRAQRIFIFILEL; KRAQRIFIFILELL;
RAQRIFIFILELLL; AQRIFIFILELLLE; QRIFIFILELLLEF;
RIFIFILELLLEFC; IFIFILELLLEFCR; FIFILELLLEFCRG;
IFILELLLEFCRGE; FILELLLEFCRGED; ILELLLEFCRGEDS;
LELLLEFCRGEDSV; ELLLEFCRGEDSVD; LLLEFCRGEDSVDG;
LLEFCRGEDSVDGK; LEFCRGEDSVDGKN; EFCRGEDSVDGKNK;
FCRGEDSVDGKNKS; CRGEDSVDGKNKST; RGEDSVDGKNKSTT;
GEDSVDGKNKSTTA; EDSVDGKNKSTTAL; DSVDGKNKSTTALP;
SVDGKNKSTTALPA; VDGKNKSTTALPAV; DGKNKSTTALPAVK;
GKNKSTTALPAVKD; KNKSTTALPAVKDS; NKSTTALPAVKDSV;
KSTTALPAVKDSVK; STTALPAVKDSVKD; TTALPAVKDSVKDS;
VSNPFFFVFPGSWV; SNPFFFVFPGSWVL; NPFFFVFPGSWVLL;
LPVYLRLLLPQDFQ; PVYLRLLLPQDFQW; VYLRLLLPQDFQWL;
YLRLLLPQDFQWLK; LRLLLPQDFQWLKL; RLLLPQDFQWLKLL;
LLLPQDFQWLKLLL; LLPQDFQWLKLLLG; LPQDFQWLKLLLGR;
PQDFQWLKLLLGRL; QDFQWLKLLLGRLL; DFQWLKLLLGRLLL;
FQWLKLLLGRLLLL; GISSLMIGITKFPL; ASISNQAWLWNCLT;
SISNQAWLWNCLTQ; ISNQAWLWNCLTQM; SNQAWLWNCLTQMS;
NQAWLWNCLTQMST; QAWLWNCLTQMSTM; AWLWNCLTQMSTMI;
WLWNCLTQMSTMIF; LWNCLTQMSTMIFC; WNCLTQMSTMIFCF;
NCLTQMSTMIFCFL; CLTQMSTMIFCFLV; ILLLIIFNTLILGI;

LLLIIFNTLILGIG; LLIIFNTLILGIGV; LIIFNTLILGIGVL;
IIFNTLILGIGVLL; IFNTLILGIGVLLC; FNTLILGIGVLLCL;
NTLILGIGVLLCLL; TLILGIGVLLCLLL; LILGIGVLLCLLLF;
ILGIGVLLCLLLFP; LGIGVLLCLLLFPR; GIGVLLCLLLFPRL;
IGVLLCLLLFPRLC; GVLLCLLLFPRLCG; VLLCLLLFPRLCGM;
LLCLLLFPRLCGML; LCLLLFPRLCGMLL; CLLLFPRLCGMLLG;
LLLFPRLCGMLLGM; LLFPRLCGMLLGMI; LFPRLCGMLLGMIY;
FPRLCGMLLGMIYL; PRLCGMLLGMIYLL; PHRNCREEQKDFLE;
HRNCREEQKDFLET; RNCREEQKDFLETP; NCREEQKDFLETPW;
CREEQKDFLETPWL; REEQKDFLETPWLD; EEQKDFLETPWLDF;
EQKDFLETPWLDFW; QKDFLETPWLDFWR; KDFLETPWLDFWRK;
DFLETPWLDFWRKL; FLETPWLDFWRKLP; LETPWLDFWRKLPG;
ETPWLDFWRKLPGQ; TPWLDFWRKLPGQL; TFIIIFNNIILIFP;
FIIIFNNIILIFPL; IIIFNNIILIFPLL; IIFNNIILIFPLLG;
IFNNIILIFPLLGP; FNNIILIFPLLGPQ; NNIILIFPLLGPQW;
NIILIFPLLGPQWL; IILIFPLLGPQWLD; ILIFPLLGPQWLDK;
LKGKVPVYILAILI; KGKVPVYILAILIV; KKLLPQEVLIKELL;
KLLPQEVLIKELLL; LLPQEVLIKELLLN; LPQEVLIKELLLNG;
PQEVLIKELLLNGC; QEVLIKELLLNGCC; EVLIKELLLNGCCL;
VLIKELLLNGCCLY; LIKELLLNGCCLYF; HLLLKHMKMAPTKR;
LLLKHMKMAPTKRK; LLKHMKMAPTKRKG; LKHMKMAPTKRKGE;
KHMKMAPTKRKGEC; HMKMAPTKRKGECP; MKMAPTKRKGECPG;
KMAPTKRKGECPGA; MAPTKRKGECPGAA; APTKRKGECPGAAP;
PTKRKGECPGAAPK; TKRKGECPGAAPKK; KRKGECPGAAPKKP;
RKGECPGAAPKKPK; KGECPGAAPKKPKE; GECPGAAPKKPKEP;
ECPGAAPKKPKEPV; CPGAAPKKPKEPVQ; PGAAPKKPKEPVQV;
GAAPKKPKEPVQVP; AAPKKPKEPVQVPK; APKKPKEPVQVPKL;
PKKPKEPVQVPKLL; KKPKEPVQVPKLLI; KPKEPVQVPKLLIK;
PKEPVQVPKLLIKG; KEPVQVPKLLIKGG; EPVQVPKLLIKGGV;
PVQVPKLLIKGGVE; VQVPKLLIKGGVEV; QVPKLLIKGGVEVL;
VPKLLIKGGVEVLE; PKLLIKGGVEVLEV; KLLIKGGVEVLEVK;
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KGGVEVLEVKTGVD; GGVEVLEVKTGVDA; GVEVLEVKTGVDAI;
VEVLEVKTGVDAIT; EVLEVKTGVDAITE; VLEVKTGVDAITEV;
LEVKTGVDAITEVE; EVKTGVDAITEVEC; VKTGVDAITEVECF;
KTGVDAITEVECFL; TGVDAITEVECFLN; GVDAITEVECFLNP;
VDAITEVECFLNPE; DAITEVECFLNPEM; AITEVECFLNPEMG;
ITEVECFLNPEMGD; TEVECFLNPEMGDP; EVECFLNPEMGDPD;
VECFLNPEMGDPDE; ECFLNPEMGDPDEN; CFLNPEMGDPDENL;
FLNPEMGDPDENLR; LNPEMGDPDENLRG; NPEMGDPDENLRGF;
PEMGDPDENLRGFS; EMGDPDENLRGFSL; MGDPDENLRGFSLK;
GDPDENLRGFSLKL; DPDENLRGFSLKLS; PDENLRGFSLKLSA;
DENLRGFSLKLSAE; ENLRGFSLKLSAEN; NLRGFSLKLSAEND;
LRGFSLKLSAENDF; RGFSLKLSAENDFS; GFSLKLSAENDFSS;
FSLKLSAENDFSSD; SLKLSAENDFSSDS; LKLSAENDFSSDSP;
KLSAENDFSSDSPE; LSAENDFSSDSPER; SAENDFSSDSPERK;
AENDFSSDSPERKM; ENDFSSDSPERKML; NDFSSDSPERKMLP;
DFSSDSPERKMLPC; FSSDSPERKMLPCY; SSDSPERKMLPCYS;
SDSPERKMLPCYST; DSPERKMLPCYSTA; SPERKMLPCYSTAR;
PERKMLPCYSTARI; ERKMLPCYSTARIP; RKMLPCYSTARIPL;
KMLPCYSTARIPLP; MLPCYSTARIPLPN; LPCYSTARIPLPNL;
PCYSTARIPLPNLN; CYSTARIPLPNLNE; YSTARIPLPNLNED;
STARIPLPNLNEDL; TARIPLPNLNEDLT; ARIPLPNLNEDLTC;
RIPLPNLNEDLTCG; IPLPNLNEDLTCGN; PLPNLNEDLTCGNL;
LPNLNEDLTCGNLL; PNLNEDLTCGNLLM; NLNEDLTCGNLLMW;
LNEDLTCGNLLMWE; NEDLTCGNLLMWEA; EDLTCGNLLMWEAV;
DLTCGNLLMWEAVT; LTCGNLLMWEAVTV; TCGNLLMWEAVTVQ;
CGNLLMWEAVTVQT; GNLLMWEAVTVQTE; NLLMWEAVTVQTEV;
LLMWEAVTVQTEVI; LMWEAVTVQTEVIG; MWEAVTVQTEVIGI;

WEAVTVQTEVIGIT; EAVTVQTEVIGITS; AVTVQTEVIGITSM;
VTVQTEVIGITSML; TVQTEVIGITSMLN; VQTEVIGITSMLNL;
QTEVIGITSMLNLH; TEVIGITSMLNLHA; EVIGITSMLNLHAG;
VIGITSMLNLHAGS; IGITSMLNLHAGSQ; GITSMLNLHAGSQK;
ITSMLNLHAGSQKV; TSMLNLHAGSQKVH; SMLNLHAGSQKVHE;
MLNLHAGSQKVHEH; LNLHAGSQKVHEHG; NLHAGSQKVHEHGG;
LHAGSQKVHEHGGG; HAGSQKVHEHGGGK; AGSQKVHEHGGGKP;
GSQKVHEHGGGKPI; SQKVHEHGGGKPIQ; QKVHEHGGGKPIQG;
KVHEHGGGKPIQGS; VHEHGGGKPIQGSN; HEHGGGKPIQGSNF;
EHGGGKPIQGSNFH; HGGGKPIQGSNFHF; GGGKPIQGSNFHFF;
GGKPIQGSNFHFFA; GKPIQGSNFHFFAV; KPIQGSNFHFFAVG;
PIQGSNFHFFAVGG; IQGSNFHFFAVGGE; QGSNFHFFAVGGEP;
GSNFHFFAVGGEPL; SNFHFFAVGGEPLE; NFHFFAVGGEPLEM;
FHFFAVGGEPLEMQ; HFFAVGGEPLEMQG; FFAVGGEPLEMQGV;
FAVGGEPLEMQGVL; AVGGEPLEMQGVLM; VGGEPLEMQGVLMN;
GGEPLEMQGVLMNY; GEPLEMQGVLMNYR; EPLEMQGVLMNYRS;
PLEMQGVLMNYRSK; LEMQGVLMNYRSKY; EMQGVLMNYRSKYP;
MQGVLMNYRSKYPD; QGVLMNYRSKYPDG; GVLMNYRSKYPDGT;
VLMNYRSKYPDGTI; LMNYRSKYPDGTIT; MNYRSKYPDGTITP;
NYRSKYPDGTITPK; YRSKYPDGTITPKN; RSKYPDGTITPKNP;
SKYPDGTITPKNPT; KYPDGTITPKNPTA; YPDGTITPKNPTAQ;
PDGTITPKNPTAQS; DGTITPKNPTAQSQ; GTITPKNPTAQSQV;
TITPKNPTAQSQVM; ITPKNPTAQSQVMN; TPKNPTAQSQVMNT;
PKNPTAQSQVMNTD; KNPTAQSQVMNTDH; NPTAQSQVMNTDHK;
PTAQSQVMNTDHKA; TAQSQVMNTDHKAY; AQSQVMNTDHKAYL;
QSQVMNTDHKAYLD; SQVMNTDHKAYLDK; QVMNTDHKAYLDKN;
VMNTDHKAYLDKNN; MNTDHKAYLDKNNA; NTDHKAYLDKNNAY;
TDHKAYLDKNNAYP; DHKAYLDKNNAYPV; HKAYLDKNNAYPVE;
KAYLDKNNAYPVEC; AYLDKNNAYPVECW; YLDKNNAYPVECWV;
LDKNNAYPVECWVP; DKNNAYPVECWVPD; KNNAYPVECWVPDP;
NNAYPVECWVPDPS; NAYPVECWVPDPSR; AYPVECWVPDPSRN;
YPVECWVPDPSRNE; PVECWVPDPSRNEN; VECWVPDPSRNENA;
ECWVPDPSRNENAR; CWVPDPSRNENARY; WVPDPSRNENARYF;
VPDPSRNENARYFG; PDPSRNENARYFGT; DPSRNENARYFGTF;
PSRNENARYFGTFT; SRNENARYFGTFTG; RNENARYFGTFTGG;
NENARYFGTFTGGE; ENARYFGTFTGGEN; NARYFGTFTGGENV;
ARYFGTFTGGENVP; RYFGTFTGGENVPP; YFGTFTGGENVPPV;
FGTFTGGENVPPVL; GTFTGGENVPPVLH; TFTGGENVPPVLHV;
FTGGENVPPVLHVT; TGGENVPPVLHVTN; GGENVPPVLHVTNT;
GENVPPVLHVTNTA; ENVPPVLHVTNTAT; NVPPVLHVTNTATT;
VPPVLHVTNTATTV; PPVLHVTNTATTVL; PVLHVTNTATTVLL;
VLHVTNTATTVLLD; LHVTNTATTVLLDE; HVTNTATTVLLDEQ;
VTNTATTVLLDEQG; TNTATTVLLDEQGV; NTATTVLLDEQGVG;
TATTVLLDEQGVGP; ATTVLLDEQGVGPL; TTVLLDEQGVGPLC;
TVLLDEQGVGPLCK; VLLDEQGVGPLCKA; LLDEQGVGPLCKAD;
LDEQGVGPLCKADS; DEQGVGPLCKADSL; EQGVGPLCKADSLY;
QGVGPLCKADSLYV; GVGPLCKADSLYVS; VGPLCKADSLYVSA;
GPLCKADSLYVSAA; PLCKADSLYVSAAD; LCKADSLYVSAADI;
CKADSLYVSAADIC; KADSLYVSAADICG; ADSLYVSAADICGL;
DSLYVSAADICGLF; SLYVSAADICGLFT; LYVSAADICGLFTN;
YVSAADICGLFTNS; VSAADICGLFTNSS; SAADICGLFTNSSG;
AADICGLFTNSSGT; ADICGLFTNSSGTQ; DICGLFTNSSGTQQ;
ICGLFTNSSGTQQW; CGLFTNSSGTQQWR; GLFTNSSGTQQWRG;
LFTNSSGTQQWRGL; FTNSSGTQQWRGLA; TNSSGTQQWRGLAR;
NSSGTQQWRGLARY; SSGTQQWRGLARYF; SGTQQWRGLARYFK;
GTQQWRGLARYFKI; TQQWRGLARYFKIR; QQWRGLARYFKIRL;
QWRGLARYFKIRLR; WRGLARYFKIRLRK; RGLARYFKIRLRKR;
GLARYFKIRLRKRS; LARYFKIRLRKRSV; ARYFKIRLRKRSVK;
RYFKIRLRKRSVKN; YFKIRLRKRSVKNP; FKIRLRKRSVKNPY;

KIRLRKRSVKNPYP; IRLRKRSVKNPYPI; RLRKRSVKNPYPIS;
LRKRSVKNPYPISF; RKRSVKNPYPISFL; KRSVKNPYPISFLL;
RSVKNPYPISFLLS; SVKNPYPISFLLSD; VKNPYPISFLLSDL;
KNPYPISFLLSDLI; NPYPISFLLSDLIN; PYPISFLLSDLINR;
YPISFLLSDLINRR; PISFLLSDLINRRT; ISFLLSDLINRRTQ;
SFLLSDLINRRTQR; FLLSDLINRRTQRV; LLSDLINRRTQRVD;
LSDLINRRTQRVDG; SDLINRRTQRVDGQ; DLINRRTQRVDGQP;
LINRRTQRVDGQPM; INRRTQRVDGQPMY; NRRTQRVDGQPMYG;
RRTQRVDGQPMYGM; RTQRVDGQPMYGME; TQRVDGQPMYGMES;
QRVDGQPMYGMESQ; RVDGQPMYGMESQV; VDGQPMYGMESQVE;
DGQPMYGMESQVEE; GQPMYGMESQVEEV; QPMYGMESQVEEVR;
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GMESQVEEVRVFDG; MESQVEEVRVFDGT; ESQVEEVRVFDGTE;
SQVEEVRVFDGTER; QVEEVRVFDGTERL; VEEVRVFDGTERLP;
EEVRVFDGTERLPG; EVRVFDGTERLPGD; VRVFDGTERLPGDP;
RVFDGTERLPGDPD; VFDGTERLPGDPDM; FDGTERLPGDPDMI;
DGTERLPGDPDMIR; GTERLPGDPDMIRY; TERLPGDPDMIRYI;
ERLPGDPDMIRYID; RLPGDPDMIRYIDK; LPGDPDMIRYIDKQ;
PGDPDMIRYIDKQG; GDPDMIRYIDKQGQ; DPDMIRYIDKQGQL;
PDMIRYIDKQGQLQ; DMIRYIDKQGQLQT; MIRYIDKQGQLQTK;
IRYIDKQGQLQTKM; RYIDKQGQLQTKML; TGAFIVHIHLINAA;
GAFIVHIHLINAAF; AFIVHIHLINAAFV; ATFKLVLFWGWCFR;
TFKLVLFWGWCFRP; FKLVLFWGWCFRPF; KLVLFWGWCFRPFK;
LVLFWGWCFRPFKT; VLFWGWCFRPFKTL; LFWGWCFRPFKTLK;
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RPFKTLKAFTQMQL; PFKTLKAFTQMQLL; FKTLKAFTQMQLLT;
KTLKAFTQMQLLTM; TLKAFTQMQLLTMG; LKAFTQMQLLTMGV;
ILFSCNIKNTFPHA; LFSCNIKNTFPHAY; FSCNIKNTFPHAYI;
SCNIKNTFPHAYII; CNIKNTFPHAYIIF; NIKNTFPHAYIIFH;
IKNTFPHAYIIFHP; KSIHTYLRIQPFLP; SIHTYLRIQPFLPF;
IHTYLRIQPFLPFN; HTYLRIQPFLPFNN; TYLRIQPFLPFNNS;
YLRIQPFLPFNNSR; LRIQPFLPFNNSRL; RIQPFLPFNNSRLY;
IQPFLPFNNSRLYI; QPFLPFNNSRLYIS; PFLPFNNSRLYISC;
FLPFNNSRLYISCK; LPFNNSRLYISCKI; PFNNSRLYISCKIS;
FNNSRLYISCKISY; NNSRLYISCKISYR; NSRLYISCKISYRP;
SRLYISCKISYRPK; RLYISCKISYRPKP; LYISCKISYRPKPN;
IYFGPKIYLSYKSS; YFGPKIYLSYKSSL; FGPKIYLSYKSSLQ;
GPKIYLSYKSSLQG; PKIYLSYKSSLQGF; KIYLSYKSSLQGFR;
IYLSYKSSLQGFRD; YLSYKSSLQGFRDR; LSYKSSLQGFRDRI;
SYKSSLQGFRDRIL; YKSSLQGFRDRILI; KSSLQGFRDRILIH;
SSLQGFRDRILIHC; SLQGFRDRILIHCN; LQGFRDRILIHCNQ;
QGFRDRILIHCNQA; GFRDRILIHCNQAW; FRDRILIHCNQAWW;
RDRILIHCNQAWWK; DRILIHCNQAWWKY; RILIHCNQAWWKYL;
ILIHCNQAWWKYLG; LIHCNQAWWKYLGS; IHCNQAWWKYLGSF;
HCNQAWWKYLGSFV; FSSCPFYIFKNNHV; SSCPFYIFKNNHVL;
SCPFYIFKNNHVLI; CPFYIFKNNHVLIY; PFYIFKNNHVLIYS;
FYIFKNNHVLIYSY; YIFKNNHVLIYSYT; PVSSFRYIENNTVQ;
VSSFRYIENNTVQK; SSFRYIENNTVQKI; SFRYIENNTVQKIK;
FRYIENNTVQKIKY; RYIENNTVQKIKYY; YIENNTVQKIKYYR;
IENNTVQKIKYYRI; ENNTVQKIKYYRIH; NNTVQKIKYYRIHF;
NTVQKIKYYRIHFR; HFFPGHMKGIYSFF; FFPGHMKGIYSFFS;
NCIYCLLTNTFLIF; CIYCLLTNTFLIFT; IYCLLTNTFLIFTF;
YCLLTNTFLIFTFC; CLLTNTFLIFTFCK; LLTNTFLIFTFCKN;
LTNTFLIFTFCKNN; TNTFLIFTFCKNNS; NTFLIFTFCKNNSI;
TFLIFTFCKNNSIC; FLIFTFCKNNSICK; LIFTFCKNNSICKV;
IFTFCKNNSICKVL; FTFCKNNSICKVLF; TFCKNNSICKVLFM;
FCKNNSICKVLFMI; CKNNSICKVLFMIL; KNNSICKVLFMILK;
NNSICKVLFMILKV; NSICKVLFMILKVI; SICKVLFMILKVIR;

ICKVLFMILKVIRL; CKVLFMILKVIRLV; KVLFMILKVIRLVF;
VLFMILKVIRLVFF; LFMILKVIRLVFFL; FMILKVIRLVFFLT;
MILKVIRLVFFLTL; ILKVIRLVFFLTLF; LKVIRLVFFLTLFT;
KVIRLVFFLTLFTL; VIRLVFFLTLFTLL; IRLVFFLTLFTLLY;
RLVFFLTLFTLLYI; LVFFLTLFTLLYIV; VFFLTLFTLLYIVL;
FFLTLFTLLYIVLK; FLTLFTLLYIVLKF; KHILTLCLYCILSN;
FPRHLLCFFRLFWA; PRHLLCFFRLFWAK; RHLLCFFRLFWAKI;
HLLCFFRLFWAKIM; LLCFFRLFWAKIML; LCFFRLFWAKIMLL;
APLNAFFYSMVWIS; PLNAFFYSMVWISS; KTKGTQLLTEIINC;
TKGTQLLTEIINCR; KGTQLLTEIINCRN; GTQLLTEIINCRNS;
TQLLTEIINCRNSM; QLLTEIINCRNSMS; LLTEIINCRNSMSM;
LTEIINCRNSMSMW; TEIINCRNSMSMWS; KEYNIMPSTHVSTN;
EYNIMPSTHVSTNK; YNIMPSTHVSTNKS; NIMPSTHVSTNKSY;
IMPSTHVSTNKSYR; MPSTHVSTNKSYRI; PSTHVSTNKSYRIF;
STHVSTNKSYRIFF; THVSTNKSYRIFFH; HVSTNKSYRIFFHK;
VSTNKSYRIFFHKF; STNKSYRIFFHKFF; TNKSYRIFFHKFFI;
NKSYRIFFHKFFIQ; KSYRIFFHKFFIQN; SYRIFFHKFFIQNL;
YRIFFHKFFIQNLS; RIFFHKFFIQNLSF; IFFHKFFIQNLSFF;
FFHKFFIQNLSFFF; FHKFFIQNLSFFFS; HKFFIQNLSFFFSS;
KFFIQNLSFFFSSI; FFIQNLSFFFSSIH; FIQNLSFFFSSIHS;
IQNLSFFFSSIHSK; QNLSFFFSSIHSKA; NLSFFFSSIHSKAG;
LSFFFSSIHSKAGK; SFFFSSIHSKAGKG; FFFSSIHSKAGKGS;
FFSSIHSKAGKGSI; FSSIHSKAGKGSIT; SSIHSKAGKGSITK;
SIHSKAGKGSITKY; IHSKAGKGSITKYS; HSKAGKGSITKYSL;
SKAGKGSITKYSLT; KAGKGSITKYSLTK; AGKGSITKYSLTKK;
GKGSITKYSLTKKL; KGSITKYSLTKKLV; IRGKVFRVFYLSFF;
RGKVFRVFYLSFFF; GKVFRVFYLSFFFG; KVFRVFYLSFFFGW;
VFRVFYLSFFFGWC; VLRICCCFFITGKH; LRICCCFFITGKHI;
RICCCFFITGKHIF; ICCCFFITGKHIFM; CCCFFITGKHIFMA;
CCFFITGKHIFMAK; IFIPFFIKGTPPGL; FIPFFIKGTPPGLP;
IPFFIKGTPPGLPL; PFFIKGTPPGLPLF; FFIKGTPPGLPLFC;
FIKGTPPGLPLFCS; IKGTPPGLPLFCSI; KGTPPGLPLFCSIG;
GTPPGLPLFCSIGW; TPPGLPLFCSIGWH; PPGLPLFCSIGWHL;
SFRSLKGVSPIIWT; FRSLKGVSPIIWTH; RSLKGVSPIIWTHH;
SLKGVSPIIWTHHC; LKGVSPIIWTHHCR; KGVSPIIWTHHCRV;
GVSPIIWTHHCRVS; VSPIIWTHHCRVSS; SPIIWTHHCRVSSV;
PIIWTHHCRVSSVR; IIWTHHCRVSSVRS; IWTHHCRVSSVRSK;
WTHHCRVSSVRSKP; THHCRVSSVRSKPN; HHCRVSSVRSKPNH;
HCRVSSVRSKPNHC; CRVSSVRSKPNHCV; RVSSVRSKPNHCVK;
VSSVRSKPNHCVKQ; SSVRSKPNHCVKQS; SVRSKPNHCVKQSM;
VRSKPNHCVKQSMQ; QSIQTKGSFLKNFL; SIQTKGSFLKNFLF;
IQTKGSFLKNFLFK; QTKGSFLKNFLFKC; TKGSFLKNFLFKCL;
KGSFLKNFLFKCLN; GSFLKNFLFKCLNL; SFLKNFLFKCLNLS;
HSMQGQCTEGFLEQ; SMQGQCTEGFLEQI; MQGQCTEGFLEQIG;
QGQCTEGFLEQIGH; GQCTEGFLEQIGHS; QCTEGFLEQIGHSL;
CTEGFLEQIGHSLQ; TEGFLEQIGHSLQY; EGFLEQIGHSLQYR;
GFLEQIGHSLQYRV; FLEQIGHSLQYRVS; LEQIGHSLQYRVSG;
EQIGHSLQYRVSGQ; QIGHSLQYRVSGQR; IGHSLQYRVSGQRG;
GHSLQYRVSGQRGK; HSLQYRVSGQRGKS; SLQYRVSGQRGKSA;
LQYRVSGQRGKSAQ; QYRVSGQRGKSAQT; YRVSGQRGKSAQTS;
RVSGQRGKSAQTSE; VSGQRGKSAQTSEL; SGQRGKSAQTSELL;
GQRGKSAQTSELLQ; QRGKSAQTSELLQV; RGKSAQTSELLQVP;
GKSAQTSELLQVPK; KSAQTSELLQVPKS; SAQTSELLQVPKSG;
ATFTSCSIFLYKVF; TFTSCSIFLYKVFI; FTSCSIFLYKVFIL;
TSCSIFLYKVFILF; SCSIFLYKVFILFI; CSIFLYKVFILFIL;
SIFLYKVFILFILS; IFLYKVFILFILSS; FLYKVFILFILSSS;
LYKVFILFILSSSP; YKVFILFILSSSPP; KVFILFILSSSPPL;
VFILFILSSSPPLS; FILFILSSSPPLSG; AFLIKGRFPQAALS;
FLIKGRFPQAALSR; LIKGRFPQAALSRP; IKGRFPQAALSRPK;

KGRFPQAALSRPKR; GRFPQAALSRPKRS; RFPQAALSRPKRSM;
FPQAALSRPKRSMS; PQAALSRPKRSMSS; QAALSRPKRSMSSM;
AALSRPKRSMSSMD; ALSRPKRSMSSMDS; LSRPKRSMSSMDSS;
SRPKRSMSSMDSSL; RPKRSMSSMDSSLL; PKRSMSSMDSSLLR;
KRSMSSMDSSLLRT; RSMSSMDSSLLRTL; SMSSMDSSLLRTLS

15 mers:
FCKNCKRIGISPNSF; CKNCKRIGISPNSFA; KNCKRIGISPNSFAR;
NCKRIGISPNSFARP; CKRIGISPNSFARPQ; KRIGISPNSFARPQK;
RIGISPNSFARPQKK; IGISPNSFARPQKKP; GISPNSFARPQKKPP;
ISPNSFARPQKKPPH; SPNSFARPQKKPPHP; PNSFARPQKKPPHPY;
NSFARPQKKPPHPYY; SFARPQKKPPHPYYL; FARPQKKPPHPYYLR;
ARPQKKPPHPYYLRE; RPQKKPPHPYYLRER; PQKKPPHPYYLRERV;
QKKPPHPYYLRERVE; KKPPHPYYLRERVEA; KPPHPYYLRERVEAE;
PPHPYYLRERVEAEA; PHPYYLRERVEAEAA; HPYYLRERVEAEAAS;
PYYLRERVEAEAASA; YYLRERVEAEAASAS; YLRERVEAEAASASY;
LRERVEAEAASASYI; RERVEAEAASASYIL; KKRPQGGAAYPWNAA;
KRPQGGAAYPWNAAK; RPQGGAAYPWNAAKP; PQEGKCMTHRGMQPN;
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KCMTHRGMQPNHDLR; CMTHRGMQPNHDLRK; MTHRGMQPNHDLRKE;
THRGMQPNHDLRKES; HRGMQPNHDLRKESA; LTGRSCLPMECSQTM;
TGRSCLPMECSQTMT; GRSCLPMECSQTMTS; RSCLPMECSQTMTSG;
SCLPMECSQTMTSGR; CLPMECSQTMTSGRK; LPMECSQTMTSGRKV;
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CSQTMTSGRKVHDRH; SQTMTSGRKVHDRHV; QTMTSGRKVHDRHVL;
TMTSGRKVHDRHVLR; MTSGRKVHDRHVLRA; ESWPCPQLNWTKAMV;
SWPCPQLNWTKAMVL; WPCPQLNWTKAMVLR; PCPQLNWTKAMVLRQ;
CPQLNWTKAMVLRQL; PQLNWTKAMVLRQLS; QLNWTKAMVLRQLSR;
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TKAMVLRQLSRQASV; KAMVLRQLSRQASVK; AMVLRQLSRQASVKV;
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RQLSRQASVKVGKTW; QLSRQASVKVGKTWT; LSRQASVKVGKTWTG;
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AQRIFIFILELLLEF; QRIFIFILELLLEFC; RIFIFILELLLEFCR;
IFIFILELLLEFCRG; FIFILELLLEFCRGE; IFILELLLEFCRGED;
FILELLLEFCRGEDS; ILELLLEFCRGEDSV; LELLLEFCRGEDSVD;
ELLLEFCRGEDSVDG; LLLEFCRGEDSVDGK; LLEFCRGEDSVDGKN;
LEFCRGEDSVDGKNK; EFCRGEDSVDGKNKS; FCRGEDSVDGKNKST;
CRGEDSVDGKNKSTT; RGEDSVDGKNKSTTA; GEDSVDGKNKSTTAL;
EDSVDGKNKSTTALP; DSVDGKNKSTTALPA; SVDGKNKSTTALPAV;
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KNKSTTALPAVKDSV; NKSTTALPAVKDSVK; KSTTALPAVKDSVKD;
STTALPAVKDSVKDS; VSNPFFFVFPGSWVL; SNPFFFVFPGSWVLL;
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SNQAWLWNCLTQMST; NQAWLWNCLTQMSTM; QAWLWNCLTQMSTMI;
AWLWNCLTQMSTMIF; WLWNCLTQMSTMIFC; LWNCLTQMSTMIFCF;
WNCLTQMSTMIFCFL; NCLTQMSTMIFCFLV; ILLLIIFNTLILGIG;
LLLIIFNTLILGIGV; LLIIFNTLILGIGVL; LIIFNTLILGIGVLL;
IIFNTLILGIGVLLC; IFNTLILGIGVLLCL; FNTLILGIGVLLCLL;
NTLILGIGVLLCLLL; TLILGIGVLLCLLLF; LILGIGVLLCLLLFP;
ILGIGVLLCLLLFPR; LGIGVLLCLLLFPRL; GIGVLLCLLLFPRLC;

IGVLLCLLLFPRLCG; GVLLCLLLFPRLCGM; VLLCLLLFPRLCGML;
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LLLFPRLCGMLLGMI; LLFPRLCGMLLGMIY; LFPRLCGMLLGMIYL;
FPRLCGMLLGMIYLL; PHRNCREEQKDFLET; HRNCREEQKDFLETP;
RNCREEQKDFLETPW; NCREEQKDFLETPWL; CREEQKDFLETPWLD;
REEQKDFLETPWLDF; EEQKDFLETPWLDFW; EQKDFLETPWLDFWR;
QKDFLETPWLDFWRK; KDFLETPWLDFWRKL; DFLETPWLDFWRKLP;
FLETPWLDFWRKLPG; LETPWLDFWRKLPGQ; ETPWLDFWRKLPGQL;
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IIFNNIILIFPLLGP; IFNNIILIFPLLGPQ; FNNIILIFPLLGPQW;
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QEVLIKELLLNGCCL; EVLIKELLLNGCCLY; VLIKELLLNGCCLYF;
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VKTGVDAITEVECFL; KTGVDAITEVECFLN; TGVDAITEVECFLNP;
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PDENLRGFSLKLSAE; DENLRGFSLKLSAEN; ENLRGFSLKLSAEND;
NLRGFSLKLSAENDF; LRGFSLKLSAENDFS; RGFSLKLSAENDFSS;
GFSLKLSAENDFSSD; FSLKLSAENDFSSDS; SLKLSAENDFSSDSP;
LKLSAENDFSSDSPE; KLSAENDFSSDSPER; LSAENDFSSDSPERK;
SAENDFSSDSPERKM; AENDFSSDSPERKML; ENDFSSDSPERKMLP;
NDFSSDSPERKMLPC; DFSSDSPERKMLPCY; FSSDSPERKMLPCYS;
SSDSPERKMLPCYST; SDSPERKMLPCYSTA; DSPERKMLPCYSTAR;
SPERKMLPCYSTARI; PERKMLPCYSTARIP; ERKMLPCYSTARIPL;
RKMLPCYSTARIPLP; KMLPCYSTARIPLPN; MLPCYSTARIPLPNL;
LPCYSTARIPLPNLN; PCYSTARIPLPNLNE; CYSTARIPLPNLNED;
YSTARIPLPNLNEDL; STARIPLPNLNEDLT; TARIPLPNLNEDLTC;
ARIPLPNLNEDLTCG; RIPLPNLNEDLTCGN; IPLPNLNEDLTCGNL;
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TCGNLLMWEAVTVQT; CGNLLMWEAVTVQTE; GNLLMWEAVTVQTEV;
NLLMWEAVTVQTEVI; LLMWEAVTVQTEVIG; LMWEAVTVQTEVIGI;
MWEAVTVQTEVIGIT; WEAVTVQTEVIGITS; EAVTVQTEVIGITSM;
AVTVQTEVIGITSML; VTVQTEVIGITSMLN; TVQTEVIGITSMLNL;
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EVIGITSMLNLHAGS; VIGITSMLNLHAGSQ; IGITSMLNLHAGSQK;
GITSMLNLHAGSQKV; ITSMLNLHAGSQKVH; TSMLNLHAGSQKVHE;
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QKVHEHGGGKPIQGS; KVHEHGGGKPIQGSN; VHEHGGGKPIQGSNF;
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AYPVECWVPDPSRNE; YPVECWVPDPSRNEN; PVECWVPDPSRNENA;
VECWVPDPSRNENAR; ECWVPDPSRNENARY; CWVPDPSRNENARYF;
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RNENARYFGTFTGGE; NENARYFGTFTGGEN; ENARYFGTFTGGENV;
NARYFGTFTGGENVP; ARYFGTFTGGENVPP; RYFGTFTGGENVPPV;
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VGPLCKADSLYVSAA; GPLCKADSLYVSAAD; PLCKADSLYVSAADI;
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ADSLYVSAADICGLF; DSLYVSAADICGLFT; SLYVSAADICGLFTN;
LYVSAADICGLFTNS; YVSAADICGLFTNSS; VSAADICGLFTNSSG;
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SRLYISCKISYRPKP; RLYISCKISYRPKPN; IYFGPKIYLSYKSSL;
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YKSSLQGFRDRILIH; KSSLQGFRDRILIHC; SSLQGFRDRILIHCN;
SLQGFRDRILIHCNQ; LQGFRDRILIHCNQA; QGFRDRILIHCNQAW;
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VSSFRYIENNTVQKI; SSFRYIENNTVQKIK; SFRYIENNTVQKIKY;
FRYIENNTVQKIKYY; RYIENNTVQKIKYYR; YIENNTVQKIKYYRI;
IENNTVQKIKYYRIH; ENNTVQKIKYYRIHF; NNTVQKIKYYRIHFR;
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IYCLLTNTFLIFTFC; YCLLTNTFLIFTFCK; CLLTNTFLIFTFCKN;
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NTFLIFTFCKNNSIC; TFLIFTFCKNNSICK; FLIFTFCKNNSICKV;
LIFTFCKNNSICKVL; IFTFCKNNSICKVLF; FTFCKNNSICKVLFM;
TFCKNNSICKVLFMI; FCKNNSICKVLFMIL; CKNNSICKVLFMILK;
KNNSICKVLFMILKV; NNSICKVLFMILKVI; NSICKVLFMILKVIR;
SICKVLFMILKVIRL; ICKVLFMILKVIRLV; CKVLFMILKVIRLVF;
KVLFMILKVIRLVFF; VLFMILKVIRLVFFL; LFMILKVIRLVFFLT;
FMILKVIRLVFFLTL; MILKVIRLVFFLTLF; ILKVIRLVFFLTLFT;
LKVIRLVFFLTLFTL; KVIRLVFFLTLFTLL; VIRLVFFLTLFTLLY;
IRLVFFLTLFTLLYI; RLVFFLTLFTLLYIV; LVFFLTLFTLLYIVL;
VFFLTLFTLLYIVLK; FFLTLFTLLYIVLKF; FPRHLLCFFRLFWAK;
PRHLLCFFRLFWAKI; RHLLCFFRLFWAKIM; HLLCFFRLFWAKIML;
LLCFFRLFWAKIMLL; APLNAFFYSMVWISS; KTKGTQLLTEIINCR;
TKGTQLLTEIINCRN; KGTQLLTEIINCRNS; GTQLLTEIINCRNSM;

TQLLTEIINCRNSMS; QLLTEIINCRNSMSM; LLTEIINCRNSMSMW;
LTEIINCRNSMSMWS; KEYNIMPSTHVSTNK; EYNIMPSTHVSTNKS;
YNIMPSTHVSTNKSY; NIMPSTHVSTNKSYR; IMPSTHVSTNKSYRI;
MPSTHVSTNKSYRIF; PSTHVSTNKSYRIFF; STHVSTNKSYRIFFH;
THVSTNKSYRIFFHK; HVSTNKSYRIFFHKF; VSTNKSYRIFFHKFF;
STNKSYRIFFHKFFI; TNKSYRIFFHKFFIQ; NKSYRIFFHKFFIQN;
KSYRIFFHKFFIQNL; SYRIFFHKFFIQNLS; YRIFFHKFFIQNLSF;
RIFFHKFFIQNLSFF; IFFHKFFIQNLSFFF; FFHKFFIQNLSFFFS;
FHKFFIQNLSFFFSS; HKFFIQNLSFFFSSI; KFFIQNLSFFFSSIH;
FFIQNLSFFFSSIHS; FIQNLSFFFSSIHSK; IQNLSFFFSSIHSKA;
QNLSFFFSSIHSKAG; NLSFFFSSIHSKAGK; LSFFFSSIHSKAGKG;
SFFFSSIHSKAGKGS; FFFSSIHSKAGKGSI; FFSSIHSKAGKGSIT;
FSSIHSKAGKGSITK; SSIHSKAGKGSITKY; SIHSKAGKGSITKYS;
IHSKAGKGSITKYSL; HSKAGKGSITKYSLT; SKAGKGSITKYSLTK;
KAGKGSITKYSLTKK; AGKGSITKYSLTKKL; GKGSITKYSLTKKLV;
IRGKVFRVFYLSFFF; RGKVFRVFYLSFFFG; GKVFRVFYLSFFFGW;
KVFRVFYLSFFFGWC; VLRICCCFFITGKHI; LRICCCFFITGKHIF;
RICCCFFITGKHIFM; ICCCFFITGKHIFMA; CCCFFITGKHIFMAK;
IFIPFFIKGTPPGLP; FIPFFIKGTPPGLPL; IPFFIKGTPPGLPLF;
PFFIKGTPPGLPLFC; FFIKGTPPGLPLFCS; FIKGTPPGLPLFCSI;
IKGTPPGLPLFCSIG; KGTPPGLPLFCSIGW; GTPPGLPLFCSIGWH;
TPPGLPLFCSIGWHL; SFRSLKGVSPIIWTH; FRSLKGVSPIIWTHH;
RSLKGVSPIIWTHHC; SLKGVSPIIWTHHCR; LKGVSPIIWTHHCRV;
KGVSPIIWTHHCRVS; GVSPIIWTHHCRVSS; VSPIIWTHHCRVSSV;
SPIIWTHHCRVSSVR; PIIWTHHCRVSSVRS; IIWTHHCRVSSVRSK;
IWTHHCRVSSVRSKP; WTHHCRVSSVRSKPN; THHCRVSSVRSKPNH;
HHCRVSSVRSKPNHC; HCRVSSVRSKPNHCV; CRVSSVRSKPNHCVK;
RVSSVRSKPNHCVKQ; VSSVRSKPNHCVKQS; SSVRSKPNHCVKQSM;
SVRSKPNHCVKQSMQ; QSIQTKGSFLKNFLF; SIQTKGSFLKNFLFK;
IQTKGSFLKNFLFKC; QTKGSFLKNFLFKCL; TKGSFLKNFLFKCLN;
KGSFLKNFLFKCLNL; GSFLKNFLFKCLNLS; HSMQGQCTEGFLEQI;
SMQGQCTEGFLEQIG; MQGQCTEGFLEQIGH; QGQCTEGFLEQIGHS;
GQCTEGFLEQIGHSL; QCTEGFLEQIGHSLQ; CTEGFLEQIGHSLQY;
TEGFLEQIGHSLQYR; EGFLEQIGHSLQYRV; GFLEQIGHSLQYRVS;
FLEQIGHSLQYRVSG; LEQIGHSLQYRVSGQ; EQIGHSLQYRVSGQR;
QIGHSLQYRVSGQRG; IGHSLQYRVSGQRGK; GHSLQYRVSGQRGKS;
HSLQYRVSGQRGKSA; SLQYRVSGQRGKSAQ; LQYRVSGQRGKSAQT;
QYRVSGQRGKSAQTS; YRVSGQRGKSAQTSE; RVSGQRGKSAQTSEL;
VSGQRGKSAQTSELL; SGQRGKSAQTSELLQ; GQRGKSAQTSELLQV;
QRGKSAQTSELLQVP; RGKSAQTSELLQVPK; GKSAQTSELLQVPKS;
KSAQTSELLQVPKSG; ATFTSCSIFLYKVFI; TFTSCSIFLYKVFIL;
FTSCSIFLYKVFILF; TSCSIFLYKVFILFI; SCSIFLYKVFILFIL;
CSIFLYKVFILFILS; SIFLYKVFILFILSS; IFLYKVFILFILSSS;
FLYKVFILFILSSSP; LYKVFILFILSSSPP; YKVFILFILSSSPPL;
KVFILFILSSSPPLS; VFILFILSSSPPLSG; AFLIKGRFPQAALSR;
FLIKGRFPQAALSRP; LIKGRFPQAALSRPK; IKGRFPQAALSRPKR;
KGRFPQAALSRPKRS; GRFPQAALSRPKRSM; RFPQAALSRPKRSMS;
FPQAALSRPKRSMSS; PQAALSRPKRSMSSM; QAALSRPKRSMSSMD;
AALSRPKRSMSSMDS; ALSRPKRSMSSMDSS; LSRPKRSMSSMDSSL;
SRPKRSMSSMDSSLL; RPKRSMSSMDSSLLR; PKRSMSSMDSSLLRT;
KRSMSSMDSSLLRTL; RSMSSMDSSLLRTLS

16 mers:
FCKNCKRIGISPNSFA; CKNCKRIGISPNSFAR; KNCKRIGISPNSFARP;
NCKRIGISPNSFARPQ; CKRIGISPNSFARPQK; KRIGISPNSFARPQKK;
RIGISPNSFARPQKKP; IGISPNSFARPQKKPP; GISPNSFARPQKKPPH;
ISPNSFARPQKKPPHP; SPNSFARPQKKPPHPY; PNSFARPQKKPPHPYY;
NSFARPQKKPPHPYYL; SFARPQKKPPHPYYLR; FARPQKKPPHPYYLRE;
ARPQKKPPHPYYLRER; RPQKKPPHPYYLRERV; PQKKPPHPYYLRERVE;
QKKPPHPYYLRERVEA; KKPPHPYYLRERVEAE; KPPHPYYLRERVEAEA;

PPHPYYLRERVEAEAA; PHPYYLRERVEAEAAS; HPYYLRERVEAEAASA;
PYYLRERVEAEAASAS; YYLRERVEAEAASASY; YLRERVEAEAASASYI;
LRERVEAEAASASYIL; KKRPQGGAAYPWNAAK; KRPQGGAAYPWNAAKP;
PQEGKCMTHRGMQPNH; QEGKCMTHRGMQPNHD; EGKCMTHRGMQPNHDL;
GKCMTHRGMQPNHDLR; KCMTHRGMQPNHDLRK; CMTHRGMQPNHDLRKE;
MTHRGMQPNHDLRKES; THRGMQPNHDLRKESA; LTGRSCLPMECSQTMT;
TGRSCLPMECSQTMTS; GRSCLPMECSQTMTSG; RSCLPMECSQTMTSGR;
SCLPMECSQTMTSGRK; CLPMECSQTMTSGRKV; LPMECSQTMTSGRKVH;
PMECSQTMTSGRKVHD; MECSQTMTSGRKVHDR; ECSQTMTSGRKVHDRH;
CSQTMTSGRKVHDRHV; SQTMTSGRKVHDRHVL; QTMTSGRKVHDRHVLR;
TMTSGRKVHDRHVLRA; ESWPCPQLNWTKAMVL; SWPCPQLNWTKAMVLR;
WPCPQLNWTKAMVLRQ; PCPQLNWTKAMVLRQL; CPQLNWTKAMVLRQLS;
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VLRQLSRQASVKVGKT; LRQLSRQASVKVGKTW; RQLSRQASVKVGKTWT;
QLSRQASVKVGKTWTG; LSRQASVKVGKTWTGT; SRQASVKVGKTWTGTK;
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QRIFIFILELLLEFCR; RIFIFILELLLEFCRG; IFIFILELLLEFCRGE;
FIFILELLLEFCRGED; IFILELLLEFCRGEDS; FILELLLEFCRGEDSV;
ILELLLEFCRGEDSVD; LELLLEFCRGEDSVDG; ELLLEFCRGEDSVDGK;
LLLEFCRGEDSVDGKN; LLEFCRGEDSVDGKNK; LEFCRGEDSVDGKNKS;
EFCRGEDSVDGKNKST; FCRGEDSVDGKNKSTT; CRGEDSVDGKNKSTTA;
RGEDSVDGKNKSTTAL; GEDSVDGKNKSTTALP; EDSVDGKNKSTTALPA;
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NKSTTALPAVKDSVKD; KSTTALPAVKDSVKDS; VSNPFFFVFPGSWVLL;
LPVYLRLLLPQDFQWL; PVYLRLLLPQDFQWLK; VYLRLLLPQDFQWLKL;
YLRLLLPQDFQWLKLL; LRLLLPQDFQWLKLLL; RLLLPQDFQWLKLLLG;
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PQDFQWLKLLLGRLLL; QDFQWLKLLLGRLLLL; ASISNQAWLWNCLTQM;
SISNQAWLWNCLTQMS; ISNQAWLWNCLTQMST; SNQAWLWNCLTQMSTM;
NQAWLWNCLTQMSTMI; QAWLWNCLTQMSTMIF; AWLWNCLTQMSTMIFC;
WLWNCLTQMSTMIFCF; LWNCLTQMSTMIFCFL; WNCLTQMSTMIFCFLV;
ILLLIIFNTLILGIGV; LLLIIFNTLILGIGVL; LLIIFNTLILGIGVLL;
LIIFNTLILGIGVLLC; IIFNTLILGIGVLLCL; IFNTLILGIGVLLCLL;
FNTLILGIGVLLCLLL; NTLILGIGVLLCLLLF; TLILGIGVLLCLLLFP;
LILGIGVLLCLLLFPR; ILGIGVLLCLLLFPRL; LGIGVLLCLLLFPRLC;
GIGVLLCLLLFPRLCG; IGVLLCLLLFPRLCGM; GVLLCLLLFPRLCGML;
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CLLLFPRLCGMLLGMI; LLLFPRLCGMLLGMIY; LLFPRLCGMLLGMIYL;
LFPRLCGMLLGMIYLL; PHRNCREEQKDFLETP; HRNCREEQKDFLETPW;
RNCREEQKDFLETPWL; NCREEQKDFLETPWLD; CREEQKDFLETPWLDF;
REEQKDFLETPWLDFW; EEQKDFLETPWLDFWR; EQKDFLETPWLDFWRK;
QKDFLETPWLDFWRKL; KDFLETPWLDFWRKLP; DFLETPWLDFWRKLPG;
FLETPWLDFWRKLPGQ; LETPWLDFWRKLPGQL; TFIIIFNNIILIFPLL;
FIIIFNNIILIFPLLG; IIIFNNIILIFPLLGP; IIFNNIILIFPLLGPQ;
IFNNIILIFPLLGPQW; FNNIILIFPLLGPQWL; NNIILIFPLLGPQWLD;
NIILIFPLLGPQWLDK; KKLLPQEVLIKELLLN; KLLPQEVLIKELLLNG;
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QEVLIKELLLNGCCLY; EVLIKELLLNGCCLYF; HLLLKHMKMAPTKRKG;
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KMAPTKRKGECPGAAP; MAPTKRKGECPGAAPK; APTKRKGECPGAAPKK;

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RKGECPGAAPKKPKEP; KGECPGAAPKKPKEPV; GECPGAAPKKPKEPVQ;
ECPGAAPKKPKEPVQV; CPGAAPKKPKEPVQVP; PGAAPKKPKEPVQVPK;
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VPKLLIKGGVEVLEVK; PKLLIKGGVEVLEVKT; KLLIKGGVEVLEVKTG;
LLIKGGVEVLEVKTGV; LIKGGVEVLEVKTGVD; IKGGVEVLEVKTGVDA;
KGGVEVLEVKTGVDAI; GGVEVLEVKTGVDAIT; GVEVLEVKTGVDAITE;
VEVLEVKTGVDAITEV; EVLEVKTGVDAITEVE; VLEVKTGVDAITEVEC;
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VECFLNPEMGDPDENL; ECFLNPEMGDPDENLR; CFLNPEMGDPDENLRG;
FLNPEMGDPDENLRGF; LNPEMGDPDENLRGFS; NPEMGDPDENLRGFSL;
PEMGDPDENLRGFSLK; EMGDPDENLRGFSLKL; MGDPDENLRGFSLKLS;
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FSLKLSAENDFSSDSP; SLKLSAENDFSSDSPE; LKLSAENDFSSDSPER;
KLSAENDFSSDSPERK; LSAENDFSSDSPERKM; SAENDFSSDSPERKML;
AENDFSSDSPERKMLP; ENDFSSDSPERKMLPC; NDFSSDSPERKMLPCY;
DFSSDSPERKMLPCYS; FSSDSPERKMLPCYST; SSDSPERKMLPCYSTA;
SDSPERKMLPCYSTAR; DSPERKMLPCYSTARI; SPERKMLPCYSTARIP;
PERKMLPCYSTARIPL; ERKMLPCYSTARIPLP; RKMLPCYSTARIPLPN;
KMLPCYSTARIPLPNL; MLPCYSTARIPLPNLN; LPCYSTARIPLPNLNE;
PCYSTARIPLPNLNED; CYSTARIPLPNLNEDL; YSTARIPLPNLNEDLT;
STARIPLPNLNEDLTC; TARIPLPNLNEDLTCG; ARIPLPNLNEDLTCGN;
RIPLPNLNEDLTCGNL; IPLPNLNEDLTCGNLL; PLPNLNEDLTCGNLLM;
LPNLNEDLTCGNLLMW; PNLNEDLTCGNLLMWE; NLNEDLTCGNLLMWEA;
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VTVQTEVIGITSMLNL; TVQTEVIGITSMLNLH; VQTEVIGITSMLNLHA;
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KVHEHGGGKPIQGSNF; VHEHGGGKPIQGSNFH; HEHGGGKPIQGSNFHF;
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PIQGSNFHFFAVGGEP; IQGSNFHFFAVGGEPL; QGSNFHFFAVGGEPLE;
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SKYPDGTITPKNPTAQ; KYPDGTITPKNPTAQS; YPDGTITPKNPTAQSQ;
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TITPKNPTAQSQVMNT; ITPKNPTAQSQVMNTD; TPKNPTAQSQVMNTDH;

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QSQVMNTDHKAYLDKN; SQVMNTDHKAYLDKNN; QVMNTDHKAYLDKNNA;
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LDKNNAYPVECWVPDP; DKNNAYPVECWVPDPS; KNNAYPVECWVPDPSR;
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VPDPSRNENARYFGTF; PDPSRNENARYFGTFT; DPSRNENARYFGTFTG;
PSRNENARYFGTFTGG; SRNENARYFGTFTGGE; RNENARYFGTFTGGEN;
NENARYFGTFTGGENV; ENARYFGTFTGGENVP; NARYFGTFTGGENVPP;
ARYFGTFTGGENVPPV; RYFGTFTGGENVPPVL; YFGTFTGGENVPPVLH;
FGTFTGGENVPPVLHV; GTFTGGENVPPVLHVT; TFTGGENVPPVLHVTN;
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VPPVLHVTNTATTVLL; PPVLHVTNTATTVLLD; PVLHVTNTATTVLLDE;
VLHVTNTATTVLLDEQ; LHVTNTATTVLLDEQG; HVTNTATTVLLDEQGV;
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TATTVLLDEQGVGPLC; ATTVLLDEQGVGPLCK; TTVLLDEQGVGPLCKA;
TVLLDEQGVGPLCKAD; VLLDEQGVGPLCKADS; LLDEQGVGPLCKADSL;
LDEQGVGPLCKADSLY; DEQGVGPLCKADSLYV; EQGVGPLCKADSLYVS;
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DSLYVSAADICGLFTN; SLYVSAADICGLFTNS; LYVSAADICGLFTNSS;
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SQVEEVRVFDGTERLP; QVEEVRVFDGTERLPG; VEEVRVFDGTERLPGD;
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DGTERLPGDPDMIRYI; GTERLPGDPDMIRYID; TERLPGDPDMIRYIDK;
ERLPGDPDMIRYIDKQ; RLPGDPDMIRYIDKQG; LPGDPDMIRYIDKQGQ;
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PFKTLKAFTQMQLLTM; FKTLKAFTQMQLLTMG; KTLKAFTQMQLLTMGV;
ILFSCNIKNTFPHAYI; LFSCNIKNTFPHAYII; FSCNIKNTFPHAYIIF;
SCNIKNTFPHAYIIFH; CNIKNTFPHAYIIFHP; KSIHTYLRIQPFLPFN;
SIHTYLRIQPFLPFNN; IHTYLRIQPFLPFNNS; HTYLRIQPFLPFNNSR;
TYLRIQPFLPFNNSRL; YLRIQPFLPFNNSRLY; LRIQPFLPFNNSRLYI;
RIQPFLPFNNSRLYIS; IQPFLPFNNSRLYISC; QPFLPFNNSRLYISCK;
PFLPFNNSRLYISCKI; FLPFNNSRLYISCKIS; LPFNNSRLYISCKISY;
PFNNSRLYISCKISYR; FNNSRLYISCKISYRP; NNSRLYISCKISYRPK;
NSRLYISCKISYRPKP; SRLYISCKISYRPKPN; IYFGPKIYLSYKSSLQ;
YFGPKIYLSYKSSLQG; FGPKIYLSYKSSLQGF; GPKIYLSYKSSLQGFR;
PKIYLSYKSSLQGFRD; KIYLSYKSSLQGFRDR; IYLSYKSSLQGFRDRI;
YLSYKSSLQGFRDRIL; LSYKSSLQGFRDRILI; SYKSSLQGFRDRILIH;
YKSSLQGFRDRILIHC; KSSLQGFRDRILIHCN; SSLQGFRDRILIHCNQ;
SLQGFRDRILIHCNQA; LQGFRDRILIHCNQAW; QGFRDRILIHCNQAWW;
GFRDRILIHCNQAWWK; FRDRILIHCNQAWWKY; RDRILIHCNQAWWKYL;
DRILIHCNQAWWKYLG; RILIHCNQAWWKYLGS; ILIHCNQAWWKYLGSF;
LIHCNQAWWKYLGSFV; FSSCPFYIFKNNHVLI; SSCPFYIFKNNHVLIY;
SCPFYIFKNNHVLIYS; CPFYIFKNNHVLIYSY; PFYIFKNNHVLIYSYT;
PVSSFRYIENNTVQKI; VSSFRYIENNTVQKIK; SSFRYIENNTVQKIKY;
SFRYIENNTVQKIKYY; FRYIENNTVQKIKYYR; RYIENNTVQKIKYYRI;
YIENNTVQKIKYYRIH; IENNTVQKIKYYRIHF; ENNTVQKIKYYRIHFR;
NCIYCLLTNTFLIFTF; CIYCLLTNTFLIFTFC; IYCLLTNTFLIFTFCK;
YCLLTNTFLIFTFCKN; CLLTNTFLIFTFCKNN; LLTNTFLIFTFCKNNS;
LTNTFLIFTFCKNNSI; TNTFLIFTFCKNNSIC; NTFLIFTFCKNNSICK;
TFLIFTFCKNNSICKV; FLIFTFCKNNSICKVL; LIFTFCKNNSICKVLF;
IFTFCKNNSICKVLFM; FTFCKNNSICKVLFMI; TFCKNNSICKVLFMIL;
FCKNNSICKVLFMILK; CKNNSICKVLFMILKV; KNNSICKVLFMILKVI;
NNSICKVLFMILKVIR; NSICKVLFMILKVIRL; SICKVLFMILKVIRLV;
ICKVLFMILKVIRLVF; CKVLFMILKVIRLVFF; KVLFMILKVIRLVFFL;
VLFMILKVIRLVFFLT; LFMILKVIRLVFFLTL; FMILKVIRLVFFLTLF;
MILKVIRLVFFLTLFT; ILKVIRLVFFLTLFTL; LKVIRLVFFLTLFTLL;
KVIRLVFFLTLFTLLY; VIRLVFFLTLFTLLYI; IRLVFFLTLFTLLYIV;
RLVFFLTLFTLLYIVL; LVFFLTLFTLLYIVLK; VFFLTLFTLLYIVLKF;
FPRHLLCFFRLFWAKI; PRHLLCFFRLFWAKIM; RHLLCFFRLFWAKIML;
HLLCFFRLFWAKIMLL; KTKGTQLLTEIINCRN; TKGTQLLTEIINCRNS;
KGTQLLTEIINCRNSM; GTQLLTEIINCRNSMS; TQLLTEIINCRNSMSM;
QLLTEIINCRNSMSMW; LLTEIINCRNSMSMWS; KEYNIMPSTHVSTNKS;
EYNIMPSTHVSTNKSY; YNIMPSTHVSTNKSYR; NIMPSTHVSTNKSYRI;
IMPSTHVSTNKSYRIF; MPSTHVSTNKSYRIFF; PSTHVSTNKSYRIFFH;
STHVSTNKSYRIFFHK; THVSTNKSYRIFFHKF; HVSTNKSYRIFFHKFF;
VSTNKSYRIFFHKFFI; STNKSYRIFFHKFFIQ; TNKSYRIFFHKFFIQN;
NKSYRIFFHKFFIQNL; KSYRIFFHKFFIQNLS; SYRIFFHKFFIQNLSF;
YRIFFHKFFIQNLSFF; RIFFHKFFIQNLSFFF; IFFHKFFIQNLSFFFS;
FFHKFFIQNLSFFFSS; FHKFFIQNLSFFFSSI; HKFFIQNLSFFFSSIH;
KFFIQNLSFFFSSIHS; FFIQNLSFFFSSIHSK; FIQNLSFFFSSIHSKA;
IQNLSFFFSSIHSKAG; QNLSFFFSSIHSKAGK; NLSFFFSSIHSKAGKG;
LSFFFSSIHSKAGKGS; SFFFSSIHSKAGKGSI; FFFSSIHSKAGKGSIT;
FFSSIHSKAGKGSITK; FSSIHSKAGKGSITKY; SSIHSKAGKGSITKYS;
SIHSKAGKGSITKYSL; IHSKAGKGSITKYSLT; HSKAGKGSITKYSLTK;
SKAGKGSITKYSLTKK; KAGKGSITKYSLTKKL; AGKGSITKYSLTKKLV;
IRGKVFRVFYLSFFFG; RGKVFRVFYLSFFFGW; GKVFRVFYLSFFFGWC;
VLRICCCFFITGKHIF; LRICCCFFITGKHIFM; RICCCFFITGKHIFMA;
ICCCFFITGKHIFMAK; IFIPFFIKGTPPGLPL; FIPFFIKGTPPGLPLF;
IPFFIKGTPPGLPLFC; PFFIKGTPPGLPLFCS; FFIKGTPPGLPLFCSI;
FIKGTPPGLPLFCSIG; IKGTPPGLPLFCSIGW; KGTPPGLPLFCSIGWH;
GTPPGLPLFCSIGWHL; SFRSLKGVSPIIWTHH; FRSLKGVSPIIWTHHC;
RSLKGVSPIIWTHHCR; SLKGVSPIIWTHHCRV; LKGVSPIIWTHHCRVS;

KGVSPIIWTHHCRVSS; GVSPIIWTHHCRVSSV; VSPIIWTHHCRVSSVR; SPIIWTHHCRVSSVRS; PIIWTHHCRVSSVRSK; IIWTHHCRVSSVRSKP; IWTHHCRVSSVRSKPN; WTHHCRVSSVRSKPNH; THHCRVSSVRSKPNHC; HHCRVSSVRSKPNHCV; HCRVSSVRSKPNHCVK; CRVSSVRSKPNHCVKQ; RVSSVRSKPNHCVKQS; VSSVRSKPNHCVKQSM; SSVRSKPNHCVKQSMQ; QSIQTKGSFLKNFLFK; SIQTKGSFLKNFLFKC; IQTKGSFLKNFLFKCL; QTKGSFLKNFLFKCLN; TKGSFLKNFLFKCLNL; KGSFLKNFLFKCLNLS; HSMQGQCTEGFLEQIG; SMQGQCTEGFLEQIGH; MQGQCTEGFLEQIGHS; QGQCTEGFLEQIGHSL; GQCTEGFLEQIGHSLQ; QCTEGFLEQIGHSLQY; CTEGFLEQIGHSLQYR; TEGFLEQIGHSLQYRV; EGFLEQIGHSLQYRVS; GFLEQIGHSLQYRVSG; FLEQIGHSLQYRVSGQ; LEQIGHSLQYRVSGQR; EQIGHSLQYRVSGQRG; QIGHSLQYRVSGQRGK; IGHSLQYRVSGQRGKS; GHSLQYRVSGQRGKSA; HSLQYRVSGQRGKSAQ; SLQYRVSGQRGKSAQT; LQYRVSGQRGKSAQTS; QYRVSGQRGKSAQTSE; YRVSGQRGKSAQTSEL; RVSGQRGKSAQTSELL; VSGQRGKSAQTSELLQ; SGQRGKSAQTSELLQV; GQRGKSAQTSELLQVP; QRGKSAQTSELLQVPK; RGKSAQTSELLQVPKS; GKSAQTSELLQVPKSG; ATFTSCSIFLYKVFIL; TFTSCSIFLYKVFILF; FTSCSIFLYKVFILFI; TSCSIFLYKVFILFIL; SCSIFLYKVFILFILS; CSIFLYKVFILFILSS; SIFLYKVFILFILSSS; IFLYKVFILFILSSSP; FLYKVFILFILSSSPP; LYKVFILFILSSSPPL; YKVFILFILSSSPPLS; KVFILFILSSSPPLSG; AFLIKGRFPQAALSRP; FLIKGRFPQAALSRPK; LIKGRFPQAALSRPKR; IKGRFPQAALSRPKRS; KGRFPQAALSRPKRSM; GRFPQAALSRPKRSMS; RFPQAALSRPKRSMSS; FPQAALSRPKRSMSSM; PQAALSRPKRSMSSMD; QAALSRPKRSMSSMDS; AALSRPKRSMSSMDSS; ALSRPKRSMSSMDSSL; LSRPKRSMSSMDSSLL; SRPKRSMSSMDSSLLR; RPKRSMSSMDSSLLRT; PKRSMSSMDSSLLRTL; KRSMSSMDSSLLRTLS
BK virus, reading frame 2
13 mers: GFPQIVLLGLRKS; FPQIVLLGLRKSL; PQIVLLGLRKSLH; QIVLLGLRKSLHT; IVLLGLRKSLHTL; VLLGLRKSLHTLT; LLGLRKSLHTLTT; EKGWRQRRPRPLI; KGWRQRRPRPLIY; GWRQRRPRPLIYY; WRQRRPRPLIYYK; RQRRPRPLIYYKK; QRRPRPLIYYKKK; RRPRPLIYYKKKG; RPRPLIYYKKKGH; PRPLIYYKKKGHR; RPLIYYKKKGHRE; PLIYYKKKGHREE; LIYYKKKGHREEL; IYYKKKGHREELL; YYKKKGHREELLT; YKKKGHREELLTH; KKKGHREELLTHG; KKGHREELLTHGM; KGHREELLTHGMQ; GHREELLTHGMQP; HREELLTHGMQPN; REELLTHGMQPNH; EELLTHGMQPNHD; ELLTHGMQPNHDL; LLTHGMQPNHDLR; LTHGMQPNHDLRK; THGMQPNHDLRKE; HGMQPNHDLRKES; GMQPNHDLRKESA; LTGECSQTMTSGR; TGECSQTMTSGRK; GECSQTMTSGRKV; ECSQTMTSGRKVH; CSQTMTSGRKVHD; SQTMTSGRKVHDS; QTMTSGRKVHDSQ; TMTSGRKVHDSQG; MTSGRKVHDSQGG; TSGRKVHDSQGGA; SGRKVHDSQGGAA; GRKVHDSQGGAAY; RKVHDSQGGAAYP; KVHDSQGGAAYPW; VHDSQGGAAYPWN; HDSQGGAAYPWNA; DSQGGAAYPWNAA; SQGGAAYPWNAAK; QGGAAYPWNAAKP; PQEGKCMTDMFCE; QEGKCMTDMFCEP; EGKCMTDMFCEPR; GKCMTDMFCEPRN; KCMTDMFCEPRNL; CMTDMFCEPRNLG; MTDMFCEPRNLGL; TDMFCEPRNLGLV; DMFCEPRNLGLVP; MFCEPRNLGLVPS; TGQRPWFCASCHD; GQRPWFCASCHDK; QRPWFCASCHDKL; RPWFCASCHDKLQ; KLVKPGLEQKKEL; LVKPGLEQKKELR; VKPGLEQKKELRG; KPGLEQKKELRGF; PGLEQKKELRGFL; GLEQKKELRGFLF; LEQKKELRGFLFL; EQKKELRGFLFLF; VIPFFLYFQVHGC; IPFFLYFQVHGCC; PFFLYFQVHGCCS; FFLYFQVHGCCSS; FLYFQVHGCCSST; LYFQVHGCCSSTF; YFQVHGCCSSTFG; FQVHGCCSSTFGG; QVHGCCSSTFGGP; VHGCCSSTFGGPS; HGCCSSTFGGPSC; GCCSSTFGGPSCQ; CCSSTFGGPSCQC; CSSTFGGPSCQCI; NCCWGGCCCYRSS; CCWGGCCCYRSSN; CWGGCCCYRSSNC; WGGCCCYRSSNCI; GGCCCYRSSNCIP; GCCCYRSSNCIPC; CCCYRSSNCIPCY; CCYRSSNCIPCYC; CYRSSNCIPCYCR; YRSSNCIPCYCRG; RSSNCIPCYCRGH; SSNCIPCYCRGHN; SNCIPCYCRGHNK; NCIPCYCRGHNKY; CIPCYCRGHNKYL; IPCYCRGHNKYLR; PCYCRGHNKYLRG; CYCRGHNKYLRGY; YCRGHNKYLRGYS; CRGHNKYLRGYSC; RGHNKYLRGYSCY; GHNKYLRGYSCYR; HNKYLRGYSCYRP; NKYLRGYSCYRPN; KYLRGYSCYRPNS; YLRGYSCYRPNSS; LRGYSCYRPNSSN; RGYSCYRPNSSNI; GYSCYRPNSSNIC; YSCYRPNSSNICC; SCYRPNSSNICCN; CYRPNSSNICCNC; YRPNSSNICCNCW; RPNSSNICCNCWC;

PNSSNICCNCWCS; NSSNICCNCWCSW; SSNICCNCWCSWG; SNICCNCWCSWGY;
NICCNCWCSWGYC; ICCNCWCSWGYCW; CCNCWCSWGYCWV; CNCWCSWGYCWVC;
NCWCSWGYCWVCC; CWCSWGYCWVCCF; WCSWGYCWVCCFN; CSWGYCWVCCFNS;
SWGYCWVCCFNSN; WGYCWVCCFNSNC; LGSQSFHCRPLSA; GSQSFHCRPLSAI;
SQSFHCRPLSAIR; QSFHCRPLSAIRH; SFHCRPLSAIRHG; FHCRPLSAIRHGF;
HCRPLSAIRHGFG; CRPLSAIRHGFGI; RPLSAIRHGFGIV; ALGSFFVCYYFPG;
LGSFFVCYYFPGF; GSFFVCYYFPGFV; SFFVCYYFPGFVA; FFVCYYFPGFVAC;
FVCYYFPGFVACY; YTFYNLTGIAEKN; TFYNLTGIAEKNR; FYNLTGIAEKNRK;
YNLTGIAEKNRKI; NLTGIAEKNRKIF; IFGGNYLDNCKCP; FGGNYLDNCKCPY;
GGNYLDNCKCPYK; GNYLDNCKCPYKL; NYLDNCKCPYKLL; QYRRSYTKNGLKK;
YRRSYTKNGLKKS; RRSYTKNGLKKST; RSYTKNGLKKSTK; SYTKNGLKKSTKC;
YTKNGLKKSTKCT; TKNGLKKSTKCTF; KNGLKKSTKCTFR; NGLKKSTKCTFRR;
GLKKSTKCTFRRV; LKKSTKCTFRRVY; KKSTKCTFRRVYR; KSTKCTFRRVYRK;
STKCTFRRVYRKN; TKCTFRRVYRKNY; KCTFRRVYRKNYC; CTFRRVYRKNYCP;
TFRRVYRKNYCPR; FRRVYRKNYCPRR; RRVYRKNYCPRRC; SKNCSSMDVAFTS;
KNCSSMDVAFTSR; NCSSMDVAFTSRP; CSSMDVAFTSRPV; SSMDVAFTSRPVR;
SMDVAFTSRPVRD; MDVAFTSRPVRDC; DVAFTSRPVRDCN; VAFTSRPVRDCNT;
AFTSRPVRDCNTC; FTSRPVRDCNTCS; RWPQPKEKESVQG; WPQPKEKESVQGQ;
PQPKEKESVQGQL; QPKEKESVQGQLP; PKEKESVQGQLPK; KEKESVQGQLPKS;
EKESVQGQLPKSQ; KESVQGQLPKSQR; ESVQGQLPKSQRN; SVQGQLPKSQRNP;
VQGQLPKSQRNPC; QGQLPKSQRNPCK; GQLPKSQRNPCKC; QLPKSQRNPCKCQ;
LPKSQRNPCKCQN; PKSQRNPCKCQNY; TQKWGIQMKTLGA; QKWGIQMKTLGAL;
KWGIQMKTLGALV; VLKMTLAVIAQRE; LKMTLAVIAQREK; KMTLAVIAQREKC;
MTLAVIAQREKCF; TLAVIAQREKCFP; LAVIAQREKCFPV; AVIAQREKCFPVT;
VIAQREKCFPVTA; IAQREKCFPVTAQ; AQREKCFPVTAQQ; QREKCFPVTAQQE;
REKCFPVTAQQEF; EKCFPVTAQQEFP; KCFPVTAQQEFPS; CFPVTAQQEFPSP;
FPVTAQQEFPSPI; LACLTFMQGHKKC; ACLTFMQGHKKCM; CLTFMQGHKKCMS;
LTFMQGHKKCMSM; TFMQGHKKCMSMV; FMQGHKKCMSMVE; MQGHKKCMSMVEE;
QGHKKCMSMVEEN; GHKKCMSMVEENL; HKKCMSMVEENLF; KKCMSMVEENLFK;
KCMSMVEENLFKA; CMSMVEENLFKAV; MSMVEENLFKAVI; SMVEENLFKAVIS;
MVEENLFKAVIST; VEENLFKAVISTS; EENLFKAVISTSL; ENLFKAVISTSLL;
ILTIRPIWTKTML; LTIRPIWTKTMLI; TIRPIWTKTMLIQ; IRPIWTKTMLIQL;
RPIWTKTMLIQLS; PIWTKTMLIQLSA; IWTKTMLIQLSAG; WTKTMLIQLSAGY;
TKTMLIQLSAGYL; KTMLIQLSAGYLI; TMLIQLSAGYLIP; MLIQLSAGYLIPV;
LIQLSAGYLIPVE; IQLSAGYLIPVEM; QLSAGYLIPVEMK; LSAGYLIPVEMKM;
SAGYLIPVEMKML; AGYLIPVEMKMLG; GYLIPVEMKMLGI; YLIPVEMKMLGIL;
LIPVEMKMLGILG; IPVEMKMLGILGL; PVEMKMLGILGLS; VEMKMLGILGLSQ;
EMKMLGILGLSQE; MKMLGILGLSQEG; KMLGILGLSQEGK; MLGILGLSQEGKM;
LGILGLSQEGKMF; GILGLSQEGKMFP; ILGLSQEGKMFPQ; LGLSQEGKMFPQY;
GLSQEGKMFPQYF; LSQEGKMFPQYFM; MNRVWGLFVKLIA; NRVWGLFVKLIAC;
RVWGLFVKLIACM; VWGLFVKLIACMF; WGLFVKLIACMFQ; GLFVKLIACMFQL;
LFVKLIACMFQLL; FVKLIACMFQLLI; VKLIACMFQLLIF; KLIACMFQLLIFV;
LIACMFQLLIFVA; IACMFQLLIFVAC; ACMFQLLIFVACL; CMFQLLIFVACLL;
MFQLLIFVACLLT; FQLLIFVACLLTA; QLLIFVACLLTAL; LLIFVACLLTALE;
LIFVACLLTALEH; IFVACLLTALEHN; FVACLLTALEHNS; VACLLTALEHNSG;
ACLLTALEHNSGE; CLLTALEHNSGEA; LLTALEHNSGEAL; LTALEHNSGEALQ;
TALEHNSGEALQD; ALEHNSGEALQDI; LEHNSGEALQDIL; EHNSGEALQDILR;
HNSGEALQDILRS; NSGEALQDILRSA; TGEPREWMGSLCM; GEPREWMGSLCMV;
EPREWMGSLCMVW; PREWMGSLCMVWN; REWMGSLCMVWNP; EWMGSLCMVWNPR;
KRLGCLMAQKDFQ; RLGCLMAQKDFQG; LGCLMAQKDFQGT; GCLMAQKDFQGTQ;
CLMAQKDFQGTQI; DILTNRDNCKPKC; ILTNRDNCKPKCF; LTNRDNCKPKCFK;
TNRDNCKPKCFKQ; NRDNCKPKCFKQV; RDNCKPKCFKQVL; DNCKPKCFKQVLL;
NCKPKCFKQVLLL; CKPKCFKQVLLLY; KPKCFKQVLLLYI; PKCFKQVLLLYIY;
KCFKQVLLLYIYI; MLLLYKPLLSLCY; LLLYKPLLSLCYF; LLYKPLLSLCYFG;
LYKPLLSLCYFGG; YKPLLSLCYFGGG; KPLLSLCYFGGGV; PLLSLCYFGGGVL;
LLSLCYFGGGVLG; LSLCYFGGGVLGL; SLCYFGGGVLGLL; LCYFGGGVLGLLK;
CYFGGGVLGLLKH; LWGSDLWESSAGA; WGSDLWESSAGAE; GSDLWESSAGAEV;
SDLWESSAGAEVS; DLWESSAGAEVSE; LWESSAGAEVSET; WESSAGAEVSETW;
ESSAGAEVSETWE; SSAGAEVSETWEE; SAGAEVSETWEEH; AGAEVSETWEEHC;

GAEVSETWEEHCD; AEVSETWEEHCDW; EVSETWEEHCDWD; VSETWEEHCDWDS;
SETWEEHCDWDSV; ETWEEHCDWDSVL; TWEEHCDWDSVLD; WEEHCDWDSVLDP;
EEHCDWDSVLDPC; EHCDWDSVLDPCP; HCDWDSVLDPCPE; CDWDSVLDPCPES;
DWDSVLDPCPESS; WDSVLDPCPESSV; DSVLDPCPESSVS; SVLDPCPESSVSE;
VLDPCPESSVSES; LDPCPESSVSESS; DPCPESSVSESSS; PCPESSVSESSSL;
CPESSVSESSSLV; PESSVSESSSLVI; ESSVSESSSLVIS; SSVSESSSLVISR;
SVSESSSLVISRI; VSESSSLVISRIH; SESSSLVISRIHF; ESSSLVISRIHFP;
SSSLVISRIHFPM; SSLVISRIHFPMH; SLVISRIHFPMHI; LVISRIHFPMHIL;
VISRIHFPMHILY; ISRIHFPMHILYF; SRIHFPMHILYFI; RIHFPMHILYFIL;
IHFPMHILYFILE; HFPMHILYFILEK; FPMHILYFILEKV; PMHILYFILEKVY;
MHILYFILEKVYI; HILYFILEKVYIL; ILYFILEKVYILI; LYFILEKVYILIS;
YFILEKVYILISE; FILEKVYILISES; ILEKVYILISESS; LEKVYILISESSL;
EKVYILISESSLS; KVYILISESSLSF; VYILISESSLSFH; YILISESSLSFHS;
ILISESSLSFHST; LISESSLSFHSTI; ISESSLSFHSTIL; SESSLSFHSTILD;
ESSLSFHSTILDC; SSLSFHSTILDCI; SLSFHSTILDCIS; LSFHSTILDCISV;
SFHSTILDCISVA; FHSTILDCISVAK; HSTILDCISVAKS; STILDCISVAKSA;
TILDCISVAKSAT; ILDCISVAKSATG; LDCISVAKSATGL; DCISVAKSATGLN;
CISVAKSATGLNQ; ISVAKSATGLNQI; SVAKSATGLNQIS; VAKSATGLNQISS;
AKSATGLNQISSS; KSATGLNQISSSN; SATGLNQISSSNK; ATGLNQISSSNKV;
TGLNQISSSNKVI; GLNQISSSNKVIP; LNQISSSNKVIPL; NQISSSNKVIPLC;
QISSSNKVIPLCK; ISSSNKVIPLCKI; SSSNKVIPLCKIL; SSNKVIPLCKILF;
SNKVIPLCKILFS; NKVIPLCKILFSS; KVIPLCKILFSSK; VIPLCKILFSSKN;
IPLCKILFSSKNS; PLCKILFSSKNSE; LCKILFSSKNSEF; CKILFSSKNSEFC;
KILFSSKNSEFCK; ILFSSKNSEFCKD; LFSSKNSEFCKDF; FSSKNSEFCKDFL;
SSKNSEFCKDFLK; SKNSEFCKDFLKY; KNSEFCKDFLKYI; NSEFCKDFLKYIL;
SEFCKDFLKYILG; EFCKDFLKYILGL; FCKDFLKYILGLK; CKDFLKYILGLKS;
KDFLKYILGLKSI; DFLKYILGLKSIC; FLKYILGLKSICL; LKYILGLKSICLT;
KYILGLKSICLTN; YILGLKSICLTNL; ILGLKSICLTNLA; LGLKSICLTNLAC;
GLKSICLTNLACR; LKSICLTNLACRV; KSICLTNLACRVL; SICLTNLACRVLG;
ICLTNLACRVLGT; CLTNLACRVLGTG; LTNLACRVLGTGY; TNLACRVLGTGYS;
NLACRVLGTGYSF; LACRVLGTGYSFI; ACRVLGTGYSFIV; CRVLGTGYSFIVT;
RVLGTGYSFIVTK; VLGTGYSFIVTKP; LGTGYSFIVTKPG; GTGYSFIVTKPGG;
TGYSFIVTKPGGN; GYSFIVTKPGGNI; YSFIVTKPGGNIW; SFIVTKPGGNIWV;
FIVTKPGGNIWVL; IVTKPGGNIWVLL; VTKPGGNIWVLLF; TKPGGNIWVLLFK;
KPGGNIWVLLFKC; PGGNIWVLLFKCF; GGNIWVLLFKCFF; GNIWVLLFKCFFS;
NIWVLLFKCFFSK; IWVLLFKCFFSKF; WVLLFKCFFSKFT; VLLFKCFFSKFTL;
LLFKCFFSKFTLT; LFKCFFSKFTLTL; FKCFFSKFTLTLP; KCFFSKFTLTLPS;
CFFSKFTLTLPSK; SLKLSKLFIPCPE; LKLSKLFIPCPEG; KLSKLFIPCPEGK;
LSKLFIPCPEGKS; SKLFIPCPEGKSF; KLFIPCPEGKSFD; LFIPCPEGKSFDS;
FIPCPEGKSFDSA; IPCPEGKSFDSAP; PCPEGKSFDSAPV; CPEGKSFDSAPVP;
PEGKSFDSAPVPF; EGKSFDSAPVPFT; GKSFDSAPVPFTS; KSFDSAPVPFTSS;
SFDSAPVPFTSSK; FDSAPVPFTSSKT; DSAPVPFTSSKTT; SAPVPFTSSKTTM;
APVPFTSSKTTMY; SIATPSSKVSLSM; IATPSSKVSLSMG; ATPSSKVSLSMGR;
TPSSKVSLSMGRF; PSSKVSLSMGRFT; SSKVSLSMGRFTF; SKVSLSMGRFTFK;
KVSLSMGRFTFKA; VSLSMGRFTFKAL; SLSMGRFTFKALP; LSMGRFTFKALPP;
SMGRFTFKALPPH; MGRFTFKALPPHK; GRFTFKALPPHKS; RFTFKALPPHKSN;
FTFKALPPHKSNN; TFKALPPHKSNNP; FKALPPHKSNNPA; KALPPHKSNNPAA;
ALPPHKSNNPAAS; LPPHKSNNPAASV; PPHKSNNPAASVV; PHKSNNPAASVVF;
HKSNNPAASVVFP; KSNNPAASVVFPL; SNNPAASVVFPLS; NNPAASVVFPLSM;
NPAASVVFPLSMG; PAASVVFPLSMGP; AASVVFPLSMGPL; ASVVFPLSMGPLN;
SVVFPLSMGPLNN; VVFPLSMGPLNNQ; VFPLSMGPLNNQY; FPLSMGPLNNQYL;
PLSMGPLNNQYLL; LSMGPLNNQYLLL; SMGPLNNQYLLLG; MGPLNNQYLLLGT;
GPLNNQYLLLGTL; PLNNQYLLLGTLK; LNNQYLLLGTLKT; NNQYLLLGTLKTI;
NQYLLLGTLKTIQ; QYLLLGTLKTIQC; YLLLGTLKTIQCK; LLLGTLKTIQCKK;
LLGTLKTIQCKKS; LGTLKTIQCKKSN; GTLKTIQCKKSNI; TLKTIQCKKSNIT;
LKTIQCKKSNITE; KTIQCKKSNITES; TIQCKKSNITESI; IQCKKSNITESIL;
QCKKSNITESILG; CKKSNITESILGS; KKSNITESILGSK; KSNITESILGSKQ;
SNITESILGSKQC; NITESILGSKQCS; ITESILGSKQCSQ; TESILGSKQCSQA;
ESILGSKQCSQAT; SILGSKQCSQATP; ILGSKQCSQATPA; LGSKQCSQATPAI;

GSKQCSQATPAIY; SKQCSQATPAIYC; KQCSQATPAIYCS; QCSQATPAIYCSS;
CSQATPAIYCSST; SQATPAIYCSSTA; QATPAIYCSSTAF; ATPAIYCSSTAFP;
RVSTLFLAKTVST; VSTLFLAKTVSTA; STLFLAKTVSTAC; FLLSAKIIAFAKC;
LLSAKIIAFAKCF; LSAKIIAFAKCFS; NSKYIPNNKNTSS; SKYIPNNKNTSSH;
KYIPNNKNTSSHF; YIPNNKNTSSHFV; IPNNKNTSSHFVS; PNNKNTSSHFVST;
NNKNTSSHFVSTA; NKNTSSHFVSTAY; KNTSSHFVSTAYS; NTSSHFVSTAYSV;
TSSHFVSTAYSVI; SSHFVSTAYSVIN; SHFVSTAYSVINF; HFVSTAYSVINFQ;
FVSTAYSVINFQD; VSTAYSVINFQDT; STAYSVINFQDTC; TAYSVINFQDTCF;
AYSVINFQDTCFV; YSVINFQDTCFVS; SVINFQDTCFVSS; VINFQDTCFVSSG;
INFQDTCFVSSGS; NFQDTCFVSSGSS; FQDTCFVSSGSSG; QDTCFVSSGSSGL;
DTCFVSSGSSGLK; TCFVSSGSSGLKS; CFVSSGSSGLKSC; FVSSGSSGLKSCS;
VSSGSSGLKSCSF; SSGSSGLKSCSFK; SGSSGLKSCSFKP; GSSGLKSCSFKPP;
MLSSIVWYGSLVK; LSSIVWYGSLVKA; SSIVWYGSLVKAL; SIVWYGSLVKALY;
IVWYGSLVKALYS; VWYGSLVKALYSK; WYGSLVKALYSKY; YGSLVKALYSKYS;
GSLVKALYSKYSL; SLVKALYSKYSLL; LVKALYSKYSLLT; VKALYSKYSLLTP;
KALYSKYSLLTPL; ALYSKYSLLTPLQ; LYSKYSLLTPLQI; YSKYSLLTPLQIK;
SKYSLLTPLQIKK; KYSLLTPLQIKKL; YSLLTPLQIKKLK; SLLTPLQIKKLKV;
LLTPLQIKKLKVH; LTPLQIKKLKVHS; TPLQIKKLKVHSF; QKLLIAETLCLCG;
KLLIAETLCLCGV; LLIAETLCLCGVK; LIAETLCLCGVKK; IAETLCLCGVKKN;
AETLCLCGVKKNI; ETLCLCGVKKNII; TLCLCGVKKNIIL; LCLCGVKKNIILC;
CLCGVKKNIILCP; LCGVKKNIILCPA; CGVKKNIILCPAH; GVKKNIILCPAHM;
VKKNIILCPAHMC; KKNIILCPAHMCL; KNIILCPAHMCLL; NIILCPAHMCLLI;
IILCPAHMCLLIK; ILCPAHMCLLIKV; LCPAHMCLLIKVT; CPAHMCLLIKVTE;
PAHMCLLIKVTEY; AHMCLLIKVTEYF; HMCLLIKVTEYFS; MCLLIKVTEYFSI;
CLLIKVTEYFSIS; LLIKVTEYFSISF; LIKVTEYFSISFL; IKVTEYFSISFLY;
KVTEYFSISFLYR; VTEYFSISFLYRI; AFSLVVYTAKQAR; FSLVVYTAKQARV;
SLVVYTAKQARVL; LVVYTAKQARVLL; VVYTAKQARVLLL; VYTAKQARVLLLN;
YTAKQARVLLLNT; TAKQARVLLLNTA; LRNWCRSEGKSLG; RNWCRSEGKSLGS;
NWCRSEGKSLGSS; WCRSEGKSLGSST; CRSEGKSLGSSTF; RSEGKSLGSSTFL;
SEGKSLGSSTFLF; EGKSLGSSTFLFF; GKSLGSSTFLFFL; KSLGSSTFLFFLG;
SLGSSTFLFFLGG; LGSSTFLFFLGGV; GSSTFLFFLGGVE; SSTFLFFLGGVEC;
ESAVASSSLANIS; SAVASSSLANISS; AVASSSLANISSW; VASSSLANISSWQ;
ASSSLANISSWQN; SSSLANISSWQNK; SSLANISSWQNKS; SLANISSWQNKSS;
LANISSWQNKSSS; ANISSWQNKSSSH; NISSWQNKSSSHF; ISSWQNKSSSHFS;
SSWQNKSSSHFSL; SWQNKSSSHFSLK; WQNKSSSHFSLKE; QNKSSSHFSLKEL;
NKSSSHFSLKELH; KSSSHFSLKELHQ; SSSHFSLKELHQD; SSHFSLKELHQDS;
SHFSLKELHQDSH; HFSLKELHQDSHS; FSLKELHQDSHSS; SLKELHQDSHSSV;
LKELHQDSHSSVP; VGTYKKNNYLGPF; GTYKKNNYLGPFN; TYKKNNYLGPFNI;
YKKNNYLGPFNIL; KKNNYLGPFNILL; KNNYLGPFNILLF; NNYLGPFNILLFI;
REFLQLFGPTIAE; EFLQLFGPTIAEF; FLQLFGPTIAEFL; LQLFGPTIAEFLQ;
QLFGPTIAEFLQL; LFGPTIAEFLQLG; FGPTIAEFLQLGL; GPTIAEFLQLGLS;
PTIAEFLQLGLSQ; TIAEFLQLGLSQT; IAEFLQLGLSQTT; AEFLQLGLSQTTV;
SSQCSSNLSKPRA; SQCSSNLSKPRAL; QCSSNLSKPRALF; CSSNLSKPRALFL;
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SKPRALFLKIFYL; KPRALFLKIFYLN; PRALFLKIFYLNA; RALFLKIFYLNAL;
ALFLKIFYLNALI; ADIACKGSAQKAF; DIACKGSAQKAFW; IACKGSAQKAFWN;
ACKGSAQKAFWNK; AIPCSTGYLGKEE; IPCSTGYLGKEEN; PCSTGYLGKEENQ;
CSTGYLGKEENQH; STGYLGKEENQHK; TGYLGKEENQHKP; GYLGKEENQHKPL;
YLGKEENQHKPLS; LGKEENQHKPLSY; GKEENQHKPLSYS; KEENQHKPLSYSR;
EENQHKPLSYSRF; ENQHKPLSYSRFQ; NQHKPLSYSRFQN; QHKPLSYSRFQNQ;
HKPLSYSRFQNQA; KPLSYSRFQNQAD; PLSYSRFQNQADE; LSYSRFQNQADEL;
SYSRFQNQADELP; YSRFQNQADELPL; SRFQNQADELPLH; RFQNQADELPLHP;
FQNQADELPLHPA; QNQADELPLHPAP; NQADELPLHPAPF; QADELPLHPAPFF;
ADELPLHPAPFFY; DELPLHPAPFFYT; ELPLHPAPFFYTK; LPLHPAPFFYTKY;
PLHPAPFFYTKYS; LHPAPFFYTKYSF; HPAPFFYTKYSFS; PAPFFYTKYSFSS;
APFFYTKYSFSSF; PFFYTKYSFSSFY; FFYTKYSFSSFYP; FYTKYSFSSFYPR;
YTKYSFSSFYPRR; TKYSFSSFYPRRP; KYSFSSFYPRRPL; YSFSSFYPRRPLC;
SFSSFYPRRPLCQ; FSSFYPRRPLCQG; SSFYPRRPLCQGE; SFYPRRPLCQGEI;
FYPRRPLCQGEIP; YPRRPLCQGEIPY; PRRPLCQGEIPYT; RRPLCQGEIPYTS;

RPLCQGEIPYTSL; PLCQGEIPYTSLN; LCQGEIPYTSLNK; CQGEIPYTSLNKL;
QGEIPYTSLNKLF; GEIPYTSLNKLFS; EIPYTSLNKLFSL; IPYTSLNKLFSLR;
PYTSLNKLFSLRE; YTSLNKLFSLRED; TSLNKLFSLREDF; SLNKLFSLREDFP;
LNKLFSLREDFPR; NKLFSLREDFPRQ; KLFSLREDFPRQL; LFSLREDFPRQLF;
FSLREDFPRQLFQ; SLREDFPRQLFQG; LREDFPRQLFQGL; REDFPRQLFQGLK;
EDFPRQLFQGLKG; DFPRQLFQGLKGP

14 mers:
GFPQIVLLGLRKSL; FPQIVLLGLRKSLH; PQIVLLGLRKSLHT;
QIVLLGLRKSLHTL; IVLLGLRKSLHTLT; VLLGLRKSLHTLTT;
EKGWRQRRPRPLIY; KGWRQRRPRPLIYY; GWRQRRPRPLIYYK;
WRQRRPRPLIYYKK; RQRRPRPLIYYKKK; QRRPRPLIYYKKKG;
RRPRPLIYYKKKGH; RPRPLIYYKKKGHR; PRPLIYYKKKGHRE;
RPLIYYKKKGHREE; PLIYYKKKGHREEL; LIYYKKKGHREELL;
IYYKKKGHREELLT; YYKKKGHREELLTH; YKKKGHREELLTHG;
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GHREELLTHGMQPN; HREELLTHGMQPNH; REELLTHGMQPNHD;
EELLTHGMQPNHDL; ELLTHGMQPNHDLR; LLTHGMQPNHDLRK;
LTHGMQPNHDLRKE; THGMQPNHDLRKES; HGMQPNHDLRKESA;
LTGECSQTMTSGRK; TGECSQTMTSGRKV; GECSQTMTSGRKVH;
ECSQTMTSGRKVHD; CSQTMTSGRKVHDS; SQTMTSGRKVHDSQ;
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TSGRKVHDSQGGAA; SGRKVHDSQGGAAY; GRKVHDSQGGAAYP;
RKVHDSQGGAAYPW; KVHDSQGGAAYPWN; VHDSQGGAAYPWNA;
HDSQGGAAYPWNAA; DSQGGAAYPWNAAK; SQGGAAYPWNAAKP;
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GKCMTDMFCEPRNL; KCMTDMFCEPRNLG; CMTDMFCEPRNLGL;
MTDMFCEPRNLGLV; TDMFCEPRNLGLVP; DMFCEPRNLGLVPS;
TGQRPWFCASCHDK; GQRPWFCASCHDKL; QRPWFCASCHDKLQ;
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LEQKKELRGFLFLF; VIPFFLYFQVHGCC; IPFFLYFQVHGCCS;
PFFLYFQVHGCCSS; FFLYFQVHGCCSST; FLYFQVHGCCSSTF;
LYFQVHGCCSSTFG; YFQVHGCCSSTFGG; FQVHGCCSSTFGGP;
QVHGCCSSTFGGPS; VHGCCSSTFGGPSC; HGCCSSTFGGPSCQ;
GCCSSTFGGPSCQC; CCSSTFGGPSCQCI; NCCWGGCCCYRSSN;
CCWGGCCCYRSSNC; CWGGCCCYRSSNCI; WGGCCCYRSSNCIP;
GGCCCYRSSNCIPC; GCCCYRSSNCIPCY; CCCYRSSNCIPCYC;
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RSSNCIPCYCRGHN; SSNCIPCYCRGHNK; SNCIPCYCRGHNKY;
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PCYCRGHNKYLRGY; CYCRGHNKYLRGYS; YCRGHNKYLRGYSC;
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HNKYLRGYSCYRPN; NKYLRGYSCYRPNS; KYLRGYSCYRPNSS;
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GYSCYRPNSSNICC; YSCYRPNSSNICCN; SCYRPNSSNICCNC;
CYRPNSSNICCNCW; YRPNSSNICCNCWC; RPNSSNICCNCWCS;
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CWCSWGYCWVCCFN; WCSWGYCWVCCFNS; CSWGYCWVCCFNSN;
SWGYCWVCCFNSNC; LGSQSFHCRPLSAI; GSQSFHCRPLSAIR;
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FHCRPLSAIRHGFG; HCRPLSAIRHGFGI; CRPLSAIRHGFGIV;
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SFFVCYYFPGFVAC; FFVCYYFPGFVACY; YTFYNLTGIAEKNR;
TFYNLTGIAEKNRK; FYNLTGIAEKNRKI; YNLTGIAEKNRKIF;
IFGGNYLDNCKCPY; FGGNYLDNCKCPYK; GGNYLDNCKCPYKL;
GNYLDNCKCPYKLL; QYRRSYTKNGLKKS; YRRSYTKNGLKKST;
RRSYTKNGLKKSTK; RSYTKNGLKKSTKC; SYTKNGLKKSTKCT;

YTKNGLKKSTKCTF; TKNGLKKSTKCTFR; KNGLKKSTKCTFRR;
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TFRRVYRKNYCPRR; FRRVYRKNYCPRRC; SKNCSSMDVAFTSR;
KNCSSMDVAFTSRP; NCSSMDVAFTSRPV; CSSMDVAFTSRPVR;
SSMDVAFTSRPVRD; SMDVAFTSRPVRDC; MDVAFTSRPVRDCN;
DVAFTSRPVRDCNT; VAFTSRPVRDCNTC; AFTSRPVRDCNTCS;
RWPQPKEKESVQGQ; WPQPKEKESVQGQL; PQPKEKESVQGQLP;
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SVQGQLPKSQRNPC; VQGQLPKSQRNPCK; QGQLPKSQRNPCKC;
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QREKCFPVTAQQEF; REKCFPVTAQQEFP; EKCFPVTAQQEFPS;
KCFPVTAQQEFPSP; CFPVTAQQEFPSPI; LACLTFMQGHKKCM;
ACLTFMQGHKKCMS; CLTFMQGHKKCMSM; LTFMQGHKKCMSMV;
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VEENLFKAVISTSL; EENLFKAVISTSLL; ILTIRPIWTKTMLI;
LTIRPIWTKTMLIQ; TIRPIWTKTMLIQL; IRPIWTKTMLIQLS;
RPIWTKTMLIQLSA; PIWTKTMLIQLSAG; IWTKTMLIQLSAGY;
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IQLSAGYLIPVEMK; QLSAGYLIPVEMKM; LSAGYLIPVEMKML;
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LGLSQEGKMFPQYF; GLSQEGKMFPQYFM; MNRVWGLFVKLIAC;
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LIACMFQLLIFVAC; IACMFQLLIFVACL; ACMFQLLIFVACLL;
CMFQLLIFVACLLT; MFQLLIFVACLLTA; FQLLIFVACLLTAL;
QLLIFVACLLTALE; LLIFVACLLTALEH; LIFVACLLTALEHN;
IFVACLLTALEHNS; FVACLLTALEHNSG; VACLLTALEHNSGE;
ACLLTALEHNSGEA; CLLTALEHNSGEAL; LLTALEHNSGEALQ;
LTALEHNSGEALQD; TALEHNSGEALQDI; ALEHNSGEALQDIL;
LEHNSGEALQDILR; EHNSGEALQDILRS; HNSGEALQDILRSA;
TGEPREWMGSLCMV; GEPREWMGSLCMVW; EPREWMGSLCMVWN;
PREWMGSLCMVWNP; REWMGSLCMVWNPR; KRLGCLMAQKDFQG;
RLGCLMAQKDFQGT; LGCLMAQKDFQGTQ; GCLMAQKDFQGTQI;
DILTNRDNCKPKCF; ILTNRDNCKPKCFK; LTNRDNCKPKCFKQ;
TNRDNCKPKCFKQV; NRDNCKPKCFKQVL; RDNCKPKCFKQVLL;
DNCKPKCFKQVLLL; NCKPKCFKQVLLLY; CKPKCFKQVLLLYI;
KPKCFKQVLLLYIY; PKCFKQVLLLYIYI; MLLLYKPLLSLCYF;
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YKPLLSLCYFGGGV; KPLLSLCYFGGGVL; PLLSLCYFGGGVLG;
LLSLCYFGGGVLGL; LSLCYFGGGVLGLL; SLCYFGGGVLGLLK;
LCYFGGGVLGLLKH; LWGSDLWESSAGAE; WGSDLWESSAGAEV;
GSDLWESSAGAEVS; SDLWESSAGAEVSE; DLWESSAGAEVSET;
LWESSAGAEVSETW; WESSAGAEVSETWE; ESSAGAEVSETWEE;

SSAGAEVSETWEEH; SAGAEVSETWEEHC; AGAEVSETWEEHCD;
GAEVSETWEEHCDW; AEVSETWEEHCDWD; EVSETWEEHCDWDS;
VSETWEEHCDWDSV; SETWEEHCDWDSVL; ETWEEHCDWDSVLD;
TWEEHCDWDSVLDP; WEEHCDWDSVLDPC; EEHCDWDSVLDPCP;
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SVLDPCPESSVSES; VLDPCPESSVSESS; LDPCPESSVSESSS;
DPCPESSVSESSSL; PCPESSVSESSSLV; CPESSVSESSSLVI;
PESSVSESSSLVIS; ESSVSESSSLVISR; SSVSESSSLVISRI;
SVSESSSLVISRIH; VSESSSLVISRIHF; SESSSLVISRIHFP;
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SLVISRIHFPMHIL; LVISRIHFPMHILY; VISRIHFPMHILYF;
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ILYFILEKVYILIS; LYFILEKVYILISE; YFILEKVYILISES;
FILEKVYILISESS; ILEKVYILISESSL; LEKVYILISESSLS;
EKVYILISESSLSF; KVYILISESSLSFH; VYILISESSLSFHS;
YILISESSLSFHST; ILISESSLSFHSTI; LISESSLSFHSTIL;
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SSLSFHSTILDCIS; SLSFHSTILDCISV; LSFHSTILDCISVA;
SFHSTILDCISVAK; FHSTILDCISVAKS; HSTILDCISVAKSA;
STILDCISVAKSAT; TILDCISVAKSATG; ILDCISVAKSATGL;
LDCISVAKSATGLN; DCISVAKSATGLNQ; CISVAKSATGLNQI;
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CRVLGTGYSFIVTK; RVLGTGYSFIVTKP; VLGTGYSFIVTKPG;
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KLSKLFIPCPEGKS; LSKLFIPCPEGKSF; SKLFIPCPEGKSFD;
KLFIPCPEGKSFDS; LFIPCPEGKSFDSA; FIPCPEGKSFDSAP;
IPCPEGKSFDSAPV; PCPEGKSFDSAPVP; CPEGKSFDSAPVPF;
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KVSLSMGRFTFKAL; VSLSMGRFTFKALP; SLSMGRFTFKALPP;
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KTIQCKKSNITESI; TIQCKKSNITESIL; IQCKKSNITESILG;
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ITESILGSKQCSQA; TESILGSKQCSQAT; ESILGSKQCSQATP;
SILGSKQCSQATPA; ILGSKQCSQATPAI; LGSKQCSQATPAIY;
GSKQCSQATPAIYC; SKQCSQATPAIYCS; KQCSQATPAIYCSS;
QCSQATPAIYCSST; CSQATPAIYCSSTA; SQATPAIYCSSTAF;
QATPAIYCSSTAFP; RVSTLFLAKTVSTA; VSTLFLAKTVSTAC;
FLLSAKIIAFAKCF; LLSAKIIAFAKCFS; NSKYIPNNKNTSSH;
SKYIPNNKNTSSHF; KYIPNNKNTSSHFV; YIPNNKNTSSHFVS;
IPNNKNTSSHFVST; PNNKNTSSHFVSTA; NNKNTSSHFVSTAY;
NKNTSSHFVSTAYS; KNTSSHFVSTAYSV; NTSSHFVSTAYSVI;
TSSHFVSTAYSVIN; SSHFVSTAYSVINF; SHFVSTAYSVINFQ;
HFVSTAYSVINFQD; FVSTAYSVINFQDT; VSTAYSVINFQDTC;
STAYSVINFQDTCF; TAYSVINFQDTCFV; AYSVINFQDTCFVS;
YSVINFQDTCFVSS; SVINFQDTCFVSSG; VINFQDTCFVSSGS;
INFQDTCFVSSGSS; NFQDTCFVSSGSSG; FQDTCFVSSGSSGL;
QDTCFVSSGSSGLK; DTCFVSSGSSGLKS; TCFVSSGSSGLKSC;
CFVSSGSSGLKSCS; FVSSGSSGLKSCSF; VSSGSSGLKSCSFK;
SSGSSGLKSCSFKP; SGSSGLKSCSFKPP; MLSSIVWYGSLVKA;
LSSIVWYGSLVKAL; SSIVWYGSLVKALY; SIVWYGSLVKALYS;
IVWYGSLVKALYSK; VWYGSLVKALYSKY; WYGSLVKALYSKYS;
YGSLVKALYSKYSL; GSLVKALYSKYSLL; SLVKALYSKYSLLT;
LVKALYSKYSLLTP; VKALYSKYSLLTPL; KALYSKYSLLTPLQ;
ALYSKYSLLTPLQI; LYSKYSLLTPLQIK; YSKYSLLTPLQIKK;
SKYSLLTPLQIKKL; KYSLLTPLQIKKLK; YSLLTPLQIKKLKV;
SLLTPLQIKKLKVH; LLTPLQIKKLKVHS; LTPLQIKKLKVHSF;
QKLLIAETLCLCGV; KLLIAETLCLCGVK; LLIAETLCLCGVKK;
LIAETLCLCGVKKN; IAETLCLCGVKKNI; AETLCLCGVKKNII;
ETLCLCGVKKNIIL; TLCLCGVKKNIILC; LCLCGVKKNIILCP;
CLCGVKKNIILCPA; LCGVKKNIILCPAH; CGVKKNIILCPAHM;
GVKKNIILCPAHMC; VKKNIILCPAHMCL; KKNIILCPAHMCLL;
KNIILCPAHMCLLI; NIILCPAHMCLLIK; IILCPAHMCLLIKV;
ILCPAHMCLLIKVT; LCPAHMCLLIKVTE; CPAHMCLLIKVTEY;
PAHMCLLIKVTEYF; AHMCLLIKVTEYFS; HMCLLIKVTEYFSI;
MCLLIKVTEYFSIS; CLLIKVTEYFSISF; LLIKVTEYFSISFL;
LIKVTEYFSISFLY; IKVTEYFSISFLYR; KVTEYFSISFLYRI;
AFSLVVYTAKQARV; FSLVVYTAKQARVL; SLVVYTAKQARVLL;
LVVYTAKQARVLLL; VVYTAKQARVLLLN; VYTAKQARVLLLNT;
YTAKQARVLLLNTA; LRNWCRSEGKSLGS; RNWCRSEGKSLGSS;
NWCRSEGKSLGSST; WCRSEGKSLGSSTF; CRSEGKSLGSSTFL;
RSEGKSLGSSTFLF; SEGKSLGSSTFLFF; EGKSLGSSTFLFFL;
GKSLGSSTFLFFLG; KSLGSSTFLFFLGG; SLGSSTFLFFLGGV;
LGSSTFLFFLGGVE; GSSTFLFFLGGVEC; ESAVASSSLANISS;

SAVASSSLANISSW; AVASSSLANISSWQ; VASSSLANISSWQN;
ASSSLANISSWQNK; SSSLANISSWQNKS; SSLANISSWQNKSS;
SLANISSWQNKSSS; LANISSWQNKSSSH; ANISSWQNKSSSHF;
NISSWQNKSSSHFS; ISSWQNKSSSHFSL; SSWQNKSSSHFSLK;
SWQNKSSSHFSLKE; WQNKSSSHFSLKEL; QNKSSSHFSLKELH;
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FSLKELHQDSHSSV; SLKELHQDSHSSVP; VGTYKKNNYLGPFN;
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GPTIAEFLQLGLSQ; PTIAEFLQLGLSQT; TIAEFLQLGLSQTT;
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SKPRALFLKIFYLN; KPRALFLKIFYLNA; PRALFLKIFYLNAL;
RALFLKIFYLNALI; ADIACKGSAQKAFW; DIACKGSAQKAFWN;
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FQNQADELPLHPAP; QNQADELPLHPAPF; NQADELPLHPAPFF;
QADELPLHPAPFFY; ADELPLHPAPFFYT; DELPLHPAPFFYTK;
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LHPAPFFYTKYSFS; HPAPFFYTKYSFSS; PAPFFYTKYSFSSF;
APFFYTKYSFSSFY; PFFYTKYSFSSFYP; FFYTKYSFSSFYPR;
FYTKYSFSSFYPRR; YTKYSFSSFYPRRP; TKYSFSSFYPRRPL;
KYSFSSFYPRRPLC; YSFSSFYPRRPLCQ; SFSSFYPRRPLCQG;
FSSFYPRRPLCQGE; SSFYPRRPLCQGEI; SFYPRRPLCQGEIP;
FYPRRPLCQGEIPY; YPRRPLCQGEIPYT; PRRPLCQGEIPYTS;
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SLNKLFSLREDFPR; LNKLFSLREDFPRQ; NKLFSLREDFPRQL;
KLFSLREDFPRQLF; LFSLREDFPRQLFQ; FSLREDFPRQLFQG;
SLREDFPRQLFQGL; LREDFPRQLFQGLK; REDFPRQLFQGLKG; EDFPRQLFQGLKGP

15 mers:
GFPQIVLLGLRKSLH; FPQIVLLGLRKSLHT; PQIVLLGLRKSLHTL;
QIVLLGLRKSLHTLT; IVLLGLRKSLHTLTT; EKGWRQRRPRPLIYY;
KGWRQRRPRPLIYYK; GWRQRRPRPLIYYKK; WRQRRPRPLIYYKKK;
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RPRPLIYYKKKGHRE; PRPLIYYKKKGHREE; RPLIYYKKKGHREEL;
PLIYYKKKGHREELL; LIYYKKKGHREELLT; IYYKKKGHREELLTH;
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HREELLTHGMQPNHD; REELLTHGMQPNHDL; EELLTHGMQPNHDLR;
ELLTHGMQPNHDLRK; LLTHGMQPNHDLRKE; LTHGMQPNHDLRKES;
THGMQPNHDLRKESA; LTGECSQTMTSGRKV; TGECSQTMTSGRKVH;
GECSQTMTSGRKVHD; ECSQTMTSGRKVHDS; CSQTMTSGRKVHDSQ;
SQTMTSGRKVHDSQG; QTMTSGRKVHDSQGG; TMTSGRKVHDSQGGA;
MTSGRKVHDSQGGAA; TSGRKVHDSQGGAAY; SGRKVHDSQGGAAYP;
GRKVHDSQGGAAYPW; RKVHDSQGGAAYPWN; KVHDSQGGAAYPWNA;
VHDSQGGAAYPWNAA; HDSQGGAAYPWNAAK; DSQGGAAYPWNAAKP;

PQEGKCMTDMFCEPR; QEGKCMTDMFCEPRN; EGKCMTDMFCEPRNL;
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MTDMFCEPRNLGLVP; TDMFCEPRNLGLVPS; TGQRPWFCASCHDKL;
GQRPWFCASCHDKLQ; KLVKPGLEQKKELRG; LVKPGLEQKKELRGF;
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GLEQKKELRGFLFLF; VIPFFLYFQVHGCCS; IPFFLYFQVHGCCSS;
PFFLYFQVHGCCSST; FFLYFQVHGCCSSTF; FLYFQVHGCCSSTFG;
LYFQVHGCCSSTFGG; YFQVHGCCSSTFGGP; FQVHGCCSSTFGGPS;
QVHGCCSSTFGGPSC; VHGCCSSTFGGPSCQ; HGCCSSTFGGPSCQC;
GCCSSTFGGPSCQCI; NCCWGGCCCYRSSNC; CCWGGCCCYRSSNCI;
CWGGCCCYRSSNCIP; WGGCCCYRSSNCIPC; GGCCCYRSSNCIPCY;
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CYRSSNCIPCYCRGH; YRSSNCIPCYCRGHN; RSSNCIPCYCRGHNK;
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WCSWGYCWVCCFNSN; CSWGYCWVCCFNSNC; LGSQSFHCRPLSAIR;
GSQSFHCRPLSAIRH; SQSFHCRPLSAIRHG; QSFHCRPLSAIRHGF;
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SFFVCYYFPGFVACY; YTFYNLTGIAEKNRK; TFYNLTGIAEKNRKI;
FYNLTGIAEKNRKIF; IFGGNYLDNCKCPYK; FGGNYLDNCKCPYKL;
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RRSYTKNGLKKSTKC; RSYTKNGLKKSTKCT; SYTKNGLKKSTKCTF;
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TKCTFRRVYRKNYCP; KCTFRRVYRKNYCPR; CTFRRVYRKNYCPRR;
TFRRVYRKNYCPRRC; SKNCSSMDVAFTSRP; KNCSSMDVAFTSRPV;
NCSSMDVAFTSRPVR; CSSMDVAFTSRPVRD; SSMDVAFTSRPVRDC;
SMDVAFTSRPVRDCN; MDVAFTSRPVRDCNT; DVAFTSRPVRDCNTC;
VAFTSRPVRDCNTCS; RWPQPKEKESVQGQL; WPQPKEKESVQGQLP;
PQPKEKESVQGQLPK; QPKEKESVQGQLPKS; PKEKESVQGQLPKSQ;
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ESVQGQLPKSQRNPC; SVQGQLPKSQRNPCK; VQGQLPKSQRNPCKC;
QGQLPKSQRNPCKCQ; GQLPKSQRNPCKCQN; QLPKSQRNPCKCQNY;
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KMTLAVIAQREKCFP; MTLAVIAQREKCFPV; TLAVIAQREKCFPVT;
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REKCFPVTAQQEFPS; EKCFPVTAQQEFPSP; KCFPVTAQQEFPSPI;
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HKKCMSMVEENLFKA; KKCMSMVEENLFKAV; KCMSMVEENLFKAVI;
CMSMVEENLFKAVIS; MSMVEENLFKAVIST; SMVEENLFKAVISTS;
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LTIRPIWTKTMLIQL; TIRPIWTKTMLIQLS; IRPIWTKTMLIQLSA;
RPIWTKTMLIQLSAG; PIWTKTMLIQLSAGY; IWTKTMLIQLSAGYL;
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IQLSAGYLIPVEMKM; QLSAGYLIPVEMKML; LSAGYLIPVEMKMLG;
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LGLSQEGKMFPQYFM; MNRVWGLFVKLIACM; NRVWGLFVKLIACMF;
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GLFVKLIACMFQLLI; LFVKLIACMFQLLIF; FVKLIACMFQLLIFV;
VKLIACMFQLLIFVA; KLIACMFQLLIFVAC; LIACMFQLLIFVACL;
IACMFQLLIFVACLL; ACMFQLLIFVACLLT; CMFQLLIFVACLLTA;
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LLIFVACLLTALEHN; LIFVACLLTALEHNS; IFVACLLTALEHNSG;
FVACLLTALEHNSGE; VACLLTALEHNSGEA; ACLLTALEHNSGEAL;
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TALEHNSGEALQDIL; ALEHNSGEALQDILR; LEHNSGEALQDILRS;
EHNSGEALQDILRSA; TGEPREWMGSLCMVW; GEPREWMGSLCMVWN;
EPREWMGSLCMVWNP; PREWMGSLCMVWNPR; KRLGCLMAQKDFQGT;
RLGCLMAQKDFQGTQ; LGCLMAQKDFQGTQI; DILTNRDNCKPKCFK;
ILTNRDNCKPKCFKQ; LTNRDNCKPKCFKQV; TNRDNCKPKCFKQVL;
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SLCYFGGGVLGLLKH; LWGSDLWESSAGAEV; WGSDLWESSAGAEVS;
GSDLWESSAGAEVSE; SDLWESSAGAEVSET; DLWESSAGAEVSETW;
LWESSAGAEVSETWE; WESSAGAEVSETWEE; ESSAGAEVSETWEEH;
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VSETWEEHCDWDSVL; SETWEEHCDWDSVLD; ETWEEHCDWDSVLDP;
TWEEHCDWDSVLDPC; WEEHCDWDSVLDPCP; EEHCDWDSVLDPCPE;
EHCDWDSVLDPCPES; HCDWDSVLDPCPESS; CDWDSVLDPCPESSV;
DWDSVLDPCPESSVS; WDSVLDPCPESSVSE; DSVLDPCPESSVSES;
SVLDPCPESSVSESS; VLDPCPESSVSESSS; LDPCPESSVSESSSL;
DPCPESSVSESSSLV; PCPESSVSESSSLVI; CPESSVSESSSLVIS;
PESSVSESSSLVISR; ESSVSESSSLVISRI; SSVSESSSLVISRIH;
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KQCSQATPAIYCSST; QCSQATPAIYCSSTA; CSQATPAIYCSSTAF;
SQATPAIYCSSTAFP; RVSTLFLAKTVSTAC; FLLSAKIIAFAKCFS;
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NTSSHFVSTAYSVIN; TSSHFVSTAYSVINF; SSHFVSTAYSVINFQ;
SHFVSTAYSVINFQD; HFVSTAYSVINFQDT; FVSTAYSVINFQDTC;
VSTAYSVINFQDTCF; STAYSVINFQDTCFV; TAYSVINFQDTCFVS;
AYSVINFQDTCFVSS; YSVINFQDTCFVSSG; SVINFQDTCFVSSGS;
VINFQDTCFVSSGSS; INFQDTCFVSSGSSG; NFQDTCFVSSGSSGL;
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TCFVSSGSSGLKSCS; CFVSSGSSGLKSCSF; FVSSGSSGLKSCSFK;
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LSSIVWYGSLVKALY; SSIVWYGSLVKALYS; SIVWYGSLVKALYSK;
IVWYGSLVKALYSKY; VWYGSLVKALYSKYS; WYGSLVKALYSKYSL;
YGSLVKALYSKYSLL; GSLVKALYSKYSLLT; SLVKALYSKYSLLTP;
LVKALYSKYSLLTPL; VKALYSKYSLLTPLQ; KALYSKYSLLTPLQI;
ALYSKYSLLTPLQIK; LYSKYSLLTPLQIKK; YSKYSLLTPLQIKKL;
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SLLTPLQIKKLKVHS; LLTPLQIKKLKVHSF; QKLLIAETLCLCGVK;
KLLIAETLCLCGVKK; LLIAETLCLCGVKKN; LIAETLCLCGVKKNI;
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16 mers:

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CSSMDVAFTSRPVRDC; SSMDVAFTSRPVRDCN; SMDVAFTSRPVRDCNT;
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DTCFVSSGSSGLKSCS; TCFVSSGSSGLKSCSF; CFVSSGSSGLKSCSFK;
FVSSGSSGLKSCSFKP; VSSGSSGLKSCSFKPP; MLSSIVWYGSLVKALY;
LSSIVWYGSLVKALYS; SSIVWYGSLVKALYSK; SIVWYGSLVKALYSKY;
IVWYGSLVKALYSKYS; VWYGSLVKALYSKYSL; WYGSLVKALYSKYSLL;
YGSLVKALYSKYSLLT; GSLVKALYSKYSLLTP; SLVKALYSKYSLLTPL;
LVKALYSKYSLLTPLQ; VKALYSKYSLLTPLQI; KALYSKYSLLTPLQIK;
ALYSKYSLLTPLQIKK; LYSKYSLLTPLQIKKL; YSKYSLLTPLQIKKLK;
SKYSLLTPLQIKKLKV; KYSLLTPLQIKKLKVH; YSLLTPLQIKKLKVHS;
SLLTPLQIKKLKVHSF; QKLLIAETLCLCGVKK; KLLIAETLCLCGVKKN;
LLIAETLCLCGVKKNI; LIAETLCLCGVKKNII; IAETLCLCGVKKNIIL;
AETLCLCGVKKNIILC; ETLCLCGVKKNIILCP; TLCLCGVKKNIILCPA;
LCLCGVKKNIILCPAH; CLCGVKKNIILCPAHM; LCGVKKNIILCPAHMC;
CGVKKNIILCPAHMCL; GVKKNIILCPAHMCLL; VKKNIILCPAHMCLLI;
KKNIILCPAHMCLLIK; KNIILCPAHMCLLIKV; NIILCPAHMCLLIKVT;
IILCPAHMCLLIKVTE; ILCPAHMCLLIKVTEY; LCPAHMCLLIKVTEYF;
CPAHMCLLIKVTEYFS; PAHMCLLIKVTEYFSI; AHMCLLIKVTEYFSIS;
HMCLLIKVTEYFSISF; MCLLIKVTEYFSISFL; CLLIKVTEYFSISFLY;
LLIKVTEYFSISFLYR; LIKVTEYFSISFLYRI; AFSLVVYTAKQARVLL;
FSLVVYTAKQARVLLL; SLVVYTAKQARVLLLN; LVVYTAKQARVLLLNT;
VVYTAKQARVLLLNTA; LRNWCRSEGKSLGSST; RNWCRSEGKSLGSSTF;
NWCRSEGKSLGSSTFL; WCRSEGKSLGSSTFLF; CRSEGKSLGSSTFLFF;
RSEGKSLGSSTFLFFL; SEGKSLGSSTFLFFLG; EGKSLGSSTFLFFLGG;
GKSLGSSTFLFFLGGV; KSLGSSTFLFFLGGVE; SLGSSTFLFFLGGVEC;
ESAVASSSLANISSWQ; SAVASSSLANISSWQN; AVASSSLANISSWQNK;
VASSSLANISSWQNKS; ASSSLANISSWQNKSS; SSSLANISSWQNKSSS;
SSLANISSWQNKSSSH; SLANISSWQNKSSSHF; LANISSWQNKSSSHFS;
ANISSWQNKSSSHFSL; NISSWQNKSSSHFSLK; ISSWQNKSSSHFSLKE;
SSWQNKSSSHFSLKEL; SWQNKSSSHFSLKELH; WQNKSSSHFSLKELHQ;
QNKSSSHFSLKELHQD; NKSSSHFSLKELHQDS; KSSSHFSLKELHQDSH;
SSSHFSLKELHQDSHS; SSHFSLKELHQDSHSS; SHFSLKELHQDSHSSV;
HFSLKELHQDSHSSVP; VGTYKKNNYLGPFNIL; GTYKKNNYLGPFNILL;
TYKKNNYLGPFNILLF; YKKNNYLGPFNILLFI; REFLQLFGPTIAEFLQ;
EFLQLFGPTIAEFLQL; FLQLFGPTIAEFLQLG; LQLFGPTIAEFLQLGL;
QLFGPTIAEFLQLGLS; LFGPTIAEFLQLGLSQ; FGPTIAEFLQLGLSQT;
GPTIAEFLQLGLSQTT; PTIAEFLQLGLSQTTV; SSQCSSNLSKPRALFL;
SQCSSNLSKPRALFLK; QCSSNLSKPRALFLKI; CSSNLSKPRALFLKIF;
SSNLSKPRALFLKIFY; SNLSKPRALFLKIFYL; NLSKPRALFLKIFYLN;
LSKPRALFLKIFYLNA; SKPRALFLKIFYLNAL; KPRALFLKIFYLNALI;
ADIACKGSAQKAFWNK; AIPCSTGYLGKEENQH; IPCSTGYLGKEENQHK;
PCSTGYLGKEENQHKP; CSTGYLGKEENQHKPL; STGYLGKEENQHKPLS;
TGYLGKEENQHKPLSY; GYLGKEENQHKPLSYS; YLGKEENQHKPLSYSR;
LGKEENQHKPLSYSRF; GKEENQHKPLSYSRFQ; KEENQHKPLSYSRFQN;
EENQHKPLSYSRFQNQ; ENQHKPLSYSRFQNQA; NQHKPLSYSRFQNQAD;
QHKPLSYSRFQNQADE; HKPLSYSRFQNQADEL; KPLSYSRFQNQADELP;
PLSYSRFQNQADELPL; LSYSRFQNQADELPLH; SYSRFQNQADELPLHP;
YSRFQNQADELPLHPA; SRFQNQADELPLHPAP; RFQNQADELPLHPAPF;

FQNQADELPLHPAPFF; QNQADELPLHPAPFFY; NQADELPLHPAPFFYT;
QADELPLHPAPFFYTK; ADELPLHPAPFFYTKY; DELPLHPAPFFYTKYS;
ELPLHPAPFFYTKYSF; LPLHPAPFFYTKYSFS; PLHPAPFFYTKYSFSS;
LHPAPFFYTKYSFSSF; HPAPFFYTKYSFSSFY; PAPFFYTKYSFSSFYP;
APFFYTKYSFSSFYPR; PFFYTKYSFSSFYPRR; FFYTKYSFSSFYPRRP;
FYTKYSFSSFYPRRPL; YTKYSFSSFYPRRPLC; TKYSFSSFYPRRPLCQ;
KYSFSSFYPRRPLCQG; YSFSSFYPRRPLCQGE; SFSSFYPRRPLCQGEI;
FSSFYPRRPLCQGEIP; SSFYPRRPLCQGEIPY; SFYPRRPLCQGEIPYT;
FYPRRPLCQGEIPYTS; YPRRPLCQGEIPYTSL; PRRPLCQGEIPYTSLN;
RRPLCQGEIPYTSLNK; RPLCQGEIPYTSLNKL; PLCQGEIPYTSLNKLF;
LCQGEIPYTSLNKLFS; CQGEIPYTSLNKLFSL; QGEIPYTSLNKLFSLR;
GEIPYTSLNKLFSLRE; EIPYTSLNKLFSLRED; IPYTSLNKLFSLREDF;
PYTSLNKLFSLREDFP; YTSLNKLFSLREDFPR; TSLNKLFSLREDFPRQ;
SLNKLFSLREDFPRQL; LNKLFSLREDFPRQLF; NKLFSLREDFPRQLFQ;
KLFSLREDFPRQLFQG; LFSLREDFPRQLFQGL; FSLREDFPRQLFQGLK;
SLREDFPRQLFQGLKG; LREDFPRQLFQGLKGP

BK virus, reading frame 3

13 mers:
ASEKASTPLLLER; SEKASTPLLLERK; EKASTPLLLERKG; KASTPLLLERKGG;
ASTPLLLERKGGG; STPLLLERKGGGR; TPLLLERKGGGRG; PLLLERKGGGRGG;
LLLERKGGGRGGL; LLERKGGGRGGLG; LERKGGGRGGLGL; ERKGGGRGGLGLL;
RKGGGRGGLGLLY; KGGGRGGLGLLYI; GGGRGGLGLLYII; GGRGGLGLLYIIK;
GRGGLGLLYIIKK; RGGLGLLYIIKKK; GGLGLLYIIKKKA; GLGLLYIIKKKAT;
LGLLYIIKKKATG; GLLYIIKKKATGR; LLYIIKKKATGRS; LYIIKKKATGRSC;
YIIKKKATGRSCL; IIKKKATGRSCLP; IKKKATGRSCLPM; KKKATGRSCLPME;
KKATGRSCLPMEC; KATGRSCLPMECS; ATGRSCLPMECSQ; TGRSCLPMECSQT;
GRSCLPMECSQTM; RSCLPMECSQTMT; SCLPMECSQTMTS; CLPMECSQTMTSG;
LPMECSQTMTSGR; PMECSQTMTSGRK; MECSQTMTSGRKV; ECSQTMTSGRKVH;
CSQTMTSGRKVHD; SQTMTSGRKVHDS; QTMTSGRKVHDSQ; TMTSGRKVHDSQG;
MTSGRKVHDSQGN; TSGRKVHDSQGNA; SGRKVHDSQGNAA; GRKVHDSQGNAAK;
RKVHDSQGNAAKP; PQEGKCMTHREEL; QEGKCMTHREELL; EGKCMTHREELLT;
GKCMTHREELLTH; KCMTHREELLTHG; CMTHREELLTHGM; MTHREELLTHGMQ;
THREELLTHGMQP; HREELLTHGMQPN; REELLTHGMQPNH; EELLTHGMQPNHD;
ELLTHGMQPNHDL; LLTHGMQPNHDLR; LTHGMQPNHDLRK; THGMQPNHDLRKE;
HGMQPNHDLRKES; GMQPNHDLRKESA; QTCFASLGILALS; TCFASLGILALSP;
CFASLGILALSPV; FASLGILALSPVK; ASLGILALSPVKL; SLGILALSPVKLD;
LGILALSPVKLDK; GILALSPVKLDKG; ILALSPVKLDKGH; LALSPVKLDKGHG;
ALSPVKLDKGHGS; LSPVKLDKGHGSA; SPVKLDKGHGSAP; PVKLDKGHGSAPA;
VKLDKGHGSAPAV; KLDKGHGSAPAVT; LDKGHGSAPAVTT; DKGHGSAPAVTTS;
KGHGSAPAVTTSF; GHGSAPAVTTSFS; HGSAPAVTTSFSE; GSAPAVTTSFSES;
SAPAVTTSFSESW; NLDWNKKKSSEDF; LDWNKKKSSEDFY; DWNKKKSSEDFYF;
WNKKKSSEDFYFY; NKKKSSEDFYFYF; KKKSSEDFYFYFR; KKSSEDFYFYFRA;
KSSEDFYFYFRAF; SSEDFYFYFRAFA; SEDFYFYFRAFAG; EDFYFYFRAFAGI;
DFYFYFRAFAGIL; RQCRREKQKYHCF; QCRREKQKYHCFT; CRREKQKYHCFTC;
RREKQKYHCFTCC; REKQKYHCFTCCK; EKQKYHCFTCCKR; KQKYHCFTCCKRL;
QKYHCFTCCKRLC; KYHCFTCCKRLCK; YHCFTCCKRLCKR; HCFTCCKRLCKRL;
CFTCCKRLCKRLL; FTCCKRLCKRLLG; TCCKRLCKRLLGK; SLFFCISRFMGAA;
LFFCISRFMGAAL; FFCISRFMGAALA; FCISRFMGAALAL; CISRFMGAALALL;
ISRFMGAALALLG; SRFMGAALALLGD; RFMGAALALLGDL; FMGAALALLGDLV;
MGAALALLGDLVA; GAALALLGDLVAS; AALALLGDLVASV; ALALLGDLVASVS;
LALLGDLVASVSE; ALLGDLVASVSEA; LLGDLVASVSEAA; LGDLVASVSEAAA;
GDLVASVSEAAAA; DLVASVSEAAAAT; LVASVSEAAAATG; VASVSEAAAATGF;
ASVSEAAAATGFS; SVSEAAAATGFSV; VSEAAAATGFSVA; SEAAAATGFSVAE;
EAAAATGFSVAEI; AAAATGFSVAEIA; AAATGFSVAEIAA; AATGFSVAEIAAG;
ATGFSVAEIAAGE; TGFSVAEIAAGEA; GFSVAEIAAGEAA; FSVAEIAAGEAAA;
SVAEIAAGEAAAA; VAEIAAGEAAAAI; AEIAAGEAAAAIE; EIAAGEAAAAIEV;
IAAGEAAAAIEVQ; AAGEAAAAIEVQI; AGEAAAAIEVQIA; GEAAAAIEVQIAS;
EAAAAIEVQIASL; AAAAIEVQIASLA; AAAIEVQIASLAT; AAIEVQIASLATV;
AIEVQIASLATVE; IEVQIASLATVEG; EVQIASLATVEGI; VQIASLATVEGIT;

QIASLATVEGITS; IASLATVEGITST; ASLATVEGITSTS; SLATVEGITSTSE;
LATVEGITSTSEA; ATVEGITSTSEAI; TVEGITSTSEAIA; VEGITSTSEAIAA;
EGITSTSEAIAAI; GITSTSEAIAAIG; ITSTSEAIAAIGL; TSTSEAIAAIGLT;
STSEAIAAIGLTP; TSEAIAAIGLTPQ; SEAIAAIGLTPQT; EAIAAIGLTPQTY;
AIAAIGLTPQTYA; IAAIGLTPQTYAV; AAIGLTPQTYAVI; AIGLTPQTYAVIA;
IGLTPQTYAVIAG; GLTPQTYAVIAGA; LTPQTYAVIAGAP; TPQTYAVIAGAPG;
PQTYAVIAGAPGA; QTYAVIAGAPGAI; TYAVIAGAPGAIA; YAVIAGAPGAIAG;
AVIAGAPGAIAGF; VIAGAPGAIAGFA; IAGAPGAIAGFAA; AGAPGAIAGFAAL;
GAPGAIAGFAALI; APGAIAGFAALIQ; PGAIAGFAALIQT; GAIAGFAALIQTV;
AIAGFAALIQTVS; IAGFAALIQTVSG; AGFAALIQTVSGI; GFAALIQTVSGIS;
FAALIQTVSGISS; AALIQTVSGISSL; ALIQTVSGISSLA; LIQTVSGISSLAQ;
IQTVSGISSLAQV; QTVSGISSLAQVG; TVSGISSLAQVGY; VSGISSLAQVGYK;
SGISSLAQVGYKF; GISSLAQVGYKFF; ISSLAQVGYKFFD; SSLAQVGYKFFDD;
SLAQVGYKFFDDW; LAQVGYKFFDDWD; AQVGYKFFDDWDH; QVGYKFFDDWDHK;
VGYKFFDDWDHKV; GYKFFDDWDHKVS; YKFFDDWDHKVST; KFFDDWDHKVSTV;
FFDDWDHKVSTVG; FDDWDHKVSTVGL; DDWDHKVSTVGLY; DWDHKVSTVGLYQ;
WDHKVSTVGLYQQ; DHKVSTVGLYQQS; HKVSTVGLYQQSG; KVSTVGLYQQSGM;
VSTVGLYQQSGMA; STVGLYQQSGMAL; TVGLYQQSGMALE; VGLYQQSGMALEL;
GLYQQSGMALELF; LYQQSGMALELFN; YQQSGMALELFNP; QQSGMALELFNPD;
QSGMALELFNPDE; SGMALELFNPDEY; GMALELFNPDEYY; MALELFNPDEYYD;
ALELFNPDEYYDI; LELFNPDEYYDIL; ELFNPDEYYDILF; LFNPDEYYDILFP;
FNPDEYYDILFPG; NPDEYYDILFPGV; PDEYYDILFPGVN; DEYYDILFPGVNT;
EYYDILFPGVNTF; YYDILFPGVNTFV; YDILFPGVNTFVN; DILFPGVNTFVNN;
ILFPGVNTFVNNI; LFPGVNTFVNNIQ; FPGVNTFVNNIQY; PGVNTFVNNIQYL;
GVNTFVNNIQYLD; VNTFVNNIQYLDP; NTFVNNIQYLDPR; TFVNNIQYLDPRH;
FVNNIQYLDPRHW; VNNIQYLDPRHWG; NNIQYLDPRHWGP; NIQYLDPRHWGPS;
IQYLDPRHWGPSL; QYLDPRHWGPSLF; YLDPRHWGPSLFA; LDPRHWGPSLFAT;
DPRHWGPSLFATI; PRHWGPSLFATIS; RHWGPSLFATISQ; HWGPSLFATISQA;
WGPSLFATISQAL; GPSLFATISQALW; PSLFATISQALWH; SLFATISQALWHV;
LFATISQALWHVI; FATISQALWHVIR; ATISQALWHVIRD; TISQALWHVIRDD;
ISQALWHVIRDDI; SQALWHVIRDDIP; QALWHVIRDDIPS; ALWHVIRDDIPSI;
LWHVIRDDIPSIT; WHVIRDDIPSITS; HVIRDDIPSITSQ; VIRDDIPSITSQE;
IRDDIPSITSQEL; RDDIPSITSQELQ; DDIPSITSQELQR; DIPSITSQELQRR;
IPSITSQELQRRT; PSITSQELQRRTE; SITSQELQRRTER; ITSQELQRRTERF;
TSQELQRRTERFF; SQELQRRTERFFR; QELQRRTERFFRD; ELQRRTERFFRDS;
LQRRTERFFRDSL; QRRTERFFRDSLA; RRTERFFRDSLAR; RTERFFRDSLARF;
TERFFRDSLARFL; ERFFRDSLARFLE; RFFRDSLARFLEE; FFRDSLARFLEET;
FRDSLARFLEETT; RDSLARFLEETTW; DSLARFLEETTWT; SLARFLEETTWTI;
LARFLEETTWTIV; ARFLEETTWTIVN; RFLEETTWTIVNA; FLEETTWTIVNAP;
LEETTWTIVNAPI; EETTWTIVNAPIN; ETTWTIVNAPINF; TTWTIVNAPINFY;
TWTIVNAPINFYN; WTIVNAPINFYNY; TIVNAPINFYNYI; IVNAPINFYNYIQ;
VNAPINFYNYIQQ; NAPINFYNYIQQY; APINFYNYIQQYY; PINFYNYIQQYYS;
INFYNYIQQYYSD; NFYNYIQQYYSDL; FYNYIQQYYSDLS; YNYIQQYYSDLSP;
NYIQQYYSDLSPI; YIQQYYSDLSPIR; IQQYYSDLSPIRP; QQYYSDLSPIRPS;
QYYSDLSPIRPSM; YYSDLSPIRPSMV; YSDLSPIRPSMVR; SDLSPIRPSMVRQ;
DLSPIRPSMVRQV; LSPIRPSMVRQVA; SPIRPSMVRQVAE; PIRPSMVRQVAER;
IRPSMVRQVAERE; RPSMVRQVAEREG; PSMVRQVAEREGT; SMVRQVAEREGTR;
MVRQVAEREGTRV; VRQVAEREGTRVH; RQVAEREGTRVHF; QVAEREGTRVHFG;
VAEREGTRVHFGH; AEREGTRVHFGHT; EREGTRVHFGHTY; REGTRVHFGHTYS;
EGTRVHFGHTYSI; GTRVHFGHTYSID; TRVHFGHTYSIDD; RVHFGHTYSIDDA;
VHFGHTYSIDDAD; HFGHTYSIDDADS; FGHTYSIDDADSI; GHTYSIDDADSIE;
HTYSIDDADSIEE; TYSIDDADSIEEV; YSIDDADSIEEVT; SIDDADSIEEVTQ;
IDDADSIEEVTQR; DDADSIEEVTQRM; DADSIEEVTQRMD; ADSIEEVTQRMDL;
DSIEEVTQRMDLR; SIEEVTQRMDLRN; IEEVTQRMDLRNQ; EEVTQRMDLRNQQ;
EVTQRMDLRNQQS; VTQRMDLRNQQSV; TQRMDLRNQQSVH; QRMDLRNQQSVHS;
RMDLRNQQSVHSG; MDLRNQQSVHSGE; DLRNQQSVHSGEF; LRNQQSVHSGEFI;
RNQQSVHSGEFIE; NQQSVHSGEFIEK; QQSVHSGEFIEKT; QSVHSGEFIEKTI;
SVHSGEFIEKTIA; VHSGEFIEKTIAP; HSGEFIEKTIAPG; SGEFIEKTIAPGG;
GEFIEKTIAPGGA; EFIEKTIAPGGAN; FIEKTIAPGGANQ; IEKTIAPGGANQR;

EKTIAPGGANQRT; KTIAPGGANQRTA; TIAPGGANQRTAP; IAPGGANQRTAPQ;
APGGANQRTAPQW; PGGANQRTAPQWM; GGANQRTAPQWML; GANQRTAPQWMLP;
ANQRTAPQWMLPL; NQRTAPQWMLPLL; QRTAPQWMLPLLL; RTAPQWMLPLLLG;
TAPQWMLPLLLGL; APQWMLPLLLGLY; PQWMLPLLLGLYG; QWMLPLLLGLYGT;
WMLPLLLGLYGTV; MLPLLLGLYGTVT; LPLLLGLYGTVTP; PLLLGLYGTVTPA;
LLLGLYGTVTPAL; LLGLYGTVTPALE; LGLYGTVTPALEA; GLYGTVTPALEAY;
LYGTVTPALEAYE; YGTVTPALEAYED; GTVTPALEAYEDG; TVTPALEAYEDGP;
VTPALEAYEDGPN; TPALEAYEDGPNQ; PALEAYEDGPNQK; ALEAYEDGPNQKK;
LEAYEDGPNQKKR; EAYEDGPNQKKRR; AYEDGPNQKKRRV; YEDGPNQKKRRVS;
EDGPNQKKRRVSR; DGPNQKKRRVSRG; GPNQKKRRVSRGS; PNQKKRRVSRGSS;
NQKKRRVSRGSSQ; QKKRRVSRGSSQK; KKRRVSRGSSQKA; KRRVSRGSSQKAK;
RRVSRGSSQKAKG; RVSRGSSQKAKGT; VSRGSSQKAKGTR; SRGSSQKAKGTRA;
RGSSQKAKGTRAS; GSSQKAKGTRASA; SSQKAKGTRASAK; SQKAKGTRASAKT;
QKAKGTRASAKTT; KAKGTRASAKTTN; AKGTRASAKTTNK; KGTRASAKTTNKR;
GTRASAKTTNKRR; TRASAKTTNKRRS; RASAKTTNKRRSR; ASAKTTNKRRSRS;
SAKTTNKRRSRSS; AKTTNKRRSRSSR; KTTNKRRSRSSRS; NWGRCYYRGRMLP;
WGRCYYRGRMLPK; GRCYYRGRMLPKP; RCYYRGRMLPKPR; CYYRGRMLPKPRN;
YYRGRMLPKPRNG; YRGRMLPKPRNGG; RGRMLPKPRNGGS; GRMLPKPRNGGSR;
PREKNASLLQHSK; REKNASLLQHSKN; EKNASLLQHSKNS; KNASLLQHSKNSP;
NASLLQHSKNSPP; ASLLQHSKNSPPQ; SLLQHSKNSPPQF; LLQHSKNSPPQFK;
GPNLWKSTDVGGC; PNLWKSTDVGGCN; NLWKSTDVGGCNC; LWKSTDVGGCNCT;
WKSTDVGGCNCTN; KSTDVGGCNCTNR; STDVGGCNCTNRG; TDVGGCNCTNRGY;
DVGGCNCTNRGYW; VGGCNCTNRGYWN; GGCNCTNRGYWNN; FPLLCCRWRTLGN;
PLLCCRWRTLGNA; LLCCRWRTLGNAG; LCCRWRTLGNAGS; CCRWRTLGNAGSA;
CRWRTLGNAGSAN; RWRTLGNAGSANE; WRTLGNAGSANEL; RTLGNAGSANELQ;
TLGNAGSANELQV; LGNAGSANELQVK; GNAGSANELQVKV; NAGSANELQVKVP;
VFWDFHRRGKCSP; FWDFHRRGKCSPS; WDFHRRGKCSPST; DFHRRGKCSPSTS;
FHRRGKCSPSTSC; HRRGKCSPSTSCD; RRGKCSPSTSCDQ; RGKCSPSTSCDQH;
GKCSPSTSCDQHS; KCSPSTSCDQHSY; CSPSTSCDQHSYH; SPSTSCDQHSYHS;
PSTSCDQHSYHSV; STSCDQHSYHSVA; TSCDQHSYHSVAR; QLWNTTVERPCKI;
LWNTTVERPCKIF; DPPEKKICKESLP; PPEKKICKESLPN; PEKKICKESLPNF;
EKKICKESLPNFL; KKICKESLPNFLF; KICKESLPNFLFA; ICKESLPNFLFAK;
PYKQENPESGWAA; YKQENPESGWAAY; KQENPESGWAAYV; QENPESGWAAYVW;
ENPESGWAAYVWY; NPESGWAAYVWYG; PESGWAAYVWYGI; ESGWAAYVWYGIP;
SGWAAYVWYGIPG; GWAAYVWYGIPGR; WAAYVWYGIPGRR; AAYVWYGIPGRRG;
WHRKTSRGPRYDK; HRKTSRGPRYDKI; RKTSRGPRYDKIY; QTGTIANQNALNR;
TGTIANQNALNRC; GTIANQNALNRCF; TIANQNALNRCFY; IANQNALNRCFYC;
ANQNALNRCFYCT; NQNALNRCFYCTY; QNALNRCFYCTYT; NALNRCFYCTYTF;
ALNRCFYCTYTFN; LNRCFYCTYTFNK; NRCFYCTYTFNKC; RCFYCTYTFNKCC;
CFYCTYTFNKCCF; FYCTYTFNKCCFC; YCTYTFNKCCFCI; CTYTFNKCCFCIS;
TYTFNKCCFCISH; YTFNKCCFCISHF; NTESLYTNATLDY; TESLYTNATLDYG;
ESLYTNATLDYGG; SLYTNATLDYGGL; LYTNATLDYGGLT; YTNATLDYGGLTF;
TNATLDYGGLTFG; NATLDYGGLTFGN; ATLDYGGLTFGNL; TLDYGGLTFGNLQ;
LDYGGLTFGNLQQ; DYGGLTFGNLQQG; YGGLTFGNLQQGL; GGLTFGNLQQGLK;
GLTFGNLQQGLKY; LTFGNLQQGLKYL; TFGNLQQGLKYLR; FGNLQQGLKYLRL;
GNLQQGLKYLRLG; NLQQGLKYLRLGK; LQQGLKYLRLGKS; QQGLKYLRLGKSI;
QGLKYLRLGKSIV; GLKYLRLGKSIVI; LKYLRLGKSIVIG; KYLRLGKSIVIGI;
YLRLGKSIVIGIQ; LRLGKSIVIGIQC; RLGKSIVIGIQCL; LGKSIVIGIQCLI;
GKSIVIGIQCLIH; KSIVIGIQCLIHV; SIVIGIQCLIHVQ; IVIGIQCLIHVQS;
VIGIQCLIHVQSL; IGIQCLIHVQSLQ; GIQCLIHVQSLQF; IQCLIHVQSLQFL;
QCLIHVQSLQFLN; CLIHVQSLQFLNP; LIHVQSLQFLNPL; IHVQSLQFLNPLL;
HVQSLQFLNPLLL; YQEYISPCIYYIS; QEYISPCIYYISS; EYISPCIYYISSL;
YISPCIYYISSLK; ISPCIYYISSLKK; SPCIYYISSLKKY; PCIYYISSLKKYT;
CIYYISSLKKYTY; IYYISSLKKYTYL; YYISSLKKYTYLS; YISSLKKYTYLSQ;
ISSLKKYTYLSQN; SSLKKYTYLSQNP; SLKKYTYLSQNPA; LKKYTYLSQNPAF;
KKYTYLSQNPAFP; KYTYLSQNPAFPS; YTYLSQNPAFPSI; TYLSQNPAFPSIQ;
YLSQNPAFPSIQQ; LSQNPAFPSIQQF; TKLAVATRSFHFV; KLAVATRSFHFVK;
LAVATRSFHFVKF; AVATRSFHFVKFF; VATRSFHFVKFFF; ATRSFHFVKFFFQ;
TRSFHFVKFFFQV; RSFHFVKFFFQVR; SFHFVKFFFQVRT; FHFVKFFFQVRTL;

HFVKFFFQVRTLS; FVKFFFQVRTLSF; VKFFFQVRTLSFV; KFFFQVRTLSFVR;
FFFQVRTLSFVRI; FFQVRTLSFVRIF; FQVRTLSFVRIFL; QVRTLSFVRIFLN;
VRTLSFVRIFLNI; RTLSFVRIFLNIF; TLSFVRIFLNIFW; LSFVRIFLNIFWA;
PSLVEIFGFFCLN; SLVEIFGFFCLNV; LVEIFGFFCLNVS; VEIFGFFCLNVSF;
EIFGFFCLNVSFL; IFGFFCLNVSFLN; FGFFCLNVSFLNL; GFFCLNVSFLNLP;
HFHLNNLSNCLNC; FHLNNLSNCLNCL; HLNNLSNCLNCLF; LNNLSNCLNCLFH;
NNLSNCLNCLFHV; NLSNCLNCLFHVL; LSNCLNCLFHVLK; SNCLNCLFHVLKA;
NCLNCLFHVLKAN; CLNCLFHVLKANP; LNCLFHVLKANPL; NCLFHVLKANPLI;
CLFHVLKANPLIQ; LFHVLKANPLIQL; FHVLKANPLIQLL; HVLKANPLIQLLS;
VLKANPLIQLLSL; LKANPLIQLLSLL; KANPLIQLLSLLH; ANPLIQLLSLLHL;
NPLIQLLSLLHLQ; PLIQLLSLLHLQK; LIQLLSLLHLQKQ; IQLLSLLHLQKQP;
QLLSLLHLQKQPC; LLSLLHLQKQPCT; LSLLHLQKQPCTD; SLLHLQKQPCTDL;
LHLAQRLAFPWVG; HLAQRLAFPWVGL; LAQRLAFPWVGLH; AQRLAFPWVGLHL;
QRLAFPWVGLHLR; RLAFPWVGLHLRL; LAFPWVGLHLRLY; AFPWVGLHLRLYH;
FPWVGLHLRLYHH; PWVGLHLRLYHHT; WVGLHLRLYHHTN; VGLHLRLYHHTNL;
GLHLRLYHHTNLI; LHLRLYHHTNLIT; HLRLYHHTNLITL; LRLYHHTNLITLQ;
RLYHHTNLITLQL; LYHHTNLITLQLV; YHHTNLITLQLVL; HHTNLITLQLVLF;
HTNLITLQLVLFF; TNLITLQLVLFFH; NLITLQLVLFFHY; LITLQLVLFFHYQ;
ITLQLVLFFHYQW; TLQLVLFFHYQWD; LQLVLFFHYQWDL; KQYSAKNQILQNP;
QYSAKNQILQNPF; VANSAAKQHLPYI; ANSAAKQHLPYIV; NSAAKQHLPYIVL;
SAAKQHLPYIVLV; AAKQHLPYIVLVQ; AKQHLPYIVLVQH; KQHLPYIVLVQHF;
QHLPYIVLVQHFH; HLPYIVLVQHFHE; LPYIVLVQHFHEL; PYIVLVQHFHELQ;
YIVLVQHFHELQI; IVLVQHFHELQIL; VLVQHFHELQILN; LVQHFHELQILNP;
VQHFHELQILNPF; QHFHELQILNPFY; HFHELQILNPFYL; FHELQILNPFYLI;
HELQILNPFYLIY; ELQILNPFYLIYD; IFLLAFLPWSYEG; FLLAFLPWSYEGY;
LLAFLPWSYEGYL; LAFLPWSYEGYLL; AFLPWSYEGYLLF; FLPWSYEGYLLFF;
LKLYLLLADKYFF; KLYLLLADKYFFD; LYLLLADKYFFDF; YLLLADKYFFDFY;
LLLADKYFFDFYF; LLADKYFFDFYFL; LADKYFFDFYFLQ; ADKYFFDFYFLQK;
SDKAGLFSDTFYT; DKAGLFSDTFYTP; KAGLFSDTFYTPL; AGLFSDTFYTPLH;
GLFSDTFYTPLHC; LFSDTFYTPLHCI; FSDTFYTPLHCIE; SDTFYTPLHCIEI;
DTFYTPLHCIEIL; TFYTPLHCIEILN; FYTPLHCIEILNT; YTPLHCIEILNTY;
TPLHCIEILNTYL; PLHCIEILNTYLI; LHCIEILNTYLII; HCIEILNTYLIIK;
CIEILNTYLIIKT; IEILNTYLIIKTH; EILNTYLIIKTHP; ILNTYLIIKTHPH;
LNTYLIIKTHPHT; NTYLIIKTHPHTL; TYLIIKTHPHTLS; YLIIKTHPHTLSL;
LIIKTHPHTLSLL; IIKTHPHTLSLLH; IKTHPHTLSLLHT; KTHPHTLSLLHTQ;
LISKTPALFLQAL; ISKTPALFLQALL; SKTPALFLQALLG; NHAPLSPLECFLL;
LQKLYVYVELKRI; GLLPFFFFWVVLS; LLPFFFFWVVLSV; LPFFFFWVVLSVE;
PFFFFWVVLSVEN; FFFFWVVLSVENL; FFFWVVLSVENLL; FFWVVLSVENLLL;
FWVVLSVENLLLL; WVVLSVENLLLLL; VVLSVENLLLLLH; VLSVENLLLLLHH;
LSVENLLLLLHHW; SVENLLLLLHHWQ; VENLLLLLHHWQT; ENLLLLLHHWQTY;
NLLLLLHHWQTYL; LLLLLHHWQTYLH; LLLLHHWQTYLHG; LLLHHWQTYLHGK;
LLHHWQTYLHGKI; LHHWQTYLHGKIN; HHWQTYLHGKINL; HWQTYLHGKINLH;
WQTYLHGKINLHP; QTYLHGKINLHPI; TYLHGKINLHPIF; YLHGKINLHPIFH;
RNSTRTPTLLFHR; NSTRTPTLLFHRL; STRTPTLLFHRLA; TRTPTLLFHRLAP;
RTPTLLFHRLAPI; TPTLLFHRLAPIK; PTLLFHRLAPIKK; TLLFHRLAPIKKI;
LLFHRLAPIKKII; LFHRLAPIKKIIT; GLLIFYYLSKYKL; LLIFYYLSKYKLV;
LIFYYLSKYKLVT; IFYYLSKYKLVTL; FYYLSKYKLVTLK; YYLSKYKLVTLKL;
ISEGSFSNYLDPP; SEGSFSNYLDPPL; EGSFSNYLDPPLQ; GSFSNYLDPPLQS;
SFSNYLDPPLQSF; FSNYLDPPLQSFF; SNYLDPPLQSFFS; AKPLCEAVNAVAI;
KPLCEAVNAVAIY; PLCEAVNAVAIYP; LCEAVNAVAIYPN; CEAVNAVAIYPNQ;
EAVNAVAIYPNQG; AVNAVAIYPNQGL; VNAVAIYPNQGLF; NAVAIYPNQGLFS;
HARAVHRRLFGTN; ARAVHRRLFGTNR; RAVHRRLFGTNRP; AVHRRLFGTNRPF;
VHRRLFGTNRPFL; HRRLFGTNRPFLA; RRLFGTNRPFLAV; RLFGTNRPFLAVQ;
LFGTNRPFLAVQG; FGTNRPFLAVQGI; GTNRPFLAVQGIW; TNRPFLAVQGIWA;
NRPFLAVQGIWAK; RPFLAVQGIWAKR; PFLAVQGIWAKRK; FLAVQGIWAKRKI;
LAVQGIWAKRKIS; AVQGIWAKRKIST; VQGIWAKRKISTN; QGIWAKRKISTNL;
ATPGSKIRLMSYL; TPGSKIRLMSYLY; PGSKIRLMSYLYI; GSKIRLMSYLYIL;
SKIRLMSYLYILL; KIRLMSYLYILLH; IRLMSYLYILLHF; RLMSYLYILLHFF;
LMSYLYILLHFFI; MSYLYILLHFFIQ; SYLYILLHFFIQS; YLYILLHFFIQSI;

LYILLHFFIQSIH; YILLHFFIQSIHS; ILLHFFIQSIHSL; LLHFFIQSIHSLH; LHFFIQSIHSLHF; HFFIQSIHSLHFI; FFIQSIHSLHFIL; FIQSIHSLHFILV; IQSIHSLHFILVA; QSIHSLHFILVAP; SIHSLHFILVAPF; IHSLHFILVAPFV; HSLHFILVAPFVR; SLHFILVAPFVRV; LHFILVAPFVRVK; HFILVAPFVRVKF; FILVAPFVRVKFL; ILVAPFVRVKFLT

14 mers:

ASEKASTPLLLERK; SEKASTPLLLERKG; EKASTPLLLERKGG; KASTPLLLERKGGG; ASTPLLLERKGGGR; STPLLLERKGGGRG; TPLLLERKGGGRGG; PLLLERKGGGRGGL; LLLERKGGGRGGLG; LLERKGGGRGGLGL; LERKGGGRGGLGLL; ERKGGGRGGLGLLY; RKGGGRGGLGLLYI; KGGGRGGLGLLYII; GGGRGGLGLLYIIK; GGRGGLGLLYIIKK; GRGGLGLLYIIKKK; RGGLGLLYIIKKKA; GGLGLLYIIKKKAT; GLGLLYIIKKKATG; LGLLYIIKKKATGR; GLLYIIKKKATGRS; LLYIIKKKATGRSC; LYIIKKKATGRSCL; YIIKKKATGRSCLP; IIKKKATGRSCLPM; IKKKATGRSCLPME; KKKATGRSCLPMEC; KKATGRSCLPMECS; KATGRSCLPMECSQ; ATGRSCLPMECSQT; TGRSCLPMECSQTM; GRSCLPMECSQTMT; RSCLPMECSQTMTS; SCLPMECSQTMTSG; CLPMECSQTMTSGR; LPMECSQTMTSGRK; PMECSQTMTSGRKV; MECSQTMTSGRKVH; ECSQTMTSGRKVHD; CSQTMTSGRKVHDS; SQTMTSGRKVHDSQ; QTMTSGRKVHDSQG; TMTSGRKVHDSQGN; MTSGRKVHDSQGNA; TSGRKVHDSQGNAA; SGRKVHDSQGNAAK; GRKVHDSQGNAAKP; PQEGKCMTHREELL; QEGKCMTHREELLT; EGKCMTHREELLTH; GKCMTHREELLTHG; KCMTHREELLTHGM; CMTHREELLTHGMQ; MTHREELLTHGMQP; THREELLTHGMQPN; HREELLTHGMQPNH; REELLTHGMQPNHD; EELLTHGMQPNHDL; ELLTHGMQPNHDLR; LLTHGMQPNHDLRK; LTHGMQPNHDLRKE; THGMQPNHDLRKES; HGMQPNHDLRKESA; QTCFASLGILALSP; TCFASLGILALSPV; CFASLGILALSPVK; FASLGILALSPVKL; ASLGILALSPVKLD; SLGILALSPVKLDK; LGILALSPVKLDKG; GILALSPVKLDKGH; ILALSPVKLDKGHG; LALSPVKLDKGHGS; ALSPVKLDKGHGSA; LSPVKLDKGHGSAP; SPVKLDKGHGSAPA; PVKLDKGHGSAPAV; VKLDKGHGSAPAVT; KLDKGHGSAPAVTT; LDKGHGSAPAVTTS; DKGHGSAPAVTTSF; KGHGSAPAVTTSFS; GHGSAPAVTTSFSE; HGSAPAVTTSFSES; GSAPAVTTSFSESW; NLDWNKKKSSEDFY; LDWNKKKSSEDFYF; DWNKKKSSEDFYFY; WNKKKSSEDFYFYF; NKKKSSEDFYFYFR; KKKSSEDFYFYFRA; KKSSEDFYFYFRAF; KSSEDFYFYFRAFA; SSEDFYFYFRAFAG; SEDFYFYFRAFAGI; EDFYFYFRAFAGIL; RQCRREKQKYHCFT; QCRREKQKYHCFTC; CRREKQKYHCFTCC; RREKQKYHCFTCCK; REKQKYHCFTCCKR; EKQKYHCFTCCKRL; KQKYHCFTCCKRLC; QKYHCFTCCKRLCK; KYHCFTCCKRLCKR; YHCFTCCKRLCKRL; HCFTCCKRLCKRLL; CFTCCKRLCKRLLG; FTCCKRLCKRLLGK; SLFFCISRFMGAAL; LFFCISRFMGAALA; FFCISRFMGAALAL; FCISRFMGAALALL; CISRFMGAALALLG; ISRFMGAALALLGD; SRFMGAALALLGDL; RFMGAALALLGDLV; FMGAALALLGDLVA; MGAALALLGDLVAS; GAALALLGDLVASV; AALALLGDLVASVS; ALALLGDLVASVSE; LALLGDLVASVSEA; ALLGDLVASVSEAA; LLGDLVASVSEAAA; LGDLVASVSEAAAA; GDLVASVSEAAAAT; DLVASVSEAAAATG; LVASVSEAAAATGF; VASVSEAAAATGFS; ASVSEAAAATGFSV; SVSEAAAATGFSVA; VSEAAAATGFSVAE; SEAAAATGFSVAEI; EAAAATGFSVAEIA; AAAATGFSVAEIAA; AAATGFSVAEIAAG; AATGFSVAEIAAGE; ATGFSVAEIAAGEA; TGFSVAEIAAGEAA; GFSVAEIAAGEAAA; FSVAEIAAGEAAAA; SVAEIAAGEAAAAI; VAEIAAGEAAAAIE; AEIAAGEAAAAIEV; EIAAGEAAAAIEVQ; IAAGEAAAAIEVQI; AAGEAAAAIEVQIA; AGEAAAAIEVQIAS; GEAAAAIEVQIASL; EAAAAIEVQIASLA; AAAAIEVQIASLAT; AAAIEVQIASLATV; AAIEVQIASLATVE; AIEVQIASLATVEG; IEVQIASLATVEGI; EVQIASLATVEGIT; VQIASLATVEGITS;

QIASLATVEGITST; IASLATVEGITSTS; ASLATVEGITSTSE;
SLATVEGITSTSEA; LATVEGITSTSEAI; ATVEGITSTSEAIA;
TVEGITSTSEAIAA; VEGITSTSEAIAAI; EGITSTSEAIAAIG;
GITSTSEAIAAIGL; ITSTSEAIAAIGLT; TSTSEAIAAIGLTP;
STSEAIAAIGLTPQ; TSEAIAAIGLTPQT; SEAIAAIGLTPQTY;
EAIAAIGLTPQTYA; AIAAIGLTPQTYAV; IAAIGLTPQTYAVI;
AAIGLTPQTYAVIA; AIGLTPQTYAVIAG; IGLTPQTYAVIAGA;
GLTPQTYAVIAGAP; LTPQTYAVIAGAPG; TPQTYAVIAGAPGA;
PQTYAVIAGAPGAI; QTYAVIAGAPGAIA; TYAVIAGAPGAIAG;
YAVIAGAPGAIAGF; AVIAGAPGAIAGFA; VIAGAPGAIAGFAA;
IAGAPGAIAGFAAL; AGAPGAIAGFAALI; GAPGAIAGFAALIQ;
APGAIAGFAALIQT; PGAIAGFAALIQTV; GAIAGFAALIQTVS;
AIAGFAALIQTVSG; IAGFAALIQTVSGI; AGFAALIQTVSGIS;
GFAALIQTVSGISS; FAALIQTVSGISSL; AALIQTVSGISSLA;
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FFDDWDHKVSTVGL; FDDWDHKVSTVGLY; DDWDHKVSTVGLYQ;
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HKVSTVGLYQQSGM; KVSTVGLYQQSGMA; VSTVGLYQQSGMAL;
STVGLYQQSGMALE; TVGLYQQSGMALEL; VGLYQQSGMALELF;
GLYQQSGMALELFN; LYQQSGMALELFNP; YQQSGMALELFNPD;
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FNPDEYYDILFPGV; NPDEYYDILFPGVN; PDEYYDILFPGVNT;
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GVNTFVNNIQYLDP; VNTFVNNIQYLDPR; NTFVNNIQYLDPRH;
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QYLDPRHWGPSLFA; YLDPRHWGPSLFAT; LDPRHWGPSLFATI;
DPRHWGPSLFATIS; PRHWGPSLFATISQ; RHWGPSLFATISQA;
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FATISQALWHVIRD; ATISQALWHVIRDD; TISQALWHVIRDDI;
ISQALWHVIRDDIP; SQALWHVIRDDIPS; QALWHVIRDDIPSI;
ALWHVIRDDIPSIT; LWHVIRDDIPSITS; WHVIRDDIPSITSQ;
HVIRDDIPSITSQE; VIRDDIPSITSQEL; IRDDIPSITSQELQ;
RDDIPSITSQELQR; DDIPSITSQELQRR; DIPSITSQELQRRT;
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QRRTERFFRDSLAR; RRTERFFRDSLARF; RTERFFRDSLARFL;
TERFFRDSLARFLE; ERFFRDSLARFLEE; RFFRDSLARFLEET;
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DSLARFLEETTWTI; SLARFLEETTWTIV; LARFLEETTWTIVN;
ARFLEETTWTIVNA; RFLEETTWTIVNAP; FLEETTWTIVNAPI;
LEETTWTIVNAPIN; EETTWTIVNAPINF; ETTWTIVNAPINFY;
TTWTIVNAPINFYN; TWTIVNAPINFYNY; WTIVNAPINFYNYI;
TIVNAPINFYNYIQ; IVNAPINFYNYIQQ; VNAPINFYNYIQQY;
NAPINFYNYIQQYY; APINFYNYIQQYYS; PINFYNYIQQYYSD;
INFYNYIQQYYSDL; NFYNYIQQYYSDLS; FYNYIQQYYSDLSP;
YNYIQQYYSDLSPI; NYIQQYYSDLSPIR; YIQQYYSDLSPIRP;
IQQYYSDLSPIRPS; QQYYSDLSPIRPSM; QYYSDLSPIRPSMV;

YYSDLSPIRPSMVR; YSDLSPIRPSMVRQ; SDLSPIRPSMVRQV;
DLSPIRPSMVRQVA; LSPIRPSMVRQVAE; SPIRPSMVRQVAER;
PIRPSMVRQVAERE; IRPSMVRQVAEREG; RPSMVRQVAEREGT;
PSMVRQVAEREGTR; SMVRQVAEREGTRV; MVRQVAEREGTRVH;
VRQVAEREGTRVHF; RQVAEREGTRVHFG; QVAEREGTRVHFGH;
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TRVHFGHTYSIDDA; RVHFGHTYSIDDAD; VHFGHTYSIDDADS;
HFGHTYSIDDADSI; FGHTYSIDDADSIE; GHTYSIDDADSIEE;
HTYSIDDADSIEEV; TYSIDDADSIEEVT; YSIDDADSIEEVTQ;
SIDDADSIEEVTQR; IDDADSIEEVTQRM; DDADSIEEVTQRMD;
DADSIEEVTQRMDL; ADSIEEVTQRMDLR; DSIEEVTQRMDLRN;
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SGEFIEKTIAPGGA; GEFIEKTIAPGGAN; EFIEKTIAPGGANQ;
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YYRGRMLPKPRNGG; YRGRMLPKPRNGGS; RGRMLPKPRNGGSR;
PREKNASLLQHSKN; REKNASLLQHSKNS; EKNASLLQHSKNSP;
KNASLLQHSKNSPP; NASLLQHSKNSPPQ; ASLLQHSKNSPPQF;
SLLQHSKNSPPQFK; GPNLWKSTDVGGCN; PNLWKSTDVGGCNC;
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KSTDVGGCNCTNRG; STDVGGCNCTNRGY; TDVGGCNCTNRGYW;
DVGGCNCTNRGYWN; VGGCNCTNRGYWNN; FPLLCCRWRTLGNA;
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WRTLGNAGSANELQ; RTLGNAGSANELQV; TLGNAGSANELQVK;
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RGKCSPSTSCDQHS; GKCSPSTSCDQHSY; KCSPSTSCDQHSYH;
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PPEKKICKESLPNF; PEKKICKESLPNFL; EKKICKESLPNFLF;

KKICKESLPNFLFA; KICKESLPNFLFAK; PYKQENPESGWAAY;
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ENPESGWAAYVWYG; NPESGWAAYVWYGI; PESGWAAYVWYGIP;
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NQNALNRCFYCTYT; QNALNRCFYCTYTF; NALNRCFYCTYTFN;
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LKYLRLGKSIVIGI; KYLRLGKSIVIGIQ; YLRLGKSIVIGIQC;
LRLGKSIVIGIQCL; RLGKSIVIGIQCLI; LGKSIVIGIQCLIH;
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IVIGIQCLIHVQSL; VIGIQCLIHVQSLQ; IGIQCLIHVQSLQF;
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CLIHVQSLQFLNPL; LIHVQSLQFLNPLL; IHVQSLQFLNPLLL;
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YISPCIYYISSLKK; ISPCIYYISSLKKY; SPCIYYISSLKKYT;
PCIYYISSLKKYTY; CIYYISSLKKYTYL; IYYISSLKKYTYLS;
YYISSLKKYTYLSQ; YISSLKKYTYLSQN; ISSLKKYTYLSQNP;
SSLKKYTYLSQNPA; SLKKYTYLSQNPAF; LKKYTYLSQNPAFP;
KKYTYLSQNPAFPS; KYTYLSQNPAFPSI; YTYLSQNPAFPSIQ;
TYLSQNPAFPSIQQ; YLSQNPAFPSIQQF; TKLAVATRSFHFVK;
KLAVATRSFHFVKF; LAVATRSFHFVKFF; AVATRSFHFVKFFF;
VATRSFHFVKFFFQ; ATRSFHFVKFFFQV; TRSFHFVKFFFQVR;
RSFHFVKFFFQVRT; SFHFVKFFFQVRTL; FHFVKFFFQVRTLS;
HFVKFFFQVRTLSF; FVKFFFQVRTLSFV; VKFFFQVRTLSFVR;
KFFFQVRTLSFVRI; FFFQVRTLSFVRIF; FFQVRTLSFVRIFL;
FQVRTLSFVRIFLN; QVRTLSFVRIFLNI; VRTLSFVRIFLNIF;
RTLSFVRIFLNIFW; TLSFVRIFLNIFWA; PSLVEIFGFFCLNV;
SLVEIFGFFCLNVS; LVEIFGFFCLNVSF; VEIFGFFCLNVSFL;
EIFGFFCLNVSFLN; IFGFFCLNVSFLNL; FGFFCLNVSFLNLP;
HFHLNNLSNCLNCL; FHLNNLSNCLNCLF; HLNNLSNCLNCLFH;
LNNLSNCLNCLFHV; NNLSNCLNCLFHVL; NLSNCLNCLFHVLK;
LSNCLNCLFHVLKA; SNCLNCLFHVLKAN; NCLNCLFHVLKANP;
CLNCLFHVLKANPL; LNCLFHVLKANPLI; NCLFHVLKANPLIQ;
CLFHVLKANPLIQL; LFHVLKANPLIQLL; FHVLKANPLIQLLS;
HVLKANPLIQLLSL; VLKANPLIQLLSLL; LKANPLIQLLSLLH;
KANPLIQLLSLLHL; ANPLIQLLSLLHLQ; NPLIQLLSLLHLQK;
PLIQLLSLLHLQKQ; LIQLLSLLHLQKQP; IQLLSLLHLQKQPC;
QLLSLLHLQKQPCT; LLSLLHLQKQPCTD; LSLLHLQKQPCTDL;
LHLAQRLAFPWVGL; HLAQRLAFPWVGLH; LAQRLAFPWVGLHL;
AQRLAFPWVGLHLR; QRLAFPWVGLHLRL; RLAFPWVGLHLRLY;
LAFPWVGLHLRLYH; AFPWVGLHLRLYHH; FPWVGLHLRLYHHT;
PWVGLHLRLYHHTN; WVGLHLRLYHHTNL; VGLHLRLYHHTNLI;
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LRLYHHTNLITLQL; RLYHHTNLITLQLV; LYHHTNLITLQLVL;
YHHTNLITLQLVLF; HHTNLITLQLVLFF; HTNLITLQLVLFFH;
TNLITLQLVLFFHY; NLITLQLVLFFHYQ; LITLQLVLFFHYQW;
ITLQLVLFFHYQWD; TLQLVLFFHYQWDL; KQYSAKNQILQNPF;

VANSAAKQHLPYIV; ANSAAKQHLPYIVL; NSAAKQHLPYIVLV;
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KQHLPYIVLVQHFH; QHLPYIVLVQHFHE; HLPYIVLVQHFHEL;
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VQHFHELQILNPFY; QHFHELQILNPFYL; HFHELQILNPFYLI;
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AFLPWSYEGYLLFF; LKLYLLLADKYFFD; KLYLLLADKYFFDF;
LYLLLADKYFFDFY; YLLLADKYFFDFYF; LLLADKYFFDFYFL;
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DKAGLFSDTFYTPL; KAGLFSDTFYTPLH; AGLFSDTFYTPLHC;
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FYTPLHCIEILNTY; YTPLHCIEILNTYL; TPLHCIEILNTYLI;
PLHCIEILNTYLII; LHCIEILNTYLIIK; HCIEILNTYLIIKT;
CIEILNTYLIIKTH; IEILNTYLIIKTHP; EILNTYLIIKTHPH;
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LHHWQTYLHGKINL; HHWQTYLHGKINLH; HWQTYLHGKINLHP;
WQTYLHGKINLHPI; QTYLHGKINLHPIF; TYLHGKINLHPIFH;
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TRTPTLLFHRLAPI; RTPTLLFHRLAPIK; TPTLLFHRLAPIKK;
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IFYYLSKYKLVTLK; FYYLSKYKLVTLKL; ISEGSFSNYLDPPL;
SEGSFSNYLDPPLQ; EGSFSNYLDPPLQS; GSFSNYLDPPLQSF;
SFSNYLDPPLQSFF; FSNYLDPPLQSFFS; AKPLCEAVNAVAIY;
KPLCEAVNAVAIYP; PLCEAVNAVAIYPN; LCEAVNAVAIYPNQ;
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VNAVAIYPNQGLFS; HARAVHRRLFGTNR; ARAVHRRLFGTNRP;
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TNRPFLAVQGIWAK; NRPFLAVQGIWAKR; RPFLAVQGIWAKRK;
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AVQGIWAKRKISTN; VQGIWAKRKISTNL; ATPGSKIRLMSYLY;
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FIQSIHSLHFILVA; IQSIHSLHFILVAP; QSIHSLHFILVAPF;
SIHSLHFILVAPFV; IHSLHFILVAPFVR; HSLHFILVAPFVRV;
SLHFILVAPFVRVK; LHFILVAPFVRVKF; HFILVAPFVRVKFL; FILVAPFVRVKFLT

15 mers:
ASEKASTPLLLERKG; SEKASTPLLLERKGG; EKASTPLLLERKGGG;
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AIEVQIASLATVEGI; IEVQIASLATVEGIT; EVQIASLATVEGITS;
VQIASLATVEGITST; QIASLATVEGITSTS; IASLATVEGITSTSE;
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GPSLFATISQALWHV; PSLFATISQALWHVI; SLFATISQALWHVIR;
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TISQALWHVIRDDIP; ISQALWHVIRDDIPS; SQALWHVIRDDIPSI;
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RFFRDSLARFLEETT; FFRDSLARFLEETTW; FRDSLARFLEETTWT;
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EYISPCIYYISSLKK; YISPCIYYISSLKKY; ISPCIYYISSLKKYT;
SPCIYYISSLKKYTY; PCIYYISSLKKYTYL; CIYYISSLKKYTYLS;
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YTYLSQNPAFPSIQQ; TYLSQNPAFPSIQQF; TKLAVATRSFHFVKF;
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VATRSFHFVKFFFQV; ATRSFHFVKFFFQVR; TRSFHFVKFFFQVRT;
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FQVRTLSFVRIFLNI; QVRTLSFVRIFLNIF; VRTLSFVRIFLNIFW;
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EGSFSNYLDPPLQSF; GSFSNYLDPPLQSFF; SFSNYLDPPLQSFFS;
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IHSLHFILVAPFVRV; HSLHFILVAPFVRVK; SLHFILVAPFVRVKF;
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16 mers:
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NALNRCFYCTYTFNKC; ALNRCFYCTYTFNKCC; LNRCFYCTYTFNKCCF;
NRCFYCTYTFNKCCFC; RCFYCTYTFNKCCFCI; CFYCTYTFNKCCFCIS;
FYCTYTFNKCCFCISH; YCTYTFNKCCFCISHF; NTESLYTNATLDYGGL;
TESLYTNATLDYGGLT; ESLYTNATLDYGGLTF; SLYTNATLDYGGLTFG;
LYTNATLDYGGLTFGN; YTNATLDYGGLTFGNL; TNATLDYGGLTFGNLQ;
NATLDYGGLTFGNLQQ; ATLDYGGLTFGNLQQG; TLDYGGLTFGNLQQGL;
LDYGGLTFGNLQQGLK; DYGGLTFGNLQQGLKY; YGGLTFGNLQQGLKYL;
GGLTFGNLQQGLKYLR; GLTFGNLQQGLKYLRL; LTFGNLQQGLKYLRLG;
TFGNLQQGLKYLRLGK; FGNLQQGLKYLRLGKS; GNLQQGLKYLRLGKSI;
NLQQGLKYLRLGKSIV; LQQGLKYLRLGKSIVI; QQGLKYLRLGKSIVIG;
QGLKYLRLGKSIVIGI; GLKYLRLGKSIVIGIQ; LKYLRLGKSIVIGIQC;
KYLRLGKSIVIGIQCL; YLRLGKSIVIGIQCLI; LRLGKSIVIGIQCLIH;
RLGKSIVIGIQCLIHV; LGKSIVIGIQCLIHVQ; GKSIVIGIQCLIHVQS;
KSIVIGIQCLIHVQSL; SIVIGIQCLIHVQSLQ; IVIGIQCLIHVQSLQF;
VIGIQCLIHVQSLQFL; IGIQCLIHVQSLQFLN; GIQCLIHVQSLQFLNP;
IQCLIHVQSLQFLNPL; QCLIHVQSLQFLNPLL; CLIHVQSLQFLNPLLL;
YQEYISPCIYYISSLK; QEYISPCIYYISSLKK; EYISPCIYYISSLKKY;
YISPCIYYISSLKKYT; ISPCIYYISSLKKYTY; SPCIYYISSLKKYTYL;
PCIYYISSLKKYTYLS; CIYYISSLKKYTYLSQ; IYYISSLKKYTYLSQN;
YYISSLKKYTYLSQNP; YISSLKKYTYLSQNPA; ISSLKKYTYLSQNPAF;
SSLKKYTYLSQNPAFP; SLKKYTYLSQNPAFPS; LKKYTYLSQNPAFPSI;
KKYTYLSQNPAFPSIQ; KYTYLSQNPAFPSIQQ; YTYLSQNPAFPSIQQF;
TKLAVATRSFHFVKFF; KLAVATRSFHFVKFFF; LAVATRSFHFVKFFFQ;
AVATRSFHFVKFFFQV; VATRSFHFVKFFFQVR; ATRSFHFVKFFFQVRT;
TRSFHFVKFFFQVRTL; RSFHFVKFFFQVRTLS; SFHFVKFFFQVRTLSF;
FHFVKFFFQVRTLSFV; HFVKFFFQVRTLSFVR; FVKFFFQVRTLSFVRI;
VKFFFQVRTLSFVRIF; KFFFQVRTLSFVRIFL; FFFQVRTLSFVRIFLN;
FFQVRTLSFVRIFLNI; FQVRTLSFVRIFLNIF; QVRTLSFVRIFLNIFW;
VRTLSFVRIFLNIFWA; PSLVEIFGFFCLNVSF; SLVEIFGFFCLNVSFL;
LVEIFGFFCLNVSFLN; VEIFGFFCLNVSFLNL; EIFGFFCLNVSFLNLP;
HFHLNNLSNCLNCLFH; FHLNNLSNCLNCLFHV; HLNNLSNCLNCLFHVL;
LNNLSNCLNCLFHVLK; NNLSNCLNCLFHVLKA; NLSNCLNCLFHVLKAN;

LSNCLNCLFHVLKANP; SNCLNCLFHVLKANPL; NCLNCLFHVLKANPLI;
CLNCLFHVLKANPLIQ; LNCLFHVLKANPLIQL; NCLFHVLKANPLIQLL;
CLFHVLKANPLIQLLS; LFHVLKANPLIQLLSL; FHVLKANPLIQLLSLL;
HVLKANPLIQLLSLLH; VLKANPLIQLLSLLHL; LKANPLIQLLSLLHLQ;
KANPLIQLLSLLHLQK; ANPLIQLLSLLHLQKQ; NPLIQLLSLLHLQKQP;
PLIQLLSLLHLQKQPC; LIQLLSLLHLQKQPCT; IQLLSLLHLQKQPCTD;
QLLSLLHLQKQPCTDL; LHLAQRLAFPWVGLHL; HLAQRLAFPWVGLHLR;
LAQRLAFPWVGLHLRL; AQRLAFPWVGLHLRLY; QRLAFPWVGLHLRLYH;
RLAFPWVGLHLRLYHH; LAFPWVGLHLRLYHHT; AFPWVGLHLRLYHHTN;
FPWVGLHLRLYHHTNL; PWVGLHLRLYHHTNLI; WVGLHLRLYHHTNLIT;
VGLHLRLYHHTNLITL; GLHLRLYHHTNLITLQ; LHLRLYHHTNLITLQL;
HLRLYHHTNLITLQLV; LRLYHHTNLITLQLVL; RLYHHTNLITLQLVLF;
LYHHTNLITLQLVLFF; YHHTNLITLQLVLFFH; HHTNLITLQLVLFFHY;
HTNLITLQLVLFFHYQ; TNLITLQLVLFFHYQW; NLITLQLVLFFHYQWD;
LITLQLVLFFHYQWDL; VANSAAKQHLPYIVLV; ANSAAKQHLPYIVLVQ;
NSAAKQHLPYIVLVQH; SAAKQHLPYIVLVQHF; AAKQHLPYIVLVQHFH;
AKQHLPYIVLVQHFHE; KQHLPYIVLVQHFHEL; QHLPYIVLVQHFHELQ;
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YIVLVQHFHELQILNP; IVLVQHFHELQILNPF; VLVQHFHELQILNPFY;
LVQHFHELQILNPFYL; VQHFHELQILNPFYLI; QHFHELQILNPFYLIY;
HFHELQILNPFYLIYD; IFLLAFLPWSYEGYLL; FLLAFLPWSYEGYLLF;
LLAFLPWSYEGYLLFF; LKLYLLLADKYFFDFY; KLYLLLADKYFFDFYF;
LYLLLADKYFFDFYFL; YLLLADKYFFDFYFLQ; LLLADKYFFDFYFLQK;
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AGLFSDTFYTPLHCIE; GLFSDTFYTPLHCIEI; LFSDTFYTPLHCIEIL;
FSDTFYTPLHCIEILN; SDTFYTPLHCIEILNT; DTFYTPLHCIEILNTY;
TFYTPLHCIEILNTYL; FYTPLHCIEILNTYLI; YTPLHCIEILNTYLII;
TPLHCIEILNTYLIIK; PLHCIEILNTYLIIKT; LHCIEILNTYLIIKTH;
HCIEILNTYLIIKTHP; CIEILNTYLIIKTHPH; IEILNTYLIIKTHPHT;
EILNTYLIIKTHPHTL; ILNTYLIIKTHPHTLS; LNTYLIIKTHPHTLSL;
NTYLIIKTHPHTLSLL; TYLIIKTHPHTLSLLH; YLIIKTHPHTLSLLHT;
LIIKTHPHTLSLLHTQ; GLLPFFFFWVVLSVEN; LLPFFFFWVVLSVENL;
LPFFFFWVVLSVENLL; PFFFFWVVLSVENLLL; FFFFWVVLSVENLLLL;
FFFWVVLSVENLLLLL; FFWVVLSVENLLLLLH; FWVVLSVENLLLLLHH;
WVVLSVENLLLLLHHW; VVLSVENLLLLLHHWQ; VLSVENLLLLLHHWQT;
LSVENLLLLLHHWQTY; SVENLLLLLHHWQTYL; VENLLLLLHHWQTYLH;
ENLLLLLHHWQTYLHG; NLLLLLHHWQTYLHGK; LLLLLHHWQTYLHGKI;
LLLLHHWQTYLHGKIN; LLLHHWQTYLHGKINL; LLHHWQTYLHGKINLH;
LHHWQTYLHGKINLHP; HHWQTYLHGKINLHPI; HWQTYLHGKINLHPIF;
WQTYLHGKINLHPIFH; RNSTRTPTLLFHRLAP; NSTRTPTLLFHRLAPI;
STRTPTLLFHRLAPIK; TRTPTLLFHRLAPIKK; RTPTLLFHRLAPIKKI;
TPTLLFHRLAPIKKII; PTLLFHRLAPIKKIIT; GLLIFYYLSKYKLVTL;
LLIFYYLSKYKLVTLK; LIFYYLSKYKLVTLKL; ISEGSFSNYLDPPLQS;
SEGSFSNYLDPPLQSF; EGSFSNYLDPPLQSFF; GSFSNYLDPPLQSFFS;
AKPLCEAVNAVAIYPN; KPLCEAVNAVAIYPNQ; PLCEAVNAVAIYPNQG;
LCEAVNAVAIYPNQGL; CEAVNAVAIYPNQGLF; EAVNAVAIYPNQGLFS;
HARAVHRRLFGTNRPF; ARAVHRRLFGTNRPFL; RAVHRRLFGTNRPFLA;
AVHRRLFGTNRPFLAV; VHRRLFGTNRPFLAVQ; HRRLFGTNRPFLAVQG;
RRLFGTNRPFLAVQGI; RLFGTNRPFLAVQGIW; LFGTNRPFLAVQGIWA;
FGTNRPFLAVQGIWAK; GTNRPFLAVQGIWAKR; TNRPFLAVQGIWAKRK;
NRPFLAVQGIWAKRKI; RPFLAVQGIWAKRKIS; PFLAVQGIWAKRKIST;
FLAVQGIWAKRKISTN; LAVQGIWAKRKISTNL; ATPGSKIRLMSYLYIL;
TPGSKIRLMSYLYILL; PGSKIRLMSYLYILLH; GSKIRLMSYLYILLHF;
SKIRLMSYLYILLHFF; KIRLMSYLYILLHFFI; IRLMSYLYILLHFFIQ;
RLMSYLYILLHFFIQS; LMSYLYILLHFFIQSI; MSYLYILLHFFIQSIH;
SYLYILLHFFIQSIHS; YLYILLHFFIQSIHSL; LYILLHFFIQSIHSLH;
YILLHFFIQSIHSLHF; ILLHFFIQSIHSLHFI; LLHFFIQSIHSLHFIL;
LHFFIQSIHSLHFILV; HFFIQSIHSLHFILVA; FFIQSIHSLHFILVAP;
FIQSIHSLHFILVAPF; IQSIHSLHFILVAPFV; QSIHSLHFILVAPFVR;

SIHSLHFILVAPFVRV; IHSLHFILVAPFVRVK; HSLHFILVAPFVRVKF; SLHFILVAPFVRVKFL; LHFILVAPFVRVKFLT; HFILVAPFVRVKFLT

BK virus reverse reading frame 1

13 mers:

MDKVLNREESMEL; DKVLNREESMELM; KVLNREESMELMD; VLNREESMELMDL; LNREESMELMDLL; NREESMELMDLLG; REESMELMDLLGL; EESMELMDLLGLE; ESMELMDLLGLER; SMELMDLLGLERA; MELMDLLGLERAA; ELMDLLGLERAAW; LMDLLGLERAAWG; MDLLGLERAAWGN; DLLGLERAAWGNL; LLGLERAAWGNLP; LGLERAAWGNLPL; GLERAAWGNLPLM; LERAAWGNLPLMR; ERAAWGNLPLMRK; RAAWGNLPLMRKA; AAWGNLPLMRKAY; AWGNLPLMRKAYL; WGNLPLMRKAYLR; GNLPLMRKAYLRK; NLPLMRKAYLRKC; LPLMRKAYLRKCK; PLMRKAYLRKCKE; LMRKAYLRKCKEF; MRKAYLRKCKEFH; RKAYLRKCKEFHP; KAYLRKCKEFHPD; AYLRKCKEFHPDK; YLRKCKEFHPDKG; LRKCKEFHPDKGG; RKCKEFHPDKGGD; KCKEFHPDKGGDE; CKEFHPDKGGDED; KEFHPDKGGDEDK; EFHPDKGGDEDKM; FHPDKGGDEDKMK; HPDKGGDEDKMKR; PDKGGDEDKMKRM; DKGGDEDKMKRMN; KGGDEDKMKRMNT; GGDEDKMKRMNTL; GDEDKMKRMNTLY; DEDKMKRMNTLYK; EDKMKRMNTLYKK; DKMKRMNTLYKKM; KMKRMNTLYKKME; MKRMNTLYKKMEQ; KRMNTLYKKMEQD; RMNTLYKKMEQDV; MNTLYKKMEQDVK; NTLYKKMEQDVKV; TLYKKMEQDVKVA; LYKKMEQDVKVAH; YKKMEQDVKVAHQ; KKMEQDVKVAHQP; KMEQDVKVAHQPD; MEQDVKVAHQPDF; EQDVKVAHQPDFG; QDVKVAHQPDFGT; DVKVAHQPDFGTW; VKVAHQPDFGTWS; KVAHQPDFGTWSS; VAHQPDFGTWSSS; AHQPDFGTWSSSE; HQPDFGTWSSSEV; QPDFGTWSSSEVC; PDFGTWSSSEVCA; DFGTWSSSEVCAD; FGTWSSSEVCADF; GTWSSSEVCADFP; TWSSSEVCADFPL; WSSSEVCADFPLC; SSSEVCADFPLCP; SSEVCADFPLCPD; SEVCADFPLCPDT; EVCADFPLCPDTL; VCADFPLCPDTLY; CADFPLCPDTLYC; ADFPLCPDTLYCK; DFPLCPDTLYCKE; FPLCPDTLYCKEW; PLCPDTLYCKEWP; LCPDTLYCKEWPI; CPDTLYCKEWPIC; PDTLYCKEWPICS; DTLYCKEWPICSK; TLYCKEWPICSKK; LYCKEWPICSKKP; YCKEWPICSKKPS; CKEWPICSKKPSV; KEWPICSKKPSVH; EWPICSKKPSVHC; WPICSKKPSVHCP; PICSKKPSVHCPC; ICSKKPSVHCPCM; CSKKPSVHCPCML; SKKPSVHCPCMLC; KKPSVHCPCMLCQ; KPSVHCPCMLCQL; PSVHCPCMLCQLR; SVHCPCMLCQLRL; VHCPCMLCQLRLR; HCPCMLCQLRLRH; CPCMLCQLRLRHL; PCMLCQLRLRHLN; CMLCQLRLRHLNR; MLCQLRLRHLNRK; LCQLRLRHLNRKF; CQLRLRHLNRKFL; QLRLRHLNRKFLR; LRLRHLNRKFLRK; RLRHLNRKFLRKE; LRHLNRKFLRKEP; RHLNRKFLRKEPL; HLNRKFLRKEPLV; LNRKFLRKEPLVW; NRKFLRKEPLVWI; RKFLRKEPLVWID; KFLRKEPLVWIDC; FLRKEPLVWIDCY; LRKEPLVWIDCYC; RKEPLVWIDCYCI; KEPLVWIDCYCID; EPLVWIDCYCIDC; PLVWIDCYCIDCF; LVWIDCYCIDCFT; VWIDCYCIDCFTQ; WIDCYCIDCFTQW; IDCYCIDCFTQWF; DCYCIDCFTQWFG; CYCIDCFTQWFGL; YCIDCFTQWFGLD; CIDCFTQWFGLDL; IDCFTQWFGLDLT; DCFTQWFGLDLTE; CFTQWFGLDLTEE; FTQWFGLDLTEET; TQWFGLDLTEETL; QWFGLDLTEETLQ; WFGLDLTEETLQW; FGLDLTEETLQWW; GLDLTEETLQWWV; LDLTEETLQWWVQ; DLTEETLQWWVQI; LTEETLQWWVQII; TEETLQWWVQIIG; EETLQWWVQIIGE; ETLQWWVQIIGET; TLQWWVQIIGETP; LQWWVQIIGETPF; QWWVQIIGETPFR; WWVQIIGETPFRD; WVQIIGETPFRDL; VQIIGETPFRDLK; QIIGETPFRDLKL; KALSNYFFYRCQP; ALSNYFFYRCQPM; LSNYFFYRCQPME; SNYFFYRCQPMEQ; NYFFYRCQPMEQK; YFFYRCQPMEQKS; FFYRCQPMEQKSG; FYRCQPMEQKSGS; YRCQPMEQKSGSP; RCQPMEQKSGSPG; CQPMEQKSGSPGG; QPMEQKSGSPGGV; PMEQKSGSPGGVP; MEQKSGSPGGVPL; EQKSGSPGGVPLM; QKSGSPGGVPLMK; KSGSPGGVPLMKN; SGSPGGVPLMKNG; GSPGGVPLMKNGM; SPGGVPLMKNGMK; PGGVPLMKNGMKI; GGVPLMKNGMKIY; GVPLMKNGMKIYF; VPLMKNGMKIYFA; PLMKNGMKIYFAM; LMKNGMKIYFAMK; MKNGMKIYFAMKI; KNGMKIYFAMKIC; NGMKIYFAMKICL; GMKIYFAMKICLP; MKIYFAMKICLPV; KIYFAMKICLPVM; IYFAMKICLPVMK; YFAMKICLPVMKK; FAMKICLPVMKKQ; AMKICLPVMKKQQ; MKICLPVMKKQQQ; KICLPVMKKQQQI; ICLPVMKKQQQIL; CLPVMKKQQQILN; LPVMKKQQQILNT; PVMKKQQQILNTQ; VMKKQQQILNTQH; MKKQQQILNTQHH; KKQQQILNTQHHP; KQQQILNTQHHPK; QQQILNTQHHPKK; QQILNTQHHPKKK; QILNTQHHPKKKE; ILNTQHHPKKKER; KTLKTFPLIYTSF; TLKTFPLIYTSFL; LKTFPLIYTSFLV; KTFPLIYTSFLVK; TFPLIYTSFLVKL; FPLIYTSFLVKLY; PLIYTSFLVKLYL; LIYTSFLVKLYLV; IYTSFLVKLYLVI; YTSFLVKLYLVIE;

TSFLVKLYLVIEP; SFLVKLYLVIEPL; FLVKLYLVIEPLP; LVKLYLVIEPLPA;
VKLYLVIEPLPAL; KLYLVIEPLPALL; LYLVIEPLPALLC; YLVIEPLPALLCI;
LVIEPLPALLCIL; VIEPLPALLCILL; IEPLPALLCILLK; EPLPALLCILLKK;
PLPALLCILLKKK; LPALLCILLKKKL; PALLCILLKKKLK; ALLCILLKKKLKF;
LLCILLKKKLKFC; LCILLKKKLKFCI; CILLKKKLKFCIK; ILLKKKLKFCIKN;
LLKKKLKFCIKNL; LKKKLKFCIKNLW; KKKLKFCIKNLWK; KKLKFCIKNLWKN;
KLKFCIKNLWKNI; LKFCIKNLWKNIL; LLLVDTCVLGIIL; LLVDTCVLGIILY;
LVDTCVLGIILYS; VDTCVLGIILYSF; LHIDIEFLQLIIS; HIDIEFLQLIISV;
IDIEFLQLIISVK; DIEFLQLIISVKS; IEFLQLIISVKSC; EFLQLIISVKSCV;
FLQLIISVKSCVP; LQLIISVKSCVPL; QLIISVKSCVPLV; LIISVKSCVPLVF;
FVRVLIRNTYYIV; VRVLIRNTYYIVP; RSMILAQKSLKKQ; SMILAQKSLKKQS;
MILAQKSLKKQSR; ILAQKSLKKQSRC; LAQKSLKKQSRCL; AQKSLKKQSRCLG;
QKSLKKQSRCLGN; RSVKSVRKKTSLI; SVKSVRKKTSLIT; VKSVRKKTSLITL;
KSVRKKTSLITLS; SVRKKTSLITLSI; VRKKTSLITLSIM; RKKTSLITLSIMK;
KKTSLITLSIMKS; KTSLITLSIMKST; TSLITLSIMKSTL; SLITLSIMKSTLQ;
LITLSIMKSTLQM; ITLSIMKSTLQML; TLSIMKSTLQMLL; LSIMKSTLQMLLF;
SIMKSTLQMLLFL; IMKSTLQMLLFLQ; MKSTLQMLLFLQK; KSTLQMLLFLQKV;
STLQMLLFLQKVK; TLQMLLFLQKVKI; LQMLLFLQKVKIK; QMLLFLQKVKIKK;
MLLFLQKVKIKKV; LLFLQKVKIKKVF; LFLQKVKIKKVFV; FLQKVKIKKVFVS;
LQKVKIKKVFVSK; QKVKIKKVFVSKQ; NNIWQVLLGCTVC; NIWQVLLGCTVCY;
IWQVLLGCTVCYL; WQVLLGCTVCYLK; QVLLGCTVCYLKW; VLLGCTVCYLKWI;
LLGCTVCYLKWIL; YLIFCTVLFSMYL; LIFCTVLFSMYLK; IFCTVLFSMYLKE;
FCTVLFSMYLKED; CTVLFSMYLKEDT; TVLFSMYLKEDTG; VLFSMYLKEDTGY;
LFSMYLKEDTGYL; FSMYLKEDTGYLK; SMYLKEDTGYLKV; MYLKEDTGYLKVP;
YLKEDTGYLKVPL; LKEDTGYLKVPLI; KEDTGYLKVPLIV; EDTGYLKVPLIVE;
DTGYLKVPLIVEK; TGYLKVPLIVEKQ; GYLKVPLIVEKQH; KGQELNQRICLQD;
GQELNQRICLQDM; QELNQRICLQDME; TKEPKYFHQAWLQ; MSILSLKPCKLDL;
ENPYKTQSSYLKK; NPYKTQSSYLKKE; PYKTQSSYLKKEF; YKTQSSYLKKEFY;
KTQSSYLKKEFYK; TQSSYLKKEFYKV; QSSYLKKEFYKVE; LILQLIYNLELLN;
ILQLIYNLELLNG; LQLIYNLELLNGR; QLIYNLELLNGRK; LIYNLELLNGRKG;
IYNLELLNGRKGW; YNLELLNGRKGWI; NLELLNGRKGWIL; LELLNGRKGWILR;
NIIYAWGNVFLIL; IIYAWGNVFLILQ; IYAWGNVFLILQE; YAWGNVFLILQEK;
AWGNVFLILQEKR; WGNVFLILQEKRI; GNVFLILQEKRIQ; NVFLILQEKRIQK;
VFLILQEKRIQKL; FLILQEKRIQKLK; LILQEKRIQKLKT; ILQEKRIQKLKTL;
LQEKRIQKLKTLD; QEKRIQKLKTLDM; EKRIQKLKTLDMD; KRIQKLKTLDMDQ;
RIQKLKTLDMDQA; IQKLKTLDMDQAL; QKLKTLDMDQALN; KLKTLDMDQALNP;
LKTLDMDQALNPN; KTLDMDQALNPNH; TLDMDQALNPNHN; LDMDQALNPNHNA;
DMDQALNPNHNAL; MDQALNPNHNALP; DQALNPNHNALPK; QALNPNHNALPKS;
ALNPNHNALPKSQ; LNPNHNALPKSQI; NPNHNALPKSQIL; PNHNALPKSQILQ;
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LPKSQILQPLLKI; PKSQILQPLLKIP; KSQILQPLLKIPK; SQILQPLLKIPKG;
QILQPLLKIPKGQ; ILQPLLKIPKGQT; LQPLLKIPKGQTP; QPLLKIPKGQTPI;
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IPKGQTPIVKSCI; PKGQTPIVKSCIC; KGQTPIVKSCICV; GQTPIVKSCICVK;
QTPIVKSCICVKA; TPIVKSCICVKAF; PIVKSCICVKAFS; IVKSCICVKAFSV;
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ICVKAFSVLKGLK; CVKAFSVLKGLKH; VKAFSVLKGLKHH; KAFSVLKGLKHHP;
AFSVLKGLKHHPQ; FSVLKGLKHHPQN; SVLKGLKHHPQNN; VLKGLKHHPQNNT;
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SLKVAYTKAAFIK; LKVAYTKAAFIKC; KVAYTKAAFIKCI; VAYTKAAFIKCIC;
AYTKAAFIKCICT; YTKAAFIKCICTI; TKAAFIKCICTIK; KAAFIKCICTIKA;
AAFIKCICTIKAP; AFIKCICTIKAPV; SILVCNCPCLSIY; ILVCNCPCLSIYL;
LVCNCPCLSIYLI; VCNCPCLSIYLII; CNCPCLSIYLIIS; NCPCLSIYLIISG;
CPCLSIYLIISGS; PCLSIYLIISGSP; CLSIYLIISGSPG; LSIYLIISGSPGS;
SIYLIISGSPGSL; IYLIISGSPGSLS; YLIISGSPGSLSV; LIISGSPGSLSVP;
IISGSPGSLSVPS; ISGSPGSLSVPSN; SGSPGSLSVPSNT; GSPGSLSVPSNTL;
SPGSLSVPSNTLT; PGSLSVPSNTLTS; GSLSVPSNTLTSS; SLSVPSNTLTSST;

LSVPSNTLTSSTW; SVPSNTLTSSTWD; VPSNTLTSSTWDS; PSNTLTSSTWDSI;
SNTLTSSTWDSIP; NTLTSSTWDSIPY; TLTSSTWDSIPYI; LTSSTWDSIPYIG;
TSSTWDSIPYIGC; SSTWDSIPYIGCP; STWDSIPYIGCPS; TWDSIPYIGCPST;
WDSIPYIGCPSTL; DSIPYIGCPSTLW; SIPYIGCPSTLWV; IPYIGCPSTLWVL;
PYIGCPSTLWVLL; YIGCPSTLWVLLF; IGCPSTLWVLLFI; GCPSTLWVLLFIR;
CPSTLWVLLFIRS; PSTLWVLLFIRSL; STLWVLLFIRSLS; TLWVLLFIRSLSK;
LWVLLFIRSLSKK; WVLLFIRSLSKKE; VLLFIRSLSKKEI; LLFIRSLSKKEIG;
GFFTDLFLRRILK; FFTDLFLRRILKY; FTDLFLRRILKYL; TDLFLRRILKYLA;
DLFLRRILKYLAR; LFLRRILKYLARP; FLRRILKYLARPL; LRRILKYLARPLH;
RRILKYLARPLHC; RILKYLARPLHCC; ILKYLARPLHCCV; LKYLARPLHCCVP;
KYLARPLHCCVPE; YLARPLHCCVPEL; LARPLHCCVPELL; ARPLHCCVPELLV;
RPLHCCVPELLVN; PLHCCVPELLVNR; LHCCVPELLVNRP; HCCVPELLVNRPQ;
CCVPELLVNRPQI; CVPELLVNRPQIS; VPELLVNRPQISA; PELLVNRPQISAA;
ELLVNRPQISAAE; LLVNRPQISAAET; LVNRPQISAAETY; VNRPQISAAETYR;
NRPQISAAETYRL; RPQISAAETYRLS; PQISAAETYRLSA; QISAAETYRLSAL;
ISAAETYRLSALQ; SAAETYRLSALQR; AAETYRLSALQRG; AETYRLSALQRGP;
ETYRLSALQRGPT; TYRLSALQRGPTP; YRLSALQRGPTPC; RLSALQRGPTPCS;
LSALQRGPTPCSS; SALQRGPTPCSSS; ALQRGPTPCSSSN; LQRGPTPCSSSNT;
QRGPTPCSSSNTV; RGPTPCSSSNTVV; GPTPCSSSNTVVA; PTPCSSSNTVVAV;
TPCSSSNTVVAVL; PCSSSNTVVAVLV; CSSSNTVVAVLVT; STGGTFSPPVKVP;
TGGTFSPPVKVPK; GGTFSPPVKVPKY; GTFSPPVKVPKYL; TFSPPVKVPKYLA;
FSPPVKVPKYLAF; SPPVKVPKYLAFS; PPVKVPKYLAFSF; PVKVPKYLAFSFL;
VKVPKYLAFSFLL; KVPKYLAFSFLLG; VPKYLAFSFLLGS; PKYLAFSFLLGSG;
KYLAFSFLLGSGT; YLAFSFLLGSGTQ; LAFSFLLGSGTQH; AFSFLLGSGTQHS;
FSFLLGSGTQHST; SFLLGSGTQHSTG; ALWSVFITWDWAV; LWSVFITWDWAVG;
WSVFITWDWAVGF; SVFITWDWAVGFL; VFITWDWAVGFLG; FITWDWAVGFLGV;
ITWDWAVGFLGVI; TWDWAVGFLGVIV; WDWAVGFLGVIVP; DWAVGFLGVIVPS;
WAVGFLGVIVPSG; AVGFLGVIVPSGY; VGFLGVIVPSGYF; GFLGVIVPSGYFD;
FLGVIVPSGYFDL; FISTPCISKGSPP; ISTPCISKGSPPT; STPCISKGSPPTA;
TPCISKGSPPTAK; PCISKGSPPTAKK; CISKGSPPTAKKW; ISKGSPPTAKKWK;
SKGSPPTAKKWKL; KGSPPTAKKWKLL; GSPPTAKKWKLLP; IGFPPPCSCTFCD;
GFPPPCSCTFCDP; FPPPCSCTFCDPA; RLSMLVIPITSVC; LSMLVIPITSVCT;
SMLVIPITSVCTV; MLVIPITSVCTVT; LVIPITSVCTVTA; VIPITSVCTVTAS;
IPITSVCTVTASH; PITSVCTVTASHI; ITSVCTVTASHIS; TSVCTVTASHISR;
SVCTVTASHISRF; VCTVTASHISRFP; CTVTASHISRFPQ; TVTASHISRFPQV;
VTASHISRFPQVR; TASHISRFPQVRS; ASHISRFPQVRSS; SHISRFPQVRSSF;
HISRFPQVRSSFK; ISRFPQVRSSFKL; SRFPQVRSSFKLG; RFPQVRSSFKLGR;
FPQVRSSFKLGRG; PQVRSSFKLGRGI; QVRSSFKLGRGIL; VRSSFKLGRGILA;
RSSFKLGRGILAV; SSFKLGRGILAVL; QGSIFLSGLSLLK; GSIFLSGLSLLKS;
SIFLSGLSLLKSF; IFLSGLSLLKSFS; FLSGLSLLKSFSA; LSGLSLLKSFSAL;
SGLSLLKSFSALS; GLSLLKSFSALSF; LSLLKSFSALSFR; SLLKSFSALSFRL;
LLKSFSALSFRLK; LKSFSALSFRLKP; KSFSALSFRLKPL; SFSALSFRLKPLR;
FSALSFRLKPLRF; SALSFRLKPLRFS; ALSFRLKPLRFSS; LSFRLKPLRFSSG;
SFRLKPLRFSSGS; FRLKPLRFSSGSP; RLKPLRFSSGSPI; LKPLRFSSGSPIS;
KPLRFSSGSPISG; PLRFSSGSPISGF; LRFSSGSPISGFR; RFSSGSPISGFRK;
FSSGSPISGFRKH; SSGSPISGFRKHS; SGSPISGFRKHST; GSPISGFRKHSTS;
SPISGFRKHSTSV; PISGFRKHSTSVI; ISGFRKHSTSVIA; SGFRKHSTSVIAS;
GFRKHSTSVIAST; FRKHSTSVIASTP; RKHSTSVIASTPV; KHSTSVIASTPVL;
HSTSVIASTPVLT; STSVIASTPVLTS; TSVIASTPVLTSR; SVIASTPVLTSRT;
VIASTPVLTSRTS; IASTPVLTSRTST; ASTPVLTSRTSTP; STPVLTSRTSTPP;
TPVLTSRTSTPPF; PVLTSRTSTPPFI; VLTSRTSTPPFIS; LTSRTSTPPFISS;
TSRTSTPPFISSF; SRTSTPPFISSFG; RTSTPPFISSFGT; TSTPPFISSFGTC;
STPPFISSFGTCT; TPPFISSFGTCTG; PPFISSFGTCTGS; PFISSFGTCTGSF;
FISSFGTCTGSFG; ISSFGTCTGSFGF; SSFGTCTGSFGFL; SFGTCTGSFGFLG;
FGTCTGSFGFLGA; GTCTGSFGFLGAA; TCTGSFGFLGAAP; CTGSFGFLGAAPG;
TGSFGFLGAAPGH; GSFGFLGAAPGHS; SFGFLGAAPGHSP; FGFLGAAPGHSPF;
GFLGAAPGHSPFL; FLGAAPGHSPFLL; LGAAPGHSPFLLV; GAAPGHSPFLLVG;
AAPGHSPFLLVGA; APGHSPFLLVGAI; PGHSPFLLVGAIF; GHSPFLLVGAIFI;
HSPFLLVGAIFIC; SPFLLVGAIFICF; PFLLVGAIFICFK; FLLVGAIFICFKS;

LLVGAIFICFKSR; LVGAIFICFKSRC; VGAIFICFKSRCY; GAIFICFKSRCYS;
AIFICFKSRCYSP; IFICFKSRCYSPV; FICFKSRCYSPVQ; ICFKSRCYSPVQA;
RQHPLRSSSLIST; QHPLRSSSLISTS; HPLRSSSLISTSW; PLRSSSLISTSWG;
LRSSSLISTSWGN; RSSSLISTSWGNS; SSSLISTSWGNSF; SSLISTSWGNSFF;
SLISTSWGNSFFY; LISTSWGNSFFYK; ISTSWGNSFFYKL; STSWGNSFFYKLS;
VHSLCNFFYTVSI; HSLCNFFYTVSII; SLCNFFYTVSIIY; LCNFFYTVSIIYT;
CNFFYTVSIIYTI; NFFYTVSIIYTIS; FFYTVSIIYTISM; FYTVSIIYTISMA;
YTVSIIYTISMAK; TVSIIYTISMAKM; VSIIYTISMAKMY; SIIYTISMAKMYT;
IIYTISMAKMYTG; IYTISMAKMYTGT; YTISMAKMYTGTF; TISMAKMYTGTFP;
ISMAKMYTGTFPF; SMAKMYTGTFPFS; MAKMYTGTFPFSY; AKMYTGTFPFSYL;
KMYTGTFPFSYLS; MYTGTFPFSYLSN; YTGTFPFSYLSNH; GPNRGKIRIILLN;
PNRGKIRIILLNI; NRGKIRIILLNII; RGKIRIILLNIII; GKIRIILLNIIIK;
KIRIILLNIIIKV; IRIILLNIIIKVY; RIILLNIIIKVYR; IILLNIIIKVYRG;
ILLNIIIKVYRGI; LLNIIIKVYRGIY; LNIIIKVYRGIYN; NIIIKVYRGIYNC;
IIIKVYRGIYNCP; IIKVYRGIYNCPG; IKVYRGIYNCPGS; KVYRGIYNCPGSF;
VYRGIYNCPGSFL; YRGIYNCPGSFLQ; RGIYNCPGSFLQK; GIYNCPGSFLQKS;
IYNCPGSFLQKSS; YNCPGSFLQKSSQ; NCPGSFLQKSSQG; CPGSFLQKSSQGV;
PGSFLQKSSQGVS; GSFLQKSSQGVSK; SFLQKSSQGVSKK; FLQKSSQGVSKKS;
LQKSSQGVSKKSF; QKSSQGVSKKSFC; KSSQGVSKKSFCS; SSQGVSKKSFCSS;
SQGVSKKSFCSSL; QGVSKKSFCSSLQ; GVSKKSFCSSLQF; VSKKSFCSSLQFL;
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QSLGNSSKQRRTP; SLGNSSKQRRTPM; LGNSSKQRRTPMP; GNSSKQRRTPMPR;
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IKVLNIINKSIYT; KVLNIINKSIYTR; VLNIINKSIYTRK; LNIINKSIYTRKQ;
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KSIYTRKQNIIVL; SIYTRKQNIIVLI; IYTRKQNIIVLIW; YTRKQNIIVLIWV;
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NIIVLIWVKQFQS; IIVLIWVKQFQSH; IVLIWVKQFQSHA; LLIEAYSGNFVIP;
LIEAYSGNFVIPI; IEAYSGNFVIPII; EAYSGNFVIPIIK; AYSGNFVIPIIKE;
YSGNFVIPIIKEL; SGNFVIPIIKELI; GNFVIPIIKELIP; NFVIPIIKELIPY;
FVIPIIKELIPYL; VIPIIKELIPYLS; SSKPSNSPRSTSN; SKPSNSPRSTSNY;
KPSNSPRSTSNYS; PSNSPRSTSNYSI; SNSPRSTSNYSIC; NSPRSTSNYSICL;
SPRSTSNYSICLR; PRSTSNYSICLRS; GTCYALYSSKGCN; TCYALYSSKGCNL;
CYALYSSKGCNLN; YALYSSKGCNLNF; ALYSSKGCNLNFY; LYSSKGCNLNFYS;
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VVLLFFPSTLSSP; VLLFFPSTLSSPL; LLFFPSTLSSPLQ; LFFPSTLSSPLQN;
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PLQNSSKSSKIKI; LQNSSKSSKIKIK; QNSSKSSKIKIKI; NSSKSSKIKIKIL;
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VPVQVLPTFTEAC; PVQVLPTFTEACR; VQVLPTFTEACRD; QVLPTFTEACRDS;
VLPTFTEACRDSW; LPTFTEACRDSWR; PTFTEACRDSWRR; TFTEACRDSWRRT;
FTEACRDSWRRTM; TEACRDSWRRTMA; EACRDSWRRTMAF; ACRDSWRRTMAFV;
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KTCLSCTFLPEVM; TCLSCTFLPEVMV; CLSCTFLPEVMVW; LSCTFLPEVMVWL;
SCTFLPEVMVWLH; CTFLPEVMVWLHS; TFLPEVMVWLHSM; FLPEVMVWLHSMG;
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MVWLHSMGKQLLP; VWLHSMGKQLLPV; WLHSMGKQLLPVS; LHSMGKQLLPVSH; HSMGKQLLPVSHA; SMGKQLLPVSHAL; MGKQLLPVSHALS; GKQLLPVSHALSF; KQLLPVSHALSFL; QLLPVSHALSFLR; LLPVSHALSFLRS; LPVSHALSFLRSW; PVSHALSFLRSWF; VSHALSFLRSWFG; SHALSFLRSWFGC; HALSFLRSWFGCI; ALSFLRSWFGCIP; LSFLRSWFGCIPL; EAEAASASTLSLK; GLAKLFGEIPILL; LAKLFGEIPILLQ; AKLFGEIPILLQF; KLFGEIPILLQFL; LFGEIPILLQFLQ

14 mers:

MDKVLNREESMELM; DKVLNREESMELMD; KVLNREESMELMDL; VLNREESMELMDLL; LNREESMELMDLLG; NREESMELMDLLGL; REESMELMDLLGLE; EESMELMDLLGLER; ESMELMDLLGLERA; SMELMDLLGLERAA; MELMDLLGLERAAW; ELMDLLGLERAAWG; LMDLLGLERAAWGN; MDLLGLERAAWGNL; DLLGLERAAWGNLP; LLGLERAAWGNLPL; LGLERAAWGNLPLM; GLERAAWGNLPLMR; LERAAWGNLPLMRK; ERAAWGNLPLMRKA; RAAWGNLPLMRKAY; AAWGNLPLMRKAYL; AWGNLPLMRKAYLR; WGNLPLMRKAYLRK; GNLPLMRKAYLRKC; NLPLMRKAYLRKCK; LPLMRKAYLRKCKE; PLMRKAYLRKCKEF; LMRKAYLRKCKEFH; MRKAYLRKCKEFHP; RKAYLRKCKEFHPD; KAYLRKCKEFHPDK; AYLRKCKEFHPDKG; YLRKCKEFHPDKGG; LRKCKEFHPDKGGD; RKCKEFHPDKGGDE; KCKEFHPDKGGDED; CKEFHPDKGGDEDK; KEFHPDKGGDEDKM; EFHPDKGGDEDKMK; FHPDKGGDEDKMKR; HPDKGGDEDKMKRM; PDKGGDEDKMKRMN; DKGGDEDKMKRMNT; KGGDEDKMKRMNTL; GGDEDKMKRMNTLY; GDEDKMKRMNTLYK; DEDKMKRMNTLYKK; EDKMKRMNTLYKKM; DKMKRMNTLYKKME; KMKRMNTLYKKMEQ; MKRMNTLYKKMEQD; KRMNTLYKKMEQDV; RMNTLYKKMEQDVK; MNTLYKKMEQDVKV; NTLYKKMEQDVKVA; TLYKKMEQDVKVAH; LYKKMEQDVKVAHQ; YKKMEQDVKVAHQP; KKMEQDVKVAHQPD; KMEQDVKVAHQPDF; MEQDVKVAHQPDFG; EQDVKVAHQPDFGT; QDVKVAHQPDFGTW; DVKVAHQPDFGTWS; VKVAHQPDFGTWSS; KVAHQPDFGTWSSS; VAHQPDFGTWSSSE; AHQPDFGTWSSSEV; HQPDFGTWSSSEVC; QPDFGTWSSSEVCA; PDFGTWSSSEVCAD; DFGTWSSSEVCADF; FGTWSSSEVCADFP; GTWSSSEVCADFPL; TWSSSEVCADFPLC; WSSSEVCADFPLCP; SSSEVCADFPLCPD; SSEVCADFPLCPDT; SEVCADFPLCPDTL; EVCADFPLCPDTLY; VCADFPLCPDTLYC; CADFPLCPDTLYCK; ADFPLCPDTLYCKE; DFPLCPDTLYCKEW; FPLCPDTLYCKEWP; PLCPDTLYCKEWPI; LCPDTLYCKEWPIC; CPDTLYCKEWPICS; PDTLYCKEWPICSK; DTLYCKEWPICSKK; TLYCKEWPICSKKP; LYCKEWPICSKKPS; YCKEWPICSKKPSV; CKEWPICSKKPSVH; KEWPICSKKPSVHC; EWPICSKKPSVHCP; WPICSKKPSVHCPC; PICSKKPSVHCPCM; ICSKKPSVHCPCML; CSKKPSVHCPCMLC; SKKPSVHCPCMLCQ; KKPSVHCPCMLCQL; KPSVHCPCMLCQLR; PSVHCPCMLCQLRL; SVHCPCMLCQLRLR; VHCPCMLCQLRLRH; HCPCMLCQLRLRHL; CPCMLCQLRLRHLN; PCMLCQLRLRHLNR; CMLCQLRLRHLNRK; MLCQLRLRHLNRKF; LCQLRLRHLNRKFL; CQLRLRHLNRKFLR; QLRLRHLNRKFLRK; LRLRHLNRKFLRKE; RLRHLNRKFLRKEP; LRHLNRKFLRKEPL; RHLNRKFLRKEPLV; HLNRKFLRKEPLVW; LNRKFLRKEPLVWI; NRKFLRKEPLVWID; RKFLRKEPLVWIDC; KFLRKEPLVWIDCY; FLRKEPLVWIDCYC; LRKEPLVWIDCYCI; RKEPLVWIDCYCID; KEPLVWIDCYCIDC; EPLVWIDCYCIDCF; PLVWIDCYCIDCFT; LVWIDCYCIDCFTQ; VWIDCYCIDCFTQW; WIDCYCIDCFTQWF; IDCYCIDCFTQWFG; DCYCIDCFTQWFGL; CYCIDCFTQWFGLD; YCIDCFTQWFGLDL; CIDCFTQWFGLDLT; IDCFTQWFGLDLTE; DCFTQWFGLDLTEE; CFTQWFGLDLTEET; FTQWFGLDLTEETL; TQWFGLDLTEETLQ; QWFGLDLTEETLQW; WFGLDLTEETLQWW; FGLDLTEETLQWWV; GLDLTEETLQWWVQ; LDLTEETLQWWVQI; DLTEETLQWWVQII; LTEETLQWWVQIIG; TEETLQWWVQIIGE; EETLQWWVQIIGET; ETLQWWVQIIGETP; TLQWWVQIIGETPF; LQWWVQIIGETPFR; QWWVQIIGETPFRD;

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SNYFFYRCQPMEQK; NYFFYRCQPMEQKS; YFFYRCQPMEQKSG;
FFYRCQPMEQKSGS; FYRCQPMEQKSGSP; YRCQPMEQKSGSPG;
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GGVPLMKNGMKIYF; GVPLMKNGMKIYFA; VPLMKNGMKIYFAM;
PLMKNGMKIYFAMK; LMKNGMKIYFAMKI; MKNGMKIYFAMKIC;
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FPLIYTSFLVKLYL; PLIYTSFLVKLYLV; LIYTSFLVKLYLVI;
IYTSFLVKLYLVIE; YTSFLVKLYLVIEP; TSFLVKLYLVIEPL;
SFLVKLYLVIEPLP; FLVKLYLVIEPLPA; LVKLYLVIEPLPAL;
VKLYLVIEPLPALL; KLYLVIEPLPALLC; LYLVIEPLPALLCI;
YLVIEPLPALLCIL; LVIEPLPALLCILL; VIEPLPALLCILLK;
IEPLPALLCILLKK; EPLPALLCILLKKK; PLPALLCILLKKKL;
LPALLCILLKKKLK; PALLCILLKKKLKF; ALLCILLKKKLKFC;
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ILLKKKLKFCIKNL; LLKKKLKFCIKNLW; LKKKLKFCIKNLWK;
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DIEFLQLIISVKSC; IEFLQLIISVKSCV; EFLQLIISVKSCVP;
FLQLIISVKSCVPL; LQLIISVKSCVPLV; QLIISVKSCVPLVF;
FVRVLIRNTYYIVP; RSMILAQKSLKKQS; SMILAQKSLKKQSR;
MILAQKSLKKQSRC; ILAQKSLKKQSRCL; LAQKSLKKQSRCLG;
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QVLLGCTVCYLKWI; VLLGCTVCYLKWIL; YLIFCTVLFSMYLK;
LIFCTVLFSMYLKE; IFCTVLFSMYLKED; FCTVLFSMYLKEDT;
CTVLFSMYLKEDTG; TVLFSMYLKEDTGY; VLFSMYLKEDTGYL;
LFSMYLKEDTGYLK; FSMYLKEDTGYLKV; SMYLKEDTGYLKVP;
MYLKEDTGYLKVPL; YLKEDTGYLKVPLI; LKEDTGYLKVPLIV;
KEDTGYLKVPLIVE; EDTGYLKVPLIVEK; DTGYLKVPLIVEKQ;
TGYLKVPLIVEKQH; KGQELNQRICLQDM; GQELNQRICLQDME;
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YKTQSSYLKKEFYK; KTQSSYLKKEFYKV; TQSSYLKKEFYKVE;
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QLIYNLELLNGRKG; LIYNLELLNGRKGW; IYNLELLNGRKGWI;
YNLELLNGRKGWIL; NLELLNGRKGWILR; NIIYAWGNVFLILQ;
IIYAWGNVFLILQE; IYAWGNVFLILQEK; YAWGNVFLILQEKR;

AWGNVFLILQEKRI; WGNVFLILQEKRIQ; GNVFLILQEKRIQK;
NVFLILQEKRIQKL; VFLILQEKRIQKLK; FLILQEKRIQKLKT;
LILQEKRIQKLKTL; ILQEKRIQKLKTLD; LQEKRIQKLKTLDM;
QEKRIQKLKTLDMD; EKRIQKLKTLDMDQ; KRIQKLKTLDMDQA;
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AFSVLKGLKHHPQN; FSVLKGLKHHPQNN; SVLKGLKHHPQNNT;
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QNNTSLKVAYTKAA; NNTSLKVAYTKAAF; NTSLKVAYTKAAFI;
TSLKVAYTKAAFIK; SLKVAYTKAAFIKC; LKVAYTKAAFIKCI;
KVAYTKAAFIKCIC; VAYTKAAFIKCICT; AYTKAAFIKCICTI;
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AAFIKCICTIKAPV; SILVCNCPCLSIYL; ILVCNCPCLSIYLI;
LVCNCPCLSIYLII; VCNCPCLSIYLIIS; CNCPCLSIYLIISG;
NCPCLSIYLIISGS; CPCLSIYLIISGSP; PCLSIYLIISGSPG;
CLSIYLIISGSPGS; LSIYLIISGSPGSL; SIYLIISGSPGSLS;
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IISGSPGSLSVPSN; ISGSPGSLSVPSNT; SGSPGSLSVPSNTL;
GSPGSLSVPSNTLT; SPGSLSVPSNTLTS; PGSLSVPSNTLTSS;
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KTLKTFPLIYTSFLVK; TLKTFPLIYTSFLVKL; LKTFPLIYTSFLVKLY;
KTFPLIYTSFLVKLYL; TFPLIYTSFLVKLYLV; FPLIYTSFLVKLYLVI;
PLIYTSFLVKLYLVIE; LIYTSFLVKLYLVIEP; IYTSFLVKLYLVIEPL;
YTSFLVKLYLVIEPLP; TSFLVKLYLVIEPLPA; SFLVKLYLVIEPLPAL;
FLVKLYLVIEPLPALL; LVKLYLVIEPLPALLC; VKLYLVIEPLPALLCI;
KLYLVIEPLPALLCIL; LYLVIEPLPALLCILL; YLVIEPLPALLCILLK;
LVIEPLPALLCILLKK; VIEPLPALLCILLKKK; IEPLPALLCILLKKKL;
EPLPALLCILLKKKLK; PLPALLCILLKKKLKF; LPALLCILLKKKLKFC;
PALLCILLKKKLKFCI; ALLCILLKKKLKFCIK; LLCILLKKKLKFCIKN;
LCILLKKKLKFCIKNL; CILLKKKLKFCIKNLW; ILLKKKLKFCIKNLWK;
LLKKKLKFCIKNLWKN; LKKKLKFCIKNLWKNI; KKKLKFCIKNLWKNIL;
LLLVDTCVLGIILYSF; LHIDIEFLQLIISVKS; HIDIEFLQLIISVKSC;
IDIEFLQLIISVKSCV; DIEFLQLIISVKSCVP; IEFLQLIISVKSCVPL;
EFLQLIISVKSCVPLV; FLQLIISVKSCVPLVF; RSMILAQKSLKKQSRC;
SMILAQKSLKKQSRCL; MILAQKSLKKQSRCLG; ILAQKSLKKQSRCLGN;
RSVKSVRKKTSLITLS; SVKSVRKKTSLITLSI; VKSVRKKTSLITLSIM;
KSVRKKTSLITLSIMK; SVRKKTSLITLSIMKS; VRKKTSLITLSIMKST;
RKKTSLITLSIMKSTL; KKTSLITLSIMKSTLQ; KTSLITLSIMKSTLQM;
TSLITLSIMKSTLQML; SLITLSIMKSTLQMLL; LITLSIMKSTLQMLLF;
ITLSIMKSTLQMLLFL; TLSIMKSTLQMLLFLQ; LSIMKSTLQMLLFLQK;
SIMKSTLQMLLFLQKV; IMKSTLQMLLFLQKVK; MKSTLQMLLFLQKVKI;
KSTLQMLLFLQKVKIK; STLQMLLFLQKVKIKK; TLQMLLFLQKVKIKKV;
LQMLLFLQKVKIKKVF; QMLLFLQKVKIKKVFV; MLLFLQKVKIKKVFVS;
LLFLQKVKIKKVFVSK; LFLQKVKIKKVFVSKQ; NNIWQVLLGCTVCYLK;
NIWQVLLGCTVCYLKW; IWQVLLGCTVCYLKWI; WQVLLGCTVCYLKWIL;
YLIFCTVLFSMYLKED; LIFCTVLFSMYLKEDT; IFCTVLFSMYLKEDTG;
FCTVLFSMYLKEDTGY; CTVLFSMYLKEDTGYL; TVLFSMYLKEDTGYLK;
VLFSMYLKEDTGYLKV; LFSMYLKEDTGYLKVP; FSMYLKEDTGYLKVPL;
SMYLKEDTGYLKVPLI; MYLKEDTGYLKVPLIV; YLKEDTGYLKVPLIVE;
LKEDTGYLKVPLIVEK; KEDTGYLKVPLIVEKQ; EDTGYLKVPLIVEKQH;
ENPYKTQSSYLKKEFY; NPYKTQSSYLKKEFYK; PYKTQSSYLKKEFYKV;
YKTQSSYLKKEFYKVE; LILQLIYNLELLNGRK; ILQLIYNLELLNGRKG;

LQLIYNLELLNGRKGW; QLIYNLELLNGRKGWI; LIYNLELLNGRKGWIL;
IYNLELLNGRKGWILR; NIIYAWGNVFLILQEK; IIYAWGNVFLILQEKR;
IYAWGNVFLILQEKRI; YAWGNVFLILQEKRIQ; AWGNVFLILQEKRIQK;
WGNVFLILQEKRIQKL; GNVFLILQEKRIQKLK; NVFLILQEKRIQKLKT;
VFLILQEKRIQKLKTL; FLILQEKRIQKLKTLD; LILQEKRIQKLKTLDM;
ILQEKRIQKLKTLDMD; LQEKRIQKLKTLDMDQ; QEKRIQKLKTLDMDQA;
EKRIQKLKTLDMDQAL; KRIQKLKTLDMDQALN; RIQKLKTLDMDQALNP;
IQKLKTLDMDQALNPN; QKLKTLDMDQALNPNH; KLKTLDMDQALNPNHN;
LKTLDMDQALNPNHNA; KTLDMDQALNPNHNAL; TLDMDQALNPNHNALP;
LDMDQALNPNHNALPK; DMDQALNPNHNALPKS; MDQALNPNHNALPKSQ;
DQALNPNHNALPKSQI; QALNPNHNALPKSQIL; ALNPNHNALPKSQILQ;
LNPNHNALPKSQILQP; NPNHNALPKSQILQPL; PNHNALPKSQILQPLL;
NHNALPKSQILQPLLK; HNALPKSQILQPLLKI; NALPKSQILQPLLKIP;
ALPKSQILQPLLKIPK; LPKSQILQPLLKIPKG; PKSQILQPLLKIPKGQ;
KSQILQPLLKIPKGQT; SQILQPLLKIPKGQTP; QILQPLLKIPKGQTPI;
ILQPLLKIPKGQTPIV; LQPLLKIPKGQTPIVK; QPLLKIPKGQTPIVKS;
PLLKIPKGQTPIVKSC; LLKIPKGQTPIVKSCI; LKIPKGQTPIVKSCIC;
KIPKGQTPIVKSCICV; IPKGQTPIVKSCICVK; PKGQTPIVKSCICVKA;
KGQTPIVKSCICVKAF; GQTPIVKSCICVKAFS; QTPIVKSCICVKAFSV;
TPIVKSCICVKAFSVL; PIVKSCICVKAFSVLK; IVKSCICVKAFSVLKG;
VKSCICVKAFSVLKGL; KSCICVKAFSVLKGLK; SCICVKAFSVLKGLKH;
CICVKAFSVLKGLKHH; ICVKAFSVLKGLKHHP; CVKAFSVLKGLKHHPQ;
VKAFSVLKGLKHHPQN; KAFSVLKGLKHHPQNN; AFSVLKGLKHHPQNNT;
FSVLKGLKHHPQNNTS; SVLKGLKHHPQNNTSL; VLKGLKHHPQNNTSLK;
LKGLKHHPQNNTSLKV; KGLKHHPQNNTSLKVA; GLKHHPQNNTSLKVAY;
LKHHPQNNTSLKVAYT; KHHPQNNTSLKVAYTK; HHPQNNTSLKVAYTKA;
HPQNNTSLKVAYTKAA; PQNNTSLKVAYTKAAF; QNNTSLKVAYTKAAFI;
NNTSLKVAYTKAAFIK; NTSLKVAYTKAAFIKC; TSLKVAYTKAAFIKCI;
SLKVAYTKAAFIKCIC; LKVAYTKAAFIKCICT; KVAYTKAAFIKCICTI;
VAYTKAAFIKCICTIK; AYTKAAFIKCICTIKA; YTKAAFIKCICTIKAP;
TKAAFIKCICTIKAPV; SILVCNCPCLSIYLII; ILVCNCPCLSIYLIIS;
LVCNCPCLSIYLIISG; VCNCPCLSIYLIISGS; CNCPCLSIYLIISGSP;
NCPCLSIYLIISGSPG; CPCLSIYLIISGSPGS; PCLSIYLIISGSPGSL;
CLSIYLIISGSPGSLS; LSIYLIISGSPGSLSV; SIYLIISGSPGSLSVP;
IYLIISGSPGSLSVPS; YLIISGSPGSLSVPSN; LIISGSPGSLSVPSNT;
IISGSPGSLSVPSNTL; ISGSPGSLSVPSNTLT; SGSPGSLSVPSNTLTS;
GSPGSLSVPSNTLTSS; SPGSLSVPSNTLTSST; PGSLSVPSNTLTSSTW;
GSLSVPSNTLTSSTWD; SLSVPSNTLTSSTWDS; LSVPSNTLTSSTWDSI;
SVPSNTLTSSTWDSIP; VPSNTLTSSTWDSIPY; PSNTLTSSTWDSIPYI;
SNTLTSSTWDSIPYIG; NTLTSSTWDSIPYIGC; TLTSSTWDSIPYIGCP;
LTSSTWDSIPYIGCPS; TSSTWDSIPYIGCPST; SSTWDSIPYIGCPSTL;
STWDSIPYIGCPSTLW; TWDSIPYIGCPSTLWV; WDSIPYIGCPSTLWVL;
DSIPYIGCPSTLWVLL; SIPYIGCPSTLWVLLF; IPYIGCPSTLWVLLFI;
PYIGCPSTLWVLLFIR; YIGCPSTLWVLLFIRS; IGCPSTLWVLLFIRSL;
GCPSTLWVLLFIRSLS; CPSTLWVLLFIRSLSK; PSTLWVLLFIRSLSKK;
STLWVLLFIRSLSKKE; TLWVLLFIRSLSKKEI; LWVLLFIRSLSKKEIG;
GFFTDLFLRRILKYLA; FFTDLFLRRILKYLAR; FTDLFLRRILKYLARP;
TDLFLRRILKYLARPL; DLFLRRILKYLARPLH; LFLRRILKYLARPLHC;
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KYLARPLHCCVPELLV; YLARPLHCCVPELLVN; LARPLHCCVPELLVNR;
ARPLHCCVPELLVNRP; RPLHCCVPELLVNRPQ; PLHCCVPELLVNRPQI;
LHCCVPELLVNRPQIS; HCCVPELLVNRPQISA; CCVPELLVNRPQISAA;
CVPELLVNRPQISAAE; VPELLVNRPQISAAET; PELLVNRPQISAAETY;
ELLVNRPQISAAETYR; LLVNRPQISAAETYRL; LVNRPQISAAETYRLS;
VNRPQISAAETYRLSA; NRPQISAAETYRLSAL; RPQISAAETYRLSALQ;
PQISAAETYRLSALQR; QISAAETYRLSALQRG; ISAAETYRLSALQRGP;
SAAETYRLSALQRGPT; AAETYRLSALQRGPTP; AETYRLSALQRGPTPC;
ETYRLSALQRGPTPCS; TYRLSALQRGPTPCSS; YRLSALQRGPTPCSSS;

RLSALQRGPTPCSSSN; LSALQRGPTPCSSSNT; SALQRGPTPCSSSNTV;
ALQRGPTPCSSSNTVV; LQRGPTPCSSSNTVVA; QRGPTPCSSSNTVVAV;
RGPTPCSSSNTVVAVL; GPTPCSSSNTVVAVLV; PTPCSSSNTVVAVLVT;
STGGTFSPPVKVPKYL; TGGTFSPPVKVPKYLA; GGTFSPPVKVPKYLAF;
GTFSPPVKVPKYLAFS; TFSPPVKVPKYLAFSF; FSPPVKVPKYLAFSFL;
SPPVKVPKYLAFSFLL; PPVKVPKYLAFSFLLG; PVKVPKYLAFSFLLGS;
VKVPKYLAFSFLLGSG; KVPKYLAFSFLLGSGT; VPKYLAFSFLLGSGTQ;
PKYLAFSFLLGSGTQH; KYLAFSFLLGSGTQHS; YLAFSFLLGSGTQHST;
LAFSFLLGSGTQHSTG; ALWSVFITWDWAVGFL; LWSVFITWDWAVGFLG;
WSVFITWDWAVGFLGV; SVFITWDWAVGFLGVI; VFITWDWAVGFLGVIV;
FITWDWAVGFLGVIVP; ITWDWAVGFLGVIVPS; TWDWAVGFLGVIVPSG;
WDWAVGFLGVIVPSGY; DWAVGFLGVIVPSGYF; WAVGFLGVIVPSGYFD;
AVGFLGVIVPSGYFDL; FISTPCISKGSPPTAK; ISTPCISKGSPPTAKK;
STPCISKGSPPTAKKW; TPCISKGSPPTAKKWK; PCISKGSPPTAKKWKL;
CISKGSPPTAKKWKLL; ISKGSPPTAKKWKLLP; RLSMLVIPITSVCTVT;
LSMLVIPITSVCTVTA; SMLVIPITSVCTVTAS; MLVIPITSVCTVTASH;
LVIPITSVCTVTASHI; VIPITSVCTVTASHIS; IPITSVCTVTASHISR;
PITSVCTVTASHISRF; ITSVCTVTASHISRFP; TSVCTVTASHISRFPQ;
SVCTVTASHISRFPQV; VCTVTASHISRFPQVR; CTVTASHISRFPQVRS;
TVTASHISRFPQVRSS; VTASHISRFPQVRSSF; TASHISRFPQVRSSFK;
ASHISRFPQVRSSFKL; SHISRFPQVRSSFKLG; HISRFPQVRSSFKLGR;
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FPQVRSSFKLGRGILA; PQVRSSFKLGRGILAV; QVRSSFKLGRGILAVL;
QGSIFLSGLSLLKSFS; GSIFLSGLSLLKSFSA; SIFLSGLSLLKSFSAL;
IFLSGLSLLKSFSALS; FLSGLSLLKSFSALSF; LSGLSLLKSFSALSFR;
SGLSLLKSFSALSFRL; GLSLLKSFSALSFRLK; LSLLKSFSALSFRLKP;
SLLKSFSALSFRLKPL; LLKSFSALSFRLKPLR; LKSFSALSFRLKPLRF;
KSFSALSFRLKPLRFS; SFSALSFRLKPLRFSS; FSALSFRLKPLRFSSG;
SALSFRLKPLRFSSGS; ALSFRLKPLRFSSGSP; LSFRLKPLRFSSGSPI;
SFRLKPLRFSSGSPIS; FRLKPLRFSSGSPISG; RLKPLRFSSGSPISGF;
LKPLRFSSGSPISGFR; KPLRFSSGSPISGFRK; PLRFSSGSPISGFRKH;
LRFSSGSPISGFRKHS; RFSSGSPISGFRKHST; FSSGSPISGFRKHSTS;
SSGSPISGFRKHSTSV; SGSPISGFRKHSTSVI; GSPISGFRKHSTSVIA;
SPISGFRKHSTSVIAS; PISGFRKHSTSVIAST; ISGFRKHSTSVIASTP;
SGFRKHSTSVIASTPV; GFRKHSTSVIASTPVL; FRKHSTSVIASTPVLT;
RKHSTSVIASTPVLTS; KHSTSVIASTPVLTSR; HSTSVIASTPVLTSRT;
STSVIASTPVLTSRTS; TSVIASTPVLTSRTST; SVIASTPVLTSRTSTP;
VIASTPVLTSRTSTPP; IASTPVLTSRTSTPPF; ASTPVLTSRTSTPPFI;
STPVLTSRTSTPPFIS; TPVLTSRTSTPPFISS; PVLTSRTSTPPFISSF;
VLTSRTSTPPFISSFG; LTSRTSTPPFISSFGT; TSRTSTPPFISSFGTC;
SRTSTPPFISSFGTCT; RTSTPPFISSFGTCTG; TSTPPFISSFGTCTGS;
STPPFISSFGTCTGSF; TPPFISSFGTCTGSFG; PPFISSFGTCTGSFGF;
PFISSFGTCTGSFGFL; FISSFGTCTGSFGFLG; ISSFGTCTGSFGFLGA;
SSFGTCTGSFGFLGAA; SFGTCTGSFGFLGAAP; FGTCTGSFGFLGAAPG;
GTCTGSFGFLGAAPGH; TCTGSFGFLGAAPGHS; CTGSFGFLGAAPGHSP;
TGSFGFLGAAPGHSPF; GSFGFLGAAPGHSPFL; SFGFLGAAPGHSPFLL;
FGFLGAAPGHSPFLLV; GFLGAAPGHSPFLLVG; FLGAAPGHSPFLLVGA;
LGAAPGHSPFLLVGAI; GAAPGHSPFLLVGAIF; AAPGHSPFLLVGAIFI;
APGHSPFLLVGAIFIC; PGHSPFLLVGAIFICF; GHSPFLLVGAIFICFK;
HSPFLLVGAIFICFKS; SPFLLVGAIFICFKSR; PFLLVGAIFICFKSRC;
FLLVGAIFICFKSRCY; LLVGAIFICFKSRCYS; LVGAIFICFKSRCYSP;
VGAIFICFKSRCYSPV; GAIFICFKSRCYSPVQ; AIFICFKSRCYSPVQA;
RQHPLRSSSLISTSWG; QHPLRSSSLISTSWGN; HPLRSSSLISTSWGNS;
PLRSSSLISTSWGNSF; LRSSSLISTSWGNSFF; RSSSLISTSWGNSFFY;
SSSLISTSWGNSFFYK; SSLISTSWGNSFFYKL; SLISTSWGNSFFYKLS;
VHSLCNFFYTVSIIYT; HSLCNFFYTVSIIYTI; SLCNFFYTVSIIYTIS;
LCNFFYTVSIIYTISM; CNFFYTVSIIYTISMA; NFFYTVSIIYTISMAK;
FFYTVSIIYTISMAKM; FYTVSIIYTISMAKMY; YTVSIIYTISMAKMYT;
TVSIIYTISMAKMYTG; VSIIYTISMAKMYTGT; SIIYTISMAKMYTGTF;

IIYTISMAKMYTGTFP; IYTISMAKMYTGTFPF; YTISMAKMYTGTFPFS;
TISMAKMYTGTFPFSY; ISMAKMYTGTFPFSYL; SMAKMYTGTFPFSYLS;
MAKMYTGTFPFSYLSN; AKMYTGTFPFSYLSNH; GPNRGKIRIILLNIII;
PNRGKIRIILLNIIIK; NRGKIRIILLNIIIKV; RGKIRIILLNIIIKVY;
GKIRIILLNIIIKVYR; KIRIILLNIIIKVYRG; IRIILLNIIIKVYRGI;
RIILLNIIIKVYRGIY; IILLNIIIKVYRGIYN; ILLNIIIKVYRGIYNC;
LLNIIIKVYRGIYNCP; LNIIIKVYRGIYNCPG; NIIIKVYRGIYNCPGS;
IIIKVYRGIYNCPGSF; IIKVYRGIYNCPGSFL; IKVYRGIYNCPGSFLQ;
KVYRGIYNCPGSFLQK; VYRGIYNCPGSFLQKS; YRGIYNCPGSFLQKSS;
RGIYNCPGSFLQKSSQ; GIYNCPGSFLQKSSQG; IYNCPGSFLQKSSQGV;
YNCPGSFLQKSSQGVS; NCPGSFLQKSSQGVSK; CPGSFLQKSSQGVSKK;
PGSFLQKSSQGVSKKS; GSFLQKSSQGVSKKSF; SFLQKSSQGVSKKSFC;
FLQKSSQGVSKKSFCS; LQKSSQGVSKKSFCSS; QKSSQGVSKKSFCSSL;
KSSQGVSKKSFCSSLQ; SSQGVSKKSFCSSLQF; SQGVSKKSFCSSLQFL;
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RYIIPNNMPQSLGNSS; YIIPNNMPQSLGNSSK; IIPNNMPQSLGNSSKQ;
IPNNMPQSLGNSSKQR; PNNMPQSLGNSSKQRR; NNMPQSLGNSSKQRRT;
NMPQSLGNSSKQRRTP; MPQSLGNSSKQRRTPM; PQSLGNSSKQRRTPMP;
QSLGNSSKQRRTPMPR; SLGNSSKQRRTPMPRI; LGNSSKQRRTPMPRIK;
GNSSKQRRTPMPRIKV; NSSKQRRTPMPRIKVL; SSKQRRTPMPRIKVLN;
SKQRRTPMPRIKVLNI; KQRRTPMPRIKVLNII; QRRTPMPRIKVLNIIN;
RRTPMPRIKVLNIINK; RTPMPRIKVLNIINKS; TPMPRIKVLNIINKSI;
PMPRIKVLNIINKSIY; MPRIKVLNIINKSIYT; PRIKVLNIINKSIYTR;
RIKVLNIINKSIYTRK; IKVLNIINKSIYTRKQ; KVLNIINKSIYTRKQN;
VLNIINKSIYTRKQNI; LNIINKSIYTRKQNII; NIINKSIYTRKQNIIV;
IINKSIYTRKQNIIVL; INKSIYTRKQNIIVLI; NKSIYTRKQNIIVLIW;
KSIYTRKQNIIVLIWV; SIYTRKQNIIVLIWVK; IYTRKQNIIVLIWVKQ;
YTRKQNIIVLIWVKQF; TRKQNIIVLIWVKQFQ; RKQNIIVLIWVKQFQS;
KQNIIVLIWVKQFQSH; QNIIVLIWVKQFQSHA; LLIEAYSGNFVIPIIK;
LIEAYSGNFVIPIIKE; IEAYSGNFVIPIIKEL; EAYSGNFVIPIIKELI;
AYSGNFVIPIIKELIP; YSGNFVIPIIKELIPY; SGNFVIPIIKELIPYL;
GNFVIPIIKELIPYLS; SSKPSNSPRSTSNYSI; SKPSNSPRSTSNYSIC;
KPSNSPRSTSNYSICL; PSNSPRSTSNYSICLR; SNSPRSTSNYSICLRS;
GTCYALYSSKGCNLNF; TCYALYSSKGCNLNFY; CYALYSSKGCNLNFYS;
YALYSSKGCNLNFYSS; ALYSSKGCNLNFYSSS; LYSSKGCNLNFYSSSS;
YSSKGCNLNFYSSSSL; SSKGCNLNFYSSSSLP; SKGCNLNFYSSSSLPS;
KGCNLNFYSSSSLPSS; GCNLNFYSSSSLPSSN; CNLNFYSSSSLPSSNF;
NLNFYSSSSLPSSNFS; LNFYSSSSLPSSNFSH; SSTHEPGNTKKKGLLT;
ESFTESFTAGKAVVLL; SFTESFTAGKAVVLLF; FTESFTAGKAVVLLFF;
TESFTAGKAVVLLFFP; ESFTAGKAVVLLFFPS; SFTAGKAVVLLFFPST;
FTAGKAVVLLFFPSTL; TAGKAVVLLFFPSTLS; AGKAVVLLFFPSTLSS;
GKAVVLLFFPSTLSSP; KAVVLLFFPSTLSSPL; AVVLLFFPSTLSSPLQ;
VVLLFFPSTLSSPLQN; VLLFFPSTLSSPLQNS; LLFFPSTLSSPLQNSS;
LFFPSTLSSPLQNSSK; FFPSTLSSPLQNSSKS; FPSTLSSPLQNSSKSS;
PSTLSSPLQNSSKSSK; STLSSPLQNSSKSSKI; TLSSPLQNSSKSSKIK;
LSSPLQNSSKSSKIKI; SSPLQNSSKSSKIKIK; SPLQNSSKSSKIKIKI;
PLQNSSKSSKIKIKIL; ALFFVPVQVLPTFTEA; LFFVPVQVLPTFTEAC;
FFVPVQVLPTFTEACR; FVPVQVLPTFTEACRD; VPVQVLPTFTEACRDS;
PVQVLPTFTEACRDSW; VQVLPTFTEACRDSWR; QVLPTFTEACRDSWRR;
VLPTFTEACRDSWRRT; LPTFTEACRDSWRRTM; PTFTEACRDSWRRTMA;
TFTEACRDSWRRTMAF; FTEACRDSWRRTMAFV; TEACRDSWRRTMAFVQ;
EACRDSWRRTMAFVQF; ACRDSWRRTMAFVQFN; CRDSWRRTMAFVQFNW;
RDSWRRTMAFVQFNWG; DSWRRTMAFVQFNWGQ; SWRRTMAFVQFNWGQG;
WRRTMAFVQFNWGQGQ; RRTMAFVQFNWGQGQD; RTMAFVQFNWGQGQDS;
ARKTCLSCTFLPEVMV; RKTCLSCTFLPEVMVW; KTCLSCTFLPEVMVWL;
TCLSCTFLPEVMVWLH; CLSCTFLPEVMVWLHS; LSCTFLPEVMVWLHSM;
SCTFLPEVMVWLHSMG; CTFLPEVMVWLHSMGK; TFLPEVMVWLHSMGKQ;
FLPEVMVWLHSMGKQL; LPEVMVWLHSMGKQLL; PEVMVWLHSMGKQLLP;
EVMVWLHSMGKQLLPV; VMVWLHSMGKQLLPVS; MVWLHSMGKQLLPVSH;

VWLHSMGKQLLPVSHA; WLHSMGKQLLPVSHAL; LHSMGKQLLPVSHALS;
HSMGKQLLPVSHALSF; SMGKQLLPVSHALSFL; MGKQLLPVSHALSFLR;
GKQLLPVSHALSFLRS; KQLLPVSHALSFLRSW; QLLPVSHALSFLRSWF;
LLPVSHALSFLRSWFG; LPVSHALSFLRSWFGC; PVSHALSFLRSWFGCI;
VSHALSFLRSWFGCIP; SHALSFLRSWFGCIPL; GLAKLFGEIPILLQFL;
LAKLFGEIPILLQFLQ

BK virus reverse reading frame 2

13 mers:
WIKFLTGKNPWSS; IKFLTGKNPWSSW; KFLTGKNPWSSWT; FLTGKNPWSSWTF;
GSVRNFTLTKGAT; SVRNFTLTKGATR; VRNFTLTKGATRI; RNFTLTKGATRIK;
LISLILEPGVAQR; ISLILEPGVAQRF; SLILEPGVAQRFV; LILEPGVAQRFVL;
ILEPGVAQRFVLI; LEPGVAQRFVLIF; EPGVAQRFVLIFL; PGVAQRFVLIFLF;
GVAQRFVLIFLFA; VAQRFVLIFLFAQ; AQRFVLIFLFAQI; QRFVLIFLFAQIP;
RFVLIFLFAQIPC; FVLIFLFAQIPCT; VLIFLFAQIPCTA; LIFLFAQIPCTAR;
IFLFAQIPCTARN; FLFAQIPCTARNG; LFAQIPCTARNGL; FAQIPCTARNGLF;
AQIPCTARNGLFV; QIPCTARNGLFVP; IPCTARNGLFVPK; PCTARNGLFVPKS;
CTARNGLFVPKSL; TARNGLFVPKSLL; ARNGLFVPKSLLC; RNGLFVPKSLLCT;
NGLFVPKSLLCTA; GLFVPKSLLCTAL; LFVPKSLLCTALA; FVPKSLLCTALAC;
VPKSLLCTALACY; PKSLLCTALACYV; KSLLCTALACYVS; SLLCTALACYVSL;
LLCTALACYVSLD; IATALTASHSGLA; VIIFFIGANLWNR; IIFFIGANLWNRR;
IFFIGANLWNRRV; FFIGANLWNRRVG; FIGANLWNRRVGV; IGANLWNRRVGVL;
GANLWNRRVGVLV; ANLWNRRVGVLVE; NLWNRRVGVLVEF; LWNRRVGVLVEFL;
RSNSRFSTLNTTQ; SNSRFSTLNTTQK; NSRFSTLNTTQKK; SRFSTLNTTQKKK;
RFSTLNTTQKKKK; FSTLNTTQKKKKG; STLNTTQKKKKGR; TLNTTQKKKKGRR;
LNTTQKKKKGRRP; RSIPYYRRKHSRG; SIPYYRRKHSRGL; IPYYRRKHSRGLK;
PYYRRKHSRGLKG; YYRRKHSRGLKGA; GCVFIIRYVFRIS; CVFIIRYVFRISI;
VFIIRYVFRISIQ; FIIRYVFRISIQC; IIRYVFRISIQCR; IRYVFRISIQCRG;
RYVFRISIQCRGV; KSKKYLSASSRYS; SKKYLSASSRYSF; KKYLSASSRYSFS;
KKSRYPSYDQGRN; KSRYPSYDQGRNA; SRYPSYDQGRNAN; RYPSYDQGRNANR;
YPSYDQGRNANRK; PSYDQGRNANRKI; SYDQGRNANRKIQ; YDQGRNANRKIQS;
DQGRNANRKIQSY; QGRNANRKIQSYI; GRNANRKIQSYIR; NGFNIWSSWKCCT;
GFNIWSSWKCCTR; FNIWSSWKCCTRT; NIWSSWKCCTRTI; IWSSWKCCTRTIY;
WSSWKCCTRTIYG; SSWKCCTRTIYGR; SWKCCTRTIYGRC; WKCCTRTIYGRCC;
KCCTRTIYGRCCL; CCTRTIYGRCCLA; CTRTIYGRCCLAA; TRTIYGRCCLAAL;
RTIYGRCCLAALF; TIYGRCCLAALFA; IYGRCCLAALFAT; WKNNTSCRVIRFV;
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FRTWNKQFRQFER; RTWNKQFRQFERL; TWNKQFRQFERLF; WNKQFRQFERLFR;
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KFRKETFKQKNPN; FRKETFKQKNPNI; RKETFKQKNPNIS; KETFKQKNPNIST;
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PITMLFPSLRYFS; ITMLFPSLRYFSP; TMLFPSLRYFSPC; KWLIQKQHLLNVY;
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IVPVCQYILSYLG; VPVCQYILSYLGP; PVCQYILSYLGPL; VCQYILSYLGPLE;
CQYILSYLGPLEV; QYILSYLGPLEVF; YILSYLGPLEVFL; ILSYLGPLEVFLC;
LSYLGPLEVFLCH; SYLGPLEVFLCHQ; YLGPLEVFLCHQT; LGPLEVFLCHQTP;
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GKDSLQIFFSGGS; NILQGLSTVVFQS; ILQGLSTVVFQSC; TGHKYQQLKHTGY;
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GAIVFSINSPECT; AIVFSINSPECTL; IVFSINSPECTLC; FLKSILCVTSSIL;
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LCVTSSILSASSI; CVTSSILSASSIL; VWPKCTRVPSLSA; WPKCTRVPSLSAT;
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AANPAIAPGAPAI; ANPAIAPGAPAIT; NPAIAPGAPAITA; PAIAPGAPAITAY;
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PIAAIASEVLVMP; IAAIASEVLVMPS; AAIASEVLVMPST; AIASEVLVMPSTV;
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VLVMPSTVARDAI; TSIAAAASPAAIS; SIAAAASPAAISA; IAAAASPAAISAT;
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ISATENPVAAAAS; SATENPVAAAASD; ATENPVAAAASDT; TENPVAAAASDTL;
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LGPSSYASRAGVTV; GPSSYASRAGVTVP; PSSYASRAGVTVPY;
SSYASRAGVTVPYR; SYASRAGVTVPYRP; YASRAGVTVPYRPR;
ASRAGVTVPYRPRS; SRAGVTVPYRPRSK; RAGVTVPYRPRSKG;
AGVTVPYRPRSKGN; GVTVPYRPRSKGNI; VTVPYRPRSKGNIH;
LAPPGAIVFSINSP; APPGAIVFSINSPE; PPGAIVFSINSPEC;
PGAIVFSINSPECT; GAIVFSINSPECTL; AIVFSINSPECTLC;
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SILCVTSSILSASS; ILCVTSSILSASSI; LCVTSSILSASSIL;
VWPKCTRVPSLSAT; WPKCTRVPSLSATC; PKCTRVPSLSATCL;
KCTRVPSLSATCLT; CTRVPSLSATCLTI; TRVPSLSATCLTIE;
RVPSLSATCLTIEG; VPSLSATCLTIEGL; PSLSATCLTIEGLI;
SLSATCLTIEGLIG; LSATCLTIEGLIGE; SATCLTIEGLIGER;
ATCLTIEGLIGERS; TCLTIEGLIGERSE; KFIGAFTIVQVVSS;
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IVQVVSSKNLAKES; VQVVSSKNLAKESL; QVVSSKNLAKESLK;
VVSSKNLAKESLKN; VSSKNLAKESLKNL; SSKNLAKESLKNLS;
SKNLAKESLKNLSV; KNLAKESLKNLSVL; NLAKESLKNLSVLL;
LAKESLKNLSVLLC; AKESLKNLSVLLCN; KESLKNLSVLLCNS;
ESLKNLSVLLCNSC; SLKNLSVLLCNSCE; LKNLSVLLCNSCEV;
KNLSVLLCNSCEVI; NLSVLLCNSCEVIE; LSVLLCNSCEVIEG;
SVLLCNSCEVIEGI; VLLCNSCEVIEGIS; LLCNSCEVIEGISS;
LCNSCEVIEGISSL; CNSCEVIEGISSLI; NSCEVIEGISSLIT;
SCEVIEGISSLITC; CEVIEGISSLITCH; EVIEGISSLITCHK;
VIEGISSLITCHKA; IEGISSLITCHKAW; EGISSLITCHKAWE;
GISSLITCHKAWEI; ISSLITCHKAWEIV; SSLITCHKAWEIVA;
SLITCHKAWEIVAN; LITCHKAWEIVANK; ITCHKAWEIVANKE;
TCHKAWEIVANKEG; CHKAWEIVANKEGP; HKAWEIVANKEGPQ;
KAWEIVANKEGPQC; AWEIVANKEGPQCL; WEIVANKEGPQCLG;
EIVANKEGPQCLGS; IVANKEGPQCLGSR; VANKEGPQCLGSRY;
ILLTKVFTPGNRIS; YSSGLNNSKAMPDC; IKAANPAIAPGAPA;

KAANPAIAPGAPAI; AANPAIAPGAPAIT; ANPAIAPGAPAITA;
NPAIAPGAPAITAY; PAIAPGAPAITAYV; GVRPIAAIASEVLV;
VRPIAAIASEVLVM; RPIAAIASEVLVMP; PIAAIASEVLVMPS;
IAAIASEVLVMPST; AAIASEVLVMPSTV; AIASEVLVMPSTVA;
IASEVLVMPSTVAR; ASEVLVMPSTVARD; SEVLVMPSTVARDA;
EVLVMPSTVARDAI; TSIAAAASPAAISA; SIAAAASPAAISAT;
IAAAASPAAISATE; AAAASPAAISATEN; AAASPAAISATENP;
AASPAAISATENPV; ASPAAISATENPVA; SPAAISATENPVAA;
PAAISATENPVAAA; AAISATENPVAAAA; AISATENPVAAAAS;
ISATENPVAAAASD; SATENPVAAAASDT; ATENPVAAAASDTL;
TENPVAAAASDTLA; ENPVAAAASDTLAT; NPVAAAASDTLATR;
PVAAAASDTLATRS; VAAAASDTLATRSP; AAAASDTLATRSPK;
AAASDTLATRSPKS; AASDTLATRSPKSA; ASDTLATRSPKSAR;
SDTLATRSPKSARA; DTLATRSPKSARAA; TLATRSPKSARAAP;
LATRSPKSARAAPM; ATRSPKSARAAPMN; TRSPKSARAAPMNL;
RSPKSARAAPMNLE; SPKSARAAPMNLEI; PKSARAAPMNLEIQ;
KSARAAPMNLEIQK; SARAAPMNLEIQKK; ARAAPMNLEIQKKR;
RAAPMNLEIQKKRD; AAPMNLEIQKKRDY; APMNLEIQKKRDYL;
PMNLEIQKKRDYLP; MNLEIQKKRDYLPR; NLEIQKKRDYLPRS;
LEIQKKRDYLPRSL; EIQKKRDYLPRSLL; IQKKRDYLPRSLLQ;
QKKRDYLPRSLLQS; KKRDYLPRSLLQSL; KRDYLPRSLLQSLL;
RDYLPRSLLQSLLQ; DYLPRSLLQSLLQQ; YLPRSLLQSLLQQV;
LPRSLLQSLLQQVK; PRSLLQSLLQQVKQ; RSLLQSLLQQVKQW;
SLLQSLLQQVKQWY; LLQSLLQQVKQWYF; LQSLLQQVKQWYFC;
QSLLQQVKQWYFCF; SLLQQVKQWYFCFS; LLQQVKQWYFCFSR;
LQQVKQWYFCFSRL; QQVKQWYFCFSRLH; QVKQWYFCFSRLHC;
VKQWYFCFSRLHCL; KQWYFCFSRLHCLH; QWYFCFSRLHCLHL;
WYFCFSRLHCLHLY; YFCFSRLHCLHLYK; FCFSRLHCLHLYKI;
CFSRLHCLHLYKIP; FSRLHCLHLYKIPA; SRLHCLHLYKIPAK;
RLHCLHLYKIPAKA; LHCLHLYKIPAKAL; HCLHLYKIPAKALK;
KSSELFFLFQSRFY; SSELFFLFQSRFYQ; SELFFLFQSRFYQL;
ELFFLFQSRFYQLS; LFFLFQSRFYQLSL; FFLFQSRFYQLSLK;
FLFQSRFYQLSLKL; LFQSRFYQLSLKLV; FQSRFYQLSLKLVV;
QSRFYQLSLKLVVT; SRFYQLSLKLVVTA; RFYQLSLKLVVTAG;
FYQLSLKLVVTAGA; YQLSLKLVVTAGAE; QLSLKLVVTAGAEP;
LSLKLVVTAGAEPW; SLKLVVTAGAEPWP; LKLVVTAGAEPWPL;
KLVVTAGAEPWPLS; LVVTAGAEPWPLSS; VVTAGAEPWPLSSL;
VTAGAEPWPLSSLT; TAGAEPWPLSSLTG; AGAEPWPLSSLTGD;
GAEPWPLSSLTGDK; AEPWPLSSLTGDKA; EPWPLSSLTGDKAK;
PWPLSSLTGDKAKI; WPLSSLTGDKAKIP; PLSSLTGDKAKIPR;
LSSLTGDKAKIPRL; SSLTGDKAKIPRLA; SLTGDKAKIPRLAK;
LTGDKAKIPRLAKH; TGDKAKIPRLAKHV; GDKAKIPRLAKHVC;
DKAKIPRLAKHVCH; KAKIPRLAKHVCHA; AKIPRLAKHVCHAL;
KIPRLAKHVCHALS; IPRLAKHVCHALSF; PRLAKHVCHALSFL;
RLAKHVCHALSFLR; LAKHVCHALSFLRS; AKHVCHALSFLRSW;
KHVCHALSFLRSWF; HVCHALSFLRSWFG; VCHALSFLRSWFGC;
CHALSFLRSWFGCI; HALSFLRSWFGCIP; ALSFLRSWFGCIPW;
LSFLRSWFGCIPWV; SFLRSWFGCIPWVS; FLRSWFGCIPWVSS;
LRSWFGCIPWVSSS; RSWFGCIPWVSSSS; SWFGCIPWVSSSSL;
GHGLAAFPCESCTF; HGLAAFPCESCTFL; GLAAFPCESCTFLP;
LAAFPCESCTFLPE; AAFPCESCTFLPEV; AFPCESCTFLPEVM;
FPCESCTFLPEVMV; PCESCTFLPEVMVW; CESCTFLPEVMVWL;
ESCTFLPEVMVWLH; SCTFLPEVMVWLHS; CTFLPEVMVWLHSM;
TFLPEVMVWLHSMG; FLPEVMVWLHSMGK; LPEVMVWLHSMGKQ;
PEVMVWLHSMGKQL; EVMVWLHSMGKQLL; VMVWLHSMGKQLLP;
MVWLHSMGKQLLPV; VWLHSMGKQLLPVA; WLHSMGKQLLPVAF;
LHSMGKQLLPVAFF; HSMGKQLLPVAFFF; SMGKQLLPVAFFFI;
MGKQLLPVAFFFII; GKQLLPVAFFFIIY; KQLLPVAFFFIIYK;
QLLPVAFFFIIYKR; LLPVAFFFIIYKRP; LPVAFFFIIYKRPR;

PVAFFFIIYKRPRP; VAFFFIIYKRPRPP; AFFFIIYKRPRPPL;
FFFIIYKRPRPPLP; FFIIYKRPRPPLPP; FIIYKRPRPPLPPP;
IIYKRPRPPLPPPF; IYKRPRPPLPPPFL; YKRPRPPLPPPFLS;
KRPRPPLPPPFLSS; RPRPPLPPPFLSSS; PRPPLPPPFLSSSK;
RPPLPPPFLSSSKG; PPLPPPFLSSSKGV; PLPPPFLSSSKGVE;
LPPPFLSSSKGVEA; PPPFLSSSKGVEAF; PPFLSSSKGVEAFS;
PFLSSSKGVEAFSE; FLSSSKGVEAFSEA; QNYLGKSLFFCNFC; NYLGKSLFFCNFCK

15 mers:
WIKFLTGKNPWSSWT; IKFLTGKNPWSSWTF; GSVRNFTLTKGATRI;
SVRNFTLTKGATRIK; LISLILEPGVAQRFV; ISLILEPGVAQRFVL;
SLILEPGVAQRFVLI; LILEPGVAQRFVLIF; ILEPGVAQRFVLIFL;
LEPGVAQRFVLIFLF; EPGVAQRFVLIFLFA; PGVAQRFVLIFLFAQ;
GVAQRFVLIFLFAQI; VAQRFVLIFLFAQIP; AQRFVLIFLFAQIPC;
QRFVLIFLFAQIPCT; RFVLIFLFAQIPCTA; FVLIFLFAQIPCTAR;
VLIFLFAQIPCTARN; LIFLFAQIPCTARNG; IFLFAQIPCTARNGL;
FLFAQIPCTARNGLF; LFAQIPCTARNGLFV; FAQIPCTARNGLFVP;
AQIPCTARNGLFVPK; QIPCTARNGLFVPKS; IPCTARNGLFVPKSL;
PCTARNGLFVPKSLL; CTARNGLFVPKSLLC; TARNGLFVPKSLLCT;
ARNGLFVPKSLLCTA; RNGLFVPKSLLCTAL; NGLFVPKSLLCTALA;
GLFVPKSLLCTALAC; LFVPKSLLCTALACY; FVPKSLLCTALACYV;
VPKSLLCTALACYVS; PKSLLCTALACYVSL; KSLLCTALACYVSLD;
VIIFFIGANLWNRRV; IIFFIGANLWNRRVG; IFFIGANLWNRRVGV;
FFIGANLWNRRVGVL; FIGANLWNRRVGVLV; IGANLWNRRVGVLVE;
GANLWNRRVGVLVEF; ANLWNRRVGVLVEFL; RSNSRFSTLNTTQKK;
SNSRFSTLNTTQKKK; NSRFSTLNTTQKKKK; SRFSTLNTTQKKKKG;
RFSTLNTTQKKKKGR; FSTLNTTQKKKKGRR; STLNTTQKKKKGRRP;
RSIPYYRRKHSRGLK; SIPYYRRKHSRGLKG; IPYYRRKHSRGLKGA;
GCVFIIRYVFRISIQ; CVFIIRYVFRISIQC; VFIIRYVFRISIQCR;
FIIRYVFRISIQCRG; IIRYVFRISIQCRGV; KSKKYLSASSRYSFS;
KKSRYPSYDQGRNAN; KSRYPSYDQGRNANR; SRYPSYDQGRNANRK;
RYPSYDQGRNANRKI; YPSYDQGRNANRKIQ; PSYDQGRNANRKIQS;
SYDQGRNANRKIQSY; YDQGRNANRKIQSYI; DQGRNANRKIQSYIR;
NGFNIWSSWKCCTRT; GFNIWSSWKCCTRTI; FNIWSSWKCCTRTIY;
NIWSSWKCCTRTIYG; IWSSWKCCTRTIYGR; WSSWKCCTRTIYGRC;
SSWKCCTRTIYGRCC; SWKCCTRTIYGRCCL; WKCCTRTIYGRCCLA;
KCCTRTIYGRCCLAA; CCTRTIYGRCCLAAL; CTRTIYGRCCLAALF;
TRTIYGRCCLAALFA; RTIYGRCCLAALFAT; WKNNTSCRVIRFVWW;
IKGFAFRTWNKQFRQ; KGFAFRTWNKQFRQF; GFAFRTWNKQFRQFE;
FAFRTWNKQFRQFER; AFRTWNKQFRQFERL; FRTWNKQFRQFERLF;
RTWNKQFRQFERLFR; TWNKQFRQFERLFRW; WNKQFRQFERLFRWK;
NKQFRQFERLFRWKC; GKFRKETFKQKNPNI; KFRKETFKQKNPNIS;
FRKETFKQKNPNIST; RKETFKQKNPNISTR; KETFKQKNPNISTRL;
ETFKQKNPNISTRLG; TFKQKNPNISTRLGY; FKQKNPNISTRLGYN;
KQKNPNISTRLGYNE; AQNIFKKILTKLRVL; QNIFKKILTKLRVLT;
KKNFTKWNDLVATAN; KNFTKWNDLVATANL; NFTKWNDLVATANLV;
IPITMLFPSLRYFSP; PITMLFPSLRYFSPC; KWLIQKQHLLNVYVQ;
KHLFKAFWFAIVPVC; HLFKAFWFAIVPVCQ; LFKAFWFAIVPVCQY;
FKAFWFAIVPVCQYI; KAFWFAIVPVCQYIL; AFWFAIVPVCQYILS;
FWFAIVPVCQYILSY; WFAIVPVCQYILSYL; FAIVPVCQYILSYLG;
AIVPVCQYILSYLGP; IVPVCQYILSYLGPL; VPVCQYILSYLGPLE;
PVCQYILSYLGPLEV; VCQYILSYLGPLEVF; CQYILSYLGPLEVFL;
QYILSYLGPLEVFLC; YILSYLGPLEVFLCH; ILSYLGPLEVFLCHQ;
LSYLGPLEVFLCHQT; SYLGPLEVFLCHQTP; GHLAKRKLGKDSLQI;
HLAKRKLGKDSLQIF; LAKRKLGKDSLQIFF; AKRKLGKDSLQIFFS;
KRKLGKDSLQIFFSG; RKLGKDSLQIFFSGG; KLGKDSLQIFFSGGS;
TGHKYQQLKHTGYQL; GHKYQQLKHTGYQLY; HKYQQLKHTGYQLYK;
KYQQLKHTGYQLYKE; YQQLKHTGYQLYKEA; QQLKHTGYQLYKEAP;
QLKHTGYQLYKEAPH; LKHTGYQLYKEAPHP; KHTGYQLYKEAPHPV;
HTGYQLYKEAPHPVH; TGYQLYKEAPHPVHL; GYQLYKEAPHPVHLA;

YQLYKEAPHPVHLAT; QLYKEAPHPVHLATL; LYKEAPHPVHLATLW;
LCWSHEVLGEHFPLL; HFHFYWDQVPSTQLD; FHFYWDQVPSTQLDK;
HFYWDQVPSTQLDKH; FYWDQVPSTQLDKHC; YWDQVPSTQLDKHCF;
WDQVPSTQLDKHCFC; DQVPSTQLDKHCFCP; QVPSTQLDKHCFCPN;
VPSTQLDKHCFCPNR; PSTQLDKHCFCPNRP; STQLDKHCFCPNRPY;
TQLDKHCFCPNRPYG; QLDKHCFCPNRPYGQ; LDKHCFCPNRPYGQY;
DKHCFCPNRPYGQYS; KHCFCPNRPYGQYSL; HCFCPNRPYGQYSLP;
CFCPNRPYGQYSLPG; FCPNRPYGQYSLPGT; CPNRPYGQYSLPGTG;
PNRPYGQYSLPGTGL; NRPYGQYSLPGTGLL; RPYGQYSLPGTGLLG;
PYGQYSLPGTGLLGF; YHQGTLTCNSLALPA; HQGTLTCNSLALPAF;
QGTLTCNSLALPAFP; GTLTCNSLALPAFPR; TLTCNSLALPAFPRV;
LTCNSLALPAFPRVL; TCNSLALPAFPRVLH; CNSLALPAFPRVLHL;
NSLALPAFPRVLHLQ; SLALPAFPRVLHLQQ; LALPAFPRVLHLQQR;
ALPAFPRVLHLQQRS; LPAFPRVLHLQQRSG; PAFPRVLHLQQRSGN;
AFPRVLHLQQRSGNY; FPRVLHLQQRSGNYC; PRVLHLQQRSGNYCL;
RVLHLQQRSGNYCLE; VFLHHAHALFVTLHE; FLHHAHALFVTLHEG;
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VQLQPPTSVDFHRLG; QLQPPTSVDFHRLGP; LQPPTSVDFHRLGPH;
QPPTSVDFHRLGPHL; PPTSVDFHRLGPHLN; PTSVDFHRLGPHLNW;
TSVDFHRLGPHLNWG; SVDFHRLGPHLNWGG; VDFHRLGPHLNWGGE;
DFHRLGPHLNWGGEF; FHRLGPHLNWGGEFL; HRLGPHLNWGGEFLL;
RLGPHLNWGGEFLLC; LGPHLNWGGEFLLCC; GPHLNWGGEFLLCCN;
PHLNWGGEFLLCCNR; HLNWGGEFLLCCNRE; LNWGGEFLLCCNREA;
NWGGEFLLCCNREAF; WGGEFLLCCNREAFF; GGEFLLCCNREAFFS;
GEFLLCCNREAFFSL; EFLLCCNREAFFSLG; FLLCCNREAFFSLGY;
LLCCNREAFFSLGYH; LCCNREAFFSLGYHC; GFHLDPPFLGLGSIL;
FHLDPPFLGLGSILP; HLDPPFLGLGSILPL; LLELLLLLLLVVLAL;
LELLLLLLLVVLALA; ELLLLLLLVVLALAR; LLLLLLLVVLALARV;
LLLLLLVVLALARVP; LLLLLVVLALARVPL; LLLLVVLALARVPLA;
LLLVVLALARVPLAF; LLVVLALARVPLAFW; LVVLALARVPLAFWE;
VVLALARVPLAFWEL; VLALARVPLAFWELP; LALARVPLAFWELPL;
ALARVPLAFWELPLD; LARVPLAFWELPLDT; ARVPLAFWELPLDTL;
RVPLAFWELPLDTLL; VPLAFWELPLDTLLF; PLAFWELPLDTLLFF;
LAFWELPLDTLLFFW; AFWELPLDTLLFFWL; FWELPLDTLLFFWLG;
WELPLDTLLFFWLGP; ELPLDTLLFFWLGPS; LPLDTLLFFWLGPSS;
PLDTLLFFWLGPSSY; LDTLLFFWLGPSSYA; DTLLFFWLGPSSYAS;
TLLFFWLGPSSYASR; LLFFWLGPSSYASRA; LFFWLGPSSYASRAG;
FFWLGPSSYASRAGV; FWLGPSSYASRAGVT; WLGPSSYASRAGVTV;
LGPSSYASRAGVTVP; GPSSYASRAGVTVPY; PSSYASRAGVTVPYR;
SSYASRAGVTVPYRP; SYASRAGVTVPYRPR; YASRAGVTVPYRPRS;
ASRAGVTVPYRPRSK; SRAGVTVPYRPRSKG; RAGVTVPYRPRSKGN;
AGVTVPYRPRSKGNI; GVTVPYRPRSKGNIH; LAPPGAIVFSINSPE;
APPGAIVFSINSPEC; PPGAIVFSINSPECT; PGAIVFSINSPECTL;
GAIVFSINSPECTLC; FLKSILCVTSSILSA; LKSILCVTSSILSAS;
KSILCVTSSILSASS; SILCVTSSILSASSI; ILCVTSSILSASSIL;
VWPKCTRVPSLSATC; WPKCTRVPSLSATCL; PKCTRVPSLSATCLT;
KCTRVPSLSATCLTI; CTRVPSLSATCLTIE; TRVPSLSATCLTIEG;
RVPSLSATCLTIEGL; VPSLSATCLTIEGLI; PSLSATCLTIEGLIG;
SLSATCLTIEGLIGE; LSATCLTIEGLIGER; SATCLTIEGLIGERS;
ATCLTIEGLIGERSE; KFIGAFTIVQVVSSK; FIGAFTIVQVVSSKN;
IGAFTIVQVVSSKNL; GAFTIVQVVSSKNLA; AFTIVQVVSSKNLAK;
FTIVQVVSSKNLAKE; TIVQVVSSKNLAKES; IVQVVSSKNLAKESL;
VQVVSSKNLAKESLK; QVVSSKNLAKESLKN; VVSSKNLAKESLKNL;
VSSKNLAKESLKNLS; SSKNLAKESLKNLSV; SKNLAKESLKNLSVL;
KNLAKESLKNLSVLL; NLAKESLKNLSVLLC; LAKESLKNLSVLLCN;
AKESLKNLSVLLCNS; KESLKNLSVLLCNSC; ESLKNLSVLLCNSCE;
SLKNLSVLLCNSCEV; LKNLSVLLCNSCEVI; KNLSVLLCNSCEVIE;
NLSVLLCNSCEVIEG; LSVLLCNSCEVIEGI; SVLLCNSCEVIEGIS;
VLLCNSCEVIEGISS; LLCNSCEVIEGISSL; LCNSCEVIEGISSLI;

CNSCEVIEGISSLIT; NSCEVIEGISSLITC; SCEVIEGISSLITCH;
CEVIEGISSLITCHK; EVIEGISSLITCHKA; VIEGISSLITCHKAW;
IEGISSLITCHKAWE; EGISSLITCHKAWEI; GISSLITCHKAWEIV;
ISSLITCHKAWEIVA; SSLITCHKAWEIVAN; SLITCHKAWEIVANK;
LITCHKAWEIVANKE; ITCHKAWEIVANKEG; TCHKAWEIVANKEGP;
CHKAWEIVANKEGPQ; HKAWEIVANKEGPQC; KAWEIVANKEGPQCL;
AWEIVANKEGPQCLG; WEIVANKEGPQCLGS; EIVANKEGPQCLGSR;
IVANKEGPQCLGSRY; IKAANPAIAPGAPAI; KAANPAIAPGAPAIT;
AANPAIAPGAPAITA; ANPAIAPGAPAITAY; NPAIAPGAPAITAYV;
GVRPIAAIASEVLVM; VRPIAAIASEVLVMP; RPIAAIASEVLVMPS;
PIAAIASEVLVMPST; IAAIASEVLVMPSTV; AAIASEVLVMPSTVA;
AIASEVLVMPSTVAR; IASEVLVMPSTVARD; ASEVLVMPSTVARDA;
SEVLVMPSTVARDAI; TSIAAAASPAAISAT; SIAAAASPAAISATE;
IAAAASPAAISATEN; AAAASPAAISATENP; AAASPAAISATENPV;
AASPAAISATENPVA; ASPAAISATENPVAA; SPAAISATENPVAAA;
PAAISATENPVAAAA; AAISATENPVAAAAS; AISATENPVAAAASD;
ISATENPVAAAASDT; SATENPVAAAASDTL; ATENPVAAAASDTLA;
TENPVAAAASDTLAT; ENPVAAAASDTLATR; NPVAAAASDTLATRS;
PVAAAASDTLATRSP; VAAAASDTLATRSPK; AAAASDTLATRSPKS;
AAASDTLATRSPKSA; AASDTLATRSPKSAR; ASDTLATRSPKSARA;
SDTLATRSPKSARAA; DTLATRSPKSARAAP; TLATRSPKSARAAPM;
LATRSPKSARAAPMN; ATRSPKSARAAPMNL; TRSPKSARAAPMNLE;
RSPKSARAAPMNLEI; SPKSARAAPMNLEIQ; PKSARAAPMNLEIQK;
KSARAAPMNLEIQKK; SARAAPMNLEIQKKR; ARAAPMNLEIQKKRD;
RAAPMNLEIQKKRDY; AAPMNLEIQKKRDYL; APMNLEIQKKRDYLP;
PMNLEIQKKRDYLPR; MNLEIQKKRDYLPRS; NLEIQKKRDYLPRSL;
LEIQKKRDYLPRSLL; EIQKKRDYLPRSLLQ; IQKKRDYLPRSLLQS;
QKKRDYLPRSLLQSL; KKRDYLPRSLLQSLL; KRDYLPRSLLQSLLQ;
RDYLPRSLLQSLLQQ; DYLPRSLLQSLLQQV; YLPRSLLQSLLQQVK;
LPRSLLQSLLQQVKQ; PRSLLQSLLQQVKQW; RSLLQSLLQQVKQWY;
SLLQSLLQQVKQWYF; LLQSLLQQVKQWYFC; LQSLLQQVKQWYFCF;
QSLLQQVKQWYFCFS; SLLQQVKQWYFCFSR; LLQQVKQWYFCFSRL;
LQQVKQWYFCFSRLH; QQVKQWYFCFSRLHC; QVKQWYFCFSRLHCL;
VKQWYFCFSRLHCLH; KQWYFCFSRLHCLHL; QWYFCFSRLHCLHLY;
WYFCFSRLHCLHLYK; YFCFSRLHCLHLYKI; FCFSRLHCLHLYKIP;
CFSRLHCLHLYKIPA; FSRLHCLHLYKIPAK; SRLHCLHLYKIPAKA;
RLHCLHLYKIPAKAL; LHCLHLYKIPAKALK; KSSELFFLFQSRFYQ;
SSELFFLFQSRFYQL; SELFFLFQSRFYQLS; ELFFLFQSRFYQLSL;
LFFLFQSRFYQLSLK; FFLFQSRFYQLSLKL; FLFQSRFYQLSLKLV;
LFQSRFYQLSLKLVV; FQSRFYQLSLKLVVT; QSRFYQLSLKLVVTA;
SRFYQLSLKLVVTAG; RFYQLSLKLVVTAGA; FYQLSLKLVVTAGAE;
YQLSLKLVVTAGAEP; QLSLKLVVTAGAEPW; LSLKLVVTAGAEPWP;
SLKLVVTAGAEPWPL; LKLVVTAGAEPWPLS; KLVVTAGAEPWPLSS;
LVVTAGAEPWPLSSL; VVTAGAEPWPLSSLT; VTAGAEPWPLSSLTG;
TAGAEPWPLSSLTGD; AGAEPWPLSSLTGDK; GAEPWPLSSLTGDKA;
AEPWPLSSLTGDKAK; EPWPLSSLTGDKAKI; PWPLSSLTGDKAKIP;
WPLSSLTGDKAKIPR; PLSSLTGDKAKIPRL; LSSLTGDKAKIPRLA;
SSLTGDKAKIPRLAK; SLTGDKAKIPRLAKH; LTGDKAKIPRLAKHV;
TGDKAKIPRLAKHVC; GDKAKIPRLAKHVCH; DKAKIPRLAKHVCHA;
KAKIPRLAKHVCHAL; AKIPRLAKHVCHALS; KIPRLAKHVCHALSF;
IPRLAKHVCHALSFL; PRLAKHVCHALSFLR; RLAKHVCHALSFLRS;
LAKHVCHALSFLRSW; AKHVCHALSFLRSWF; KHVCHALSFLRSWFG;
HVCHALSFLRSWFGC; VCHALSFLRSWFGCI; CHALSFLRSWFGCIP;
HALSFLRSWFGCIPW; ALSFLRSWFGCIPWV; LSFLRSWFGCIPWVS;
SFLRSWFGCIPWVSS; FLRSWFGCIPWVSSS; LRSWFGCIPWVSSSS;
RSWFGCIPWVSSSSL; GHGLAAFPCESCTFL; HGLAAFPCESCTFLP;
GLAAFPCESCTFLPE; LAAFPCESCTFLPEV; AAFPCESCTFLPEVM;
AFPCESCTFLPEVMV; FPCESCTFLPEVMVW; PCESCTFLPEVMVWL;
CESCTFLPEVMVWLH; ESCTFLPEVMVWLHS; SCTFLPEVMVWLHSM;

CTFLPEVMVWLHSMG; TFLPEVMVWLHSMGK; FLPEVMVWLHSMGKQ;
LPEVMVWLHSMGKQL; PEVMVWLHSMGKQLL; EVMVWLHSMGKQLLP;
VMVWLHSMGKQLLPV; MVWLHSMGKQLLPVA; VWLHSMGKQLLPVAF;
WLHSMGKQLLPVAFF; LHSMGKQLLPVAFFF; HSMGKQLLPVAFFFI;
SMGKQLLPVAFFFII; MGKQLLPVAFFFIIY; GKQLLPVAFFFIIYK;
KQLLPVAFFFIIYKR; QLLPVAFFFIIYKRP; LLPVAFFFIIYKRPR;
LPVAFFFIIYKRPRP; PVAFFFIIYKRPRPP; VAFFFIIYKRPRPPL;
AFFFIIYKRPRPPLP; FFFIIYKRPRPPLPP; FFIIYKRPRPPLPPP;
FIIYKRPRPPLPPPF; IIYKRPRPPLPPPFL; IYKRPRPPLPPPFLS;
YKRPRPPLPPPFLSS; KRPRPPLPPPFLSSS; RPRPPLPPPFLSSSK;
PRPPLPPPFLSSSKG; RPPLPPPFLSSSKGV; PPLPPPFLSSSKGVE;
PLPPPFLSSSKGVEA; LPPPFLSSSKGVEAF; PPPFLSSSKGVEAFS;
PPFLSSSKGVEAFSE; PFLSSSKGVEAFSEA; QNYLGKSLFFCNFCK

16 mers:
WIKFLTGKNPWSSWTF; GSVRNFTLTKGATRIK; LISLILEPGVAQRFVL;
ISLILEPGVAQRFVLI; SLILEPGVAQRFVLIF; LILEPGVAQRFVLIFL;
ILEPGVAQRFVLIFLF; LEPGVAQRFVLIFLFA; EPGVAQRFVLIFLFAQ;
PGVAQRFVLIFLFAQI; GVAQRFVLIFLFAQIP; VAQRFVLIFLFAQIPC;
AQRFVLIFLFAQIPCT; QRFVLIFLFAQIPCTA; RFVLIFLFAQIPCTAR;
FVLIFLFAQIPCTARN; VLIFLFAQIPCTARNG; LIFLFAQIPCTARNGL;
IFLFAQIPCTARNGLF; FLFAQIPCTARNGLFV; LFAQIPCTARNGLFVP;
FAQIPCTARNGLFVPK; AQIPCTARNGLFVPKS; QIPCTARNGLFVPKSL;
IPCTARNGLFVPKSLL; PCTARNGLFVPKSLLC; CTARNGLFVPKSLLCT;
TARNGLFVPKSLLCTA; ARNGLFVPKSLLCTAL; RNGLFVPKSLLCTALA;
NGLFVPKSLLCTALAC; GLFVPKSLLCTALACY; LFVPKSLLCTALACYV;
FVPKSLLCTALACYVS; VPKSLLCTALACYVSL; PKSLLCTALACYVSLD;
VIIFFIGANLWNRRVG; IIFFIGANLWNRRVGV; IFFIGANLWNRRVGVL;
FFIGANLWNRRVGVLV; FIGANLWNRRVGVLVE; IGANLWNRRVGVLVEF;
GANLWNRRVGVLVEFL; RSNSRFSTLNTTQKKK; SNSRFSTLNTTQKKKK;
NSRFSTLNTTQKKKKG; SRFSTLNTTQKKKKGR; RFSTLNTTQKKKKGRR;
FSTLNTTQKKKKGRRP; RSIPYYRRKHSRGLKG; SIPYYRRKHSRGLKGA;
GCVFIIRYVFRISIQC; CVFIIRYVFRISIQCR; VFIIRYVFRISIQCRG;
FIIRYVFRISIQCRGV; KKSRYPSYDQGRNANR; KSRYPSYDQGRNANRK;
SRYPSYDQGRNANRKI; RYPSYDQGRNANRKIQ; YPSYDQGRNANRKIQS;
PSYDQGRNANRKIQSY; SYDQGRNANRKIQSYI; YDQGRNANRKIQSYIR;
NGFNIWSSWKCCTRTI; GFNIWSSWKCCTRTIY; FNIWSSWKCCTRTIYG;
NIWSSWKCCTRTIYGR; IWSSWKCCTRTIYGRC; WSSWKCCTRTIYGRCC;
SSWKCCTRTIYGRCCL; SWKCCTRTIYGRCCLA; WKCCTRTIYGRCCLAA;
KCCTRTIYGRCCLAAL; CCTRTIYGRCCLAALF; CTRTIYGRCCLAALFA;
TRTIYGRCCLAALFAT; IKGFAFRTWNKQFRQF; KGFAFRTWNKQFRQFE;
GFAFRTWNKQFRQFER; FAFRTWNKQFRQFERL; AFRTWNKQFRQFERLF;
FRTWNKQFRQFERLFR; RTWNKQFRQFERLFRW; TWNKQFRQFERLFRWK;
WNKQFRQFERLFRWKC; GKFRKETFKQKNPNIS; KFRKETFKQKNPNIST;
FRKETFKQKNPNISTR; RKETFKQKNPNISTRL; KETFKQKNPNISTRLG;
ETFKQKNPNISTRLGY; TFKQKNPNISTRLGYN; FKQKNPNISTRLGYNE;
AQNIFKKILTKLRVLT; KKNFTKWNDLVATANL; KNFTKWNDLVATANLV;
IPITMLFPSLRYFSPC; KHLFKAFWFAIVPVCQ; HLFKAFWFAIVPVCQY;
LFKAFWFAIVPVCQYI; FKAFWFAIVPVCQYIL; KAFWFAIVPVCQYILS;
AFWFAIVPVCQYILSY; FWFAIVPVCQYILSYL; WFAIVPVCQYILSYLG;
FAIVPVCQYILSYLGP; AIVPVCQYILSYLGPL; IVPVCQYILSYLGPLE;
VPVCQYILSYLGPLEV; PVCQYILSYLGPLEVF; VCQYILSYLGPLEVFL;
CQYILSYLGPLEVFLC; QYILSYLGPLEVFLCH; YILSYLGPLEVFLCHQ;
ILSYLGPLEVFLCHQT; LSYLGPLEVFLCHQTP; GHLAKRKLGKDSLQIF;
HLAKRKLGKDSLQIFF; LAKRKLGKDSLQIFFS; AKRKLGKDSLQIFFSG;
KRKLGKDSLQIFFSGG; RKLGKDSLQIFFSGGS; TGHKYQQLKHTGYQLY;
GHKYQQLKHTGYQLYK; HKYQQLKHTGYQLYKE; KYQQLKHTGYQLYKEA;
YQQLKHTGYQLYKEAP; QQLKHTGYQLYKEAPH; QLKHTGYQLYKEAPHP;
LKHTGYQLYKEAPHPV; KHTGYQLYKEAPHPVH; HTGYQLYKEAPHPVHL;
TGYQLYKEAPHPVHLA; GYQLYKEAPHPVHLAT; YQLYKEAPHPVHLATL;

QLYKEAPHPVHLATLW; HFHFYWDQVPSTQLDK; FHFYWDQVPSTQLDKH;
HFYWDQVPSTQLDKHC; FYWDQVPSTQLDKHCF; YWDQVPSTQLDKHCFC;
WDQVPSTQLDKHCFCP; DQVPSTQLDKHCFCPN; QVPSTQLDKHCFCPNR;
VPSTQLDKHCFCPNRP; PSTQLDKHCFCPNRPY; STQLDKHCFCPNRPYG;
TQLDKHCFCPNRPYGQ; QLDKHCFCPNRPYGQY; LDKHCFCPNRPYGQYS;
DKHCFCPNRPYGQYSL; KHCFCPNRPYGQYSLP; HCFCPNRPYGQYSLPG;
CFCPNRPYGQYSLPGT; FCPNRPYGQYSLPGTG; CPNRPYGQYSLPGTGL;
PNRPYGQYSLPGTGLL; NRPYGQYSLPGTGLLG; RPYGQYSLPGTGLLGF;
YHQGTLTCNSLALPAF; HQGTLTCNSLALPAFP; QGTLTCNSLALPAFPR;
GTLTCNSLALPAFPRV; TLTCNSLALPAFPRVL; LTCNSLALPAFPRVLH;
TCNSLALPAFPRVLHL; CNSLALPAFPRVLHLQ; NSLALPAFPRVLHLQQ;
SLALPAFPRVLHLQQR; LALPAFPRVLHLQQRS; ALPAFPRVLHLQQRSG;
LPAFPRVLHLQQRSGN; PAFPRVLHLQQRSGNY; AFPRVLHLQQRSGNYC;
FPRVLHLQQRSGNYCL; PRVLHLQQRSGNYCLE; VFLHHAHALFVTLHEG;
PLFVQLQPPTSVDFHR; LFVQLQPPTSVDFHRL; FVQLQPPTSVDFHRLG;
VQLQPPTSVDFHRLGP; QLQPPTSVDFHRLGPH; LQPPTSVDFHRLGPHL;
QPPTSVDFHRLGPHLN; PPTSVDFHRLGPHLNW; PTSVDFHRLGPHLNWG;
TSVDFHRLGPHLNWGG; SVDFHRLGPHLNWGGE; VDFHRLGPHLNWGGEF;
DFHRLGPHLNWGGEFL; FHRLGPHLNWGGEFLL; HRLGPHLNWGGEFLLC;
RLGPHLNWGGEFLLCC; LGPHLNWGGEFLLCCN; GPHLNWGGEFLLCCNR;
PHLNWGGEFLLCCNRE; HLNWGGEFLLCCNREA; LNWGGEFLLCCNREAF;
NWGGEFLLCCNREAFF; WGGEFLLCCNREAFFS; GGEFLLCCNREAFFSL;
GEFLLCCNREAFFSLG; EFLLCCNREAFFSLGY; FLLCCNREAFFSLGYH;
LLCCNREAFFSLGYHC; GFHLDPPFLGLGSILP; FHLDPPFLGLGSILPL;
LLELLLLLLLVVLALA; LELLLLLLLVVLALAR; ELLLLLLLVVLALARV;
LLLLLLLVVLALARVP; LLLLLLVVLALARVPL; LLLLLVVLALARVPLA;
LLLLVVLALARVPLAF; LLLVVLALARVPLAFW; LLVVLALARVPLAFWE;
LVVLALARVPLAFWEL; VVLALARVPLAFWELP; VLALARVPLAFWELPL;
LALARVPLAFWELPLD; ALARVPLAFWELPLDT; LARVPLAFWELPLDTL;
ARVPLAFWELPLDTLL; RVPLAFWELPLDTLLF; VPLAFWELPLDTLLFF;
PLAFWELPLDTLLFFW; LAFWELPLDTLLFFWL; AFWELPLDTLLFFWLG;
FWELPLDTLLFFWLGP; WELPLDTLLFFWLGPS; ELPLDTLLFFWLGPSS;
LPLDTLLFFWLGPSSY; PLDTLLFFWLGPSSYA; LDTLLFFWLGPSSYAS;
DTLLFFWLGPSSYASR; TLLFFWLGPSSYASRA; LLFFWLGPSSYASRAG;
LFFWLGPSSYASRAGV; FFWLGPSSYASRAGVT; FWLGPSSYASRAGVTV;
WLGPSSYASRAGVTVP; LGPSSYASRAGVTVPY; GPSSYASRAGVTVPYR;
PSSYASRAGVTVPYRP; SSYASRAGVTVPYRPR; SYASRAGVTVPYRPRS;
YASRAGVTVPYRPRSK; ASRAGVTVPYRPRSKG; SRAGVTVPYRPRSKGN;
RAGVTVPYRPRSKGNI; AGVTVPYRPRSKGNIH; LAPPGAIVFSINSPEC;
APPGAIVFSINSPECT; PPGAIVFSINSPECTL; PGAIVFSINSPECTLC;
FLKSILCVTSSILSAS; LKSILCVTSSILSASS; KSILCVTSSILSASSI;
SILCVTSSILSASSIL; VWPKCTRVPSLSATCL; WPKCTRVPSLSATCLT;
PKCTRVPSLSATCLTI; KCTRVPSLSATCLTIE; CTRVPSLSATCLTIEG;
TRVPSLSATCLTIEGL; RVPSLSATCLTIEGLI; VPSLSATCLTIEGLIG;
PSLSATCLTIEGLIGE; SLSATCLTIEGLIGER; LSATCLTIEGLIGERS;
SATCLTIEGLIGERSE; KFIGAFTIVQVVSSKN; FIGAFTIVQVVSSKNL;
IGAFTIVQVVSSKNLA; GAFTIVQVVSSKNLAK; AFTIVQVVSSKNLAKE;
FTIVQVVSSKNLAKES; TIVQVVSSKNLAKESL; IVQVVSSKNLAKESLK;
VQVVSSKNLAKESLKN; QVVSSKNLAKESLKNL; VVSSKNLAKESLKNLS;
VSSKNLAKESLKNLSV; SSKNLAKESLKNLSVL; SKNLAKESLKNLSVLL;
KNLAKESLKNLSVLLC; NLAKESLKNLSVLLCN; LAKESLKNLSVLLCNS;
AKESLKNLSVLLCNSC; KESLKNLSVLLCNSCE; ESLKNLSVLLCNSCEV;
SLKNLSVLLCNSCEVI; LKNLSVLLCNSCEVIE; KNLSVLLCNSCEVIEG;
NLSVLLCNSCEVIEGI; LSVLLCNSCEVIEGIS; SVLLCNSCEVIEGISS;
VLLCNSCEVIEGISSL; LLCNSCEVIEGISSLI; LCNSCEVIEGISSLIT;
CNSCEVIEGISSLITC; NSCEVIEGISSLITCH; SCEVIEGISSLITCHK;
CEVIEGISSLITCHKA; EVIEGISSLITCHKAW; VIEGISSLITCHKAWE;
IEGISSLITCHKAWEI; EGISSLITCHKAWEIV; GISSLITCHKAWEIVA;
ISSLITCHKAWEIVAN; SSLITCHKAWEIVANK; SLITCHKAWEIVANKE;

LITCHKAWEIVANKEG; ITCHKAWEIVANKEGP; TCHKAWEIVANKEGPQ;
CHKAWEIVANKEGPQC; HKAWEIVANKEGPQCL; KAWEIVANKEGPQCLG;
AWEIVANKEGPQCLGS; WEIVANKEGPQCLGSR; EIVANKEGPQCLGSRY;
IKAANPAIAPGAPAIT; KAANPAIAPGAPAITA; AANPAIAPGAPAITAY;
ANPAIAPGAPAITAYV; GVRPIAAIASEVLVMP; VRPIAAIASEVLVMPS;
RPIAAIASEVLVMPST; PIAAIASEVLVMPSTV; IAAIASEVLVMPSTVA;
AAIASEVLVMPSTVAR; AIASEVLVMPSTVARD; IASEVLVMPSTVARDA;
ASEVLVMPSTVARDAI; TSIAAAASPAAISATE; SIAAAASPAAISATEN;
IAAAASPAAISATENP; AAAASPAAISATENPV; AAASPAAISATENPVA;
AASPAAISATENPVAA; ASPAAISATENPVAAA; SPAAISATENPVAAAA;
PAAISATENPVAAAAS; AAISATENPVAAAASD; AISATENPVAAAASDT;
ISATENPVAAAASDTL; SATENPVAAAASDTLA; ATENPVAAAASDTLAT;
TENPVAAAASDTLATR; ENPVAAAASDTLATRS; NPVAAAASDTLATRSP;
PVAAAASDTLATRSPK; VAAAASDTLATRSPKS; AAAASDTLATRSPKSA;
AAASDTLATRSPKSAR; AASDTLATRSPKSARA; ASDTLATRSPKSARAA;
SDTLATRSPKSARAAP; DTLATRSPKSARAAPM; TLATRSPKSARAAPMN;
LATRSPKSARAAPMNL; ATRSPKSARAAPMNLE; TRSPKSARAAPMNLEI;
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KSARAAPMNLEIQKKR; SARAAPMNLEIQKKRD; ARAAPMNLEIQKKRDY;
RAAPMNLEIQKKRDYL; AAPMNLEIQKKRDYLP; APMNLEIQKKRDYLPR;
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QKKRDYLPRSLLQSLL; KKRDYLPRSLLQSLLQ; KRDYLPRSLLQSLLQQ;
RDYLPRSLLQSLLQQV; DYLPRSLLQSLLQQVK; YLPRSLLQSLLQQVKQ;
LPRSLLQSLLQQVKQW; PRSLLQSLLQQVKQWY; RSLLQSLLQQVKQWYF;
SLLQSLLQQVKQWYFC; LLQSLLQQVKQWYFCF; LQSLLQQVKQWYFCFS;
QSLLQQVKQWYFCFSR; SLLQQVKQWYFCFSRL; LLQQVKQWYFCFSRLH;
LQQVKQWYFCFSRLHC; QQVKQWYFCFSRLHCL; QVKQWYFCFSRLHCLH;
VKQWYFCFSRLHCLHL; KQWYFCFSRLHCLHLY; QWYFCFSRLHCLHLYK;
WYFCFSRLHCLHLYKI; YFCFSRLHCLHLYKIP; FCFSRLHCLHLYKIPA;
CFSRLHCLHLYKIPAK; FSRLHCLHLYKIPAKA; SRLHCLHLYKIPAKAL;
RLHCLHLYKIPAKALK; KSSELFFLFQSRFYQL; SSELFFLFQSRFYQLS;
SELFFLFQSRFYQLSL; ELFFLFQSRFYQLSLK; LFFLFQSRFYQLSLKL;
FFLFQSRFYQLSLKLV; FLFQSRFYQLSLKLVV; LFQSRFYQLSLKLVVT;
FQSRFYQLSLKLVVTA; QSRFYQLSLKLVVTAG; SRFYQLSLKLVVTAGA;
RFYQLSLKLVVTAGAE; FYQLSLKLVVTAGAEP; YQLSLKLVVTAGAEPW;
QLSLKLVVTAGAEPWP; LSLKLVVTAGAEPWPL; SLKLVVTAGAEPWPLS;
LKLVVTAGAEPWPLSS; KLVVTAGAEPWPLSSL; LVVTAGAEPWPLSSLT;
VVTAGAEPWPLSSLTG; VTAGAEPWPLSSLTGD; TAGAEPWPLSSLTGDK;
AGAEPWPLSSLTGDKA; GAEPWPLSSLTGDKAK; AEPWPLSSLTGDKAKI;
EPWPLSSLTGDKAKIP; PWPLSSLTGDKAKIPR; WPLSSLTGDKAKIPRL;
PLSSLTGDKAKIPRLA; LSSLTGDKAKIPRLAK; SSLTGDKAKIPRLAKH;
SLTGDKAKIPRLAKHV; LTGDKAKIPRLAKHVC; TGDKAKIPRLAKHVCH;
GDKAKIPRLAKHVCHA; DKAKIPRLAKHVCHAL; KAKIPRLAKHVCHALS;
AKIPRLAKHVCHALSF; KIPRLAKHVCHALSFL; IPRLAKHVCHALSFLR;
PRLAKHVCHALSFLRS; RLAKHVCHALSFLRSW; LAKHVCHALSFLRSWF;
AKHVCHALSFLRSWFG; KHVCHALSFLRSWFGC; HVCHALSFLRSWFGCI;
VCHALSFLRSWFGCIP; CHALSFLRSWFGCIPW; HALSFLRSWFGCIPWV;
ALSFLRSWFGCIPWVS; LSFLRSWFGCIPWVSS; SFLRSWFGCIPWVSSS;
FLRSWFGCIPWVSSSS; LRSWFGCIPWVSSSSL; GHGLAAFPCESCTFLP;
HGLAAFPCESCTFLPE; GLAAFPCESCTFLPEV; LAAFPCESCTFLPEVM;
AAFPCESCTFLPEVMV; AFPCESCTFLPEVMVW; FPCESCTFLPEVMVWL;
PCESCTFLPEVMVWLH; CESCTFLPEVMVWLHS; ESCTFLPEVMVWLHSM;
SCTFLPEVMVWLHSMG; CTFLPEVMVWLHSMGK; TFLPEVMVWLHSMGKQ;
FLPEVMVWLHSMGKQL; LPEVMVWLHSMGKQLL; PEVMVWLHSMGKQLLP;
EVMVWLHSMGKQLLPV; VMVWLHSMGKQLLPVA; MVWLHSMGKQLLPVAF;
VWLHSMGKQLLPVAFF; WLHSMGKQLLPVAFFF; LHSMGKQLLPVAFFFI;
HSMGKQLLPVAFFFII; SMGKQLLPVAFFFIIY; MGKQLLPVAFFFIIYK;
GKQLLPVAFFFIIYKR; KQLLPVAFFFIIYKRP; QLLPVAFFFIIYKRPR;

LLPVAFFFIIYKRPRP; LPVAFFFIIYKRPRPP; PVAFFFIIYKRPRPPL; VAFFFIIYKRPRPPLP; AFFFIIYKRPRPPLPP; FFFIIYKRPRPPLPPP; FFIIYKRPRPPLPPPF; FIIYKRPRPPLPPPFL; IIYKRPRPPLPPPFLS; IYKRPRPPLPPPFLSS; YKRPRPPLPPPFLSSS; KRPRPPLPPPFLSSSK; RPRPPLPPPFLSSSKG; PRPPLPPPFLSSSKGV; RPPLPPPFLSSSKGVE; PPLPPPFLSSSKGVEA; PLPPPFLSSSKGVEAF; LPPPFLSSSKGVEAFS; PPPFLSSSKGVEAFSE; PPFLSSSKGVEAFSEA
BK virus, reverse reading frame 3
13 mers:
QGRIHGAHGPFRP; KSCLGKSSLNEKS; SCLGKSSLNEKSL; CLGKSSLNEKSLF; LGKSSLNEKSLFK; GKSSLNEKSLFKE; KSSLNEKSLFKEV; FSSLPRYPVLQGM; SSLPRYPVLQGMA; SLPRYPVLQGMAY; LPRYPVLQGMAYL; PRYPVLQGMAYLF; RYPVLQGMAYLFQ; YPVLQGMAYLFQK; PVLQGMAYLFQKA; VLQGMAYLFQKAF; LQGMAYLFQKAFC; QGMAYLFQKAFCA; GMAYLFQKAFCAL; MAYLFQKAFCALP; AYLFQKAFCALPL; YLFQKAFCALPLH; LFQKAFCALPLHA; FQKAFCALPLHAM; QKAFCALPLHAMS; KAFCALPLHAMSA; KIFKKRALGLDRL; IFKKRALGLDRLL; FKKRALGLDRLLL; KKRALGLDRLLLH; RNSAMVGPNNWRN; NSAMVGPNNWRNS; SAMVGPNNWRNSL; AMVGPNNWRNSLQ; MVGPNNWRNSLQR; VGPNNWRNSLQRS; GPNNWRNSLQRSK; PNNWRNSLQRSKA; NNWRNSLQRSKAL; NWRNSLQRSKALR; VPTYGTEEWESWW; PTYGTEEWESWWS; TYGTEEWESWWSS; YGTEEWESWWSSF; GTEEWESWWSSFN; TEEWESWWSSFNE; EEWESWWSSFNEK; EWESWWSSFNEKW; WESWWSSFNEKWD; ESWWSSFNEKWDE; SWWSSFNEKWDED; WWSSFNEKWDEDL; WSSFNEKWDEDLF; SSFNEKWDEDLFC; SFNEKWDEDLFCH; FNEKWDEDLFCHE; NEKWDEDLFCHED; EKWDEDLFCHEDM; KWDEDLFCHEDMF; WDEDLFCHEDMFA; DEDLFCHEDMFAS; EDLFCHEDMFASD; DLFCHEDMFASDE; LFCHEDMFASDEE; FCHEDMFASDEEA; CHEDMFASDEEAT; HEDMFASDEEATA; EDMFASDEEATAD; DMFASDEEATADS; MFASDEEATADSQ; FASDEEATADSQH; ASDEEATADSQHS; SDEEATADSQHST; DEEATADSQHSTP; EEATADSQHSTPP; EATADSQHSTPPK; ATADSQHSTPPKK; TADSQHSTPPKKK; ADSQHSTPPKKKR; DSQHSTPPKKKRK; SQHSTPPKKKRKV; QHSTPPKKKRKVE; HSTPPKKKRKVED; STPPKKKRKVEDP; TPPKKKRKVEDPK; PPKKKRKVEDPKD; PKKKRKVEDPKDF; KKKRKVEDPKDFP; KKRKVEDPKDFPS; KRKVEDPKDFPSD; RKVEDPKDFPSDL; KVEDPKDFPSDLH; VEDPKDFPSDLHQ; EDPKDFPSDLHQF; DPKDFPSDLHQFL; PKDFPSDLHQFLS; KDFPSDLHQFLSQ; DFPSDLHQFLSQA; FPSDLHQFLSQAV; PSDLHQFLSQAVF; SDLHQFLSQAVFS; DLHQFLSQAVFSN; LHQFLSQAVFSNR; HQFLSQAVFSNRT; QFLSQAVFSNRTL; FLSQAVFSNRTLA; LSQAVFSNRTLAC; SQAVFSNRTLACF; QAVFSNRTLACFA; AVFSNRTLACFAV; VFSNRTLACFAVY; FSNRTLACFAVYT; SNRTLACFAVYTT; NRTLACFAVYTTK; RTLACFAVYTTKE; TLACFAVYTTKEK; LACFAVYTTKEKA; ACFAVYTTKEKAQ; CFAVYTTKEKAQI; FAVYTTKEKAQIL; AVYTTKEKAQILY; VYTTKEKAQILYK; YTTKEKAQILYKK; TTKEKAQILYKKL; TKEKAQILYKKLM; KEKAQILYKKLME; EKAQILYKKLMEK; KAQILYKKLMEKY; AQILYKKLMEKYS; QILYKKLMEKYSV; ILYKKLMEKYSVT; LYKKLMEKYSVTF; YKKLMEKYSVTFI; KKLMEKYSVTFIS; KLMEKYSVTFISR; LMEKYSVTFISRH; MEKYSVTFISRHM; EKYSVTFISRHMC; KYSVTFISRHMCA; YSVTFISRHMCAG; SVTFISRHMCAGH; VTFISRHMCAGHN; TFISRHMCAGHNI; FISRHMCAGHNII; ISRHMCAGHNIIF; SRHMCAGHNIIFF; RHMCAGHNIIFFL; HMCAGHNIIFFLT; MCAGHNIIFFLTP; CAGHNIIFFLTPH; AGHNIIFFLTPHR; GHNIIFFLTPHRH; HNIIFFLTPHRHR; NIIFFLTPHRHRV; IIFFLTPHRHRVS; IFFLTPHRHRVSA; FFLTPHRHRVSAI; FLTPHRHRVSAIN; LTPHRHRVSAINN; TPHRHRVSAINNF; PHRHRVSAINNFC; HRHRVSAINNFCQ; RHRVSAINNFCQK; HRVSAINNFCQKL; RVSAINNFCQKLC; VSAINNFCQKLCT; SAINNFCQKLCTF; AINNFCQKLCTFS; INNFCQKLCTFSF; NNFCQKLCTFSFL; NFCQKLCTFSFLI; FCQKLCTFSFLIC; CQKLCTFSFLICK; QKLCTFSFLICKG; KLCTFSFLICKGV; LCTFSFLICKGVN; CTFSFLICKGVNK; TFSFLICKGVNKE; FSFLICKGVNKEY; SFLICKGVNKEYL; FLICKGVNKEYLL; LICKGVNKEYLLY; ICKGVNKEYLLYS; CKGVNKEYLLYSA; KGVNKEYLLYSAL; GVNKEYLLYSALT; VNKEYLLYSALTR; NKEYLLYSALTRD; KEYLLYSALTRDP; EYLLYSALTRDPY; YLLYSALTRDPYH; LLYSALTRDPYHT; LYSALTRDPYHTI; YSALTRDPYHTIE; SALTRDPYHTIEE; ALTRDPYHTIEES; LTRDPYHTIEESI; TRDPYHTIEESIQ; RDPYHTIEESIQG; DPYHTIEESIQGG;

PYHTIEESIQGGL; YHTIEESIQGGLK; HTIEESIQGGLKE; TIEESIQGGLKEH;
IEESIQGGLKEHD; EESIQGGLKEHDF; ESIQGGLKEHDFS; SIQGGLKEHDFSP;
IQGGLKEHDFSPE; QGGLKEHDFSPEE; GGLKEHDFSPEEP; GLKEHDFSPEEPE;
LKEHDFSPEEPEE; KEHDFSPEEPEET; EHDFSPEEPEETK; HDFSPEEPEETKQ;
DFSPEEPEETKQV; FSPEEPEETKQVS; SPEEPEETKQVSW; PEEPEETKQVSWK;
EEPEETKQVSWKL; EPEETKQVSWKLI; PEETKQVSWKLIT; EETKQVSWKLITE;
ETKQVSWKLITEY; TKQVSWKLITEYA; KQVSWKLITEYAV; QVSWKLITEYAVE;
VSWKLITEYAVET; SWKLITEYAVETK; WKLITEYAVETKC; KLITEYAVETKCE;
LITEYAVETKCED; ITEYAVETKCEDV; TEYAVETKCEDVF; EYAVETKCEDVFL;
YAVETKCEDVFLL; AVETKCEDVFLLL; VETKCEDVFLLLG; ETKCEDVFLLLGM;
TKCEDVFLLLGMY; KCEDVFLLLGMYL; CEDVFLLLGMYLE; EDVFLLLGMYLEF;
DVFLLLGMYLEFQ; VFLLLGMYLEFQY; FLLLGMYLEFQYN; LLLGMYLEFQYNV;
LLGMYLEFQYNVE; LGMYLEFQYNVEE; GMYLEFQYNVEEC; MYLEFQYNVEECK;
YLEFQYNVEECKK; LEFQYNVEECKKC; EFQYNVEECKKCQ; FQYNVEECKKCQK;
QYNVEECKKCQKK; YNVEECKKCQKKD; NVEECKKCQKKDQ; VEECKKCQKKDQP;
EECKKCQKKDQPY; ECKKCQKKDQPYH; CKKCQKKDQPYHF; KKCQKKDQPYHFK;
KCQKKDQPYHFKY; CQKKDQPYHFKYH; QKKDQPYHFKYHE; KKDQPYHFKYHEK;
KDQPYHFKYHEKH; DQPYHFKYHEKHF; QPYHFKYHEKHFA; PYHFKYHEKHFAN;
YHFKYHEKHFANA; HFKYHEKHFANAI; FKYHEKHFANAII; KYHEKHFANAIIF;
YHEKHFANAIIFA; HEKHFANAIIFAE; EKHFANAIIFAES; KHFANAIIFAESK;
HFANAIIFAESKN; FANAIIFAESKNQ; ANAIIFAESKNQK; NAIIFAESKNQKS;
AIIFAESKNQKSI; IIFAESKNQKSIC; IFAESKNQKSICQ; FAESKNQKSICQQ;
AESKNQKSICQQA; ESKNQKSICQQAV; SKNQKSICQQAVD; KNQKSICQQAVDT;
NQKSICQQAVDTV; QKSICQQAVDTVL; KSICQQAVDTVLA; SICQQAVDTVLAK;
ICQQAVDTVLAKK; CQQAVDTVLAKKR; QQAVDTVLAKKRV; QAVDTVLAKKRVD;
AVDTVLAKKRVDT; VDTVLAKKRVDTL; DTVLAKKRVDTLH; TVLAKKRVDTLHM;
VLAKKRVDTLHMT; LAKKRVDTLHMTR; AKKRVDTLHMTRE; KKRVDTLHMTREE;
KRVDTLHMTREEM; RVDTLHMTREEML; VDTLHMTREEMLT; DTLHMTREEMLTE;
TLHMTREEMLTER; LHMTREEMLTERF; HMTREEMLTERFN; MTREEMLTERFNH;
TREEMLTERFNHI; REEMLTERFNHIL; EEMLTERFNHILD; EMLTERFNHILDK;
MLTERFNHILDKM; LTERFNHILDKMD; TERFNHILDKMDL; ERFNHILDKMDLI;
RFNHILDKMDLIF; FNHILDKMDLIFG; NHILDKMDLIFGA; HILDKMDLIFGAH;
ILDKMDLIFGAHG; LDKMDLIFGAHGN; DKMDLIFGAHGNA; KMDLIFGAHGNAV;
MDLIFGAHGNAVL; DLIFGAHGNAVLE; LIFGAHGNAVLEQ; IFGAHGNAVLEQY;
FGAHGNAVLEQYM; GAHGNAVLEQYMA; AHGNAVLEQYMAG; HGNAVLEQYMAGV;
GNAVLEQYMAGVA; NAVLEQYMAGVAW; AVLEQYMAGVAWL; VLEQYMAGVAWLH;
LEQYMAGVAWLHC; EQYMAGVAWLHCL; QYMAGVAWLHCLL; YMAGVAWLHCLLP;
MAGVAWLHCLLPK; AGVAWLHCLLPKM; GVAWLHCLLPKMD; VAWLHCLLPKMDS;
AWLHCLLPKMDSV; WLHCLLPKMDSVI; LHCLLPKMDSVIF; HCLLPKMDSVIFD;
CLLPKMDSVIFDF; LLPKMDSVIFDFL; LPKMDSVIFDFLH; PKMDSVIFDFLHC;
KMDSVIFDFLHCI; MDSVIFDFLHCIV; DSVIFDFLHCIVF; SVIFDFLHCIVFN;
VIFDFLHCIVFNV; IFDFLHCIVFNVP; FDFLHCIVFNVPK; DFLHCIVFNVPKR;
FLHCIVFNVPKRR; LHCIVFNVPKRRY; HCIVFNVPKRRYW; CIVFNVPKRRYWL;
IVFNVPKRRYWLF; VFNVPKRRYWLFK; FNVPKRRYWLFKG; NVPKRRYWLFKGP;
VPKRRYWLFKGPI; PKRRYWLFKGPID; KRRYWLFKGPIDS; RRYWLFKGPIDSG;
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LNVNLPMERLTFE; NVNLPMERLTFEL; VNLPMERLTFELG; NLPMERLTFELGV;
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YMVVFEDVKGTGA; MVVFEDVKGTGAE; VVFEDVKGTGAES; VFEDVKGTGAESK;
FEDVKGTGAESKD; EDVKGTGAESKDL; DVKGTGAESKDLP; VKGTGAESKDLPS;

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14 mers:
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AQILYKKLMEKYSV; QILYKKLMEKYSVT; ILYKKLMEKYSVTF;
LYKKLMEKYSVTFI; YKKLMEKYSVTFIS; KKLMEKYSVTFISR;
KLMEKYSVTFISRH; LMEKYSVTFISRHM; MEKYSVTFISRHMC;
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FISRHMCAGHNIIF; ISRHMCAGHNIIFF; SRHMCAGHNIIFFL;
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IFFLTPHRHRVSAI; FFLTPHRHRVSAIN; FLTPHRHRVSAINN;
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SFLICKGVNKEYLL; FLICKGVNKEYLLY; LICKGVNKEYLLYS;
ICKGVNKEYLLYSA; CKGVNKEYLLYSAL; KGVNKEYLLYSALT;
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KEYLLYSALTRDPY; EYLLYSALTRDPYH; YLLYSALTRDPYHT;
LLYSALTRDPYHTI; LYSALTRDPYHTIE; YSALTRDPYHTIEE;
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PYHTIEESIQGGLK; YHTIEESIQGGLKE; HTIEESIQGGLKEH;
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ESIQGGLKEHDFSP; SIQGGLKEHDFSPE; IQGGLKEHDFSPEE;
QGGLKEHDFSPEEP; GGLKEHDFSPEEPE; GLKEHDFSPEEPEE;
LKEHDFSPEEPEET; KEHDFSPEEPEETK; EHDFSPEEPEETKQ;
HDFSPEEPEETKQV; DFSPEEPEETKQVS; FSPEEPEETKQVSW;
SPEEPEETKQVSWK; PEEPEETKQVSWKL; EEPEETKQVSWKLI;
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HMTREEMLTERFNH; MTREEMLTERFNHI; TREEMLTERFNHIL;
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FRPVADFATDIQSR; RPVADFATDIQSRI; PVADFATDIQSRIV;
VADFATDIQSRIVE; ADFATDIQSRIVEW; DFATDIQSRIVEWK;
FATDIQSRIVEWKE; ATDIQSRIVEWKER; TDIQSRIVEWKERL;
DIQSRIVEWKERLD; IQSRIVEWKERLDS; QSRIVEWKERLDSE;
SRIVEWKERLDSEI; RIVEWKERLDSEIS; IVEWKERLDSEISM;
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VYTVFTSTKFQQKL; NKNKNPLSSFFCSS; KNKNPLSSFFCSSP;
NKNPLSSFFCSSPG; KNPLSSFFCSSPGF; NPLSSFFCSSPGFT;
PLSSFFCSSPGFTN; LSSFFCSSPGFTNF; SSFFCSSPGFTNFH;
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RPRFLGSQNMSVMH; PRFLGSQNMSVMHF; RFLGSQNMSVMHFP;
FLGSQNMSVMHFPS; AAPPCESCTFLPEV; APPCESCTFLPEVM;
PPCESCTFLPEVMV; PCESCTFLPEVMVW; CESCTFLPEVMVWL;
ESCTFLPEVMVWLH; SCTFLPEVMVWLHS; CTFLPEVMVWLHSP;
TFLPEVMVWLHSPV; FLPEVMVWLHSPVS; LPEVMVWLHSPVSH;
PEVMVWLHSPVSHA; EVMVWLHSPVSHAL; VMVWLHSPVSHALS;
MVWLHSPVSHALSF; VWLHSPVSHALSFL; WLHSPVSHALSFLR;
LHSPVSHALSFLRS; HSPVSHALSFLRSW; SPVSHALSFLRSWF;
PVSHALSFLRSWFG; VSHALSFLRSWFGC; SHALSFLRSWFGCI;
HALSFLRSWFGCIP; ALSFLRSWFGCIPW; LSFLRSWFGCIPWV;
SFLRSWFGCIPWVS; FLRSWFGCIPWVSS; LRSWFGCIPWVSSS;
RSWFGCIPWVSSSS; SWFGCIPWVSSSSL; WFGCIPWVSSSSLW;
FGCIPWVSSSSLWP; GCIPWVSSSSLWPF; CIPWVSSSSLWPFF;
IPWVSSSSLWPFFL; YIRGRGRLCLHPFS; IRGRGRLCLHPFSQ;
RGRGRLCLHPFSQV; GRGRLCLHPFSQVV; RGRLCLHPFSQVVR;
GRLCLHPFSQVVRV; RLCLHPFSQVVRVW; LCLHPFSQVVRVWR;
CLHPFSQVVRVWRL; LHPFSQVVRVWRLF; HPFSQVVRVWRLFL;
PFSQVVRVWRLFLR; FSQVVRVWRLFLRP; SQVVRVWRLFLRPS;
QVVRVWRLFLRPSK; VVRVWRLFLRPSKT; VRVWRLFLRPSKTI;
RVWRLFLRPSKTIW; VWRLFLRPSKTIWG; WRLFLRPSKTIWGN;
RLFLRPSKTIWGNP; LFLRPSKTIWGNPY; FLRPSKTIWGNPYS;
LRPSKTIWGNPYSF; RPSKTIWGNPYSFA; PSKTIWGNPYSFAI;
SKTIWGNPYSFAIF; KTIWGNPYSFAIFA; TIWGNPYSFAIFAK

15 mers:
KSCLGKSSLNEKSLF; SCLGKSSLNEKSLFK; CLGKSSLNEKSLFKE;
LGKSSLNEKSLFKEV; FSSLPRYPVLQGMAY; SSLPRYPVLQGMAYL;
SLPRYPVLQGMAYLF; LPRYPVLQGMAYLFQ; PRYPVLQGMAYLFQK;
RYPVLQGMAYLFQKA; YPVLQGMAYLFQKAF; PVLQGMAYLFQKAFC;
VLQGMAYLFQKAFCA; LQGMAYLFQKAFCAL; QGMAYLFQKAFCALP;
GMAYLFQKAFCALPL; MAYLFQKAFCALPLH; AYLFQKAFCALPLHA;
YLFQKAFCALPLHAM; LFQKAFCALPLHAMS; FQKAFCALPLHAMSA;
KIFKKRALGLDRLLL; IFKKRALGLDRLLLH; RNSAMVGPNNWRNSL;
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MVGPNNWRNSLQRSK; VGPNNWRNSLQRSKA; GPNNWRNSLQRSKAL;
PNNWRNSLQRSKALR; VPTYGTEEWESWWSS; PTYGTEEWESWWSSF;
TYGTEEWESWWSSFN; YGTEEWESWWSSFNE; GTEEWESWWSSFNEK;
TEEWESWWSSFNEKW; EEWESWWSSFNEKWD; EWESWWSSFNEKWDE;
WESWWSSFNEKWDED; ESWWSSFNEKWDEDL; SWWSSFNEKWDEDLF;
WWSSFNEKWDEDLFC; WSSFNEKWDEDLFCH; SSFNEKWDEDLFCHE;
SFNEKWDEDLFCHED; FNEKWDEDLFCHEDM; NEKWDEDLFCHEDMF;
EKWDEDLFCHEDMFA; KWDEDLFCHEDMFAS; WDEDLFCHEDMFASD;
DEDLFCHEDMFASDE; EDLFCHEDMFASDEE; DLFCHEDMFASDEEA;
LFCHEDMFASDEEAT; FCHEDMFASDEEATA; CHEDMFASDEEATAD;
HEDMFASDEEATADS; EDMFASDEEATADSQ; DMFASDEEATADSQH;
MFASDEEATADSQHS; FASDEEATADSQHST; ASDEEATADSQHSTP;
SDEEATADSQHSTPP; DEEATADSQHSTPPK; EEATADSQHSTPPKK;
EATADSQHSTPPKKK; ATADSQHSTPPKKKR; TADSQHSTPPKKKRK;
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QHSTPPKKKRKVEDP; HSTPPKKKRKVEDPK; STPPKKKRKVEDPKD;
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KDFPSDLHQFLSQAV; DFPSDLHQFLSQAVF; FPSDLHQFLSQAVFS;
PSDLHQFLSQAVFSN; SDLHQFLSQAVFSNR; DLHQFLSQAVFSNRT;
LHQFLSQAVFSNRTL; HQFLSQAVFSNRTLA; QFLSQAVFSNRTLAC;
FLSQAVFSNRTLACF; LSQAVFSNRTLACFA; SQAVFSNRTLACFAV;
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FSNRTLACFAVYTTK; SNRTLACFAVYTTKE; NRTLACFAVYTTKEK;
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EKAQILYKKLMEKYS; KAQILYKKLMEKYSV; AQILYKKLMEKYSVT;
QILYKKLMEKYSVTF; ILYKKLMEKYSVTFI; LYKKLMEKYSVTFIS;
YKKLMEKYSVTFISR; KKLMEKYSVTFISRH; KLMEKYSVTFISRHM;
LMEKYSVTFISRHMC; MEKYSVTFISRHMCA; EKYSVTFISRHMCAG;
KYSVTFISRHMCAGH; YSVTFISRHMCAGHN; SVTFISRHMCAGHNI;
VTFISRHMCAGHNII; TFISRHMCAGHNIIF; FISRHMCAGHNIIFF;
ISRHMCAGHNIIFFL; SRHMCAGHNIIFFLT; RHMCAGHNIIFFLTP;
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NIIFFLTPHRHRVSA; IIFFLTPHRHRVSAI; IFFLTPHRHRVSAIN;
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VSAINNFCQKLCTFS; SAINNFCQKLCTFSF; AINNFCQKLCTFSFL;
INNFCQKLCTFSFLI; NNFCQKLCTFSFLIC; NFCQKLCTFSFLICK;
FCQKLCTFSFLICKG; CQKLCTFSFLICKGV; QKLCTFSFLICKGVN;
KLCTFSFLICKGVNK; LCTFSFLICKGVNKE; CTFSFLICKGVNKEY;
TFSFLICKGVNKEYL; FSFLICKGVNKEYLL; SFLICKGVNKEYLLY;
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VNKEYLLYSALTRDP; NKEYLLYSALTRDPY; KEYLLYSALTRDPYH;
EYLLYSALTRDPYHT; YLLYSALTRDPYHTI; LLYSALTRDPYHTIE;
LYSALTRDPYHTIEE; YSALTRDPYHTIEES; SALTRDPYHTIEESI;
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YHTIEESIQGGLKEH; HTIEESIQGGLKEHD; TIEESIQGGLKEHDF;
IEESIQGGLKEHDFS; EESIQGGLKEHDFSP; ESIQGGLKEHDFSPE;
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GGLKEHDFSPEEPEE; GLKEHDFSPEEPEET; LKEHDFSPEEPEETK;
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DFSPEEPEETKQVSW; FSPEEPEETKQVSWK; SPEEPEETKQVSWKL;
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EDVFLLLGMYLEFQY; DVFLLLGMYLEFQYN; VFLLLGMYLEFQYNV;
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LGMYLEFQYNVEECK; GMYLEFQYNVEECKK; MYLEFQYNVEECKKC;
YLEFQYNVEECKKCQ; LEFQYNVEECKKCQK; EFQYNVEECKKCQKK;
FQYNVEECKKCQKKD; QYNVEECKKCQKKDQ; YNVEECKKCQKKDQP;

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HFKYHEKHFANAIIF; FKYHEKHFANAIIFA; KYHEKHFANAIIFAE;
YHEKHFANAIIFAES; HEKHFANAIIFAESK; EKHFANAIIFAESKN;
KHFANAIIFAESKNQ; HFANAIIFAESKNQK; FANAIIFAESKNQKS;
ANAIIFAESKNQKSI; NAIIFAESKNQKSIC; AIIFAESKNQKSICQ;
IIFAESKNQKSICQQ; IFAESKNQKSICQQA; FAESKNQKSICQQAV;
AESKNQKSICQQAVD; ESKNQKSICQQAVDT; SKNQKSICQQAVDTV;
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TVLAKKRVDTLHMTR; VLAKKRVDTLHMTRE; LAKKRVDTLHMTREE;
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MTREEMLTERFNHIL; TREEMLTERFNHILD; REEMLTERFNHILDK;
EEMLTERFNHILDKM; EMLTERFNHILDKMD; MLTERFNHILDKMDL;
LTERFNHILDKMDLI; TERFNHILDKMDLIF; ERFNHILDKMDLIFG;
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FGAHGNAVLEQYMAG; GAHGNAVLEQYMAGV; AHGNAVLEQYMAGVA;
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SVIFDFLHCIVFNVP; VIFDFLHCIVFNVPK; IFDFLHCIVFNVPKR;
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LNVNLPMERLTFELG; NVNLPMERLTFELGV; VNLPMERLTFELGVA;
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DQYMVVFEDVKGTGA; QYMVVFEDVKGTGAE; YMVVFEDVKGTGAES;
MVVFEDVKGTGAESK; VVFEDVKGTGAESKD; VFEDVKGTGAESKDL;
FEDVKGTGAESKDLP; EDVKGTGAESKDLPS; DVKGTGAESKDLPSG;

VKGTGAESKDLPSGH; KGTGAESKDLPSGHG; GTGAESKDLPSGHGI;
TGAESKDLPSGHGIN; GAESKDLPSGHGINN; AESKDLPSGHGINNL;
ESKDLPSGHGINNLD; SKDLPSGHGINNLDS; KDLPSGHGINNLDSL;
DLPSGHGINNLDSLR; LPSGHGINNLDSLRD; PSGHGINNLDSLRDY;
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IWFRPVADFATDIQS; WFRPVADFATDIQSR; FRPVADFATDIQSRI;
RPVADFATDIQSRIV; PVADFATDIQSRIVE; VADFATDIQSRIVEW;
ADFATDIQSRIVEWK; DFATDIQSRIVEWKE; FATDIQSRIVEWKER;
ATDIQSRIVEWKERL; TDIQSRIVEWKERLD; DIQSRIVEWKERLDS;
IQSRIVEWKERLDSE; QSRIVEWKERLDSEI; SRIVEWKERLDSEIS;
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EWKERLDSEISMYTF; WKERLDSEISMYTFS; KERLDSEISMYTFSR;
ERLDSEISMYTFSRM; RLDSEISMYTFSRMK; LDSEISMYTFSRMKY;
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GKCILDITREEDSET; KCILDITREEDSETE; CILDITREEDSETED;
ILDITREEDSETEDS; LDITREEDSETEDSG; DITREEDSETEDSGH;
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VSDTSAPAEDSQRSD; SDTSAPAEDSQRSDP; DTSAPAEDSQRSDPH;
TSAPAEDSQRSDPHS; SAPAEDSQRSDPHSQ; APAEDSQRSDPHSQE;
PAEDSQRSDPHSQEL; AEDSQRSDPHSQELH; EDSQRSDPHSQELHL;
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LQLSLFVNISYHIWV; QLSLFVNISYHIWVP; LSLFVNISYHIWVPW;
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VNISYHIWVPWKSFC; NISYHIWVPWKSFCA; ISYHIWVPWKSFCAI;
SYHIWVPWKSFCAIK; YHIWVPWKSFCAIKH; HIWVPWKSFCAIKHP;
IWVPWKSFCAIKHPN; WVPWKSFCAIKHPNL; VPWKSFCAIKHPNLF;
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WVRILYRSFSQADLK; VRILYRSFSQADLKI; RILYRSFSQADLKIS;
ILYRSFSQADLKISC; LYRSFSQADLKISCK; YRSFSQADLKISCKA;
RSFSQADLKISCKAS; SFSQADLKISCKASP; FSQADLKISCKASPL;
SQADLKISCKASPLL; QADLKISCKASPLLC; ADLKISCKASPLLCS;
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KASPLLCSRAVSKQA; ASPLLCSRAVSKQAT; SPLLCSRAVSKQATN;
PLLCSRAVSKQATNI; LLCSRAVSKQATNIS; LCSRAVSKQATNISS;
NIQAISFTKRPHTLF; IQAISFTKRPHTLFI; QHCGSCVGHMKYWGN;
HCGSCVGHMKYWGNI; CGSCVGHMKYWGNIF; GSCVGHMKYWGNIFP;
SCVGHMKYWGNIFPS; CVGHMKYWGNIFPSC; VGHMKYWGNIFPSCE;
GHMKYWGNIFPSCES; HMKYWGNIFPSCESP; MKYWGNIFPSCESPK;
KYWGNIFPSCESPKI; YWGNIFPSCESPKIP; WGNIFPSCESPKIPS;
GNIFPSCESPKIPSI; NIFPSCESPKIPSIF; IFPSCESPKIPSIFI;
FPSCESPKIPSIFIS; PSCESPKIPSIFIST; SCESPKIPSIFISTG;
CESPKIPSIFISTGI; ESPKIPSIFISTGIR; SPKIPSIFISTGIRY;
PKIPSIFISTGIRYP; KIPSIFISTGIRYPA; IPSIFISTGIRYPAL;
PSIFISTGIRYPALN; SIFISTGIRYPALNW; IFISTGIRYPALNWI;
FISTGIRYPALNWIS; ISTGIRYPALNWISI; STGIRYPALNWISIV;
TGIRYPALNWISIVF; GIRYPALNWISIVFV; IRYPALNWISIVFVQ;
RYPALNWISIVFVQI; YPALNWISIVFVQIG; PALNWISIVFVQIGL;
ALNWISIVFVQIGLM; LNWISIVFVQIGLMV; NWISIVFVQIGLMVS;
WISIVFVQIGLMVSI; ISIVFVQIGLMVSIH; SIVFVQIGLMVSIHY;
IVFVQIGLMVSIHYL; VFVQIGLMVSIHYLG; FVQIGLMVSIHYLGL;
VQIGLMVSIHYLGLG; QIGLMVSIHYLGLGC; IGLMVSIHYLGLGCW;
GLMVSIHYLGLGCWV; LMVSIHYLGLGCWVF; MVSIHYLGLGCWVFR;
VSIHYLGLGCWVFRG; SIHYLGLGCWVFRGY; IHYLGLGCWVFRGYS;
HYLGLGCWVFRGYST; YLGLGCWVFRGYSTI; LGLGCWVFRGYSTIR;
GLGCWVFRGYSTIRV; LGCWVFRGYSTIRVL; HSLHFQGFSTYSKEV;
SLHFQGFSTYSKEVE; LHFQGFSTYSKEVEI; HFQGFSTYSKEVEIT;
FQGFSTYSKEVEITA; QGFSTYSKEVEITAL; GFSTYSKEVEITALN;

FSTYSKEVEITALNR; STYSKEVEITALNRF; TYSKEVEITALNRFS;
YSKEVEITALNRFSS; SKEVEITALNRFSST; KEVEITALNRFSSTM;
EVEITALNRFSSTML; VEITALNRFSSTMLM; EITALNRFSSTMLMH;
ITALNRFSSTMLMHF; TALNRFSSTMLMHFL; PCMKVKHASYSNNLC;
CMKVKHASYSNNLCL; MKVKHASYSNNLCLY; KVKHASYSNNLCLYS;
VKHASYSNNLCLYSY; KHASYSNNLCLYSYS; HASYSNNLCLYSYSL;
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GNSCCAVTGKHFSLW; NSCCAVTGKHFSLWA; SCCAVTGKHFSLWAI;
CCAVTGKHFSLWAIT; CAVTGKHFSLWAITA; AVTGKHFSLWAITAK;
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CESCTFLPEVMVWLH; ESCTFLPEVMVWLHS; SCTFLPEVMVWLHSP;
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16 mers:
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FSSLPRYPVLQGMAYL; SSLPRYPVLQGMAYLF; SLPRYPVLQGMAYLFQ;
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VDTVLAKKRVDTLHMT; DTVLAKKRVDTLHMTR; TVLAKKRVDTLHMTRE;
VLAKKRVDTLHMTREE; LAKKRVDTLHMTREEM; AKKRVDTLHMTREEML;
KKRVDTLHMTREEMLT; KRVDTLHMTREEMLTE; RVDTLHMTREEMLTER;

VDTLHMTREEMLTERF; DTLHMTREEMLTERFN; TLHMTREEMLTERFNH;
LHMTREEMLTERFNHI; HMTREEMLTERFNHIL; MTREEMLTERFNHILD;
TREEMLTERFNHILDK; REEMLTERFNHILDKM; EEMLTERFNHILDKMD;
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TQIFPPGLVTMNEYPV; QIFPPGLVTMNEYPVP; IFPPGLVTMNEYPVPK;
FPPGLVTMNEYPVPKT; PPGLVTMNEYPVPKTL; PGLVTMNEYPVPKTLQ;
GLVTMNEYPVPKTLQA; LVTMNEYPVPKTLQAR; VTMNEYPVPKTLQARF;

TMNEYPVPKTLQARFV; MNEYPVPKTLQARFVR; NEYPVPKTLQARFVRQ;
EYPVPKTLQARFVRQI; YPVPKTLQARFVRQID; PVPKTLQARFVRQIDF;
VPKTLQARFVRQIDFR; PKTLQARFVRQIDFRP; KTLQARFVRQIDFRPK;
TLQARFVRQIDFRPKI; LQARFVRQIDFRPKIY; QARFVRQIDFRPKIYL;
ARFVRQIDFRPKIYLR; RFVRQIDFRPKIYLRK; FVRQIDFRPKIYLRKS;
VRQIDFRPKIYLRKSL; RQIDFRPKIYLRKSLQ; QIDFRPKIYLRKSLQN;
IDFRPKIYLRKSLQNS; DFRPKIYLRKSLQNSE; FRPKIYLRKSLQNSEF;
RPKIYLRKSLQNSEFL; PKIYLRKSLQNSEFLL; KIYLRKSLQNSEFLLE;
IYLRKSLQNSEFLLEK; YLRKSLQNSEFLLEKR; LRKSLQNSEFLLEKRI;
RKSLQNSEFLLEKRIL; KSLQNSEFLLEKRILQ; SLQNSEFLLEKRILQS;
LQNSEFLLEKRILQSG; QNSEFLLEKRILQSGM; NSEFLLEKRILQSGMT;
SEFLLEKRILQSGMTL; EFLLEKRILQSGMTLL; FLLEKRILQSGMTLLL;
LLEKRILQSGMTLLLL; LEKRILQSGMTLLLLL; EKRILQSGMTLLLLLI;
KRILQSGMTLLLLLIW; RILQSGMTLLLLLIWF; ILQSGMTLLLLLIWFR;
LQSGMTLLLLLIWFRP; QSGMTLLLLLIWFRPV; SGMTLLLLLIWFRPVA;
GMTLLLLLIWFRPVAD; MTLLLLLIWFRPVADF; TLLLLLIWFRPVADFA;
LLLLLIWFRPVADFAT; LLLLIWFRPVADFATD; LLLIWFRPVADFATDI;
LLIWFRPVADFATDIQ; LIWFRPVADFATDIQS; IWFRPVADFATDIQSR;
WFRPVADFATDIQSRI; FRPVADFATDIQSRIV; RPVADFATDIQSRIVE;
PVADFATDIQSRIVEW; VADFATDIQSRIVEWK; ADFATDIQSRIVEWKE;
DFATDIQSRIVEWKER; FATDIQSRIVEWKERL; ATDIQSRIVEWKERLD;
TDIQSRIVEWKERLDS; DIQSRIVEWKERLDSE; IQSRIVEWKERLDSEI;
QSRIVEWKERLDSEIS; SRIVEWKERLDSEISM; RIVEWKERLDSEISMY;
IVEWKERLDSEISMYT; VEWKERLDSEISMYTF; EWKERLDSEISMYTFS;
WKERLDSEISMYTFSR; KERLDSEISMYTFSRM; ERLDSEISMYTFSRMK;
RLDSEISMYTFSRMKY; LDSEISMYTFSRMKYN; DSEISMYTFSRMKYNI;
SEISMYTFSRMKYNIC; EISMYTFSRMKYNICM; ISMYTFSRMKYNICMG;
SMYTFSRMKYNICMGK; MYTFSRMKYNICMGKC; YTFSRMKYNICMGKCI;
TFSRMKYNICMGKCIL; FSRMKYNICMGKCILD; SRMKYNICMGKCILDI;
RMKYNICMGKCILDIT; MKYNICMGKCILDITR; KYNICMGKCILDITRE;
YNICMGKCILDITREE; NICMGKCILDITREED; ICMGKCILDITREEDS;
CMGKCILDITREEDSE; MGKCILDITREEDSET; GKCILDITREEDSETE;
KCILDITREEDSETED; CILDITREEDSETEDS; ILDITREEDSETEDSG;
LDITREEDSETEDSGH; DITREEDSETEDSGHG; ITREEDSETEDSGHGS;
TREEDSETEDSGHGSS; REEDSETEDSGHGSST; EEDSETEDSGHGSSTE;
EDSETEDSGHGSSTES; DSETEDSGHGSSTESQ; SETEDSGHGSSTESQS;
ETEDSGHGSSTESQSQ; TEDSGHGSSTESQSQC; EDSGHGSSTESQSQCS;
DSGHGSSTESQSQCSS; SGHGSSTESQSQCSSQ; GHGSSTESQSQCSSQV;
HGSSTESQSQCSSQVS; GSSTESQSQCSSQVSD; SSTESQSQCSSQVSDT;
STESQSQCSSQVSDTS; TESQSQCSSQVSDTSA; ESQSQCSSQVSDTSAP;
SQSQCSSQVSDTSAPA; QSQCSSQVSDTSAPAE; SQCSSQVSDTSAPAED;
QCSSQVSDTSAPAEDS; CSSQVSDTSAPAEDSQ; SSQVSDTSAPAEDSQR;
SQVSDTSAPAEDSQRS; QVSDTSAPAEDSQRSD; VSDTSAPAEDSQRSDP;
SDTSAPAEDSQRSDPH; DTSAPAEDSQRSDPHS; TSAPAEDSQRSDPHSQ;
SAPAEDSQRSDPHSQE; APAEDSQRSDPHSQEL; PAEDSQRSDPHSQELH;
AEDSQRSDPHSQELHL; EDSQRSDPHSQELHLC; DSQRSDPHSQELHLCK;
SQRSDPHSQELHLCKG; QRSDPHSQELHLCKGF; RSDPHSQELHLCKGFQ;
SDPHSQELHLCKGFQC; DPHSQELHLCKGFQCF; PHSQELHLCKGFQCFK;
HSQELHLCKGFQCFKR; SQELHLCKGFQCFKRP; QELHLCKGFQCFKRPK;
ELHLCKGFQCFKRPKT; LHLCKGFQCFKRPKTP; HLCKGFQCFKRPKTPP;
LCKGFQCFKRPKTPPP; CKGFQCFKRPKTPPPK; MYMYNKSTCLKHFGLQ;
YMYNKSTCLKHFGLQL; MYNKSTCLKHFGLQLS; YNKSTCLKHFGLQLSL;
NKSTCLKHFGLQLSLF; KSTCLKHFGLQLSLFV; STCLKHFGLQLSLFVN;
TCLKHFGLQLSLFVNI; CLKHFGLQLSLFVNIS; LKHFGLQLSLFVNISY;
KHFGLQLSLFVNISYH; HFGLQLSLFVNISYHI; FGLQLSLFVNISYHIW;
GLQLSLFVNISYHIWV; LQLSLFVNISYHIWVP; QLSLFVNISYHIWVPW;
LSLFVNISYHIWVPWK; SLFVNISYHIWVPWKS; LFVNISYHIWVPWKSF;
FVNISYHIWVPWKSFC; VNISYHIWVPWKSFCA; NISYHIWVPWKSFCAI;
ISYHIWVPWKSFCAIK; SYHIWVPWKSFCAIKH; YHIWVPWKSFCAIKHP;

HIWVPWKSFCAIKHPN; IWVPWKSFCAIKHPNL; WVPWKSFCAIKHPNLF;
VPWKSFCAIKHPNLFY; PWKSFCAIKHPNLFYL; WKSFCAIKHPNLFYLG;
KSFCAIKHPNLFYLGF; SFCAIKHPNLFYLGFH; FCAIKHPNLFYLGFHT;
CAIKHPNLFYLGFHTI; AIKHPNLFYLGFHTIH; IKHPNLFYLGFHTIHR;
KHPNLFYLGFHTIHRL; HPNLFYLGFHTIHRLP; PNLFYLGFHTIHRLPI;
NLFYLGFHTIHRLPIH; LFYLGFHTIHRLPIHS; FYLGFHTIHRLPIHSL;
YLGFHTIHRLPIHSLG; LGFHTIHRLPIHSLGS; GFHTIHRLPIHSLGSP;
FHTIHRLPIHSLGSPV; HTIHRLPIHSLGSPVY; TIHRLPIHSLGSPVYK;
IHRLPIHSLGSPVYKV; HRLPIHSLGSPVYKVT; QKGNWVRILYRSFSQA;
KGNWVRILYRSFSQAD; GNWVRILYRSFSQADL; NWVRILYRSFSQADLK;
WVRILYRSFSQADLKI; VRILYRSFSQADLKIS; RILYRSFSQADLKISC;
ILYRSFSQADLKISCK; LYRSFSQADLKISCKA; YRSFSQADLKISCKAS;
RSFSQADLKISCKASP; SFSQADLKISCKASPL; FSQADLKISCKASPLL;
SQADLKISCKASPLLC; QADLKISCKASPLLCS; ADLKISCKASPLLCSR;
DLKISCKASPLLCSRA; LKISCKASPLLCSRAV; KISCKASPLLCSRAVS;
ISCKASPLLCSRAVSK; SCKASPLLCSRAVSKQ; CKASPLLCSRAVSKQA;
KASPLLCSRAVSKQAT; ASPLLCSRAVSKQATN; SPLLCSRAVSKQATNI;
PLLCSRAVSKQATNIS; LLCSRAVSKQATNISS; NIQAISFTKRPHTLFI;
QHCGSCVGHMKYWGNI; HCGSCVGHMKYWGNIF; CGSCVGHMKYWGNIFP;
GSCVGHMKYWGNIFPS; SCVGHMKYWGNIFPSC; CVGHMKYWGNIFPSCE;
VGHMKYWGNIFPSCES; GHMKYWGNIFPSCESP; HMKYWGNIFPSCESPK;
MKYWGNIFPSCESPKI; KYWGNIFPSCESPKIP; YWGNIFPSCESPKIPS;
WGNIFPSCESPKIPSI; GNIFPSCESPKIPSIF; NIFPSCESPKIPSIFI;
IFPSCESPKIPSIFIS; FPSCESPKIPSIFIST; PSCESPKIPSIFISTG;
SCESPKIPSIFISTGI; CESPKIPSIFISTGIR; ESPKIPSIFISTGIRY;
SPKIPSIFISTGIRYP; PKIPSIFISTGIRYPA; KIPSIFISTGIRYPAL;
IPSIFISTGIRYPALN; PSIFISTGIRYPALNW; SIFISTGIRYPALNWI;
IFISTGIRYPALNWIS; FISTGIRYPALNWISI; ISTGIRYPALNWISIV;
STGIRYPALNWISIVF; TGIRYPALNWISIVFV; GIRYPALNWISIVFVQ;
IRYPALNWISIVFVQI; RYPALNWISIVFVQIG; YPALNWISIVFVQIGL;
PALNWISIVFVQIGLM; ALNWISIVFVQIGLMV; LNWISIVFVQIGLMVS;
NWISIVFVQIGLMVSI; WISIVFVQIGLMVSIH; ISIVFVQIGLMVSIHY;
SIVFVQIGLMVSIHYL; IVFVQIGLMVSIHYLG; VFVQIGLMVSIHYLGL;
FVQIGLMVSIHYLGLG; VQIGLMVSIHYLGLGC; QIGLMVSIHYLGLGCW;
IGLMVSIHYLGLGCWV; GLMVSIHYLGLGCWVF; LMVSIHYLGLGCWVFR;
MVSIHYLGLGCWVFRG; VSIHYLGLGCWVFRGY; SIHYLGLGCWVFRGYS;
IHYLGLGCWVFRGYST; HYLGLGCWVFRGYSTI; YLGLGCWVFRGYSTIR;
LGLGCWVFRGYSTIRV; GLGCWVFRGYSTIRVL; HSLHFQGFSTYSKEVE;
SLHFQGFSTYSKEVEI; LHFQGFSTYSKEVEIT; HFQGFSTYSKEVEITA;
FQGFSTYSKEVEITAL; QGFSTYSKEVEITALN; GFSTYSKEVEITALNR;
FSTYSKEVEITALNRF; STYSKEVEITALNRFS; TYSKEVEITALNRFSS;
YSKEVEITALNRFSST; SKEVEITALNRFSSTM; KEVEITALNRFSSTML;
EVEITALNRFSSTMLM; VEITALNRFSSTMLMH; EITALNRFSSTMLMHF;
ITALNRFSSTMLMHFL; PCMKVKHASYSNNLCL; CMKVKHASYSNNLCLY;
MKVKHASYSNNLCLYS; KVKHASYSNNLCLYSY; VKHASYSNNLCLYSYS;
KHASYSNNLCLYSYSL; HASYSNNLCLYSYSLP; ASYSNNLCLYSYSLPH;
SYSNNLCLYSYSLPHQ; IGEGNSCCAVTGKHFS; GEGNSCCAVTGKHFSL;
EGNSCCAVTGKHFSLW; GNSCCAVTGKHFSLWA; NSCCAVTGKHFSLWAI;
SCCAVTGKHFSLWAIT; CCAVTGKHFSLWAITA; CAVTGKHFSLWAITAK;
AVTGKHFSLWAITAKV; VTGKHFSLWAITAKVI; TGKHFSLWAITAKVIF;
GKHFSLWAITAKVIFS; KHFSLWAITAKVIFST; FWHLHGFLWLFGSCPW;
WHLHGFLWLFGSCPWT; HLHGFLWLFGSCPWTL; LHGFLWLFGSCPWTLS;
HGFLWLFGSCPWTLSF; GFLWLFGSCPWTLSFS; FLWLFGSCPWTLSFSF;
LWLFGSCPWTLSFSFG; WLFGSCPWTLSFSFGW; LFGSCPWTLSFSFGWG;
FGSCPWTLSFSFGWGH; GSCPWTLSFSFGWGHL; SCPWTLSFSFGWGHLH;
CPWTLSFSFGWGHLHM; PWTLSFSFGWGHLHML; WTLSFSFGWGHLHMLQ;
TLSFSFGWGHLHMLQE; LSFSFGWGHLHMLQEQ; SFSFGWGHLHMLQEQV;
FSFGWGHLHMLQEQVL; SFGWGHLHMLQEQVLQ; FGWGHLHMLQEQVLQS;
GWGHLHMLQEQVLQSR; WGHLHMLQEQVLQSRT; GHLHMLQEQVLQSRTG;

HLHMLQEQVLQSRTGL; LHMLQEQVLQSRTGLE; HMLQEQVLQSRTGLEV;
MLQEQVLQSRTGLEVK; LQEQVLQSRTGLEVKA; QEQVLQSRTGLEVKAT;
EQVLQSRTGLEVKATS; QVLQSRTGLEVKATSI; VLQSRTGLEVKATSIE;
LQSRTGLEVKATSIEE; QSRTGLEVKATSIEEQ; SRTGLEVKATSIEEQF;
RTGLEVKATSIEEQFF; TGLEVKATSIEEQFFD; TLLNVHFVDFLSPFFV;
LLLYCQHHLYYKYGQN; LLYCQHHLYYKYGQNV; LYCQHHLYYKYGQNVH;
YCQHHLYYKYGQNVHG; CQHHLYYKYGQNVHGY; QHHLYYKYGQNVHGYL;
HHLYYKYGQNVHGYLP; HLYYKYGQNVHGYLPF; LYYKYGQNVHGYLPFQ;
YYKYGQNVHGYLPFQL; YKYGQNVHGYLPFQLL; KYGQNVHGYLPFQLLV;
QKYLHQETEYHSTHLG; TIPKPCLIADRGLQWK; IPKPCLIADRGLQWKL;
PKPCLIADRGLQWKLC; KPCLIADRGLQWKLCD; PCLIADRGLQWKLCDP;
CLIADRGLQWKLCDPN; LIADRGLQWKLCDPNH; IADRGLQWKLCDPNHQ;
ADRGLQWKLCDPNHQR; DRGLQWKLCDPNHQRT; RGLQWKLCDPNHQRTY;
GLQWKLCDPNHQRTYT; LQWKLCDPNHQRTYTL; QWKLCDPNHQRTYTLL;
WKLCDPNHQRTYTLLE; KLCDPNHQRTYTLLEL; LCDPNHQRTYTLLELR;
CDPNHQRTYTLLELRN; PQEHQQLQHMFEELGL; QQQPPQQQFQPLKILW;
QQPPQQQFQPLKILWQ; QPPQQQFQPLKILWQQ; PPQQQFQPLKILWQQQ;
PQQQFQPLKILWQQQP; QQQFQPLKILWQQQPQ; QQFQPLKILWQQQPQI;
QFQPLKILWQQQPQIH; FQPLKILWQQQPQIHW; QPLKILWQQQPQIHWQ;
PLKILWQQQPQIHWQL; LKILWQQQPQIHWQLG; KILWQQQPQIHWQLGP;
ILWQQQPQIHWQLGPP; LWQQQPQIHWQLGPPK; WQQQPQIHWQLGPPKV;
QQQPQIHWQLGPPKVL; QQPQIHWQLGPPKVLE; QPQIHWQLGPPKVLEQ;
PQIHWQLGPPKVLEQH; QIHWQLGPPKVLEQHP; TWKYKKKGITYLGVFY;
WKYKKKGITYLGVFYR; KYKKKGITYLGVFYRV; YKKKGITYLGVFYRVF;
KKKGITYLGVFYRVFY; KKGITYLGVFYRVFYS; KGITYLGVFYRVFYSR;
SSGTFVFPVYTVFTST; SGTFVFPVYTVFTSTK; GTFVFPVYTVFTSTKF;
TFVFPVYTVFTSTKFQ; FVFPVYTVFTSTKFQQ; VFPVYTVFTSTKFQQK;
FPVYTVFTSTKFQQKL; NKNKNPLSSFFCSSPG; KNKNPLSSFFCSSPGF;
NKNPLSSFFCSSPGFT; KNPLSSFFCSSPGFTN; NPLSSFFCSSPGFTNF;
PLSSFFCSSPGFTNFH; LGTRPRFLGSQNMSVM; GTRPRFLGSQNMSVMH;
TRPRFLGSQNMSVMHF; RPRFLGSQNMSVMHFP; PRFLGSQNMSVMHFPS;
AAPPCESCTFLPEVMV; APPCESCTFLPEVMVW; PPCESCTFLPEVMVWL;
PCESCTFLPEVMVWLH; CESCTFLPEVMVWLHS; ESCTFLPEVMVWLHSP;
SCTFLPEVMVWLHSPV; CTFLPEVMVWLHSPVS; TFLPEVMVWLHSPVSH;
FLPEVMVWLHSPVSHA; LPEVMVWLHSPVSHAL; PEVMVWLHSPVSHALS;
EVMVWLHSPVSHALSF; VMVWLHSPVSHALSFL; MVWLHSPVSHALSFLR;
VWLHSPVSHALSFLRS; WLHSPVSHALSFLRSW; LHSPVSHALSFLRSWF;
HSPVSHALSFLRSWFG; SPVSHALSFLRSWFGC; PVSHALSFLRSWFGCI;
VSHALSFLRSWFGCIP; SHALSFLRSWFGCIPW; HALSFLRSWFGCIPWV;
ALSFLRSWFGCIPWVS; LSFLRSWFGCIPWVSS; SFLRSWFGCIPWVSSS;
FLRSWFGCIPWVSSSS; LRSWFGCIPWVSSSSL; RSWFGCIPWVSSSSLW;
SWFGCIPWVSSSSLWP; WFGCIPWVSSSSLWPF; FGCIPWVSSSSLWPFF;
GCIPWVSSSSLWPFFL; YIRGRGRLCLHPFSQV; IRGRGRLCLHPFSQVV;
RGRGRLCLHPFSQVVR; GRGRLCLHPFSQVVRV; RGRLCLHPFSQVVRVW;
GRLCLHPFSQVVRVWR; RLCLHPFSQVVRVWRL; LCLHPFSQVVRVWRLF;
CLHPFSQVVRVWRLFL; LHPFSQVVRVWRLFLR; HPFSQVVRVWRLFLRP;
PFSQVVRVWRLFLRPS; FSQVVRVWRLFLRPSK; SQVVRVWRLFLRPSKT;
QVVRVWRLFLRPSKTI; VVRVWRLFLRPSKTIW; VRVWRLFLRPSKTIWG;
RVWRLFLRPSKTIWGN; VWRLFLRPSKTIWGNP; WRLFLRPSKTIWGNPY;
RLFLRPSKTIWGNPYS; LFLRPSKTIWGNPYSF; FLRPSKTIWGNPYSFA;
LRPSKTIWGNPYSFAI; RPSKTIWGNPYSFAIF; PSKTIWGNPYSFAIFA;
SKTIWGNPYSFAIFAK

Preferred BK virus fragments of VP2-3 capable of interacting with one or more MHC class 2 molecules are listed in Table P.

Table P: Prediction of BK virus VP2-3 protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed.

Allele	pos	peptide	core	1-log50k(aff)	aff(nM)	B.L.Identity
DRB1_0101	36	AAIEVQIASLATVEG	VQIASLATV	0.7655	13	SB BK VP2-3
DRB1_0101	37	AIEVQIASLATVEGI	IASLATVEG	0.7653	13	SB BK VP2-3
DRB1_0101	38	IEVQIASLATVEGIT	IASLATVEG	0.7535	14	SB BK VP2-3
DRB1_0101	39	EVQIASLATVEGITT	IASLATVEG	0.7419	16	SB BK VP2-3
DRB1_0101	216	QDYYSNLSPIRPSMV	YSNLSPIRP	0.7369	17	SB BK VP2-3
DRB1_0101	258	VTQRMDLRNKESVHS	VTQRMDLRN	0.7362	17	SB BK VP2-3
DRB1_0101	259	TQRMDLRNKESVHSG	LRNKESVHS	0.7390	17	SB BK VP2-3
DRB1_0101	260	QRMDLRNKESVHSGE	LRNKESVHS	0.7399	17	SB BK VP2-3
DRB1_0101	261	RMDLRNKESVHSGEF	LRNKESVHS	0.7383	17	SB BK VP2-3
DRB1_0101	262	MDLRNKESVHSGEFI	LRNKESVHS	0.7362	17	SB BK VP2-3
DRB1_0101	217	DYYSNLSPIRPSMVR	YSNLSPIRP	0.7308	18	SB BK VP2-3
DRB1_0101	82	AALIQTVTGISSLAQ	IQTVTGISS	0.7316	18	SB BK VP2-3
DRB1_0101	83	ALIQTVTGISSLAQV	VTGISSLAQ	0.7288	19	SB BK VP2-3
DRB1_0101	40	VQIASLATVEGITTT	IASLATVEG	0.7231	20	SB BK VP2-3
DRB1_0101	66	QTYAVIAGAPGAIAG	IAGAPGAIA	0.7250	20	SB BK VP2-3
DRB1_0101	65	PQTYAVIAGAPGAIA	VIAGAPGAI	0.7203	21	SB BK VP2-3
DRB1_0101	67	TYAVIAGAPGAIAGF	IAGAPGAIA	0.7196	21	SB BK VP2-3
DRB1_0101	68	YAVIAGAPGAIAGFA	IAGAPGAIA	0.7188	21	SB BK VP2-3
DRB1_0101	213	NYIQDYYSNLSPIRP	YYSNLSPIR	0.7087	23	SB BK VP2-3
DRB1_0101	214	YIQDYYSNLSPIRPS	YSNLSPIRP	0.7104	23	SB BK VP2-3
DRB1_0101	215	IQDYYSNLSPIRPSM	YSNLSPIRP	0.7116	23	SB BK VP2-3
DRB1_0101	219	YSNLSPIRPSMVRQV	YSNLSPIRP	0.7018	25	SB BK VP2-3
DRB1_0101	84	LIQTVTGISSLAQVG	VTGISSLAQ	0.7012	25	SB BK VP2-3
DRB1_0101	69	AVIAGAPGAIAGFAA	IAGAPGAIA	0.6972	26	SB BK VP2-3
DRB1_0101	85	IQTVTGISSLAQVGY	VTGISSLAQ	0.7004	26	SB BK VP2-3
DRB1_0101	24	FSVAEIAAGEAAAAI	IAAGEAAAA	0.6947	27	SB BK VP2-3
DRB1_0101	26	VAEIAAGEAAAAIEV	IAAGEAAAA	0.6967	27	SB BK VP2-3
DRB1_0101	27	AEIAAGEAAAAIEVQ	IAAGEAAAA	0.6963	27	SB BK VP2-3
DRB1_0101	25	SVAEIAAGEAAAAIE	IAAGEAAAA	0.6933	28	SB BK VP2-3
DRB1_0101	34	AAAAIEVQIASLATV	EVQIASLAT	0.6919	28	SB BK VP2-3
DRB1_0101	35	AAAIEVQIASLATVE	VQIASLATV	0.6928	28	SB BK VP2-3
DRB1_0101	23	GFSVAEIAAGEAAAA	VAEIAAGEA	0.6867	30	SB BK VP2-3
DRB1_0101	292	QWMLPLLLGLYGTVT	QWMLPLLLG	0.6800	32	SB BK VP2-3
DRB1_0101	1	MGAALALLGDLVASV	MGAALALLG	0.6779	33	SB BK VP2-3
DRB1_0101	296	PLLLGLYGTVTPALE	LLGLYGTVT	0.6771	33	SB BK VP2-3
DRB1_0101	289	TAPQWMLPLLLGLYG	PQWMLPLLL	0.6746	34	SB BK VP2-3
DRB1_0101	295	LPLLLGLYGTVTPAL	LLGLYGTVT	0.6709	35	SB BK VP2-3
DRB1_0101	218	YYSNLSPIRPSMVRQ	YSNLSPIRP	0.6689	36	SB BK VP2-3
DRB1_0101	293	WMLPLLLGLYGTVTP	LLGLYGTVT	0.6559	41	SB BK VP2-3
DRB1_0101	294	MLPLLLGLYGTVTPA	LLGLYGTVT	0.6545	42	SB BK VP2-3
DRB1_0101	220	SNLSPIRPSMVRQVA	IRPSMVRQV	0.6515	43	SB BK VP2-3
DRB1_0101	288	RTAPQWMLPLLLGLY	PQWMLPLLL	0.6514	43	SB BK VP2-3
DRB1_0101	86	QTVTGISSLAQVGYR	VTGISSLAQ	0.6515	43	SB BK VP2-3
DRB1_0101	9	GDLVASVSEAAAATG	LVASVSEAA	0.6476	45	SB BK VP2-3
DRB1_0101	287	QRTAPQWMLPLLLGL	PQWMLPLLL	0.6469	46	SB BK VP2-3
DRB1_0101	290	APQWMLPLLLGLYGT	QWMLPLLLG	0.6444	47	SB BK VP2-3
DRB1_0101	263	DLRNKESVHSGEFIE	LRNKESVHS	0.6362	51	WB BK VP2-3
DRB1_0101	264	LRNKESVHSGEFIEK	LRNKESVHS	0.6346	52	WB BK VP2-3
DRB1_0101	42	IASLATVEGITTTSE	IASLATVEG	0.6326	53	WB BK VP2-3
DRB1_0101	5	LALLGDLVASVSEAA	LGDLVASVS	0.6322	53	WB BK VP2-3
DRB1_0101	170	RDDIPAITSQELQRR	IPAITSQEL	0.6313	54	WB BK VP2-3

DRB1_0101	171	DDIPAITSQELQRRT	IPAITSQEL	0.6309	54	WB BK VP2-3
DRB1_0101	186	ERFFRDSLARFLEET	FRDSLARFL	0.6320	54	WB BK VP2-3
DRB1_0101	184	RTERFFRDSLARFLE	FRDSLARFL	0.6295	55	WB BK VP2-3
DRB1_0101	185	TERFFRDSLARFLEE	FRDSLARFL	0.6304	55	WB BK VP2-3
DRB1_0101	183	RRTERFFRDSLARFL	FFRDSLARF	0.6285	56	WB BK VP2-3
DRB1_0101	187	RFFRDSLARFLEETT	FRDSLARFL	0.6286	56	WB BK VP2-3
DRB1_0101	70	VIAGAPGAIAGFAAL	IAGAPGAIA	0.6277	56	WB BK VP2-3
DRB1_0101	75	PGAIAGFAALIQTVT	IAGFAALIQ	0.6288	56	WB BK VP2-3
DRB1_0101	76	GAIAGFAALIQTVTG	FAALIQTVT	0.6280	56	WB BK VP2-3
DRB1_0101	41	QIASLATVEGITTTS	IASLATVEG	0.6263	57	WB BK VP2-3
DRB1_0101	6	ALLGDLVASVSEAAA	LVASVSEAA	0.6253	58	WB BK VP2-3
DRB1_0101	221	NLSPIRPSMVRQVAE	IRPSMVRQV	0.6218	60	WB BK VP2-3
DRB1_0101	297	LLLGLYGTVTPALEA	LLGLYGTVT	0.6216	60	WB BK VP2-3
DRB1_0101	222	LSPIRPSMVRQVAER	IRPSMVRQV	0.6206	61	WB BK VP2-3
DRB1_0101	291	PQWMLPLLLGLYGTV	PQWMLPLLL	0.6197	61	WB BK VP2-3
DRB1_0101	298	LLGLYGTVTPALEAY	LLGLYGTVT	0.6201	61	WB BK VP2-3
DRB1_0101	79	AGFAALIQTVTGISS	FAALIQTVT	0.6202	61	WB BK VP2-3
DRB1_0101	8	LGDLVASVSEAAAAT	LVASVSEAA	0.6196	61	WB BK VP2-3
DRB1_0101	155	PSLFATISQALWHVI	LFATISQAL	0.6154	64	WB BK VP2-3
DRB1_0101	28	EIAAGEAAAAIEVQI	IAAGEAAAA	0.6146	65	WB BK VP2-3
DRB1_0101	286	NQRTAPQWMLPLLLG	PQWMLPLLL	0.6139	65	WB BK VP2-3
DRB1_0101	151	RHWGPSLFATISQAL	RHWGPSLFA	0.6126	66	WB BK VP2-3
DRB1_0101	275	FIEKTIAPGGANQRT	IAPGGANQR	0.6093	69	WB BK VP2-3
DRB1_0101	29	IAAGEAAAAIEVQIA	IAAGEAAAA	0.6093	69	WB BK VP2-3
DRB1_0101	7	LLGDLVASVSEAAAA	LVASVSEAA	0.6068	70	WB BK VP2-3
DRB1_0101	11	LVASVSEAAAATGFS	VSEAAAATG	0.6048	72	WB BK VP2-3
DRB1_0101	152	HWGPSLFATISQALW	LFATISQAL	0.6052	72	WB BK VP2-3
DRB1_0101	276	IEKTIAPGGANQRTA	IAPGGANQR	0.6053	72	WB BK VP2-3
DRB1_0101	154	GPSLFATISQALWHV	LFATISQAL	0.6040	73	WB BK VP2-3
DRB1_0101	111	TVGLYQQSGMALELF	LYQQSGMAL	0.6024	74	WB BK VP2-3
DRB1_0101	10	DLVASVSEAAAATGF	VSEAAAATG	0.6015	75	WB BK VP2-3
DRB1_0101	112	VGLYQQSGMALELFN	LYQQSGMAL	0.6010	75	WB BK VP2-3
DRB1_0101	277	EKTIAPGGANQRTAP	IAPGGANQR	0.6011	75	WB BK VP2-3
DRB1_0101	71	IAGAPGAIAGFAALI	IAGAPGAIA	0.6015	75	WB BK VP2-3
DRB1_0101	153	WGPSLFATISQALWH	LFATISQAL	0.5994	76	WB BK VP2-3
DRB1_0101	223	SPIRPSMVRQVAERE	IRPSMVRQV	0.6003	76	WB BK VP2-3
DRB1_0101	110	STVGLYQQSGMALEL	LYQQSGMAL	0.5977	78	WB BK VP2-3
DRB1_0101	78	IAGFAALIQTVTGIS	FAALIQTVT	0.5963	79	WB BK VP2-3
DRB1_0101	77	AIAGFAALIQTVTGI	FAALIQTVT	0.5949	80	WB BK VP2-3
DRB1_0101	278	KTIAPGGANQRTAPQ	IAPGGANQR	0.5943	81	WB BK VP2-3
DRB1_0101	2	GAALALLGDLVASVS	LALLGDLVA	0.5930	82	WB BK VP2-3
DRB1_0101	3	AALALLGDLVASVSE	LGDLVASVS	0.5912	83	WB BK VP2-3
DRB1_0101	81	FAALIQTVTGISSLA	IQTVTGISS	0.5912	83	WB BK VP2-3
DRB1_0101	173	IPAITSQELQRRTER	ITSQELQRR	0.5853	89	WB BK VP2-3
DRB1_0101	172	DIPAITSQELQRRTE	ITSQELQRR	0.5840	90	WB BK VP2-3
DRB1_0101	88	VTGISSLAQVGYRFF	VTGISSLAQ	0.5828	91	WB BK VP2-3
DRB1_0101	80	GFAALIQTVTGISSL	IQTVTGISS	0.5817	92	WB BK VP2-3
DRB1_0101	274	EFIEKTIAPGGANQR	IEKTIAPGG	0.5781	96	WB BK VP2-3
DRB1_0101	320	KRRVSRGSSQKAKGT	VSRGSSQKA	0.5786	96	WB BK VP2-3
DRB1_0101	167	HVIRDDIPAITSQEL	IRDDIPAIT	0.5761	98	WB BK VP2-3
DRB1_0101	109	VSTVGLYQQSGMALE	LYQQSGMAL	0.5756	99	WB BK VP2-3
DRB1_0101	64	TPQTYAVIAGAPGAI	YAVIAGAPG	0.5756	99	WB BK VP2-3
DRB1_0101	321	RRVSRGSSQKAKGTR	VSRGSSQKA	0.5746	100	WB BK VP2-3
DRB1_0101	323	VSRGSSQKAKGTRAS	VSRGSSQKA	0.5730	101	WB BK VP2-3
DRB1_0101	319	KKRRVSRGSSQKAKG	VSRGSSQKA	0.5712	104	WB BK VP2-3
DRB1_0101	318	QKKRRVSRGSSQKAK	VSRGSSQKA	0.5695	105	WB BK VP2-3
DRB1_0101	87	TVTGISSLAQVGYRF	VTGISSLAQ	0.5702	105	WB BK VP2-3
DRB1_0101	299	LGLYGTVTPALEAYE	LYGTVTPAL	0.5689	106	WB BK VP2-3
DRB1_0101	4	ALALLGDLVASVSEA	LGDLVASVS	0.5688	106	WB BK VP2-3
DRB1_0101	317	NQKKRRVSRGSSQKA	RVSRGSSQK	0.5685	107	WB BK VP2-3
DRB1_0101	12	VASVSEAAAATGFSV	VSEAAAATG	0.5666	109	WB BK VP2-3
DRB1_0101	169	IRDDIPAITSQELQR	IPAITSQEL	0.5628	113	WB BK VP2-3

DRB1_0101	285	ANQRTAPQWMLPLLL	RTAPQWMLP	0.5629	113	WB BK VP2-3
DRB1_0101	33	EAAAAIEVQIASLAT	IEVQIASLA	0.5628	113	WB BK VP2-3
DRB1_0101	74	APGAIAGFAALIQTV	IAGFAALIQ	0.5631	113	WB BK VP2-3
DRB1_0101	168	VIRDDIPAITSQELQ	IPAITSQEL	0.5596	117	WB BK VP2-3
DRB1_0101	212	YNYIQDYYSNLSPIR	IQDYYSNLS	0.5601	117	WB BK VP2-3
DRB1_0101	72	AGAPGAIAGFAALIQ	AIAGFAALI	0.5598	117	WB BK VP2-3
DRB1_0101	73	GAPGAIAGFAALIQT	IAGFAALIQ	0.5602	117	WB BK VP2-3
DRB1_0101	108	KVSTVGLYQQSGMAL	TVGLYQQSG	0.5550	123	WB BK VP2-3
DRB1_0101	156	SLFATISQALWHVIR	LFATISQAL	0.5526	127	WB BK VP2-3
DRB1_0101	13	ASVSEAAAATGFSVA	VSEAAAATG	0.5482	133	WB BK VP2-3
DRB1_0101	113	GLYQQSGMALELFNP	LYQQSGMAL	0.5426	141	WB BK VP2-3
DRB1_0101	157	LFATISQALWHVIRD	LFATISQAL	0.5415	143	WB BK VP2-3
DRB1_0101	188	FFRDSLARFLEETTW	FRDSLARFL	0.5345	154	WB BK VP2-3
DRB1_0101	43	ASLATVEGITTTSEA	LATVEGITT	0.5345	154	WB BK VP2-3
DRB1_0101	149	DPRHWGPSLFATISQ	RHWGPSLFA	0.5298	162	WB BK VP2-3
DRB1_0101	148	LDPRHWGPSLFATIS	RHWGPSLFA	0.5294	163	WB BK VP2-3
DRB1_0101	57	AIAAIGLTPQTYAVI	IAAIGLTPQ	0.5280	165	WB BK VP2-3
DRB1_0101	189	FRDSLARFLEETTWT	FRDSLARFL	0.5271	167	WB BK VP2-3
DRB1_0101	279	TIAPGGANQRTAPQW	IAPGGANQR	0.5252	170	WB BK VP2-3
DRB1_0101	174	PAITSQELQRRTERF	ITSQELQRR	0.5214	177	WB BK VP2-3
DRB1_0101	114	LYQQSGMALELFNPD	LYQQSGMAL	0.5213	178	WB BK VP2-3
DRB1_0101	199	ETTWTIVNAPINFYN	IVNAPINFY	0.5209	178	WB BK VP2-3
DRB1_0101	58	IAAIGLTPQTYAVIA	LTPQTYAVI	0.5203	180	WB BK VP2-3
DRB1_0101	147	YLDPRHWGPSLFATI	RHWGPSLFA	0.5192	182	WB BK VP2-3
DRB1_0101	56	EAIAAIGLTPQTYAV	IAAIGLTPQ	0.5190	182	WB BK VP2-3
DRB1_0101	200	TTWTIVNAPINFYNY	IVNAPINFY	0.5185	183	WB BK VP2-3
DRB1_0101	198	EETTWTIVNAPINFY	WTIVNAPIN	0.5179	184	WB BK VP2-3
DRB1_0101	224	PIRPSMVRQVAEREG	IRPSMVRQV	0.5170	186	WB BK VP2-3
DRB1_0101	63	LTPQTYAVIAGAPGA	YAVIAGAPG	0.5172	186	WB BK VP2-3
DRB1_0101	225	IRPSMVRQVAEREGT	IRPSMVRQV	0.5152	190	WB BK VP2-3
DRB1_0101	209	INFYNYIQDYYSNLS	YNYIQDYYS	0.5135	193	WB BK VP2-3
DRB1_0101	55	SEAIAAIGLTPQTYA	IAAIGLTPQ	0.5133	194	WB BK VP2-3
DRB1_0101	210	NFYNYIQDYYSNLSP	IQDYYSNLS	0.5129	195	WB BK VP2-3
DRB1_0101	145	IQYLDPRHWGPSLFA	IQYLDPRHW	0.5100	201	WB BK VP2-3
DRB1_0101	300	GLYGTVTPALEAYED	LYGTVTPAL	0.5097	201	WB BK VP2-3
DRB1_0101	322	RVSRGSSQKAKGTRA	VSRGSSQKA	0.5073	207	WB BK VP2-3
DRB1_0101	201	TWTIVNAPINFYNYI	IVNAPINFY	0.5050	212	WB BK VP2-3
DRB1_0101	202	WTIVNAPINFYNYIQ	IVNAPINFY	0.5004	223	WB BK VP2-3
DRB1_0101	140	TFVNNIQYLDPRHWG	IQYLDPRHW	0.4969	231	WB BK VP2-3
DRB1_0101	327	SSQKAKGTRASAKTT	QKAKGTRAS	0.4971	231	WB BK VP2-3
DRB1_0101	139	NTFVNNIQYLDPRHW	VNNIQYLDP	0.4965	232	WB BK VP2-3
DRB1_0101	45	LATVEGITTTSEAIA	VEGITTTSE	0.4966	232	WB BK VP2-3
DRB1_0101	62	GLTPQTYAVIAGAPG	TPQTYAVIA	0.4959	234	WB BK VP2-3
DRB1_0101	280	IAPGGANQRTAPQWM	IAPGGANQR	0.4948	237	WB BK VP2-3
DRB1_0101	54	TSEAIAAIGLTPQTY	IAAIGLTPQ	0.4931	241	WB BK VP2-3
DRB1_0101	142	VNNIQYLDPRHWGPS	IQYLDPRHW	0.4908	247	WB BK VP2-3
DRB1_0101	211	FYNYIQDYYSNLSPI	IQDYYSNLS	0.4889	252	WB BK VP2-3
DRB1_0101	53	TTSEAIAAIGLTPQT	IAAIGLTPQ	0.4889	252	WB BK VP2-3
DRB1_0101	141	FVNNIQYLDPRHWGP	IQYLDPRHW	0.4885	253	WB BK VP2-3
DRB1_0101	143	NNIQYLDPRHWGPSL	IQYLDPRHW	0.4867	258	WB BK VP2-3
DRB1_0101	44	SLATVEGITTTSEAI	VEGITTTSE	0.4868	258	WB BK VP2-3
DRB1_0101	59	AAIGLTPQTYAVIAG	LTPQTYAVI	0.4849	263	WB BK VP2-3
DRB1_0101	326	GSSQKAKGTRASAKT	QKAKGTRAS	0.4838	267	WB BK VP2-3
DRB1_0101	14	SVSEAAAATGFSVAE	VSEAAAATG	0.4826	270	WB BK VP2-3
DRB1_0101	150	PRHWGPSLFATISQA	WGPSLFATI	0.4823	271	WB BK VP2-3
DRB1_0101	301	LYGTVTPALEAYEDG	LYGTVTPAL	0.4803	277	WB BK VP2-3
DRB1_0101	129	EYYDILFPGVNTFVN	LFPGVNTFV	0.4778	284	WB BK VP2-3
DRB1_0101	60	AIGLTPQTYAVIAGA	LTPQTYAVI	0.4766	288	WB BK VP2-3
DRB1_0101	146	QYLDPRHWGPSLFAT	RHWGPSLFA	0.4756	291	WB BK VP2-3
DRB1_0101	52	TTTSEAIAAIGLTPQ	SEAIAAIGL	0.4719	303	WB BK VP2-3
DRB1_0101	130	YYDILFPGVNTFVNN	LFPGVNTFV	0.4703	308	WB BK VP2-3
DRB1_0101	128	DEYYDILFPGVNTFV	YYDILFPGV	0.4673	318	WB BK VP2-3

DRB1_0101	325	RGSSQKAKGTRASAK	QKAKGTRAS	0.4649	327	WB BK VP2-3
DRB1_0101	131	YDILFPGVNTFVNNI	LFPGVNTFV	0.4632	333	WB BK VP2-3
DRB1_0101	46	ATVEGITTTSEAIAA	VEGITTTSE	0.4606	342	WB BK VP2-3
DRB1_0101	15	VSEAAAATGFSVAEI	VSEAAAATG	0.4598	345	WB BK VP2-3
DRB1_0101	328	SQKAKGTRASAKTTN	QKAKGTRAS	0.4565	358	WB BK VP2-3
DRB1_0101	132	DILFPGVNTFVNNIQ	LFPGVNTFV	0.4558	361	WB BK VP2-3
DRB1_0101	61	IGLTPQTYAVIAGAP	LTPQTYAVI	0.4557	361	WB BK VP2-3
DRB1_0101	324	SRGSSQKAKGTRASA	QKAKGTRAS	0.4547	365	WB BK VP2-3
DRB1_0101	329	QKAKGTRASAKTTNK	QKAKGTRAS	0.4538	369	WB BK VP2-3
DRB1_0101	22	TGFSVAEIAAGEAAA	FSVAEIAAG	0.4532	371	WB BK VP2-3
DRB1_0101	32	GEAAAAIEVQIASLA	AAAIEVQIA	0.4528	372	WB BK VP2-3
DRB1_0101	21	ATGFSVAEIAAGEAA	FSVAEIAAG	0.4520	376	WB BK VP2-3
DRB1_0101	20	AATGFSVAEIAAGEA	FSVAEIAAG	0.4471	396	WB BK VP2-3
DRB1_0101	227	PSMVRQVAEREGTHV	MVRQVAERE	0.4426	416	WB BK VP2-3
DRB1_0101	101	FFSDWDHKVSTVGLY	WDHKVSTVG	0.4398	429	WB BK VP2-3
DRB1_0101	100	RFFSDWDHKVSTVGL	WDHKVSTVG	0.4393	431	WB BK VP2-3
DRB1_0101	103	SDWDHKVSTVGLYQQ	WDHKVSTVG	0.4367	443	WB BK VP2-3
DRB1_0101	158	FATISQALWHVIRDD	ISQALWHVI	0.4312	471	WB BK VP2-3
DRB1_0101	175	AITSQELQRRTERFF	ITSQELQRR	0.4287	483	WB BK VP2-3
DRB1_0101	49	EGITTTSEAIAAIGL	ITTTSEAIA	0.4284	485	WB BK VP2-3
DRB1_0101	102	FSDWDHKVSTVGLYQ	WDHKVSTVG	0.4283	486	WB BK VP2-3
DRB1_0301	182	QRRTERFFRDSLARF	RFFRDSLAR	0.4487	390	WB BK VP2-3
DRB1_0301	183	RRTERFFRDSLARFL	FFRDSLARF	0.4472	396	WB BK VP2-3
DRB1_0301	186	ERFFRDSLARFLEET	FFRDSLARF	0.4469	397	WB BK VP2-3
DRB1_0301	184	RTERFFRDSLARFLE	FFRDSLARF	0.4468	398	WB BK VP2-3
DRB1_0301	185	TERFFRDSLARFLEE	FFRDSLARF	0.4464	399	WB BK VP2-3
DRB1_0401	213	NYIQDYYSNLSPIRP	YYSNLSPIR	0.5927	82	WB BK VP2-3
DRB1_0401	212	YNYIQDYYSNLSPIR	IQDYYSNLS	0.5864	88	WB BK VP2-3
DRB1_0401	214	YIQDYYSNLSPIRPS	YYSNLSPIR	0.5789	95	WB BK VP2-3
DRB1_0401	215	IQDYYSNLSPIRPSM	YYSNLSPIR	0.5767	97	WB BK VP2-3
DRB1_0401	216	QDYYSNLSPIRPSMV	YYSNLSPIR	0.5674	108	WB BK VP2-3
DRB1_0401	258	VTQRMDLRNKESVHS	VTQRMDLRN	0.5284	164	WB BK VP2-3
DRB1_0401	259	TQRMDLRNKESVHSG	LRNKESVHS	0.5237	173	WB BK VP2-3
DRB1_0401	260	QRMDLRNKESVHSGE	LRNKESVHS	0.5240	173	WB BK VP2-3
DRB1_0401	261	RMDLRNKESVHSGEF	LRNKESVHS	0.5213	178	WB BK VP2-3
DRB1_0401	262	MDLRNKESVHSGEFI	LRNKESVHS	0.5168	187	WB BK VP2-3
DRB1_0401	5	LALLGDLVASVSEAA	LLGDLVASV	0.5166	187	WB BK VP2-3
DRB1_0401	6	ALLGDLVASVSEAAA	LVASVSEAA	0.5140	192	WB BK VP2-3
DRB1_0401	7	LLGDLVASVSEAAAA	LVASVSEAA	0.5130	194	WB BK VP2-3
DRB1_0401	8	LGDLVASVSEAAAAT	LVASVSEAA	0.5130	194	WB BK VP2-3
DRB1_0401	9	GDLVASVSEAAAATG	LVASVSEAA	0.5118	197	WB BK VP2-3
DRB1_0401	82	AALIQTVTGISSLAQ	LIQTVTGIS	0.5068	208	WB BK VP2-3
DRB1_0401	217	DYYSNLSPIRPSMVR	YYSNLSPIR	0.4779	284	WB BK VP2-3
DRB1_0401	83	ALIQTVTGISSLAQV	VTGISSLAQ	0.4763	289	WB BK VP2-3
DRB1_0401	84	LIQTVTGISSLAQVG	VTGISSLAQ	0.4711	306	WB BK VP2-3
DRB1_0401	218	YYSNLSPIRPSMVRQ	YYSNLSPIR	0.4694	312	WB BK VP2-3
DRB1_0401	198	EETTWTIVNAPINFY	WTIVNAPIN	0.4557	361	WB BK VP2-3
DRB1_0401	199	ETTWTIVNAPINFYN	IVNAPINFY	0.4556	362	WB BK VP2-3
DRB1_0401	200	TTWTIVNAPINFYNY	IVNAPINFY	0.4527	373	WB BK VP2-3
DRB1_0401	85	IQTVTGISSLAQVGY	VTGISSLAQ	0.4432	414	WB BK VP2-3
DRB1_0401	202	WTIVNAPINFYNYIQ	IVNAPINFY	0.4421	418	WB BK VP2-3
DRB1_0401	201	TWTIVNAPINFYNYI	IVNAPINFY	0.4401	427	WB BK VP2-3
DRB1_0401	81	FAALIQTVTGISSLA	LIQTVTGIS	0.4399	428	WB BK VP2-3
DRB1_0401	36	AAIEVQIASLATVEG	IEVQIASLA	0.4327	463	WB BK VP2-3
DRB1_0401	132	DILFPGVNTFVNNIQ	GVNTFVNNI	0.4289	483	WB BK VP2-3
DRB1_0404	213	NYIQDYYSNLSPIRP	IQDYYSNLS	0.5128	195	WB BK VP2-3
DRB1_0404	82	AALIQTVTGISSLAQ	LIQTVTGIS	0.4868	258	WB BK VP2-3
DRB1_0404	198	EETTWTIVNAPINFY	TTWTIVNAP	0.4822	271	WB BK VP2-3
DRB1_0404	215	IQDYYSNLSPIRPSM	IQDYYSNLS	0.4815	273	WB BK VP2-3

DRB1_0404	295	LPLLLGLYGTVTPAL	LLGLYGTVT	0.4754	292	WB BK VP2-3
DRB1_0404	214	YIQDYYSNLSPIRPS	IQDYYSNLS	0.4645	328	WB BK VP2-3
DRB1_0404	296	PLLLGLYGTVTPALE	LLGLYGTVT	0.4620	337	WB BK VP2-3
DRB1_0404	293	WMLPLLLGLYGTVTP	LLGLYGTVT	0.4571	356	WB BK VP2-3
DRB1_0404	294	MLPLLLGLYGTVTPA	LLGLYGTVT	0.4547	365	WB BK VP2-3
DRB1_0404	36	AAIEVQIASLATVEG	IEVQIASLA	0.4515	378	WB BK VP2-3
DRB1_0404	200	TTWTIVNAPINFYNY	IVNAPINFY	0.4472	396	WB BK VP2-3
DRB1_0404	194	ARFLEETTWTIVNAP	FLEETTWTI	0.4467	398	WB BK VP2-3
DRB1_0404	212	YNYIQDYYSNLSPIR	IQDYYSNLS	0.4449	406	WB BK VP2-3
DRB1_0404	199	ETTWTIVNAPINFYN	IVNAPINFY	0.4444	408	WB BK VP2-3
DRB1_0404	81	FAALIQTVTGISSLA	LIQTVTGIS	0.4428	415	WB BK VP2-3
DRB1_0404	292	QWMLPLLLGLYGTVT	MLPLLLGLY	0.4376	439	WB BK VP2-3
DRB1_0404	297	LLLGLYGTVTPALEA	LGLYGTVTP	0.4365	445	WB BK VP2-3
DRB1_0404	84	LIQTVTGISSLAQVG	LIQTVTGIS	0.4287	483	WB BK VP2-3
DRB1_0404	38	IEVQIASLATVEGIT	IASLATVEG	0.4281	487	WB BK VP2-3
DRB1_0404	78	IAGFAALIQTVTGIS	AALIQTVTG	0.4270	493	WB BK VP2-3
DRB1_0404	196	FLEETTWTIVNAPIN	TTWTIVNAP	0.4258	499	WB BK VP2-3
DRB1_0405	213	NYIQDYYSNLSPIRP	IQDYYSNLS	0.5630	113	WB BK VP2-3
DRB1_0405	212	YNYIQDYYSNLSPIR	IQDYYSNLS	0.5391	146	WB BK VP2-3
DRB1_0405	209	INFYNYIQDYYSNLS	YNYIQDYYS	0.5339	155	WB BK VP2-3
DRB1_0405	96	QVGYRFFSDWDHKVS	YRFFSDWDH	0.5285	164	WB BK VP2-3
DRB1_0405	210	NFYNYIQDYYSNLSP	IQDYYSNLS	0.5274	166	WB BK VP2-3
DRB1_0405	196	FLEETTWTIVNAPIN	EETTWTIVN	0.5259	169	WB BK VP2-3
DRB1_0405	214	YIQDYYSNLSPIRPS	IQDYYSNLS	0.5183	184	WB BK VP2-3
DRB1_0405	215	IQDYYSNLSPIRPSM	IQDYYSNLS	0.5155	189	WB BK VP2-3
DRB1_0405	135	FPGVNTFVNNIQYLD	VNTFVNNIQ	0.5129	194	WB BK VP2-3
DRB1_0405	211	FYNYIQDYYSNLSPI	IQDYYSNLS	0.5093	202	WB BK VP2-3
DRB1_0405	198	EETTWTIVNAPINFY	WTIVNAPIN	0.5089	203	WB BK VP2-3
DRB1_0405	136	PGVNTFVNNIQYLDP	VNTFVNNIQ	0.5073	207	WB BK VP2-3
DRB1_0405	95	AQVGYRFFSDWDHKV	YRFFSDWDH	0.5059	210	WB BK VP2-3
DRB1_0405	132	DILFPGVNTFVNNIQ	FPGVNTFVN	0.5008	222	WB BK VP2-3
DRB1_0405	133	ILFPGVNTFVNNIQY	VNTFVNNIQ	0.4983	228	WB BK VP2-3
DRB1_0405	97	VGYRFFSDWDHKVST	YRFFSDWDH	0.4930	241	WB BK VP2-3
DRB1_0405	194	ARFLEETTWTIVNAP	EETTWTIVN	0.4887	253	WB BK VP2-3
DRB1_0405	197	LEETTWTIVNAPINF	WTIVNAPIN	0.4832	268	WB BK VP2-3
DRB1_0405	199	ETTWTIVNAPINFYN	WTIVNAPIN	0.4813	274	WB BK VP2-3
DRB1_0405	195	RFLEETTWTIVNAPI	EETTWTIVN	0.4799	278	WB BK VP2-3
DRB1_0405	94	LAQVGYRFFSDWDHK	GYRFFSDWD	0.4772	286	WB BK VP2-3
DRB1_0405	93	SLAQVGYRFFSDWDH	GYRFFSDWD	0.4758	291	WB BK VP2-3
DRB1_0405	134	LFPGVNTFVNNIQYL	VNTFVNNIQ	0.4752	292	WB BK VP2-3
DRB1_0405	193	LARFLEETTWTIVNA	EETTWTIVN	0.4694	312	WB BK VP2-3
DRB1_0405	158	FATISQALWHVIRDD	QALWHVIRD	0.4626	335	WB BK VP2-3
DRB1_0405	157	LFATISQALWHVIRD	SQALWHVIR	0.4616	339	WB BK VP2-3
DRB1_0405	200	TTWTIVNAPINFYNY	IVNAPINFY	0.4599	345	WB BK VP2-3
DRB1_0405	98	GYRFFSDWDHKVSTV	YRFFSDWDH	0.4557	361	WB BK VP2-3
DRB1_0405	192	SLARFLEETTWTIVN	FLEETTWTI	0.4451	405	WB BK VP2-3
DRB1_0405	137	GVNTFVNNIQYLDPR	VNTFVNNIQ	0.4315	469	WB BK VP2-3
DRB1_0405	138	VNTFVNNIQYLDPRH	VNTFVNNIQ	0.4315	469	WB BK VP2-3
DRB1_0701	155	PSLFATISQALWHVI	LFATISQAL	0.6499	44	SB BK VP2-3
DRB1_0701	154	GPSLFATISQALWHV	LFATISQAL	0.6324	53	WB BK VP2-3
DRB1_0701	153	WGPSLFATISQALWH	LFATISQAL	0.6252	58	WB BK VP2-3
DRB1_0701	152	HWGPSLFATISQALW	LFATISQAL	0.6229	59	WB BK VP2-3
DRB1_0701	151	RHWGPSLFATISQAL	WGPSLFATI	0.6204	61	WB BK VP2-3
DRB1_0701	219	YSNLSPIRPSMVRQV	LSPIRPSMV	0.6186	62	WB BK VP2-3
DRB1_0701	220	SNLSPIRPSMVRQVA	LSPIRPSMV	0.6184	62	WB BK VP2-3
DRB1_0701	216	QDYYSNLSPIRPSMV	YYSNLSPIR	0.6145	65	WB BK VP2-3
DRB1_0701	217	DYYSNLSPIRPSMVR	LSPIRPSMV	0.6117	67	WB BK VP2-3
DRB1_0701	218	YYSNLSPIRPSMVRQ	LSPIRPSMV	0.6108	67	WB BK VP2-3
DRB1_0701	194	ARFLEETTWTIVNAP	FLEETTWTI	0.6047	72	WB BK VP2-3
DRB1_0701	191	DSLARFLEETTWTIV	FLEETTWTI	0.6040	73	WB BK VP2-3

DRB1_0701	193	LARFLEETTWTIVNA	FLEETTWTI	0.6028	73	WB BK VP2-3
DRB1_0701	192	SLARFLEETTWTIVN	FLEETTWTI	0.6024	74	WB BK VP2-3
DRB1_0701	156	SLFATISQALWHVIR	LFATISQAL	0.5732	101	WB BK VP2-3
DRB1_0701	157	LFATISQALWHVIRD	LFATISQAL	0.5709	104	WB BK VP2-3
DRB1_0701	195	RFLEETTWTIVNAPI	LEETTWTIV	0.5523	127	WB BK VP2-3
DRB1_0701	221	NLSPIRPSMVRQVAE	LSPIRPSMV	0.5258	169	WB BK VP2-3
DRB1_0701	222	LSPIRPSMVRQVAER	LSPIRPSMV	0.5249	171	WB BK VP2-3
DRB1_0701	196	FLEETTWTIVNAPIN	FLEETTWTI	0.5082	205	WB BK VP2-3
DRB1_0701	58	IAAIGLTPQTYAVIA	LTPQTYAVI	0.4999	224	WB BK VP2-3
DRB1_0701	57	AIAAIGLTPQTYAVI	AIGLTPQTY	0.4992	226	WB BK VP2-3
DRB1_0701	59	AAIGLTPQTYAVIAG	LTPQTYAVI	0.4959	234	WB BK VP2-3
DRB1_0701	60	AIGLTPQTYAVIAGA	LTPQTYAVI	0.4955	235	WB BK VP2-3
DRB1_0701	61	IGLTPQTYAVIAGAP	LTPQTYAVI	0.4924	243	WB BK VP2-3
DRB1_0701	190	RDSLARFLEETTWTI	RDSLARFLE	0.4903	248	WB BK VP2-3
DRB1_0701	167	HVIRDDIPAITSQEL	VIRDDIPAI	0.4747	294	WB BK VP2-3
DRB1_0701	131	YDILFPGVNTFVNNI	LFPGVNTFV	0.4730	299	WB BK VP2-3
DRB1_0701	168	VIRDDIPAITSQELQ	IPAITSQEL	0.4729	300	WB BK VP2-3
DRB1_0701	132	DILFPGVNTFVNNIQ	LFPGVNTFV	0.4725	301	WB BK VP2-3
DRB1_0701	169	IRDDIPAITSQELQR	IPAITSQEL	0.4681	316	WB BK VP2-3
DRB1_0701	170	RDDIPAITSQELQRR	IPAITSQEL	0.4671	319	WB BK VP2-3
DRB1_0701	171	DDIPAITSQELQRRT	IPAITSQEL	0.4635	332	WB BK VP2-3
DRB1_0701	129	EYYDILFPGVNTFVN	LFPGVNTFV	0.4503	383	WB BK VP2-3
DRB1_0701	130	YYDILFPGVNTFVNN	FPGVNTFVN	0.4488	389	WB BK VP2-3
DRB1_0701	133	ILFPGVNTFVNNIQY	FPGVNTFVN	0.4334	459	WB BK VP2-3
DRB1_0701	158	FATISQALWHVIRDD	ISQALWHVI	0.4279	488	WB BK VP2-3
DRB1_0802	214	YIQDYYSNLSPIRPS	YSNLSPIRP	0.4370	442	WB BK VP2-3
DRB1_0802	213	NYIQDYYSNLSPIRP	YYSNLSPIR	0.4360	447	WB BK VP2-3
DRB1_0802	215	IQDYYSNLSPIRPSM	YSNLSPIRP	0.4360	447	WB BK VP2-3
DRB1_0802	216	QDYYSNLSPIRPSMV	YSNLSPIRP	0.4358	448	WB BK VP2-3
DRB1_0901	110	STVGLYQQSGMALEL	YQQSGMALE	0.4827	270	WB BK VP2-3
DRB1_0901	111	TVGLYQQSGMALELF	YQQSGMALE	0.4750	293	WB BK VP2-3
DRB1_0901	112	VGLYQQSGMALELFN	YQQSGMALE	0.4750	293	WB BK VP2-3
DRB1_0901	109	VSTVGLYQQSGMALE	LYQQSGMAL	0.4737	297	WB BK VP2-3
DRB1_0901	36	AAIEVQIASLATVEG	VQIASLATV	0.4709	306	WB BK VP2-3
DRB1_0901	35	AAAIEVQIASLATVE	VQIASLATV	0.4664	322	WB BK VP2-3
DRB1_0901	198	EETTWTIVNAPINFY	WTIVNAPIN	0.4656	324	WB BK VP2-3
DRB1_0901	199	ETTWTIVNAPINFYN	WTIVNAPIN	0.4657	324	WB BK VP2-3
DRB1_0901	37	AIEVQIASLATVEGI	VQIASLATV	0.4650	326	WB BK VP2-3
DRB1_0901	34	AAAAIEVQIASLATV	IEVQIASLA	0.4647	328	WB BK VP2-3
DRB1_0901	38	IEVQIASLATVEGIT	VQIASLATV	0.4639	331	WB BK VP2-3
DRB1_0901	297	LLLGLYGTVTPALEA	LYGTVTPAL	0.4627	335	WB BK VP2-3
DRB1_0901	200	TTWTIVNAPINFYNY	WTIVNAPIN	0.4612	340	WB BK VP2-3
DRB1_0901	296	PLLLGLYGTVTPALE	LYGTVTPAL	0.4611	341	WB BK VP2-3
DRB1_0901	299	LGLYGTVTPALEAYE	LYGTVTPAL	0.4598	346	WB BK VP2-3
DRB1_0901	298	LLGLYGTVTPALEAY	LYGTVTPAL	0.4531	372	WB BK VP2-3
DRB1_0901	113	GLYQQSGMALELFNP	YQQSGMALE	0.4451	405	WB BK VP2-3
DRB1_0901	183	RRTERFFRDSLARFL	FFRDSLARF	0.4413	422	WB BK VP2-3
DRB1_0901	184	RTERFFRDSLARFLE	FRDSLARFL	0.4404	426	WB BK VP2-3
DRB1_0901	186	ERFFRDSLARFLEET	FRDSLARFL	0.4393	431	WB BK VP2-3
DRB1_0901	185	TERFFRDSLARFLEE	FRDSLARFL	0.4382	436	WB BK VP2-3
DRB1_0901	187	RFFRDSLARFLEETT	FRDSLARFL	0.4306	474	WB BK VP2-3
DRB1_0901	295	LPLLLGLYGTVTPAL	LGLYGTVTP	0.4290	482	WB BK VP2-3
DRB1_0901	65	PQTYAVIAGAPGAIA	VIAGAPGAI	0.4281	487	WB BK VP2-3
DRB1_0901	66	QTYAVIAGAPGAIAG	VIAGAPGAI	0.4279	488	WB BK VP2-3
DRB1_0901	67	TYAVIAGAPGAIAGF	VIAGAPGAI	0.4259	499	WB BK VP2-3
DRB1_1302	135	FPGVNTFVNNIQYLD	VNTFVNNIQ	0.7008	25	SB BK VP2-3
DRB1_1302	136	PGVNTFVNNIQYLDP	FVNNIQYLD	0.6940	27	SB BK VP2-3
DRB1_1302	137	GVNTFVNNIQYLDPR	FVNNIQYLD	0.6861	30	SB BK VP2-3
DRB1_1302	138	VNTFVNNIQYLDPRH	FVNNIQYLD	0.6825	31	SB BK VP2-3

DRB1_1302	139	NTFVNNIQYLDPRHW	FVNNIQYLD	0.6608	39	SB BK VP2-3
DRB1_1302	213	NYIQDYYSNLSPIRP	IQDYYSNLS	0.6338	53	WB BK VP2-3
DRB1_1302	216	QDYYSNLSPIRPSMV	YSNLSPIRP	0.6265	57	WB BK VP2-3
DRB1_1302	215	IQDYYSNLSPIRPSM	YSNLSPIRP	0.6245	58	WB BK VP2-3
DRB1_1302	214	YIQDYYSNLSPIRPS	YSNLSPIRP	0.6230	59	WB BK VP2-3
DRB1_1302	217	DYYSNLSPIRPSMVR	YSNLSPIRP	0.6216	60	WB BK VP2-3
DRB1_1302	293	WMLPLLLGLYGTVTP	LLGLYGTVT	0.6200	61	WB BK VP2-3
DRB1_1302	296	PLLLGLYGTVTPALE	LGLYGTVTP	0.6167	63	WB BK VP2-3
DRB1_1302	294	MLPLLLGLYGTVTPA	LGLYGTVTP	0.6126	66	WB BK VP2-3
DRB1_1302	295	LPLLLGLYGTVTPAL	LGLYGTVTP	0.6083	69	WB BK VP2-3
DRB1_1302	297	LLLGLYGTVTPALEA	LGLYGTVTP	0.6067	70	WB BK VP2-3
DRB1_1302	140	TFVNNIQYLDPRHWG	FVNNIQYLD	0.5962	79	WB BK VP2-3
DRB1_1302	36	AAIEVQIASLATVEG	VQIASLATV	0.5884	86	WB BK VP2-3
DRB1_1302	141	FVNNIQYLDPRHWGP	FVNNIQYLD	0.5710	104	WB BK VP2-3
DRB1_1302	37	AIEVQIASLATVEGI	VQIASLATV	0.5647	111	WB BK VP2-3
DRB1_1302	38	IEVQIASLATVEGIT	VQIASLATV	0.5646	111	WB BK VP2-3
DRB1_1302	218	YYSNLSPIRPSMVRQ	YSNLSPIRP	0.5481	133	WB BK VP2-3
DRB1_1302	199	ETTWTIVNAPINFYN	IVNAPINFY	0.5463	135	WB BK VP2-3
DRB1_1302	200	TTWTIVNAPINFYNY	IVNAPINFY	0.5452	137	WB BK VP2-3
DRB1_1302	198	EETTWTIVNAPINFY	WTIVNAPIN	0.5445	138	WB BK VP2-3
DRB1_1302	298	LLGLYGTVTPALEAY	LGLYGTVTP	0.5383	148	WB BK VP2-3
DRB1_1302	219	YSNLSPIRPSMVRQV	YSNLSPIRP	0.5366	150	WB BK VP2-3
DRB1_1302	201	TWTIVNAPINFYNYI	IVNAPINFY	0.5349	153	WB BK VP2-3
DRB1_1302	79	AGFAALIQTVTGISS	FAALIQTVT	0.5306	161	WB BK VP2-3
DRB1_1302	34	AAAAIEVQIASLATV	IEVQIASLA	0.5257	169	WB BK VP2-3
DRB1_1302	202	WTIVNAPINFYNYIQ	IVNAPINFY	0.5240	172	WB BK VP2-3
DRB1_1302	35	AAAIEVQIASLATVE	VQIASLATV	0.5233	174	WB BK VP2-3
DRB1_1302	299	LGLYGTVTPALEAYE	LGLYGTVTP	0.5095	202	WB BK VP2-3
DRB1_1302	40	VQIASLATVEGITTT	IASLATVEG	0.5094	202	WB BK VP2-3
DRB1_1302	80	GFAALIQTVTGISSL	IQTVTGISS	0.5080	205	WB BK VP2-3
DRB1_1302	39	EVQIASLATVEGITT	IASLATVEG	0.5076	206	WB BK VP2-3
DRB1_1302	81	FAALIQTVTGISSLA	IQTVTGISS	0.5054	211	WB BK VP2-3
DRB1_1302	78	IAGFAALIQTVTGIS	FAALIQTVT	0.4783	283	WB BK VP2-3
DRB1_1302	82	AALIQTVTGISSLAQ	IQTVTGISS	0.4693	312	WB BK VP2-3
DRB1_1302	83	ALIQTVTGISSLAQV	IQTVTGISS	0.4437	411	WB BK VP2-3
DRB1_1302	109	VSTVGLYQQSGMALE	VGLYQQSGM	0.4417	420	WB BK VP2-3
DRB1_1302	132	DILFPGVNTFVNNIQ	FPGVNTFVN	0.4394	431	WB BK VP2-3
DRB1_1302	133	ILFPGVNTFVNNIQY	VNTFVNNIQ	0.4339	457	WB BK VP2-3
DRB1_1302	203	TIVNAPINFYNYIQD	IVNAPINFY	0.4317	468	WB BK VP2-3
DRB1_1302	110	STVGLYQQSGMALEL	VGLYQQSGM	0.4274	490	WB BK VP2-3
DRB1_1501	259	TQRMDLRNKESVHSG	LRNKESVHS	0.5055	211	WB BK VP2-3
DRB1_1501	258	VTQRMDLRNKESVHS	TQRMDLRNK	0.4963	233	WB BK VP2-3
DRB1_1501	260	QRMDLRNKESVHSGE	LRNKESVHS	0.4888	252	WB BK VP2-3
DRB1_1501	261	RMDLRNKESVHSGEF	LRNKESVHS	0.4818	272	WB BK VP2-3
DRB1_1501	292	QWMLPLLLGLYGTVT	MLPLLLGLY	0.4818	272	WB BK VP2-3
DRB1_1501	293	WMLPLLLGLYGTVTP	LLGLYGTVT	0.4703	308	WB BK VP2-3
DRB1_1501	262	MDLRNKESVHSGEFI	LRNKESVHS	0.4652	326	WB BK VP2-3
DRB1_1501	294	MLPLLLGLYGTVTPA	LLGLYGTVT	0.4567	357	WB BK VP2-3
DRB1_1501	295	LPLLLGLYGTVTPAL	LLGLYGTVT	0.4514	378	WB BK VP2-3
DRB1_1501	296	PLLLGLYGTVTPALE	LLGLYGTVT	0.4387	434	WB BK VP2-3
DRB4_0101	213	NYIQDYYSNLSPIRP	IQDYYSNLS	0.4336	458	WB BK VP2-3
DRB5_0101	216	QDYYSNLSPIRPSMV	YYSNLSPIR	0.5417	142	WB BK VP2-3
DRB5_0101	214	YIQDYYSNLSPIRPS	YSNLSPIRP	0.5315	159	WB BK VP2-3
DRB5_0101	215	IQDYYSNLSPIRPSM	YSNLSPIRP	0.5316	159	WB BK VP2-3
DRB5_0101	213	NYIQDYYSNLSPIRP	YYSNLSPIR	0.5308	160	WB BK VP2-3
DRB5_0101	217	DYYSNLSPIRPSMVR	YSNLSPIRP	0.5081	205	WB BK VP2-3
DRB5_0101	218	YYSNLSPIRPSMVRQ	YYSNLSPIR	0.4623	336	WB BK VP2-3
DRB5_0101	174	PAITSQELQRRTERF	ITSQELQRR	0.4449	406	WB BK VP2-3
DRB5_0101	173	IPAITSQELQRRTER	ITSQELQRR	0.4422	418	WB BK VP2-3

Preferred BK virus fragments of VP1 capable of interacting with one or more MHC class 2 molecules are listed in Table Q.

Table Q: Prediction of BK virus VP1 protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed.

Allel	pos	peptide	core	1-log50k(aff)	aff(nM)	Bind level	Identity
DRB1_0101	164	QGVLMNYRTKYPQGT	LMNYRTKYP	0.7782	11	SB	VP1
DRB1_0101	165	GVLMNYRTKYPQGTI	YRTKYPQGT	0.7768	11	SB	VP1
DRB1_0101	166	VLMNYRTKYPQGTIT	YRTKYPQGT	0.7796	11	SB	VP1
DRB1_0101	167	LMNYRTKYPQGTITP	YRTKYPQGT	0.7798	11	SB	VP1
DRB1_0101	168	MNYRTKYPQGTITPK	YRTKYPQGT	0.7778	11	SB	VP1
DRB1_0101	118	KTEVIGITSMLNLHA	VIGITSMLN	0.7623	13	SB	VP1
DRB1_0101	119	TEVIGITSMLNLHAG	VIGITSMLN	0.7621	13	SB	VP1
DRB1_0101	233	PPVLHVTNTATTVLL	VTNTATTVL	0.7280	19	SB	VP1
DRB1_0101	234	PVLHVTNTATTVLLD	VTNTATTVL	0.7252	20	SB	VP1
DRB1_0101	235	VLHVTNTATTVLLDE	VTNTATTVL	0.7244	20	SB	VP1
DRB1_0101	232	VPPVLHVTNTATTVL	VLHVTNTAT	0.7197	21	SB	VP1
DRB1_0101	236	LHVTNTATTVLLDEQ	VTNTATTVL	0.7207	21	SB	VP1
DRB1_0101	121	VIGITSMLNLHAGSQ	VIGITSMLN	0.7107	23	SB	VP1
DRB1_0101	120	EVIGITSMLNLHAGS	VIGITSMLN	0.7035	25	SB	VP1
DRB1_0101	266	ADICGLFTNSSGTQQ	ICGLFTNSS	0.7009	25	SB	VP1
DRB1_0101	262	YVSAADICGLFTNSS	YVSAADICG	0.6956	27	SB	VP1
DRB1_0101	117	VKTEVIGITSMLNLH	VIGITSMLN	0.6913	28	SB	VP1
DRB1_0101	116	TVKTEVIGITSMLNL	VIGITSMLN	0.6903	29	SB	VP1
DRB1_0101	115	VTVKTEVIGITSMLN	EVIGITSML	0.6842	30	SB	VP1
DRB1_0101	169	NYRTKYPQGTITPKN	YRTKYPQGT	0.6853	30	SB	VP1
DRB1_0101	265	AADICGLFTNSSGTQ	ICGLFTNSS	0.6859	30	SB	VP1
DRB1_0101	170	YRTKYPQGTITPKNP	YRTKYPQGT	0.6835	31	SB	VP1
DRB1_0101	264	SAADICGLFTNSSGT	ICGLFTNSS	0.6829	31	SB	VP1
DRB1_0101	263	VSAADICGLFTNSSG	ICGLFTNSS	0.6809	32	SB	VP1
DRB1_0101	305	FLLSDLINRRTQKVD	LINRRTQKV	0.6730	34	SB	VP1
DRB1_0101	304	SFLLSDLINRRTQKV	LSDLINRRT	0.6723	35	SB	VP1
DRB1_0101	105	TCGNLLMWEAVTVKT	LLMWEAVTV	0.6651	37	SB	VP1
DRB1_0101	106	CGNLLMWEAVTVKTE	LLMWEAVTV	0.6660	37	SB	VP1
DRB1_0101	107	GNLLMWEAVTVKTEV	LLMWEAVTV	0.6675	37	SB	VP1
DRB1_0101	306	LLSDLINRRTQKVDG	LINRRTQKV	0.6610	39	SB	VP1
DRB1_0101	307	LSDLINRRTQKVDGQ	LINRRTQKV	0.6620	39	SB	VP1
DRB1_0101	308	SDLINRRTQKVDGQP	LINRRTQKV	0.6493	44	SB	VP1
DRB1_0101	122	IGITSMLNLHAGSQK	ITSMLNLHA	0.6472	45	SB	VP1
DRB1_0101	108	NLLMWEAVTVKTEVI	MWEAVTVKT	0.6381	50	WB	VP1
DRB1_0101	237	HVTNTATTVLLDEQG	VTNTATTVL	0.6362	51	WB	VP1
DRB1_0101	267	DICGLFTNSSGTQQW	ICGLFTNSS	0.6283	56	WB	VP1
DRB1_0101	268	ICGLFTNSSGTQQWR	ICGLFTNSS	0.6286	56	WB	VP1
DRB1_0101	104	LTCGNLLMWEAVTVK	LLMWEAVTV	0.6269	57	WB	VP1
DRB1_0101	317	KVDGQPMYGMESQVE	VDGQPMYGM	0.6232	59	WB	VP1
DRB1_0101	318	VDGQPMYGMESQVEE	MYGMESQVE	0.6230	59	WB	VP1
DRB1_0101	238	VTNTATTVLLDEQGV	VTNTATTVL	0.6202	61	WB	VP1
DRB1_0101	252	VGPLCKADSLYVSAA	LCKADSLYV	0.6161	64	WB	VP1
DRB1_0101	253	GPLCKADSLYVSAAD	LCKADSLYV	0.6146	65	WB	VP1
DRB1_0101	250	QGVGPLCKADSLYVS	LCKADSLYV	0.6129	66	WB	VP1
DRB1_0101	251	GVGPLCKADSLYVSA	LCKADSLYV	0.6115	67	WB	VP1
DRB1_0101	109	LLMWEAVTVKTEVIG	MWEAVTVKT	0.6104	68	WB	VP1
DRB1_0101	249	EQGVGPLCKADSLYV	VGPLCKADS	0.6000	76	WB	VP1
DRB1_0101	123	GITSMLNLHAGSQKV	ITSMLNLHA	0.5940	81	WB	VP1
DRB1_0101	124	ITSMLNLHAGSQKVH	ITSMLNLHA	0.5895	85	WB	VP1
DRB1_0101	320	GQPMYGMESQVEEVR	MYGMESQVE	0.5805	94	WB	VP1

DRB1_0101	103	DLTCGNLLMWEAVTV	LTCGNLLMW	0.5786	96	WB VP1
DRB1_0101	319	DGQPMYGMESQVEEV	MYGMESQVE	0.5779	96	WB VP1
DRB1_0101	315	TQKVDGQPMYGMESQ	VDGQPMYGM	0.5631	113	WB VP1
DRB1_0101	309	DLINRRTQKVDGQPM	LINRRTQKV	0.5612	115	WB VP1
DRB1_0101	314	RTQKVDGQPMYGMES	VDGQPMYGM	0.5605	116	WB VP1
DRB1_0101	316	QKVDGQPMYGMESQV	VDGQPMYGM	0.5604	116	WB VP1
DRB1_0101	321	QPMYGMESQVEEVRV	MYGMESQVE	0.5604	116	WB VP1
DRB1_0101	310	LINRRTQKVDGQPMY	LINRRTQKV	0.5595	117	WB VP1
DRB1_0101	161	LEMQGVLMNYRTKYP	MQGVLMNYR	0.5570	121	WB VP1
DRB1_0101	158	GDPLEMQGVLMNYRT	MQGVLMNYR	0.5484	132	WB VP1
DRB1_0101	256	CKADSLYVSAADICG	ADSLYVSAA	0.5470	135	WB VP1
DRB1_0101	257	KADSLYVSAADICGL	YVSAADICG	0.5462	136	WB VP1
DRB1_0101	84	RKMLPCYSTARIPLP	RKMLPCYST	0.5450	137	WB VP1
DRB1_0101	258	ADSLYVSAADICGLF	YVSAADICG	0.5446	138	WB VP1
DRB1_0101	259	DSLYVSAADICGLFT	YVSAADICG	0.5443	138	WB VP1
DRB1_0101	159	DPLEMQGVLMNYRTK	MQGVLMNYR	0.5441	139	WB VP1
DRB1_0101	260	SLYVSAADICGLFTN	YVSAADICG	0.5396	146	WB VP1
DRB1_0101	81	SPDRKMLPCYSTARI	RKMLPCYST	0.5323	158	WB VP1
DRB1_0101	110	LMWEAVTVKTEVIGI	MWEAVTVKT	0.5308	160	WB VP1
DRB1_0101	231	NVPPVLHVTNTATTV	LHVTNTATT	0.5288	164	WB VP1
DRB1_0101	177	GTITPKNPTAQSQVM	ITPKNPTAQ	0.5283	165	WB VP1
DRB1_0101	82	PDRKMLPCYSTARIP	RKMLPCYST	0.5256	170	WB VP1
DRB1_0101	254	PLCKADSLYVSAADI	LCKADSLYV	0.5231	174	WB VP1
DRB1_0101	162	EMQGVLMNYRTKYPQ	LMNYRTKYP	0.5203	179	WB VP1
DRB1_0101	80	DSPDRKMLPCYSTAR	RKMLPCYST	0.5206	179	WB VP1
DRB1_0101	255	LCKADSLYVSAADIC	LCKADSLYV	0.5180	184	WB VP1
DRB1_0101	294	KRSVKNPYPISFLLS	VKNPYPISF	0.5180	184	WB VP1
DRB1_0101	313	RRTQKVDGQPMYGME	VDGQPMYGM	0.5170	186	WB VP1
DRB1_0101	157	GGDPLEMQGVLMNYR	LEMQGVLMN	0.5164	187	WB VP1
DRB1_0101	295	RSVKNPYPISFLLSD	VKNPYPISF	0.5161	188	WB VP1
DRB1_0101	312	NRRTQKVDGQPMYGM	KVDGQPMYG	0.5163	188	WB VP1
DRB1_0101	160	PLEMQGVLMNYRTKY	MQGVLMNYR	0.5148	190	WB VP1
DRB1_0101	269	CGLFTNSSGTQQWRG	FTNSSGTQQ	0.5138	193	WB VP1
DRB1_0101	292	LRKRSVKNPYPISFL	VKNPYPISF	0.5094	202	WB VP1
DRB1_0101	163	MQGVLMNYRTKYPQG	LMNYRTKYP	0.5072	207	WB VP1
DRB1_0101	230	ENVPPVLHVTNTATT	VLHVTNTAT	0.5053	211	WB VP1
DRB1_0101	293	RKRSVKNPYPISFLL	VKNPYPISF	0.5053	211	WB VP1
DRB1_0101	270	GLFTNSSGTQQWRGL	FTNSSGTQQ	0.5035	215	WB VP1
DRB1_0101	175	PQGTITPKNPTAQSQ	ITPKNPTAQ	0.5026	217	WB VP1
DRB1_0101	176	QGTITPKNPTAQSQV	ITPKNPTAQ	0.5007	222	WB VP1
DRB1_0101	291	RLRKRSVKNPYPISF	LRKRSVKNP	0.5005	222	WB VP1
DRB1_0101	125	TSMLNLHAGSQKVHE	MLNLHAGSQ	0.4968	231	WB VP1
DRB1_0101	62	DNLRGYSQHLSAENA	LRGYSQHLS	0.4929	241	WB VP1
DRB1_0101	83	DRKMLPCYSTARIPL	MLPCYSTAR	0.4902	249	WB VP1
DRB1_0101	87	LPCYSTARIPLPNLN	YSTARIPLP	0.4891	252	WB VP1
DRB1_0101	85	KMLPCYSTARIPLPN	YSTARIPLP	0.4865	259	WB VP1
DRB1_0101	349	IRYIDRQGQLQTKMV	YIDRQGQLQ	0.4856	261	WB VP1
DRB1_0101	111	MWEAVTVKTEVIGIT	MWEAVTVKT	0.4847	264	WB VP1
DRB1_0101	88	PCYSTARIPLPNLNE	YSTARIPLP	0.4819	272	WB VP1
DRB1_0101	86	MLPCYSTARIPLPNL	YSTARIPLP	0.4817	273	WB VP1
DRB1_0101	23	VQVPKLLIKGGVEVL	LLIKGGVEV	0.4803	277	WB VP1
DRB1_0101	61	DDNLRGYSQHLSAEN	LRGYSQHLS	0.4800	278	WB VP1
DRB1_0101	179	ITPKNPTAQSQVMNT	ITPKNPTAQ	0.4786	282	WB VP1
DRB1_0101	285	ARYFKIRLRKRSVKN	FKIRLRKRS	0.4787	282	WB VP1
DRB1_0101	155	AVGGDPLEMQGVLMN	GDPLEMQGV	0.4780	284	WB VP1
DRB1_0101	284	LARYFKIRLRKRSVK	FKIRLRKRS	0.4764	289	WB VP1
DRB1_0101	178	TITPKNPTAQSQVMN	ITPKNPTAQ	0.4755	291	WB VP1
DRB1_0101	282	RGLARYFKIRLRKRS	YFKIRLRKR	0.4754	292	WB VP1
DRB1_0101	283	GLARYFKIRLRKRSV	FKIRLRKRS	0.4744	295	WB VP1
DRB1_0101	173	KYPQGTITPKNPTAQ	PQGTITPKN	0.4716	304	WB VP1
DRB1_0101	174	YPQGTITPKNPTAQS	ITPKNPTAQ	0.4716	304	WB VP1
DRB1_0101	224	GTYTGGENVPPVLHV	YTGGENVPP	0.4697	310	WB VP1

DRB1_0101	322	PMYGMESQVEEVRVF	MYGMESQVE	0.4691	312	WB VP1
DRB1_0101	156	VGGDPLEMQGVLMNY	LEMQGVLMN	0.4685	314	WB VP1
DRB1_0101	25	VPKLLIKGGVEVLEV	LLIKGGVEV	0.4678	317	WB VP1
DRB1_0101	24	QVPKLLIKGGVEVLE	LLIKGGVEV	0.4674	318	WB VP1
DRB1_0101	22	PVQVPKLLIKGGVEV	VPKLLIKGG	0.4668	320	WB VP1
DRB1_0101	261	LYVSAADICGLFTNS	YVSAADICG	0.4665	321	WB VP1
DRB1_0101	26	PKLLIKGGVEVLEVK	LLIKGGVEV	0.4633	332	WB VP1
DRB1_0101	151	FHFFAVGGDPLEMQG	VGGDPLEMQ	0.4633	333	WB VP1
DRB1_0101	323	MYGMESQVEEVRVFD	MYGMESQVE	0.4626	335	WB VP1
DRB1_0101	150	NFHFFAVGGDPLEMQ	AVGGDPLEM	0.4611	340	WB VP1
DRB1_0101	223	FGTYTGGENVPPVLH	YTGGENVPP	0.4596	346	WB VP1
DRB1_0101	297	VKNPYPISFLLSDLI	VKNPYPISF	0.4588	349	WB VP1
DRB1_0101	63	NLRGYSQHLSAENAF	YSQHLSAEN	0.4583	351	WB VP1
DRB1_0101	152	HFFAVGGDPLEMQGV	VGGDPLEMQ	0.4576	354	WB VP1
DRB1_0101	286	RYFKIRLRKRSVKNP	FKIRLRKRS	0.4564	358	WB VP1
DRB1_0101	64	LRGYSQHLSAENAFE	YSQHLSAEN	0.4559	360	WB VP1
DRB1_0101	220	TRYFGTYTGGENVPP	YFGTYTGGE	0.4546	365	WB VP1
DRB1_0101	301	YPISFLLSDLINRRT	ISFLLSDLI	0.4540	368	WB VP1
DRB1_0101	126	SMLNLHAGSQKVHEN	MLNLHAGSQ	0.4520	376	WB VP1
DRB1_0101	34	VEVLEVKTGVDAITE	VKTGVDAIT	0.4507	381	WB VP1
DRB1_0101	33	GVEVLEVKTGVDAIT	VEVLEVKTG	0.4499	385	WB VP1
DRB1_0101	226	YTGGENVPPVLHVTN	YTGGENVPP	0.4471	397	WB VP1
DRB1_0101	303	ISFLLSDLINRRTQK	LSDLINRRT	0.4468	397	WB VP1
DRB1_0101	153	FFAVGGDPLEMQGVL	VGGDPLEMQ	0.4446	407	WB VP1
DRB1_0101	225	TYTGGENVPPVLHVT	YTGGENVPP	0.4439	410	WB VP1
DRB1_0101	302	PISFLLSDLINRRTQ	LSDLINRRT	0.4439	411	WB VP1
DRB1_0101	36	VLEVKTGVDAITEVE	VKTGVDAIT	0.4399	429	WB VP1
DRB1_0101	35	EVLEVKTGVDAITEV	VKTGVDAIT	0.4395	430	WB VP1
DRB1_0101	37	LEVKTGVDAITEVEC	VKTGVDAIT	0.4381	437	WB VP1
DRB1_0101	127	MLNLHAGSQKVHENG	MLNLHAGSQ	0.4375	440	WB VP1
DRB1_0101	229	GENVPPVLHVTNTAT	NVPPVLHVT	0.4368	443	WB VP1
DRB1_0101	60	PDDNLRGYSQHLSAE	LRGYSQHLS	0.4346	454	WB VP1
DRB1_0101	59	DPDDNLRGYSQHLSA	LRGYSQHLS	0.4337	458	WB VP1
DRB1_0101	65	RGYSQHLSAENAFES	YSQHLSAEN	0.4335	459	WB VP1
DRB1_0101	27	KLLIKGGVEVLEVKT	LIKGGVEVL	0.4331	461	WB VP1
DRB1_0101	221	RYFGTYTGGENVPPV	YTGGENVPP	0.4318	468	WB VP1
DRB1_0101	296	SVKNPYPISFLLSDL	VKNPYPISF	0.4317	468	WB VP1
DRB1_0101	222	YFGTYTGGENVPPVL	YTGGENVPP	0.4313	470	WB VP1
DRB1_0101	271	LFTNSSGTQQWRGLA	FTNSSGTQQ	0.4313	470	WB VP1
DRB1_0101	58	GDPDDNLRGYSQHLS	NLRGYSQHL	0.4305	474	WB VP1
DRB1_0101	281	WRGLARYFKIRLRKR	WRGLARYFK	0.4285	485	WB VP1
DRB1_0101	276	SGTQQWRGLARYFKI	WRGLARYFK	0.4263	496	WB VP1
DRB1_0101	154	FAVGGDPLEMQGVLM	VGGDPLEMQ	0.4261	498	WB VP1
DRB1_0101	277	GTQQWRGLARYFKIR	WRGLARYFK	0.4259	498	WB VP1
DRB1_0101	275	SSGTQQWRGLARYFK	QQWRGLARY	0.4258	499	WB VP1
DRB1_0401	118	KTEVIGITSMLNLHA	VIGITSMLN	0.5278	165	WB VP1
DRB1_0401	119	TEVIGITSMLNLHAG	ITSMLNLHA	0.5243	172	WB VP1
DRB1_0401	266	ADICGLFTNSSGTQQ	ICGLFTNSS	0.5078	206	WB VP1
DRB1_0401	265	AADICGLFTNSSGTQ	ICGLFTNSS	0.5038	215	WB VP1
DRB1_0401	120	EVIGITSMLNLHAGS	ITSMLNLHA	0.4938	239	WB VP1
DRB1_0401	121	VIGITSMLNLHAGSQ	ITSMLNLHA	0.4931	241	WB VP1
DRB1_0401	262	YVSAADICGLFTNSS	YVSAADICG	0.4874	256	WB VP1
DRB1_0401	264	SAADICGLFTNSSGT	ICGLFTNSS	0.4849	263	WB VP1
DRB1_0401	263	VSAADICGLFTNSSG	ICGLFTNSS	0.4805	276	WB VP1
DRB1_0401	287	YFKIRLRKRSVKNPY	RLRKRSVKN	0.4585	350	WB VP1
DRB1_0401	304	SFLLSDLINRRTQKV	LLSDLINRR	0.4554	362	WB VP1
DRB1_0401	288	FKIRLRKRSVKNPYP	RKRSVKNPY	0.4485	390	WB VP1
DRB1_0401	122	IGITSMLNLHAGSQK	ITSMLNLHA	0.4473	395	WB VP1
DRB1_0401	291	RLRKRSVKNPYPISF	RKRSVKNPY	0.4444	408	WB VP1
DRB1_0401	232	VPPVLHVTNTATTVL	PVLHVTNTA	0.4431	414	WB VP1
DRB1_0401	115	VTVKTEVIGITSMLN	VKTEVIGIT	0.4422	418	WB VP1

DRB1_0401	289	KIRLRKRSVKNPYPI	RKRSVKNPY	0.4410	424	WB VP1
DRB1_0401	117	VKTEVIGITSMLNLH	VIGITSMLN	0.4404	426	WB VP1
DRB1_0401	268	ICGLFTNSSGTQQWR	ICGLFTNSS	0.4395	430	WB VP1
DRB1_0401	267	DICGLFTNSSGTQQW	ICGLFTNSS	0.4385	435	WB VP1
DRB1_0401	230	ENVPPVLHVTNTATT	PVLHVTNTA	0.4370	442	WB VP1
DRB1_0401	290	IRLRKRSVKNPYPIS	RKRSVKNPY	0.4334	460	WB VP1
DRB1_0401	231	NVPPVLHVTNTATTV	PVLHVTNTA	0.4332	461	WB VP1
DRB1_0401	301	YPISFLLSDLINRRT	LLSDLINRR	0.4287	483	WB VP1
DRB1_0401	116	TVKTEVIGITSMLNL	VIGITSMLN	0.4285	485	WB VP1
DRB1_0401	300	PYPISFLLSDLINRR	ISFLLSDLI	0.4265	495	WB VP1
DRB1_0404	121	VIGITSMLNLHAGSQ	ITSMLNLHA	0.6731	34	SB VP1
DRB1_0404	122	IGITSMLNLHAGSQK	MLNLHAGSQ	0.6665	37	SB VP1
DRB1_0404	124	ITSMLNLHAGSQKVH	MLNLHAGSQ	0.6499	44	SB VP1
DRB1_0404	123	GITSMLNLHAGSQKV	MLNLHAGSQ	0.6491	45	SB VP1
DRB1_0404	163	MQGVLMNYRTKYPQG	LMNYRTKYP	0.6123	66	WB VP1
DRB1_0404	125	TSMLNLHAGSQKVHE	MLNLHAGSQ	0.6117	67	WB VP1
DRB1_0404	161	LEMQGVLMNYRTKYP	MQGVLMNYR	0.6109	67	WB VP1
DRB1_0404	164	QGVLMNYRTKYPQGT	LMNYRTKYP	0.6092	69	WB VP1
DRB1_0404	162	EMQGVLMNYRTKYPQ	LMNYRTKYP	0.6059	71	WB VP1
DRB1_0404	165	GVLMNYRTKYPQGTI	LMNYRTKYP	0.6046	72	WB VP1
DRB1_0404	126	SMLNLHAGSQKVHEN	MLNLHAGSQ	0.5148	190	WB VP1
DRB1_0404	127	MLNLHAGSQKVHENG	MLNLHAGSQ	0.5132	194	WB VP1
DRB1_0404	166	VLMNYRTKYPQGTIT	LMNYRTKYP	0.5108	199	WB VP1
DRB1_0404	266	ADICGLFTNSSGTQQ	ICGLFTNSS	0.5092	202	WB VP1
DRB1_0404	265	AADICGLFTNSSGTQ	ICGLFTNSS	0.5081	205	WB VP1
DRB1_0404	167	LMNYRTKYPQGTITP	LMNYRTKYP	0.5069	208	WB VP1
DRB1_0404	304	SFLLSDLINRRTQKV	LLSDLINRR	0.4931	241	WB VP1
DRB1_0404	301	YPISFLLSDLINRRT	LLSDLINRR	0.4876	256	WB VP1
DRB1_0404	119	TEVIGITSMLNLHAG	ITSMLNLHA	0.4851	263	WB VP1
DRB1_0404	302	PISFLLSDLINRRTQ	LLSDLINRR	0.4821	271	WB VP1
DRB1_0404	303	ISFLLSDLINRRTQK	LLSDLINRR	0.4816	273	WB VP1
DRB1_0404	118	KTEVIGITSMLNLHA	VIGITSMLN	0.4807	275	WB VP1
DRB1_0404	46	ITEVECFLNPEMGDP	TEVECFLNP	0.4807	275	WB VP1
DRB1_0404	47	TEVECFLNPEMGDPD	FLNPEMGDP	0.4801	277	WB VP1
DRB1_0404	48	EVECFLNPEMGDPDD	FLNPEMGDP	0.4754	292	WB VP1
DRB1_0404	50	ECFLNPEMGDPDDNL	FLNPEMGDP	0.4751	293	WB VP1
DRB1_0404	49	VECFLNPEMGDPDDN	FLNPEMGDP	0.4745	295	WB VP1
DRB1_0404	267	DICGLFTNSSGTQQW	LFTNSSGTQ	0.4682	315	WB VP1
DRB1_0404	268	ICGLFTNSSGTQQWR	LFTNSSGTQ	0.4665	321	WB VP1
DRB1_0404	84	RKMLPCYSTARIPLP	MLPCYSTAR	0.4629	334	WB VP1
DRB1_0404	105	TCGNLLMWEAVTVKT	LMWEAVTVK	0.4618	338	WB VP1
DRB1_0404	106	CGNLLMWEAVTVKTE	LMWEAVTVK	0.4597	346	WB VP1
DRB1_0404	232	VPPVLHVTNTATTVL	LHVTNTATT	0.4584	351	WB VP1
DRB1_0404	300	PYPISFLLSDLINRR	FLLSDLINR	0.4582	351	WB VP1
DRB1_0404	120	EVIGITSMLNLHAGS	ITSMLNLHA	0.4575	354	WB VP1
DRB1_0404	107	GNLLMWEAVTVKTEV	LMWEAVTVK	0.4552	363	WB VP1
DRB1_0404	233	PPVLHVTNTATTVLL	LHVTNTATT	0.4466	398	WB VP1
DRB1_0404	230	ENVPPVLHVTNTATT	VLHVTNTAT	0.4465	399	WB VP1
DRB1_0404	108	NLLMWEAVTVKTEVI	LMWEAVTVK	0.4456	403	WB VP1
DRB1_0404	305	FLLSDLINRRTQKVD	LLSDLINRR	0.4431	414	WB VP1
DRB1_0404	192	NTDHKAYLDKNNAYP	KAYLDKNNA	0.4422	418	WB VP1
DRB1_0404	193	TDHKAYLDKNNAYPV	YLDKNNAYP	0.4402	427	WB VP1
DRB1_0404	231	NVPPVLHVTNTATTV	LHVTNTATT	0.4401	428	WB VP1
DRB1_0404	194	DHKAYLDKNNAYPVE	YLDKNNAYP	0.4393	431	WB VP1
DRB1_0404	85	KMLPCYSTARIPLPN	YSTARIPLP	0.4335	459	WB VP1
DRB1_0404	234	PVLHVTNTATTVLLD	LHVTNTATT	0.4328	463	WB VP1
DRB1_0404	195	HKAYLDKNNAYPVEC	YLDKNNAYP	0.4303	476	WB VP1
DRB1_0404	196	KAYLDKNNAYPVECW	YLDKNNAYP	0.4288	483	WB VP1
DRB1_0404	104	LTCGNLLMWEAVTVK	LLMWEAVTV	0.4272	492	WB VP1
DRB1_0405	205	YPVECWIPDPSRNEN	WIPDPSRNE	0.4758	291	WB VP1

DRB1_0405	204	AYPVECWIPDPSRNE	ECWIPDPSR	0.4737	297	WB VP1
DRB1_0405	118	KTEVIGITSMLNLHA	VIGITSMLN	0.4649	327	WB VP1
DRB1_0405	119	TEVIGITSMLNLHAG	VIGITSMLN	0.4617	338	WB VP1
DRB1_0405	88	PCYSTARIPLPNLNE	YSTARIPLP	0.4515	378	WB VP1
DRB1_0405	206	PVECWIPDPSRNENT	WIPDPSRNE	0.4387	434	WB VP1
DRB1_0405	115	VTVKTEVIGITSMLN	TVKTEVIGI	0.4272	492	WB VP1
DRB1_0701	232	VPPVLHVTNTATTVL	VLHVTNTAT	0.7832	10	SB VP1
DRB1_0701	233	PPVLHVTNTATTVLL	VTNTATTVL	0.7867	10	SB VP1
DRB1_0701	234	PVLHVTNTATTVLLD	VTNTATTVL	0.7821	11	SB VP1
DRB1_0701	235	VLHVTNTATTVLLDE	VTNTATTVL	0.7792	11	SB VP1
DRB1_0701	236	LHVTNTATTVLLDEQ	VTNTATTVL	0.7807	11	SB VP1
DRB1_0701	237	HVTNTATTVLLDEQG	VTNTATTVL	0.6865	30	SB VP1
DRB1_0701	238	VTNTATTVLLDEQGV	VTNTATTVL	0.6833	31	SB VP1
DRB1_0701	304	SFLLSDLINRRTQKV	LSDLINRRT	0.5382	148	WB VP1
DRB1_0701	308	SDLINRRTQKVDGQP	LINRRTQKV	0.5370	150	WB VP1
DRB1_0701	305	FLLSDLINRRTQKVD	LINRRTQKV	0.5365	151	WB VP1
DRB1_0701	306	LLSDLINRRTQKVDG	LINRRTQKV	0.5340	155	WB VP1
DRB1_0701	307	LSDLINRRTQKVDGQ	LINRRTQKV	0.5332	156	WB VP1
DRB1_0701	231	NVPPVLHVTNTATTV	VLHVTNTAT	0.4751	293	WB VP1
DRB1_0701	107	GNLLMWEAVTVKTEV	LLMWEAVTV	0.4593	347	WB VP1
DRB1_0701	105	TCGNLLMWEAVTVKT	LLMWEAVTV	0.4539	368	WB VP1
DRB1_0701	106	CGNLLMWEAVTVKTE	LLMWEAVTV	0.4530	372	WB VP1
DRB1_0701	104	LTCGNLLMWEAVTVK	LLMWEAVTV	0.4517	377	WB VP1
DRB1_0701	103	DLTCGNLLMWEAVTV	LTCGNLLMW	0.4475	395	WB VP1
DRB1_0701	230	ENVPPVLHVTNTATT	VLHVTNTAT	0.4461	401	WB VP1
DRB1_0701	309	DLINRRTQKVDGQPM	LINRRTQKV	0.4383	436	WB VP1
DRB1_0701	310	LINRRTQKVDGQPMY	LINRRTQKV	0.4370	442	WB VP1
DRB1_0701	285	ARYFKIRLRKRSVKN	YFKIRLRKR	0.4289	483	WB VP1
DRB1_0701	249	EQGVGPLCKADSLYV	PLCKADSLY	0.4260	498	WB VP1
DRB1_0802	282	RGLARYFKIRLRKRS	RGLARYFKI	0.5826	91	WB VP1
DRB1_0802	283	GLARYFKIRLRKRSV	FKIRLRKRS	0.5827	91	WB VP1
DRB1_0802	284	LARYFKIRLRKRSVK	FKIRLRKRS	0.5824	92	WB VP1
DRB1_0802	285	ARYFKIRLRKRSVKN	FKIRLRKRS	0.5816	92	WB VP1
DRB1_0802	286	RYFKIRLRKRSVKNP	FKIRLRKRS	0.5825	92	WB VP1
DRB1_0802	287	YFKIRLRKRSVKNPY	FKIRLRKRS	0.4907	247	WB VP1
DRB1_0802	288	FKIRLRKRSVKNPYP	FKIRLRKRS	0.4905	248	WB VP1
DRB1_0901	84	RKMLPCYSTARIPLP	LPCYSTARI	0.5150	190	WB VP1
DRB1_0901	85	KMLPCYSTARIPLPN	YSTARIPLP	0.5124	195	WB VP1
DRB1_0901	86	MLPCYSTARIPLPNL	YSTARIPLP	0.4991	226	WB VP1
DRB1_0901	87	LPCYSTARIPLPNLN	YSTARIPLP	0.4968	231	WB VP1
DRB1_0901	88	PCYSTARIPLPNLNE	YSTARIPLP	0.4598	345	WB VP1
DRB1_1101	276	SGTQQWRGLARYFKI	WRGLARYFK	0.5202	180	WB VP1
DRB1_1101	277	GTQQWRGLARYFKIR	WRGLARYFK	0.5200	180	WB VP1
DRB1_1101	278	TQQWRGLARYFKIRL	WRGLARYFK	0.5165	187	WB VP1
DRB1_1101	275	SSGTQQWRGLARYFK	QQWRGLARY	0.5148	191	WB VP1
DRB1_1101	279	QQWRGLARYFKIRLR	WRGLARYFK	0.5146	191	WB VP1
DRB1_1101	281	WRGLARYFKIRLRKR	WRGLARYFK	0.4569	357	WB VP1
DRB1_1101	280	QWRGLARYFKIRLRK	WRGLARYFK	0.4404	426	WB VP1
DRB1_1302	161	LEMQGVLMNYRTKYP	VLMNYRTKY	0.6366	51	WB VP1
DRB1_1302	162	EMQGVLMNYRTKYPQ	VLMNYRTKY	0.6357	51	WB VP1
DRB1_1302	163	MQGVLMNYRTKYPQG	VLMNYRTKY	0.6190	62	WB VP1
DRB1_1302	164	QGVLMNYRTKYPQGT	VLMNYRTKY	0.6178	63	WB VP1
DRB1_1302	160	PLEMQGVLMNYRTKY	QGVLMNYRT	0.6118	67	WB VP1
DRB1_1302	233	PPVLHVTNTATTVLL	VTNTATTVL	0.6016	75	WB VP1
DRB1_1302	234	PVLHVTNTATTVLLD	VTNTATTVL	0.5831	91	WB VP1
DRB1_1302	232	VPPVLHVTNTATTVL	VLHVTNTAT	0.5808	93	WB VP1
DRB1_1302	235	VLHVTNTATTVLLDE	VTNTATTVL	0.5658	110	WB VP1

DRB1_1302	284	LARYFKIRLRKRSVK	FKIRLRKRS	0.5521	127	WB VP1
DRB1_1302	165	GVLMNYRTKYPQGTI	VLMNYRTKY	0.5482	133	WB VP1
DRB1_1302	285	ARYFKIRLRKRSVKN	FKIRLRKRS	0.5453	137	WB VP1
DRB1_1302	286	RYFKIRLRKRSVKNP	FKIRLRKRS	0.5448	138	WB VP1
DRB1_1302	287	YFKIRLRKRSVKNPY	IRLRKRSVK	0.5427	141	WB VP1
DRB1_1302	236	LHVTNTATTVLLDEQ	VTNTATTVL	0.5416	143	WB VP1
DRB1_1302	288	FKIRLRKRSVKNPYP	IRLRKRSVK	0.5351	153	WB VP1
DRB1_1302	117	VKTEVIGITSMLNLH	IGITSMLNL	0.5226	175	WB VP1
DRB1_1302	166	VLMNYRTKYPQGTIT	VLMNYRTKY	0.5220	176	WB VP1
DRB1_1302	116	TVKTEVIGITSMLNL	EVIGITSML	0.5120	196	WB VP1
DRB1_1302	282	RGLARYFKIRLRKRS	LARYFKIRL	0.4951	236	WB VP1
DRB1_1302	118	KTEVIGITSMLNLHA	IGITSMLNL	0.4947	237	WB VP1
DRB1_1302	283	GLARYFKIRLRKRSV	FKIRLRKRS	0.4916	245	WB VP1
DRB1_1302	304	SFLLSDLINRRTQKV	LLSDLINRR	0.4893	251	WB VP1
DRB1_1302	305	FLLSDLINRRTQKVD	LINRRTQKV	0.4877	255	WB VP1
DRB1_1302	119	TEVIGITSMLNLHAG	IGITSMLNL	0.4792	280	WB VP1
DRB1_1302	120	EVIGITSMLNLHAGS	IGITSMLNL	0.4786	282	WB VP1
DRB1_1302	91	STARIPLPNLNEDLT	ARIPLPNLN	0.4726	301	WB VP1
DRB1_1302	237	HVTNTATTVLLDEQG	VTNTATTVL	0.4703	308	WB VP1
DRB1_1302	95	IPLPNLNEDLTCGNL	LPNLNEDLT	0.4680	316	WB VP1
DRB1_1302	93	ARIPLPNLNEDLTCG	LPNLNEDLT	0.4675	318	WB VP1
DRB1_1302	94	RIPLPNLNEDLTCGN	LPNLNEDLT	0.4673	318	WB VP1
DRB1_1302	159	DPLEMQGVLMNYRTK	QGVLMNYRT	0.4669	320	WB VP1
DRB1_1302	92	TARIPLPNLNEDLTC	LPNLNEDLT	0.4645	328	WB VP1
DRB1_1302	158	GDPLEMQGVLMNYRT	LEMQGVLMN	0.4643	329	WB VP1
DRB1_1302	289	KIRLRKRSVKNPYPI	RKRSVKNPY	0.4576	354	WB VP1
DRB1_1302	290	IRLRKRSVKNPYPIS	RKRSVKNPY	0.4565	358	WB VP1
DRB1_1302	306	LLSDLINRRTQKVDG	LINRRTQKV	0.4527	373	WB VP1
DRB1_1302	122	IGITSMLNLHAGSQK	IGITSMLNL	0.4502	383	WB VP1
DRB1_1302	115	VTVKTEVIGITSMLN	VKTEVIGIT	0.4481	392	WB VP1
DRB1_1302	114	AVTVKTEVIGITSML	VKTEVIGIT	0.4425	417	WB VP1
DRB1_1302	238	VTNTATTVLLDEQGV	VTNTATTVL	0.4366	444	WB VP1
DRB1_1302	307	LSDLINRRTQKVDGQ	LINRRTQKV	0.4354	450	WB VP1
DRB1_1302	23	VQVPKLLIKGGVEVL	LLIKGGVEV	0.4322	466	WB VP1
DRB1_1302	266	ADICGLFTNSSGTQQ	LFTNSSGTQ	0.4320	466	WB VP1
DRB1_1302	267	DICGLFTNSSGTQQW	FTNSSGTQQ	0.4291	481	WB VP1
DRB1_1501	283	GLARYFKIRLRKRSV	YFKIRLRKR	0.6573	41	SB VP1
DRB1_1501	282	RGLARYFKIRLRKRS	YFKIRLRKR	0.6478	45	SB VP1
DRB1_1501	284	LARYFKIRLRKRSVK	YFKIRLRKR	0.6478	45	SB VP1
DRB1_1501	285	ARYFKIRLRKRSVKN	YFKIRLRKR	0.6480	45	SB VP1
DRB1_1501	281	WRGLARYFKIRLRKR	ARYFKIRLR	0.6307	54	WB VP1
DRB1_1501	286	RYFKIRLRKRSVKNP	YFKIRLRKR	0.5738	101	WB VP1
DRB1_1501	279	QQWRGLARYFKIRLR	WRGLARYFK	0.5664	109	WB VP1
DRB1_1501	287	YFKIRLRKRSVKNPY	YFKIRLRKR	0.5644	111	WB VP1
DRB1_1501	301	YPISFLLSDLINRRT	FLLSDLINR	0.5442	139	WB VP1
DRB1_1501	280	QWRGLARYFKIRLRK	ARYFKIRLR	0.5432	140	WB VP1
DRB1_1501	302	PISFLLSDLINRRTQ	FLLSDLINR	0.5326	157	WB VP1
DRB1_1501	303	ISFLLSDLINRRTQK	FLLSDLINR	0.5312	160	WB VP1
DRB1_1501	304	SFLLSDLINRRTQKV	LLSDLINRR	0.5284	165	WB VP1
DRB1_1501	300	PYPISFLLSDLINRR	FLLSDLINR	0.5247	171	WB VP1
DRB1_1501	305	FLLSDLINRRTQKVD	FLLSDLINR	0.5067	208	WB VP1
DRB1_1501	104	LTCGNLLMWEAVTVK	LLMWEAVTV	0.5050	212	WB VP1
DRB1_1501	105	TCGNLLMWEAVTVKT	LLMWEAVTV	0.5048	212	WB VP1
DRB1_1501	107	GNLLMWEAVTVKTEV	LLMWEAVTV	0.5033	216	WB VP1
DRB1_1501	106	CGNLLMWEAVTVKTE	LLMWEAVTV	0.5029	217	WB VP1
DRB1_1501	161	LEMQGVLMNYRTKYP	MQGVLMNYR	0.4970	231	WB VP1
DRB1_1501	278	TQQWRGLARYFKIRL	WRGLARYFK	0.4915	245	WB VP1
DRB1_1501	275	SSGTQQWRGLARYFK	TQQWRGLAR	0.4823	271	WB VP1
DRB1_1501	276	SGTQQWRGLARYFKI	TQQWRGLAR	0.4818	272	WB VP1
DRB1_1501	163	MQGVLMNYRTKYPQG	MQGVLMNYR	0.4769	287	WB VP1
DRB1_1501	299	NPYPISFLLSDLINR	ISFLLSDLI	0.4742	296	WB VP1

DRB1_1501	162	EMQGVLMNYRTKYPQ	MQGVLMNYR	0.4707	307	WB VP1
DRB1_1501	288	FKIRLRKRSVKNPYP	IRLRKRSVK	0.4578	353	WB VP1
DRB1_1501	277	GTQQWRGLARYFKIR	WRGLARYFK	0.4564	358	WB VP1
DRB1_1501	108	NLLMWEAVTVKTEVI	LLMWEAVTV	0.4524	374	WB VP1
DRB1_1501	160	PLEMQGVLMNYRTKY	MQGVLMNYR	0.4445	408	WB VP1
DRB1_1501	122	IGITSMLNLHAGSQK	ITSMLNLHA	0.4316	469	WB VP1
DRB4_0101	205	YPVECWIPDPSRNEN	VECWIPDPS	0.5233	174	WB VP1
DRB4_0101	203	NAYPVECWIPDPSRN	VECWIPDPS	0.5154	189	WB VP1
DRB4_0101	204	AYPVECWIPDPSRNE	VECWIPDPS	0.5145	191	WB VP1
DRB4_0101	202	NNAYPVECWIPDPSR	VECWIPDPS	0.5002	223	WB VP1
DRB4_0101	201	KNNAYPVECWIPDPS	YPVECWIPD	0.4824	271	WB VP1
DRB4_0101	206	PVECWIPDPSRNENT	VECWIPDPS	0.4517	377	WB VP1
DRB4_0101	207	VECWIPDPSRNENTR	VECWIPDPS	0.4492	388	WB VP1
DRB5_0101	285	ARYFKIRLRKRSVKN	FKIRLRKRS	0.6288	55	WB VP1
DRB5_0101	284	LARYFKIRLRKRSVK	FKIRLRKRS	0.6287	56	WB VP1
DRB5_0101	282	RGLARYFKIRLRKRS	YFKIRLRKR	0.6211	60	WB VP1
DRB5_0101	283	GLARYFKIRLRKRSV	FKIRLRKRS	0.6196	61	WB VP1
DRB5_0101	286	RYFKIRLRKRSVKNP	FKIRLRKRS	0.5991	77	WB VP1
DRB5_0101	287	YFKIRLRKRSVKNPY	FKIRLRKRS	0.5403	145	WB VP1
DRB5_0101	281	WRGLARYFKIRLRKR	WRGLARYFK	0.4956	235	WB VP1
DRB5_0101	288	FKIRLRKRSVKNPYP	FKIRLRKRS	0.4834	267	WB VP1
DRB5_0101	164	QGVLMNYRTKYPQGT	LMNYRTKYP	0.4622	337	WB VP1
DRB5_0101	165	GVLMNYRTKYPQGTI	YRTKYPQGT	0.4558	361	WB VP1
DRB5_0101	177	GTITPKNPTAQSQVM	ITPKNPTAQ	0.4497	386	WB VP1
DRB5_0101	71	LSAENAFESDSPDRK	AFESDSPDR	0.4477	394	WB VP1
DRB5_0101	72	SAENAFESDSPDRKM	FESDSPDRK	0.4472	396	WB VP1
DRB5_0101	73	AENAFESDSPDRKML	FESDSPDRK	0.4469	397	WB VP1
DRB5_0101	173	KYPQGTITPKNPTAQ	QGTITPKNP	0.4468	398	WB VP1
DRB5_0101	74	ENAFESDSPDRKMLP	FESDSPDRK	0.4464	400	WB VP1
DRB5_0101	275	SSGTQQWRGLARYFK	TQQWRGLAR	0.4455	403	WB VP1
DRB5_0101	174	YPQGTITPKNPTAQS	ITPKNPTAQ	0.4442	409	WB VP1
DRB5_0101	276	SGTQQWRGLARYFKI	WRGLARYFK	0.4440	410	WB VP1
DRB5_0101	279	QQWRGLARYFKIRLR	WRGLARYFK	0.4423	417	WB VP1
DRB5_0101	277	GTQQWRGLARYFKIR	WRGLARYFK	0.4408	424	WB VP1
DRB5_0101	278	TQQWRGLARYFKIRL	WRGLARYFK	0.4408	424	WB VP1
DRB5_0101	176	QGTITPKNPTAQSQV	ITPKNPTAQ	0.4392	432	WB VP1
DRB5_0101	175	PQGTITPKNPTAQSQ	ITPKNPTAQ	0.4390	433	WB VP1
DRB5_0101	166	VLMNYRTKYPQGTIT	YRTKYPQGT	0.4344	455	WB VP1
DRB5_0101	168	MNYRTKYPQGTITPK	YRTKYPQGT	0.4342	456	WB VP1
DRB5_0101	75	NAFESDSPDRKMLPC	FESDSPDRK	0.4294	480	WB VP1

Preferred BK virus fragments of small T antigen capable of interacting with one or more MHC class 2 molecules are listed in Table R.

Table R: Prediction of BK virus small t protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed.

Allele	pos	peptide	core	1-log50k(aff)	aff(nM)	B.L.	Identity
DRB1_0101	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.6972	26	SB	Small t
DRB1_0101	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.6958	27	SB	Small t
DRB1_0101	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.6940	27	SB	Small t
DRB1_0101	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.6954	27	SB	Small t
DRB1_0101	18	GLERAAWGNLPLMRK	ERAAWGNLP	0.6928	28	SB	Small t
DRB1_0101	24	WGNLPLMRKAYLKKC	WGNLPLMRK	0.6020	74	WB	Small t
DRB1_0101	23	AWGNLPLMRKAYLKK	WGNLPLMRK	0.6000	76	WB	Small t
DRB1_0101	110	PCMLCQLRLRHLNRK	LCQLRLRHL	0.5884	86	WB	Small t
DRB1_0101	111	CMLCQLRLRHLNRKF	LCQLRLRHL	0.5833	91	WB	Small t
DRB1_0101	108	HCPCMLCQLRLRHLN	LCQLRLRHL	0.5732	101	WB	Small t
DRB1_0101	107	VHCPCMLCQLRLRHL	PCMLCQLRL	0.5712	104	WB	Small t
DRB1_0101	109	CPCMLCQLRLRHLNR	LCQLRLRHL	0.5711	104	WB	Small t
DRB1_0101	11	MELMDLLGLERAAWG	MDLLGLERA	0.5102	200	WB	Small t
DRB1_0101	113	LCQLRLRHLNRKFLR	LCQLRLRHL	0.5082	205	WB	Small t
DRB1_0101	112	MLCQLRLRHLNRKFL	LCQLRLRHL	0.5077	206	WB	Small t
DRB1_0101	121	LNRKFLRKEPLVWID	LRKEPLVWI	0.4900	249	WB	Small t
DRB1_0101	120	HLNRKFLRKEPLVWI	FLRKEPLVW	0.4888	252	WB	Small t
DRB1_0101	12	ELMDLLGLERAAWGN	MDLLGLERA	0.4876	256	WB	Small t
DRB1_0101	122	NRKFLRKEPLVWIDC	LRKEPLVWI	0.4836	267	WB	Small t
DRB1_0101	8	EESMELMDLLGLERA	LMDLLGLER	0.4834	268	WB	Small t
DRB1_0101	123	RKFLRKEPLVWIDCY	LRKEPLVWI	0.4822	271	WB	Small t
DRB1_0101	9	ESMELMDLLGLERAA	LMDLLGLER	0.4823	271	WB	Small t
DRB1_0101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4796	279	WB	Small t
DRB1_0101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4754	292	WB	Small t
DRB1_0101	10	SMELMDLLGLERAAW	MDLLGLERA	0.4730	299	WB	Small t
DRB1_0101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4724	302	WB	Small t
DRB1_0101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4699	310	WB	Small t
DRB1_0101	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4690	313	WB	Small t
DRB1_0101	2	DKVLNREESMELMDL	LNREESMEL	0.4683	315	WB	Small t
DRB1_0101	3	KVLNREESMELMDLL	LNREESMEL	0.4672	319	WB	Small t
DRB1_0101	125	FLRKEPLVWIDCYCI	LRKEPLVWI	0.4622	337	WB	Small t
DRB1_0101	13	LMDLLGLERAAWGNL	LGLERAAWG	0.4572	355	WB	Small t
DRB1_0101	1	MDKVLNREESMELMD	LNREESMEL	0.4521	376	WB	Small t
DRB1_0101	124	KFLRKEPLVWIDCYC	LRKEPLVWI	0.4493	387	WB	Small t
DRB1_0101	14	MDLLGLERAAWGNLP	LGLERAAWG	0.4451	405	WB	Small t
DRB1_0101	5	LNREESMELMDLLGL	LNREESMEL	0.4397	429	WB	Small t
DRB1_0101	126	LRKEPLVWIDCYCID	LRKEPLVWI	0.4391	432	WB	Small t
DRB1_0101	7	REESMELMDLLGLER	MELMDLLGL	0.4355	449	WB	Small t
DRB1_0101	91	DTLYCKEWPICSKKP	YCKEWPICS	0.4339	457	WB	Small t
DRB1_0101	92	TLYCKEWPICSKKPS	YCKEWPICS	0.4323	465	WB	Small t
DRB1_0101	140	DCFTQWFGLDLTEET	FTQWFGLDL	0.4291	482	WB	Small t
DRB1_0401	92	TLYCKEWPICSKKPS	YCKEWPICS	0.5564	121	WB	Small t
DRB1_0401	91	DTLYCKEWPICSKKP	YCKEWPICS	0.5500	130	WB	Small t
DRB1_0401	90	PDTLYCKEWPICSKK	YCKEWPICS	0.5447	138	WB	Small t
DRB1_0401	89	CPDTLYCKEWPICSK	YCKEWPICS	0.5423	141	WB	Small t
DRB1_0401	88	LCPDTLYCKEWPICS	LYCKEWPIC	0.5400	145	WB	Small t
DRB1_0401	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5015	220	WB	Small t
DRB1_0401	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4994	225	WB	Small t
DRB1_0401	46	GGDEDKMKRMNTLYK	KMKRMNTLY	0.4992	226	WB	Small t
DRB1_0401	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4991	226	WB	Small t

DRB1_0401	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4948	237	WB Small t
DRB1_0401	94	YCKEWPICSKKPSVH	YCKEWPICS	0.4689	313	WB Small t
DRB1_0401	93	LYCKEWPICSKKPSV	YCKEWPICS	0.4677	317	WB Small t
DRB1_0405	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.5687	106	WB Small t
DRB1_0405	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.5662	109	WB Small t
DRB1_0405	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5447	138	WB Small t
DRB1_0405	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.5432	140	WB Small t
DRB1_0405	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5413	143	WB Small t
DRB1_0405	152	EETLQWWVQIIGETP	LQWWVQIIG	0.5365	151	WB Small t
DRB1_0405	151	TEETLQWWVQIIGET	LQWWVQIIG	0.5328	157	WB Small t
DRB1_0405	150	LTEETLQWWVQIIGE	LQWWVQIIG	0.5314	159	WB Small t
DRB1_0405	153	ETLQWWVQIIGETPF	LQWWVQIIG	0.5290	163	WB Small t
DRB1_0405	149	DLTEETLQWWVQIIG	TLQWWVQII	0.5260	169	WB Small t
DRB1_0405	18	GLERAAWGNLPLMRK	RAAWGNLPL	0.5095	202	WB Small t
DRB1_0405	19	LERAAWGNLPLMRKA	RAAWGNLPL	0.4956	235	WB Small t
DRB1_0405	137	YCIDCFTQWFGLDLT	FTQWFGLDL	0.4951	236	WB Small t
DRB1_0405	139	IDCFTQWFGLDLTEE	TQWFGLDLT	0.4864	259	WB Small t
DRB1_0405	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4857	261	WB Small t
DRB1_0405	52	MKRMNTLYKKMEQDV	MKRMNTLYK	0.4857	261	WB Small t
DRB1_0405	138	CIDCFTQWFGLDLTE	TQWFGLDLT	0.4851	263	WB Small t
DRB1_0405	155	LQWWVQIIGETPFRD	LQWWVQIIG	0.4691	312	WB Small t
DRB1_0405	140	DCFTQWFGLDLTEET	TQWFGLDLT	0.4671	319	WB Small t
DRB1_0405	69	AHQPDFGTWNSSEVC	FGTWNSSEV	0.4648	327	WB Small t
DRB1_0405	68	VAHQPDFGTWNSSEV	QPDFGTWNS	0.4624	336	WB Small t
DRB1_0405	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.4570	356	WB Small t
DRB1_0405	71	QPDFGTWNSSEVCAD	FGTWNSSEV	0.4550	364	WB Small t
DRB1_0405	17	LGLERAAWGNLPLMR	RAAWGNLPL	0.4515	378	WB Small t
DRB1_0405	70	HQPDFGTWNSSEVCA	FGTWNSSEV	0.4467	398	WB Small t
DRB1_0405	154	TLQWWVQIIGETPFR	LQWWVQIIG	0.4465	399	WB Small t
DRB1_0405	16	LLGLERAAWGNLPLM	RAAWGNLPL	0.4465	399	WB Small t
DRB1_0405	15	DLLGLERAAWGNLPL	ERAAWGNLP	0.4401	427	WB Small t
DRB1_0405	136	CYCIDCFTQWFGLDL	IDCFTQWFG	0.4322	465	WB Small t
DRB1_0405	141	CFTQWFGLDLTEETL	TQWFGLDLT	0.4323	465	WB Small t
DRB1_0405	72	PDFGTWNSSEVCADF	FGTWNSSEV	0.4300	477	WB Small t
DRB1_0701	95	CKEWPICSKKPSVHC	ICSKKPSVH	0.4880	255	WB Small t
DRB1_0701	96	KEWPICSKKPSVHCP	ICSKKPSVH	0.4829	269	WB Small t
DRB1_0701	97	EWPICSKKPSVHCPC	ICSKKPSVH	0.4823	271	WB Small t
DRB1_0701	98	WPICSKKPSVHCPCM	ICSKKPSVH	0.4807	276	WB Small t
DRB1_0701	94	YCKEWPICSKKPSVH	PICSKKPSV	0.4738	297	WB Small t
DRB1_0701	70	HQPDFGTWNSSEVCA	FGTWNSSEV	0.4721	303	WB Small t
DRB1_0701	71	QPDFGTWNSSEVCAD	FGTWNSSEV	0.4716	304	WB Small t
DRB1_0701	68	VAHQPDFGTWNSSEV	DFGTWNSSE	0.4709	306	WB Small t
DRB1_0701	69	AHQPDFGTWNSSEVC	FGTWNSSEV	0.4705	308	WB Small t
DRB1_0701	72	PDFGTWNSSEVCADF	FGTWNSSEV	0.4685	314	WB Small t
DRB1_1101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4550	364	WB Small t
DRB1_1101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4498	385	WB Small t
DRB1_1101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4495	386	WB Small t
DRB1_1101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4483	391	WB Small t
DRB1_1101	46	GGDEDKMKRMNTLYK	EDKMKRMNT	0.4433	413	WB Small t
DRB1_1101	18	GLERAAWGNLPLMRK	AWGNLPLMR	0.4312	471	WB Small t
DRB1_1101	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.4311	471	WB Small t
DRB1_1101	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.4288	483	WB Small t
DRB1_1101	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.4279	488	WB Small t
DRB1_1302	18	GLERAAWGNLPLMRK	LERAAWGNL	0.5752	99	WB Small t
DRB1_1302	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.5714	103	WB Small t
DRB1_1302	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.5704	104	WB Small t
DRB1_1302	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.5702	105	WB Small t
DRB1_1302	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.5531	126	WB Small t

DRB1_1302	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5012	221	WB Small t
DRB1_1302	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4986	227	WB Small t
DRB1_1302	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4966	232	WB Small t
DRB1_1302	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4940	239	WB Small t
DRB1_1302	24	WGNLPLMRKAYLKKC	WGNLPLMRK	0.4926	242	WB Small t
DRB1_1302	23	AWGNLPLMRKAYLKK	WGNLPLMRK	0.4885	253	WB Small t
DRB1_1302	153	ETLQWWVQIIGETPF	WWVQIIGET	0.4827	270	WB Small t
DRB1_1302	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4800	278	WB Small t
DRB1_1302	155	LQWWVQIIGETPFRD	VQIIGETPF	0.4679	317	WB Small t
DRB1_1302	154	TLQWWVQIIGETPFR	VQIIGETPF	0.4659	323	WB Small t
DRB1_1302	113	LCQLRLRHLNRKFLR	LRLRHLNRK	0.4607	342	WB Small t
DRB1_1302	112	MLCQLRLRHLNRKFL	LRLRHLNRK	0.4561	360	WB Small t
DRB1_1302	114	CQLRLRHLNRKFLRK	LRLRHLNRK	0.4549	364	WB Small t
DRB1_1302	156	QWWVQIIGETPFRDL	VQIIGETPF	0.4401	427	WB Small t
DRB1_1302	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4272	492	WB Small t
DRB1_1501	111	CMLCQLRLRHLNRKF	LRLRHLNRK	0.5327	157	WB Small t
DRB1_1501	110	PCMLCQLRLRHLNRK	QLRLRHLNR	0.5274	166	WB Small t
DRB1_1501	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5229	174	WB Small t
DRB1_1501	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.5190	182	WB Small t
DRB1_1501	24	WGNLPLMRKAYLKKC	LMRKAYLKK	0.5176	185	WB Small t
DRB1_1501	113	LCQLRLRHLNRKFLR	LRLRHLNRK	0.5166	187	WB Small t
DRB1_1501	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.5153	190	WB Small t
DRB1_1501	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5147	191	WB Small t
DRB1_1501	112	MLCQLRLRHLNRKFL	LRLRHLNRK	0.5140	192	WB Small t
DRB1_1501	23	AWGNLPLMRKAYLKK	LPLMRKAYL	0.5076	206	WB Small t
DRB1_1501	25	GNLPLMRKAYLKKCK	LMRKAYLKK	0.5063	209	WB Small t
DRB1_1501	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.5026	217	WB Small t
DRB1_1501	26	NLPLMRKAYLKKCKE	LMRKAYLKK	0.4961	233	WB Small t
DRB1_1501	114	CQLRLRHLNRKFLRK	LRLRHLNRK	0.4919	244	WB Small t
DRB1_1501	27	LPLMRKAYLKKCKEF	LMRKAYLKK	0.4850	263	WB Small t
DRB1_1501	13	LMDLLGLERAAWGNL	LMDLLGLER	0.4683	315	WB Small t
DRB1_1501	11	MELMDLLGLERAAWG	LMDLLGLER	0.4651	326	WB Small t
DRB1_1501	115	QLRLRHLNRKFLRKE	LRLRHLNRK	0.4643	329	WB Small t
DRB1_1501	120	HLNRKFLRKEPLVWI	FLRKEPLVW	0.4621	337	WB Small t
DRB1_1501	121	LNRKFLRKEPLVWID	FLRKEPLVW	0.4374	440	WB Small t
DRB1_1501	28	PLMRKAYLKKCKEFH	LMRKAYLKK	0.4332	461	WB Small t
DRB1_1501	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4331	461	WB Small t
DRB1_1501	123	RKFLRKEPLVWIDCY	FLRKEPLVW	0.4300	477	WB Small t
DRB1_1501	10	SMELMDLLGLERAAW	LMDLLGLER	0.4261	497	WB Small t
DRB4_0101	94	YCKEWPICSKKPSVH	YCKEWPICS	0.5706	104	WB Small t
DRB4_0101	112	MLCQLRLRHLNRKFL	LRLRHLNRK	0.5364	151	WB Small t
DRB4_0101	113	LCQLRLRHLNRKFLR	LRLRHLNRK	0.5342	155	WB Small t
DRB4_0101	111	CMLCQLRLRHLNRKF	LRLRHLNRK	0.5331	156	WB Small t
DRB4_0101	110	PCMLCQLRLRHLNRK	LCQLRLRHL	0.5322	158	WB Small t
DRB4_0101	95	CKEWPICSKKPSVHC	ICSKKPSVH	0.5323	158	WB Small t
DRB4_0101	114	CQLRLRHLNRKFLRK	LRLRHLNRK	0.5291	163	WB Small t
DRB4_0101	96	KEWPICSKKPSVHCP	ICSKKPSVH	0.5267	167	WB Small t
DRB4_0101	97	EWPICSKKPSVHCPC	ICSKKPSVH	0.5247	171	WB Small t
DRB4_0101	98	WPICSKKPSVHCPCM	ICSKKPSVH	0.5172	186	WB Small t
DRB4_0101	115	QLRLRHLNRKFLRKE	LRLRHLNRK	0.4556	361	WB Small t
DRB4_0101	116	LRLRHLNRKFLRKEP	LRLRHLNRK	0.4510	380	WB Small t
DRB4_0101	100	ICSKKPSVHCPCMLC	ICSKKPSVH	0.4432	413	WB Small t
DRB4_0101	99	PICSKKPSVHCPCML	ICSKKPSVH	0.4374	440	WB Small t
DRB5_0101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4763	289	WB Small t
DRB5_0101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4758	290	WB Small t
DRB5_0101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4726	301	WB Small t
DRB5_0101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4617	338	WB Small t
DRB5_0101	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4567	357	WB Small t
DRB5_0101	112	MLCQLRLRHLNRKFL	LRLRHLNRK	0.4397	429	WB Small t

DRB5_0101	114	CQLRLRHLNRKFLRK	LRHLNRKFL	0.4398	429	WB Small t
DRB5_0101	53	KRMNTLYKKMEQDVK	KRMNTLYKK	0.4284	485	WB Small t
DRB5_0101	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.4268	494	WB Small t

Preferred BK virus fragments of large T antigen capable of interacting with one or more MHC class 2 molecules are listed in Table S.

Table S: Prediction of BK virus Large T protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII/database. The MHC class 2 molecules for which no binders were found are not listed.

Allele	pos	peptide	core	1-log50k(aff)	aff(nM)	B.L.	Identity
DRB1_0101	566	LEKRILQSGMTLLLL	LQSGMTLLL	0.7526	15	SB	Large T
DRB1_0101	567	EKRILQSGMTLLLLL	LQSGMTLLL	0.7519	15	SB	Large T
DRB1_0101	568	KRILQSGMTLLLLLI	LQSGMTLLL	0.7525	15	SB	Large T
DRB1_0101	569	RILQSGMTLLLLLIW	LQSGMTLLL	0.7504	15	SB	Large T
DRB1_0101	565	LLEKRILQSGMTLLL	KRILQSGMT	0.7441	16	SB	Large T
DRB1_0101	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.6972	26	SB	Large T
DRB1_0101	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.6958	27	SB	Large T
DRB1_0101	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.6940	27	SB	Large T
DRB1_0101	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.6954	27	SB	Large T
DRB1_0101	18	GLERAAWGNLPLMRK	ERAAWGNLP	0.6928	28	SB	Large T
DRB1_0101	570	ILQSGMTLLLLLIWF	LQSGMTLLL	0.6646	38	SB	Large T
DRB1_0101	571	LQSGMTLLLLLIWFR	LQSGMTLLL	0.6561	41	SB	Large T
DRB1_0101	383	NAVLEQYMAGVAWLH	EQYMAGVAW	0.6528	43	SB	Large T
DRB1_0101	387	EQYMAGVAWLHCLLP	YMAGVAWLH	0.6516	43	SB	Large T
DRB1_0101	385	VLEQYMAGVAWLHCL	YMAGVAWLH	0.6507	44	SB	Large T
DRB1_0101	384	AVLEQYMAGVAWLHC	YMAGVAWLH	0.6486	45	SB	Large T
DRB1_0101	386	LEQYMAGVAWLHCLL	YMAGVAWLH	0.6483	45	SB	Large T
DRB1_0101	441	LLDLCGGKALNVNLP	LCGGKALNV	0.6340	52	WB	Large T
DRB1_0101	144	LHQFLSQAVFSNRTL	LHQFLSQAV	0.6329	53	WB	Large T
DRB1_0101	143	DLHQFLSQAVFSNRT	LHQFLSQAV	0.6318	54	WB	Large T
DRB1_0101	442	LDLCGGKALNVNLPM	LCGGKALNV	0.6310	54	WB	Large T
DRB1_0101	439	AGLLDLCGGKALNVN	LCGGKALNV	0.6263	57	WB	Large T
DRB1_0101	440	GLLDLCGGKALNVNL	LCGGKALNV	0.6223	60	WB	Large T
DRB1_0101	438	AAGLLDLCGGKALNV	LLDLCGGKA	0.6207	61	WB	Large T
DRB1_0101	142	SDLHQFLSQAVFSNR	LHQFLSQAV	0.6178	62	WB	Large T
DRB1_0101	141	PSDLHQFLSQAVFSN	LHQFLSQAV	0.6165	63	WB	Large T
DRB1_0101	533	YPVPKTLQARFVRQI	PKTLQARFV	0.6160	64	WB	Large T
DRB1_0101	534	PVPKTLQARFVRQID	LQARFVRQI	0.6136	65	WB	Large T
DRB1_0101	140	FPSDLHQFLSQAVFS	LHQFLSQAV	0.6083	69	WB	Large T
DRB1_0101	138	KDFPSDLHQFLSQAV	FPSDLHQFL	0.6036	73	WB	Large T
DRB1_0101	139	DFPSDLHQFLSQAVF	LHQFLSQAV	0.6019	74	WB	Large T
DRB1_0101	24	WGNLPLMRKAYLKKC	WGNLPLMRK	0.6020	74	WB	Large T
DRB1_0101	23	AWGNLPLMRKAYLKK	WGNLPLMRK	0.6000	76	WB	Large T
DRB1_0101	517	NKRTQIFPPGLVTMN	IFPPGLVTM	0.5951	80	WB	Large T
DRB1_0101	518	KRTQIFPPGLVTMNE	IFPPGLVTM	0.5907	84	WB	Large T
DRB1_0101	428	GPIDSGKTTLAAGLL	IDSGKTTLA	0.5880	86	WB	Large T
DRB1_0101	519	RTQIFPPGLVTMNEY	IFPPGLVTM	0.5871	87	WB	Large T
DRB1_0101	520	TQIFPPGLVTMNEYP	IFPPGLVTM	0.5843	90	WB	Large T
DRB1_0101	268	KQVSWKLITEYAVET	WKLITEYAV	0.5795	95	WB	Large T
DRB1_0101	269	QVSWKLITEYAVETK	LITEYAVET	0.5780	96	WB	Large T
DRB1_0101	284	CEDVFLLLGMYLEFQ	VFLLLGMYL	0.5771	97	WB	Large T
DRB1_0101	285	EDVFLLLGMYLEFQY	VFLLLGMYL	0.5774	97	WB	Large T
DRB1_0101	535	VPKTLQARFVRQIDF	LQARFVRQI	0.5743	100	WB	Large T
DRB1_0101	536	PKTLQARFVRQIDFR	LQARFVRQI	0.5746	100	WB	Large T
DRB1_0101	270	VSWKLITEYAVETKC	LITEYAVET	0.5715	103	WB	Large T
DRB1_0101	147	FLSQAVFSNRTLACF	SQAVFSNRT	0.5698	105	WB	Large T
DRB1_0101	388	QYMAGVAWLHCLLPK	YMAGVAWLH	0.5680	107	WB	Large T
DRB1_0101	603	ERLDSEISMYTFSRM	LDSEISMYT	0.5669	108	WB	Large T
DRB1_0101	389	YMAGVAWLHCLLPKM	YMAGVAWLH	0.5664	109	WB	Large T
DRB1_0101	448	KALNVNLPMERLTFE	LNVNLPMER	0.5655	110	WB	Large T
DRB1_0101	444	LCGGKALNVNLPMER	LCGGKALNV	0.5641	112	WB	Large T

DRB1_0101	446	GGKALNVNLPMERLT	LNVNLPMER	0.5640	112	WB Large T
DRB1_0101	425	LFKGPIDSGKTTLAA	IDSGKTTLA	0.5627	113	WB Large T
DRB1_0101	447	GKALNVNLPMERLTF	LNVNLPMER	0.5619	114	WB Large T
DRB1_0101	427	KGPIDSGKTTLAAGL	IDSGKTTLA	0.5613	115	WB Large T
DRB1_0101	599	VEWKERLDSEISMYT	KERLDSEIS	0.5611	115	WB Large T
DRB1_0101	445	CGGKALNVNLPMERL	LNVNLPMER	0.5598	117	WB Large T
DRB1_0101	490	GHGINNLDSLRDYLD	INNLDSLRD	0.5597	117	WB Large T
DRB1_0101	271	SWKLITEYAVETKCE	LITEYAVET	0.5583	119	WB Large T
DRB1_0101	489	SGHGINNLDSLRDYL	INNLDSLRD	0.5574	120	WB Large T
DRB1_0101	491	HGINNLDSLRDYLDG	INNLDSLRD	0.5573	120	WB Large T
DRB1_0101	424	WLFKGPIDSGKTTLA	KGPIDSGKT	0.5567	121	WB Large T
DRB1_0101	487	LPSGHGINNLDSLRD	LPSGHGINN	0.5568	121	WB Large T
DRB1_0101	530	MNEYPVPKTLQARFV	YPVPKTLQA	0.5570	121	WB Large T
DRB1_0101	426	FKGPIDSGKTTLAAG	IDSGKTTLA	0.5562	122	WB Large T
DRB1_0101	600	EWKERLDSEISMYTF	LDSEISMYT	0.5562	122	WB Large T
DRB1_0101	602	KERLDSEISMYTFSR	LDSEISMYT	0.5560	122	WB Large T
DRB1_0101	488	PSGHGINNLDSLRDY	INNLDSLRD	0.5554	123	WB Large T
DRB1_0101	601	WKERLDSEISMYTFS	LDSEISMYT	0.5538	125	WB Large T
DRB1_0101	272	WKLITEYAVETKCED	LITEYAVET	0.5514	128	WB Large T
DRB1_0101	531	NEYPVPKTLQARFVR	PKTLQARFV	0.5518	128	WB Large T
DRB1_0101	521	QIFPPGLVTMNEYPV	FPPGLVTMN	0.5507	129	WB Large T
DRB1_0101	443	DLCGGKALNVNLPME	LCGGKALNV	0.5488	132	WB Large T
DRB1_0101	228	VNKEYLLYSALTRDP	YLLYSALTR	0.5454	137	WB Large T
DRB1_0101	145	HQFLSQAVFSNRTLA	SQAVFSNRT	0.5437	139	WB Large T
DRB1_0101	374	MDLIFGAHGNAVLEQ	IFGAHGNAV	0.5440	139	WB Large T
DRB1_0101	375	DLIFGAHGNAVLEQY	IFGAHGNAV	0.5439	139	WB Large T
DRB1_0101	229	NKEYLLYSALTRDPY	LYSALTRDP	0.5434	140	WB Large T
DRB1_0101	146	QFLSQAVFSNRTLAC	SQAVFSNRT	0.5423	141	WB Large T
DRB1_0101	373	KMDLIFGAHGNAVLE	IFGAHGNAV	0.5366	150	WB Large T
DRB1_0101	564	FLLEKRILQSGMTLL	KRILQSGMT	0.5369	150	WB Large T
DRB1_0101	372	DKMDLIFGAHGNAVL	IFGAHGNAV	0.5366	151	WB Large T
DRB1_0101	230	KEYLLYSALTRDPYH	LYSALTRDP	0.5334	156	WB Large T
DRB1_0101	449	ALNVNLPMERLTFEL	NVNLPMERL	0.5320	158	WB Large T
DRB1_0101	286	DVFLLLGMYLEFQYN	LLGMYLEFQ	0.5310	160	WB Large T
DRB1_0101	232	YLLYSALTRDPYHII	LYSALTRDP	0.5298	162	WB Large T
DRB1_0101	338	ICQQAVDTVLAKKRV	QQAVDTVLA	0.5273	166	WB Large T
DRB1_0101	430	IDSGKTTLAAGLLDL	IDSGKTTLA	0.5269	167	WB Large T
DRB1_0101	149	SQAVFSNRTLACFAV	FSNRTLACF	0.5259	169	WB Large T
DRB1_0101	337	SICQQAVDTVLAKKR	QQAVDTVLA	0.5252	170	WB Large T
DRB1_0101	148	LSQAVFSNRTLACFA	FSNRTLACF	0.5244	172	WB Large T
DRB1_0101	231	EYLLYSALTRDPYHI	LYSALTRDP	0.5238	173	WB Large T
DRB1_0101	522	IFPPGLVTMNEYPVP	IFPPGLVTM	0.5236	173	WB Large T
DRB1_0101	532	EYPVPKTLQARFVRQ	PKTLQARFV	0.5222	176	WB Large T
DRB1_0101	429	PIDSGKTTLAAGLLD	IDSGKTTLA	0.5198	180	WB Large T
DRB1_0101	516	LNKRTQIFPPGLVTM	RTQIFPPGL	0.5156	189	WB Large T
DRB1_0101	287	VFLLLGMYLEFQYNV	VFLLLGMYL	0.5144	191	WB Large T
DRB1_0101	11	MELMDLLGLERAAWG	MDLLGLERA	0.5102	200	WB Large T
DRB1_0101	473	VFEDVKGTGAESKDL	VKGTGAESK	0.5100	201	WB Large T
DRB1_0101	474	FEDVKGTGAESKDLP	VKGTGAESK	0.5088	203	WB Large T
DRB1_0101	537	KTLQARFVRQIDFRP	LQARFVRQI	0.5092	203	WB Large T
DRB1_0101	475	EDVKGTGAESKDLPS	VKGTGAESK	0.5068	208	WB Large T
DRB1_0101	195	NIIFFLTPHRHRVSA	IFFLTPHRH	0.5062	209	WB Large T
DRB1_0101	335	QKSICQQAVDTVLAK	ICQQAVDTV	0.5063	209	WB Large T
DRB1_0101	194	HNIIFFLTPHRHRVS	IFFLTPHRH	0.5053	211	WB Large T
DRB1_0101	336	KSICQQAVDTVLAKK	ICQQAVDTV	0.5051	212	WB Large T
DRB1_0101	334	NQKSICQQAVDTVLA	ICQQAVDTV	0.5035	215	WB Large T
DRB1_0101	450	LNVNLPMERLTFELG	NVNLPMERL	0.5031	216	WB Large T
DRB1_0101	527	LVTMNEYPVPKTLQA	MNEYPVPKT	0.5027	217	WB Large T
DRB1_0101	528	VTMNEYPVPKTLQAR	YPVPKTLQA	0.5012	221	WB Large T
DRB1_0101	371	LDKMDLIFGAHGNAV	LDKMDLIFG	0.4990	226	WB Large T
DRB1_0101	572	QSGMTLLLLLIWFRP	MTLLLLLIW	0.4975	230	WB Large T
DRB1_0101	282	TKCEDVFLLLGMYLE	VFLLLGMYL	0.4937	239	WB Large T

DRB1_0101	283	KCEDVFLLLGMYLEF	VFLLLGMYL	0.4920	244	WB Large T
DRB1_0101	376	LIFGAHGNAVLEQYM	FGAHGNAVL	0.4919	244	WB Large T
DRB1_0101	394	AWLHCLLPKMDSVIF	LLPKMDSVI	0.4910	246	WB Large T
DRB1_0101	604	RLDSEISMYTFSRMK	LDSEISMYT	0.4900	249	WB Large T
DRB1_0101	605	LDSEISMYTFSRMKY	LDSEISMYT	0.4889	252	WB Large T
DRB1_0101	12	ELMDLLGLERAAWGN	MDLLGLERA	0.4876	256	WB Large T
DRB1_0101	472	VVFEDVKGTGAESKD	VKGTGAESK	0.4858	261	WB Large T
DRB1_0101	471	MVVFEDVKGTGAESK	FEDVKGTGA	0.4853	262	WB Large T
DRB1_0101	340	QQAVDTVLAKKRVDT	VDTVLAKKR	0.4843	265	WB Large T
DRB1_0101	172	ILYKKLMEKYSVTFI	YKKLMEKYS	0.4836	267	WB Large T
DRB1_0101	339	CQQAVDTVLAKKRVD	VDTVLAKKR	0.4837	267	WB Large T
DRB1_0101	8	EESMELMDLLGLERA	LMDLLGLER	0.4834	268	WB Large T
DRB1_0101	9	ESMELMDLLGLERAA	LMDLLGLER	0.4823	271	WB Large T
DRB1_0101	395	WLHCLLPKMDSVIFD	LPKMDSVIF	0.4815	273	WB Large T
DRB1_0101	256	EHDFNPEEPEETKQV	FNPEEPEET	0.4804	276	WB Large T
DRB1_0101	152	VFSNRTLACFAVYTT	TLACFAVYT	0.4803	277	WB Large T
DRB1_0101	257	HDFNPEEPEETKQVS	FNPEEPEET	0.4796	279	WB Large T
DRB1_0101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4796	279	WB Large T
DRB1_0101	255	KEHDFNPEEPEETKQ	FNPEEPEET	0.4792	280	WB Large T
DRB1_0101	396	LHCLLPKMDSVIFDF	LPKMDSVIF	0.4778	284	WB Large T
DRB1_0101	254	LKEHDFNPEEPEETK	FNPEEPEET	0.4775	285	WB Large T
DRB1_0101	150	QAVFSNRTLACFAVY	FSNRTLACF	0.4767	288	WB Large T
DRB1_0101	563	EFLLEKRILQSGMTL	KRILQSGMT	0.4767	288	WB Large T
DRB1_0101	226	KGVNKEYLLYSALTR	EYLLYSALT	0.4763	289	WB Large T
DRB1_0101	548	DFRPKIYLRKSLQNS	FRPKIYLRK	0.4755	291	WB Large T
DRB1_0101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4754	292	WB Large T
DRB1_0101	549	FRPKIYLRKSLQNSE	YLRKSLQNS	0.4751	293	WB Large T
DRB1_0101	171	QILYKKLMEKYSVTF	YKKLMEKYS	0.4745	295	WB Large T
DRB1_0101	253	GLKEHDFNPEEPEET	GLKEHDFNP	0.4744	295	WB Large T
DRB1_0101	196	IIFFLTPHRHRVSAI	LTPHRHRVS	0.4734	298	WB Large T
DRB1_0101	397	HCLLPKMDSVIFDFL	LPKMDSVIF	0.4735	298	WB Large T
DRB1_0101	10	SMELMDLLGLERAAW	MDLLGLERA	0.4730	299	WB Large T
DRB1_0101	578	LLLLIWFRPVADFSK	LIWFRPVAD	0.4729	300	WB Large T
DRB1_0101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4724	302	WB Large T
DRB1_0101	562	SEFLLEKRILQSGMT	LEKRILQSG	0.4722	302	WB Large T
DRB1_0101	579	LLLIWFRPVADFSKD	LIWFRPVAD	0.4723	302	WB Large T
DRB1_0101	551	PKIYLRKSLQNSEFL	YLRKSLQNS	0.4719	303	WB Large T
DRB1_0101	523	FPPGLVTMNEYPVPK	FPPGLVTMN	0.4709	306	WB Large T
DRB1_0101	197	IFFLTPHRHRVSAIN	LTPHRHRVS	0.4697	310	WB Large T
DRB1_0101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4699	310	WB Large T
DRB1_0101	550	RPKIYLRKSLQNSEF	YLRKSLQNS	0.4698	310	WB Large T
DRB1_0101	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4690	313	WB Large T
DRB1_0101	2	DKVLNREESMELMDL	LNREESMEL	0.4683	315	WB Large T
DRB1_0101	577	LLLLLIWFRPVADFS	LIWFRPVAD	0.4684	315	WB Large T
DRB1_0101	153	FSNRTLACFAVYTTK	LACFAVYTT	0.4677	317	WB Large T
DRB1_0101	3	KVLNREESMELMDLL	LNREESMEL	0.4672	319	WB Large T
DRB1_0101	281	ETKCEDVFLLLGMYL	EDVFLLLGM	0.4666	321	WB Large T
DRB1_0101	573	SGMTLLLLLIWFRPV	MTLLLLLIW	0.4649	327	WB Large T
DRB1_0101	493	INNLDSLRDYLDGSV	INNLDSLRD	0.4638	331	WB Large T
DRB1_0101	524	PPGLVTMNEYPVPKT	LVTMNEYPV	0.4635	332	WB Large T
DRB1_0101	525	PGLVTMNEYPVPKTL	MNEYPVPKT	0.4633	333	WB Large T
DRB1_0101	151	AVFSNRTLACFAVYT	FSNRTLACF	0.4625	336	WB Large T
DRB1_0101	492	GINNLDSLRDYLDGS	INNLDSLRD	0.4622	336	WB Large T
DRB1_0101	227	GVNKEYLLYSALTRD	YLLYSALTR	0.4619	338	WB Large T
DRB1_0101	529	TMNEYPVPKTLQARF	YPVPKTLQA	0.4598	345	WB Large T
DRB1_0101	459	LTFELGVAIDQYMVV	LGVAIDQYM	0.4589	349	WB Large T
DRB1_0101	457	ERLTFELGVAIDQYM	LTFELGVAI	0.4584	351	WB Large T
DRB1_0101	398	CLLPKMDSVIFDFLH	LPKMDSVIF	0.4578	353	WB Large T
DRB1_0101	552	KIYLRKSLQNSEFLL	YLRKSLQNS	0.4575	354	WB Large T
DRB1_0101	13	LMDLLGLERAAWGNL	LGLERAAWG	0.4572	355	WB Large T
DRB1_0101	575	MTLLLLLIWFRPVAD	MTLLLLLIW	0.4574	355	WB Large T
DRB1_0101	451	NVNLPMERLTFELGV	NVNLPMERL	0.4555	362	WB Large T

DRB1_0101	193	GHNIIFFLTPHRHRV	IFFLTPHRH	0.4529	372	WB Large T
DRB1_0101	1	MDKVLNREESMELMD	LNREESMEL	0.4521	376	WB Large T
DRB1_0101	432	SGKTTLAAGLLDLCG	KTTLAAGLL	0.4504	382	WB Large T
DRB1_0101	233	LLYSALTRDPYHIIE	LYSALTRDP	0.4500	384	WB Large T
DRB1_0101	377	IFGAHGNAVLEQYMA	IFGAHGNAV	0.4493	387	WB Large T
DRB1_0101	273	KLITEYAVETKCEDV	LITEYAVET	0.4490	388	WB Large T
DRB1_0101	458	RLTFELGVAIDQYMV	LGVAIDQYM	0.4476	394	WB Large T
DRB1_0101	234	LYSALTRDPYHIIEE	LYSALTRDP	0.4472	396	WB Large T
DRB1_0101	422	RYWLFKGPIDSGKTT	WLFKGPIDS	0.4473	396	WB Large T
DRB1_0101	421	RRYWLFKGPIDSGKT	WLFKGPIDS	0.4465	399	WB Large T
DRB1_0101	274	LITEYAVETKCEDVF	LITEYAVET	0.4460	401	WB Large T
DRB1_0101	14	MDLLGLERAAWGNLP	LGLERAAWG	0.4451	405	WB Large T
DRB1_0101	476	DVKGTGAESKDLPSG	VKGTGAESK	0.4428	415	WB Large T
DRB1_0101	477	VKGTGAESKDLPSGH	VKGTGAESK	0.4412	422	WB Large T
DRB1_0101	526	GLVTMNEYPVPKTLQ	MNEYPVPKT	0.4408	424	WB Large T
DRB1_0101	174	YKKLMEKYSVTFISR	LMEKYSVTF	0.4406	425	WB Large T
DRB1_0101	390	MAGVAWLHCLLPKMD	VAWLHCLLP	0.4407	425	WB Large T
DRB1_0101	173	LYKKLMEKYSVTFIS	LMEKYSVTF	0.4405	426	WB Large T
DRB1_0101	5	LNREESMELMDLLGL	LNREESMEL	0.4397	429	WB Large T
DRB1_0101	580	LLIWFRPVADFSKDI	WFRPVADFS	0.4370	442	WB Large T
DRB1_0101	391	AGVAWLHCLLPKMDS	VAWLHCLLP	0.4368	443	WB Large T
DRB1_0101	7	REESMELMDLLGLER	MELMDLLGL	0.4355	449	WB Large T
DRB1_0101	341	QAVDTVLAKKRVDTL	VDTVLAKKR	0.4341	456	WB Large T
DRB1_0101	431	DSGKTTLAAGLLDLC	KTTLAAGLL	0.4339	457	WB Large T
DRB1_0101	155	NRTLACFAVYTTKEK	LACFAVYTT	0.4312	471	WB Large T
DRB1_0101	192	AGHNIIFFLTPHRHR	IFFLTPHRH	0.4310	472	WB Large T
DRB1_0101	538	TLQARFVRQIDFRPK	LQARFVRQI	0.4309	472	WB Large T
DRB1_0101	266	ETKQVSWKLITEYAV	VSWKLITEY	0.4307	473	WB Large T
DRB1_0101	267	TKQVSWKLITEYAVE	WKLITEYAV	0.4303	475	WB Large T
DRB1_0101	539	LQARFVRQIDFRPKI	LQARFVRQI	0.4290	482	WB Large T
DRB1_0101	225	CKGVNKEYLLYSALT	VNKEYLLYS	0.4288	483	WB Large T
DRB1_0101	677	KGFQCFKRPKTPPPK	FKRPKTPPP	0.4281	487	WB Large T
DRB1_0101	333	KNQKSICQQAVDTVL	ICQQAVDTV	0.4261	498	WB Large T
DRB1_0101	72	PDFGTWNSSEVPTYG	FGTWNSSEV	0.4258	499	WB Large T
DRB1_0401	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5015	220	WB Large T
DRB1_0401	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4994	225	WB Large T
DRB1_0401	46	GGDEDKMKRMNTLYK	KMKRMNTLY	0.4992	226	WB Large T
DRB1_0401	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4991	226	WB Large T
DRB1_0401	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4948	237	WB Large T
DRB1_0401	192	AGHNIIFFLTPHRHR	IIFFLTPHR	0.4859	261	WB Large T
DRB1_0401	194	HNIIFFLTPHRHRVS	IIFFLTPHR	0.4856	261	WB Large T
DRB1_0401	193	GHNIIFFLTPHRHRV	IIFFLTPHR	0.4820	272	WB Large T
DRB1_0401	191	CAGHNIIFFLTPHRH	IIFFLTPHR	0.4700	309	WB Large T
DRB1_0401	190	MCAGHNIIFFLTPHR	MCAGHNIIF	0.4533	371	WB Large T
DRB1_0404	194	HNIIFFLTPHRHRVS	IIFFLTPHR	0.5594	118	WB Large T
DRB1_0404	193	GHNIIFFLTPHRHRV	IIFFLTPHR	0.5580	119	WB Large T
DRB1_0404	284	CEDVFLLLGMYLEFQ	FLLLGMYLE	0.5487	132	WB Large T
DRB1_0404	286	DVFLLLGMYLEFQYN	LLGMYLEFQ	0.5479	133	WB Large T
DRB1_0404	285	EDVFLLLGMYLEFQY	LLGMYLEFQ	0.5470	135	WB Large T
DRB1_0404	288	FLLLGMYLEFQYNVE	LLGMYLEFQ	0.5425	141	WB Large T
DRB1_0404	287	VFLLLGMYLEFQYNV	LLGMYLEFQ	0.5417	142	WB Large T
DRB1_0404	192	AGHNIIFFLTPHRHR	IIFFLTPHR	0.5303	161	WB Large T
DRB1_0404	191	CAGHNIIFFLTPHRH	IIFFLTPHR	0.5272	167	WB Large T
DRB1_0404	575	MTLLLLLIWFRPVAD	LLLLIWFRP	0.5188	182	WB Large T
DRB1_0404	389	YMAGVAWLHCLLPKM	VAWLHCLLP	0.5113	198	WB Large T
DRB1_0404	387	EQYMAGVAWLHCLLP	YMAGVAWLH	0.5087	203	WB Large T
DRB1_0404	576	TLLLLLIWFRPVADF	LLLLIWFRP	0.5091	203	WB Large T
DRB1_0404	190	MCAGHNIIFFLTPHR	HNIIFFLTP	0.5052	211	WB Large T
DRB1_0404	390	MAGVAWLHCLLPKMD	VAWLHCLLP	0.5054	211	WB Large T
DRB1_0404	175	KKLMEKYSVTFISRH	LMEKYSVTF	0.5033	216	WB Large T

DRB1_0404	391	AGVAWLHCLLPKMDS	VAWLHCLLP	0.5004	223	WB Large T
DRB1_0404	577	LLLLLIWFRPVADFS	LLIWFRPVA	0.5001	223	WB Large T
DRB1_0404	388	QYMAGVAWLHCLLPK	VAWLHCLLP	0.4995	225	WB Large T
DRB1_0404	195	NIIFFLTPHRHRVSA	IIFFLTPHR	0.4985	227	WB Large T
DRB1_0404	179	EKYSVTFISRHMCAG	YSVTFISRH	0.4981	228	WB Large T
DRB1_0404	177	LMEKYSVTFISRHMC	YSVTFISRH	0.4969	231	WB Large T
DRB1_0404	176	KLMEKYSVTFISRHM	YSVTFISRH	0.4952	236	WB Large T
DRB1_0404	178	MEKYSVTFISRHMCA	YSVTFISRH	0.4940	239	WB Large T
DRB1_0404	578	LLLLIWFRPVADFSK	LLIWFRPVA	0.4909	247	WB Large T
DRB1_0404	196	IIFFLTPHRHRVSAI	IIFFLTPHR	0.4866	258	WB Large T
DRB1_0404	574	GMTLLLLLIWFRPVA	LLLLIWFRP	0.4835	267	WB Large T
DRB1_0404	371	LDKMDLIFGAHGNAV	MDLIFGAHG	0.4592	348	WB Large T
DRB1_0404	290	LLGMYLEFQYNVEEC	LLGMYLEFQ	0.4448	406	WB Large T
DRB1_0404	289	LLLGMYLEFQYNVEE	LLGMYLEFQ	0.4447	407	WB Large T
DRB1_0404	372	DKMDLIFGAHGNAVL	IFGAHGNAV	0.4437	411	WB Large T
DRB1_0405	575	MTLLLLLIWFRPVAD	LLIWFRPVA	0.7757	11	SB Large T
DRB1_0405	576	TLLLLLIWFRPVADF	LIWFRPVAD	0.7721	12	SB Large T
DRB1_0405	577	LLLLLIWFRPVADFS	LIWFRPVAD	0.7733	12	SB Large T
DRB1_0405	578	LLLLIWFRPVADFSK	LIWFRPVAD	0.7738	12	SB Large T
DRB1_0405	579	LLLIWFRPVADFSKD	LIWFRPVAD	0.7712	12	SB Large T
DRB1_0405	85	YGTEEWESWWSSFNE	WESWWSSFN	0.7453	16	SB Large T
DRB1_0405	87	TEEWESWWSSFNEKW	WESWWSSFN	0.7451	16	SB Large T
DRB1_0405	86	GTEEWESWWSSFNEK	WESWWSSFN	0.7381	17	SB Large T
DRB1_0405	88	EEWESWWSSFNEKWD	WESWWSSFN	0.7402	17	SB Large T
DRB1_0405	84	TYGTEEWESWWSSFN	TEEWESWWS	0.7216	20	SB Large T
DRB1_0405	580	LLIWFRPVADFSKDI	LIWFRPVAD	0.6804	32	SB Large T
DRB1_0405	581	LIWFRPVADFSKDIQ	LIWFRPVAD	0.6771	33	SB Large T
DRB1_0405	89	EWESWWSSFNEKWDE	WESWWSSFN	0.6771	33	SB Large T
DRB1_0405	90	WESWWSSFNEKWDED	WESWWSSFN	0.6504	44	SB Large T
DRB1_0405	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.5687	106	WB Large T
DRB1_0405	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.5662	109	WB Large T
DRB1_0405	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5447	138	WB Large T
DRB1_0405	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.5432	140	WB Large T
DRB1_0405	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5413	143	WB Large T
DRB1_0405	490	GHGINNLDSLRDYLD	INNLDSLRD	0.5182	184	WB Large T
DRB1_0405	491	HGINNLDSLRDYLDG	INNLDSLRD	0.5113	198	WB Large T
DRB1_0405	18	GLERAAWGNLPLMRK	RAAWGNLPL	0.5095	202	WB Large T
DRB1_0405	487	LPSGHGINNLDSLRD	GHGINNLDS	0.4979	229	WB Large T
DRB1_0405	19	LERAAWGNLPLMRKA	RAAWGNLPL	0.4956	235	WB Large T
DRB1_0405	488	PSGHGINNLDSLRDY	INNLDSLRD	0.4948	237	WB Large T
DRB1_0405	489	SGHGINNLDSLRDYL	INNLDSLRD	0.4858	261	WB Large T
DRB1_0405	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4857	261	WB Large T
DRB1_0405	52	MKRMNTLYKKMEQDV	MKRMNTLYK	0.4857	261	WB Large T
DRB1_0405	391	AGVAWLHCLLPKMDS	VAWLHCLLP	0.4831	269	WB Large T
DRB1_0405	91	ESWWSSFNEKWDEDL	WSSFNEKWD	0.4812	274	WB Large T
DRB1_0405	390	MAGVAWLHCLLPKMD	VAWLHCLLP	0.4697	310	WB Large T
DRB1_0405	387	EQYMAGVAWLHCLLP	YMAGVAWLH	0.4648	327	WB Large T
DRB1_0405	68	VAHQPDFGTWNSSEV	QPDFGTWNS	0.4624	336	WB Large T
DRB1_0405	418	VPKRRYWLFKGPIDS	YWLFKGPID	0.4620	337	WB Large T
DRB1_0405	388	QYMAGVAWLHCLLPK	VAWLHCLLP	0.4614	339	WB Large T
DRB1_0405	420	KRRYWLFKGPIDSGK	YWLFKGPID	0.4599	345	WB Large T
DRB1_0405	419	PKRRYWLFKGPIDSG	YWLFKGPID	0.4586	350	WB Large T
DRB1_0405	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.4570	356	WB Large T
DRB1_0405	69	AHQPDFGTWNSSEVP	FGTWNSSEV	0.4571	356	WB Large T
DRB1_0405	389	YMAGVAWLHCLLPKM	VAWLHCLLP	0.4547	365	WB Large T
DRB1_0405	421	RRYWLFKGPIDSGKT	YWLFKGPID	0.4540	368	WB Large T
DRB1_0405	417	NVPKRRYWLFKGPID	RYWLFKGPI	0.4530	372	WB Large T
DRB1_0405	17	LGLERAAWGNLPLMR	RAAWGNLPL	0.4515	378	WB Large T
DRB1_0405	16	LLGLERAAWGNLPLM	RAAWGNLPL	0.4465	399	WB Large T
DRB1_0405	493	INNLDSLRDYLDGSV	INNLDSLRD	0.4409	424	WB Large T
DRB1_0405	492	GINNLDSLRDYLDGS	INNLDSLRD	0.4405	426	WB Large T

DRB1_0405	15	DLLGLERAAWGNLPL	ERAAWGNLP	0.4401	427	WB Large T
DRB1_0405	70	HQPDFGTWNSSEVPT	FGTWNSSEV	0.4392	432	WB Large T
DRB1_0405	653	CSSQVSDTSAPDSEN	QVSDTSAPD	0.4296	479	WB Large T
DRB1_0405	654	SSQVSDTSAPDSENP	QVSDTSAPD	0.4282	486	WB Large T
DRB1_0701	412	HCVVFNVPKRRYWLF	VFNVPKRRY	0.5438	139	WB Large T
DRB1_0701	413	CVVFNVPKRRYWLFK	VPKRRYWLF	0.5406	144	WB Large T
DRB1_0701	414	VVFNVPKRRYWLFKG	VPKRRYWLF	0.5149	190	WB Large T
DRB1_0701	415	VFNVPKRRYWLFKGP	VPKRRYWLF	0.5009	221	WB Large T
DRB1_0701	71	QPDFGTWNSSEVPTY	FGTWNSSEV	0.4820	272	WB Large T
DRB1_0701	72	PDFGTWNSSEVPTYG	FGTWNSSEV	0.4789	281	WB Large T
DRB1_0701	68	VAHQPDFGTWNSSEV	DFGTWNSSE	0.4709	306	WB Large T
DRB1_0701	69	AHQPDFGTWNSSEVP	FGTWNSSEV	0.4658	324	WB Large T
DRB1_0701	70	HQPDFGTWNSSEVPT	FGTWNSSEV	0.4657	324	WB Large T
DRB1_0701	416	FNVPKRRYWLFKGPI	VPKRRYWLF	0.4627	335	WB Large T
DRB1_0701	194	HNIIFFLTPHRHRVS	IFFLTPHRH	0.4550	364	WB Large T
DRB1_0701	195	NIIFFLTPHRHRVSA	IFFLTPHRH	0.4521	375	WB Large T
DRB1_0701	193	GHNIIFFLTPHRHRV	IFFLTPHRH	0.4386	434	WB Large T
DRB1_0701	176	KLMEKYSVTFISRHM	YSVTFISRH	0.4346	454	WB Large T
DRB1_0701	196	IIFFLTPHRHRVSAI	IFFLTPHRH	0.4331	461	WB Large T
DRB1_0701	177	LMEKYSVTFISRHMC	YSVTFISRH	0.4315	469	WB Large T
DRB1_0701	387	EQYMAGVAWLHCLLP	YMAGVAWLH	0.4303	475	WB Large T
DRB1_0701	386	LEQYMAGVAWLHCLL	YMAGVAWLH	0.4292	481	WB Large T
DRB1_0701	192	AGHNIIFFLTPHRHR	IFFLTPHRH	0.4288	483	WB Large T
DRB1_0701	197	IFFLTPHRHRVSAIN	IFFLTPHRH	0.4289	483	WB Large T
DRB1_0901	229	NKEYLLYSALTRDPY	YLLYSALTR	0.4376	439	WB Large T
DRB1_0901	230	KEYLLYSALTRDPYH	YLLYSALTR	0.4372	441	WB Large T
DRB1_0901	72	PDFGTWNSSEVPTYG	WNSSEVPTY	0.4364	445	WB Large T
DRB1_0901	71	QPDFGTWNSSEVPTY	FGTWNSSEV	0.4355	449	WB Large T
DRB1_0901	228	VNKEYLLYSALTRDP	YLLYSALTR	0.4325	464	WB Large T
DRB1_0901	384	AVLEQYMAGVAWLHC	LEQYMAGVA	0.4270	493	WB Large T
DRB1_0901	383	NAVLEQYMAGVAWLH	LEQYMAGVA	0.4259	499	WB Large T
DRB1_1101	232	YLLYSALTRDPYHII	YSALTRDPY	0.4594	347	WB Large T
DRB1_1101	233	LLYSALTRDPYHIIE	YSALTRDPY	0.4586	350	WB Large T
DRB1_1101	231	EYLLYSALTRDPYHI	YSALTRDPY	0.4552	363	WB Large T
DRB1_1101	229	NKEYLLYSALTRDPY	YLLYSALTR	0.4548	364	WB Large T
DRB1_1101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4550	364	WB Large T
DRB1_1101	230	KEYLLYSALTRDPYH	YSALTRDPY	0.4537	369	WB Large T
DRB1_1101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4498	385	WB Large T
DRB1_1101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4495	386	WB Large T
DRB1_1101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4483	391	WB Large T
DRB1_1101	46	GGDEDKMKRMNTLYK	EDKMKRMNT	0.4433	413	WB Large T
DRB1_1101	18	GLERAAWGNLPLMRK	AWGNLPLMR	0.4312	471	WB Large T
DRB1_1101	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.4311	471	WB Large T
DRB1_1101	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.4288	483	WB Large T
DRB1_1101	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.4279	488	WB Large T
DRB1_1302	18	GLERAAWGNLPLMRK	LERAAWGNL	0.5752	99	WB Large T
DRB1_1302	21	RAAWGNLPLMRKAYL	WGNLPLMRK	0.5714	103	WB Large T
DRB1_1302	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.5704	104	WB Large T
DRB1_1302	19	LERAAWGNLPLMRKA	WGNLPLMRK	0.5702	105	WB Large T
DRB1_1302	20	ERAAWGNLPLMRKAY	WGNLPLMRK	0.5531	126	WB Large T
DRB1_1302	285	EDVFLLLGMYLEFQY	FLLLGMYLE	0.5498	130	WB Large T
DRB1_1302	445	CGGKALNVNLPMERL	LNVNLPMER	0.5476	134	WB Large T
DRB1_1302	446	GGKALNVNLPMERLT	LNVNLPMER	0.5454	137	WB Large T
DRB1_1302	566	LEKRILQSGMTLLLL	ILQSGMTLL	0.5431	140	WB Large T
DRB1_1302	444	LCGGKALNVNLPMER	GKALNVNLP	0.5427	141	WB Large T
DRB1_1302	565	LLEKRILQSGMTLLL	ILQSGMTLL	0.5420	142	WB Large T
DRB1_1302	447	GKALNVNLPMERLTF	LNVNLPMER	0.5392	146	WB Large T
DRB1_1302	284	CEDVFLLLGMYLEFQ	FLLLGMYLE	0.5383	148	WB Large T

DRB1_1302	283	KCEDVFLLLGMYLEF	FLLLGMYLE	0.5363	151	WB Large T
DRB1_1302	567	EKRILQSGMTLLLLL	ILQSGMTLL	0.5327	157	WB Large T
DRB1_1302	282	TKCEDVFLLLGMYLE	VFLLLGMYL	0.5292	163	WB Large T
DRB1_1302	568	KRILQSGMTLLLLLI	ILQSGMTLL	0.5282	165	WB Large T
DRB1_1302	286	DVFLLLGMYLEFQYN	FLLLGMYLE	0.5258	169	WB Large T
DRB1_1302	409	DFLHCVVFNVPKRRY	VVFNVPKRR	0.5112	198	WB Large T
DRB1_1302	411	LHCVVFNVPKRRYWL	VFNVPKRRY	0.5079	205	WB Large T
DRB1_1302	410	FLHCVVFNVPKRRYW	VFNVPKRRY	0.5074	206	WB Large T
DRB1_1302	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5012	221	WB Large T
DRB1_1302	448	KALNVNLPMERLTFE	LNVNLPMER	0.4996	225	WB Large T
DRB1_1302	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4986	227	WB Large T
DRB1_1302	609	ISMYTFSRMKYNICM	MYTFSRMKY	0.4969	231	WB Large T
DRB1_1302	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4966	232	WB Large T
DRB1_1302	412	HCVVFNVPKRRYWLF	VFNVPKRRY	0.4955	235	WB Large T
DRB1_1302	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4940	239	WB Large T
DRB1_1302	564	FLLEKRILQSGMTLL	KRILQSGMT	0.4938	239	WB Large T
DRB1_1302	608	EISMYTFSRMKYNIC	ISMYTFSRM	0.4935	240	WB Large T
DRB1_1302	24	WGNLPLMRKAYLKKC	WGNLPLMRK	0.4926	242	WB Large T
DRB1_1302	23	AWGNLPLMRKAYLKK	WGNLPLMRK	0.4885	253	WB Large T
DRB1_1302	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4800	278	WB Large T
DRB1_1302	487	LPSGHGINNLDSLRD	HGINNLDSL	0.4764	289	WB Large T
DRB1_1302	489	SGHGINNLDSLRDYL	INNLDSLRD	0.4752	293	WB Large T
DRB1_1302	488	PSGHGINNLDSLRDY	INNLDSLRD	0.4736	298	WB Large T
DRB1_1302	569	RILQSGMTLLLLLIW	LQSGMTLLL	0.4720	303	WB Large T
DRB1_1302	287	VFLLLGMYLEFQYNV	FLLLGMYLE	0.4711	306	WB Large T
DRB1_1302	413	CVVFNVPKRRYWLFK	VFNVPKRRY	0.4581	352	WB Large T
DRB1_1302	522	IFPPGLVTMNEYPVP	PGLVTMNEY	0.4560	360	WB Large T
DRB1_1302	490	GHGINNLDSLRDYLD	INNLDSLRD	0.4532	371	WB Large T
DRB1_1302	523	FPPGLVTMNEYPVPK	PGLVTMNEY	0.4489	389	WB Large T
DRB1_1302	232	YLLYSALTRDPYHII	YSALTRDPY	0.4367	444	WB Large T
DRB1_1302	491	HGINNLDSLRDYLDG	INNLDSLRD	0.4358	448	WB Large T
DRB1_1302	570	ILQSGMTLLLLLIWF	ILQSGMTLL	0.4330	462	WB Large T
DRB1_1302	449	ALNVNLPMERLTFEL	LNVNLPMER	0.4326	463	WB Large T
DRB1_1302	607	SEISMYTFSRMKYNI	ISMYTFSRM	0.4327	463	WB Large T
DRB1_1302	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4272	492	WB Large T
DRB1_1501	192	AGHNIIFFLTPHRHR	IIFFLTPHR	0.6526	43	SB Large T
DRB1_1501	193	GHNIIFFLTPHRHRV	IIFFLTPHR	0.6507	44	SB Large T
DRB1_1501	575	MTLLLLLIWFRPVAD	LLLLLIWFR	0.6509	44	SB Large T
DRB1_1501	574	GMTLLLLLIWFRPVA	LLLLLIWFR	0.6462	46	SB Large T
DRB1_1501	191	CAGHNIIFFLTPHRH	IIFFLTPHR	0.6427	48	SB Large T
DRB1_1501	194	HNIIFFLTPHRHRVS	IIFFLTPHR	0.6416	48	SB Large T
DRB1_1501	576	TLLLLLIWFRPVADF	LLLLLIWFR	0.6127	66	WB Large T
DRB1_1501	577	LLLLLIWFRPVADFS	LLIWFRPVA	0.5958	79	WB Large T
DRB1_1501	190	MCAGHNIIFFLTPHR	NIIFFLTPH	0.5914	83	WB Large T
DRB1_1501	573	SGMTLLLLLIWFRPV	LLLLLIWFR	0.5875	87	WB Large T
DRB1_1501	195	NIIFFLTPHRHRVSA	IIFFLTPHR	0.5848	89	WB Large T
DRB1_1501	572	QSGMTLLLLLIWFRP	LLLLLIWFR	0.5640	112	WB Large T
DRB1_1501	196	IIFFLTPHRHRVSAI	IIFFLTPHR	0.5515	128	WB Large T
DRB1_1501	578	LLLLIWFRPVADFSK	LLIWFRPVA	0.5410	144	WB Large T
DRB1_1501	571	LQSGMTLLLLLIWFR	TLLLLLIWF	0.5272	167	WB Large T
DRB1_1501	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.5229	174	WB Large T
DRB1_1501	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.5190	182	WB Large T
DRB1_1501	24	WGNLPLMRKAYLKKC	LMRKAYLKK	0.5176	185	WB Large T
DRB1_1501	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.5153	190	WB Large T
DRB1_1501	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.5147	191	WB Large T
DRB1_1501	23	AWGNLPLMRKAYLKK	LPLMRKAYL	0.5076	206	WB Large T
DRB1_1501	25	GNLPLMRKAYLKKCK	LMRKAYLKK	0.5063	209	WB Large T
DRB1_1501	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.5026	217	WB Large T
DRB1_1501	26	NLPLMRKAYLKKCKE	LMRKAYLKK	0.4961	233	WB Large T
DRB1_1501	548	DFRPKIYLRKSLQNS	DFRPKIYLR	0.4942	238	WB Large T
DRB1_1501	227	GVNKEYLLYSALTRD	YLLYSALTR	0.4878	255	WB Large T

DRB1_1501	228	VNKEYLLYSALTRDP	YLLYSALTR	0.4864	259	WB Large T
DRB1_1501	229	NKEYLLYSALTRDPY	YLLYSALTR	0.4863	259	WB Large T
DRB1_1501	230	KEYLLYSALTRDPYH	YLLYSALTR	0.4859	260	WB Large T
DRB1_1501	27	LPLMRKAYLKKCKEF	LMRKAYLKK	0.4850	263	WB Large T
DRB1_1501	409	DFLHCVVFNVPKRRY	CVVFNVPKR	0.4823	271	WB Large T
DRB1_1501	410	FLHCVVFNVPKRRYW	CVVFNVPKR	0.4819	272	WB Large T
DRB1_1501	226	KGVNKEYLLYSALTR	VNKEYLLYS	0.4792	280	WB Large T
DRB1_1501	411	LHCVVFNVPKRRYWL	CVVFNVPKR	0.4791	280	WB Large T
DRB1_1501	543	FVRQIDFRPKIYLRK	DFRPKIYLR	0.4749	293	WB Large T
DRB1_1501	544	VRQIDFRPKIYLRKS	DFRPKIYLR	0.4739	297	WB Large T
DRB1_1501	542	RFVRQIDFRPKIYLR	VRQIDFRPK	0.4731	299	WB Large T
DRB1_1501	408	FDFLHCVVFNVPKRR	CVVFNVPKR	0.4728	300	WB Large T
DRB1_1501	579	LLLIWFRPVADFSKD	LLIWFRPVA	0.4695	311	WB Large T
DRB1_1501	13	LMDLLGLERAAWGNL	LMDLLGLER	0.4683	315	WB Large T
DRB1_1501	549	FRPKIYLRKSLQNSE	YLRKSLQNS	0.4683	315	WB Large T
DRB1_1501	11	MELMDLLGLERAAWG	LMDLLGLER	0.4651	326	WB Large T
DRB1_1501	142	SDLHQFLSQAVFSNR	LHQFLSQAV	0.4611	341	WB Large T
DRB1_1501	413	CVVFNVPKRRYWLFK	CVVFNVPKR	0.4554	362	WB Large T
DRB1_1501	169	KAQILYKKLMEKYSV	ILYKKLMEK	0.4523	375	WB Large T
DRB1_1501	170	AQILYKKLMEKYSVT	ILYKKLMEK	0.4511	379	WB Large T
DRB1_1501	546	QIDFRPKIYLRKSLQ	DFRPKIYLR	0.4502	383	WB Large T
DRB1_1501	419	PKRRYWLFKGPIDSG	WLFKGPIDS	0.4498	385	WB Large T
DRB1_1501	418	VPKRRYWLFKGPIDS	KRRYWLFKG	0.4458	402	WB Large T
DRB1_1501	547	IDFRPKIYLRKSLQN	FRPKIYLRK	0.4373	440	WB Large T
DRB1_1501	420	KRRYWLFKGPIDSGK	WLFKGPIDS	0.4350	452	WB Large T
DRB1_1501	414	VVFNVPKRRYWLFKG	PKRRYWLFK	0.4334	460	WB Large T
DRB1_1501	28	PLMRKAYLKKCKEFH	LMRKAYLKK	0.4332	461	WB Large T
DRB1_1501	51	KMKRMNTLYKKMEQD	MKRMNTLYK	0.4331	461	WB Large T
DRB1_1501	172	ILYKKLMEKYSVTFI	ILYKKLMEK	0.4319	467	WB Large T
DRB1_1501	550	RPKIYLRKSLQNSEF	YLRKSLQNS	0.4316	469	WB Large T
DRB1_1501	545	RQIDFRPKIYLRKSL	DFRPKIYLR	0.4312	471	WB Large T
DRB1_1501	580	LLIWFRPVADFSKDI	LLIWFRPVA	0.4297	479	WB Large T
DRB1_1501	412	HCVVFNVPKRRYWLF	CVVFNVPKR	0.4294	480	WB Large T
DRB1_1501	10	SMELMDLLGLERAAW	LMDLLGLER	0.4261	497	WB Large T
DRB4_0101	609	ISMYTFSRMKYNICM	FSRMKYNIC	0.5682	107	WB Large T
DRB4_0101	611	MYTFSRMKYNICMGK	FSRMKYNIC	0.5289	163	WB Large T
DRB4_0101	608	EISMYTFSRMKYNIC	ISMYTFSRM	0.5272	167	WB Large T
DRB4_0101	612	YTFSRMKYNICMGKC	FSRMKYNIC	0.5271	167	WB Large T
DRB4_0101	610	SMYTFSRMKYNICMG	FSRMKYNIC	0.5243	172	WB Large T
DRB4_0101	576	TLLLLLIWFRPVADF	LIWFRPVAD	0.4721	302	WB Large T
DRB4_0101	194	HNIIFFLTPHRHRVS	IFFLTPHRH	0.4700	309	WB Large T
DRB4_0101	193	GHNIIFFLTPHRHRV	IFFLTPHRH	0.4668	320	WB Large T
DRB4_0101	192	AGHNIIFFLTPHRHR	IFFLTPHRH	0.4660	323	WB Large T
DRB4_0101	195	NIIFFLTPHRHRVSA	IFFLTPHRH	0.4640	330	WB Large T
DRB4_0101	541	ARFVRQIDFRPKIYL	VRQIDFRPK	0.4637	331	WB Large T
DRB4_0101	577	LLLLLIWFRPVADFS	LIWFRPVAD	0.4628	334	WB Large T
DRB4_0101	191	CAGHNIIFFLTPHRH	IIFFLTPHR	0.4583	351	WB Large T
DRB4_0101	613	TFSRMKYNICMGKCI	FSRMKYNIC	0.4575	354	WB Large T
DRB4_0101	542	RFVRQIDFRPKIYLR	VRQIDFRPK	0.4556	362	WB Large T
DRB4_0101	578	LLLLIWFRPVADFSK	LIWFRPVAD	0.4526	373	WB Large T
DRB4_0101	614	FSRMKYNICMGKCIL	FSRMKYNIC	0.4368	443	WB Large T
DRB4_0101	579	LLLIWFRPVADFSKD	LIWFRPVAD	0.4362	446	WB Large T
DRB4_0101	539	LQARFVRQIDFRPKI	VRQIDFRPK	0.4355	449	WB Large T
DRB4_0101	575	MTLLLLLIWFRPVAD	LLLIWFRPV	0.4344	455	WB Large T
DRB4_0101	538	TLQARFVRQIDFRPK	FVRQIDFRP	0.4341	456	WB Large T
DRB4_0101	540	QARFVRQIDFRPKIY	VRQIDFRPK	0.4260	498	WB Large T
DRB5_0101	543	FVRQIDFRPKIYLRK	RQIDFRPKI	0.6349	52	WB Large T
DRB5_0101	544	VRQIDFRPKIYLRKS	FRPKIYLRK	0.6346	52	WB Large T
DRB5_0101	545	RQIDFRPKIYLRKSL	FRPKIYLRK	0.6343	52	WB Large T
DRB5_0101	546	QIDFRPKIYLRKSLQ	FRPKIYLRK	0.6326	53	WB Large T

DRB5_0101	547	IDFRPKIYLRKSLQN	FRPKIYLRK	0.6322	53	WB Large T
DRB5_0101	411	LHCVVFNVPKRRYWL	VVFNVPKRR	0.5655	110	WB Large T
DRB5_0101	412	HCVVFNVPKRRYWLF	VVFNVPKRR	0.5631	113	WB Large T
DRB5_0101	410	FLHCVVFNVPKRRYW	VVFNVPKRR	0.5614	115	WB Large T
DRB5_0101	409	DFLHCVVFNVPKRRY	VVFNVPKRR	0.5437	139	WB Large T
DRB5_0101	548	DFRPKIYLRKSLQNS	FRPKIYLRK	0.5361	151	WB Large T
DRB5_0101	549	FRPKIYLRKSLQNSE	FRPKIYLRK	0.5359	152	WB Large T
DRB5_0101	255	KEHDFNPEEPEETKQ	FNPEEPEET	0.5183	183	WB Large T
DRB5_0101	254	LKEHDFNPEEPEETK	FNPEEPEET	0.5181	184	WB Large T
DRB5_0101	256	EHDFNPEEPEETKQV	FNPEEPEET	0.5168	186	WB Large T
DRB5_0101	253	GLKEHDFNPEEPEET	GLKEHDFNP	0.5161	188	WB Large T
DRB5_0101	257	HDFNPEEPEETKQVS	FNPEEPEET	0.5162	188	WB Large T
DRB5_0101	408	FDFLHCVVFNVPKRR	CVVFNVPKR	0.5052	211	WB Large T
DRB5_0101	413	CVVFNVPKRRYWLFK	VVFNVPKRR	0.5006	222	WB Large T
DRB5_0101	84	TYGTEEWESWWSSFN	TEEWESWWS	0.4988	227	WB Large T
DRB5_0101	85	YGTEEWESWWSSFNE	WESWWSSFN	0.4977	229	WB Large T
DRB5_0101	88	EEWESWWSSFNEKWD	WESWWSSFN	0.4975	230	WB Large T
DRB5_0101	87	TEEWESWWSSFNEKW	WESWWSSFN	0.4963	233	WB Large T
DRB5_0101	86	GTEEWESWWSSFNEK	WESWWSSFN	0.4952	235	WB Large T
DRB5_0101	677	KGFQCFKRPKTPPPK	FQCFKRPKT	0.4816	273	WB Large T
DRB5_0101	49	EDKMKRMNTLYKKME	MKRMNTLYK	0.4763	289	WB Large T
DRB5_0101	50	DKMKRMNTLYKKMEQ	MKRMNTLYK	0.4758	290	WB Large T
DRB5_0101	48	DEDKMKRMNTLYKKM	MKRMNTLYK	0.4726	301	WB Large T
DRB5_0101	414	VVFNVPKRRYWLFKG	VVFNVPKRR	0.4695	311	WB Large T
DRB5_0101	47	GDEDKMKRMNTLYKK	MKRMNTLYK	0.4617	338	WB Large T
DRB5_0101	194	HNIIFFLTPHRHRVS	FFLTPHRHR	0.4587	350	WB Large T
DRB5_0101	46	GGDEDKMKRMNTLYK	DKMKRMNTL	0.4567	357	WB Large T
DRB5_0101	193	GHNIIFFLTPHRHRV	FFLTPHRHR	0.4542	367	WB Large T
DRB5_0101	195	NIIFFLTPHRHRVSA	FFLTPHRHR	0.4419	419	WB Large T
DRB5_0101	119	TADSQHSTPPKKKRK	QHSTPPKKK	0.4363	446	WB Large T
DRB5_0101	120	ADSQHSTPPKKKRKV	QHSTPPKKK	0.4331	461	WB Large T
DRB5_0101	259	FNPEEPEETKQVSWK	FNPEEPEET	0.4320	467	WB Large T
DRB5_0101	53	KRMNTLYKKMEQDVK	KRMNTLYKK	0.4284	485	WB Large T
DRB5_0101	22	AAWGNLPLMRKAYLK	WGNLPLMRK	0.4268	494	WB Large T

Preferred BK virus fragments of Agnoprotein capable of interacting with one or more MHC class 2 molecules are listed in Table T.

Table T: Prediction of BK virus Agnoprotein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) using the http://www.cbs.dtu.dk/services/NetMHCII / database. The MHC class 2 molecules for which no binders were found are not listed.

Allele	pos	peptide	core	1-log50k(aff)	affinity(nM)	Bind Level	Identity
DRB1_0101	8	LVVLRQLSRQASVKV	LRQLSRQAS	0.6877	29	SB	Agno
DRB1_0101	9	VVLRQLSRQASVKVG	LSRQASVKV	0.6820	31	SB	Agno
DRB1_0101	10	VLRQLSRQASVKVGK	LSRQASVKV	0.6587	40	SB	Agno
DRB1_0101	11	LRQLSRQASVKVGKT	LSRQASVKV	0.6595	40	SB	Agno
DRB1_0101	5	PKNLVVLRQLSRQAS	VLRQLSRQA	0.6455	46	SB	Agno
DRB1_0101	7	NLVVLRQLSRQASVK	VLRQLSRQA	0.6439	47	SB	Agno
DRB1_0101	6	KNLVVLRQLSRQASV	VLRQLSRQA	0.6410	49	SB	Agno
DRB1_0101	12	RQLSRQASVKVGKTW	LSRQASVKV	0.6369	51	WB	Agno
DRB1_0101	14	LSRQASVKVGKTWTG	LSRQASVKV	0.6206	61	WB	Agno
DRB1_0101	18	ASVKVGKTWTGTKKR	VKVGKTWTG	0.5679	107	WB	Agno
DRB1_0101	17	QASVKVGKTWTGTKK	VKVGKTWTG	0.5669	108	WB	Agno
DRB1_0101	15	SRQASVKVGKTWTGT	VKVGKTWTG	0.5640	112	WB	Agno
DRB1_0101	16	RQASVKVGKTWTGTK	VKVGKTWTG	0.5640	112	WB	Agno
DRB1_0101	4	EPKNLVVLRQLSRQA	PKNLVVLRQ	0.5604	116	WB	Agno
DRB1_0101	13	QLSRQASVKVGKTWT	LSRQASVKV	0.5447	138	WB	Agno
DRB1_0101	19	SVKVGKTWTGTKKRA	VKVGKTWTG	0.4852	263	WB	Agno
DRB1_0101	20	VKVGKTWTGTKKRAQ	VKVGKTWTG	0.4749	293	WB	Agno
DRB1_0401	8	LVVLRQLSRQASVKV	VLRQLSRQA	0.4745	295	WB	Agno
DRB1_0401	10	VLRQLSRQASVKVGK	LSRQASVKV	0.4500	384	WB	Agno
DRB1_0401	9	VVLRQLSRQASVKVG	LSRQASVKV	0.4476	394	WB	Agno
DRB1_0401	11	LRQLSRQASVKVGKT	LSRQASVKV	0.4393	431	WB	Agno
DRB1_0401	12	RQLSRQASVKVGKTW	LSRQASVKV	0.4380	437	WB	Agno
DRB1_0405	55	DGKNKSTTALPAVKD	NKSTTALPA	0.4704	308	WB	Agno
DRB1_0405	56	GKNKSTTALPAVKDS	TTALPAVKD	0.4657	324	WB	Agno
DRB1_0405	57	KNKSTTALPAVKDSV	TTALPAVKD	0.4367	443	WB	Agno
DRB1_0405	58	NKSTTALPAVKDSVK	TTALPAVKD	0.4330	462	WB	Agno
DRB1_1101	8	LVVLRQLSRQASVKV	LRQLSRQAS	0.4614	340	WB	Agno
DRB1_1101	5	PKNLVVLRQLSRQAS	PKNLVVLRQ	0.4605	343	WB	Agno
DRB1_1101	6	KNLVVLRQLSRQASV	LRQLSRQAS	0.4594	347	WB	Agno
DRB1_1101	9	VVLRQLSRQASVKVG	LRQLSRQAS	0.4595	347	WB	Agno
DRB1_1101	7	NLVVLRQLSRQASVK	LRQLSRQAS	0.4579	352	WB	Agno
DRB1_1302	5	PKNLVVLRQLSRQAS	VVLRQLSRQ	0.5120	196	WB	Agno
DRB1_1302	8	LVVLRQLSRQASVKV	LRQLSRQAS	0.5035	215	WB	Agno
DRB1_1302	6	KNLVVLRQLSRQASV	LRQLSRQAS	0.5031	216	WB	Agno
DRB1_1302	9	VVLRQLSRQASVKVG	LRQLSRQAS	0.4904	248	WB	Agno
DRB1_1302	7	NLVVLRQLSRQASVK	LRQLSRQAS	0.4893	251	WB	Agno
DRB1_1302	3	CEPKNLVVLRQLSRQ	LVVLRQLSR	0.4329	462	WB	Agno
DRB1_1501	5	PKNLVVLRQLSRQAS	LVVLRQLSR	0.6754	34	SB	Agno
DRB1_1501	6	KNLVVLRQLSRQASV	LVVLRQLSR	0.6742	34	SB	Agno
DRB1_1501	4	EPKNLVVLRQLSRQA	LVVLRQLSR	0.6596	40	SB	Agno
DRB1_1501	3	CEPKNLVVLRQLSRQ	LVVLRQLSR	0.6209	60	WB	Agno
DRB1_1501	7	NLVVLRQLSRQASVK	LVVLRQLSR	0.6093	69	WB	Agno
DRB1_1501	8	LVVLRQLSRQASVKV	LVVLRQLSR	0.6010	75	WB	Agno
DRB1_1501	2	FCEPKNLVVLRQLSR	NLVVLRQLS	0.5977	78	WB	Agno
DRB1_1501	9	VVLRQLSRQASVKVG	LRQLSRQAS	0.4406	425	WB	Agno
DRB4_0101	35	RIFIFILELLLEFCR	ILELLLEFC	0.4266	494	WB	Agno

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

Table U: 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 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 V.

Table V: Prediction of Borrelia burgdorferi OspA protein specific MHC class1, 8- , 9- ,10-, 11-mer peptide binders for 42 MHC class 1 alleles (see figure 11) 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 X.

Table X: Prediction of Borrelia garinii FlaB protein specific MHC class 2, 15-mer peptide binders for 14 MHC class 2 alleles (see figure 11) 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

Preferred Mycobacterium tuberculosis fragments of CFP10 protein (Rv3874) capable of interacting with one or more class 1 and/or one or more class 2 MHC molecules are listed in Table Y.

Table Y: Prediction of MHC class 1 and 2 Mycobacterium tuberculosis CFP10 peptide binders. Prediction of 8-, 9-, 10-, 11-, 13-, 14-, 15-, 16-mer peptides were using the program displayed in figure 2

8 mers: MAEMKTDA; AEMKTDAA; EMKTDAAT; MKTDAATL; KTDAATLA; TDAATLAQ; DAATLAQE; AATLAQEA; ATLAQEAG; TLAQEAGN; LAQEAGNF; AQEAGNFE; QEAGNFER; EAGNFERI; AGNFERIS; GNFERISG; NFERISGD; FERISGDL; ERISGDLK; RISGDLKT; ISGDLKTQ; SGDLKTQI; GDLKTQID; DLKTQIDQ; LKTQIDQV; KTQIDQVE; TQIDQVES; QIDQVEST; IDQVESTA; DQVESTAG; QVESTAGS; VESTAGSL; ESTAGSLQ; STAGSLQG; TAGSLQGQ; AGSLQGQW; GSLQGQWR; SLQGQWRG; LQGQWRGA; QGQWRGAA; GQWRGAAG; QWRGAAGT; WRGAAGTA; RGAAGTAA; GAAGTAAQ; AAGTAAQA; AGTAAQAA; GTAAQAAV; TAAQAAVV; AAQAAVVR; AQAAVVRF; QAAVVRFQ; AAVVRFQE; AVVRFQEA; VVRFQEAA; VRFQEAAN; RFQEAANK; FQEAANKQ; QEAANKQK; EAANKQKQ; AANKQKQE; ANKQKQEL; NKQKQELD; KQKQELDE; QKQELDEI; KQELDEIS; QELDEIST; ELDEISTN; LDEISTNI; DEISTNIR; EISTNIRQ; ISTNIRQA; STNIRQAG; TNIRQAGV; NIRQAGVQ; IRQAGVQY; RQAGVQYS; QAGVQYSR; AGVQYSRA; GVQYSRAD; VQYSRADE; QYSRADEE; YSRADEEQ; SRADEEQQ; RADEEQQQ; ADEEQQQA; DEEQQQAL; EEQQQALS; EQQQALSS; QQQALSSQ; QQALSSQM; QALSSQMG; ALSSQMGF
9 mers: MAEMKTDAA; AEMKTDAAT; EMKTDAATL; MKTDAATLA; KTDAATLAQ; TDAATLAQE; DAATLAQEA; AATLAQEAG; ATLAQEAGN; TLAQEAGNF; LAQEAGNFE; AQEAGNFER; QEAGNFERI; EAGNFERIS; AGNFERISG; GNFERISGD; NFERISGDL; FERISGDLK; ERISGDLKT; RISGDLKTQ; ISGDLKTQI; SGDLKTQID; GDLKTQIDQ; DLKTQIDQV; LKTQIDQVE; KTQIDQVES; TQIDQVEST; QIDQVESTA; IDQVESTAG; DQVESTAGS; QVESTAGSL; VESTAGSLQ; ESTAGSLQG; STAGSLQGQ; TAGSLQGQW; AGSLQGQWR; GSLQGQWRG; SLQGQWRGA; LQGQWRGAA; QGQWRGAAG; GQWRGAAGT; QWRGAAGTA; WRGAAGTAA; RGAAGTAAQ; GAAGTAAQA; AAGTAAQAA; AGTAAQAAV; GTAAQAAVV; TAAQAAVVR; AAQAAVVRF; AQAAVVRFQ; QAAVVRFQE; AAVVRFQEA; AVVRFQEAA; VVRFQEAAN; VRFQEAANK; RFQEAANKQ; FQEAANKQK; QEAANKQKQ; EAANKQKQE; AANKQKQEL; ANKQKQELD; NKQKQELDE; KQKQELDEI; QKQELDEIS; KQELDEIST; QELDEISTN; ELDEISTNI; LDEISTNIR; DEISTNIRQ; EISTNIRQA; ISTNIRQAG; STNIRQAGV; TNIRQAGVQ; NIRQAGVQY; IRQAGVQYS; RQAGVQYSR; QAGVQYSRA; AGVQYSRAD; GVQYSRADE; VQYSRADEE; QYSRADEEQ; YSRADEEQQ; SRADEEQQQ; RADEEQQQA; ADEEQQQAL; DEEQQQALS; EEQQQALSS; EQQQALSSQ; QQQALSSQM; QQALSSQMG; QALSSQMGF;
10 mers: MAEMKTDAAT; AEMKTDAATL; EMKTDAATLA; MKTDAATLAQ; KTDAATLAQE; TDAATLAQEA; DAATLAQEAG; AATLAQEAGN; ATLAQEAGNF; TLAQEAGNFE; LAQEAGNFER; AQEAGNFERI; QEAGNFERIS; EAGNFERISG; AGNFERISGD; GNFERISGDL; NFERISGDLK; FERISGDLKT; ERISGDLKTQ; RISGDLKTQI; ISGDLKTQID; SGDLKTQIDQ; GDLKTQIDQV; DLKTQIDQVE; LKTQIDQVES; KTQIDQVEST; TQIDQVESTA; QIDQVESTAG; IDQVESTAGS; DQVESTAGSL; QVESTAGSLQ; VESTAGSLQG; ESTAGSLQGQ; STAGSLQGQW; TAGSLQGQWR; AGSLQGQWRG; GSLQGQWRGA; SLQGQWRGAA; LQGQWRGAAG; QGQWRGAAGT; GQWRGAAGTA; QWRGAAGTAA; WRGAAGTAAQ; RGAAGTAAQA; GAAGTAAQAA; AAGTAAQAAV; AGTAAQAAVV; GTAAQAAVVR; TAAQAAVVRF; AAQAAVVRFQ; AQAAVVRFQE; QAAVVRFQEA; AAVVRFQEAA; AVVRFQEAAN; VVRFQEAANK; VRFQEAANKQ; RFQEAANKQK; FQEAANKQKQ; QEAANKQKQE; EAANKQKQEL;

AANKQKQELD; ANKQKQELDE; NKQKQELDEI; KQKQELDEIS; QKQELDEIST;
KQELDEISTN; QELDEISTNI; ELDEISTNIR; LDEISTNIRQ; DEISTNIRQA;
EISTNIRQAG; ISTNIRQAGV; STNIRQAGVQ; TNIRQAGVQY; NIRQAGVQYS;
IRQAGVQYSR; RQAGVQYSRA; QAGVQYSRAD; AGVQYSRADE; GVQYSRADEE;
VQYSRADEEQ; QYSRADEEQQ; YSRADEEQQQ; SRADEEQQQA; RADEEQQQAL;
ADEEQQQALS; DEEQQQALSS; EEQQQALSSQ; EQQQALSSQM; QQQALSSQMG;
QQALSSQMGF;

11 mers:
MAEMKTDAATL; AEMKTDAATLA; EMKTDAATLAQ; MKTDAATLAQE; KTDAATLAQEA;
TDAATLAQEAG; DAATLAQEAGN; AATLAQEAGNF; ATLAQEAGNFE; TLAQEAGNFER;
LAQEAGNFERI; AQEAGNFERIS; QEAGNFERISG; EAGNFERISGD; AGNFERISGDL;
GNFERISGDLK; NFERISGDLKT; FERISGDLKTQ; ERISGDLKTQI; RISGDLKTQID;
ISGDLKTQIDQ; SGDLKTQIDQV; GDLKTQIDQVE; DLKTQIDQVES; LKTQIDQVEST;
KTQIDQVESTA; TQIDQVESTAG; QIDQVESTAGS; IDQVESTAGSL; DQVESTAGSLQ;
QVESTAGSLQG; VESTAGSLQGQ; ESTAGSLQGQW; STAGSLQGQWR; TAGSLQGQWRG;
AGSLQGQWRGA; GSLQGQWRGAA; SLQGQWRGAAG; LQGQWRGAAGT; QGQWRGAAGTA;
GQWRGAAGTAA; QWRGAAGTAAQ; WRGAAGTAAQA; RGAAGTAAQAA; GAAGTAAQAAV;
AAGTAAQAAVV; AGTAAQAAVVR; GTAAQAAVVRF; TAAQAAVVRFQ; AAQAAVVRFQE;
AQAAVVRFQEA; QAAVVRFQEAA; AAVVRFQEAAN; AVVRFQEAANK; VVRFQEAANKQ;
VRFQEAANKQK; RFQEAANKQKQ; FQEAANKQKQE; QEAANKQKQEL; EAANKQKQELD;
AANKQKQELDE; ANKQKQELDEI; NKQKQELDEIS; KQKQELDEIST; QKQELDEISTN;
KQELDEISTNI; QELDEISTNIR; ELDEISTNIRQ; LDEISTNIRQA; DEISTNIRQAG;
EISTNIRQAGV; ISTNIRQAGVQ; STNIRQAGVQY; TNIRQAGVQYS; NIRQAGVQYSR;
IRQAGVQYSRA; RQAGVQYSRAD; QAGVQYSRADE; AGVQYSRADEE; GVQYSRADEEQ;
VQYSRADEEQQ; QYSRADEEQQQ; YSRADEEQQQA; SRADEEQQQAL; RADEEQQQALS;
ADEEQQQALSS; DEEQQQALSSQ; EEQQQALSSQM; EQQQALSSQMG; QQQALSSQMGF

13 mers:
MAEMKTDAATLAQ; AEMKTDAATLAQE; EMKTDAATLAQEA; MKTDAATLAQEAG;
KTDAATLAQEAGN; TDAATLAQEAGNF; DAATLAQEAGNFE; AATLAQEAGNFER;
ATLAQEAGNFERI; TLAQEAGNFERIS; LAQEAGNFERISG; AQEAGNFERISGD;
QEAGNFERISGDL; EAGNFERISGDLK; AGNFERISGDLKT; GNFERISGDLKTQ;
NFERISGDLKTQI; FERISGDLKTQID; ERISGDLKTQIDQ; RISGDLKTQIDQV;
ISGDLKTQIDQVE; SGDLKTQIDQVES; GDLKTQIDQVEST; DLKTQIDQVESTA;
LKTQIDQVESTAG; KTQIDQVESTAGS; TQIDQVESTAGSL; QIDQVESTAGSLQ;
IDQVESTAGSLQG; DQVESTAGSLQGQ; QVESTAGSLQGQW; VESTAGSLQGQWR;
ESTAGSLQGQWRG; STAGSLQGQWRGA; TAGSLQGQWRGAA; AGSLQGQWRGAAG;
GSLQGQWRGAAGT; SLQGQWRGAAGTA; LQGQWRGAAGTAA; QGQWRGAAGTAAQ;
GQWRGAAGTAAQA; QWRGAAGTAAQAA; WRGAAGTAAQAAV; RGAAGTAAQAAVV;
GAAGTAAQAAVVR; AAGTAAQAAVVRF; AGTAAQAAVVRFQ; GTAAQAAVVRFQE;
TAAQAAVVRFQEA; AAQAAVVRFQEAA; AQAAVVRFQEAAN; QAAVVRFQEAANK;
AAVVRFQEAANKQ; AVVRFQEAANKQK; VVRFQEAANKQKQ; VRFQEAANKQKQE;
RFQEAANKQKQEL; FQEAANKQKQELD; QEAANKQKQELDE; EAANKQKQELDEI;
AANKQKQELDEIS; ANKQKQELDEIST; NKQKQELDEISTN; KQKQELDEISTNI;
QKQELDEISTNIR; KQELDEISTNIRQ; QELDEISTNIRQA; ELDEISTNIRQAG;
LDEISTNIRQAGV; DEISTNIRQAGVQ; EISTNIRQAGVQY; ISTNIRQAGVQYS;
STNIRQAGVQYSR; TNIRQAGVQYSRA; NIRQAGVQYSRAD; IRQAGVQYSRADE;
RQAGVQYSRADEE; QAGVQYSRADEEQ; AGVQYSRADEEQQ; GVQYSRADEEQQQ;
VQYSRADEEQQQA; QYSRADEEQQQAL; YSRADEEQQQALS; SRADEEQQQALSS;
RADEEQQQALSSQ; ADEEQQQALSSQM; DEEQQQALSSQMG; EEQQQALSSQMGF;

14 mers:
MAEMKTDAATLAQE; AEMKTDAATLAQEA; EMKTDAATLAQEAG; MKTDAATLAQEAGN;
KTDAATLAQEAGNF; TDAATLAQEAGNFE; DAATLAQEAGNFER; AATLAQEAGNFERI;
ATLAQEAGNFERIS; TLAQEAGNFERISG; LAQEAGNFERISGD; AQEAGNFERISGDL;
QEAGNFERISGDLK; EAGNFERISGDLKT; AGNFERISGDLKTQ; GNFERISGDLKTQI;
NFERISGDLKTQID; FERISGDLKTQIDQ; ERISGDLKTQIDQV; RISGDLKTQIDQVE;
ISGDLKTQIDQVES; SGDLKTQIDQVEST; GDLKTQIDQVESTA; DLKTQIDQVESTAG;
LKTQIDQVESTAGS; KTQIDQVESTAGSL; TQIDQVESTAGSLQ; QIDQVESTAGSLQG;
IDQVESTAGSLQGQ; DQVESTAGSLQGQW; QVESTAGSLQGQWR; VESTAGSLQGQWRG;
ESTAGSLQGQWRGA; STAGSLQGQWRGAA; TAGSLQGQWRGAAG; AGSLQGQWRGAAGT;

GSLQGQWRGAAGTA; SLQGQWRGAAGTAA; LQGQWRGAAGTAAQ; QGQWRGAAGTAAQA;
GQWRGAAGTAAQAA; QWRGAAGTAAQAAV; WRGAAGTAAQAAVV; RGAAGTAAQAAVVR;
GAAGTAAQAAVVRF; AAGTAAQAAVVRFQ; AGTAAQAAVVRFQE; GTAAQAAVVRFQEA;
TAAQAAVVRFQEAA; AAQAAVVRFQEAAN; AQAAVVRFQEAANK; QAAVVRFQEAANKQ;
AAVVRFQEAANKQK; AVVRFQEAANKQKQ; VVRFQEAANKQKQE; VRFQEAANKQKQEL;
RFQEAANKQKQELD; FQEAANKQKQELDE; QEAANKQKQELDEI; EAANKQKQELDEIS;
AANKQKQELDEIST; ANKQKQELDEISTN; NKQKQELDEISTNI; KQKQELDEISTNIR;
QKQELDEISTNIRQ; KQELDEISTNIRQA; QELDEISTNIRQAG; ELDEISTNIRQAGV;
LDEISTNIRQAGVQ; DEISTNIRQAGVQY; EISTNIRQAGVQYS; ISTNIRQAGVQYSR;
STNIRQAGVQYSRA; TNIRQAGVQYSRAD; NIRQAGVQYSRADE; IRQAGVQYSRADEE;
RQAGVQYSRADEEQ; QAGVQYSRADEEQQ; AGVQYSRADEEQQQ; GVQYSRADEEQQQA;
VQYSRADEEQQQAL; QYSRADEEQQQALS; YSRADEEQQQALSS; SRADEEQQQALSSQ;
RADEEQQQALSSQM; ADEEQQQALSSQMG; DEEQQQALSSQMGF

15 mers:
MAEMKTDAATLAQEA; AEMKTDAATLAQEAG; EMKTDAATLAQEAGN; MKTDAATLAQEAGNF;
KTDAATLAQEAGNFE; TDAATLAQEAGNFER; DAATLAQEAGNFERI; AATLAQEAGNFERIS;
ATLAQEAGNFERISG; TLAQEAGNFERISGD; LAQEAGNFERISGDL; AQEAGNFERISGDLK;
QEAGNFERISGDLKT; EAGNFERISGDLKTQ; AGNFERISGDLKTQI; GNFERISGDLKTQID;
NFERISGDLKTQIDQ; FERISGDLKTQIDQV; ERISGDLKTQIDQVE; RISGDLKTQIDQVES;
ISGDLKTQIDQVEST; SGDLKTQIDQVESTA; GDLKTQIDQVESTAG; DLKTQIDQVESTAGS;
LKTQIDQVESTAGSL; KTQIDQVESTAGSLQ; TQIDQVESTAGSLQG; QIDQVESTAGSLQGQ;
IDQVESTAGSLQGQW; DQVESTAGSLQGQWR; QVESTAGSLQGQWRG; VESTAGSLQGQWRGA;
ESTAGSLQGQWRGAA; STAGSLQGQWRGAAG; TAGSLQGQWRGAAGT; AGSLQGQWRGAAGTA;
GSLQGQWRGAAGTAA; SLQGQWRGAAGTAAQ; LQGQWRGAAGTAAQA; QGQWRGAAGTAAQAA;
GQWRGAAGTAAQAAV; QWRGAAGTAAQAAVV; WRGAAGTAAQAAVVR; RGAAGTAAQAAVVRF;
GAAGTAAQAAVVRFQ; AAGTAAQAAVVRFQE; AGTAAQAAVVRFQEA; GTAAQAAVVRFQEAA;
TAAQAAVVRFQEAAN; AAQAAVVRFQEAANK; AQAAVVRFQEAANKQ; QAAVVRFQEAANKQK;
AAVVRFQEAANKQKQ; AVVRFQEAANKQKQE; VVRFQEAANKQKQEL; VRFQEAANKQKQELD;
RFQEAANKQKQELDE; FQEAANKQKQELDEI; QEAANKQKQELDEIS; EAANKQKQELDEIST;
AANKQKQELDEISTN; ANKQKQELDEISTNI; NKQKQELDEISTNIR; KQKQELDEISTNIRQ;
QKQELDEISTNIRQA; KQELDEISTNIRQAG; QELDEISTNIRQAGV; ELDEISTNIRQAGVQ;
LDEISTNIRQAGVQY; DEISTNIRQAGVQYS; EISTNIRQAGVQYSR; ISTNIRQAGVQYSRA;
STNIRQAGVQYSRAD; TNIRQAGVQYSRADE; NIRQAGVQYSRADEE; IRQAGVQYSRADEEQ;
RQAGVQYSRADEEQQ; QAGVQYSRADEEQQQ; AGVQYSRADEEQQQA; GVQYSRADEEQQQAL;
VQYSRADEEQQQALS; QYSRADEEQQQALSS; YSRADEEQQQALSSQ; SRADEEQQQALSSQM;
RADEEQQQALSSQMG; ADEEQQQALSSQMGF

16 mers:
MAEMKTDAATLAQEAG; AEMKTDAATLAQEAGN; EMKTDAATLAQEAGNF;
MKTDAATLAQEAGNFE; KTDAATLAQEAGNFER; TDAATLAQEAGNFERI;
DAATLAQEAGNFERIS; AATLAQEAGNFERISG; ATLAQEAGNFERISGD;
TLAQEAGNFERISGDL; LAQEAGNFERISGDLK; AQEAGNFERISGDLKT;
QEAGNFERISGDLKTQ; EAGNFERISGDLKTQI; AGNFERISGDLKTQID;
GNFERISGDLKTQIDQ; NFERISGDLKTQIDQV; FERISGDLKTQIDQVE;
ERISGDLKTQIDQVES; RISGDLKTQIDQVEST; ISGDLKTQIDQVESTA;
SGDLKTQIDQVESTAG; GDLKTQIDQVESTAGS; DLKTQIDQVESTAGSL;
LKTQIDQVESTAGSLQ; KTQIDQVESTAGSLQG; TQIDQVESTAGSLQGQ;
QIDQVESTAGSLQGQW; IDQVESTAGSLQGQWR; DQVESTAGSLQGQWRG;
QVESTAGSLQGQWRGA; VESTAGSLQGQWRGAA; ESTAGSLQGQWRGAAG;
STAGSLQGQWRGAAGT; TAGSLQGQWRGAAGTA; AGSLQGQWRGAAGTAA;
GSLQGQWRGAAGTAAQ; SLQGQWRGAAGTAAQA; LQGQWRGAAGTAAQAA;
QGQWRGAAGTAAQAAV; GQWRGAAGTAAQAAVV; QWRGAAGTAAQAAVVR;
WRGAAGTAAQAAVVRF; RGAAGTAAQAAVVRFQ; GAAGTAAQAAVVRFQE;
AAGTAAQAAVVRFQEA; AGTAAQAAVVRFQEAA; GTAAQAAVVRFQEAAN;
TAAQAAVVRFQEAANK; AAQAAVVRFQEAANKQ; AQAAVVRFQEAANKQK;
QAAVVRFQEAANKQKQ; AAVVRFQEAANKQKQE; AVVRFQEAANKQKQEL;
VVRFQEAANKQKQELD; VRFQEAANKQKQELDE; RFQEAANKQKQELDEI;
FQEAANKQKQELDEIS; QEAANKQKQELDEIST; EAANKQKQELDEISTN;
AANKQKQELDEISTNI; ANKQKQELDEISTNIR; NKQKQELDEISTNIRQ;
KQKQELDEISTNIRQA; QKQELDEISTNIRQAG; KQELDEISTNIRQAGV;

QELDEISTNIRQAGVQ; ELDEISTNIRQAGVQY; LDEISTNIRQAGVQYS;
DEISTNIRQAGVQYSR; EISTNIRQAGVQYSRA; ISTNIRQAGVQYSRAD;
STNIRQAGVQYSRADE; TNIRQAGVQYSRADEE; NIRQAGVQYSRADEEQ;
IRQAGVQYSRADEEQQ; RQAGVQYSRADEEQQQ; QAGVQYSRADEEQQQA;
AGVQYSRADEEQQQAL; GVQYSRADEEQQQALS; VQYSRADEEQQQALSS;
QYSRADEEQQQALSSQ; YSRADEEQQQALSSQM; SRADEEQQQALSSQMG;
RADEEQQQALSSQMGF

INDEX TO SEQUENCE LIST

	SEQ ID NO
Bcl-2 fragments (class I)	44893-45800
BclX(L) fragments (class I)	45801-46593
Cancer antigens	44889-44892
BK virus antigens	1-6
BK virus 8-11 mers class I	7-24956
Bcl-2 fragments (class II)	46594-47133
BclX(L) fragments (class II)	47134-47645
BK 13-16 mers class II	24957-44888
Survivin fragments (class I)	47646-48180
Mcl-1 fragments (class II)	48181-49526
Borrelia OspC 8-11 mers and 13-16 mers	49527-51126
Borrelia OspA fragments	51127-51380
Borrelia FlaB fragments	51381-51540
Mycobacterium tuberculosis CFP10 8-11 mers mers and 13-16 mers	51541-52252

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

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
Illustration of selected reaction groups

Figure 6
Illustration of selected cleavable linkers

Figure 7
Prediction of MHC class 1 mouse virus LCMV gp 1 protein nonamer peptide binders for H-2Kd using the Syfpeithi database. Peptides are ranked according to their binding score. Only peptides with binding scores above the value of 11 are listed.

Figure 8. Size exclusion chromatography of folded HLA-A*0201-β2m –QLFEELQEL peptide-complex. Purification of HLA-A*0201-β2m –QLFEELQEL 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 9. 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 peptide-complex
Lane 3: Folded HLA-A*0201-β2m –QLFEELQEL peptide-complex incubated with molar excess Streptavidin.

Figure 10. Composition of Fluorescein-linker molecule. (A) Schematic representation of an example of a Fluorescein-linker molecule. (B) Composition of a L15 linker.

Figure 11
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 12
Prediction of MHC class 1 mouse virus LCMV gp 1 protein nonamer peptide binders for H-2Kd using the Syfpeithi database. Peptides are ranked according to their binding score. Only peptides with binding scores above the value of 11 are listed.

Figure 13
Full List of HLA Class I alleles assigned as of January 2007 from http://www.anthonynolan.org.uk/HIG/lists/class1list.html

Figure 14
List of top 30 HLA class 1 alleles in different human ethnic groups

Figure 15
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. 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 16
PBL from a breast cancer patient was analyzed by flow cytometry to identify Bcl-X(L)173–182 (peptide YLNDHLEPWI) 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 17

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 peptide or an irrelevant peptide (BA4697–105, GLQHWVPEL) 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 18

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) 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 19. 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) 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 20. 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)) or (B) MHC Dextramers containing peptides from CMV pp65 antigen (HLA-A*0201(NLVPMVATV)).

5

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.

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 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 8).
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 9) 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 was added to the 3' end of the *DRA1*0101-fos* template. Covalently bound peptide AGFKGEQGPKGEP 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 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 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 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 example describes how an activated divinylsylfone-dextran(270kDa)(VS-dex270) was coupled with streptavidin (SA) and 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 example describes how an activated divinylsylfone-dextran(270kDa)(VS-dex270) was coupled with streptavidin (SA) and 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 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.
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 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 peptide or the negative control peptide GLAGDVSAV were generated as described elsewhere herein. The fluorophore in this example was Fluorescein-linker molecules as shown in figure 10. 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 10B. 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 10 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) 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 10 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 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 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) 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 42) 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 10 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 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 peptide or the negative control peptide GLAGDVSAV 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) 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 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) 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 (a.a. 289-297) [SEQ ID NO: 1], 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 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 BK virus peptide binders.

This example describes the total approach, applied to the BK virus genome. It thus involves the translation of the genome in both directions, i.e. in six possible reading frames.
Prediction of MHC class1 BK virus 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 BK virus-specific T-cells. Prediction is carried out using the total approach. Thus, the 8-, 9-, 10- and 11-mer peptide sequences are generated from six amino acid sequences representing direct translation of the BK virus genome sequence in all six reading frames. The 8-, 9-, 10- and 11-mer peptide sequences are derived from the genome sequence by application of the software program described in (figure 2). The 8-, 9-, 10- and 11-mer peptide sequences are shown in table I.

Example 15 Prediction of MHC class 2 BK virus peptide binders.

This example describes the total approach, applied to the BK virus genome. It thus involves the translation of the genome in both directions, i.e. in six possible reading frames.
Prediction of MHC class 2 BK virus 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 BK virus-specific T-cells. Prediction is carried out using the total approach. Thus, the 13-, 14-, 15- and 16-mer peptide sequences are generated from six amino acid sequences representing direct translation of the BK virus genome sequence in all six reading frames. The 13-, 14-, 15- and 16-mer peptide sequences are derived from the genome sequence by application of the software program described in (figure 2). The 13-, 14-, 15- and 16-mer peptide sequences are shown in table O.

Example 16 Prediction of MHC class 1 peptide binders for BK Agnoprotein using directed approach

This example describes the directed approach, applied to a known protein sequence, the Agnoprotein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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 11).

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 table N. 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 17 Prediction of MHC class 1 peptide binders for BK small t protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the small t protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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 11).

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 table L. 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 peptide binders for BK Large T protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the Large T protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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 11).

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 table M. 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 Prediction of MHC class 1 peptide binders for BK VP1 protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the VP1 protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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 11).

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 table K. 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 20 Prediction of MHC class 1 peptide binders for BK VP2-3 protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the VP2-3 protein encoded by the human genome. The purpose is to predict BK virus 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 BK virus 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 11).

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 table J. 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 21 Prediction of MHC class 1 peptide binders for human cancer protein Bcl-2 using directed approach

This example describes the directed approach, applied to a known protein sequence, the cancer protein Bcl-2 encoded by the human genome. The purpose is to predict Bcl-2 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 Bcl-2 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 11).

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 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 22 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 11).

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 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 23 Prediction of MHC class 1 human cancer protein Survivin peptide binders

This example describes the prediction of MHC class1 human Survivin 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 human Survivin specific T-cells. Prediction of the 8-, 9-, 10- and 11-mer peptide sequences are carried out using the peptide generation software program described in figure 2. The outcome is shown in table F.

Example 24 Prediction of MHC class 2 peptide binders for BK Agnoprotein using directed approach

This example describes the directed approach, applied to a known protein sequence, the Agnoprotein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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/NetMHC/ database (figure 11).

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 table T. 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 25. Prediction of MHC class 2 peptide binders for BK small t protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the small t protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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/NetMHC/ database (figure 11).

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 table R. 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 26. Prediction of MHC class 2 peptide binders for BK Large T protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the Large T protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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/NetMHC/ database (figure 11).

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 table S. 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 27. Prediction of MHC class 2 peptide binders for BK VP1 protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the VP1 protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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/NetMHC/ database (figure 11).

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 table Q. 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 28. Prediction of MHC class 2 peptide binders for BK VP2-3 protein using directed approach

This example describes the directed approach, applied to a known protein sequence, the VP2-3 protein encoded by the BK virus genome. The purpose is to predict BK virus 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 BK virus 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/NetMHC/ database (figure 11).

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 table P. 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 29 Prediction of MHC class 2 human cancer protein Mcl-1 peptide binders

This example describes the prediction of MHC class 2 human Mcl-1 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 human Mcl-1 specific T-cells. Prediction of the 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 G.

Example 30 Prediction of MHC class 2 peptide binders for human cancer protein Bcl-2 using directed approach

This example describes the directed approach, applied to a known protein sequence, the cancer protein Bcl-2 encoded by the human genome. The purpose is to predict Bcl-2 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 Bcl-2 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 11).

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 table E. 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 31 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 11).

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 table D. 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 32 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. 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 U.

Example 33 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 is 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. 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 11).

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 table V. 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 34 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 is 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. 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 11).

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 table X.

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 35 Prediction of MHC class 1 and 2 Mycobacterium tuberculosis CFP10 peptide binders

This example describes the prediction of MHC class 1 and 2 Mycobacterium tuberculosis CFP10 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 Mycobacterium tuberculosis CFP10 specific T-cells. 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 Y.

Example 36 Prediction of MHC class 1 LCMV gp1 nonamer peptide binders for mouse H-2Kd. An example of non-human MHC peptide binding motifs.

This example describes the directed approach, applied to the known protein sequence of a mouse virus protein LCMV gp1 in context of mouse MHC class 1.
Prediction of LCMV gp1 peptide sequences that binds to the MHC class 1 molecule H-2Kd for use in construction of MHC'mers designed to be used for as analytical, diagnostic, prognostic, therapeutic and vaccine purposes, through the interaction of the MHC'mers with LCMV specific mouse T-cells. Prediction is carried out using the known preferences of the given H-2 molecules for peptide binding as laid down in the prediction program found on www.syfpeithi.de. The generated 9-mer peptides are ranked according to their binding efficiency to the individual HLA class 1 molecules. The output is shown in figure 2.

Example 37. Test of predicted BclX(L) 10-mer binding peptide functionality in ELISPOT

In example 22 the best binding BclX(L) 10-mer peptide for HLA-A*0201 was identified to be YLNRHLHTWI. 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 (YLNRHLHTWI), 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 15 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.

Example 38. Test of predicted BclX(L) 10-mer binding peptide functionality in Flow cytometry

In example 22 the best binding BclX(L) 10-mer peptide for HLA-A*0201 was identified to be YLNRHLHTWI. 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 16) 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.

Example 39. 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 38 were sorted out during the flow cytometric analysis using the MHC Dextramer HLA-A*0201/YLNRHLHTWI. 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.

Example 40. Demonstration of specific cytolytic activity of isolated BclX(L) specific CD8 T-cells

The ten expanded T cell clones isolated by Flow sorting as shown in example 39 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) 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 17). 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 8).

Example 41. 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 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) 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 18. 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.

Example 42 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 43

This is an example of how MHC multimers may be used for detection of cancer specific T cells in blood samples from patients.
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 cancer, thus, immune monitoring of a cancer. MHC multimers carrying cancer specific peptides is in this example used to detect the presence of cancer specific T cells in the blood from cancer patients.

Purified MHC-peptide complexes consisting of HLA-A*1101 heavy chain, human beta2microglobulin and peptide derived from a region in Survivin (Table F) 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 contains 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:

1. APC-SA conjugated 270 kDa dextran coupled with HLA-A*1101 in complex with beta2microglobulin and the peptide DLAQCFFCFK derived from Survivin.
2. APC-SA conjugated 270 kDa dextran coupled with HLA- A*1101 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran was used to determine the presence of Survivin specific T cells in the blood from cancer patients by flow cytometry following a standard flow cytometry protocol.
Blood from a cancer patient is isolated and 100 ul of this blood is incubated with 10 µl of 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 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 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 the MHC(peptide)/APC dextran construct 1 described above and thereby the presence of Survivin specific T cells in the blood. Blood analysed with MHC(peptide)/APC dextran construct 2 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Survivin specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of Survivin specific T cells in the blood of cancer.

Example 44

This is an example of how MHC multimers may be used for detection of cancer specific T cells in blood samples from patients.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA, used for direct detection of TCR in flow Cytometry. The antigen origin is cancer, thus, immune monitoring of a cancer. MHC multimers carrying cancer specific peptides is in this example used to detect the presence of cancer specific T cells in the blood from cancer patients.

Purified MHC-peptide complexes consisting of HLA-A*1101 heavy chain, human beta2microglobulin and peptide derived from a region in Survivin (Table F) 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:

3. APC-SA coupled with HLA-A*1101 in complex with beta2microglobulin and the peptide DLAQCFFCFK derived from Survivin.
4. APC-SA coupled with HLA-A*1101 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Survivin specific T cells in the blood from cancer patients by flow cytometry following a standard flow cytometry protocol.
Blood from a cancer patient is isolated and 100 ul of this blood is incubated with either of the 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 the SA-MHC(peptide)/APC tetramers 3 described above and thereby the presence of Survivin specific T cells in the blood. 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 test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Survivin specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of Survivin specific T cells in the blood of cancer patients.

Example 45

This is an example of how MHC multimers may be used for detection of cancer specific T cells in blood samples from patients.
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 cancer, thus, immune monitoring of a cancer.
MHC multimers carrying cancer specific peptides is in this example used to detect the presence of cancer specific T cells in the blood from cancer patients.

Purified MHC-peptide complexes consisting of HLA-A*1101 heavy chain, human beta2microglobulin and peptide derived a region in Survivin (Table F) 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:

5. APC-multimerisation domain coupled with HLA-A*1101 in complex with beta2microglobulin and the peptide DLAQCFFCFK derived from Survivin.
6. APC-multimerisation domain coupled with HLA-A*1101 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Survivin specific T cells in the blood from cancer patients by flow cytometry following a standard flow cytometry protocol.
Blood from a cancer patient is isolated and 100 ul of this blood is incubated with either of the 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 the MHC(peptide)/APC multimers 5 described above and thereby the presence of Survivin specific T cells in the blood. Blood analysed with MHC(peptide)/APC multimer 6 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the Survivin specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of Survivin specific T cells in the blood of cancer patients.

Example 46

This is an example of how MHC multimers may be used for detection of Epstein-Barr Virus (EBV) specific T cells in blood samples from humans infected with EBV.
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 EBV, thus, immune monitoring of EBV infection MHC multimers carrying EBV specific peptides is in this example used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus.

Purified MHC-peptide complexes consisting of HLA-B*0702 heavy chain, human beta2microglobulin and peptide derived from a region in EBV nuclear antigen (EBNA) 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:

7. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0702 in complex with beta2microglobulin and the peptide RPPIFIRRL derived from EBNA 3A.
8. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0702 in complex with beta2microglobulin and the peptide QPRAPIRPI derived from EBNA 6.
9. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0702 in complex with beta2microglobulin and the HIV peptide TPGPGVRYPL.

The binding of the above described MHC(peptide)/APC dextran is used to determine the presence of EBV specific T cells in the blood from EBV infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with EBV infection is isolated and 100 ul of this blood is incubated with 10 µl of 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 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. 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 construct 1 or 2 described above and thereby the presence of EBV specific T cells indicate that the patient are infected with Epstein-Barr virus. Blood analysed with MHC(peptide)/APC dextran construct 3 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the EBV specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus.

Example 47

This is an example of how MHC multimers may be used for detection of Epstein-Barr Virus (EBV) specific T cells in blood samples from humans infected with EBV.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is EBV, thus, immune monitoring of EBV infection MHC multimers carrying EBV specific peptides is in this example used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus.

Purified MHC-peptide complexes consisting of HLA-B*0702 heavy chain, human beta2microglobulin and peptide derived from a region in EBV nuclear antigen (EBNA) 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:

10. APC-SA coupled with HLA-B*0702 in complex with beta2microglobulin and the peptide RPPIFIRRL derived from EBNA 3A.
11. APC-SA coupled with HLA-B*0702 in complex with beta2microglobulin and the peptide QPRAPIRPI derived from EBNA 6.
12. APC-SA coupled with HLA- B*0702 in complex with beta2microglobulin and the HIV peptide TPGPGVRYPL.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of EBV specific T cells in the blood from Epstein-Barr virus infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with EBV is isolated and 100 ul of this blood is incubated with either of the 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 4 or 5 described above and thereby the presence of EBV specific T cells will indicate that the patient are infected with Epstein-Barr virus. Blood analysed with SA- MHC(peptide)/APC tetramers 6 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC tetramer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the EBV specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus

Example 48

This is an example of how MHC multimers may be used for detection of Epstein-Barr Virus (EBV) specific T cells in blood samples from humans infected with EBV.
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 EBV, thus, immune monitoring of EBV infection
MHC multimers carrying EBV specific peptides is in this example used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus.

Purified MHC-peptide complexes consisting of HLA-B*0702 heavy chain, human beta2microglobulin and peptide derived a region in EBV nuclear antigen (EBNA) 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-B*0702 in complex with beta2microglobulin and the peptide RPPIFIRRL derived from EBNA 3A.
14. APC-multimerisation domain coupled with HLA-B*0702 in complex with beta2microglobulin and the peptide QPRAPIRPI derived from EBNA 6.
15. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the HIV peptide TPGPGVRYPL.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of EBV specific T cells in the blood from EBV infected individuals by flow cytometry following a standard flow cytometry protocol.

Blood from a patient with EBV infection is isolated and 100 ul of this blood is incubated with either of the 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 7 or 8 described above and thereby the presence of EBV specific T cells will indicate that the patient are infected with Epstein-Barr virus. Blood analysed with MHC(peptide)/APC multimer 9 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the EBV specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of EBV specific T cells in the blood of patients infected with Epstein-Barr virus.

Example 49

This is an example of how MHC multimers may be used for detection of influenza matrix peptide in blood samples from humans infected with influenza.
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 Influenza, thus, immune monitoring of influenza. The MHC multimer used are MHC complexes coupled to labeled dextran.
MHC multimers carrying influenza specific peptides is in this example used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from a region in influenza matrix peptide (Flu-MP) 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 contains 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:

16. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide GILGFVFTL derived from Flu-MP.

17. APC-SA conjugated 270 kDa dextran coupled with HLA- A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV.

The binding of the above described MHC(peptide)/APC dextran was used to determine the presence of influenza specific T cells in the blood from influenza infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a influenza infected patient is isolated and 100 ul of this blood is incubated with 10 µl of 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 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 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 the MHC(peptide)/APC dextran construct 1 described above and thereby the presence of influenza specific T cells indicate that the patient are infected with influenza virus.
Blood analysed with MHC(peptide)/APC dextran construct 2 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the influenza specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Example 50

This is an example of how MHC multimers may be used for detection of influenza matrix peptide in blood samples from humans infected with influenza.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is Influenza, thus, immune monitoring of influenza.
The MHC multimer used are MHC complexes coupled to labeled dextran.
MHC multimers carrying influenza specific peptides is in this example used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from a region in influenza matrix peptide (Flu-MP) 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:

18. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide GILGFVFTL derived from Flu-MP.
19. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of influenza specific T cells in the blood from influenza infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a cancer patient is isolated and 100 ul of this blood is incubated with either of the 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 the SA-MHC(peptide)/APC tetramers 3 described above and thereby the presence of influenza specific T cells will indicate that the patient are infected with influenza virus. 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 test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the influenza specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Example 51

This is an example of how MHC multimers may be used for detection of influenza matrix peptide in blood samples from humans infected with influenza.
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 Influenza, thus, immune monitoring of influenza.
The MHC multimer used are MHC complexes coupled to labeled dextran.
MHC multimers carrying influenza specific peptides is in this example used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived a region in influenza matrix peptide (Flu-MP) 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:

20. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide GILGFVFTL derived from Flu-MP.
21. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of influenza specific T cells in the blood from influenza infected by flow cytometry following a standard flow cytometry protocol.
Blood from a influenza infected patient is isolated and 100 ul of this blood is incubated with either of the 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 the MHC(peptide)/APC multimers 5 described above and thereby the presence of influenza specific T cells will indicate that the patient are infected with influenza virus. Blood analysed with MHC(peptide)/APC multimer 6 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the influenza specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of influenza specific T cells in the blood of patients infected with influenza virus.

Example 52

This is an example of how MHC multimers may be used for detection of Multiple sclerosis (MS) specific T cells in blood samples from MS patients.
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 MS, thus, immune monitoring of MS.
MHC multimers carrying MS specific peptides is in this example used to detect the presence of MS specific T cells in the blood of MS patients.

Purified MHC-peptide complexes consisting of HLA-DR2 heavy chains and peptide derived from a region in Myelin Basic Protein (MBP) in MS or a negative control peptide are generated 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 was 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 was 3.8x10e-8 M. The following MHC(peptide)/APC dextran constructs are made:

22. APC-SA conjugated 270 kDa dextran coupled with HLA-DR2 in complex with the peptide MBP 83-102 YDENPVVHFF KNIVTPRTPP derived from Multiple sclerosis.
23. APC-SA conjugated 270 kDa dextran coupled with HLA-DR2 in complex with the peptide MBP 144-163 VDAQGTLSKIFKLGGRDSRS derived from Multiple sclerosis.
24. APC-SA conjugated 270 kDa dextran coupled with HLA-DR2 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran was used to determine the presence of MS specific T cells in the blood from MS patients by flow cytometry following a standard flow cytometry protocol.
Blood from a MS patient is isolated and 100 ul of this blood is incubated with 10 µl of 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 CD4/PE (clone MT310 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 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-CD4/PE and either of the MHC(peptide)/APC dextran construct 1 or 2 described above and thereby the presence of MS specific T cells in the blood. Blood analysed with MHC(peptide)/APC dextran construct 3 show no staining of CD3 and CD4 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the MS specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of MS specific T cells in the blood of MS patients.

Example 53

This is an example of how MHC multimers may be used for detection of Multiple sclerosis (MS) specific T cells in blood samples from MS patients.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA, used for direct detection of TCR in flow Cytometry. The antigen origin is MS, thus, immune monitoring of MS.
MHC multimers carrying MS specific peptides is in this example used to detect the presence of MS specific T cells in the blood of MS patients.

Purified MHC-peptide complexes consisting of HLA-DR2 heavy chains and peptide derived from a region in Myelin Basic Protein (MBP) in MS or a negative control peptide are generated as described elsewhere herein. Biotinylated MHC-peptide

complexes are then coupled SA labelled with APC. MHC-peptide complexes are added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes are 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:

25. APC-SA coupled with HLA-DR2 in complex with the peptide MBP 83-102 YDENPVVHFFKNIVTPRTPP derived from Multiple sclerosis.
26. APC-SA coupled with HLA-DR2 in complex with the peptide MBP 144-163 VDAQGTLSKIFKLGGRDSRS derived from Multiple sclerosis.
27. APC-SA coupled with HLA-DR2 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of MS specific T cells in the blood from MS patients by flow cytometry following a standard flow cytometry protocol.
Blood from a MS patient is isolated and 100 ul of this blood is incubated with either of the 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 CD4/PE (clone MT310 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-CD4/PE and either of the SA-MHC(peptide)/APC tetramers 4 or 5 described above and thereby the presence of MS specific T cells in the blood. Blood analysed with SA-MHC(peptide)/APC tetramers 6 should show no staining of CD3 and CD4 positive cells with this SA-MHC(peptide)/APC tetramer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the MS specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of MS specific T cells in the blood of MS patients.

Example 54

This is an example of how MHC multimers may be used for detection of Multiple sclerosis (MS) specific T cells in blood samples from MS patients.
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 MS, thus, immune monitoring of MS.
MHC multimers carrying MS specific peptides is in this example used to detect the presence of MS specific T cells in the blood of MS patients.

Purified MHC-peptide complexes consisting of HLA-DR2 heavy chains and peptide derived from a region in Myelin Basic Protein (MBP) in MS or a negative control

peptide are generated. MHC-peptide complexes are then coupled to a multimerisation domain together with APC.
The following MHC(peptide)/APC multimers are made:

28. APC-multimerisation domain coupled with HLA-DR2 in complex with the peptide MBP 83-102 YDENPVVHFFKNIVTPRTPP derived from Multiple sclerosis.
29. APC-multimerisation domain coupled with HLA-DR2 in complex with the peptide MBP 144-163 VDAQGTLSKIFKLGGRDSRS derived from Multiple sclerosis.
30. APC-multimerisation domain coupled with HLA-DR2 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of MS specific T cells in the blood from MS patients by flow cytometry following a standard flow cytometry protocol.
Blood from a MS patient is isolated and 100 ul of this blood is incubated with either of the 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 CD4/PE (clone MT310 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-CD4/PE and either of the MHC(peptide)/APC multimers 7 or 8 described above and thereby the presence of MS specific T cells in the blood. Blood analysed with MHC(peptide)/APC multimer 9 should show no staining of CD3 and CD4 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the MS specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of MS specific T cells in the blood of MS patients.

Example 55

This is an example of how MHC multimers may be used for detection of Rheumatoid arthritis (RA) specific T cells in blood samples from RA patients.
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 RA, thus, immune monitoring of RA.
MHC multimers carrying RA specific peptides is in this example used to detect the presence of RA specific T cells in the blood of MS patients.

Purified MHC-peptide complexes consisting of HLA-DR4 heavy chains and peptide derived from a region in Collagen Type II (CII) in RA or a negative control peptide are

generated 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 was 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 was 3.8x10e-8 M. The following MHC(peptide)/APC dextran constructs are made:

31. APC-SA conjugated 270 kDa dextran coupled with HLA-DR4 in complex with the peptide CII 261-273 AGFKGEQGPKGEP derived from Rheumatoid arthritis
32. APC-SA conjugated 270 kDa dextran coupled with HLA-DR4 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran was used to determine the presence of RA specific T cells in the blood from RA patients by flow cytometry following a standard flow cytometry protocol.
Blood from a RA patient is isolated and 100 ul of this blood is incubated with 10 µl of 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 CD4/PE (clone MT310 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 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-CD4/PE and the MHC(peptide)/APC dextran construct 1 described above and thereby the presence of RA specific T cells in the blood. Blood analysed with MHC(peptide)/APC dextran construct 2 show no staining of CD3 and CD4 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the RA specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of RA specific T cells in the blood of RA patients.

Example 56

This is an example of how MHC multimers may be used for detection of Rheumatoid arthritis (RA) specific T cells in blood samples from RA patientsIn this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is RA, thus, immune monitoring of RA.
MHC multimers carrying RA specific peptides is in this example used to detect the presence of RA specific T cells in the blood of RA patients.

Purified MHC-peptide complexes consisting of HLA-DR4 heavy chains and peptide derived from a region in Collagen type II (CII) in RA or a negative control peptide are generated as described elsewhere herein. Biotinylated MHC-peptide complexes are then coupled SA labelled with APC. MHC-peptide complexes are added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes are 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:

33. APC-SA coupled with HLA-DR4 in complex with the peptide CII 261-273 AGFKGEQGPKGEP derived from Rheumatoid arthritis.
34. APC-SA coupled with HLA-DR4 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of RA specific T cells in the blood from RA patients by flow cytometry following a standard flow cytometry protocol.
Blood from a RA patient is isolated and 100 ul of this blood is incubated with either of the 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 CD4/PE (clone MT310 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-CD4/PE and the SA-MHC(peptide)/APC tetramers 3 described above and thereby the presence of RA specific T cells in the blood. Blood analysed with SA-MHC(peptide)/APC tetramers 4 should show no staining of CD3 and CD4 positive cells with this SA-MHC(peptide)/APC tetramer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the RA specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of RA specific T cells in the blood of RA patients.

Example 57

This is an example of how MHC multimers may be used for detection of Rheumatoid arthritis (RA) specific T cells in blood samples from RA patients.
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 RA, thus, immune monitoring of RA.
MHC multimers carrying RA specific peptides is in this example used to detect the presence of RA specific T cells in the blood of MS patients.
This is an example of how MHC multimers may be used for detection of Rheumatoid arthritis (RA) specific T cells in blood samples from RA patients. The MHC multimer used are MHC complexes coupled to

MHC multimers carrying RA specific peptides is in this example used to detect the presence of RA specific T cells in the blood of RA patients.

Purified MHC-peptide complexes consisting of HLA-DR4 heavy chains and peptide derived from a region in Myelin Basic Protein (MBP) in MS or a negative control peptide are generated. MHC-peptide complexes are then coupled to a multimerisation domain together with APC.
The following MHC(peptide)/APC multimers are made:

35. APC-multimerisation domain coupled with HLA-DR4 in complex with the peptide CII 261-273 AGFKGEQGPKGEP derived from Rheumatoid arthritis.
36. APC-multimerisation domain coupled with HLA-DR4 in complex with a non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of RA specific T cells in the blood from RA patients by flow cytometry following a standard flow cytometry protocol.
Blood from a RA patient is isolated and 100 ul of this blood is incubated with either of the 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 CD4/PE (clone MT310 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-CD4/PE and the MHC(peptide)/APC multimers 5 described above and thereby the presence of RA specific T cells in the blood. Blood analysed with MHC(peptide)/APC multimer 6 should show no staining of CD3 and CD4 positive cells with this SA- MHC(peptide)/APC multimers.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the RA specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of RA specific T cells in the blood of RA patients.

Example 58

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with

Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis Antigen 85B (Ag85B) 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 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 are made:

37. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KLVANNTRL derived from Ag85B.
38. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide YLLDGLRAQ derived from Ag85B.
39. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTSELPQW derived from Ag85B.
40. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 59

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled the multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis Antigen 85B (Ag85B) 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:

41. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KLVANNTRL derived from Ag85B.
42. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide YLLDGLRAQ derived from Ag85B.
43. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTSELPQW derived from Ag85B.
44. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 5, 6 or 7 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with SA-MHC(peptide)/APC tetramers 8 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 60

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis. The MHC multimer used are MHC complexes coupled to
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis Antigen 85B (Ag85B) or a negative control peptide are 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:

45. APC-multimerisation domian coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide KLVANNTRL derived from Ag85B.
46. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide YLLDGLRAQ derived from Ag85B.
47. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FLTSELPQW derived from Ag85B.
48. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 9, 10 or 11 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC multimer 12 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 61

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*0801 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis Antigen 85B (Ag85B) 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 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 are made:

49. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide MGRDIKVQF derived from Ag85B.
50. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide DIKVQFQSG derived from Ag85B.
51. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide ENFVRSSNL derived from Ag85B.
52. APC-SA conjugated 270 kDa dextran coupled with HLA-B*0801 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 13, 14 or 15 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC dextran construct 16 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 62

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled the multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis

Antigen 85B (Ag85B) 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:

53. APC-SA coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide MGRDIKVQF derived from Ag85B.
54. APC-SA coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide DIKVQFQSG derived from Ag85B.
55. APC-SA coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide ENFVRSSNL derived from Ag85B.
56. APC-SA coupled with HLA-B*0801 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 17, 18 or 19 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with SA-MHC(peptide)/APC tetramers 20 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 63

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.

TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*0801 heavy chain, human beta2microglobulin and peptide derived from regions in Mycobacterium tuberculosis Antigen 85B (Ag85B) or a negative control peptide are 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:

57. APC-multimerisation domaln coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide MGRDIKVQF derived from Ag85B.
58. APC-multimerisation domain coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide DIKVQFQSG derived from Ag85B.
59. APC-multimerisation domain coupled with HLA-B*0801 in complex with beta2microglobulin and the peptide ENFVRSSNL derived from Ag85B.
60. APC-multimerisation domain coupled with HLA-B*0801 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Ag85B specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 21, 22 or 23 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC multimer 24 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 64

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*44 heavy chain, human beta2microglobulin and peptide derived from regions in antigen Mtb39 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 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 are made:

61. APC-SA conjugated 270 kDa dextran coupled with HLA-B*44 in complex with beta2microglobulin and the peptide MWAQDAAAMF derived from Mtb39.
62. APC-SA conjugated 270 kDa dextran coupled with HLA-B*44 in complex with beta2microglobulin and the peptide AAERGPGQML derived from Mtb39.
63. APC-SA conjugated 270 kDa dextran coupled with HLA-B*44 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Mtb39 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 25 or 26 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC dextran construct 27 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 65

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled the multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*44 heavy chain, human beta2microglobulin and peptide derived from regions in antigen Mtb39 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 SA labelled with APC. MHC-peptide complexes are added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes are 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:

64. APC-SA coupled with HLA-B*44 in complex with beta2microglobulin and the peptide MWAQDAAAMF derived from Ag85B.
65. APC-SA coupled with HLA-B*44 in complex with beta2microglobulin and the peptide AAERGPGQML derived from Ag85B.
66. APC-SA coupled with HLA-B*44 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of Mtb39 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 28 or 29 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with SA-MHC(peptide)/APC tetramers 30 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 66

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*44 heavy chain, human beta2microglobulin and peptide derived from regions in antigen Mtb39 or a negative control peptide are 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:

67. APC-multimerisation domain coupled with HLA-B*44 in complex with beta2microglobulin and the peptide MWAQDAAAMF derived from Mtb39.
68. APC-multimerisation domain coupled coupled with HLA-B*44 in complex with beta2microglobulin and the peptide AAERGPGQML derived from Mtb39.
69. APC-multimerisation domain coupled coupled with HLA-B*44 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of Mtb39 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 31 or 32 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC multimer 33 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 67

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*14 heavy chain, human beta2microglobulin and peptide derived from regions in culture filtrate protein 10 (CFP10) antigen (Table Y) 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 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 are made:

70. APC-SA conjugated 270 kDa dextran coupled with HLA-B*14 in complex with beta2microglobulin and the peptide RADEEQQQAL derived from CFP10.
71. APC-SA conjugated 270 kDa dextran coupled with HLA-B*14 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of CFP10 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 the MHC(peptide)/APC dextran constructs 34 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC dextran construct 25 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 68

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled the multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*14 heavy chain, human beta2microglobulin and peptide derived from regions in culture filtrate protein 10 (CFP10) antigen (Table Y) 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 SA labelled with APC. MHC-peptide complexes are added in an amount corresponding to a ratio of 5 MHC-peptide molecules per SA molecule. Then SA/APC carrying four MHC complexes are 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:

72. APC-SA coupled with HLA-B*14 in complex with beta2microglobulin and the peptide RADEEQQQAL derived from CFP10.
73. APC-SA coupled with HLA-B*44 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of CFP10 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 the SA-MHC(peptide)/APC tetramers 36 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with SA-MHC(peptide)/APC tetramers 37 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 69

This is an example of how MHC multimers may be used for diagnosis of Tuberculosis (TB) in blood samples from humans infected with Mycobacterium tuberculosis.
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 TB, thus, immune monitoring of TB.
TB is caused by infection by Mycobacterium tuberculosis. During acute infection TB 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 TB specific T cells may thereby act as a surrogate marker for infection with Mycobacterium tuberculosis. MHC multimers carrying TB specific peptides is in this example used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Purified MHC-peptide complexes consisting of HLA-B*14 heavy chain, human beta2microglobulin and peptide derived from regions in culture filtrate protein 10 (CFP10) antigen (Table Y) or a negative control peptide are 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:

74. APC-multimerisation domain coupled with HLA-B*14 in complex with beta2microglobulin and the peptide RADEEQQQAL derived from CFP10.
75. APC-multimerisation domain coupled coupled with HLA-B*14 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of CFP10 specific T cells in the blood from TB infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with TB 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 the MHC(peptide)/APC multimers 38 described above and thereby the presence of TB specific T cells will indicate that the patient are infected with Mycobacterium tuberculosis. Blood analysed with MHC(peptide)/APC multimer 39 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 TB specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of TB specific T cells in the blood of patients infected with Mycobacterium tuberculosis.

Example 70

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 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 V) or Flagellin B (Table X) 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:

76. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
77. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
78. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B
79. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B
80. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B
81. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

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 19.
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 71

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 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 V) or Flagellin B (Table X) 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:

82. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
83. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
84. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B.
85. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B.
86. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B.
87. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

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 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.
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 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 V) or Flagellin B (Table X) 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:

88. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ALIACKQNV derived from OspA.
89. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide FTKEDTIT derived from OspA.
90. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SIQIEIEQL derived from Fla B.
91. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLNEVEKVL derived from Fla B.
92. APC-multimerisation domain coupled coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide SLAKIENAI derived from Fla B.
93. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

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 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.
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 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 U) 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:

94. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
95. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide ELANKAIGK derived from OspC.
96. 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 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.
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 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 U) 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:

97. APC-SA coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
98. APC-SA coupled with HLA-A*0301 in complex with beta2microglobulin and the peptide ELANKAIGK derived from OspC.
99. 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 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.

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 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 U) 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:

100. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide TLITEKLSK derived from OspC.
101. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide ELANKAIG derived from OspC.
102. 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 76

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.
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 CMV, thus, immune monitoring of CMV.
MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from a region in CMV internal matrix protein pp65 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:

103. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLVPMVATV derived from CMV pp65.
104. APC-SA conjugated 270 kDa dextran coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

The binding of the above described MHC(peptide)/APC dextran is used to determine the presence of CMV pp65 specific T cells in the blood from CMV infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with CMV infection is isolated and 100 ul of this blood is incubated with 10 µl of 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 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 construct 1 described above and thereby the presence of CMV specific T cells indicate that the patient are infected with Cytomegalovirus. Blood analysed with MHC(peptide)/APC dextran construct 2 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct. The result is shown I figure 20

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 77

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.
In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is CMV, thus, immune monitoring of CMV.
MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived from a region in CMV internal matrix protein pp65 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:

105. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLVPMVATV derived from CMV pp65.
106. APC-SA coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of CMV pp65 specific T cells in the blood from Cytomegalovirus infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with CMV is isolated and 100 ul of this blood is incubated with either of the 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 the SA-MHC(peptide)/APC tetramers 3 described above and thereby the presence of CMV specific T cells will indicate that the patient are infected with Cytomegalovirus. 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 test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 78

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.
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 CMV, thus, immune monitoring of CMV.
MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.
Purified MHC-peptide complexes consisting of HLA-A*0201 heavy chain, human beta2microglobulin and peptide derived a region in CMV internal matrix protein pp65 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:

107. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the peptide NLVPMVATV derived from CMV pp65.
108. APC-multimerisation domain coupled with HLA-A*0201 in complex with beta2microglobulin and the non-sense peptide GLAGDVSAV.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of CMV pp65 specific T cells in the blood from CMV infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with CMV infection is isolated and 100 ul of this blood is incubated with either of the 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 the MHC(peptide)/APC multimers 5 described above and thereby the presence of CMV specific T cells will indicate that the patient are infected with Cytomegalovirus. Blood analysed with MHC(peptide)/APC multimer 6 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 79

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.
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 CMV, thus, immune monitoring of CMV.
MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Purified MHC-peptide complexes consisting of HLA-A*2402 heavy chain, human beta2microglobulin and peptide derived from a region in CMV internal matrix protein pp65 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:

109. APC-SA conjugated 270 kDa dextran coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide QYDPVAALF derived from CMV pp65.
110. APC-SA conjugated 270 kDa dextran coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide VYALPLKML derived from CMV pp65.
111. APC-SA conjugated 270 kDa dextran coupled with HLA-A*2402 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran is used to determine the presence of CMV pp65 specific T cells in the blood from CMV infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with CMV infection is isolated and 100 ul of this blood is incubated with 10 µl of 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 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. 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 7 or 8 described above and thereby the presence of CMV specific T cells indicate that the patient are infected with Cytomegalovirus. Blood analysed with MHC(peptide)/APC dextran construct 9 show no staining of CD3 and CD8 positive cells with this MHC(peptide)/APC dextran construct.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the MHC(peptide)/APC dextran constructs can be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 80

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.

In this example the MHC multimer used are MHC complexes coupled to fluorophor-labelled multimerisation domain Streptavidin (SA), used for direct detection of TCR in flow cytometry. The antigen origin is CMV, thus, immune monitoring of CMV. MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Purified MHC-peptide complexes consisting of HLA-A*2402 heavy chain, human beta2microglobulin and peptide derived from a region in CMV internal matrix protein pp65 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:

112. APC-SA coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide QYDPVAALF derived from CMV pp65.
113. APC-SA coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide VYALPLKML derived from CMV pp65.
114. APC-SA coupled with HLA-A*2402 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC dextran can be used to determine the presence of CMV pp65 specific T cells in the blood from Cytomegalovirus infected individuals by flow cytometry following a standard flow cytometry protocol.

Blood from a patient with CMV is isolated and 100 ul of this blood is incubated with either of the 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 10 or 11 described above and thereby the presence of CMV specific T cells will indicate that the patient are infected with Cytomegalovirus. 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 test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the APC-SA coupled MHC(peptide) constructs may be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 81

This is an example of how MHC multimers may be used for detection of Cytomegalovirus (CMV) specific T cells in blood samples from humans infected with CMV.
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 CMV, thus, immune monitoring of CMV.
MHC multimers carrying CMV specific peptides is in this example used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Purified MHC-peptide complexes consisting of HLA-A*2402 heavy chain, human beta2microglobulin and peptide derived a region in CMV internal matrix protein pp65 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:

115. APC-multimerisation domain coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide QYDPVAALF derived from CMV pp65.
116. APC-multimerisation domain coupled with HLA-A*2402 in complex with beta2microglobulin and the peptide VYALPLKML derived from CMV pp65.
117. APC-multimerisation domain coupled with HLA-A*2402 in complex with beta2microglobulin and the non-sense peptide.

The binding of the above described MHC(peptide)/APC multimers can be used to determine the presence of CMV pp65 specific T cells in the blood from CMV infected individuals by flow cytometry following a standard flow cytometry protocol.
Blood from a patient with CMV infection is isolated and 100 ul of this blood is incubated with either of the 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 or 14 described above and thereby the presence of CMV specific T cells will indicate that the patient are infected with Cytomegalovirus. Blood analysed with MHC(peptide)/APC multimer 15 should show no staining of CD3 and CD8 positive cells with this SA- MHC(peptide)/APC multimer.

The sensitivity of the above described test may be enhanced by addition of labeled antibodies specific for activation markers expressed in or on the surface of the CMV specific T cells.

We conclude that the APC-multimerisation domain coupled MHC(peptide) constructs may be used to detect the presence of CMV specific T cells in the blood of patients infected with Cytomegalovirus.

Example 82

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. 20. 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 83

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples from Multiple Sclerosis (MS) 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 MS, thus, immune monitoring of MS.
The example provides a sensitive assay for the detection of T-cells reactive to the antigen Myelin Basic Protein (MBP), 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 Multiple Sclerosis 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 antigen, MBP 83-102 (YDENPVVHFF KNIVTPRTPP) or 144-163 (VDAQGTLSKIFKLGGRDSRS), 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 Multiple Sclerosis patients.

Example 84

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples from Multiple Sclerosis (MS) patients by ELISPOT.

This is an example of indirect detection of TCR, where individual cells are immobilized and measured by a chromogen assay. Antigenic peptide origin is MS, thus, immune monitoring of MS.

The example provides a sensitive assay for the detection of T-cells reactive to the antigen Myelin Oligodendrocyte Glycoprotein (MOG), 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 abovePBMCs from Multiple Sclerosis 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 antigen, MOG 1-20 (GQFRVIGPRHPIRALVGDEV) or 41-60 (RPPFSRVVHLYRNGKDQDGD), 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 Multiple Sclerosis patients.

Example 85

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples from Rheumatoid Arthritis (RA) patients by ELISPOT.
This is an example of indirect detection of TCR, where individual cells are immobilized and measured by a chromogen assay. Antigenic peptide origin is RA, thus, immune monitoring of RA.
The example provides a sensitive assay for the detection of T-cells reactive to the antigen type II collagen (CII) 261-273, 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 Rheumatoid Arthritis 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 antigen, CII 261-273 (AGFKGEQGPKGEP), 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 Rheumatoid Arthritis patients.'

Example 86

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samples from Melanoma 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 Melanoma, thus, immune monitoring of cancer.
The example provides a sensitive assay for the detection of T-cells reactive to the antigen MELAN-A/MART-1 27-35, 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 Melanoma 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 antigen, MELAN-A/MART-1 27-35 (AAGIGILTV), 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 Melanoma patients.

Example 87

This is an example of measurement of antigen reactive T-Cells by IFN-γ capture in blood samplesby 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 42, 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 88.

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 89

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.

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ITEMS

The present invention is further disclosed herein below by citation of the following, non-limiting items of the invention.

1. A MHC complex comprising one or more functional MHC molecule(s) capable of binding a peptide P,

wherein, when more than one MHC molecule is present, the MHC complex further comprises a multimerization domain preferably comprising at least one binding entity and/or a carrier,

wherein, when the multimerization domain is present, the more than one functional MHC molecules are attached either to the at least one binding entity and/or to the carrier,

wherein, when the more than one functional MHC molecules are attached to the carrier, the MHC molecules are either attached directly to the carrier or attached to the carrier via one or more binding entities.

2. The MHC complex according to item 1, wherein the MHC molecule is a vertebrate MHC molecule such as a human, a murine, a rat, a porcine, a bovine or an avian molecule.

3. The MHC complex according to item 1 or 2, wherein the MHC molecule is a human MHC molecule.

4. The MHC complex according to any one of items 1-3, wherein the MHC molecule is

a MHC Class I molecule selected from the group consisting of a heavy chain, a heavy chain combined with a β_2m, a heavy chain combined with a peptide, and a heavy chain/β_2m dimer with a peptide;

or a MHC Class II molecule selected from the group consisting of an α/β dimer, an α/β dimer with a peptide, α/β dimer combined through an affinity tag and a α/β dimer combined through an affinity tag with a peptide;

or a MHC Class I like molecule or MHC Class II like molecule.

5. The MHC complex according to any one of items 1-4, wherein the MHC molecule is a peptide free MHC molecule.

6. The MHC complex according to any one of items 1-5, wherein more than one MHC molecule is present, and wherein at least two of said MHC molecules are different.

7. The MHC complex according to any one of items 1-5, wherein more than one MHC molecule is present, and wherein the MHC molecules are the same.

8. The MHC complex according to any one of items 1-7, wherein at least two of the peptides harboured by the MHC complexes are different.

9. The MHC complex according to any one of items 1-7, wherein the peptides harboured by the MHC complexes are the same.

10. The MHC complex according to any one of items 1-9, wherein the MHC molecule(s) are attached to the carrier directly.

11. The MHC complex according to any one of items 1-9, wherein the MHC molecule(s) are attached to the carrier via one or more binding entities.

12. The MHC complex according to item 11, wherein each binding entity has attached thereto from 1 to 10 MHC molecules.

13. The MHC complex according to item 11, wherein each binding entity has attached thereto from 1 to 8 MHC molecules.

14. The MHC complex according to item 11, wherein each binding entity has attached thereto from 1 to 6 MHC molecules.

15. The MHC complex according to item 11, wherein each binding entity has attached thereto from 1 to 4 MHC molecules.

16. The MHC complex according to item 11, wherein each binding entity has attached thereto from 1 to 3 MHC molecules.

17. The MHC complex according to item 11, wherein each binding entity has attached thereto 1 or 2 MHC molecules.

18. The MHC complex according to any one of items 1-17, wherein the total number of MHC molecules of the construct is from 1 to 100.

19. The MHC complex according to any one of items 1-17, wherein the total number of MHC molecules of the construct is from 1 to 50.

20. The MHC complex according to any one of items 1-17, wherein the total number of MHC molecules of the construct is from 1 to 25.

21. The MHC complex according to item 1, wherein the binding entity is selected from 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).

22. The MHC complex according to any one of items 1-21, further comprising one or more biologically active molecules.

23. The MHC complex according to clam 22, wherein the biologically active molecules is selected from proteins, co-stimulatory molecules, cell modulating molecules,

receptors, accessory molecules, adhesion molecules, natural ligands, and toxic molecules, and
antibodies and recombinant binding molecules thereto, and
combinations thereof.

24. The MHC complex according to items 22 or 23, wherein the biologically active molecule is attached to the carrier either directly or via one or more of the binding entities.

25. The MHC complex according to any one of items 22-24, wherein the biologically active molecule is 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 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 antibodies thereto, or antibody derivatives or fragments thereof, and combinations thereof.

26. The MHC complex according to any of items 1-25 further comprising one or more labelling compounds.

27. The MHC complex according to item 26, wherein one or more labelling compounds are attached to the carrier.

28. The MHC complex according to item 26, wherein one or more labelling compounds are attached to one or more of the binding entities.

29. The MHC complex according to item 26, wherein one or more labelling compounds are attached to the MHC molecule(s).

30. The MHC complex according to item 26, wherein one or more labelling compounds are attached to the carrier and/or one or more of the binding entities and/or one or more of the MHC molecules.

31. The MHC complex according to any one of items 26-30, wherein the labelling compound is directly or indirectly detectable.

32. The MHC complex according to any of items 26-31, wherein the labelling compound is a fluorescent label, an enzyme label, a radioisotope, a chemiluminescent label, a bioluminescent label, a polymer, a metal particle, a hapten, an antibody, or a dye.

33. The MHC complex according to any one of items 26-32, wherein the labelling compound

is selected from fluorescent labels such as 5-(and 6)-carboxyfluorescein, 5- or 6-carboxyfluorescein, 6-(fluorescein)-5-(and 6)-carboxamido hexanoic acid, fluorescein isothiocyanate (F)TC), 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, or

is selected from enzymatic labels such as 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), or

is selected from luminiscence labels such as luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines, or

is selected from radioactivity labels such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor.

34. The MHC complex according to any one of items 1-33, wherein the carrier is selected from

polysaccharides including dextrans, carboxy methyl dextran, dextran polyaldehyde, carboxymethyl dextran lactone, and cyclodextrins,

pullulans, schizophyllan, scleroglucan, xanthan, gellan, O-ethylamino guaran, chitins and chitosans indlucing 6-O-carboxymethyl chitin and N-carboxymethyl chitosan,

derivatised cellolosics including carboxymethyl cellulose, carboxymethyl hydroxyethyl cellulose, hydroxyethyl cellulose, 6-amino-6-deoxy cellulose and O-ethylamine cellulose,

hydroxylated starch, hydroxypropyl starch, hydroxyethyl starch, carrageenans, alginates, and agarose,

synthetic polysaccharides including ficoll and carboxymethylated ficoll,

vinyl polymers including poly(acrylic acid), poly(acryl amides), poly(acrylic esters), poly(2-hydroxy ethyl methacrylate), poly(methyl methacrylate), poly(maleic acid), poly-(maleic anhydride), , poly(acrylamide), poly(ethyl-co-vinyl acetate), poly(methacrylic acid), poly(vinylalcohol), poly(vinyl alcohol-co-vinyl chloroacetate), aminated poly(vinyl alcohol), and co block polymers thereof,

poly ethylene glycol (PEG) or polypropylene glycol or poly(ethylene oxide-co-propylene oxides) containing polymer backbones including linear, comb-shaped or StarBurst™ dendrimers,

poly amino acids including polylysines, polyglutamic acid, polyurethanes, poly(ethylene imines), pluriol.

proteins including albumins, immunoglobulins, and virus-like proteins (VLP), and

polynucleotides, DNA, PNA, LNA, oligonucleotides and oligonucleotide dendrimer constructs.

35. The MHC complex according to any one of items 1-34, wherein the carrier is a soluble carrier.

36. The MHC complex according to any one of items 1-35 in soluble form.

37. The MHC complex according to any one of items 1-36 immobilised onto a solid or semi-solid support.

38. The MHC complex according to item 37, immobilised directly to the solid or semi-solid support.

39. The MHC complex according to item 37, immobilised to the solid or semi-solid support via a linker, a spacer, or an antibody, an antibody derivative or a fragment therof.

40. The MHC complex according to any one of items 37-39, wherein the support is selected from 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, and chips.

41. The MHC complex according to item 40, wherein the support is selected from beads and particles.

42. The MHC complex according to item 41, wherein the beads and particles are polymeric beads, polymeric particles, magnetic beads, magnetic particles, supermagnetic beads, or supermagnetic particles.

43. The MHC complex according to any one of items 1-42 for use in a flow cytometric method.

44. The MHC complex according to any one of items 1-42 for use in a histological method.

45. The MHC complex according to any one of items 1-42 for use in a cytological method.

46. A method for detecting the presence of MHC recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex according to items 1-42, and
(c) determining any binding of the MHC complex, which binding indicates the presence of MHC recognising cells.

47. A method for monitoring MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex according to items 1-42, and
(c) determining any binding of the MHC complex, thereby monitoring MHC recognising cells.

48. A method for establishing a prognosis of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex according to items 1-42, and
(c) determining any binding of the MHC complex, thereby establishing a prognosis of a disease involving MHC recognising cells.

49. A method for determining the status of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex according to items 1-42, and
(c) determining any binding of the MHC complex, thereby determining the status of a disease involving MHC recognising cells.

50. A method for diagnosing a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells,
(b) contacting the sample with a MHC complex according to items 1-42, and
(c) determining any binding of the MHC complex, thereby diagnosing a disease involving MHC recognising cells.

51. A method for determining the effectiveness of a medicament against a disease involving MHC 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 complex according to items 1-42, and
(c) determining any binding of the MHC complex, thereby determining the effectiveness of the medicament.

52. The method according to any one of items 46-51, wherein the MHC recognising cells are involved in a disease of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft versus host and host versus graft) origin.

53. The method according to item 52, wherein the disease is a chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostatic cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis, AIDS, measles, pox, chicken pox, rubella or herpes.

54. The method according to any one of items 46-53, wherein the MHC recognising cells selected from subpopulations of CD3+ T-cells, gamma,delta T-cells, alpha,beta T-cells, CD4+ T-cells, T helper cels, CD8+ T-cells, Suppressor T-cells, CD8+ cytotoxic T-cells, CTLs, NK cells, NKT cells, LAK cells, and MAK.

55. The method according to any one of items 46-51, wherein the sample is selected from histological material, cytological material, primary tumours, secondary organ metastasis, fine needle aspirates, spleen tissue, bone marrow specimens, cell smears, exfoliative cytological specimens, touch preparations, oral swabs, laryngeal swabs, vaginal swabs, bronchial lavage, gastric lavage, from the umbilical cord, and from body fluids such as blood (e.g. from a peripheral blood mononuclear cell (PBMC) population isolated from blood or from other blood-derived preparations such as leukopheresis products), from sputum samples, expectorates, and bronchial aspirates.

56. The method according to any one of items 46-55, wherein the determination of the binding is carried out by inspection in a microscope, by light, by fluorescence, by electron transmission, or by flow cytometry.

57. The method according to any one of items 46-56, wherein the sample is mounted on a support.

58. The method according to item 57, wherein the support is a solid or semi-solid support.

59. The method according to item 57 or 58, wherein the support is selected from glass slides, microtiter plates having one or more wells, beads, particles, membranes, filters, filter membranes, polymer slides, polymer membranes, chamber slides, dishes, and petridishes.

60. A composition comprising a MHC complex according to any one of items 1-42 in a solubilising medium.

61. The composition according to item 60, wherein the MHC complex comprises peptide filled MHC molecules.

62. The composition according to item 60, wherein the MHC complex comprises peptide free MHC molecules.

63. The composition according to item 62, wherein peptides to fill the peptide free MHC molecules, and the MHC complex comprising peptide free molecules are provided separately.

64. A composition comprising a MHC complex according to any one of items 1-42, wherein the MHC complex is immobilised onto a solid or semi-solid support.

65. The composition according to item 64, wherein the support is selected from glass slides, microtiter plates having one or more wells, beads, particles, membranes, filters, filter membranes, polymer slides, polymer membranes, chamber slides, dishes, and petridishes.

66. The composition according to item 64 or 65, wherein the beads and particles are polymeric beads, polymeric particles, magnetic beads, magnetic particles, supermagnetic beads, or supermagnetic particles.

67. The composition according to item 64, wherein the MHC complex comprises peptide filled MHC molecules.

68. The composition according to item 64, wherein the MHC complex comprises peptide free MHC molecules.

69. The composition according to item 68, wherein peptides to fill the peptide free MHC molecules, and the MHC complex comprising peptide free molecules are provided separately.

70. Use of a MHC complex according to any one of items 1-42 as a detection system.

71. Use of a MHC complex according to any one of items 1-42 for diagnosing a disease involving MHC recognising cells.

72. Use of a MHC complex according to any one of items 1-42 for monitoring a disease involving MHC recognising cells.

73. Use of a MHC complex according to any one of items 1-42 for establishing a prognosis for a disease involving MHC recognising cells.

74. Use of a MHC complex according to any one of items 1-42 for determining the status of a disease involving MHC recognising cells.

75. Use of a MHC complex according to any one of items 1-42 for determining the effectiveness of a medicament against a disease involving MHC recognising cells.

76. Use according to any one of items 71, wherein the the MHC recognising cells are involved in a disease of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft-versus-host and host-versus-graft) origin.

77. Use according to item 76, wherein the disease is a chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal

carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostatic cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis, AIDS, measles, pox, chicken pox, rubella or herpes.

78. Use according to any one of items 70-77, wherein the MHC recognising cells are selected from subpopulations of CD3+ T-cells, gamma,delta T-cells, alpha,beta T-cells, CD4+ T-cells, T helper cels, CD8+ T-cells, Suppressor T-cells, CD8+ cytotoxic T-cells, CTLs, NK cells, NKT cells, LAK cells, and MAK.

79. The MHC complex according to any one of items 1-42 for use as a therapeutic composition.

80. The MHC complex according to any one of items 1-42 for use in in vivo therapy.

81. The MHC complex according to any one of items 1-42 for use in ex vivo therapy.

82. A therapeutic composition comprising as active ingredient a MHC complex as defined in any one of items 1-42.

83. The therapeutic composition according to item 82, wherein the MHC complex is immobilised to a biodegradable solid or semi-solid support.

84. The therapeutic composition according to item 82 or 83, wherein the MHC complex comprises

a carrier having attached thereto one or more MHC molecules, said MHC molecules being attached to the carrier either directly or via one or more binding entities.

85. The therapeutic composition according to item 82 or 83, wherein the MHC molecule is a vertebrate MHC molecule such as a human, a murine, a rat, a porcine, a bovine or an avian molecule.

86. The therapeutic composition according to any one of items 82-85, wherein the MHC molecule is a human MHC molecule.

87. The therapeutic composition according to any one of items 82-86, wherein the MHC molecule is

a MHC Class I molecule selected from the group consisting of a heavy chain, a heavy chain combined with a β_2m, a heavy chain combined with a peptide, and a heavy chain/$\square_2$m dimer with a peptide;

or a MHC Class II molecule selected from the group consisting of an α/β dimer, an α/β dimer with a peptide, α/β dimer combined through an affinity tag and a α/β dimer combined through an affinity tag with a peptide

or a MHC Class I like molecule or a MHC Class II like molecule.

88. The therapeutic composition according to any one of items 82-87, wherein the MHC molecule is a peptide free MHC molecule.

89. The therapeutic composition according to any one of items 82-88, wherein at least two of the MHC molecules are different.

90. The therapeutic composition according to any one of items 82-88, wherein the MHC molecules are the same.

91. The therapeutic composition according to any one of items 82-88, wherein at least two of the peptides harboured by the MHC molecules are different.

92. The therapeutic composition according to any one of items 82-88, wherein the peptides harboured by the MHC molecules are the same.

93. The therapeutic composition according to any one of items 82-92, wherein the MHC molecules are attached to the carrier directly.

94. The therapeutic composition according to any one of items 82-92, wherein the MHC molecules are attached to the carrier via one or more binding entities.

95. The therapeutic composition according to item 94, wherein each binding entity has attached thereto from 1 to 10 MHC molecules.

96. The therapeutic composition according to item 94, wherein each binding entity has attached thereto from 1 to 8 MHC molecules.

97. The therapeutic composition according to item 94, wherein each binding entity has attached thereto from 1 to 6 MHC molecules.

98. The therapeutic composition according to item 94, wherein each binding entity has attached thereto from 1 to 4 MHC molecules.

99. The therapeutic composition according to item 94, wherein each binding entity has attached thereto from 1 to 3 MHC molecules.

100. The therapeutic composition according to item 94, wherein each binding entity has attached thereto 1 or 2 MHC molecules.

101. The therapeutic composition according to any one of items 82-100, wherein the total number of MHC molecules of the construct is from 1 to 100.

102. The therapeutic composition according to any one of items 82-100, wherein the total number of MHC molecules of the construct is from 1 to 50.

103. The therapeutic composition according to any one of items 82-100, wherein the total number of MHC molecules of the construct is from 1 to 25.

104. The therapeutic composition according to item 94, wherein the binding entity is selected from 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).

105. The therapeutic composition according to any one of items 82-104 further comprising one or more biologically active molecules.

106. The therapeutic composition according to item 105, wherein the biologically active molecules is selected from proteins, co-stimulatory molecules, cell modulating molecules, receptors, accessory molecules, adhesion molecules, natural ligands, and toxic molecules, and
antibodies and recombinant binding molecules thereto, and
combinations thereof.

107. The therapeutic composition according to item 105 or 106, wherein the biologically active molecule is attached to the carrier either directly or via one or more of the binding entities.

108. The therapeutic composition according to any one of items 105-107, wherein the biologically active molecule is 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 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 antibodies thereto, or antibody derivatives or fragments thereof, and combinations thereof.

109. The therapeutic composition according to any one of items 82-108, wherein the carrier is selected from

polysaccharides including dextrans, carboxy methyl dextran, dextran polyaldehyde, carboxymethyl dextran lactone, and cyclodextrins,

pullulans, schizophyllan, scleroglucan, xanthan, gellan, O-ethylamino guaran, chitins and chitosans indlucing 6-O-carboxymethyl chitin and N-carboxymethyl chitosan,

derivatised cellolosics including carboxymethyl cellulose, carboxymethyl hydroxyethyl cellulose, hydroxyethyl cellulose, 6-amino-6-deoxy cellulose and O-ethylamine cellulose,

hydroxylated starch, hydroxypropyl starch, hydroxyethyl starch, carrageenans, alginates, and agarose,

synthetic polysaccharides including ficoll and carboxymethylated ficoll,

vinyl polymers including poly(acrylic acid), poly(acryl amides), poly(acrylic esters), poly(2-hydroxy ethyl methacrylate), poly(methyl methacrylate), poly(maleic acid), poly-(maleic anhydride), , poly(acrylamide), poly(ethyl-co-vinyl acetate), poly(methacrylic acid), poly(vinylalcohol), poly(vinyl alcohol-co-vinyl chloroacetate), aminated poly(vinyl alcohol), and co block polymers thereof,

poly ethylene glycol (PEG) or polypropylene glycol or poly(ethylene oxide-co-propylene oxides) containing polymer backbones including linear, comb-shaped or StarBurst™ dendrimers,

poly amino acids including polylysines, polyglutamic acid, polyurethanes, poly(ethylene imines), pluriol.

proteins including albumins, immunoglobulins, and virus-like proteins (VLP), and

polynucleotides, DNA, PNA, LNA, oligonucleotides and oligonucleotide dendrimer constructs.

110. The therapeutic composition according to any one of items 82-109, wherein the carrier is a soluble carrier.

111. The therapeutic composition according to any one of items 82-110 further comprising one or more adjuvants and/or excipients.

112. The therapeutic composition according to item 111, wherein the adjuvant is selected from saponins such as Quil A and Qs-21, oil in water emulsions such as MF59, MPL, PLG, PLGA, aluminium salts, calcium phosphate, water in oil emulsions such as IFA (Freund's incomplete adjuvant) and CFA (Freund's complete adjuvant), interleukins such as IL-1β, IL-2, IL-7, IL-12, and INFγ, Adju-Phos®, glucan, antigen formulation, biodegradable microparticles, Cholera Holotoxin, liposomes, DDE, DHEA, DMPC, DMPG, DOC/Alum Complex, ISCOMs®, muramyl dipeptide, monophosphoryl

lipid A, muramyl tripeptide, and phospatidylethanolamine In a preferred embodiment, the adjuvant is selected from saponins such as Quil A and Qs-21, MF59, MPL, PLG, PLGA, calcium phosphate, and aluminium salts.

113. The therapeutic composition according to item 113, wherein the excipient is selected from diluents, buffers, suspending agents, wetting agents, solubilising agents, pH-adjusting agents, dispersing agents, preserving agents, and/or colorants.

114. The therapeutic composition according to any one of items 82-113 for the treatment, prevention, stabilisation, or alleviation of disease involving MHC recognising cells.

115. The therapeutic composition according to item 114, wherein the MHC recognising cells are involved in a disease of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft versus host and host versus graft) origin.

116. The therapeutic composition according to item 115, wherein the disease is a chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, prostatic cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis, AIDS, measles, pox, chicken pox, rubella or herpes.

117. The therapeutic composition according to any one of items 82-116 formulated for parenteral administration, including intravenous, intramuscular, intraarticular, subcutaneous, intradermal, epicutantous/transdermal, and intraperitoneal administration, for infusion, for oral administration, for nasal administration, for rectal administration, or for topic administration.

118. A therapeutic composition comprising as active ingredient an effective amount of MHC recognising cells, the MHC recognising cells being obtained by

bringing a sample from a subject comprising MHC recognising cells into contact with the MHC complex according to any one of items 1-42, whereby the MHC recognising cells become bound to the MHC complex,

isolating the bound MHC complex and the MHC recognising cells, and

expanding such MHC recognising cells to a clinically relevant number.

119. The therapeutic composition according to item 118, wherein the isolated MHC recognising cells are liberated from the MHC complex prior to expansion.

120. The therapeutic composition according to items 118 or 119, wherein the MHC complex is immobilised onto a solid or semi-solid support.

121. The therapeutic composition according to item 120, wherein the MHC complex is immobilised onto the solid or semi-solid support prior to contact with the sample.

122. The therapeutic composition according to item 120, wherein the MHC complex is immobilised onto the solid or semi-solid support following contact with the sample.

123. The therapeutic composition according to any one of items 118-122, wherein the expansion is carried out in the presence of one or more MHC complexes, optionally one or more biologically active molecules and optionally feeder cells such as dendritic cells or feeder cells.

124. The therapeutic composition according to any one of items 120-123, wherein the MHC complex is immobilised onto the solid or semi-solid support directly.

125. The therapeutic composition according to any one of items 120-124, wherein the MHC complex is immobilised to the solid or semi-solid support via a linker, a spacer, or an antibody, an antibody derivative or a fragment thereof.

126. The therapeutic composition according to any one of items 120-125, wherein the solid or semi-solid support is selected from particles, beads, biodegradable particles, sheets, gels, filters, membranes, fibres, capillaries, needles, microtitre strips, tubes, plates or wells, combs, pipette tips, micro arrays, chips, and microtiter plates having one or more wells.

127. The therapeutic composition according to any one of items 120-126, wherein the solid support is selected from particles and beads.

128. The therapeutic composition according to item 127, wherein the particles and beads are polymeric, magnetic or superparamagnetic.

129. The therapeutic composition according to any one of items 118-128, wherein the isolation is performed by applying a magnetic field or by flow cytometry.

130. The therapeutic composition according to any one of items 118-128, wherein the MHC complex comprises

a carrier having attached thereto one or more MHC molecules, said MHC molecules being attached to the carrier either directly or via one or more binding entities.

131. The therapeutic composition according to any one of items 118-130, wherein the MHC molecule is a vertebrate MHC molecule such as a human, a murine, a rat, a porcine, a bovine or an avian molecule.

132. The therapeutic composition according to any one of items 118-131, wherein the MHC molecule is a human MHC molecule.

133. The therapeutic composition according to any one of items 118-132, wherein the MHC molecule is

a MHC Class I molecule selected from the group consisting of a heavy chain, a heavy chain combined with a β_2m, a heavy chain combined with a peptide, and a heavy chain/β_2m dimer with a peptide;

or a MHC Class II molecule selected from the group consisting of an $\tilde{\alpha}\beta$ dimer, an $\tilde{\alpha}\beta$dimer with a peptide, $\tilde{\beta}\beta$ dimer combined through an affinity tag and a $\tilde{\beta}\beta$ dimer combined through an affinity tag with a peptide;

or a MHC Class I like molecule or a MHC Class II molecule.

134. The therapeutic composition according to any one of items 118-133, wherein the MHC molecule is a peptide free MHC molecule.

135. The therapeutic composition according to any one of items 118-134, wherein at least two of the MHC molecules are different.

136. The therapeutic composition according to any one of items 118-135, wherein the MHC molecules are the same.

137. The therapeutic composition according to any one of items 118-136, wherein at least two of the peptides harboured by the MHC molecules are different.

138. The therapeutic composition according to any one of items 118-137, wherein the peptides harboured by the MHC molecules are the same.

139. The therapeutic composition according to any one of items 118-138, wherein the MHC molecules are attached to the carrier directly.

140. The therapeutic composition according to any one of items 118-138, wherein the MHC molecules are attached to the carrier via one or more binding entities.

141. The therapeutic composition according to item 140, wherein each binding entity has attached thereto from 1 to 10 MHC molecules.

142. The therapeutic composition according to item 140, wherein each binding entity has attached thereto from 1 to 8 MHC molecules.

143. The therapeutic composition according to item 140, wherein each binding entity has attached thereto from 1 to 6 MHC molecules.

144. The therapeutic composition according to item 140, wherein each binding entity has attached thereto from 1 to 4 MHC molecules.

145. The therapeutic composition according to item 140, wherein each binding entity has attached thereto from 1 to 3 MHC molecules.

146. The therapeutic composition according to item 140, wherein each binding entity has attached thereto 1 or 2 MHC molecules.

147. The therapeutic composition according to any one of items 118-146, wherein the total number of MHC molecules of the construct is from 1 to 100.

148. The therapeutic composition according to any one of items 118-146, wherein the total number of MHC molecules of the construct is from 1 to 50.

149. The therapeutic composition according to any one of items 118-146, wherein the total number of MHC molecules of the construct is from 1 to 25.

150. The therapeutic composition according to item 140, wherein the binding entity is selected from streptavidin 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).

151. The therapeutic composition according to any one of items 118-150 further comprising one or more biologically active molecules.

152. The therapeutic composition according to item 151, wherein the biologically active molecules is selected from proteins, co-stimulatory molecules, cell modulating molecules, receptors, accessory molecules, adhesion molecules, natural ligands, and toxic molecules, and
antibodies and recombinant binding molecules thereto, and
combinations thereof.

153. The therapeutic composition according to item 150 or 151, wherein the biologically active molecule is attached to the carrier either directly or via one or more of the binding entities.

154. The therapeutic composition according to any one of items 151-153, wherein the biologically active molecule is 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 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 antibodies thereto, or antibody derivatives or fragments thereof, and combinations thereof.

155. The therapeutic composition according to any one of items 118-154, wherein the carrier is selected from

polysaccharides including dextrans, carboxy methyl dextran, dextran polyaldehyde, carboxymethyl dextran lactone, and cyclodextrins,

pullulans, schizophyllan, scleroglucan, xanthan, gellan, O-ethylamino guaran, chitins and chitosans indlucing 6-O-carboxymethyl chitin and N-carboxymethyl chitosan,

derivatised cellolosics including carboxymethyl cellulose, carboxymethyl hydroxyethyl cellulose, hydroxyethyl cellulose, 6-amino-6-deoxy cellulose and O-ethylamine cellulose,

hydroxylated starch, hydroxypropyl starch, hydroxyethyl starch, carrageenans, alginates, and agarose,

synthetic polysaccharides including ficoll and carboxymethylated ficoll,

vinyl polymers including poly(acrylic acid), poly(acryl amides), poly(acrylic esters), poly(2-hydroxy ethyl methacrylate), poly(methyl methacrylate), poly(maleic acid), poly-(maleic anhydride), , poly(acrylamide), poly(ethyl-co-vinyl acetate), poly(methacrylic acid), poly(vinylalcohol), poly(vinyl alcohol-co-vinyl chloroacetate), aminated poly(vinyl alcohol), and co block polymers thereof,

poly ethylene glycol (PEG) or polypropylene glycol or poly(ethylene oxide-co-propylene oxides) containing polymer backbones including linear, comb-shaped or StarBurst™ dendrimers,

poly amino acids including polylysines, polyglutamic acid, polyurethanes, poly(ethylene imines), pluriol.

proteins including albumins, immunoglobulins, and virus-like proteins (VLP), and

polynucleotides, DNA, PNA, LNA, oligonucleotides and oligonucleotide dendrimer constructs.

156. The therapeutic composition according to any one of items 118-155 further comprising one or more labelling compounds.

157. The therapeutic composition according to item 156, wherein one or more labelling compounds are attached to the carrier.

158. The therapeutic composition according to item 156, wherein one or more labelling compounds are attached to one or more of the binding entities.

159. The therapeutic composition according to item 156, wherein one or more labelling compounds are attached to the one or more MHC molecules.

160. The therapeutic composition according to item 156, wherein one or more labelling compounds are attached to the carrier and/or one or more of the binding entities and/or one or more of the MHC molecules.

161. The therapeutic composition according to any one of items 156-160, wherein the labelling compound is directly or indirectly detectable.

162. The therapeutic composition according to any one of items 156-161, wherein the labelling compound is a fluorescent label, an enzyme label, a radioisotope, a chemiluminescent label, a bioluminescent label, a polymer, a metal particle, a hapten, an antibody, or a dye.

163. The therapeutic composition according to any one of items 156-162, wherein the labelling compound

is selected from fluorescent labels such as 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+,

from haptens such as DNP, biotin, and digoxiginin, or

is selected from haptens such as DNP, fluorescein isothiocyanate (FITC), biotin, and digoxiginin, or

is selected from enzymatic labels such as 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), or

is selected from luminiscence labels such as luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines, or

is selected from radioactivity labels such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor.

164. The therapeutic composition according to any one of items 118-163, wherein the carrier is a soluble carrier.

165. The therapeutic composition according to any one of items 118-164 further comprising one or more excipients.

166. The therapeutic composition according to items 165, wherein the excipient is selected from diluents, buffers, suspending agents, wetting agents, solubilising agents, pH-adjusting agents, dispersing agents, preserving agents, and/or colorants.

167. The therapeutic composition according to any one of items 118-166 for the treatment, prevention, stabilisation, or alleviation of a disease involving MHC recognising cells.

168. The therapeutic composition according to item 167, wherein MHC recognising cells are involved in a disease of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft versus host and host versus graft) origin.

169. The therapeutic composition according to item 167 or 168, wherein the disease is a chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, prostatic cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis, AIDS, measles, pox, chicken pox, rubella or herpes.

170. The therapeutic composition according to any one of items 118-169 formulated for parenteral administration, including intravenous, intramuscular, intraarticular, subcutaneous, intradermal, epicutantous/transdermal, and intraperitoneal administration, for infusion, for oral administration, for nasal administration, for rectal administration, or for topic administration.

171. The therapeutic composition according to any one of items 82-170 for use in in vivo therapy.

172. A method of treating an animal, including a human being, comprising administering a therapeutic composition according to any one of items 82-170 in an effective amount.

173. A method of up-regulating, down-regulating, modulate an immune response in an animal, including a human being, comprising administering a therapeutic composition according to any one of items 82-170 in an effective amount.

174. A method of inducing anergy of a cell in an animal, including a human being, comprising administering a therapeutic composition according to any one of items 82-170 in an effective amount.

175. An adoptive cellular immunotherapeutic method comprising administrating to an animal, including a human being, a therapeutic composition according to any one of items 82-170.

176. A method of obtaining MHC recognising cells comprising

bringing into contact a MHC complex according to any one of items 1-42 and a sample suspected of comprising MHC recognising cells under conditions whereby the MHC recognising cells bind to the MHC complex, and
isolating the bound MHC complex and MHC recognising cells.

177. The method according to item 176, wherein the isolation is carried out by applying a magnetic field or by flow cytometry.

178. A method for producing a therapeutic composition according to any one of items 82-170, comprising

providing a MHC complex as defined in items 1-42,
solubilising or dispersing the MHC complex in a medium suitable for therapeutic substances, and optionally adding other adjuvants and/or excipients.

179. A method for producing a therapeutic composition according to any one of items 118-170, comprising

obtaining MHC recognising cells using a MHC complex according to any one of items 1-42,
expanding such MHC recognising cells to a clinically relevant number,
formulating the obtained cells in a medium suitable for administration, and
optionally adding adjuvants and/or excipients.

180. Use of a MHC complex according to any one of items 1-42 for ex vivo expansion of MHC recognising cells.

181. Use according to item 180, wherein the MHC complex is in soluble form.

182. Use according to item 180, wherein the MHC complex is immobilised onto a solid or semi-solid support.

183. Use according to item 182, wherein the solid or semi-solid support is selected from 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, and slides.

184. Use according to item 182 or 183, wherein the solid or semi-solid support is selected from beads and particles.

185. Use according to item 184, wherein the solid or semi-solid support is selected from polymeric, magnetic or superparamagnetic particles and beads.

186. Use according to any one of items 180-185, wherein the MHC complex further comprises one or more biologically active molecules.

187. Use according to any one of items 180-186, wherein wherein the biologically active molecule is 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 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 antibodies thereto, or antibody derivatives or fragments thereof, and combinations thereof.

187. Use of a MHC molecule in a histological method.

188. Use of a MHC molecule in a cytological method.

189. Use of a MHC molecule according to item 187 or 188 in a method for determining the presence of MHC recognising cells in a sample, in which method the MHC recognising cells of the sample are mounted on a support.

190. Use of a MHC molecule according to item 187 or 188, in a method for monitoring the presence of MHC recognising cells in a sample, in which method the MHC recognising cells of the sample are mounted on a support.

191. Use of a MHC molecule according to item 187 or 188 in a method for determining the status of a disease involving MHC recognising cells, in which method the MHC recognising cells of the sample are mounted on a support.

192. Use of a MHC molecule according to item 187 or 188 in a method for establishing a prognosis of a disease involving MHC recognising cells, in which method the MHC recognising cells of the sample are mounted on a support.

193. Use of a MHC molecule according to any one of items 187-192, wherein the support is a solid or semi-solid support.

194. Use of a MHC molecule according to any one of items 187-193, wherein the support is selected from glass slides, membranes, filters, polymer slides, chamber slides, dishes, and petridishes.

195. Use according to any one of items 187-194, wherein the sample is selected from histological material, cytological material, primary tumours, secondary organ

metastasis, fine needle aspirates, spleen tissue, bone marrow specimens, cell smears, exfoliative cytological specimens, touch preparations, oral swabs, laryngeal swabs, vaginal swabs, bronchial lavage, gastric lavage, from the umbilical cord, and from body fluids such as blood (e.g. from a peripheral blood mononuclear cell (PBMC) population isolated from blood or from other blood-derived preparations such as leukopheresis products), from sputum samples, expectorates, and bronchial aspirates.

196. The use according to any one of items 187-195, wherein the MHC molecule is

a MHC Class I molecule selected from the group consisting of a heavy chain, a heavy chain combined with a β_2m, a heavy chain combined with a peptide, and a heavy chain/β_2m dimer with a peptide;

or a MHC Class II molecule selected from the group consisting of an α/β dimer, an α/β dimer with a peptide, α/β dimer combined through an affinity tag and a α/β dimer combined through an affinity tag with a peptide;

or a MHC Class I like molecule or a MHC Class II like molecule.

197. The use according to any one of items 187-196, wherein the MHC molecule is a vertebrate MHC molecule such as a human, a murine, a rat, a porcine, a bovine or an avian molecule.

198. The use according to any one of items 187-197, wherein the MHC molecule is a human MHC molecule.

199. The use according to any one of items 187-198, wherein the MHC molecule is a peptide free MHC molecule.

200. The use according to any one of items 187-199, wherein the MHC molecule is attached to a binding entity.

201. Use according to item 200, wherein the binding entity has attached thereto from 1 to 10 MHC molecules, such as from 1 to 9, from 1 to 8, from 1 to 7, from 1 to 6, from 1 to 5, from 1 to 4, from 1 to 3, or 1 or 2 MHC molecules.

202. Use according to item 200, wherein the binding entity is selected from streptavidin 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).

203. Use according to any one of items 187-202, wherein the MHC molecule further comprises a labelling compound.

204. Use according to item 203, wherein the labelling compound can be detected directly or indirectly.

205. Use according to item 203 or 204, wherein the labelling compound is a fluorescent label, an enzyme label, a radioisotope, a chemiluminescent label, a bioluminescent label, a polymer, a metal particle, a hapten, an antibody, or a dye.

206. Use according to any one of items 203-205, wherein the labelling compound is selected from

5-(and 6)-carboxyfluorescein, 5- or 6-carboxyfluorescein, 6-(fluorescein)-5-(and 6)-carboxamido hexanoic acid, fluorescein isothiocyanate (FITC), rhodamine, tetramethyl-rhodamine, and dyes such as Cy2, Cy3, and Cy5, optionally substituted coumarin including AMCA, PerCP, phycobiliproteins including R-phycoerythrin (RPE) and allophycoerythrin (APC), Texas Red, Princeton 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,, or

is selected from enzymatic labels such as 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), or

is selected from luminiscence labels such as luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines, or

is selected from radioactivity labels such as incorporated isotopes of iodide, cobalt, selenium, tritium, and phosphor.

207. The use according to any one of items 203-206, wherein the labelling compound is attached to the MHC molecule and/or the binding entity.

208. A method for detecting the presence of MHC recognising cells in a sample comprising the steps of

(a) providing a sample suspected of comprising MHC recognising cells mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, which binding indicates the presence of MHC recognising cells.

209. A method for monitoring MHC recognising cells comprising the steps of

(a) providing a sample suspected comprising MHC recognising cells mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, thereby monitoring MHC recognising cells.

210. A method for the prognosis of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected comprising MHC recognising cells mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, thereby establishing a prognosis of a disease involving MHC recognising cells.

211. A method for determining the status of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected comprising MHC recognising cells mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, thereby determining the status of a disease involving MHC recognising cells.

212. A method for the diagnosis of a disease involving MHC recognising cells comprising the steps of

(a) providing a sample suspected comprising MHC recognising cells mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, thereby diagnosing a disease involving MHC recognising cells.

213. A method for the effectiveness of a medicament against a disease involving MHC recognising cells comprising the steps of

(a) providing a sample from a subject receiving treatment with a medicament mounted on a support,
(b) contacting the sample with a MHC molecule as defined in items 187-207, and
(c) determining any binding of the MHC molecule, thereby determining the effectiveness of the medicament.

214. The method according to any one of items 208-213, wherein the MHC recognising cells are involved in a disease of inflammatory, auto-immune, allergic, viral, cancerous, infectious, allo- or xenogene (graft-versus-host and host-versus-graft) origin.

215. The method according to item 214, wherein the disease is a chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostatic cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis, AIDS, measles, pox, chicken pox, rubella or herpes.

216. The method according to any one of items 208-214, wherein the MHC recognising cells are selected from subpopulations of CD3+ T-cells, gamma,delta T-cells, alpha,beta T-cells, CD4+ T-cells, T helper cels, CD8+ T-cells, Suppressor T-cells, CD8+ cytotoxic T-cells, CTLs, NK cells, NKT cells, LAK cells, and MAK.

217. The method or use according to any one of items 201-216, wherein the sample is selected from histological material, cytological material, primary tumours, secondary organ metastasis, fine needle aspirates, spleen tissue, bone marrow specimens, cell smears, exfoliative cytological specimens, touch preparations, oral swabs, laryngeal swabs, vaginal swabs, bronchial lavage, gastric lavage, from the umbilical cord, and from body fluids such as blood (e.g. from a peripheral blood mononuclear cell (PBMC) population isolated from blood or from other blood-derived preparations such as R

Claims

1. 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 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 $1 < n \geq 100$.

89. The MHC multimer according to claim 1, wherein $1 < n \geq 1000$.

90. The MHC multimer according to claim 1, wherein $n \geq 1{,}000{,}000{,}000$.

91. The MHC multimer according to claim 1, wherein $n \geq 1{,}000{,}000{,}000{,}000{,}000{,}000$ (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 one of the polypeptides 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 2 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 2 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, polyacrylamide 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 2).

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 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 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, and protein kinases.

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 796, wherein the peptide P originates from and/or is isolated from

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 783, 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, respectively.

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 multimeres 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,
ii) providing a population of T cells, and
iii) measuring the number, activity or state of T cells specific for said 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 individual components thereof,
ii) providing a population T cells, and
iii) measuring the number, activity or state T cells specific for said 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 thereof,
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 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 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 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 are determined from the result of the interaction of said MHC multimer with said T cells.

1111. The method of claim 1110 where the result of the interaction of said MHC multimer 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 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 virus.

1234. The method of claims 1231, wherein the infection is caused by a parasite.

1235. The method of claims 1231, wherein the infection is caused by a worm.

1236. The method of claims 1231, wherein the infection is caused by an insect.

1237. The method of claims 1231, wherein the infection is caused by a protozoan.

1238. The method of claims 1231, wherein the infection is caused by a Flagellate.

1239. The method of claims 1231, wherein the infection is caused by Entamoeba histolytica.

1240. The method of claims 1231, wherein the infection is caused by Giardia.

1241. The method of claims 1231, wherein the infection is caused by Trichomonas.

1242. The method of claims 1231, wherein the infection is caused by Leishmania.

1243. The method of claims 1231, wherein the infection is caused by Trypanosomes.

1244. The method of claims 1231, wherein the infection is caused by Trichomonas vaginalis.

1245. The method of claims 1231, wherein the infection is caused by Plasmodium.

1246. The method of claims 1231, wherein the infection is caused by an archaeo.

1247. The method of claims 1231, wherein the infection is caused by a fungus.

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 of transplantation related disease.

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 of the outcome of an organ transplantation in an individual, such as an animal, for example a human being.

1270. The method of any of the claims 1093 to 1095, wherein the outcome of an organ transplantation 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 MHC multimers comprising antigenic peptides from antigens selected from the group consisting of HA-1, HA-8, USP9Y, SMCY, TPR-protein, HB-1Y, GAD64, Collagen, 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, Collagen, human cartilage glycoprotein 39, beta-amyloid, Abeta42, APP, Presenilin 1.

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, and

administering said MHC monomer or MHC multimer 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 the MHC multimer is administered alone to said individual.

1279. The method according to claim 1277, wherein the MHC multimer is administered together with one or more adjuvant(s) to said individual.

1280. The method according to claim 1277, wherein 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 the MHC multimer is administered to said individual cutaneously.

1282. The method according to claim 1277, wherein the MHC multimer is administered to said individual subcutaneously (SC).

1283. The method according to claim 1277, wherein the MHC multimer is administered to said individual by intramuscular (IM) administration.

1284. The method according to claim 1277, wherein the MHC multimer is administered to said individual by intravenous (IV) administration.

1285. The method according to claim 1277, wherein the MHC multimer is administered to said individual by Per-oral (PO) administration.

1286. The method according to claim 1277, wherein the MHC multimer is administered to said individual inter peritoneally.

1287. The method according to claim 1277, wherein the MHC multimer is administered to said individual pulmonally.

1288. The method according to claim 1277, wherein the MHC multimer is administered to said individual vaginally.

1289. The method according to claim 1277, wherein 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 immune monitoring one or more cancer diseases comprising the step of monitoring one or more cancer antigen specific T-cells, said method comprising the steps of

providing a MHC monomer or MHC multimer, or individual components thereof, according to any of the claims 1 to 797,

providing a population of cancer antigen specific T cells, or individual cancer antigen specific T cells, and

measuring the number and/or presence of cancer antigen specific T cells specific for the peptide P of the MHC monomer or MHC multimer, thereby immune monitoring said one or more cancer diseases.

1293. A method for diagnosing one or more cancer diseases comprising immune monitoring of cancer antigen specific T cells, said method comprising the steps of

providing the MHC multimer or individual components thereof according to any of the claims 1 to 797,

providing a population of cancer antigen specific T cells, or individual cancer antigen specific T cells, and

measuring the number and/or presence of T cells specific for the peptide P of the MHC monomer or MHC multimer, thereby diagnosing said one or more cancer diseases.

1294. The method of any of claims 1292 and 1293, wherein the monitoring of antigen specific T cells comprises detection of antigen specific T cells specific for the peptide P of the MHC multimer.

1295. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises counting of antigen specific T cells specific for the peptide P of the MHC multimer.

1296. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises sorting of antigen specific T cells specific for the peptide P of the MHC multimer.

1297. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises isolation of antigen specific T cells specific for the peptide P of the MHC multimer.

1298. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises flow cytometry.

1299. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises ELISPOT.

1300. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises LDA.

1301. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises QUantaferon-like analysis.

1302. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises IHC.

1303. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises LDA.

1304. The method of any of claims 1292 and 1293, wherein the measurement of antigen specific T cells comprises microscopy.

1305. The method of any of the claims 1292 and 1293, wherein the method comprises one or more marker molecules in addition to the MHC multimer.

1306. The method of claim 1305, wherein the one or more marker molecules comprises one or more antibodies and/or antibody fragments.

1307. The method of claim 1305, wherein the one or more marker molecules comprises one or more aptamers.

1308. The method of claim 1305, wherein the one or more marker molecules comprises one or more proteins.

1309. The method of claim 1305, wherein the one or more marker molecules comprises one or more peptides.

1310. The method of claim 1305, wherein the one or more marker molecules comprises one or more small organic molecules.

1311. The method of claim 1305, wherein the one or more marker molecules comprises one or more natural compounds such as one or more steroids.

1312. The method of claim 1305, wherein the one or more marker molecules comprises one or more non-peptide polymers.

1313. The method of any of the claims 1292 and 1293, wherein the method comprises one or more labelling molecules.

1314. The method of claim 1313, wherein the one or more labelling molecules comprises one or more labelling molecules that results in directly detectable T cells.

1315. The method of claim 1313, wherein the one or more labelling molecules comprises one or more labelling molecules that results in indirectly detectable T cells.

1316. The method of claim 1313, wherein the one or more labelling molecules are attached via one or more linkers.

1317. The method of claim 1313, wherein the one or more labelling molecules comprises one or more fluorescent labels.

1318. The method of claim 1317, 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+.

1319. The method of claim 1313, wherein the one or more labelling molecules comprises one or more enzyme labels.

1320. The method of claim 1319, 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),

1321. The method of claim 1313, wherein the one or more labelling molecules comprises one or more radioisotopes.

1322. The method of claim 1321, wherein the one or more radioisotopes can be selected from the group consisting of isotopes of iodide, cobalt, selenium, tritium, and/or phosphor.

1323. The method of claim 1313, wherein the one or more labelling molecules comprises one or more chemiluminescent labels.

1324. The method of claim 1313, wherein the one or more labelling molecules comprises one or more luminescent labels.

1325. The method of claim 1324, wherein the one or more luminescent labels can be selected from the group consisting of luminol, isoluminol, acridinium esters, 1,2-dioxetanes and pyridopyridazines.

1326. The method of claim 1313, wherein the one or more labelling molecules comprises one or more polymers.

1327. The method of claim 1313, wherein the one or more labelling molecules comprises one or more metal particles.

1328. The method of claim 1313, wherein the one or more labelling molecules comprises one or more haptens.

1329. The method of claim 1328, wherein the one or more haptens can be selected from the group consisting of DNP, biotin, and digoxiginin.

1330. The method of claim 1313, wherein the one or more labelling molecules comprises one or more antibodies.

1331. The method of claim 1313, wherein the one or more labelling molecules comprises one or more dyes.

1332. The method of any of the claims 1292 and 1293, wherein the method comprises flow cytometry or flow cytometry-like analysis.

1333. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of TCRs attached to a lipid bilayer.

1334. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more individual T cells in a fluid sample.

1335. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more populations of T cells in a fluid sample.

1336. The method of claim 1335, where in the direct detection of one or more individual T cells in a fluid sample comprises flow cytometry.

1337. The method of claim 1335, where in the direct detection of one or more populations of T cells in a fluid sample comprises flow cytometry.

1338. The method of claim 1335, where in the direct detection of one or more individual T cells in a fluid sample comprises microscopy.

1339. The method of claim 1335, where in the direct detection of one or more populations of T cells in a fluid sample comprises microscopy.

1340. The method of claim 1335, 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.

1341. The method of claim 1335, 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.

1342. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more individual immobilized T cells.

1343. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more populations of immobilized T cells.

1344. The method of claim 1342, 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.

1345. The method of claim 1343, 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.

1346. The method of claim 1342, wherein the immobilization of one or more individual T cells are directly immobilized on the solid support.

1347. The method of claim 1343, wherein the immobilization of one or more populations of T cells are directly immobilized on the solid support.

1348. The method of claim 1342, wherein the immobilization of one or more individual T cells are directly immobilized through a linker on the solid support.

1349. The method of claim 1342, wherein the immobilization of one or more individual T cells are directly immobilized through a linker on the solid support.

1350. The method of any of the claims 1292 and 1293, wherein the direct detection of one or more individual immobilized T cells comprises phenotyping a T cell sample using MHC multimer beads.

1351. The method of any of the claims 1292 and 1293, wherein the direct detection of one or more populations of immobilized T cells comprises phenotyping a T cell sample using MHC multimer beads.

1352. The method of any of the claims 1292 and 1293, 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.

1353. The method of any of the claims 1292 and 1293, 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.

1354. The method of any of claims 1350 to 1353, wherein the direct detection of one or more individual immobilized T cells is followed by sorting of said T cells.

1355. The method of any of claims 1350 to 1353, wherein the direct detection one or more populations of immobilized T cells is followed by sorting of said T cells.

1356. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more individual T cells in a solid tissue either in vitro or in vivo.

1357. The method of any of the claims 1292 and 1293, wherein the method comprises direct detection of one or more populations of T cells in a solid tissue either in vitro or in vivo.

1358. The method of any of the claims 1292 to 1293, wherein the method comprises indirect detection of one or more populations of T cells in a sample.

1359. The method of any of the claims 1292 to 1293, wherein the method comprises indirect detection of one or more individual T cells in a sample.

1360. The method of any of the claims 1292 to 1293, wherein the method comprises indirect detection of one or more individual T cells in a sample by measurement of activation.

1361. The method of any of the claims 1292 to 1293, wherein the method comprises indirect detection of one or more populations of T cells in a sample by measurement of activation.

1362. The method of claims 1359 and 1360, wherein the indirect detection of one or more individual T cells in a sample comprises measurement of secretion of soluble factors.

1363. The method of claims 1358 and 1361, wherein the indirect detection of one or more populations of T cells in a sample comprises measurement of secretion of soluble factors.

1364. The method of claims 1362 and 1363, wherein the measurement of secretion of soluble factors comprises measurement of extracellular secreted soluble factors.

1365. The method of claim 1364, wherein the measurement of extracellular secreted soluble factors comprises analysis of a fluid sample.

1366. The method of claim 1364, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells by capture of extracellular secreted soluble factor on a solid support.

1367. The method of claim 1364, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells immobilized to solid support in a defined pattern.

1368. The method of claim 1364, wherein the measurement of extracellular secreted soluble factors comprises detection of T cells by measurement of effect of extracellular secreted soluble factor.

1369. The method of claim 1363, wherein the measurement of secretion of soluble factors comprises measurement of intracellular secreted soluble factors.

1370. The method of 1362, wherein the indirect detection of individual or populations of T cells in a sample comprises measurement of expression of one or more receptors.

1371. The method of 1362, wherein the indirect detection of individual or populations of T cells in a sample comprises measurement of T cell effector function.

1372. The method of any of the claims 1292 to 1293, wherein the method comprises indirect detection of individual or populations of T cells in a sample by measurement of T cell proliferation.

1373. The method of any of the claims 1292 to 1293, 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.

1374. The method of any of the claims 1292 to 1293, wherein the method comprises immunohistochemistry or immunohistochemistry-like analysis.

1375. The method of any of claims 1292 and 1293, wherein the method comprises ELISA or ELISA-like analysis.

1376. The method of any of the claims 1292 to 1293, wherein the antigen specific T cells are isolated using MHC multimers immobilized on a solid surface.

1377. The method of claim 1376, wherein the solid phase is beads.

1378. The method of claim 1376, wherein the solid phase is immunotubes.

1379. The method of claim 1376, wherein the solid phase is microtiter plates.

1380. The method of claim 1376, wherein the solid phase is microchips.

1381. The method of claim 1376, wherein the solid phase is microarrays.

1382. The method of claim 1376, wherein the solid phase is test strips.

1383. The method of any of the claims 1292 to 1293, wherein the method comprises blocking of the sample with a protein solution such as BSA or skim milk.

1384. The method of any of the claims 1292 to 1293, wherein the method comprises blocking of the MHC multimer with a protein solution such as BSA or skim milk.

1385. The method of any of the claims 1292 to 1293, wherein the method comprises mixing of MHC multimer coated beads with the cell sample.

1386. The method of any of the claims 1292 to 1293, wherein the method comprises incubation of MHC multimer coated beads with the cell sample.

1387. The method of any of the claims 1292 to 1293, wherein the method comprises a washing step after incubation of MHC multimer coated beads with the cell sample.

1388. The method of any of the claims 1292 to 1293, wherein the method comprises release of the immobilized T cells from the beads.

1389. The method of claim 1388, wherein the T cells are released by cleavage of the linker.

1390. The method of claim 1388, wherein the T cells are released by changing the pH.

1391. The method of claim 1388, wherein the T cells are released by changing the salt concentration.

1392. The method of claim 1388, wherein the T cells are released by addition of one or more competitive binders.

1393. The method of claim 1388, wherein the T cells are released by a method that does not disrupts the integrity of the cells.

1394. The method of any of the claims 1292 to 1293, wherein the method comprises manipulation of the T cells after release from the beads.

1395. The method of claim 1394, wherein the manipulation is induction of apoptosis.

1396. The method of claim 1394, wherein the manipulation is induction of proliferation.

1397. The method of claim 1394, wherein the manipulation is induction of differentiation.

1398. The method of any of the claims 1292 to 1293, 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.

1399. The method of any of the claims 1292 to 1293, 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.

1400. The method of any of the claims 1292 to 1293, wherein the sample to be analysed is acquired from cell suspensions derived from tissue samples or cell lines.

1401. The method of claims 1292 to 1293 for use in diagnosis of cancer.

1402. The method of any of the claims 1292 to 1293 for use in monitoring a cancer vaccine response.

1403. The method of any of the claims 1292 to 1293 for use in development of a cancer vaccine.

1404. The method of any of the claims 1292 to 1293, wherein T cells are specific for cancer antigens are detected.

1405. The method of any of the claims 1292 to 1293, wherein the method comprises derivatives of MHC multimers.

1406. The method of any of the claims 1292 to 1293, wherein T cells are specific for cancer associated proteins are detected.

1407. The method of claim 1406, wherein the cancer associated proteins comprises 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 and Protein kinases, in relation to clinical manifestations such as 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 and bladder cancer.

1408. A method for performing a cancer vaccination of an individual in need thereof, said method comprising the steps of

providing a MHC monomer or MHC multimer according to any of the claims 1 to 797, and

administering said MHC multimer to said individual, thereby performing a cancer vaccination of the said individual.

1409. The method according to claim 1408, wherein the MHC multimer is administered alone to said individual.

1410. The method according to claim 1408, wherein the MHC multimer is administered together with one or more adjuvant(s) to said individual.

1411. The method according to claim 1408, wherein the MHC multimer is administered to said individual more than once such as twice or three times.

1412. The method according to claim 1408, wherein the MHC multimer is administered to said individual cutaneously.

1413. The method according to claim 1408, wherein the MHC multimer is administered to said individual subcutaneously (SC).

1414. The method according to claim 1408, wherein the MHC multimer is administered to said individual by intramuscular (IM) administration.

1415. The method according to claim 1408, wherein the MHC multimer is administered to said individual by intravenous (IV) administration.

1416. The method according to claim 1408, wherein the MHC multimer is administered to said individual by Per-oral (PO) administration.

1417. The method according to claim 1408, wherein the MHC multimer is administered to said individual inter peritoneally.

1418. The method according to claim 1408, wherein the MHC multimer is administered to said individual pulmonally.

1419. The method according to claim 1408, wherein the MHC multimer is administered to said individual vaginally.

1420. The method according to claim 1408, wherein the MHC multimer is administered to said individual rectally.

1421. The method according to claim 1408, wherein the cancer vaccination is a therapeutic vaccination i.e. vaccination "teaching" the immune system to fight an existing infection or disease.

1422. A method for performing a cancer therapeutic treatment of an individual comprising the steps of

Providing the MHC multimer according to claim 1-797, and

Isolation of T cells specific for said MHC multimer, and

Optionally manipulation of said T cell and

Introduction of said T cells into the same or a different individual to obtain a cancer therapeutic treatment.

1423. A method for minimization of undesired binding of the MHC multimer according to any of the claims 1 to 782.

1424. The method of claim 1423, wherein the method comprises mutagenesis of the MHC multimer.

1425. The method of claim 1424, wherein the method comprises mutagenesis in areas of the MHC multimer responsible for binding to unwanted cells.

1426. The method of claim 1424, wherein the method comprises mutagenesis in the α3-domain of the α-chain of MHC I molecules.

1427. The method of claim 1424, wherein the method comprises mutagenesis in a sub domain in the β2 domain of the β-chain of MHC II molecules.

1428. The method of claim 1424, wherein the method comprises mutagenesis in areas of MHC multimeres 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.

1429. The method of any of the claims 1424 to 1428, wherein the mutation is a substitution.

1430. The method of any of the claims 1424 to 1428, wherein the mutation is an insertion.

1431. The method of any of the claims 1424 to 1428, wherein the mutation is a deletion.

1432. The method of any of the claims 1424 to 1431, wherein the one or more target residues are natural amino acids.

1433. The method of any of the claims 1424 to 1431, wherein the one or more target residues are non-natural amino acids.

1434. The method of any of the claims 1424 to 1431, wherein the target residues are a combination of natural and non-natural amino acids.

1435. The method of any of the claims 1424 to 1434, wherein a single amino acid is mutated.

1436. The method of any of the claims 1424 to 1434, wherein more than one amino acid is mutated.

1437. The method for minimization of undesired binding of the MHC multimer according to claim 1423, wherein the method comprises chemical alterations in the MHC multimer.

1438. The method of claim 1437, wherein the method comprises one or more chemical alterations of surface areas of the MHC multimer responsible for binding to unwanted cells.

1439. The method of claim 1437, wherein the method comprises one or more chemical alterations in the α3-domain of the α-chain of MHC I molecules.

1440. The method of claim 1437, 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.

1441. The method of claim 1437, wherein the method comprises one or more chemical alterations of surface areas of MHC multimeres 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.

1442. The method of any of the claims 1437 to 1441, wherein a single amino acid is altered.

1443. The method of any of the claims 1437 to 1441, wherein more than one amino acid is altered.

1444. The method of claim 1423, wherein the method comprises the addition of one or more components of a MHC multimer, predicted to be responsible for the undesired binding.

1445. The method of claim 1444, wherein the added component is one or more MHC multimers that contain nonsense peptides.

1446. The method of claim 1444, wherein the added component is one or more soluble MHC multimeres not coupled to a multimerization domain, and with or without peptide bound in the peptide binding cleft.

1447. The method of claim 1444, wherein the added component is individual components of the MHC multimer.

1448. The method of claim 1447, 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.

1449. The method of claim 1447, wherein the one or more individual subunits are folded.

1450. The method of claim 1447, wherein the one or more individual subunits are un-folded.

1451. The method of claim 1447, wherein the individual subunits are folded and un-folded.

1452. The method of claim 1447, 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.

1453. The method of claim 1447, 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.

1454. The method of any of the claims 1447 to 1453, wherein the added component is not labelled.

1455. The method of any of the claims 1447 to 1453, wherein the added component is labelled with a label different from the label of the MHC multimer used for analysis.

1456. The method of claim 1423, wherein one or more reagents able to identify specific cell types are included.

1457. The method of claim 1456, wherein the one or more reagents comprises gating reagents for use in flow cytometry experiments.

1458. The method of claim 1457, wherein the flow cytometry experiment comprises removal of signals from MHC multimer stained cells not expressing the specific TCR by introducing an exclusion gate.

1459. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD3.

1460. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD8.

1461. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD3 and CD8.

1462. The method of claim 1461, wherein the CD3 and CD8 are labelled with distinct labels such as fluorochromes.

1463. The method of claim 1461, wherein the CD3 and CD8 are labelled with the same labels such as fluorochromes.

1464. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD4.

1465. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD3 and CD4.

1466. The method of claim 1465, wherein the CD3 and CD4 are labelled with distinct labels such as fluorochromes.

1467. The method of claim 1465, wherein the CD3 and CD4 are labelled with the same labels such as fluorochromes.

1468. The method of claim 1457, wherein the one or more reagents comprises fluorescent antibodies directed against specific surface markers.

1469. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD2.

1470. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD27 and/or CD28.

1471. The method of claim 1457, wherein the one or more gating reagents comprises anti-Foxp3.

1472. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD45RA.

1473. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD45RO.

1474. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CD62L.

1475. The method of claim 1457, wherein the one or more gating reagents comprises reagents binding to CCR7.

1476. The method of any of the claims 1456 to 1475, wherein the reagent identifies specific cell types by selection.

1477. The method of any of the claims 1456 to 1475, wherein the reagent identifies specific cell types by exclusion.

1478. The method of claim 1477, wherein the reagent identifies CD45 expressed on red blood cells.

1479. The method of claim 1477, wherein the reagent identifies CD19 expressed on B cells.

1480. The method of claim 1477, wherein the reagent identifies CD56 expressed on NK cells.

1481. The method of claim 1477, wherein the reagent identifies CD4 expressed on T helper cells.

1482. The method of claim 1477, wherein the reagent identifies CD8 expressed on cytotoxic T cells.

1483. The method of claim 1477, wherein the reagent identifies CD14 expressed on monocytes.

1484. The method of claim 1477, wherein the reagent identifies CD15 expressed on granulocytes.

1485. The method of claim 1477, wherein the reagent identifies CD15 expressed on monocytes.

1486. The method of claim 1423 further comprising co-staining with reagents according to any of the claims 1 to 782.

1487. 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.

1488. 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.

1489. 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.

1490. 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.

1491. 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.

1492. 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.

1493. The method of any of the claims 1487 to 1492, further comprising a positive control (recognizing the MHC multimers comprising correctly folded MHC).

1494. The method of claim 1493, wherein the positive control comprises one or more beads with immobilized TCR's.

1495. The method of claim 1493, wherein the positive control comprises one or more "solid support" scaffolds with immobilized TCR's.

1496. The method of claim 1493, wherein the positive control comprises a solid surface with immobilized TCR's.

1497. The method of claim 1496, wherein the solid surface is a microtiter plate.

1498. The method of claim 1493, wherein the positive control comprises one or more micelles with immobilized TCR's.

1499. The method of claim 1493, wherein the positive control comprises one or more liposomes with immobilized TCR's.

1500. The method of claim 1493, wherein the positive control comprises soluble TCR's.

1501. The method of any of the claims 1494 to 1500, wherein the TCR's are full-length.

1502. The method of any of the claims 1494 to 1500, wherein the TCR's are truncated.

1503. The method of any of the claims 1494 to 1500, wherein the TCR's are full-length or truncated.

1504. The method of any of the claims 1494 to 1500, wherein the TCR's only comprises the extracellular domains.

1505. The method of any of the claims 1494 to 1500, wherein the TCR's are recombinant.

1506. The method of any of the claims 1494 to 1500, wherein the TCR's are chemically modified.

1507. The method of any of the claims 1494 to 1500, wherein the TCR's are enzymatically modified.

1508. The method of claim 1493, wherein the positive control comprises one or more beads with immobilized aptamers.

1509. The method of claim 1493, wherein the positive control comprises one or more "solid support" scaffolds with immobilized aptamers.

1510. The method of claim 1493, wherein the positive control comprises a solid surface with immobilized aptamers.

1511. The method of claim 1510, wherein the solid surface is a microtiter plate.

1512. The method of claim 1493, wherein the positive control comprises one or more micelles with immobilized aptamers.

1513. The method of claim 1493, wherein the positive control comprises one or more liposomes with immobilized aptamers.

1514. The method of claim 1493, wherein the positive control comprises one or more soluble aptamers.

1515. The method of claim 1493, wherein the positive control comprises one or more beads with immobilized antibody specific for the MCH mutimer.

1516. The method of claim 1493, wherein the positive control comprises one or more "solid support" scaffolds with immobilized antibody specific for the MCH mutimer.

1517. The method of claim 1493, wherein the positive control comprises a solid surface with immobilized antibody specific for the MCH mutimer.

1518. The method of claim 1517, wherein the solid surface is a microtiter plate.

1519. The method of claim 1493, wherein the positive control comprises one or more micelles with immobilized antibody specific for the MCH mutimer.

1520. The method of claim 1493, wherein the positive control comprises one or more liposomes with immobilized antibody specific for the MCH mutimer.

1521. The method of claim 1493, wherein the positive control comprises one or more soluble antibody specific for the MCH mutimer.

1522. The method of claim 1493, wherein the positive control comprises one or more beads with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1523. The method of claim 1493, wherein the positive control comprises one or more "solid support" scaffolds with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1524. The method of claim 1493, wherein the positive control comprises a solid surface with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1525. The method of claim 1524, wherein the solid surface is a microtiter plate.

1526. The method of claim 1493, wherein the positive control comprises one or more micelles with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1527. The method of claim 1493, wherein the positive control comprises one or more liposomes with immobilized molecule that recognize correctly folded MHC-peptide complexes.

1528. The method of claim 1493, wherein the positive control comprises one or more soluble molecule that recognize correctly folded MHC-peptide complexes.

1529. The method of claim 1493, wherein the positive control comprises one or more cell lines that display MHC multimer-binding molecules that recognize the MHC-peptide complexes.

1530. The method of claim 1529, wherein the cell line is a T-cell line.

1531. The method of claim 1529, wherein the MHC multimer-binding molecules are TCR's.

1532. The method of claim 1493, wherein the positive control comprises cells from blood samples that carry receptor molecules specific for the MHC multimer.

1533. The method of claim 1493, wherein the positive control comprises cells from preparations of purified lymphocytes (HPBMCs) that carry receptor molecules specific for the MHC multimer.

1534. The method of claim 1493, wherein the positive control comprises cells from bodily fluids that carry receptor molecules specific for the MHC multimer.

1535. The method of claim 1493, wherein the positive control comprises cells from bodily fluids that carry receptor molecules specific for the MHC multimer.

1536. The method of claim 1493, wherein the said method comprises density-gradient centrifugation (e.g. in CsCl).

1537. The method of claim 1493, wherein the said method comprises size exclusion chromatography.

1538. The method of claim 1493, wherein the said method comprises PAGE.

1539. The method of claim 1493, wherein the said method comprises chromatography.

1540. The method of any of the claims 1487 to 1492, wherein the MHC multimer binding is visualized with a labelled secondary component that binds the MHC multimer

1541. The method of claim 1540, wherein the label of the secondary component is selected from the group consisting of fluorophores, chromophores, chemiluminescent labels, bioluminescent labels, radioactive labels, enzyme labels.

1542. The method of any of the claims 1540 and 1541, 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.

1543. The method of claim 1541, 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.

1544. The method of any of the claims 1487 to 1543, wherein a negative control is included

1545. The method of claim 1544, wherein the method comprises MHC multimeres carrying nonsense peptides

1546. The method of claim 1544, wherein the method comprises MHC multimeres carrying nonsense chemically modified peptides

1547. The method of claim 1544, wherein the method comprises MHC multimeres carrying naturally occurring peptides different from the peptide used for analysis of specific T cells in the sample

1548. The method of claim 1544, wherein the method comprises empty MHC multimeres

1549. The method of claim 1544, wherein the method comprises MHC heavy chain or MHC multimers comprising MHC heavy chain and not the MHC light chain

1550. The method of claim 1549, wherein the MHC heavy chain is MHC I

1551. The method of claim 1549, wherein the MHC heavy chain is MHC II

1552. The method of claims 1550 and 1551, wherein the MHC heavy chain is truncated

1553. The method of claims 1550 and 1551, wherein the MHC heavy chain is full-length.

1554. The method of claims 1550 and 1551, wherein the MHC heavy chain is folded.

1555. The method of claims 1550 and 1551, wherein the MHC heavy chain is un-folded.

1556. The method of claim 1550, 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.

1557. The method of claim 1551, 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.

1558. The method of claim 1557, wherein the method comprises Beta2microglobulin.

1559. The method of claim 1544, wherein the method comprises subunits of beta2microglobulin.

1560. The method of claim 1544, wherein the method comprises MHC multimers comprising Beta2microglobulin.

1561. The method of claim 1544, wherein the method comprises MHC multimers comprising subunits of beta2microglobulin.

1562. The method of claims 1558 to 1562, wherein the Beta2microglobulin is un-folded.

1563. The method of claims 1558 to 1562, wherein the Beta2microglobulin is folded.

1564. The method of claims 1558 to 1562, wherein the subunit of Beta2microglobulin is un-folded.

1565. The method of claims 1558 to 1562, wherein the subunit of Beta2microglobulin is folded.

1566. The method of claim 1544, wherein the method comprises MHC-like complexes.

1567. The method of claim 1566, wherein the MHC-like complexes are folded.

1568. The method of claim 1566, wherein the MHC-like complexes are un-folded.

1569. The method of claim 1566, wherein the MHC-like complexes are CD1 molecules.

1570. The method of claim 1567, wherein the method comprises multimerization domains without MHC or MHC-like molecules.

1571. The method of claim 1544, wherein the method comprises one or more multimerization domains selected from the group consisting of dextran, streptavidin, IgG, coiled-coil-domain, liposomes.

1572. The method of claim 1544, wherein the method comprises one or more labels selected from the group FITC, PE, APC, pacific blue, cascade yellow.

1573. The method of any of the claims 1487 to 1492, wherein a negative and a positive control is included.

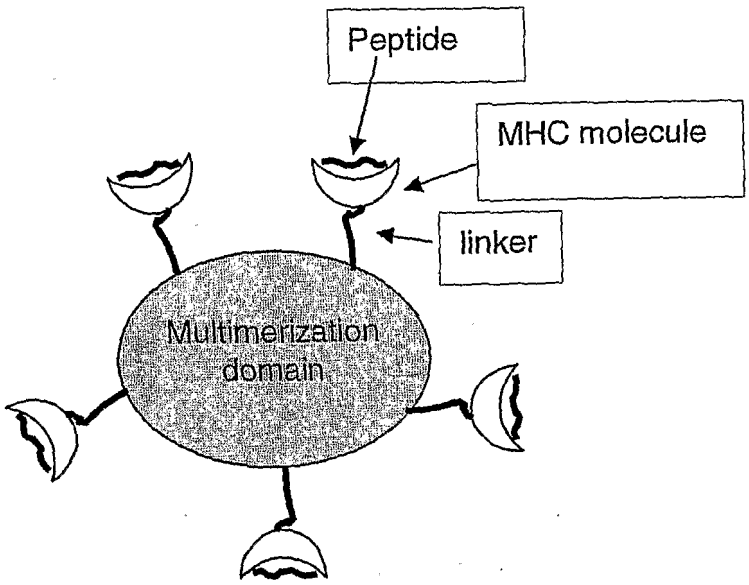


Figure 1. Schematic representation of MHC multimer

Figure 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)
```

Figure 2 cont.

```
        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
```

Figure 2 cont.

```
    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
```

Figure 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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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
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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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

Figure 3 cont.

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
HLA-HHLA-JHLA-KHLA-LHLA-P
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

Figure 3 cont.

H*0204J*0201
H*0205
H*0206
H*0301

Figure 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

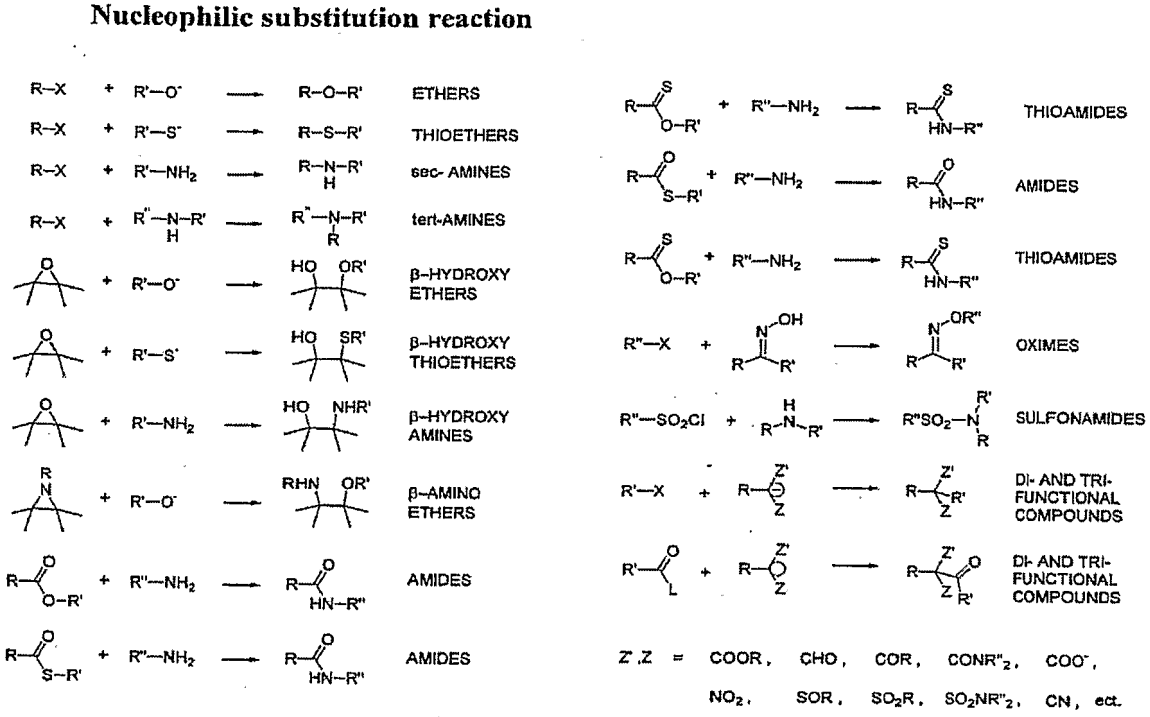
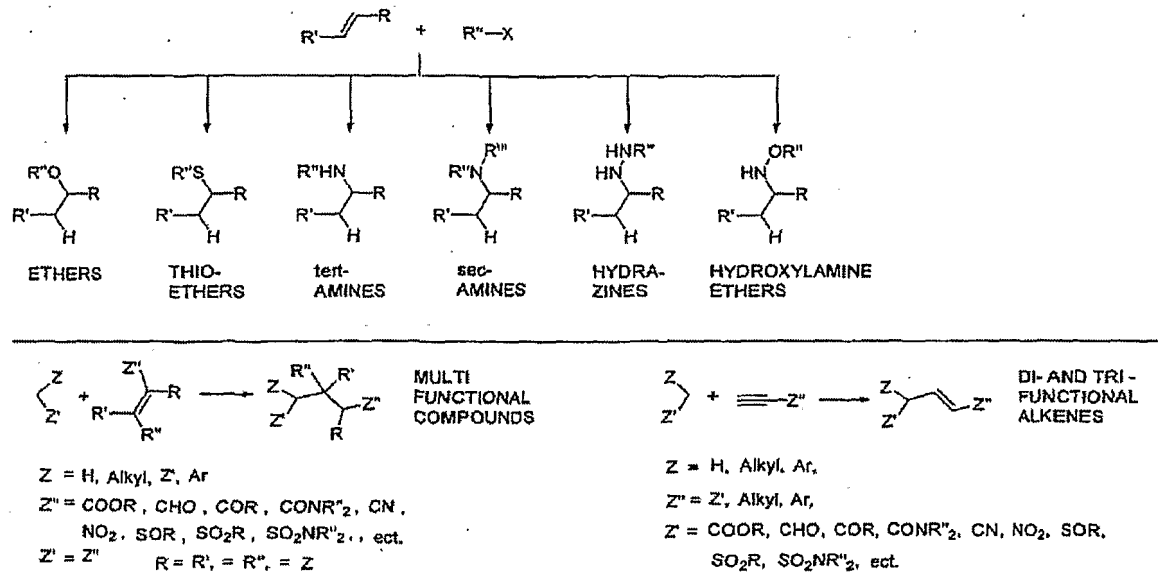


Figure 5. Reactive groups and the bonds formed upon their reaction.

B

Addition to carbon-carbon multiplebonds



Cycloaddition to multiple bounds

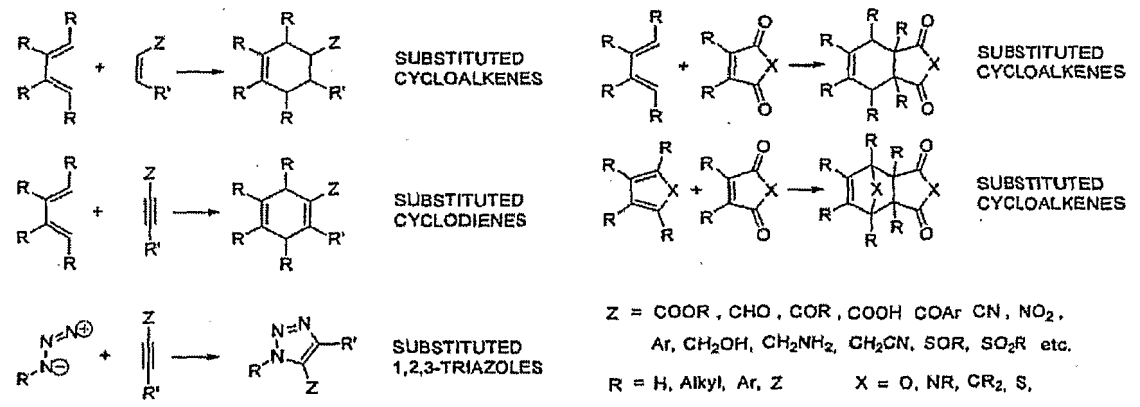


Figure 5, continued. Reactive groups and the bonds formed upon their reaction.

C

Addition to carbon-hetero multiple bonds

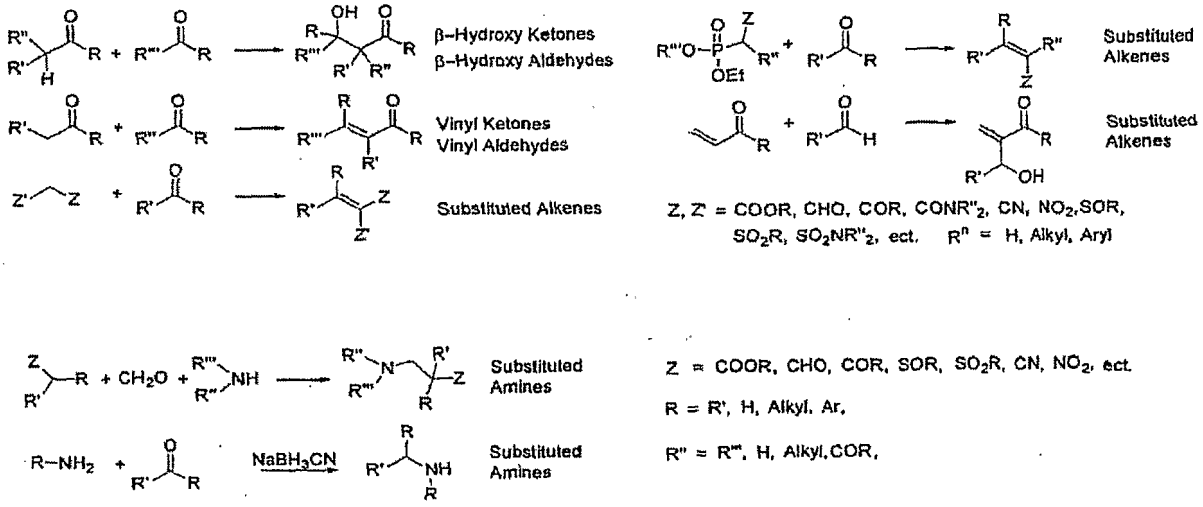
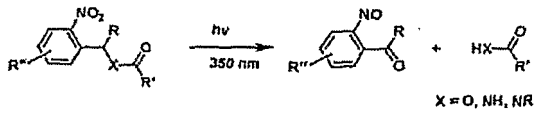
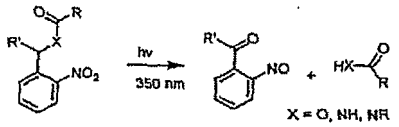


Figure 5, continued. Reactive groups and the bonds formed upon their reaction.

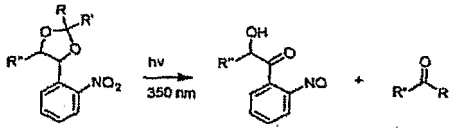
A. Linker for the formation of Ketones, Aldehydes, Amides and Acids



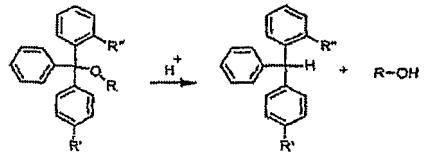
B. Linker for the formation of Ketones, Amides and Acids



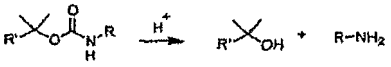
C. Linker for the formation of Aldehydes and Ketones



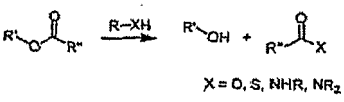
D. Linker for the formation of Alcohols and Acids



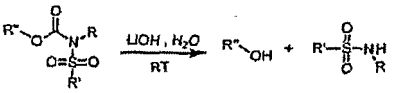
E. Linker for the formation of Amines and Alcohols



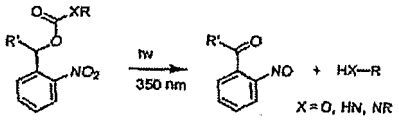
F. Linker for the formation of Esters, Thioesters , Amides and Alcohols



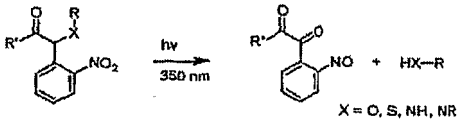
G. Linker for the formation of Sulfonamides and Alcohols



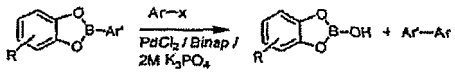
H. Linker for the formation of Ketones, Amines and Alcohols



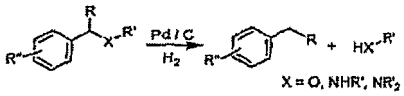
I. Linker for the formation of Ketones, Amines, Alcohols and Mercaptanes



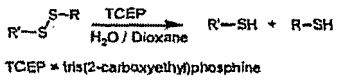
J. Linker for the formation of Biaryl and Bihetaryl



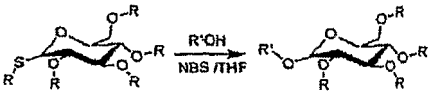
K. Linker for the formation of Benzyles, Amines, Anilins Alcohols and Phenoles



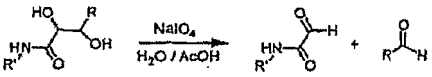
L. Linker for the formation of Mercaptanes



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

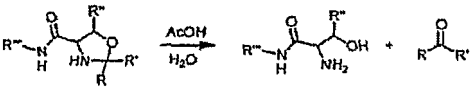


Figure 6. Cleavable linkers, conditions for cleaving them and the resulting products of the cleavage.

Figure 7

Prediction of MHC class 1 mouse virus LCMV gp 1 protein nonamer peptide binders for H-2Kd using the Syfpeithi database

Pos 1 2 3 4 5 6 7 8 9score
179 S F S D A Q S A L22
289 G Y C L T K W M I22
65 M Y G L D G P D I21
139 T F D H T L M S I21
30 I V L I I I T S I20
41 V Y N F A T C G I20
105 H Y I S M G K S G19
43 N F A T C G I L A18
108 S M G K S G L E L18
143 T L M S I V S S L18
175 Q Y N L S F S D A18
226 C S Q T S Y Q Y L18
13 M F E A L P H I I17
33 I I I T S I K A V17
73 I Y K G V Y Q F K17
84 E F D M S H L N L17
230 S Y Q Y L I I Q N17
48 G I L A L V S F L16
50 L A L V S F L F L16
75 K G V Y Q F K S V16
99 S V N N S H H Y I16
147 I V S S L H L S I16
208 K Y M R S G W G W16
227 S Q T S Y Q Y L I16
9 Q I V T M F E A L15
25 I N I V I I V L I15
92 L T M P N A C S V15
160 N Y K P V S C D F15
246 T Y A G P F R I S15
284 V E S P G G Y C L15
290 Y C L T K W M I L15
294 K W M I L A A E L15
54 S F L F L A G K S14
258 F A Q E K T K F L14
12 T M F E A L P H I13
19 H I I D E V I N I13
27 I V I I V L I I I13
82 S V E F D M S H L13
116 L T F T N D S I L13
145 M S I V S S L H L13
156 R G N S N Y K P V13
170 N G I T I Q Y N L13
178 L S F S D A Q S A13
240 T W E N H C T Y A13

Figure 7 cont.

257 L F A Q E K T K F13
262 K T K F L T R R L13
264 K F L T R R L A G13
276 W T L S D S S G V13
20 I I D E V I N I V12
21 I D E V I N I V I12
22 D E V I N I V I I12
24 V I N I V I I V L12
26 N I V I I V L I I12
37 S I K A V Y N F A12
56 L F L A G K S C G12
106 Y I S M G K S G L12
115 E L T F T N D S I12
126 H N H C N L T S A12
136 N K K T F D H T L12
140 F D H T L M S I V12
166 C D F N N G I T I12
232 Q Y L I I Q N R T12
3 P S R E M G Q I V11
42 Y N F A T C G I L11
44 F A T C G I L A L11
45 A T C G I L A L V11
69 D G P D I Y K G V11
77 V Y Q F K S V E F11
79 Q F K S V E F D M11
123 I L N H N H C N L11
167 D F N N G I T I Q11
190 C K T F R G R V L11
192 T F R G R V L D M11
196 R V L D M F R T A11
270 L A G T F T W T L11
2 L P S R E M G Q I10
8 G Q I V T M F E A10
16 A L P H I I D E V10
17 L P H I I D E V I10
23 E V I N I V I I V10
51 A L V S F L F L A10
60 G K S C G M Y G L10
146 S I V S S L H L S10
164 V S C D F N N G I10
181 S D A Q S A L S Q10
185 S A L S Q C K T F10
189 Q C K T F R G R V10
223 T T W C S Q T S Y10
228 Q T S Y Q Y L I I10
245 C T Y A G P F R I10
251 F R I S R V L F A10
273 T F T W T L S D S10

Figure 7 cont.

129 C N L T S A F N K9
133 S A F N K K T F D9
200 M F R T A F G G K9
212 S G W G W A G S D9
248 A G P F R I S R V9
249 G P F R I S R V L9
263 T K F L T R R L A9
269 R L A G T F T W T9
279 S D S S G V E S P9
117 T F T N D S I L N8
204 A F G G K Y M R S8
209 Y M R S G W G W A8
250 P F R I S R V L F8
267 T R R L A G T F T8
292 L T K W M I L A A8
15 E A L P H I I D E7
88 S H L N L T M P N7
112 S G L E L T F T N7
142 H T L M S I V S S7
217 A G S D G K T T W7
254 S R V L F A Q E K7
278 L S D S S G V E S7
282 S G V E S P G G Y7
291 C L T K W M I L A7
32 L I I I T S I K A6
55 F L F L A G K S C6
59 A G K S C G M Y G6
89 H L N L T M P N A6
96 N A C S V N N S H6
122 S I L N H N H C N6
132 T S A F N K K T F6
134 A F N K K T F D H6
137 K K T F D H T L M6
149 S S L H L S I R G6
162 K P V S C D F N N6
182 D A Q S A L S Q C6
186 A L S Q C K T F R6
202 R T A F G G K Y M6
203 T A F G G K Y M R6
216 W A G S D G K T T6
218 G S D G K T T W C6
220 D G K T T W C S Q6
224 T W C S Q T S Y Q6
275 T W T L S D S S G6
6 E M G Q I V T M F5
34 I I T S I K A V Y5
36 T S I K A V Y N F5
40 A V Y N F A T C G5

Figure 7 cont.

61 K S C G M Y G L D5
81 K S V E F D M S H5
90 L N L T M P N A C5
109 M G K S G L E L T5
111 K S G L E L T F T5
150 S L H L S I R G N5
151 L H L S I R G N S5
154 S I R G N S N Y K5
159 S N Y K P V S C D5
173 T I Q Y N L S F S5
215 G W A G S D G K T5
234 L I I Q N R T W E5
255 R V L F A Q E K T5
271 A G T F T W T L S5
280 D S S G V E S P G5
283 G V E S P G G Y C5
286 S P G G Y C L T K5
295 W M I L A A E L K5
1 T L P S R E M G Q4
5 R E M G Q I V T M4
28 V I I V L I I I T4
39 K A V Y N F A T C4
46 T C G I L A L V S4
62 S C G M Y G L D G4
66 Y G L D G P D I Y4
68 L D G P D I Y K G4
71 P D I Y K G V Y Q4
78 Y Q F K S V E F D4
93 T M P N A C S V N4
95 P N A C S V N N S4
113 G L E L T F T N D4
114 L E L T F T N D S4
118 F T N D S I L N H4
119 T N D S I L N H N4
172 I T I Q Y N L S F4
188 S Q C K T F R G R4
210 M R S G W G W A G4
213 G W G W A G S D G4
219 S D G K T T W C S4
235 I I Q N R T W E N4
243 N H C T Y A G P F4
247 Y A G P F R I S R4
259 A Q E K T K F L T4
268 R R L A G T F T W4
272 G T F T W T L S D4
274 F T W T L S D S S4
277 T L S D S S G V E4
287 P G G Y C L T K W4

Figure 7 cont.

296 M I L A A E L K C4
7 M G Q I V T M F E3
29 I I V L I I I T S3
35 I T S I K A V Y N3
38 I K A V Y N F A T3
47 C G I L A L V S F3
49 I L A L V S F L F3
64 G M Y G L D G P D3
67 G L D G P D I Y K3
85 F D M S H L N L T3
87 M S H L N L T M P3
107 I S M G K S G L E3
110 G K S G L E L T F3
130 N L T S A F N K K3
138 K T F D H T L M S3
152 H L S I R G N S N3
155 I R G N S N Y K P3
161 Y K P V S C D F N3
169 N N G I T I Q Y N3
174 I Q Y N L S F S D3
176 Y N L S F S D A Q3
191 K T F R G R V L D3
194 R G R V L D M F R3
199 D M F R T A F G G3
221 G K T T W C S Q T3
236 I Q N R T W E N H3
244 H C T Y A G P F R3
252 R I S R V L F A Q3
253 I S R V L F A Q E3
260 Q E K T K F L T R3
261 E K T K F L T R R3
266 L T R R L A G T F3
281 S S G V E S P G G3
285 E S P G G Y C L T3
288 G G Y C L T K W M3
4 S R E M G Q I V T2
57 F L A G K S C G M2
58 L A G K S C G M Y2
76 G V Y Q F K S V E2
97 A C S V N N S H H2
100 V N N S H H Y I S2
101 N N S H H Y I S M2
102 N S H H Y I S M G2
103 S H H Y I S M G K2
127 N H C N L T S A F2
135 F N K K T F D H T2
144 L M S I V S S L H2
153 L S I R G N S N Y2

Figure 7 cont.

157 G N S N Y K P V S2
158 N S N Y K P V S C2
165 S C D F N N G I T2
168 F N N G I T I Q Y2
184 Q S A L S Q C K T2
187 L S Q C K T F R G2
193 F R G R V L D M F2
197 V L D M F R T A F2
205 F G G K Y M R S G2
206 G G K Y M R S G W2
222 K T T W C S Q T S2
229 T S Y Q Y L I I Q2
237 Q N R T W E N H C2
256 V L F A Q E K T K2
11 V T M F E A L P H1
31 V L I I I T S I K1
70 G P D I Y K G V Y1
72 D I Y K G V Y Q F1
74 Y K G V Y Q F K S1
80 F K S V E F D M S1
83 V E F D M S H L N1
86 D M S H L N L T M1
98 C S V N N S H H Y1
104 H H Y I S M G K S1
124 L N H N H C N L T1
131 L T S A F N K K T1
177 N L S F S D A Q S1
183 A Q S A L S Q C K1
195 G R V L D M F R T1
201 F R T A F G G K Y1
211 R S G W G W A G S1
231 Y Q Y L I I Q N R1
239 R T W E N H C T Y1
242 E N H C T Y A G P1
293 T K W M I L A A E1
10 I V T M F E A L P0
14 F E A L P H I I D0
18 P H I I D E V I N0
52 L V S F L F L A G0
63 C G M Y G L D G P0
120 N D S I L N H N H0
121 D S I L N H N H C0
125 N H N H C N L T S0
148 V S S L H L S I R0
163 P V S C D F N N G0
171 G I T I Q Y N L S0
180 F S D A Q S A L S0
225 W C S Q T S Y Q Y0

Figure 7 cont.

233 Y L I I Q N R T W0
238 N R T W E N H C T0
241 W E N H C T Y A G0
265 F L T R R L A G T0
91 N L T M P N A C S-1
94 M P N A C S V N N-1
128 H C N L T S A F N-1
198 L D M F R T A F G-1
214 W G W A G S D G K-1
53 V S F L F L A G K-2
141 D H T L M S I V S-2
207 G K Y M R S G W G-2

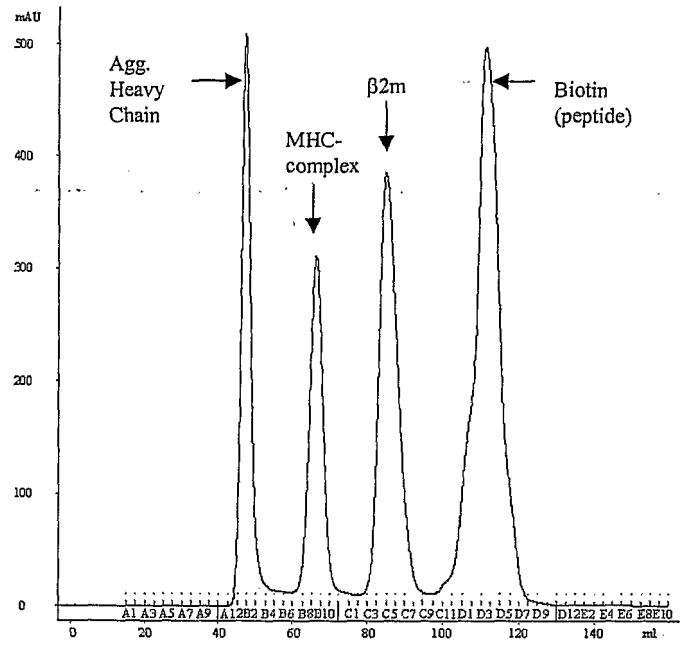


Figure 8.. Size exclusion chromatography of folded HLA-A*0201-β2m-QLFEELQEL-complex.

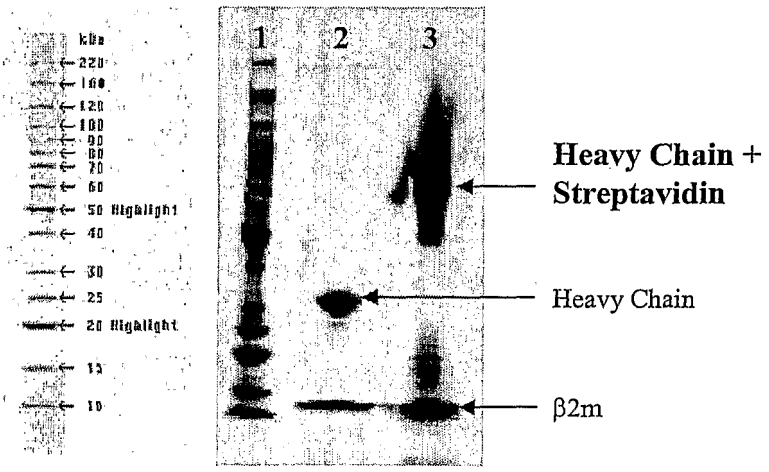
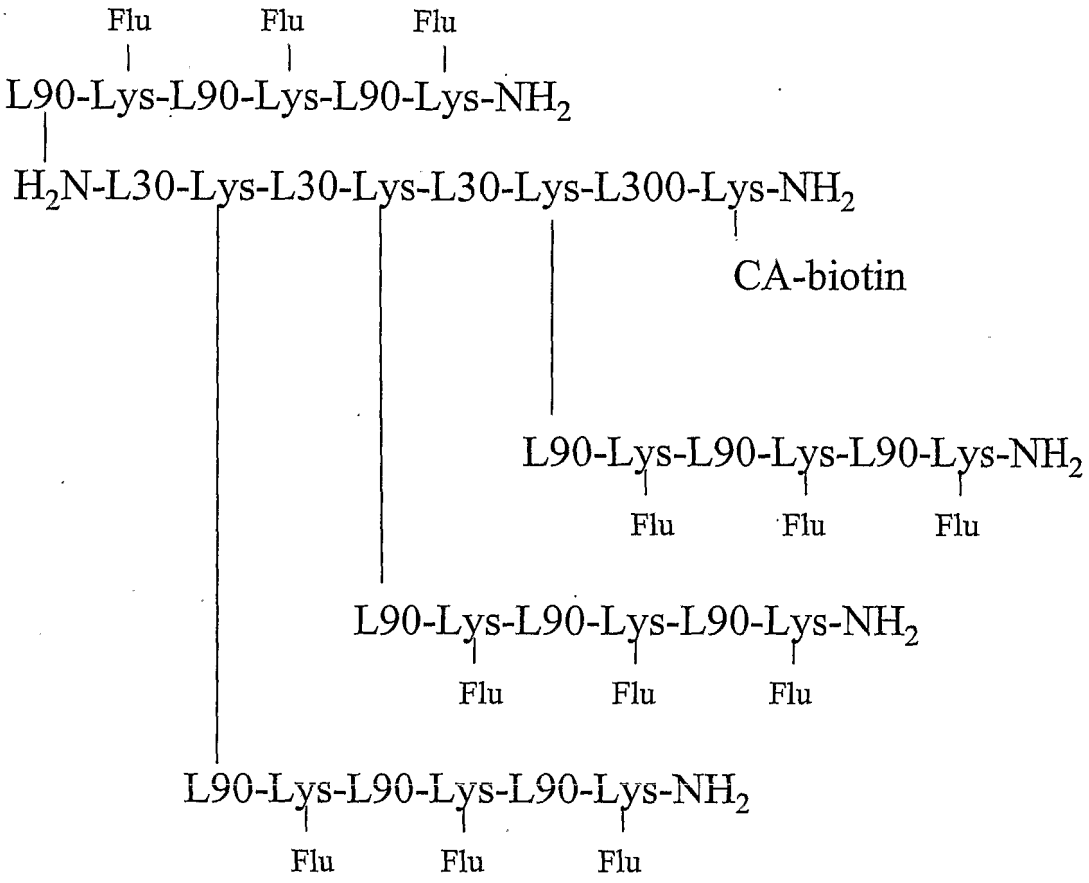


Figure 9. MHC-SHIFT Assay

A



B

L15 linker composition:

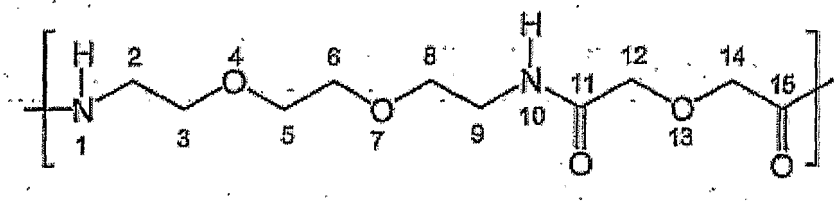


Figure 10. Composition of a Fluorescein-linker molecule

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

Figure 11 HLA alleles of the NetMHC databases

Pos	1	2	3	4	5	6	7	8	9	score
179	S	F	S	D	A	Q	S	A	L	22
289	G	Y	C	L	T	K	W	M	I	22
65	M	Y	G	L	D	G	P	D	I	21
139	T	F	D	H	T	L	M	S	I	21
30	I	V	L	I	I	I	T	S	I	20
41	V	Y	N	F	A	T	C	G	I	20
105	H	Y	I	S	M	G	K	S	G	19
43	N	F	A	T	C	G	I	L	A	18
108	S	M	G	K	S	G	L	E	L	18
143	T	L	M	S	I	V	S	S	L	18
175	Q	Y	N	L	S	F	S	D	A	18
226	C	S	Q	T	S	Y	Q	Y	L	18
13	M	F	E	A	L	P	H	I	I	17
33	I	I	I	T	S	I	K	A	V	17
73	I	Y	K	G	V	Y	Q	F	K	17
84	E	F	D	M	S	H	L	N	L	17
230	S	Y	Q	Y	L	I	I	Q	N	17
48	G	I	L	A	L	V	S	F	L	16
50	L	A	L	V	S	F	L	F	L	16
75	K	G	V	Y	Q	F	K	S	V	16
99	S	V	N	N	S	H	H	Y	I	16
147	I	V	S	S	L	H	L	S	I	16
208	K	Y	M	R	S	G	W	G	W	16
227	S	Q	T	S	Y	Q	Y	L	I	16
9	Q	I	V	T	M	F	E	A	L	15
25	I	N	I	V	I	I	V	L	I	15
92	L	T	M	P	N	A	C	S	V	15
160	N	Y	K	P	V	S	C	D	F	15
246	T	Y	A	G	P	F	R	I	S	15
284	V	E	S	P	G	G	Y	C	L	15
290	Y	C	L	T	K	W	M	I	L	15
294	K	W	M	I	L	A	A	E	L	15
54	S	F	L	F	L	A	G	K	S	14
258	F	A	Q	E	K	T	K	F	L	14
12	T	M	F	E	A	L	P	H	I	13
19	H	I	I	D	E	V	I	N	I	13
27	I	V	I	I	V	L	I	I	I	13
82	S	V	E	F	D	M	S	H	L	13
116	L	T	F	T	N	D	S	I	L	13
145	M	S	I	V	S	S	L	H	L	13
156	R	G	N	S	N	Y	K	P	V	13
170	N	G	I	T	I	Q	Y	N	L	13
178	L	S	F	S	D	A	Q	S	A	13
240	T	W	E	N	H	C	T	Y	A	13
257	L	F	A	Q	E	K	T	K	F	13
262	K	T	K	F	L	T	R	R	L	13
264	K	F	L	T	R	R	L	A	G	13
276	W	T	L	S	D	S	S	G	V	13
20	I	I	D	E	V	I	N	I	V	12
21	I	D	E	V	I	N	I	V	I	12
22	D	E	V	I	N	I	V	I	I	12
24	V	I	N	I	V	I	I	V	L	12
26	N	I	V	I	I	V	L	I	I	12
37	S	I	K	A	V	Y	N	F	A	12
56	L	F	L	A	G	K	S	C	G	12
106	Y	I	S	M	G	K	S	G	L	12
115	E	L	T	F	T	N	D	S	I	12
126	H	N	H	C	N	L	T	S	A	12
136	N	K	K	T	F	D	H	T	L	12
140	F	D	H	T	L	M	S	I	V	12
166	C	D	F	N	N	G	I	T	I	12
232	Q	Y	L	I	I	Q	N	R	T	12

Figure 12
Prediction of MHC class 1 mouse virus LCMV gp 1 protein nonamer peptide binders for H-2Kd using the Syfpeithi database

Figure 13

HLA-A	HLA-B	HLA-C	HLA-E	HLA-F	HLA-G
A*01010101	B*070201	Cw*010201	E*01010101	F*01010101	G*01010101
A*01010102N	B*070202	Cw*010202	E*01010102	F*01010102	G*01010102
A*010102	B*070203	Cw*010203	E*01010103	F*01010103	G*01010103
A*010103	B*070204	Cw*010204	E*01030101	F*01010104	G*01010104
A*010104	B*0703	Cw*0103	E*01030102	F*01010105	G*01010105
A*0102	B*0704	Cw*0104	E*010302	F*01010106	G*01010201
A*0103	B*070501	Cw*0105	E*010303	F*01010107	G*01010202
A*0104N	B*070502	Cw*0106	E*010304	F*01010108	G*010103
A*0106	B*070503	Cw*0107	E*0104	F*01010201	G*010104
A*0107	B*0706	Cw*0108		F*01010202	G*010105
A*0108	B*0707	Cw*0109		F*01010203	G*010106
A*0109	B*0708	Cw*0110		F*01010204	G*010107
A*0110	B*0709	Cw*0111		F*01010205	G*010108
A*0111N	B*0710	Cw*0112		F*01010301	G*010109
A*0112	B*0711	Cw*0113		F*01010302	G*010110
A*0113	B*0712	Cw*020201		F*01010303	G*0102
A*0114	B*0713	Cw*020202		F*01010304	G*0103
A*0115N	B*0714	Cw*020203		F*0102	G*010401
A*0116N	B*0715	Cw*020205		F*01030101	G*010402
A*0117	B*0716	Cw*0203		F*01030102	G*010403
A*0118N	B*0717	Cw*0204		F*0104	G*0105N
A*0119	B*0718	Cw*0205			G*0106
A*0120	B*0719	Cw*0206			G*0107
A*02010101	B*0720	Cw*0207			
A*02010102L	B*0721	Cw*0208			
A*020102	B*0722	Cw*0209			
A*020103	B*0723	Cw*0210			
A*020104	B*0724	Cw*0211			
A*020105	B*0725	Cw*0212			
A*020106	B*0726	Cw*0213			
A*020107	B*0727	Cw*0214			
A*020108	B*0728	Cw*0215			
A*020109	B*0729	Cw*0216			
A*020110	B*0730	Cw*0217			
A*020111	B*0731	Cw*030201			
A*020112	B*0732	Cw*030202			
A*0202	B*0733	Cw*030301			
A*020301	B*0734	Cw*030302			
A*020302	B*0735	Cw*030303			
A*0204	B*0736	Cw*030304			
A*0205	B*0737	Cw*030305			
A*020601	B*0738	Cw*030401			
A*020602	B*0739	Cw*030402			
A*020603	B*0740	Cw*030403			
A*0207	B*0741	Cw*030404			
A*0208	B*0742	Cw*030405			
A*0209	B*0743	Cw*0305			
A*0210	B*0744	Cw*0306			
A*0211	B*0745	Cw*0307			
A*0212	B*0746	Cw*0308			
A*0213	B*0747	Cw*0309			
A*0214	B*0748	Cw*0310			
A*0215N	B*0749N	Cw*031101			
A*0216	B*0750	Cw*031102			
A*021701	B*0751	Cw*0312			
A*021702	B*080101	Cw*0313			
A*0218	B*080102	Cw*0314			
A*0219	B*080103	Cw*0315			
A*022001	B*0802	Cw*0316			
A*022002	B*0803	Cw*0317			
A*0221	B*0804	Cw*0318			
A*0222	B*0805	Cw*0319			
A*0224	B*0806	Cw*0320N			
A*0225	B*0807	Cw*0321			

Figure 13 cont.

A*0226	B*0808N	Cw*0322Q
A*0227	B*0809	Cw*0323
A*0228	B*0810	Cw*0324
A*0229	B*0811	Cw*0325
A*0230	B*0812	Cw*0326
A*0231	B*0813	Cw*0327
A*0232N	B*0814	Cw*0328
A*0233	B*0815	Cw*0329
A*0234	B*0816	Cw*0330
A*023501	B*0817	Cw*0331
A*023502	B*0818	Cw*0332
A*0236	B*0819N	Cw*0333
A*0237	B*0820	Cw*0334
A*0238	B*0821	Cw*0335
A*0239	B*0822	Cw*04010101
A*0240	B*0823	Cw*04010102
A*0241	B*0824	Cw*040102
A*0242	B*0825	Cw*040103
A*0243N	B*0826	Cw*040104
A*0244	B*0827	Cw*0403
A*0245	B*0828	Cw*040401
A*0246	B*0829	Cw*040402
A*0247	B*0830N	Cw*0405
A*0248	B*0831	Cw*0406
A*0249	B*1301	Cw*0407
A*0250	B*130201	Cw*0408
A*0251	B*130202	Cw*0409N
A*0252	B*130203	Cw*0410
A*0253N	B*1303	Cw*0411
A*0254	B*1304	Cw*0412
A*0255	B*1306	Cw*0413
A*0256	B*1307N	Cw*0414
A*0257	B*1308	Cw*0415
A*0258	B*1309	Cw*0416
A*0259	B*1310	Cw*0417
A*0260	B*1311	Cw*0418
A*0261	B*1312	Cw*0419
A*0262	B*1313	Cw*0420
A*0263	B*1314	Cw*0421
A*0264	B*1315	Cw*0423
A*0265	B*1316	Cw*0424
A*0266	B*1317	Cw*050101
A*0267	B*1401	Cw*050102
A*0268	B*140201	Cw*050103
A*0269	B*140202	Cw*0502
A*0270	B*1403	Cw*0503
A*0271	B*1404	Cw*0504
A*0272	B*1405	Cw*0505
A*0273	B*140601	Cw*0506
A*027401	B*140602	Cw*0507N
A*027402	B*1407N	Cw*0508
A*0275	B*15010101	Cw*0509
A*0276	B*15010102N	Cw*0510
A*0277	B*150102	Cw*0511
A*0278	B*150103	Cw*0512
A*0279	B*150104	Cw*0513
A*0280	B*1502	Cw*0514
A*0281	B*1503	Cw*0515
A*0282N	B*1504	Cw*06020101
A*0283N	B*1505	Cw*06020102
A*0284	B*1506	Cw*060202
A*0285	B*1507	Cw*0603
A*0286	B*1508	Cw*0604
A*0287	B*1509	Cw*0605
A*0288N	B*1510	Cw*0606

Figure 13 cont.

A*0289	B*151101	Cw*0607
A*0290	B*151102	Cw*0608
A*0291	B*151103	Cw*0609
A*0292	B*1512	Cw*0610
A*0293	B*1513	Cw*0611
A*0294N	B*1514	Cw*0612
A*0295	B*1515	Cw*0613
A*0296	B*1516	Cw*0614
A*0297	B*15170101	Cw*070101
A*0299	B*15170102	Cw*070102
A*03010101	B*151702	Cw*070103
A*03010102N	B*1518	Cw*070104
A*03010103	B*1519	Cw*070105
A*030102	B*1520	Cw*070106
A*030103	B*1521	Cw*070107
A*030104	B*1523	Cw*07020101
A*030105	B*1524	Cw*07020102
A*0302	B*1525	Cw*07020103
A*0303N	B*1526N	Cw*0703
A*0304	B*1527	Cw*070401
A*0305	B*1528	Cw*070402
A*0306	B*1529	Cw*0705
A*0307	B*1530	Cw*0706
A*0308	B*1531	Cw*0707
A*0309	B*1532	Cw*0708
A*0310	B*1533	Cw*0709
A*0311N	B*1534	Cw*0710
A*0312	B*1535	Cw*0711
A*0313	B*1536	Cw*0712
A*0314	B*1537	Cw*0713
A*0315	B*1538	Cw*0714
A*0316	B*1539	Cw*0715
A*031	B*1540	Cw*0716
A*0318	B*1542	Cw*0717
A*0319	B*1543	Cw*0718
A*0320	B*1544	Cw*0719
A*0321N	B*1545	Cw*0720
A*0322	B*1546	Cw*0721
A*0323	B*1547	Cw*0722
A*0324	B*1548	Cw*0723
A*0325	B*1549	Cw*0724
A*0326	B*1550	Cw*0725
A*110101	B*1551	Cw*0726
A*110102	B*1552	Cw*0727
A*110103	B*1553	Cw*0728
A*110104	B*1554	Cw*0729
A*110105	B*1555	Cw*0730
A*110106	B*1556	Cw*0731
A*110201	B*1557	Cw*0732N
A*110202	B*1558	Cw*0733N
A*1103	B*1560	Cw*0734
A*1104	B*1561	Cw*0735
A*1105	B*1562	Cw*0736
A*1106	B*1563	Cw*0737
A*1107	B*1564	Cw*0738
A*1108	B*1565	Cw*0739
A*1109	B*1566	Cw*0740
A*1110	B*1567	Cw*0741
A*1111	B*1568	Cw*0742
A*1112	B*1569	Cw*0743
A*1113	B*1570	Cw*0744
A*1114	B*1571	Cw*0745
A*1115	B*1572	Cw*080101
A*1116	B*1573	Cw*080102
A*1117	B*1574	Cw*0802

Figure 13 cont.

A*1118	B*1575	Cw*0803
A*1119	B*1576	Cw*0804
A*1120	B*1577	Cw*0805
A*1121N	B*1578	Cw*0806
A*1122	B*1579N	Cw*0807
A*1123	B*1580	Cw*0808
A*1124	B*1581	Cw*0809
A*1125	B*1582	Cw*0810
A*1126	B*1583	Cw*0811
A*1127	B*1584	Cw*0812
A*1128	B*1585	Cw*0813
A*1129	B*1586	Cw*0814
A*2301	B*1587	Cw*120201
A*2302	B*1588	Cw*120202
A*2303	B*1589	Cw*120203
A*2304	B*1590	Cw*12030101
A*2305	B*1591	Cw*12030102
A*2306	B*1592	Cw*120302
A*2307N	B*1593	Cw*120303
A*2308N	B*1594N	Cw*120304
A*2309	B*1595	Cw*120401
A*2310	B*1596	Cw*120402
A*2311N	B*1597	Cw*1205
A*2312	B*1598	Cw*1206
A*2313	B*1599	Cw*1207
A*2314	B*9501	Cw*1208
A*24020101	B*9502	Cw*1209
A*24020102L	B*9503	Cw*1210
A*240202	B*9504	Cw*1211
A*240203	B*9505	Cw*1212
A*240204	B*950	Cw*1213
A*240205	B*9507	Cw*1214
A*240206	B*9508	Cw*1215
A*240207	B*9509	Cw*1216
A*240208	B*9510	Cw*1217
A*240209	B*9511N	Cw*1218
A*240210	B*9512	Cw*1219
A*240211	B*9513	Cw*140201
A*240212	B*9514	Cw*140202
A*240213	B*9515	Cw*140203
A*240301	B*9516	Cw*140204
A*240302	B*9517	Cw*1403
A*2404	B*9518	Cw*1404
A*2405	B*9519	Cw*1405
A*2406	B*9520	Cw*1406
A*2407	B*9521	Cw*1407N
A*2408	B*9522	Cw*1408
A*2409N	B*180101	Cw*150201
A*2410	B*180102	Cw*150202
A*2411N	B*180103	Cw*150203
A*2413	B*1802	Cw*1503
A*2414	B*1803	Cw*1504
A*2415	B*1804	Cw*150501
A*2417	B*1805	Cw*150502
A*2418	B*1806	Cw*150503
A*2419	B*1807	Cw*150504
A*2420	B*1808	Cw*1506
A*2421	B*1809	Cw*1507
A*2422	B*1810	Cw*1508
A*2423	B*1811	Cw*1509
A*2424	B*1812	Cw*1510
A*2425	B*1813	Cw*1511
A*2426	B*1814	Cw*1512
A*2427	B*1815	Cw*1513
A*2428	B*1817N	Cw*1514

Figure 13 cont.

A*2429	B*1818	Cw*1515
A*2430	B*1819	Cw*1516
A*2431	B*1820	Cw*1517
A*2432	B*1821	Cw*160101
A*2433	B*1822	Cw*160102
A*2434	B*1823N	Cw*1602
A*2435	B*1824	Cw*160401
A*2436N	B*2701	Cw*1606
A*2437	B*2702	Cw*1607
A*2438	B*2703	Cw*1608
A*2439	B*270401	Cw*1609
A*2440N	B*270402	Cw*1701
A*2441	B*270502	Cw*1702
A*2442	B*270503	Cw*1703
A*2443	B*270504	Cw*1704
A*2444	B*270505	Cw*1801
A*2445N	B*270506	Cw*1802
A*2446	B*270507	
A*2447	B*270508	
A*2448N	B*270509	
A*2449	B*2706	
A*2450	B*2707	
A*2451	B*2708	
A*2452	B*2709	
A*2453	B*2710	
A*2454	B*2711	
A*2455	B*2712	
A*2456	B*2713	
A*2457	B*2714	
A*2458	B*2715	
A*2459	B*2716	
A*2460N	B*2717	
A*2461	B*2718	
A*2462	B*2719	
A*2463	B*2720	
A*2464	B*2721	
A*2465	B*2723	
A*2466	B*2724	
A*2467	B*2725	
A*2468	B*2726	
A*250101	B*2727	
A*250102	B*2728	
A*2502	B*2729	
A*2503	B*2730	
A*2504	B*2731	
A*2505	B*2732	
A*2506	B*2733	
A*260101	B*2734	
A*260102	B*2735	
A*260103	B*2736	
A*260104	B*350101	
A*2602	B*350102	
A*2603	B*350103	
A*2604	B*350104	
A*2605	B*350105	
A*2606	B*350106	
A*260701	B*350201	
A*260702	B*350202	
A*2608	B*3503	
A*2609	B*350401	
A*2610	B*350402	
A*2611N	B*3505	
A*2612	B*3506	
A*2613	B*3507	
A*2614	B*350801	

Figure 13 cont.

A*2615	B*350802
A*2616	B*350901
A*2617	B*350902
A*2618	B*3510
A*2619	B*3511
A*2620	B*3512
A*2621	B*3513
A*2622	B*351401
A*2623	B*351402
A*2624	B*3515
A*2625N	B*3516
A*2626	B*3517
A*2627	B*3518
A*2628	B*3519
A*2629	B*3520
A*2630	B*3521
A*2631	B*3522
A*2632	B*3523
A*2633	B*3524
A*2634	B*3525
A*29010101	B*3526
A*29010102N	B*3527
A*290201	B*3528
A*290202	B*3529
A*290203	B*3530
A*2903	B*3531
A*2904	B*3532
A*2905	B*3533
A*2906	B*3534
A*2907	B*3535
A*2908N	B*3536
A*2909	B*3537
A*2910	B*3538
A*2911	B*3539
A*2912	B*3540N
A*2913	B*3541
A*2914	B*3542
A*2915	B*3543
A*2916	B*3544
A*300101	B*3545
A*300102	B*3546
A*300201	B*3547
A*300202	B*3548
A*300203	B*3549
A*3003	B*3550
A*3004	B*3551
A*3006	B*3552
A*3007	B*3553N
A*3008	B*3554
A*3009	B*3555
A*3010	B*3556
A*3011	B*3557
A*3012	B*3558
A*3013	B*3559
A*3014L	B*3560
A*3015	B*3561
A*3016	B*3562
A*3017	B*3563
A*3018	B*3564
A*3019	B*3565Q
A*310102	B*3566
A*3102	B*3567
A*3103	B*3568
A*3104	B*3569
A*3105	B*3570

Figure 13 cont.

A*3106	B*3571
A*3107	B*3572
A*3108	B*370101
A*3109	B*370102
A*3110	B*370103
A*3111	B*370104
A*3112	B*3702
A*3113	B*3703N
A*3114N	B*3704
A*3115	B*3705
A*3201	B*3706
A*3202	B*3707
A*3203	B*3708
A*3204	B*3709
A*3205	B*3710
A*3206	B*3711
A*3207	B*3712
A*3208	B*380101
A*3209	B*380102
A*3210	B*380201
A*3211Q	B*380202
A*3212	B*3803
A*3213	B*3804
A*3214	B*3805
A*3301	B*3806
A*330301	B*3807
A*330302	B*3808
A*3304	B*3809
A*3305	B*3810
A*3306	B*3811
A*3307	B*3812
A*3308	B*3813
A*3309	B*3814
A*3401	B*3815
A*3402	B*39010101
A*3403	B*39010102L
A*3404	B*390103
A*3405	B*390104
A*3406	B*390201
A*3407	B*390202
A*3408	B*3903
A*3601	B*3904
A*3602	B*3905
A*3603	B*390601
A*3604	B*390602
A*4301	B*3907
A*6601	B*3908
A*6602	B*3909
A*6603	B*3910
A*6604	B*3911
A*6605	B*3912
A*6606	B*391301
A*680101	B*391302
A*680102	B*3914
A*680103	B*3915
A*680104	B*3916
A*680105	B*3917
A*68020101	B*3918
A*68020102	B*3919
A*680301	B*3920
A*680302	B*3922
A*6804	B*3923
A*6805	B*3924
A*6806	B*3925N

Figure 13 cont.

A*6807	B*3926
A*6808	B*3927
A*6809	B*3928
A*6810	B*3929
A*6811N	B*3930
A*6812	B*3931
A*6813	B*3932
A*6814	B*3933
A*6815	B*3934
A*6816	B*3935
A*6817	B*3936
A*6818N	B*3937
A*6819	B*3938Q
A*6820	B*3939
A*6821	B*3940N
A*6822	B*3941
A*6823	B*400101
A*6824	B*400102
A*6825	B*400103
A*6826	B*400104
A*6827	B*400105
A*6828	B*400201
A*6829	B*400202
A*6830	B*400203
A*6831	B*4003
A*6832	B*4004
A*6833	B*4005
A*6834	B*40060101
A*6835	B*40060102
A*6836	B*400602
A*6901	B*4007
A*7401	B*4008
A*7402	B*4009
A*7403	B*4010
A*7404	B*4011
A*7405	B*4012
A*7406	B*4013
A*7407	B*401401
A*7408	B*401402
A*7409	B*401403
A*7410	B*4015
A*7411	B*4016
A*7412N	B*4018
A*8001	B*4019
A*9201	B*4020
A*9202	B*4021
A*9203	B*4022N
A*9204	B*4023
A*9205	B*4024
A*9206	B*4025
A*9207	B*4026
A*9208	B*4027
A*9209	B*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

Figure 13 cont.

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

Figure 13 cont.

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

Figure 13 cont.

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

Figure 13 cont.

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

Figure 13 cont.

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

Figure 13 cont.

B*7803
B*7804
B*7805
B*8101
B*8102
B*8201
B*8202
B*8301

HLA-H	HLA-J	HLA-K	HLA-L	HLA-P
H*01010101	J*01010101	K*01010101	L*01010101	P*01010101
H*01010102	J*01010102	K*01010102	L*01010102	P*01010102
H*01010103	J*01010103	K*01010103	L*01010103	P*02010101
H*0102	J*01010104	K*01010104	L*010102	P*02010102
H*02010101	J*01010105	K*0102	L*0102	
H*02010102	J*01010106	K*0103		
H*0202	J*01010107			
H*0203	J*01010108			
H*0204	J*0201			
H*0205				
H*0206				
H*0301				

Figure 14.

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/

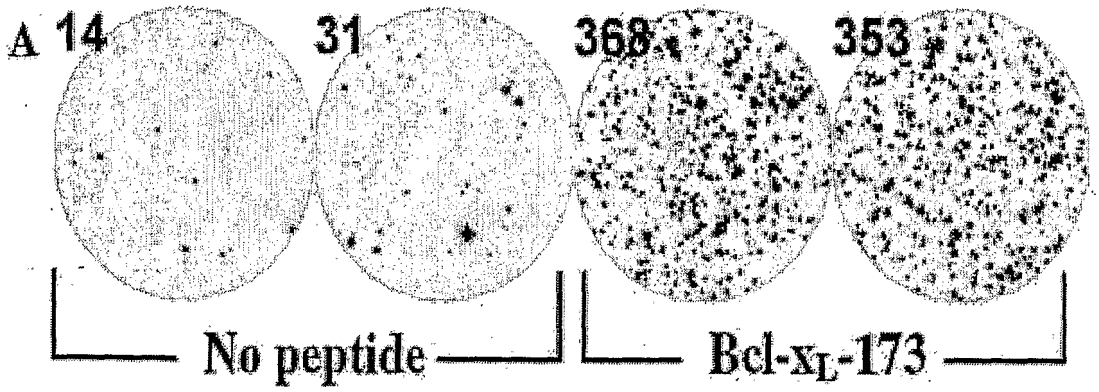


Figure 15

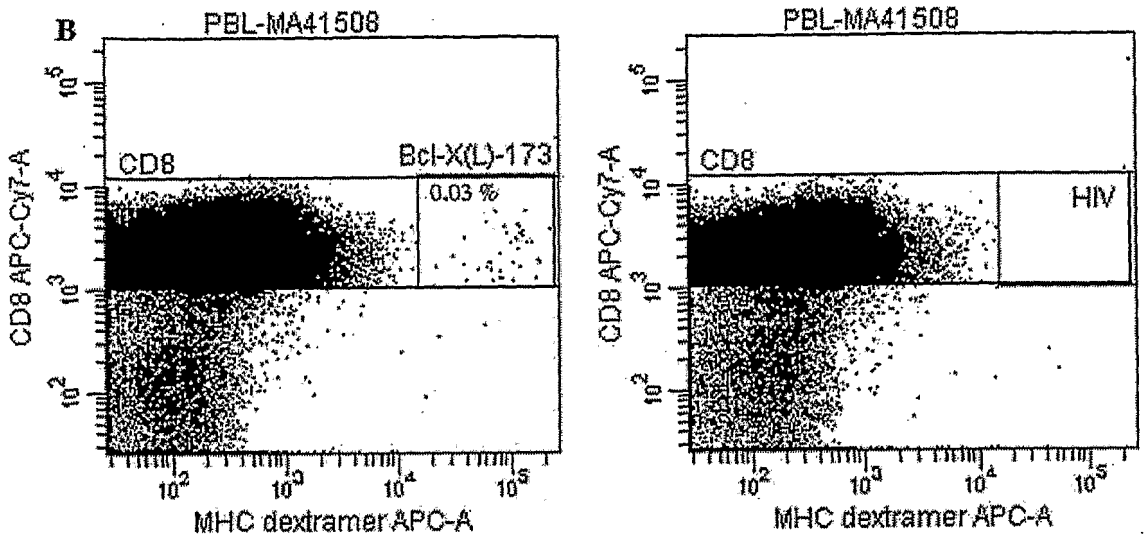

B
PBL-MA41508
CD8
Bcl-X(L)-173
0.03 %
CD8 APC-Cy7-A
MHC dextramer APC-A
PBL-MA41508
CD8
HIV
CD8 APC-Cy7-A
MHC dextramer APC-A

Figure 16

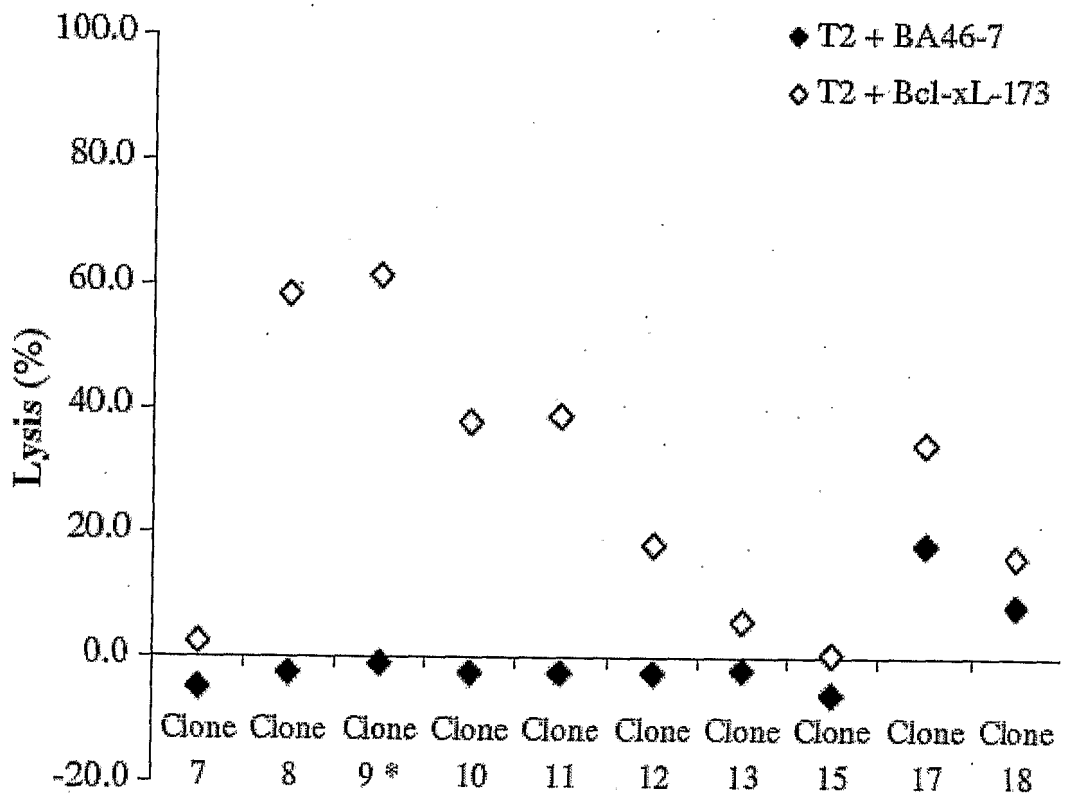

100.0
80.0
60.0
40.0
20.0
0.0
-20.0
Lysis (%)
T2 + BA46-7
T2 + Bcl-xL-173
Clone 7
Clone 8
Clone 9 *
Clone 10
Clone 11
Clone 12
Clone 13
Clone 15
Clone 17
Clone 18

Figure 17

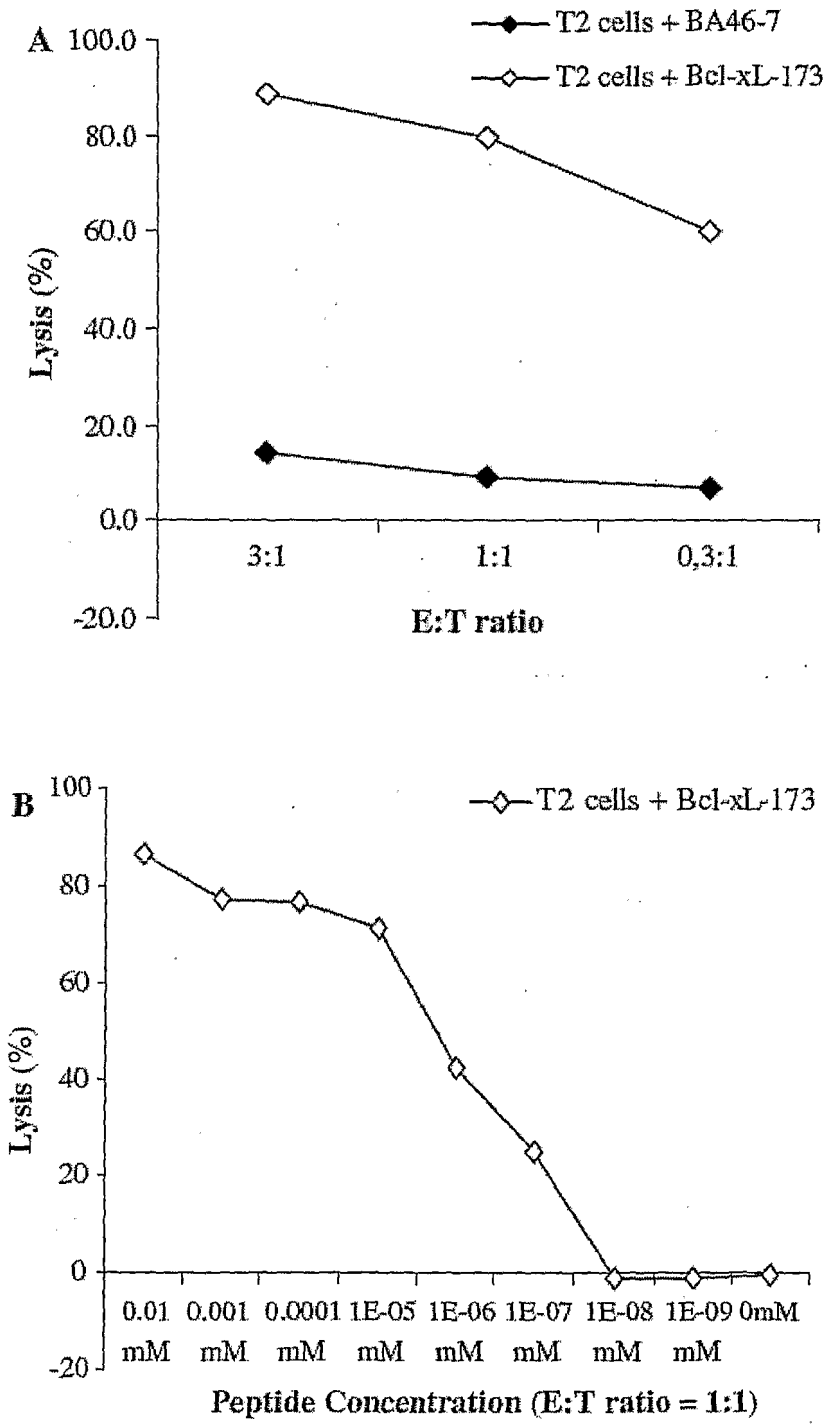

A
100.0
80.0
60.0
40.0
20.0
0.0
-20.0
Lysis (%)
T2 cells + BA46-7
T2 cells + Bcl-xL-173
3:1
1:1
0,3:1
E:T ratio
B
100
80
60
40
20
0
-20
Lysis (%)
T2 cells + Bcl-xL-173
0.01 mM
0.001 mM
0.0001 mM
1E-05 mM
1E-06 mM
1E-07 mM
1E-08 mM
1E-09 mM
0mM
Peptide Concentration (E:T ratio = 1:1)

Figure 18

Figure 19.

Detection of Borrelia specific T cells using MHC dextramers

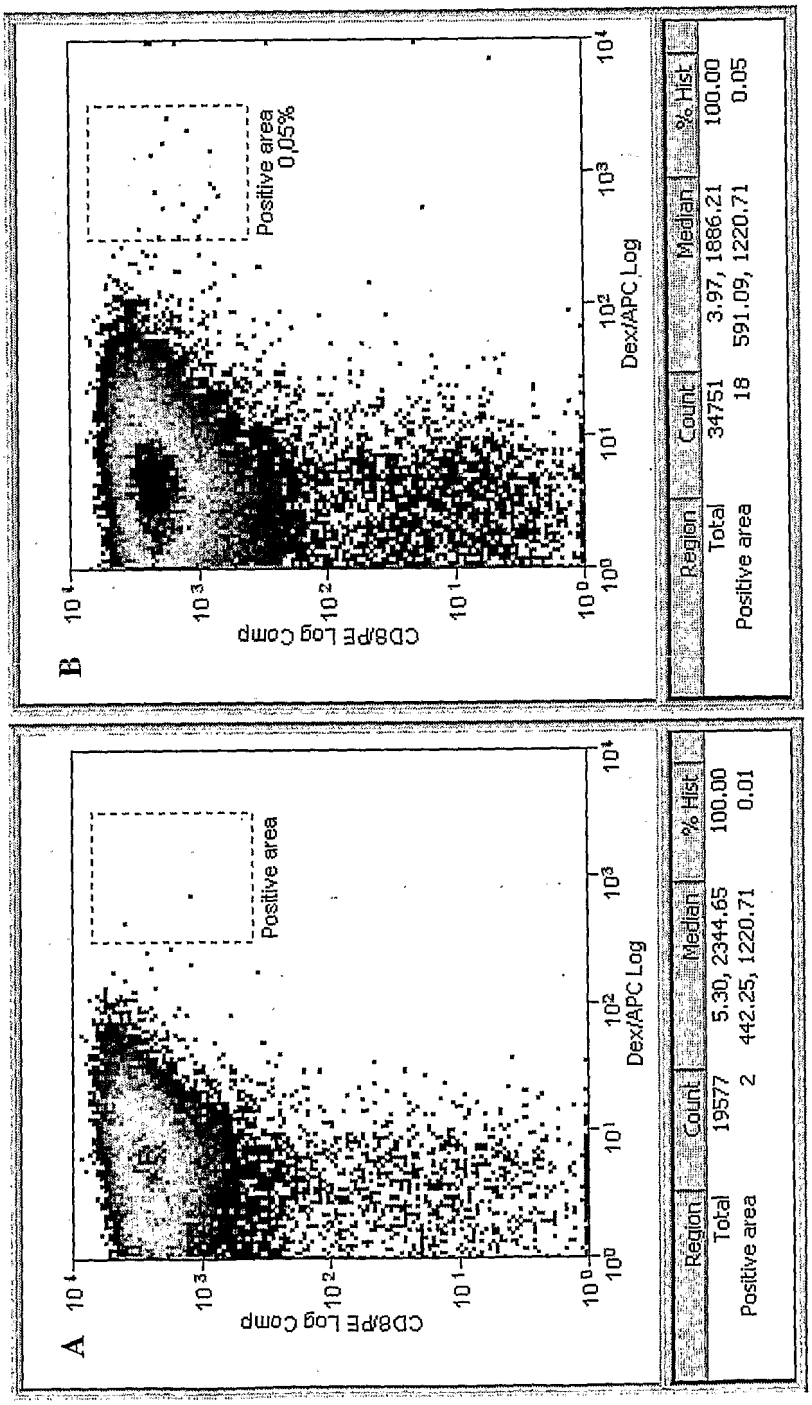


Figure 20.

Detection of CMV specific T cells using MHC dextramers

A